Probabilistic Models in the Study of Language

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Contents

About the exercises

Here is the scheme with which I have categorized exercises:

- ♣ An easy exercise
- † An exercise of medium difficulty
- ‡ A hard exercise
- * A short pen-and-paper exercise
- ** A medium-length pen-and-paper exercise
- *** A long pen-and-paper exercise
- ♡ An exercise that is especially recommended
- ⌨ An exercise that will require some computer programming (well, there may be clever ways around having to program in some cases)

NOTE: I am far from doing a complete characterization, so don't read too much into the absence of a symbol of a given category.

```
> roundN <- function(x,decimals=2,fore=5) sprintf(paste("%",fore,".",decimals,"f",sep=
```

Chapter 2

Univariate Probability

This chapter briefly introduces the fundamentals of univariate probability theory, density estimation, and evaluation of estimated probability densities.

2.1 What are probabilities, and what do they have to do with language?

We'll begin by addressing a question which is both philosophical and practical, and may be on the minds of many readers: *What are probabilities, and what do they have to do with language?* We'll start with the classic but non-linguistic example of coin-flipping, and then look at an analogous example from the study of language.

Coin flipping

You and your friend meet at the park for a game of tennis. In order to determine who will serve first, you jointly decide to flip a coin. Your friend produces a quarter and tells you that it is a fair coin. What exactly does your friend mean by this?

A translation of your friend's statement into the language of probability theory would be that the tossing of the coin is an EXPERIMENT—a repeatable procedure whose outcome may be uncertain—in which the probability of the coin landing with heads face up is equal to the probability of it landing with tails face up, at $\frac{1}{2}$. In mathematical notation we would express this translation as $P(\text{Heads}) = P(\text{Tails}) = \frac{1}{2}$. This mathematical translation is a partial answer to the question of what probabilities are. The translation is not, however, a complete answer to the question of what your friend means, until we give a semantics to statements of probability theory that allows them to be interpreted as pertaining to facts about the world. This is the philosophical problem posed by probability theory.

Two major classes of answer have been given to this philosophical problem, corresponding to two major schools of thought in the application of probability theory to real problems in the world. One school of thought, the *frequentist* school, considers the probability of an event to denote its limiting, or asymptotic, frequency over an arbitrarily large number of repeated

trials. For a frequentist, to say that $P(\text{Heads}) = \frac{1}{2}$ means that if you were to toss the coin many, many times, the proportion of Heads outcomes would be guaranteed to eventually approach 50%.

The second, *Bayesian* school of thought considers the probability of an event E to be a principled measure of the strength of one's belief that E will result. For a Bayesian, to say that $P(\text{Heads})$ for a fair coin is 0.5 (and thus equal to $P(\text{Tails})$) is to say that you believe that Heads and Tails are equally likely outcomes if you flip the coin. A popular and slightly more precise variant of Bayesian philosophy frames the interpretation of probabilities in terms of rational betting behavior, defining the probability π that someone ascribes to an event as the maximum amount of money they would be willing to pay for a bet that pays one unit of money. For a fair coin, a rational better would be willing to pay no more than fifty cents for a bet that pays \$1 if the coin comes out heads.[1]

The debate between these interpretations of probability rages, and we're not going to try and resolve it here, but it is useful to know about it, in particular because the frequentist and Bayesian schools of thought have developed approaches to inference that reflect these philosophical foundations and, in some cases, are considerably different in approach. Fortunately, for the cases in which it makes sense to talk about both reasonable belief and asymptotic frequency, it's been proven that the two schools of thought lead to the same rules of probability. If you're further interested in this, I encourage you to read Cox (1946), a beautiful, short paper.

An example of probabilities in language: word ordering

There were two parts to formalizing the notion of probability in the coin-flipping example: (1) delimiting the world of possible outcomes, and (2) assigning probabilities to each possible outcome. Each of these steps involves a simplification. Step 1 ignores such details as the angle between the "vertical" axis of the coin's face and magnetic north which results from the flip, and omits such possibilities as that the coin will land on its edge, that it will be snatched up by an owl, and so forth. Step 2 omits contingent information such as the relative orientation of the coin upon its being flipped, how hard it is flipped, the air currents, and so forth. With these simplifications, however, comes a great deal of analytical traction and power. Cases such as these, in which we can delimit a world of possible outcomes and express probabilities over those outcomes on the basis of incomplete knowledge, are ubiquitous in science, and are also ubiquitous in language. As a simple example analogous to coin flipping, let us consider the choice of how to order the words in an English BINOMIAL (Malkiel, 1959; Cooper and Ross, 1975; Benor and Levy, 2006, inter alia), such as *principal and interest*, where both orders are observed in naturally occurring usage. For a linguist to claim that this binomial has no ordering preference can be translated into the language of probability theory as stating that we are equally likely to observe (in some set of contexts of English

[1] This definition in turn raises the question of what "rational betting behavior" is. The standard response to this question defines rational betting as betting behavior that will never enter into a combination of bets that is guaranteed to lose money, and will never fail to enter into a combination of bets that is guaranteed to make money. The arguments involved are called "Dutch Book arguments" (Jeffrey, 2004).

usage) the phrases *principal and interest* and *interest and principal*; if we abbreviate these two orderings as `p` and `i` (we might denote the union of the two orderings as {*interest, principal*}) then mathematically our linguist is saying that $P(\texttt{p}) = P(\texttt{i}) = \frac{1}{2}$.

2.2 Sample Spaces

The underlying foundation of any probability distribution is the SAMPLE SPACE—a set of possible OUTCOMES, conventionally denoted Ω. For example, the sample space for orderings of the unordered binomial pair {*principal, interest*} is

$$\Omega = \{\texttt{p}, \texttt{i}\} \tag{2.1}$$

If we were to observe two tokens of the binomial, then the sample space would be

$$\Omega = \{\texttt{pp}, \texttt{pi}, \texttt{ip}, \texttt{ii}\} \tag{2.2}$$

In general, sample spaces can be finite (e.g., the set of all syntactic categories), countably infinite (e.g., the set of integers, the set of all phrase-structure trees), or uncountably infinite (e.g., the set of real numbers).

2.3 Events and probability spaces

An EVENT is simply a subset of a sample space. In the interpretation of probability distributions as beliefs, events are often interpreted as PROPOSITIONS.

> What is the sample space corresponding to the roll of a single six-sided die? What is the event that the die roll comes up even?

It follows that the negation of an event E (that is, E not happening) is simply $\Omega - E$.

A PROBABILITY SPACE P on Ω is a function from events in Ω to real numbers such that the following three axioms hold:

1. $P(E) \geq 0$ for all $E \subset \Omega$ (NON-NEGATIVITY).
2. If E_1 and E_2 are disjoint, then $P(E_1 \cup E_2) = P(E_1) + P(E_2)$ (DISJOINT UNION).
3. $P(\Omega) = 1$ (PROPERNESS).

These axioms allow us to express the probabilities of some events in terms of others.

2.4 Conditional Probability, Bayes' rule, and Independence

The CONDITIONAL PROBABILITY of event B given that A has occurred/is known is defined as follows:

$$P(B|A) \equiv \frac{P(A \cap B)}{P(A)}$$

We'll use another type of word-ordering example to illustrate this concept. In Old English, the object in a transitive sentence could appear either preverbally or postverbally. It is also well-documented in many languages that the "weight" of a noun phrase (as measured, for example, by number of words or syllables) can affect its preferred position in a clause, and that pronouns are "light" (Hawkins, 1994; Wasow, 2002). Suppose that among transitive sentences in a corpus of historical English, the frequency distribution of object position and pronominality is as follows:

(1)

	Pronoun	**Not Pronoun**
Object **Preverbal**	0.224	0.655
Object **Postverbal**	0.014	0.107

For the moment, we will interpret these frequencies directly as probabilities. (We'll see more on this in Chapter 4.) What is the conditional probability of pronominality given that an object is postverbal?

In our case, event A is **Postverbal**, and B is **Pronoun**. The quantity $P(A \cap B)$ is already listed explicity in the lower-right cell of table I: 0.014. We now need the quantity $P(A)$. For this we need to calculate the MARGINAL TOTAL of row 2 of Table I: $0.014 + 0.107 = 0.121$. We can then calculate:

$$\begin{aligned} P(\textbf{Pronoun}|\textbf{Postverbal}) &= \frac{P(\textbf{Postverbal} \cap \textbf{Pronoun})}{P(\textbf{Postverbal})} \\ &= \frac{0.014}{0.014 + 0.107} = 0.116 \end{aligned}$$

The chain rule

If we have events $E_1, E_2, \ldots, E_n$, then we can recursively apply the definition of conditional independence to the probability of all these events occurring—$P(E_1 \cap E_2 \cap \cdots \cap E_n)$—to obtain

$$P(E_1 \cap E_2 \cap \cdots \cap E_n) = P(E_n|E_1 \cap E_2 \cap \cdots \cap E_{n-1}) \ldots P(E_2|E_1)P(E_1) \qquad (2.3)$$

Equation 2.3 is known as the CHAIN RULE, and using it to decompose a complex probability distribution is known as CHAIN RULE DECOMPOSITION.

2.4.1 Bayes' rule

BAYES' RULE (also called Bayes' theorem) is simply the expression of a conditional probability in terms of the converse conditional probability and the two relevant unconditional probabilities:

$$P(A|B) = \frac{P(B|A)P(A)}{P(B)} \tag{2.4}$$

Bayes' rule can also be extended to more complex conjunctions of events/propositions:

$$P(A|B,I) = \frac{P(B|A,I)P(A|I)}{P(B|I)} \tag{2.5}$$

Although Bayes' rule is a simple mathematical truth, it acquires profound conceptual and practical power when viewed as a way of updating beliefs (encoded as probability distributions) in the face of new information. Specifically, suppose belief in A is of interest. One's initial, or PRIOR, beliefs in A are quantified by $P(A|I)$. Bayes' rule then expresses how beliefs should change when B is learned. In particular, the POSTERIOR belief $P(A|B,I)$ in A equals the prior belief times the ratio between (i) the LIKELIHOOD $P(B|A,I)$ of B under A and I and (ii) the likelihood of B under I alone. This use of Bayes' rule is often called BAYESIAN INFERENCE, and it serves as the cornerstone of (fittingly) Bayesian statistics.

We will see many examples of Bayesian inference throughout this book, but let us work through a simple example to illustrate its basic workings. We will return to the domain of Old English word order, but now focus on the relationship between an object NP's word order and its ANIMACY (assuming every object is either animate or inanimate) rather than its pronominality. Suppose we have the following probabilities:

$$\begin{aligned} P(\text{Object } \mathbf{Animate}) &= 0.4 \\ P(\text{Object } \mathbf{Postverbal}|\text{Object } \mathbf{Animate}) &= 0.7 \\ P(\text{Object } \mathbf{Postverbal}|\text{Object } \mathbf{Inanimate}) &= 0.8 \end{aligned} \tag{2.6}$$

and that we want to compute how likely an object is to be animate given that it is expressed postverbally—that is, $P(\text{Object } \mathbf{Animate}|\text{Object } \mathbf{Postverbal})$ (e.g., a comprehender may know at some point in a sentence that the object will appear postverbally, but hasn't yet heard the object spoken). Although we aren't given a probability table as in Example I, we actually have all the information necessary to compute this probability using Bayes' rule. We go through the calculations step by step below, simplifying the notation by using **Anim** and **Inanim** respectively to denote animacy and inanimacy of the object, and **PreV** and **PostV** respectively to denote preverbal and postverbal positioning of the object.

$$P(\mathbf{Anim}|\mathbf{PostV}) = \frac{P(\mathbf{PostV}|\mathbf{Anim})P(\mathbf{Anim})}{P(\mathbf{PostV})} \tag{2.7}$$

We have been given the value of the two terms in the numerator, but let us leave the numerator alone for the moment and focus on the denominator, which we weren't given in the problem specification. At first, it may not be obvious how to compute the denominator. However, we can Axiom 2 of probability theory (disjoint union) to express $P(\mathbf{PostV})$ as the sum of the probabilities $P(\mathbf{PostV} \cap \mathbf{Anim})$ and $P(\mathbf{PostV} \cap \mathbf{Inanim})$:

$$P(\mathbf{PostV}) = P(\mathbf{PostV} \cap \mathbf{Anim}) + P(\mathbf{PostV} \cap \mathbf{Inanim})$$

Although these probabilities were not specified directly either, we can use the definition of conditional probability to turn them into forms that *were* specified:

$$\begin{aligned} P(\mathbf{PostV} \cap \mathbf{Anim}) &= P(\mathbf{PostV}|\mathbf{Anim})P(\mathbf{Anim}) \\ P(\mathbf{PostV} \cap \mathbf{Inanim}) &= P(\mathbf{PostV}|\mathbf{Inanim})P(\mathbf{Inanim}) \end{aligned} \tag{2.8}$$

Now we can plug this result back into Equation (2.7):

$$P(\mathbf{Anim}|\mathbf{PostV}) = \frac{P(\mathbf{PostV}|\mathbf{Anim})P(\mathbf{Anim})}{P(\mathbf{PostV}|\mathbf{Anim})P(\mathbf{Anim}) + P(\mathbf{PostV}|\mathbf{Inanim})P(\mathbf{Inanim})} \tag{2.9}$$

At this point, it is worth reflecting on the expanded form Bayes' rule for this problem that we see in Equation (2.9). First, note that we have rewritten the initial form of Bayes' rule into a formula all of whose terms we have immediate access to in the probability specifications given in (2.6). (We were not given $P(\mathbf{Inanim})$, but the axioms of probability theory—disjoint union together with properness—allow us to easily determine that its value is 0.6.) Hence we can immediately calculate the correct answer to our problem:

$$P(\mathbf{Anim}|\mathbf{PostV}) = \frac{0.7 \times 0.4}{0.7 \times 0.4 + 0.8 \times 0.6} = 0.3684 \tag{2.10}$$

Second, note that in the right-hand side of Equation (2.9), the numerator appears as one of the two terms being summed in the denominator. This is quite often the case in applications of Bayes' rule. It was the fact that **Anim** and **Inanim** constitute an exhaustive partition of our sample space that allowed us to break down $P(\mathbf{PostV})$ in the way we did in Equation (2.8). More generally, it is quite common for the most complex step of applying Bayes' rule to be breaking the sample space into an exhaustive partition $A_1, A_2, \ldots, A_n$, and re-expressing Equation (2.11) through a summation over the members of this exhaustive partition:

$$P(A|B) = \frac{P(B|A)P(A)}{\sum_{j=1}^{n} P(B|A_j)P(A_j)} \tag{2.11}$$

A closely related third point is that computation of the denominator is usually the most complex and difficult part of applying Bayes' rule. Fortunately, there are often tricks that

one can apply either to avoid this computation or to drastically simplify it; you will see several examples of these tricks later in the book.

Finally, it is worthwhile to compare the probabilities of the object being animate before (Equation (2.6)) versus after (Equation (2.10)) obtaining the knowledge that the object follows the verb. Inspection of these two probabilities reveals that the object is postverbal *reduces* the probability by a small amount, from 0.4 to about 0.37. Inspection of the two conditional probabilities in the problem specification also reveals that inanimate objects are some more likely to be realized postverbally (probability 0.7) than animate objects are (probability 0.8). In fact, the shift induced in probability of object animacy from learning that the object is postverbal directly follows from the differential preference for postverbal realization of inanimate versus animate objects. If the object were inanimate, it would *predict more strongly* than if the object were animate that the object should be postverbal. Hence, learning that the object is in fact postverbal goes some way toward disconfirming the possibility that the object may turn out to be animate, while strengthening the possibility that it may turn out to be inanimate.

2.4.2 (Conditional) Independence

Events A and B are said to be Conditionally Independent given information C if

$$P(A \cap B|C) = P(A|C)P(B|C) \tag{2.12}$$

This form of conditional independence is often denoted symbolically as $A \perp B \mid C$.

A more philosophical way of interpreting conditional independence is that if we are in the state of knowledge denoted by C, then conditional independence of A and B means that knowing A tells us nothing more about the probability of B, and vice versa. The simple statement that A and B are conditionally independent is often used; this should be interpreted that A and B are conditionally independent given an implicit state C of "not knowing anything at all" ($C = \emptyset$).

It's crucial to keep in mind that if A and B are conditionally dependent given C, that does not guarantee they will not be conditionally independent given some other set of knowledge D. As an example, suppose that your friend gives you a pouch with three coins of identical shape. One coin is two-headed, one coin is two-tailed, and one coin is a regular fair coin; this information constitutes your state of knowledge C. You are to randomly select a coin from the pouch and, without inspecting it, flip it twice; the outcomes of the flips correspond to events A and B. Given this state of affairs, A and B are clearly *not* conditionally independent given C. For example, $P(B|A = \text{Heads}, C) > P(B|C)$: knowing that $A = \text{Heads}$ rules out the third coin and therefore makes it more likely that the second coin flip B will also come out heads. Suppose, however, that you inspect the coin before flipping it twice; call the new state of knowledge obtained after inspecting the coin D. We *do* have $A \perp B \mid D$: the conditional dependence between A and B given C derived from the uncertainty as to which of the three coins you selected, and once that uncertainty is removed, the dependency is broken and independence is obtained.

Likewise, it is also possible (though less common in real-world circumstances) for conditional independence between events to be *lost* when new knowledge is gained—see Exercise 2.2.

2.5 Discrete random variables and probability mass functions

A DISCRETE RANDOM VARIABLE X is literally a function from the sample space Ω of a probability space to a finite, or countably infinite, set of real numbers ($\mathbb{R}$).[2] Together with the function P mapping elements $\omega \in \Omega$ to probabilities, a random variable determines a PROBABILITY MASS FUNCTION $P(X(\omega))$, or $P(X)$ for short, which maps real numbers to probabilities. For any value x in the range of the random variable X, suppose that A is the part of the sample space all of whose members X maps to x. The probability that X will take on the value x is therefore simply the value that the original probability function assigns to A:

$$P(X = x) = P(A)$$

Technically speaking, the two P's in this equation are different—the first applies to values in the range of the random variable X, whereas the second applies to subsets of the sample space.

The relationship between the sample space Ω, a probability space P on Ω, and a discrete random variable X on Ω can be a bit subtle, so we'll illustrate it by returning to our example of collecting two tokens of {*principal, interest*}. Once again, the sample space is $\Omega = \{\texttt{pp}, \texttt{pi}, \texttt{ip}, \texttt{ii}\}$. Consider the function X that maps every possible pair of observations—that is, every point in the sample space—to *the total number of* `p` *outcomes obtained*. Suppose further that there is no ordering preference for the binomial, so that for each point ω in the sample space we have $P(\{\omega\}) = \frac{1}{2} \times \frac{1}{2} = \frac{1}{4}$. The total number of `p` outcomes is a random variable X, and we can make a table of the relationship between $\omega \in \Omega$, $X(\omega)$, and $P(X)$:

ω	$X(\omega)$	$P(X)$
`pp`	2	$\frac{1}{4}$
`pi`	1	$\frac{1}{2}$
`ip`	1	
`ii`	0	$\frac{1}{4}$

Notice that the random variable X serves to *partition* the sample space into equivalence classes: for each possible real number y mapped to by X, all elements of Ω mapped to y are in that equivalence class. Intuitively, a random variable can be thought of as focusing

[2] A set S is COUNTABLY INFINITE if a one-to-one mapping exists between the integers $0, 1, 2, \ldots$ and S.

attention on only the distinctions within the sample space that are of interest to us for a particular application. In the example above, the sample space consisted of ordered pairs of {*principal,interest*} binomials, but the random variable X restricts our attention to the observed *frequency* of each of the two binomial forms, throwing out the information about which binomial is observed first and which is observed second.

2.5.1 Bernoulli trials and the Bernoulli distribution

Perhaps the simplest interesting kind of event space is one that contains two outcomes, which we will arbitrarily label "success" and "failure" and respectively associate the integers 1 and 0. A BERNOULLI TRIAL is an experiment (in the sense of Section 2.1) with these two possible outcomes. This leads us to our first PARAMETRIC FAMILY OF PROBABILITY DISTRIBUTIONS, the BERNOULLI DISTRIBUTION. A parametric family of probability distributions is an infinite collection of probability distributions that vary only in the value of a fixed number of PARAMETERS characterizing the family. The Bernoulli distribution is perhaps the simplest of these families, being characterized by a single parameter, which we will denote by π. π is the probability of achieving success on a single Bernoulli trial, and can take any value between 0 and 1 (inclusive); π is sometimes called the "success parameter". The Bernoulli distribution thus has a probability mass function of the form

$$P(X = x) = \begin{cases} \pi & \text{if } x = 1 \\ 1 - \pi & \text{if } x = 0 \\ 0 & \text{otherwise} \end{cases}$$

A random variable that follows a Bernoulli distribution is often called a BERNOULLI RANDOM VARIABLE. For example, the flipping of a fair coin (with heads mapped to 1 and tails to 0) or the ordering outcome of an English binomial with no ordering preference can be modeled as a Bernoulli random variable with parameter $\pi = 0.5$.

2.5.2 Multinomial trials

We can also generalize the Bernoulli trial to the case where there are $r \geq 2$ possible outcomes; for convenience we can label the outcomes $c_1, \ldots, c_r$. This is a MULTINOMIAL TRIAL, and just as the Bernoulli distribution has 1 parameter, the distribution for multinomial trials has $r - 1$ parameters $\pi_1, \ldots, \pi_{r-1}$ determining the probability that a trial will fall into each of the classes:

$$P(X = x) = \begin{cases} \pi_1 & \text{if } x = c_1 \\ \pi_2 & \text{if } x = c_2 \\ \vdots & \vdots \\ \pi_{r-1} & \text{if } x = c_{r-1} \\ 1 - \sum_{i=1}^{r-1} \pi_i & \text{if } x = c_r \\ 0 & \text{otherwise} \end{cases} \tag{2.13}$$

We can make Equation (2.13) more symmetric by defining $\pi_r \stackrel{\text{def}}{=} 1 - \sum_{i=1}^{r-1} \pi_i$, which allows us to replace the second-to-last line of 2.13 with

$$P(X = x) = \pi_r \quad \text{if } x = c_r$$

but you should keep in mind that π_r is not an independent parameter, since it is fully determined by the other parameters.

Example. You decide to pull *Alice in Wonderland* off your bookshelf, open to a random page, put your finger down randomly on that page, and record the letter that your finger is resting on (ignoring the outcome and trying again if your finger rests on punctuation or a space). This procedure can be modeled as a multinomial trial with 26 possible outcomes, and to a first approximation the parameters of the associated distribution can simply be the relative frequencies of the different letters (ignoring the differing widths and heights of the letters). In *Alice in Wonderland*, 12.6% of the letters are `e`, 9.9% are `t`, 8.2% are `a`, and so forth; so we could write the parameters of our model as $\pi_{\texttt{e}} = 0.126$, $\pi_{\texttt{t}} = 0.099$, $\pi_{\texttt{a}} = 0.082$, and so forth.

The probability distribution for multinomial trials discussed here is a special case of the more general MULTINOMIAL DISTRIBUTION introduced in Section 3.4.1.

2.6 Cumulative distribution functions

A random variable X determines a probability mass function $P(X)$ on the real numbers. This probability mass function in turn determines a CUMULATIVE DISTRIBUTION FUNCTION F, defined as

$$F(x) \stackrel{\text{def}}{=} P(X \leq x)$$

We give a very simple illustration with the Bernoulli distribution. A Bernoulli random variable with parameter π has the following (very simple!) cumulative distribution function:

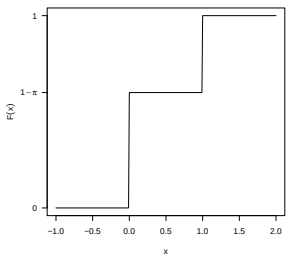


Figure 2.1: The cumulative distribution function for a Bernoulli random variable with parameter π

$$F(x) = \begin{cases} 0 & x < 0 \\ \pi & 0 \leq x < 1 \\ 1 & x \geq 1 \end{cases}$$

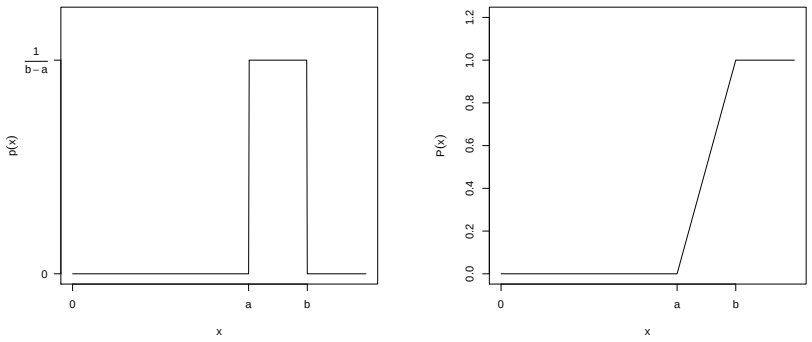
which is illustrated in Figure 2.1.

A probability mass function uniquely determines a cumulative distribution function, and vice versa.

Note that the cumulative distribution function is monotonically increasing in the range of the random variable. This means that the cumulative distribution function has an *inverse*, the QUANTILE FUNCTION, which maps a probability $0 \leq p \leq 1$ into the lowest possible number x such that $P(X \leq x) \geq p$.

2.7 Continuous random variables and probability density functions

Limiting a random variable to take on at most a countably infinite set of values is often too strong a constraint: in many cases, we want to allow outcomes to range along a continuum of real values, which is uncountably infinite. This type of outcome requires different treatment, with CONTINUOUS RANDOM VARIABLES. Instead of a discrete random variable's probability mass function, a continuous random variable has a PROBABILITY DENSITY FUNCTION $p(x)$ that assigns non-negative density to every real number. For example, the amount of time that an infant lives before it hears a parasitic gap in its native language would be naturally modeled as a continuous random variable (with $p(x) > 0$ only for $x > 0$). If we plot the probability density function (pdf) as a curve over the real number line, then the properness requirement of probability theory ensures that the total area under the curve is equal to 1 (see example in Section 2.7.1):



(a) Probability density function (b) Cumulative distribution function

Figure 2.2: The probability density function and cumulative distribution function of the uniform distribution with parameters a and b

$$\int_{-\infty}^{\infty} p(x)\, dx = 1$$

2.7.1 The uniform distribution

The simplest parametrized family of continuous probability distributions is the UNIFORM DISTRIBUTION, defined by parameters a and b bounding a continuous region $[a, b]$ within which the density function $p(x)$ is constant, and outside of which $p(x) = 0$. Since the area under the pdf curve must total 1, we must have the probability density function

$$P(x|a, b) = \begin{cases} \frac{1}{b-a} & a \leq x \leq b \\ 0 & \text{otherwise} \end{cases} \tag{2.14}$$

$p(x) = \frac{1}{b-a}$ when $x \in [a, b]$. We sometimes denote that a random variable X is distributed uniformly on the interval $[a, b]$ with the following notation:

$$X \sim \mathcal{U}(a, b)$$

Figure 2.2 shows plots of the pdf and cdf of the uniform distribution.

Example: although the uniform distribution is the simplest example of a continuous probability distribution, it is not the continuous distribution that has the most obvious or widespread applications in linguistics. One area in which uniform distributions would be most applicable, however, is historical applications, particularly as pertains to inferring event times such as the dates of recovered documents or of divergence between related languages. The

written language of Ancient Aramaic, for example, is known to have been in use from roughly 1000 B.C.E. to 500 B.C.E. (Beyer, 1986). With only this information, a crude estimate of the distribution over Ancient Aramaic document dates might be a uniform distribution on the interval [-1000,-500] (though this estimate would fail to incorporate additional information likely available from the documents themselves). Suppose a scholar consults two documents of Ancient Aramaic from unrelated sources, and finds that the date of the first document is 850 B.C.E. What is the probability that the other document dates to within fifty years of the first? Anything in the range [-900,-800] qualifies, so the probability we want is:

$$\begin{aligned} P(X \in [-900, -800]) &= \int_{-900}^{-800} \frac{1}{-500 - (-1000)} \, \mathrm{d}x \\ &= \frac{-800 - (-900)}{-500 - (-1000)} = \frac{1}{5} \end{aligned}$$

2.7.2 Change of variables for continuous probability densities

Typically, the range of a continuous random variables is some kind of metric space used to quantify events in the real world. In many cases, there may be more than one possible metric of interest. In phonetics, for example, pitch is sometimes expressed directly in units of frequency, namely Hertz (cycles per second), but sometimes measured in log-Hertz instead. The justifications for log-Hertz measurement include that in music relative changes in pitch are constant in frequency *ratio*, so that adding a constant value c to a log-Hertz measurement yields the same change in musical pitch regardless of starting frequency; and that in many cases vowels tend to be constant in the ratios among their first three formats (e.g., Lloyd (1890); Peterson (1961); Miller (1989); Hillenbrand et al. (1995)). [3] If one wants to convert a probability density from one unit of measurement to another, one needs to make a CHANGE OF VARIABLES.

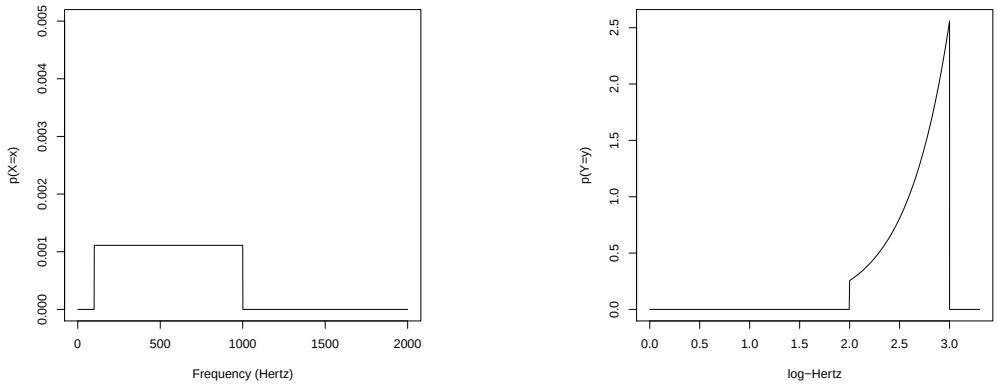
In general, if some random variable X has the probability density p and the random variable Y is defined such that $X = g(Y)$, then the probability density of Y is

$$p(Y = y) = p(X = g(y)) \frac{dg}{dy}(g(y))$$

or, more succinctly, For example, suppose that one has a random variable X with a uniform distribution over the Hertz frequency range [100,1000]. To convert this to a distribution over log-frequencies, let us call the new random variable Y defined that $Y = log_{10}X$, so that the log-Hertz range of Y is [2,3]. This means that $X = g(y) = 10^Y$ and so $\frac{dg}{dy} = 10^Y \log 10$ (see Section A.5). Figures **??** and **??** illustrate this probability density in the two units of measurement.

This example illustrates an important point: that the pdf of a continuous random variable does *not* need to be bounded above by 1; changing variables from Hertz to log-Hertz led to

[3] A formant is a peak of energy in the acoustic frequency spectrum of a vowel production.



a density as high as 2.5. Since the range in which the density exceeds 1 is small (in the log-Hertz scale), this is not a problem as the total probability mass still integrates to 1. Note that technically, since probability mass is unitless but continuous probability densities are over variables that have units, probability densities have units—in the case of the uniform distribution in the example above, the unit is "per cycle per second". And in fact, for *any* continuous probability function there will always be some change of variables based on a new unit of measurement that will lead to density exceeding 1 somewhere on the range of the new random variable! This is in contrast to the probability mass function of a discrete random variable, which is unitless must be bounded above by 1.

2.7.3 Cumulative distribution functions for continuous random variables

With a continuous random variable, the probability of any specific point in $\mathbb{R}$ is zero; the primary interest is on the probability that the outcome of the random variable will fall into a given *region* of $\mathbb{R}$, which is more naturally expressed via the cumulative distribution function (cdf) $F(x)$, defined once again as $P(X \leq x)$, or

$$F(x) = \int_{-\infty}^{x} p(x)\, dx$$

What is especially useful about the cumulative distribution function is that the probability that X will fall into a continuous *region* $[x, y]$ of the real number line can be expressed as the difference between the cdf at y and at x:

$$
\begin{aligned}
P(x \leq X \leq y) &= \int_x^y p(x)\,dx \\
&= \int_{-\infty}^y p(x)\,dx - \int_{-\infty}^x p(x)\,dx \\
&= F(y) - F(x)
\end{aligned}
$$

Because of this property, and the fact that the probability of an outcome occurring at any specific point x is 0 for a continuous random variable, the cumulative distribution is in many cases more important than the density when working with continuous random variables.

2.8 Normalized and unnormalized probability distributions

It is quite common to wind up defining a "probability" mass function F (or density function f) that adheres to the first two axioms listed in Section 2.3—non-negativity and disjoint union—but that does not adhere to the third axiom of properness. Such a function F is called an UNNORMALIZED or IMPROPER PROBABILITY DISTRIBUTION. In these cases, from F a normalized, or proper, probability distribution P can be defined as

$$
P(X = x) = \frac{1}{Z} F(x) \tag{2.15}
$$

where

$$
Z \stackrel{\text{def}}{=} \sum_x F(x)
$$

for discrete densities, and

$$
Z \stackrel{\text{def}}{=} \int_{-\infty}^{\infty} f(x)\,dx
$$

for continuous densities, when Z is finite. Here, Z is generally called the NORMALIZING CONSTANT or PARTITION FUNCTION.

When we have a function $F(X)$ that we wish to use as an unnormalized probability distribution, we will often write that

$$
P(x) \propto F(x) \tag{2.16}
$$

which is read as "$P(x)$ is proportional to $F(x)$".

Example: suppose that we wanted to construct a probability distribution over total orderings of three constituents S, O, V (e.g., the subject, object, and verb of a simple transitive clause), and characterize the probability distribution purely on the basis of the relative strengths of preference for linear precedence between every possible pair of constituents. There are three possible pairs of these constituents—SO,SV, and OV—so we will introduce one parameter for each of these pairs to indicate the relative strength of preference for one linear ordering versus another. Thus we will have one parameter, γ_1 indicating the preference for S to precede O; we will denote this event as $S \prec O$, with $\prec$ to be read as "precedes". A second parameter γ_2 will indicating the preference for S to precede V, and a third parameter γ_3 indicating the preference for O to precede V. For simplicity, we'll let each γ_i range between 0 and 1, and encourage the intuitive analogy between these three parameters and the success parameters of three separate Bernoulli trials. That is, the word orders SOV, SVO, and VSO could be thought of as "successes" for the Bernoulli trial, and we would want them together to have something like probability γ_1, whereas the word orders OSV, OVS, and VOS could be thought of as "failures" for this Bernoulli trial, and we would want them to have something like probability $1 - \gamma_1$. So we'll define a mass function F that assigns to any word order the product of (i) all the "success" parameters for precedences that are satisfied, and (ii) all the "failure" parameters for precedences that are violated. For example, we would have:

$$F(SOV) = \gamma_1\gamma_2\gamma_3$$

since this word ordering satisfies all the three precedences,

$$F(SVO) = \gamma_1\gamma_2(1 - \gamma_3)$$

since this word ordering violates $O \prec V$ but satisfies the other two precedences, and so forth.

However, there is one crucial disanalogy between the present case and the case of three separate Bernoulli trials. In three separate Bernoulli trials, there are eight logically possible outcomes, but in the case of ordering three constituents, there are only six logically possible outcomes. There are two combinations of constituent-pair precedence which are contradictory:

$$(1) S \prec O, V \prec S, O \prec V \qquad\qquad (2) O \prec S, S \prec V, V \prec O$$

As a result, the mass function F is improper: in general, it does not assign total mass of 1 to the six possible constituent orderings.

We can construct a proper probability distribution out of F, however, by computing its normalizing constant and then defining a probability distribution as described in Equation 2.15. In Table 2.1 we make totally explicit the eight logically possible combinations of

	S_O	S_V	O_V	Outcome X	$F(X)$
1	$\prec$	$\prec$	$\prec$	SOV	$\gamma_1\gamma_2\gamma_3$
2	$\prec$	$\prec$	$\succ$	SVO	$\gamma_1\gamma_2(1-\gamma_3)$
3	$\prec$	$\succ$	$\prec$	**impossible**	$\gamma_1(1-\gamma_2)\gamma_3$
4	$\prec$	$\succ$	$\succ$	VSO	$\gamma_1(1-\gamma_2)(1-\gamma_3)$
5	$\succ$	$\prec$	$\prec$	OSV	$(1-\gamma_1)\gamma_2\gamma_3$
6	$\succ$	$\prec$	$\succ$	**impossible**	$(1-\gamma_1)\gamma_2(1-\gamma_3)$
7	$\succ$	$\succ$	$\prec$	OVS	$(1-\gamma_1)(1-\gamma_2)\gamma_3$
8	$\succ$	$\succ$	$\succ$	VOS	$(1-\gamma_1)(1-\gamma_2)(1-\gamma_3)$

Table 2.1: The unnormalized distribution for {S,O,V} constituent-order model

Order	SOV	SVO	VSO	OSV	OVS	VOS
# Languages	566	488	95	25	11	4
Relative frequencies	0.476	0.410	0.080	0.021	0.009	0.003
Probabilities in constituent-order model	0.414	0.414	0.103	0.046	0.011	0.011

Table 2.2: Empirical frequencies of dominant constituent ordering among {S,O,V} for 1189 languages, taken from the World Atlas of Language Structures (Dryer, 2011; languages reported as lacking dominant order omitted). Model probabilities are for $\gamma_1 = 0.9, \gamma_2 = 0.8, \gamma_3 = 0.5$).

three pairwise precedences, the two that are contradictory, and the values assigned by F to each of the eight.

Since the set of all eight together would give a proper distribution, a simple way of expressing the normalizing constant is as $1 - F(X_3) - F(X_6)$.

This is an interesting model: because it has only three parameters, it is not as expressive as an arbitrary multinomial distribution over six classes (we would need five parameters for that; see Section 2.5.2). It's an empirical question whether it's good for modeling the kind of word-order frequencies across the languages of the world. The first two rows of Table 2.2 show the empirical frequencies of the six logically possible orderings of subject, object, and verb; the two subject-initial orderings are by far the most common, with VSO a distant third and the other orders all quite rare. If we wanted to produce a probability distribution that looked like empirical frequencies, intuitively we might set γ_1 close to 1, since S nearly always precedes O; γ_2 close to 1 as well, since S nearly always precedes V, but lower than γ_1, since the former generalization is stronger than the second; and γ_3 around $\frac{1}{2}$, since V precedes O about as often as it follows it. The third row of Table 2.2 shows the probabilities in the constituent-order model obtained with such a setting, of $\gamma_1 = 0.9, \gamma_2 = 0.8, \gamma_3 = 0.5$. It is a pretty good qualitative fit: it fails to differentiate SOV from SVO probability but reproduces the overall shape of the empirical relative frequency distribution reasonably well. In fact, this three-parameter constituent-order model can achieve even better fits to word-order-

frequency data than we see in Table 2.2; the principles according to which the optimal fit can be determined will be introduced in Chapter 4, and the model is revisited in Exercise 4.6.

Problem 2.6 in the end of this chapter revisits the question of whether the parameters γ_i really turn out to be the probabilities of satisfaction or violation of each individual constituent-pair precedence relation for the probability distribution resulting from our choice of the unnormalized mass function F.

2.9 Expected values and variance

We now turn to two fundamental quantities of probability distributions: EXPECTED VALUE and VARIANCE.

2.9.1 Expected value

The expected value of a random variable X, which is denoted in many forms including $E(X)$, $E[X]$, $\langle X \rangle$, and μ, is also known as the EXPECTATION or MEAN. For a discrete random variable X under probability distribution P, it's defined as

$$E(X) = \sum_i x_i P(X = x_i) \tag{2.17}$$

For a Bernoulli random variable X with parameter π, for example, the possible outcomes are 0 and 1, so we have

$$\begin{aligned} E(X) &= 0 \times \overbrace{(1-\pi)}^{P(X=0)} \quad + \quad 1 \times \overbrace{\pi}^{P(X=1)} \\ &= \pi \end{aligned}$$

For a continuous random variable X under cpd p, the expectation is defined using integrals instead of sums, as

$$E(X) = \int_{-\infty}^{\infty} x \; p(x) dx \tag{2.18}$$

For example, a uniformly-distributed random variable X with parameters a and b has expectation right in the middle of the interval, at $\frac{a+b}{2}$ (see Exercise 2.8).

2.9.2 Variance

The variance is a measure of how broadly distributed the r.v. tends to be. It's defined as the expectation of the squared deviation from the mean:

$$\text{Var}(X) = E[(X - E(X))^2] \tag{2.19}$$

or equivalently

$$\text{Var}(X) = E[X^2] - E[X]^2 \tag{2.20}$$

(see Exercise 3.1). The variance is often denoted σ^2 and its positive square root, σ, is known as the STANDARD DEVIATION.

If you *rescale* a random variable by defining $Y = a + bX$, then $\text{Var}(Y) = b^2X$. This is part of what is known as LINEARITY OF THE EXPECTATION, which will be introduced in full in Section 3.3.1.

Variance of Bernoulli and uniform distributions

The variance of a Bernoulli-distributed random variable needs to be calculated explicitly, by using the definition in Equation (2.20) and summing over the possible outcomes as in Equation (2.17) (recall that the expectation for a Bernoulli random variable is π):

$$\begin{aligned}
\text{Var}(X) = E[((X) - E(X))^2] &= \sum_{x \in \{0,1\}} (x - \pi)^2 \; P(x) \\
&= (\pi - 0)^2 \overbrace{(1-\pi)}^{P(X=0)} \quad + \quad (1-\pi)^2 \times \overbrace{\pi}^{P(X=1)} \\
&= \pi(1-\pi)\left[\pi + (1-\pi)\right] \\
\text{Var}(X) &= \pi(1-\pi)
\end{aligned}$$

Note that the variance is largest at $\pi = 0.5$ and zero when $\pi = 0$ or $\pi = 1$.

The uniform distribution also needs its variance explicitly calculated; its variance is $\frac{(b-a)^2}{12}$ (see Exercise 2.9).

2.10 The normal distribution

We're now in a position to introduce the NORMAL DISTRIBUTION, which is likely to be the most common continuous distribution you'll encounter. It is characterized by two parameters, the expected value μ and the variance σ^2. (Sometimes the STANDARD DEVIATION σ is used instead of the variance to parameterize the normal distribution.) Its probability density function is:

$$p(x) = \frac{1}{\sqrt{2\pi\sigma^2}} \exp\left[-\frac{(x-\mu)^2}{2\sigma^2}\right] \tag{2.21}$$

This expression seems intimidating at first glance, but it will become familiar with time.[4] It can be divided into three components:

[4] $\exp[x]$ is another way of writing e^x; it's used when the expression in the exponent is complex enough to warrant typesetting in normal-size font.

- $\frac{1}{\sqrt{2\pi\sigma^2}}$ is a normalizing constant (see Section 2.8).
- The denominator within the exponential, $2\sigma^2$, can be thought of a scaling factor determined by the variance of the normal distribution.
- The numerator within the exponential, $(x-\mu)^2$, is the square of the Euclidean distance of x from the mean. The exponent is negative, so the probability density is exponentially decreasing in the square of the distance from the mean.

The normal distribution doesn't have a closed-form cumulative density function, but the approximate cumulative density can be calculated numerically and is available in most statistical software packages. Figure 2.3 shows probability density and cumulative distribution functions for normal distributions with different means and variances.

Example: normal distributions are often used for modeling the variability in acoustic dimensions for production and perception in phonetics. Suppose that you are about to record an adult male native speaker of American English pronouncing the vowel [i]. Data from Peterson and Barney (1952) indicate that the F1 formant frequency for this vowel as pronounced by this group may reasonably be modeled as normally distributed with mean 267Hz and standard deviation 36.9Hz. What is the probability that the recording will have F1 frequency falling between 225Hz and 267Hz (lower than average but not egregiously low)? We follow the logic of Section 2.7.3 in expressing the answer in terms of the cumulative distribution function:

$$P(225\text{Hz} \leq \text{F1} \leq 267\text{Hz}) = \int_{225}^{267} p(x)\,\mathrm{d}x \tag{2.22}$$

$$= \int_{-\infty}^{267} p(x)\,\mathrm{d}x - \int_{-\infty}^{225} p(x)\,\mathrm{d}x \tag{2.23}$$

$$= F(267) - F(225) \tag{2.24}$$

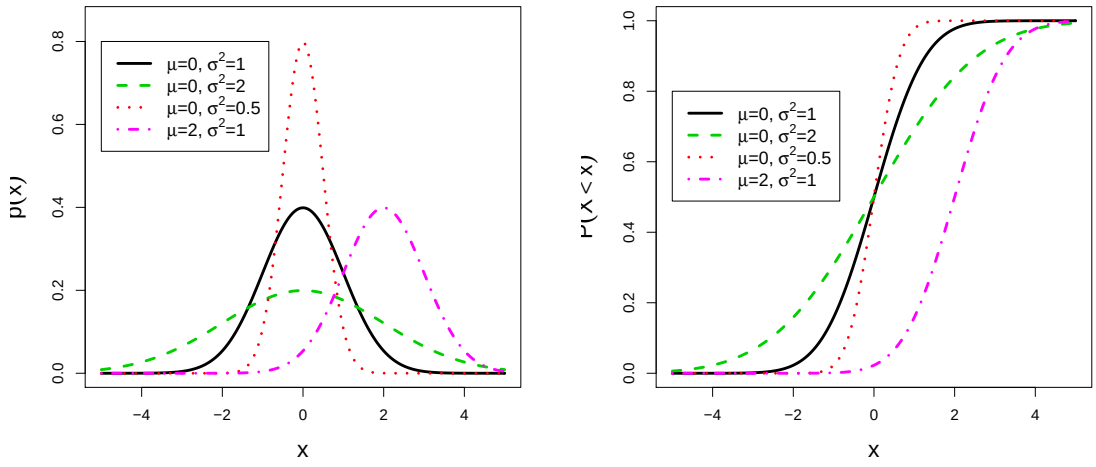
With the use of standard statistical software we can find the values of the cumulative distributions function at 267 and 225, which gives us our answer:

$$= 0.5 - 0.12 = 0.38 \tag{2.25}$$

(Note that because the normal distribution is symmetric around its mean, the cumulative distribution function applied to the mean will always be equal to 0.5.)

2.10.1 Standard normal random variables

A normal distribution with mean 0 and variance 1 is called the STANDARD NORMAL DISTRIBUTION, and a random variable following this distribution is called a STANDARD NORMAL RANDOM VARIABLE. The density function for a standard normal random variable is $p(x) = \frac{1}{\sqrt{2\pi}} e^{\left[-x^2/2\right]}$.



(a) Probability density function

(b) Cumulative distribution function

Figure 2.3: The normal distribution: density and cumulative distribution functions

2.11 Estimating probability densities

Thus far we have concerned ourselves with definitions in probability theory and a few important probability distributions. Most of the time, however, we are in the situation of not knowing the precise distribution from which a set of data have arisen, but of having to infer a probability distribution from the observed data. This is the topic of STATISTICAL INFERENCE. We conclude this chapter by briefly describing some simple techniques for estimating probability densities and evaluating the quality of those estimated densities.

2.11.1 Discrete probability densities: relative-frequency estimation

Suppose that we are interested in estimating the Bernoulli parameter π associated with the ordering preference of the English binomial {*interest,principal*} on the basis of ten tokens collected from a corpus, with "success" arbitrarily associated with the ordering *principal and interest*. Seven of them are *principal and interest* and three are *interest and principal*. The simplest way for us to estimate the underlying Bernoulli distribution is to equate relative frequency of occurrence with probability. In this case, we have seven of ten success so we estimate $\hat{\pi} = \frac{7}{10}$.[5] This process is called RELATIVE FREQUENCY ESTIMATION.

We can generalize relative frequency estimation for use with multinomial trials. Suppose that we observe N outcomes of a categorical variable that can take on some finite number r

[5]The $\hat{}$ symbol above the π indicates that this is an *estimate* of the parameter π which may or not be the true underlying parameter value.

	⟨SB, DO⟩	⟨SB, IO⟩	⟨DO, SB⟩	⟨DO, IO⟩	⟨IO, SB⟩	⟨IO, DO⟩	Total
Count	478	59	1	3	20	9	570
Relative Freq.	0.839	0.104	0.001	0.005	0.035	0.016	

Table 2.3: Frequency of grammatical functions on ordered pairs of full NPs in German newspaper text, drawn from the NEGRA-II corpus (Kempen and Harbusch, 2004). **SB** denotes "subject", **DO** denotes "direct object", and **IO** denotes direct object.

of different values. Table 2.3, for example, shows the counts of full NP pairs (presented in the order in which they appear in the clause) obtained in a sample of a corpus of German newspaper text.

In terms of probability theory, this categorical variable can be viewed as a discrete multinomial-trial random variable, for which we have observed N outcomes (570, in the case of Table 2.3). Once again we simply divide the count of each outcome by the total count, as shown in the bottom line of Table 2.3. We will see in Section 4.3.1 that, in addition to being highly intuitive, relative frequency estimation for multinomial outcomes has a deep theoretical justification.

2.11.2 Estimating continuous densities: histograms and kernel density estimation

What about for continuous variables? Figure 2.4a plots the frequency of occurrence of F0 formant frequency of the vowel ɑ by adult male speakers in the classic study of Peterson and Barney (1952).[6] It is immediately apparent that relative frequency estimation is not suitable for continuous densities; and if we were to treat the distribution over F0 formants as a discrete distribution, we would run into the problem of data sparsity. For example, we would estimate that $P(\text{F0} = 119\text{Hz}) = 0$ even though there are many observations close to 119Hz.

One common technique for continuous density estimation is the use of HISTOGRAMS. Constructing a histogram involves dividing the range of the random variable into K equally-spaced bins and counting the number of observations that fall into each bin; K can be chosen as seems appropriate to the dataset. These counts can then be normalized by the total number of observations to achieve an estimate of the probability density. Figures 2.4b and 2.4c show histograms of adult male speaker F0 frequency for 38-bin histograms of width 5Hz, starting at 95Hz and 94Hz respectively. Although the histogram determines a valid continuous density, it has two weakness. First, it assigns zero probability to a number of intervals for which the data seem to suggest possible outcomes (e.g., the 150–155Hz interval in Figure 2.4b, and the 245–250Hz interval in Figure 2.4c). Second, the shape of the histogram is quite sensitive to the exact positioning of the bins—this is apparent in the substantially different shape of the two histograms in the 100–150Hz range.

A generally preferable approach is KERNEL DENSITY ESTIMATION. A KERNEL is simply

[6]The measurements reported in this dataset are rounded off to the nearest Hertz, so in Figure 2.4a they are jittered to break ties.

a weighting function that serves as a measure of the relevance of each observation to any given point of interest on the range of a random variable. Technically, a kernel K simply takes an observation x_i and returns a non-negative function $K(x_i, \cdot)$ which distributes a total probability mass of 1 over the range of the random variable.[7] Hence we have

$$\sum_x K(x_i, x) = 1 \tag{2.26}$$

in the discrete case, or

$$\int_x K(x_i, x)\, dx = 1 \tag{2.27}$$

in the continuous case. If one has only a single observation x_1 of the outcome of a random variable X, then the kernel density estimate of the probability density over X is simply $P(X = x) = K(x_1, x)$. In general, if one has n observations $x_1, \ldots, x_n$, then the kernel density estimate for a point x is the *average* of the densities assigned to x by the kernel function obtained from each observation:

$$\hat{p}(x) = \frac{1}{n} \sum_{i=1}^{n} K(x_i, x) \tag{2.28}$$

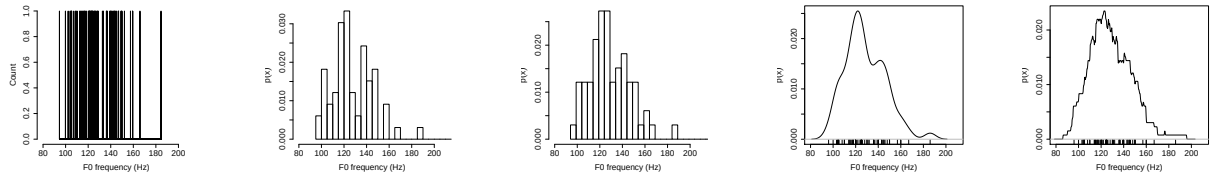
It is up to the researcher to choose the particular kernel function. Here, we give an example for a continuous random variable; in the next section we give an example for discrete kernel density estimation.

For continuous random variables, the NORMAL KERNEL is perhaps the most popular kernel; for an observation x_i it simply allocates its probability mass according to a normal density function with mean x_i and standard deviation σ. The standard deviation is sometimes called the BANDWIDTH of the kernel and denoted as b. The kernel density estimate from a set of observations $x_1, \ldots, x_n$ using bandwidth b would be:

$$\hat{p}(X = x) = \frac{1}{n\sqrt{2\pi b^2}} \sum_{i=1}^{n} \exp\left[-\frac{(x - x_i)^2}{2b^2}\right]$$

Figure 2.4d shows the kernel density estimate of adult male-speaker F0 frequency distribution for $b = 5$, with the observations themselves superimposed on the F0-axis (just like Figure 2.4a). Note that the kernel density estimate gives non-zero probability density to the entire number line, and it is visibly non-zero for the entire span between the lowest and highest observations; yet much of the nuance of the data's empirical distribution is still retained.

[7] Although a kernel serves as a type of distance metric, it is not necessarily a true distance; in particular, it need not observe the triangle inequality.



(a) Raw observations (b) 5Hz-bin histogram starting at 95Hz (c) 5Hz-bin histogram starting at 94Hz (d) Normal-kernel density estimate, $b = 5$ (e) Rectangular-kernel density estimate, $b = 20$

Figure 2.4: Adult male native English speaker F0 measurements for the vowel ɑ from Peterson and Barney (1952), together with histograms and a kernel density estimate of the underlying distribution

Of course, there are many other possible kernel functions for continuous data than the normal kernel. Another simple example is the RECTANGULAR kernel, which for an observation x_i distributes a probability mass of 1 through a uniform distribution centered on x_i with width b. Figure 2.4e shows the result of applying this kernel with bandwidth $b = 3$ to the same F0 data.[8]

One of the difficulties in kernel density estimation is the choice of bandwidth. This choice is ultimately up to the researcher, but in the next section we will introduce some principles that can help determine how good a given choice of bandwidth may be. Exercise 2.11 also addresses this issue.

Histogram- and kernel-based density estimation is often called NON-PARAMETRIC ESTIMATION. The term "non-parametric" turns up in many places in probability and statistics. In density estimation, a non-parametric method is one whose estimated densities can grow arbitrarily complex as the amount of data used for estimation continues to grow. This contrasts with PARAMETRIC ESTIMATION, in which estimation is limited to a pre-specified parametric family of models (covered in Chapter 4).

2.11.3 Kernel estimation for discrete densities

Kernel density estimation can also be useful for estimating discrete probability distributions in which the number of possible outcomes is large in comparison to the number of observations, or even countably infinite. This is a common situation in the study of language. For example, there has been considerable recent interest in estimating probability densities over possible phonological forms for lexical items (e.g., Hayes and Wilson, 2007), to account for phenomena such as gradience in speaker judgments of nonce word well-formedness. One way of placing a density over the set of possible phonological forms is to define a kernel over pairs of phoneme sequences.

[8] In case you try using the `density()` function in `R` to do rectangular kernel density estimation, the bandwidth is defined differently—as the standard deviation of the kernel's density function—and you need to adjust the chosen bandwidth accordingly.

As a simple example, let us consider the space of possible consonant-vowel-consonant (CVC) lexical forms composed of the six phonemes /t/,/p/,/k/,/æ/,/ʌ/, and/ʊ/. There are 27 possible such forms, and 18 of them occur in the English lexicon. Let us base our kernel on the string-edit distance $D(x, x')$ between forms x and x', which for these three-phoneme sequences is simply the number of positions at which two strings differ—for example, $D(/\text{pæt}/, /\text{tʊt}/) = 2$. Less similar phoneme sequences should have a lower score in our kernel, so let us define our kernel as

$$K(x, x') \propto \frac{1}{(1 + D(x, x'))^3}$$

We have used proportionality rather than equality here because of the requirement (Equation (2.26)) that the kernel sum to 1 over the complete space of possible outcomes $\{x_j\}$. We can renormalize the kernel just as we renormalize a probability distribution (see Section 2.8), by defining for each observation x_i a normalizing coefficient $Z_i = \sum_{x_j} \frac{1}{(1+D(x_i,x_j))^3}$, and dividing in this normalizing coefficient:

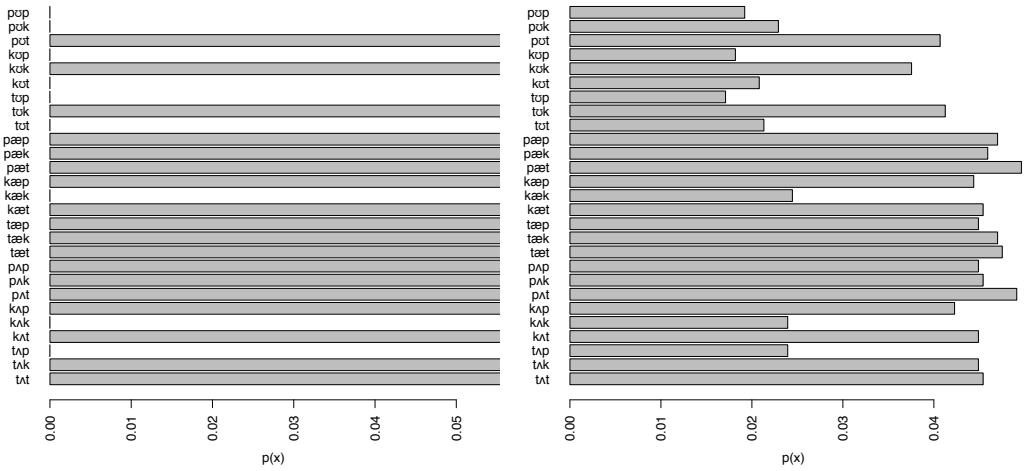
$$K(x_i, x') = \frac{1}{Z_i} \frac{1}{(1 + D(x, x'))^3}$$

For our example, it turns out that $Z_i = 2.32$ for all sequences x_i.

Figure 2.5 shows the relative-frequency and kernel-density estimates for our toy problem. Figure 2.5a shows the 18 forms in the English lexicon, and a relative-frequency estimate of the distribution over possible forms if each such entry from the English lexicon is counted as a single observation. Figure 2.5b shows the kernel density estimate. The unattested lexical forms now have non-zero probability, and furthermore the probability of both attested and unattested forms depends on how densely their neighborhoods in phonological space are occupied.

2.11.4 Kernel density estimation and exemplar models

As is made explicit in Equation (2.28), computing the probability of an outcome using kernel density estimation (KDE) involves iterating explicitly over the entire set of observations $\boldsymbol{y}$. From a computational point of view, a distinctive property of KDE is that it requires the storage and access of complete datasets. In theoretical linguistics, psycholinguistics, and computational linguistics, models with this requirement are often called EXEMPLAR MODELS. Exemplar models have received considerable attention in these fields as candidate models of language acquisition and use. For example, Bailey and Hahn (2001) adapted the exemplar model of Nosofsky (1986) to the problem of inducing probability distributions over possible lexical forms (Section 2.11.3). In syntax, the Data-Oriented Parsing model (Scha, 1990; Bod, 1992, 1998, 2006) is perhaps the best known formalized exemplar model. A point that cannot be over-emphasized is that the core substance of an exemplar model consists of (a) the representation of the space of possible exemplars, and (b) the metric of similarity



(a) Relative frequency estimation (b) Kernel density estimate

Figure 2.5: Kernel density estimation for lexical forms

between points in the exemplar representation space. In kernel density estimation, the choice of kernel constitutes the metric of similarity.

One of the common criticisms of exemplar-based models is on the grounds that it is psychologically implausible to imagine that all the exemplars in a language user's experience are retained, and are exhaustively accessed whenever the probability of a given point in the exemplar representation space is needed. We won't take sides on this issue here. However, in future chapters we do consider methods that do not have the requirement of exhaustive storage and recall of the dataset.

2.11.5 Evaluating estimated probability densities

You now have basic tools for estimating probability densities from data. Even after this brief introduction to density estimation it should be painfully obvious that there are many ways to estimate a density from a given dataset. From the standpoint of modeling linguistic cognition, this is in fact advantageous because different approaches to estimation encode different *learning biases*. This means that density estimation procedures as models of human language learning can be evaluated in terms of how closely they reflect the inferences made by language learners from exposure to finite data.

There are many times, however, when you will also be interested in evaluating how well a particular density estimate intrinsically encodes the data from which it is derived. Here we cover two approaches to this type of evaluation that enjoy wide currency: CLASSIFICATION ACCURACY and LIKELIHOOD.

Classification accuracy

For discrete random variables, the simplest method of evaluating the performance of a density estimate is CLASSIFICATION ACCURACY. Prerequisite to this notion is the notion of PREDICTION: for a given context (i.e. conditioning on some known information), what value of a discrete random variable X do I expect? Suppose that I have a probability density estimate based on some observations $\boldsymbol{y}$ and I expect to see n new observations. My predictions for the observed outcomes in these new observations (before I actually see them) can be labeled $\hat{y}_1, \ldots, \hat{y}_n$. My classification accuracy is simply the proportion of these predictions that turn out to be correct. For example, suppose that for the German grammatical function ordering data of Section 2.11.1 I expect to see three new observations. Without any further information, the most sensible thing for me to do is simply to predict $\langle \mathbf{SB}, \mathbf{DO} \rangle$ all three times, since I estimated it to be the most likely outcome. If the actual outcomes are $\langle \mathbf{SB}, \mathbf{DO} \rangle, \langle \mathbf{SB}, \mathbf{IO} \rangle, \langle \mathbf{SB}, \mathbf{DO} \rangle$, then my classification accuracy is $\frac{2}{3}$.

When we obtain a dataset all at once, then a common practice for evaluating the classification accuracy of a density estimation technique for making predictions from that data is to remove a small part of the dataset and use the rest to construct the density estimate. We then evaluate the classification accuracy of the density estimate on the small part of the dataset that was removed. For example, in the German word order data we might draw 10% of the data (57 observations)—say 45 of $\langle \mathbf{SB}, \mathbf{DO} \rangle$, 7 of $\langle \mathbf{SB}, \mathbf{IO} \rangle$, 3 of $\langle \mathbf{IO}, \mathbf{SB} \rangle$, and two of $\langle \mathbf{IO}, \mathbf{DO} \rangle$. In the remaining 90% of the data, $\langle \mathbf{SB}, \mathbf{DO} \rangle$ remains the most likely outcome, so we predict that for all 57 of the removed observations. Our classification accuracy is thus $\frac{45}{57} \approx 0.79$. This approach is called HELD-OUT EVALUATION.

Of course, held-out evaluation has some disadvantages as well, notably that the evaluation is based on only a small fraction of available data and hence will be noisy. Another widely used technique is CROSS-VALIDATION, in which we split our dataset into k equally sized portions. We then produce k different held-out evaluations of classification accuracy, each portion in turn serving as the held-out portion of the dataset, and average the classification accuracy across the folds. As a simple example, suppose we collected a corpus of {*night, day*} binomials, with 160 examples of *day and night* (`d`) and 140 examples of *night and day* (`n`). On 4-fold cross-validation, we might obtain the following outcomes:

Fold	# `d` held out	# `n` held out	Prediction	Accuracy
1	34	41	`n`	0.45
2	40	35	`d`	0.53
3	48	27	`d`	0.36
4	38	37	`d`	0.51
Total				0.46

If computing the predictions from observed data is fast, then the best kind of cross-validation is generally LEAVE-ONE-OUT cross-validation, where there are as many folds as there are observations.

Likelihood-based evaluation

Classification accuracy is "brittle" in the sense that it discards a great deal of information from a density estimate. As a simple example, for the binomial $\{night, day\}$ the best classification decision is d if $\hat{P}(\texttt{d}) > 0.5$; but $\hat{P}(\texttt{d}) = 0.51$ and $\hat{P}(\texttt{d}) = 0.99$ are very different distributions, and we'd like to distinguish the types of predictions they make. Furthermore, classification accuracy doesn't even make sense in the continuous random variable setting. We can address both these problems, however, via the concept of LIKELIHOOD, which we briefly encountered in Section 2.4.1. The likelihood under a density estimate $\hat{P}$ of a set of data $\boldsymbol{y}$ is simply

$$P(\boldsymbol{y}|\hat{P}) \tag{2.29}$$

The likelihood is sometimes viewed as a function of a set of observations $\boldsymbol{y}$, and sometimes (see Chapter 4) viewed as a property of the estimate itself $\hat{P}$. If the observations y_i are assumed to be independent of one another, then we can rewrite the likelihood as

$$P(\boldsymbol{y}|\hat{P}) = \prod_{i=1}^{n} P(y_i|\hat{P}) \tag{2.30}$$

Since likelihoods can be very small, and datasets can be very large, explicitly computing the product in Equation (2.30) can lead to problems with computational underflow. This can be avoided by computing the LOG-LIKELIHOOD; in log-space you are extremely unlikely to have computational underflow or overflow problems. Since the log of a product is the sum of a log, you'll usually see log-likelihood computed as in Equation (2.31) below:

$$\log P(\boldsymbol{y}|\hat{P}) = \sum_{i=1}^{n} \log P(y_i|\hat{P}) \tag{2.31}$$

Likelihood can be evaluated with respect to the data used to estimate the density, with respect to held-out data, or using cross-validation. Evaluating log-likelihood from the data used to estimate the model is, however, a dangerous enterprise. This is illustrated in Figures 2.6 through 2.8, for the example from Section 2.11.2 of estimating F0 formant frequency through normal-kernel density estimation. Figure 2.6 illustrates the change in estimated probability density as a result of choosing different bandwidths. The narrower the bandwidth, the more of the probability mass is focused around the observations themselves. As a result, the log-likelihood of the data used to estimate the density increases monotonically as the bandwidth decreases (Figure 2.7). The likelihood as evaluated with six-fold cross-validation, on the other hand reaches a maximum at bandwidth $b \approx 10$Hz (Figure 2.8). The discrepancy between the shapes of the curves in Figures 2.7 and 2.8 for $b < 10$—and also of the generally much higher log-likelihoods in the former figure—reveals that the narrow-bandwidth density estimates are OVERFITTING—intuitively, they mimic the observed data too closely and generalize too little. The cross-validated likelihood reveals that the assessment of The ability

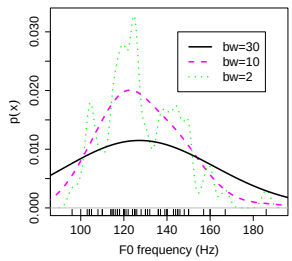


Figure 2.6: F0 formant kernel density estimates for normal kernels of different bandwidths.

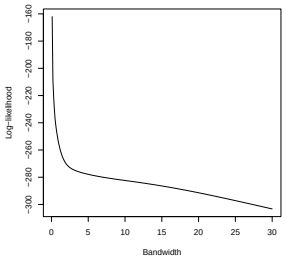


Figure 2.7: Overfitting when evaluating on training set: F0 formant log-likelihood increases unboundedly.

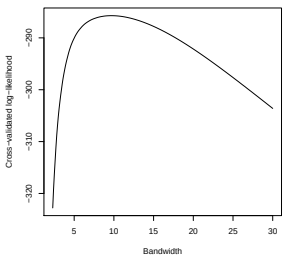
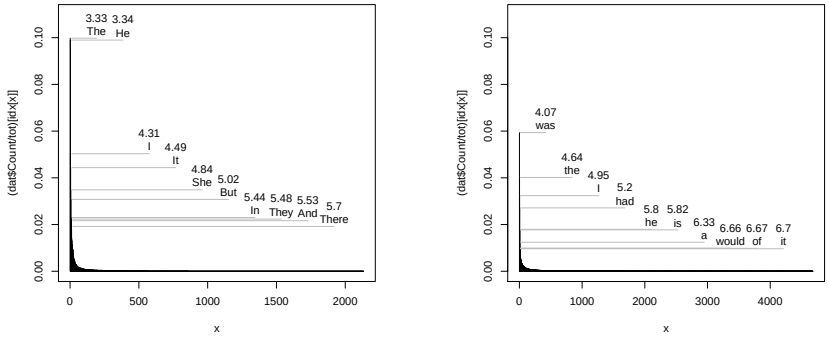


Figure 2.8: Cross-validated log-likelihood reveals the optimal bandwidth.



(a) First words

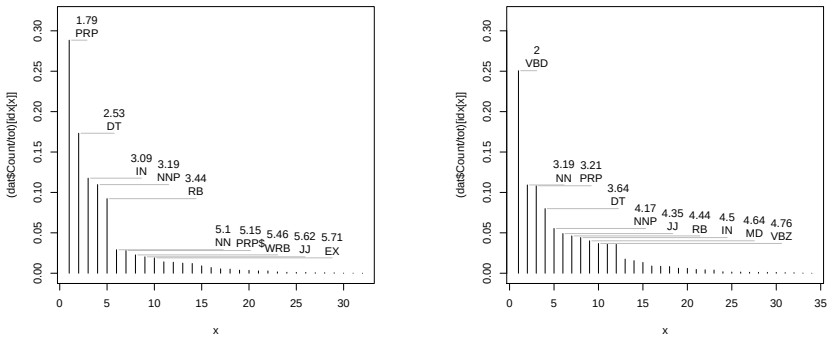
(b) Second words

Figure 2.9: The relative frequency distributions of the first and second words of sentences of the parsed Brown corpus

of the narrow-bandwidth density estimate to closely mimic observed data is a kind of *complexity* of the estimation process. Finding a balance between complexity and generalization is a hallmark issue of statistical inference, and we will see this issue arise again in numerous contexts throughout the book.

2.12 Surprisal, entropy, and relative entropy

One of the most fundamental views of probability is as quantifying our degree of uncertainty about events whose outcomes are unknown. Intuitively, the more uncertain we are as to an event's outcome, the more broadly distributed will be the probability mass over the event's possible outcomes. Likewise, we can say that learning the event's outcome gives us *information* about the world that we did not previously have. The quantity of information



(a) First-word POS (b) Second-word POS

Figure 2.10: The relative frequency distributions of the parts of speech of the first and second words of sentences of the parsed Brown corpus

conveyed by the outcome x of a discrete random variable is often measured by the SURPRISAL, alternatively called the SHANNON INFORMATION CONTENT or SELF-INFORMATION, of the outcome, defined as $\frac{1}{\log_2 P(x)}$ or equivalently $-\log_2 P(x)$; the unit of surprisal is the BIT, which is the amount of information conveyed by the flip of a fair coin. The surprisal of an event is the minimum number of bits required to convey the event's occurrence given knowledge of the underlying probability distribution from which the event was generated.

As an example, Figure **??** shows the relative frequencies (in descending order) of all words observed as the first word of at least one sentence in the parsed Brown corpus, excluding punctuation (Marcus et al., 1994). The ten most common of these words are labeled in the graph. If we oversimplify slightly and take these relative frequencies to be the true underlying word probabilities, we can compute the surprisal value that each word would have if it is seen as the first word in a new sentence drawn at random from the same corpus. These surprisal values appear above each of the ten labeled words. We can see that although there are thousands of different words attested to start sentences in this corpus, none of the ten most common conveys more than six bits of information (for reference, $2^6 = 64$).

The expected surprisal of a discrete random variable X, or the average information that an outcome of X conveys, is known as its ENTROPY $H(X)$, defined as:

$$H(X) = \sum_x P(x) \log_2 \frac{1}{P(x)} \tag{2.32}$$

or equivalently

$$= -\sum_x P(x) \log_2 P(x) \tag{2.33}$$

Applying this definition we find that the entropy of the distribution over first words in the sentence is 7.21, considerably higher than the entropy for second words, which is 9.51. The

precise values of these figures should be taken with a considerable grain of salt, because the data are quite sparse (most words only occur a handful of times, and many possible words don't appear at all), but they suggest that there is considerably more uncertainty about the second word in a sentence than about the first word of the sentence (recall, of course, that these probabilities do not at this point take into account any information about the context in which the word appears other than how many words preceded it in the sentence). Figure 2.10 shows relative frequency plots for the parts of speech of these first and second words (note, interestingly, that while PRP, or preposition, is the most frequent part of speech for first words, the most frequent word is a determiner). Repeating the calculation for parts of speech yields entropies of 3.33 and 3.8 for the first and second words respectively. Once again the entropy for the second word is greater than the first word, though by a smaller amount than in the word-level calculation (perhaps due to the fact that second words are likelier than first words to be open-class parts of speech, which are much easier to predict at the part-of-speech level than at the word-specific level).

Finally, consider the case where one has two different probability distributions P and Q over the same event space. Note that in the definition of entropy in Equation (2.32) the same probability function is used twice; one could imagine carrying out a similar calculation using each of P and Q once:

$$\sum_x P(x) \log_2 \frac{1}{Q(x)} \tag{2.34}$$

$$\tag{2.35}$$

This is known as CROSS ENTROPY. It is useful to think of the distribution Q appearing inside the logarithm as a *guess* distribution and the other distribution P as the *true*, or *reference*, distribution. Cross entropy quantifies how many bits are required on average to convey an event drawn from P when one does not know P and one's best guess of the distribution is Q. To determine how much worse this is than using the true distribution (and it is never better!), we can subtract out the entropy of P; this gives us what is called the RELATIVE ENTROPY or KULLBACK-LEIBLER DIVERGENCE (or KL divergence) from Q to P:

$$D(P||Q) = \sum_x P(x) \log_2 \frac{P(x)}{Q(x)} \tag{2.36}$$

The KL divergence can be thought of as the penalty, in bits, incurred by coding outcomes from P using Q. It is never negative and is zero *only* when $P = Q$. In our most recent example, if we call the two distributions over part-of-speech tags P_1 for first words and P_2 for second words, we find that the KL divergence $D(P_1||P_2) = 0.92$. (there are some parts of speech appearing in the second-word position which do not appear in the first-word position, such as the possessive clitic *'s*, which is represented as a separate word in the Penn Treebank, so that we cannot take the KL divergence from P_1 to P_2; it would be infinite.) This KL divergence is well over a third the size of the entropy of the true distributions, indicating that the part of speech distributions are very different for first and second words.

Surprisal, entropy, and relative entropy are essential conceptual building blocks in INFORMATION THEORY (Shannon, 1948), which among many other important ideas and results includes the SOURCE CODING THEOREM, which gives theoretical bounds on the compressibility of any information source, and the NOISY CHANNEL THEOREM, which gives theoretical bounds on the possible rate of error-free information transfer in noisy communication systems. Cover and Thomas (1991) is an authoritative text on many key areas of information theory; MacKay (2003) is another accessible text covering these two theorems.

```
> roundN <- function(x,decimals=2,fore=5) sprintf(paste("%",fore,".",decimals,"f",sep=
```

2.13 Exercises

Exercise 2.1: Conditional independence and set intersection†

Show that if A and B are conditionally independent given C and $P(A|C) > 0$, then $P(B|A \cap C) = P(B|C)$. **Hint:** one natural solution involves making use of the definition of conditional independence in two different ways.

Exercise 2.2: Loss of conditional independence**

Give an example in words where two events A and B are conditionally independent given some state of knowledge C, but when another piece of knowledge D is learned, A and B lose conditional independence.

Exercise 2.3: `tea` in *Wonderland*♣

1. You obtain infinitely many copies of the text *Alice in Wonderland* and decide to play a word game with it. You cut apart each page of each copy into individual letters, throw all the letters in a bag, shake the bag, and draw three letters at random from the bag. What is the probability that you will be able to spell `tea`? What about `tee`? [Hint: see Section 2.5.2; perhaps peek at Section A.8 as well.]

2. Why did the problem specify that you obtained infinitely many copies of the text? Suppose that you obtained only one copy of the text? Would you have enough information to compute the probability of being able to spell `tea`? Why?

Exercise 2.4: Bounds on probability density functions*

- Discrete random variables are governed by probability mass functions, which are bounded below by zero and above by 1 (that is, every value a probability mass function must be at least zero and no more than 1). Why must a probability mass function be bounded above by 1?

- Continuous random variables are governed by probability density functions, which are bounded below by zero. What are probability density functions bounded above by? Why?

Exercise 2.5: Probabilities in the constituent-order model♣

For the constituent-order example given in 2.8, let $\gamma_1 = 0.6$, $\gamma_2 = 0.4$, and $\gamma_3 = 0.3$. Compute the probabilities of all six possible word orders.

Exercise 2.6: Parameters of the constituent-order model**

In the constituent-order example given in 2.8, I mentioned that we would like to interpret the probability of each parameter γ_i analogously to the success parameter of a single Bernoulli trial, so that the probability that $S \prec O$ is γ_1, the probability that $S \prec V$ is γ_2, and the probability that $O \prec V$ is γ_3. Given the mass function F actually used in the example, is the probability that $S \prec O$ actually γ_1? Show your work.

Exercise 2.7: More on the constituent-order model

Play around with specific parameter values for the constituent-order model to get a feel for it. We know that it is more constrained than a general six-class multinomial distribution, since it has only three parameters instead of five. Qualitatively speaking, what kinds of distributions over the six logically possible word orders is it incapable of modeling?

Exercise 2.8: Expectation of a uniform random variable*

Prove mathematically that the expectation of a uniform random variable X on $[a, b]$ is $E(X) = \frac{a+b}{2}$. (This involves a simple integration; consult A.6 if you need a refresher.)

Exercise 2.9: Variance of a uniform random variable**

Prove that the variance of a continuous, uniformly distributed random variable X on $[a, b]$ is $\frac{(b-a)^2}{12}$. [Sections 2.7.1 and 2.9.2]

Exercise 2.10: Normal distributions♣

For adult female native speakers of American English, the distribution of first-formant frequencies for the vowel [ɛ] is reasonably well modeled as a normal distribution with mean 608Hz and standard deviation 77.5Hz. What is the probability that the first-formant frequency of an utterance of [ɛ] for a randomly selected adult female native speaker of American English will be between 555Hz and 697Hz?

Exercise 2.11: Assessing optimal kernel bandwidth through cross-validation†,⌨

Use leave-one-out cross-validation to calculate the cross-validated likelihood of kernel density estimates (using a normal kernel) of adult male speaker [ɑ] and [i] F2 formants from the Peterson and Barney dataset. Plot the cross-validated likelihood as a function of kernel bandwidth. Are the bandwidths that work best for [ɑ] and [i] similar to each other? Explain your results.

Exercise 2.12: Kernel density estimation and change of variables

Complete Exercise 2.11, but this time change the formant frequency measurements from Hertz to log-Hertz before carrying out bandwidth selection. Once you're done, compare the optimal bandwidths and the corresponding density estimates obtained using log-Hertz

measurements with that obtained using Hertz measurements. How different are they?

Exercise 2.13: Kernels in discrete linguistic spaces[‡]

Construct your own kernel over the space of 27 CVC lexical forms used in Section 2.11.3. With the 18 attested forms listed in that section, use leave-one-out cross-validation to compute the cross-validated likelihood of your kernel. Does it do better or worse than the original kernel?

Exercise 2.14: Exemplar-based model of phonotactic knowledge[‡]

The file `syllCounts` contains phonetic representations of attested word-initial syllables in disyllabic words of English, based on the CELEX lexical database, together with their frequencies of occurrence. Find a partner in your class. Each of you should independently construct a kernel over the phonetic representations of these word-initial syllables. Using ten-fold cross-validation, compute the cross-validated likelihood of kernel density estimtes using each of your kernels. Compare the results, noting which syllables each kernel did better on. Now join forces and try to construct a third kernel which combines the best qualities of your two kernels, and (hopefully) has a higher cross-validated likelihood than either one.

Chapter 3

Multivariate Probability

3.1 Joint probability mass and density functions

Recall that a basic probability distribution is defined over a random variable, and a random variable maps from the sample space to the real numbers.What about when you are interested in the outcome of an event that is not naturally characterizable as a single real-valued number, such as the two formants of a vowel?

The answer is simple: probability mass and density functions can be generalized over multiple random variables at once. If all the random variables are discrete, then they are governed by a JOINT PROBABILITY MASS FUNCTION; if all the random variables are continuous, then they are governed by a JOINT PROBABILITY DENSITY FUNCTION. There are many things we'll have to say about the joint distribution of collections of random variables which hold equally whether the random variables are discrete, continuous, or a mix of both. [1] In these cases we will simply use the term "joint density" with the implicit understanding that in some cases it is a probability mass function.

Notationally, for random variables $X_1, X_2, \cdots, X_N$, the joint density is written as

$$p(X_1 = x_1, X_2 = x_2, \cdots, X_N = x_n) \tag{3.1}$$

or simply

$$p(x_1, x_2, \cdots, x_n) \tag{3.2}$$

for short.

[1] If some of the random variables are discrete and others are continuous, then technically it is a probability density function rather than a probability mass function that they follow; but whenever one is required to compute the total probability contained in some part of the range of the joint density, one must sum on the discrete dimensions and integrate on the continuous dimensions.

3.1.1 Joint cumulative distribution functions

For a single random variable, the cumulative distribution function is used to indicate the probability of the outcome falling on a segment of the real number line. For a collection of N random variables $X_1, \ldots, X_N$ (or density), the analogous notion is the JOINT CUMULATIVE DISTRIBUTION FUNCTION, which is defined with respect to regions of N-dimensional space. The joint cumulative distribution function, which is sometimes notated as $F(x_1, \cdots, x_n)$, is defined as the probability of the set of random variables all falling at or below the specified values of X_i:[2]

$$F(x_1, \cdots, x_n) \stackrel{\text{def}}{=} P(X_1 \leq x_1, \cdots, X_N \leq x_n)$$

The natural thing to do is to use the joint cpd to describe the probabilities of rectangular volumes. For example, suppose X is the f_1 formant and Y is the f_2 formant of a given utterance of a vowel. The probability that the vowel will lie in the region $480\text{Hz} \leq f_1 \leq 530\text{Hz}, 940\text{Hz} \leq f_2 \leq 1020\text{Hz}$ is given below:

$$\begin{aligned} &P(480\text{Hz} \leq f_1 \leq 530\text{Hz}, 940\text{Hz} \leq f_2 \leq 1020\text{Hz}) = \\ &\qquad F(530\text{Hz}, 1020\text{Hz}) - F(530\text{Hz}, 940\text{Hz}) - F(480\text{Hz}, 1020\text{Hz}) + F(480\text{Hz}, 940\text{Hz}) \end{aligned}$$

and visualized in Figure 3.1 using the code below.

3.2 Marginalization

Often we have direct access to a joint density function but we are more interested in the probability of an outcome of a subset of the random variables in the joint density. Obtaining this probability is called MARGINALIZATION, and it involves taking a weighted sum[3] over the possible outcomes of the random variables that are not of interest. For two variables X, Y:

[2] Technically, the definition of the multivariate cumulative distribution function is

$$F(x_1, \cdots, x_n) \stackrel{\text{def}}{=} P(X_1 \leq x_1, \cdots, X_N \leq x_n) = \sum_{\vec{x} \leq \langle x_1, \cdots, x_N \rangle} p(\vec{x}) \quad \text{[Discrete]} \tag{3.3}$$

$$F(x_1, \cdots, x_n) \stackrel{\text{def}}{=} P(X_1 \leq x_1, \cdots, X_N \leq x_n) = \int_{-\infty}^{x_1} \cdots \int_{-\infty}^{x_N} p(\vec{x}) dx_N \cdots dx_1 \quad \text{[Continuous]} \tag{3.4}$$

[3] or integral in the continuous case

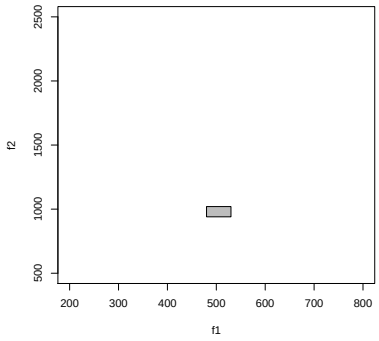


Figure 3.1: The probability of the formants of a vowel landing in the grey rectangle can be calculated using the joint cumulative distribution function.

$$\begin{aligned} P(X = x) &= \sum_y P(x, y) \\ &= \sum_y P(X = x|Y = y)P(y) \end{aligned}$$

In this case $P(X)$ is often called a *marginal density* and the process of calculating it from the joint density $P(X, Y)$ is known as *marginalization*.

As an example, consider once again the historical English example of Section 2.4. We can now recognize the table in I as giving the joint density over two binary-valued random variables: the position of the object with respect to the verb, which we can denote as X, and the pronominality of the object NP, which we can denote as Y. From the joint density given in that section we can calculate the marginal density of X:

$$P(X = x) = \begin{cases} 0.224 + 0.655 = 0.879 & x = \textbf{Preverbal} \\ 0.014 + 0.107 = 0.121 & x = \textbf{Postverbal} \end{cases} \tag{3.5}$$

Additionally, if you now look at the old English example of Section 2.4.1 and how we calculated the denominator of Equation 2.7, you will see that it involved marginalization over the animacy of the object NP. Repeating Bayes' rule for reference:

$$P(A|B) = \frac{P(B|A)P(A)}{P(B)}$$

It is very common to need to explicitly marginalize over A to obtain the marginal probability for B in the computation of the denominator of the right-hand side.

3.3 Linearity of expectation, covariance, correlation, and variance f sums of random variables

3.3.1 Linearity of the expectation

Linearity of the expectation is an extremely important property and can expressed in two parts. First, if you *rescale* a random variable, its expectation rescales in the exact same way. Mathematically, if $Y = a + bX$, then $E(Y) = a + bE(X)$.

Second, the expectation of the sum of random variables is the sum of the expectations. That is, if $Y = \sum_i X_i$, then $E(Y) = \sum_i E(X_i)$. This holds regardless of any conditional dependencies that hold among the X_i.

We can put together these two pieces to express the expectation of a linear combination of random variables. If $Y = a + \sum_i b_i X_i$, then

$$E(Y) = a + \sum_i b_i E(X_i) \tag{3.6}$$

This is incredibly convenient. We'll demonstrate this convenience when we introduc the binomial distribution in Section 3.4.

3.3.2 Covariance

The COVARIANCE between two random variables X and Y is a measure of how tightly the outcomes of X and Y tend to pattern together. It defined as follows:

$$\text{Cov}(X, Y) = E[(X - E(X))(Y - E(Y))]$$

When the covariance is positive, X tends to be high when Y is high, and vice versa; when the covariance is negative, X tends to be high when Y is low, and vice versa.

As a simple example of covariance we'll return once again to the Old English example of Section 2.4; we repeat the joint density for this example below, with the marginal densities in the row and column margins:

(1)

		Coding for Y		
		0	1	
Coding for X		**Pronoun**	**Not Pronoun**	
0	Object **Preverbal**	0.224	0.655	.879
1	Object **Postverbal**	0.014	0.107	.121
		.238	.762	

We can compute the covariance by treating each of X and Y as a Bernoulli random variable, using arbitrary codings of 1 for **Postverbal** and **Not Pronoun**, and 0 for **Preverbal** and

Pronoun. As a result, we have $E(X) = 0.121$, $E(Y) = 0.762$. The covariance between the two can then be computed as follows:

$$\begin{aligned}
&(0 - 0.121) \times (0 - .762) \times .224 && \text{(for X=0,Y=0)} \\
+&(1 - 0.121) \times (0 - .762) \times 0.014 && \text{(for X=1,Y=0)} \\
+&(0 - 0.121) \times (1 - .762) \times 0.655 && \text{(for X=0,Y=1)} \\
+&(1 - 0.121) \times (1 - .762) \times 0.107 && \text{(for X=1,Y=1)} \\
=&0.014798
\end{aligned}$$

If X and Y are conditionally independent given our state of knowledge, then $\text{Cov}(X, Y)$ is zero (Exercise 3.2 asks you to prove this).

3.3.3 Covariance and scaling random variables

What happens to $Cov(X, Y)$ when you scale X? Let $Z = a + bX$. It turns out that the covariance with Y increases by b (Exercise 3.4 asks you to prove this):

$$\text{Cov}(Z, Y) = b\text{Cov}(X, Y)$$

As an important consequence of this, rescaling a random variable by $Z = a + bX$ rescales its variance by b^2: $\text{Var}(Z) = b^2\text{Var}(X)$ (see Exercise 3.3).

3.3.4 Correlation

We just saw that the covariance of word length with frequency was much higher than with log frequency. However, the covariance cannot be compared directly across different pairs of random variables, because we also saw that random variables on different scales (e.g., those with larger versus smaller ranges) have different covariances due to the scale. For this reason, it is commmon to use the CORRELATION ρ as a standardized form of covariance:

$$\rho_{XY} = \frac{Cov(X, Y)}{\sqrt{Var(X)Var(Y)}}$$

```
[1]  0.020653248 -0.018862690 -0.009377172  0.022384614
```

In the word order & pronominality example above, where we found that the covariance of verb-object word order and object pronominality was 0.01, we can re-express this relationship as a correlation. We recall that the variance of a Bernoulli random variable with success parameter π is $\pi(1-\pi)$, so that verb-object word order has variance 0.11 and object pronominality has variance 0.18. The correlation between the two random variables is thus $\frac{0.01}{\sqrt{0.11 \times 0.18}} = 0.11$.

If X and Y are independent, then their covariance (and hence correlation) is zero.

3.3.5 Variance of the sum of random variables

It is quite often useful to understand how the variance of a sum of random variables is dependent on their joint distribution. Let $Z = X_1 + \cdots + X_n$. Then

$$\text{Var}(Z) = \sum_{i=1}^{n} \text{Var}(X_i) + \sum_{i \neq j} \text{Cov}(X_i, X_j) \tag{3.7}$$

Since the covariance between conditionally independent random variables is zero, it follows that the variance of the sum of pairwise independent random variables is the sum of their variances.

3.4 The binomial distribution

We're now in a position to introduce one of the most important probability distributions for linguistics, the BINOMIAL DISTRIBUTION. The binomial distribution family is characterized by two parameters, n and π, and a binomially distributed random variable Y is defined as the sum of n identical, independently distributed (i.i.d.) Bernoulli random variables, each with parameter π.

For example, it is intuitively obvious that the mean of a binomially distributed r.v. Y with parameters n and π is πn. However, it takes some work to show this explicitly by summing over the possible outcomes of Y and their probabilities. On the other hand, Y can be re-expressed as the sum of n BERNOULLI RANDOM VARIABLES X_i. The resulting probability density function is, for $k = 0, 1, \ldots, n$: [4]

$$P(Y = k) = \binom{n}{k} \pi^k (1 - \pi)^{n-k} \tag{3.8}$$

We'll also illustrate the utility of the linearity of expectation by deriving the expectation of Y. The mean of each X_i is trivially π, so we have:

$$E(Y) = \sum_{i}^{n} E(X_i) \tag{3.9}$$

$$= \sum_{i}^{n} \pi = \pi n \tag{3.10}$$

which makes intuitive sense.

Finally, since a binomial random variable is the sum of n mutually independent Bernoulli random variables and the variance of a Bernoulli random variable is $\pi(1 - \pi)$, the variance of a binomial random variable is $n\pi(1 - \pi)$.

[4] Note that $\binom{n}{k}$ is pronounced "n choose k", and is defined as $\frac{n!}{k!(n-k)!}$. In turn, $n!$ is pronounced "n factorial", and is defined as $n \times (n-1) \times \cdots \times 1$ for $n = 1, 2, \ldots$, and as 1 for $n = 0$.

3.4.1 The multinomial distribution

The MULTINOMIAL DISTRIBUTION is the generalization of the binomial distribution to $r \geq 2$ possible outcomes. (It can also be seen as the generalization of the distribution over multinomial trials introduced in Section 2.5.2 to the case of $n \geq 1$ trials.) The r-class multinomial is a sequence of r random variables $X_1, \ldots, X_r$ whose joint distribution is characterized by r parameters: a size parameter n denoting the number of trials, and $r-1$ parameters $\pi_1, \ldots, \pi_{r-1}$, where π_i denotes the probability that the outcome of a single trial will fall into the i-th class. (The probability that a single trial will fall into the r-th class is $\pi_r \stackrel{\text{def}}{=} 1 - \sum_{i=1}^{r-1} \pi_i$, but this is not a real parameter of the family because it's completely determined by the other parameters.) The (joint) probability mass function of the multinomial looks like this:

$$P(X_1 = n_1, \cdots, X_r = n_r) = \binom{n}{n_1 \cdots n_r} \prod_{i=1}^{r} \pi_i \tag{3.11}$$

where n_i is the number of trials that fell into the r-th class, and $\binom{n}{n_1 \cdots n_r} = \frac{n!}{n_1! \ldots n_r!}$.

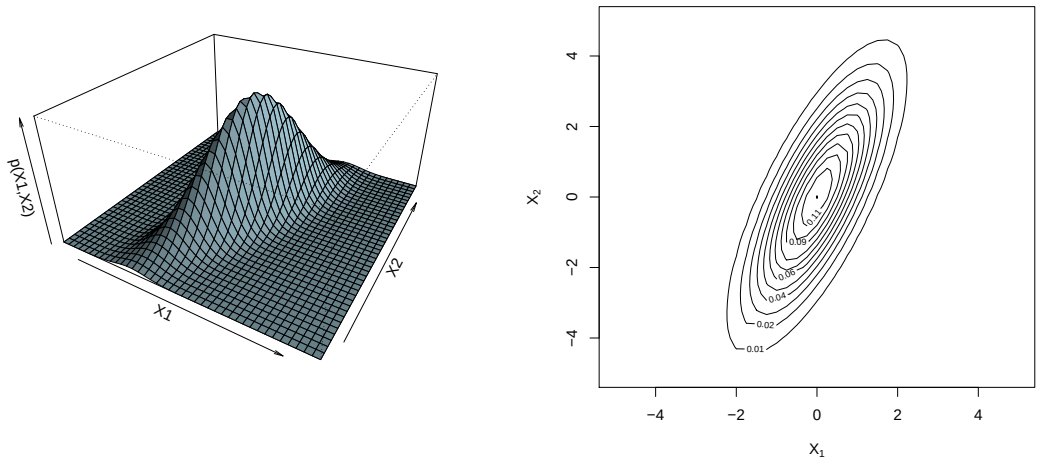
3.5 Multivariate normal distributions

Finally, we turn to the MULTIVARIATE NORMAL DISTRIBUTION. Recall that the univariate normal distribution placed a probability density over outcomes of a single continuous random variable X that was characterized by two parameters—mean μ and variance σ^2. The multivariate normal distribution in N dimensions, in contrast, places a joint probability density on N real-valued random variables $X_1, \ldots, X_N$, and is characterized by two sets of parameters: (1) a mean vector μ of length N, and (2) a symmetric COVARIANCE MATRIX (or variance-covariance matrix) $\boldsymbol{\Sigma}$ in which the entry in the i-th row and j-th column expresses the covariance between X_i and X_j. Since the covariance of a random variable with itself is its variance, the diagonal entries of $\boldsymbol{\Sigma}$ are the variances of the individual X_i and must be non-negative. In this situation we sometimes say that $X_1, \ldots, X_N$ are JOINTLY NORMALLY DISTRIBUTED.

The probability density function for the multivariate normal distribution is most easily expressed using matrix notation (Section A.9); the symbol $\mathbf{x}$ stands for the vector $\langle x_1, \ldots, x_n \rangle$:

$$p(\mathbf{x}) = \frac{1}{\sqrt{(2\pi)^N |\boldsymbol{\Sigma}|}} \exp\left[-\frac{(\mathbf{x} - \mu)^{\mathrm{T}} \boldsymbol{\Sigma}^{-1} (\mathbf{x} - \mu)}{2} \right] \tag{3.12}$$

For example, a bivariate normal distribution ($N = 2$) over random variables X_1 and X_2 has two means μ_1, μ_2, and the covariance matrix contains two variance terms (one for X_1 and one for X_2), and one *covariance term* showing the correlation between X_1 and Y_2. The covariance matrix would look like $\begin{pmatrix} \sigma_{11}^2 & \sigma_{12}^2 \\ \sigma_{12}^2 & \sigma_{22}^2 \end{pmatrix}$. Once again, the terms σ_{11}^2 and σ_{22}^2 are



(a) Perspective plot (b) Contour plot

Figure 3.2: Visualizing the multivariate normal distribution

simply the variances of X_1 and X_2 respectively (the subscripts appear doubled for notational consistency). The term σ_{12}^2 is the covariance between the two axes. [5] Figure 3.2 visualizes a bivariate normal distribution with $\mu = (0, 0)$ and $\mathbf{\Sigma} = \begin{pmatrix} 1 & 1.5 \\ 1.5 & 4 \end{pmatrix}$. Because the variance is larger in the X_2 axis, probability density falls off more rapidly along the X_1 axis. Also note that the major axis of the ellipses of constant probability in Figure 3.2b does not lie right on the X_2 axis, but rather is at an angle reflecting the positive covariance.

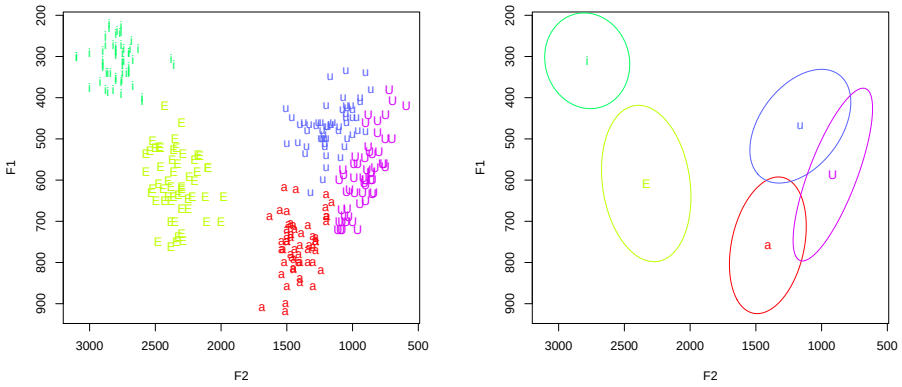
The multivariate normal distribution is very useful in modeling multivariate data such as the distribution of multiple formant frequencies in vowel production. As an example, Figure 3.3 shows how a large number of raw recordings of five vowels in American English can be summarized by five "characteristic ellipses", one for each vowel. The center of each ellipse is placed at the empirical mean for the vowel, and the shape of the ellipse reflects the empirical covariance matrix for that vowel.

In addition, multivariate normal distributions plays an important role in almost all hierarchical models, covered starting in Chapter 8.

[5] The probability density function works out to be

$$p(x_1, x_2) = \frac{1}{2\pi\sqrt{\sigma_{11}^2\sigma_{22}^2 - \sigma_{12}^4}} \exp\left[\frac{(x_1-\mu_1)^2\sigma_{22}^2 - 2(x_1-\mu_1)(x_2-\mu_2)\sigma_{12}^2 + (x_2-\mu_2)^2\sigma_{11}^2}{\sigma_{11}^2\sigma_{22}^2 - \sigma_{12}^4}\right]$$

Note that if σ_{11} is much larger than σ_{22}, then $x_2 - \mu_2$ will be more important than $x_1 - \mu_1$ in the exponential. This reflects the fact that if the variance is much larger on the X_1 axis than on the X_2 axis, a fixed amount of deviation from the mean is much less probable along the x_2 axis.



(a) Raw recordings of five vowels by adult female speakers

(b) Representation as multivariate normal distributions. The character is placed at the empirical mean for each vowel, and the covariance structure of each vowel is represented by an equiprobability ellipse

Figure 3.3: F1 and F2 formant frequency representations using multivariate normal distributions, based on the data of Peterson and Barney (1952)

3.5.1 The sum of jointly normal random variables

Yet another attractive property of the multivariate normal distribution is that the sum of a set of jointly normal random variables is itself a normal random variable. The mean and variance of the sum can be computed based on the formulae given in Sections 3.3.1 and 3.3.5. So if $\langle X_1, \ldots, X_n \rangle$ are jointly normal with mean $\langle \mu_1, \ldots, \mu_n \rangle$ and covariance matrix Σ, then $Z = X_1 + \cdots + X_n$ is normally distributed with mean $\sum_{i=1}^{n} \mu_i$ and variance $\sum_{i=1}^{n} \sigma_i^2 + \sum_{i \neq j} \sigma_{ij}$.

3.6 The central limit theorem

The CENTRAL LIMIT THEOREM is a powerful result from probability theory that states that the sum of a large quantity of i.i.d. random variables will have an approximately normal distribution, *regardless of the distribution of the individual random variables.* More formally, suppose that we have n i.i.d. random variables X_i, with $Y = X_1 + \cdots + X_n$. From linearity of the variance, we know that Y's mean is $\mu_Y = nE[X_i]$, and its variance is $\sigma_Y^2 = n\sigma_{X_i}^2$. The central limit theorem states that as the number n of random variables grows, the distribution of the random variable $Z = \frac{Y - \mu_Y}{\sigma_Y}$ approaches that of a standard normal random variable.

The central limit theorem traditionally serves as the basis for using the normal distribution to model the outcome of a complex process with many underlying contributing factors. Exercise 3.12 explores a simple example illustrating the truth of the theorem, showing how a binomial distribution with large n can be approximated by the normal distribution.

3.7 Joint entropy, conditional entropy, and mutual information

In Section 2.12 we introduced the basic information-theoretic ideas of surprisal and entropy. With multivariate probability, there is not much more to say about surprisal: all there is to say is that the surprisal of the joint outcome of multiple random variables is the log of the inverse of the joint probability of outcomes:

$$\log \frac{1}{P(x_1, x_2, \ldots, x_n)} \qquad \text{or} \qquad -\log P(x_1, x_2, \ldots, x_n). \tag{3.13}$$

However, there is much more to say about entropies. In the rest of this section we will limit the discussion to cases where there are two random variables X and Y, but most of what is discussed can be generated to collections of arbitrary quantities of random variables.

We begin by defining the JOINT ENTROPY of X and Y analogously from the surprisal of a joint outcome:

$$H(X, Y) = \sum_{x,y} P(x, y) \log \frac{1}{P(x, y)} \tag{3.14}$$

What gets really interesting is when we break down the joint entropy into its constituent parts. We start by imagining situations in which we obtain knowledge of X while remaining ignorant of Y. The average entropy that Y will have after we learn about X is called the CONDITIONAL ENTROPY of Y given X and is notated as follows:

$$H(Y|X) = \sum_{x} P(x) \sum_{y} P(y|x) \log_2 \frac{1}{P(y|x)} \tag{3.15}$$

where $P(x)$ is the marginal probability of x. Note that this equation follows simply from the definition of expectation. Recall that in Section 2.12 we showed the distributions and entropies of non-punctuation words and their corresponding parts of speech. Returning to this example and slightly modifying the dataset (now excluding all sentences in which either the first or the second word was a punctuation term, a more stringent criterion), we find that the entropy of the part of speech for the second word is 3.66 and that its conditional entropy given the first word's part of speech is 2.43. That is, the first word removes about a third of the entropy of the second word!

Next, we can ask how much information we would lose regarding the joint distribution of X and Y if we were to treat the two variables as independent. Recall once again from Section 2.12 that the KL divergence from Q to P measures the penalty incurred by using Q to approximate P. Here, let us define $Q(x, y) = P_X(x)P_Y(y)$ where P_X and P_Y are the marginal probabilities for X and Y respectively. The KL divergence from Q to P is known as the MUTUAL INFORMATION between X and Y and is defined as

$$I(X; Y) = \sum_{x,y} P(x, y) \log \frac{P(x, y)}{P_X(x)P_Y(y)} \tag{3.16}$$

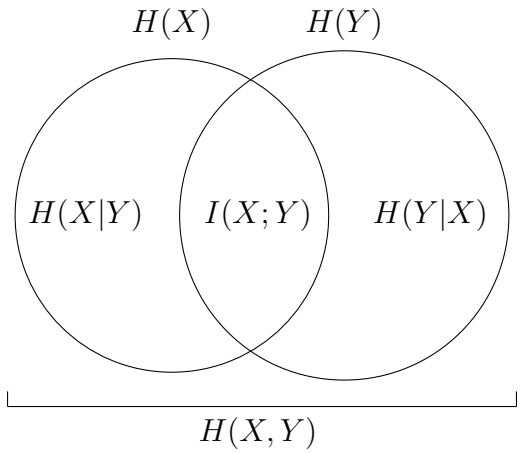


Figure 3.4: Entropy and mutual information for two random variables as a Venn diagram. Circle sizes and positions reflect the entropies of our example, where X is the first-word part of speech and Y is the second-word part of speech.

In our example, the mutual information between the parts of speech for the first and second words comes out to 1.23. You may notice that the three numbers we have just seen stand in a very simple relationship: $3.66 = 2.43 + 1.23$. This is no coincidence! In general, given any two random variables X and Y, the entropy of Y can *always* be decomposed as precisely the sum of the mutual information—which measures how much X tells you about Y—and the conditional entropy—which measures how much X *doesn't* tell you about Y:

$$H(Y) = I(X;Y) + H(Y|X) \qquad \text{and likewise} \qquad H(X) = I(X;Y) + H(X|Y). \tag{3.17}$$

There is one more remarkable decomposition to be had. In our example, the entropy of the first-word part of speech is 3.38, and the joint entropy for the two words is 5.81. In general, the joint entropy of X and Y is the sum of the individual variables' entropies minus the mutual information—which measures the *redundancy* between X and Y:

$$H(X,Y) = H(X) + H(Y) - I(X;Y) \tag{3.18}$$

In our case, 3.38 + 3.66 - 1.23 = 5.81. This decomposition arises from the original definition of mutual information as the coding penalty incurred for assuming independence between two variables.

In closing this section, let us notice that mutual information comes up in both an *asymmetric* decomposition—in the decomposition of $H(Y)$ as how much information X gives about Y—and in a *symmetric* decomposition—in the relationship between a joint entropy and the marginal entropies. For two random variables, the complete set of relations among the joint entropies, individual-variable entropies, conditional entropies, and mutual information can be depicted in a Venn diagram, as in Figure 3.4. The relations described in this section are well worth reviewing repeatedly, until they become second nature.

3.8 Exercises

Exercise 3.1: Simpler formula for variance.

Show from the definition of the variance as $\text{Var}(X) \equiv E[(X - E(X))^2]$ that it can equivalently be written as $\text{Var}(X) = E[X^2] - E[X]^2$, which we stated without proof in Section 2.9.2. [Section 3.3.1]

Exercise 3.2: Covariance of conditionally independent random variables.

Use linearity of the expectation to prove that if two random variables X and Y are conditionally independent given your state of knowledge, then $\text{Cov}(X, Y) = 0$ under this state of knowledge. (**Hint:** you can rewrite $\sum_{x,y} Xp(X = x)Yp(Y = y)$ as $\sum_x Xp(X = x) \sum_y Yp(Y = y)$, since X and $p(X = x)$ are constant with respect to y.)

Exercise 3.3: ♣

- What is the covariance of a random variable X with itself?
- Now show that if you rescale a random variable X by defining $Z = a + bX$, then $\text{Var}(Z) = b^2\text{Var}(X)$.

Exercise 3.4

Show that if you rescale X as $Z = a + bX$, then $\text{Cov}(Z, Y) = b\text{Cov}(X, Y)$.

Exercise 3.5

Prove Equation 3.7—that is, that $\text{Var}(X_1 + \cdots + X_n) = \sum_{i=1}^n \text{Var}(X_i) + \sum_{i \neq j} \text{Cov}(X_i, X_j)$.

Exercise 3.6

Let's return to coin flipping, but use a different process to generate a sequence of coin flips. Suppose I start flipping a coin with success parameter π, and every time it comes up tails I keep on flipping, but the first time it comes up heads I stop. The random variable of interest is the length of the sequence of coin flips. The GEOMETRIC DISTRIBUTION characterizes the probability density on this random variable. The probability mass function of the geometric distribution has the form

$$P(X = k) = (1 - \pi)^a \pi^b, k \in \{1, 2, \cdots\}$$

for some choice of a and b. Complete the specification of the distribution (i.e., say what a and b are are) and justify it.

Exercise 3.7

The file `brown-counts-lengths-nsyll` contains the following properties for each word type found in the parsed Brown corpus:

- The token frequency of the word;

- The length of the word in letters;
- The number of syllables in the word, as determined by the CMU Pronouncing dictionary (*http://www.speech.cs.cmu.edu/cgi-bin/cmudict*).

Plot histograms of the number of syllables for word, over (a) **word types** and (b) **word tokens**. Which of the histograms looks more binomially-distributed? Which looks more geometrically-distributed? Try to find a good fit (by eyeball assessment) to each of the histograms by choosing binomial or geometric parameters that match the data as well as you can.

Exercise 3.8

The NEGATIVE BINOMIAL distribution is a generalization of the geometric distribution in which you are interested in how many coin flips you can make before you achieve a total of r successes (where the successes are included in the total number of flips). The distribution is characterized by two parameters: the required number of successes r, and the probability p of success on any given coin flip. (The geometric distribution is a negative binomial distribution for which $r = 1$.) If the total number of coin flips obtained in a given trial is k, then the probability mass function for a negative binomial distribution with parameters p, r has the form

$$P(X = k; r, p) = \binom{a}{b}(1-p)^c p^d, k \in \{r, r+1, \cdots\}$$

for some choice of a, b, c, d. Complete the specification of the distribution (i.e., say what a, b, c, d are) and justify it.

Exercise 3.9: Linearity of expectation

You put two coins in a pouch; one coin is weighted such that it lands heads $\frac{5}{6}$ of the time when it's flipped, and the other coin is weighted such that it lands heads $\frac{1}{3}$ of the time when it's flipped. You shake the pouch, choose one of the coins from it at random and flip it twice. Write out both the marginal density for the outcome of the first flip and the joint density for the outcome of the two coin flips. Define the random variable X as the number of heads resulting from the two coin flips. Use linearity of the expectation to compute $E(X)$. Then compute $E(X)$ directly from the joint density to confirm that linearity of the expectation holds.

Exercise 3.10

Explain why rescaling a random variable by $Z = a + bX$ changes the variance by a factor of b^2, so that $\text{Var}(Z) = b^2 \text{Var}(X)$. (See Section 3.3.3.)

Exercise 3.11

You are planning on conducting a word recognition study using the lexical-decision paradigm, in which a participant is presented a letter sequence on a computer screen and

then presses a key on the keyboard as soon as she recognizes it as either a word (the key `F`) or a non-word (the key `J`). The distribution of measured response times for non-words in this study is the sum of two independent random variables: X, the elapsed time from the appearance of the letter string on the screen to the participant's successful pressing of a key; and Y, the time elapsed between the pressing of the key and the successful recording of the key press by the computer (this distribution is governed by the polling rate and reliability of the keyboard). Suppose that X has mean 600 and standard deviation 80, and Y has mean 15 and standard deviation 9 (all measured in milliseconds). What are the mean and standard deviation of recorded reaction times $(X + Y)$? [Section 3.3.5]

Exercise 3.12

Test the validity of the central limit theorem. Choose your own probability distribution, generate n i.i.d. random variables, add them together repeatedly, and standardize them (subtract out the mean and divide by the standard deviation). Use these multiple trials to generate estimated probability density and cumulative distribution functions. Compare these to the density and cumulative distribution function of the standard normal distribution. Do this for at least (a) the uniform and (b) the Bernoulli distribution. You're also welcome to use other distributions or invent your own.

1

Chapter 4

Parameter Estimation

Thus far we have concerned ourselves primarily with *probability theory*: what events may occur with what probabilities, given a model family and choices for the parameters. This is useful only in the case where we know the precise model family and parameter values for the situation of interest. But this is the exception, not the rule, for both scientific inquiry and human learning & inference. Most of the time, we are in the situation of processing data whose generative source we are uncertain about. In Chapter 2 we briefly covered elementary density estimation, using relative-frequency estimation, histograms and kernel density estimation. In this chapter we delve more deeply into the theory of probability density estimation, focusing on inference within parametric families of probability distributions (see discussion in Section 2.11.2). We start with some important properties of estimators, then turn to basic frequentist parameter estimation (maximum-likelihood estimation and corrections for bias), and finally basic Bayesian parameter estimation.

4.1 Introduction

Consider the situation of the first exposure of a native speaker of American English to an English variety with which she has no experience (e.g., Singaporean English), and the problem of inferring the probability of use of active versus passive voice in this variety with a simple transitive verb such as *hit*:

(1) The ball hit the window. (Active)

(2) The window was hit by the ball. (Passive)

There is ample evidence that this probability is contingent on a number of features of the utterance and discourse context (e.g., Weiner and Labov, 1983), and in Chapter 6 we cover how to construct such richer models, but for the moment we simplify the problem by assuming that active/passive variation can be modeled with a binomial distribution (Section 3.4) with parameter π characterizing the probability that a given potentially transitive clause eligible

for passivization will in fact be realized as a passive.[1] The question faced by the native American English speaker is thus, what inferences should we make about π on the basis of limited exposure to the new variety? This is the problem of PARAMETER ESTIMATION, and it is a central part of statistical inference. There are many different techniques for parameter estimation; any given technique is called an ESTIMATOR, which is applied to a set of data to construct an estimate. Let us briefly consider two simple estimators for our example.

Estimator 1. Suppose that our American English speaker has been exposed to n transitive sentences of the variety, and m of them have been realized in the passive voice in eligible clauses. A natural estimate of the binomial parameter π would be m/n. Because m/n is the relative frequency of the passive voice, this is known as the RELATIVE FREQUENCY ESTIMATE (RFE; see Section 2.11.1). In addition to being intuitive, we will see in Section 4.3.1 that the RFE can be derived from deep and general principles of optimality in estimation procedures. However, RFE also has weaknesses. For instance, it makes no use of the speaker's knowledge of her native English variety. In addition, when n is small, the RFE is unreliable: imagine, for example, trying to estimate π from only two or three sentences from the new variety.

Estimator 2. Our speaker presumably knows the probability of a passive in American English; call this probability q. An extremely simple estimate of π would be to ignore all new evidence and set $\pi = q$, regardless of how much data she has on the new variety. Although this option may not be as intuitive as Estimator 1, it has certain advantages: it is extremely reliable and, if the new variety is not too different from American English, reasonably accurate as well. On the other hand, once the speaker has had considerable exposure to the new variety, this approach will almost certainly be inferior to relative frequency estimation. (See Exercise to be included with this chapter.)

In light of this example, Section 4.2 describes how to assess the quality of an estimator in conceptually intuitive yet mathematically precise terms. In Section 4.3, we cover FREQUENTIST approaches to parameter estimation, which involve procedures for constructing point estimates of parameters. In particular we focus on maximum-likelihood estimation and close variants, which for multinomial data turns out to be equivalent to Estimator 1 above.In Section 4.4, we cover BAYESIAN approaches to parameter estimation, which involve placing probability distributions over the range of possible parameter values. The Bayesian estimation technique we will cover can be thought of as intermediate between Estimators 1 and 2.

4.2 Desirable properties for estimators

In this section we briefly cover three key properties of any estimator, and discuss the desirability of these properties.

[1] By this probability we implicitly conditionalize on the use of a transitive verb that is eligible for passivization, excluding intransitives and also unpassivizable verbs such as *weigh*.

4.2.1 Consistency

An estimator is CONSISTENT if the estimate $\hat{\theta}$ it constructs is guaranteed to converge to the true parameter value θ as the quantity of data to which it is applied increases. Figure 4.1 demonstrates that Estimator 1 in our example is consistent: as the sample size increases, the probability that the relative-frequency estimate $\hat{\pi}$ falls into a narrow band around the true parameter π grows asymptotically toward 1 (this behavior can also be proved rigorously; see Section 4.3.1). Estimator 2, on the other hand, is not consistent (so long as the American English parameter q differs from π), because it ignores the data completely. Consistency is nearly always a desirable property for a statistical estimator.

4.2.2 Bias

If we view the collection (or *sampling*) of data from which to estimate a population parameter as a stochastic process, then the parameter estimate $\hat{\theta}_\eta$ resulting from applying a pre-determined estimator η to the resulting data can be viewed as a continuous random variable (Section 3.1). As with any random variable, we can take its expectation. In general, it is intuitively desirable that the expected value of the estimate be equal (or at least close) to the true parameter value θ, but this will not always be the case. The BIAS of an estimator η is defined as the deviation of the expectation from the true value: $E[\hat{\theta}_\eta] - \theta$. All else being equal, the smaller the bias in an estimator the more preferable. An estimator for which the bias is zero—that is, $E[\theta_\eta] = \theta$—is called UNBIASED.

Is Estimator 1 in our passive-voice example biased? The relative-frequency estimate $\hat{\pi}$ is $\frac{m}{n}$, so $E[\hat{\pi} = E[\frac{m}{n}]$. Since n is fixed, we can move it outside of the expectation (see linearity of the expectation in Section 3.3.1) to get

$$E[\hat{\pi}] = \frac{1}{n} E[m]$$

But m is just the number of passive-voice utterances heard, and since m is binomially distributed, $E[m] = \pi n$. This means that

$$\begin{aligned} E[\hat{\pi}] &= \frac{1}{n} \pi n \\ &= \pi \end{aligned}$$

So Estimator 1 is unbiased. Estimator 2, on the other hand, has bias $q - \pi$.

4.2.3 Variance (and efficiency)

Suppose that our speaker has decided to use Estimator 1 to estimate the probability π of a passive, and has been exposed to n utterances. The intuition is extremely strong that she should use *all* n utterances to form her relative-frequency estimate $\hat{\pi}$, rather than, say, using

only the first $n/2$. But why is this the case? Regardless of how many utterances she uses with Estimator 1, her estimate will be unbiased (think about this carefully if you are not immediately convinced). But our intuitions suggest that an estimate using less data is less reliable: it is likely to vary more dramatically due to pure freaks of chance.

It is useful to quantify this notion of reliability using a natural statistical metric: the VARIANCE of the estimator, $\text{Var}(\hat{\theta})$ (Section 4.2.3). All else being equal, an estimator with smaller variance is preferable to one with greater variance. This idea, combined with a bit more simple algebra, quantitatively explains the intuition that more data is better for Estimator 1:

$$\begin{aligned}\text{Var}(\hat{\pi}) &= \text{Var}\left(\frac{m}{n}\right) \\ &= \frac{1}{n^2}\text{Var}(m) \qquad \text{(From scaling a random variable, Section 3.3.3)}\end{aligned}$$

Since m is binomially distributed, and the variance of the binomial distribution is $n\pi(1-\pi)$ (Section 3.4), so we have

$$\text{Var}(\hat{\pi}) = \frac{\pi(1-\pi)}{n} \tag{4.1}$$

So variance is inversely proportional to the sample size n, which means that relative frequency estimation is more reliable when used with larger samples, consistent with intuition.

It is almost always the case that each of bias and variance comes at the cost of the other. This leads to what is sometimes called BIAS-VARIANCE TRADEOFF: one's choice of estimator may depend on the relative importance of expected accuracy versus reliability in the task at hand. The bias-variance tradeoff is very clear in our example. Estimator 1 is unbiased, but has variance that can be quite high when samples size n is small. Estimator 2 is biased, but it has zero variance. Which of the two estimators is preferable is likely to depend on the sample size. If our speaker anticipates that she will have very few examples of transitive sentences in the new English variety to go on, and also anticipates that the new variety will not be hugely different from American English, she may well prefer (and with good reason) the small bias of Estimator 2 to the large variance of Estimator 1. The lower-variance of two estimators is called the more EFFICIENT estimator, and the EFFICIENCY of one estimator η_1 relative to another estimator η_2 is the ratio of their variances, $\text{Var}(\hat{\theta}_{\eta_1})/\text{Var}(\hat{\theta}_{\eta_2})$.

4.3 Frequentist parameter estimation and prediction

We have just covered a simple example of parameter estimation and discussed key properties of estimators, but the estimators we covered were (while intuitive) given no theoretical underpinning. In the remainder of this chapter, we will cover a few major mathematically motivated estimation techniques of general utility. This section covers FREQUENTIST estimation techniques. In frequentist statistics, an estimator gives a point estimate for the parameter(s)

of interest, and estimators are preferred or dispreferred on the basis of their general behavior, notably with respect to the properties of consistency, bias, and variance discussed in Section 4.2. We start with the most widely-used estimation technique, MAXIMUM-LIKELIHOOD ESTIMATION.

4.3.1 Maximum Likelihood Estimation

We encountered the notion of the LIKELIHOOD in Chapter 2, a basic measure of the quality of a set of predictions with respect to observed data. In the context of parameter estimation, the likelihood is naturally viewed as a function of the parameters $\boldsymbol{\theta}$ to be estimated, and is defined as in Equation (2.29)—the joint probability of a set of observations, conditioned on a choice for $\boldsymbol{\theta}$—repeated here:

$$\text{Lik}(\boldsymbol{\theta}; \boldsymbol{y}) \equiv P(\boldsymbol{y}|\boldsymbol{\theta}) \tag{4.2}$$

Since good predictions are better, a natural approach to parameter estimation is to choose the set of parameter values that yields the best predictions—that is, the parameter that *maximizes the likelihood* of the observed data. This value is called the MAXIMUM LIKELIHOOD ESTIMATE (MLE), defined formally as:[2]

$$\hat{\boldsymbol{\theta}}_{MLE} \stackrel{\text{def}}{=} \arg\max_{\boldsymbol{\theta}} \text{Lik}(\boldsymbol{\theta}; \boldsymbol{y}) \tag{4.3}$$

In nearly all cases, the MLE is consistent (Cramer, 1946), and gives intuitive results. In many common cases, it is also unbiased. For estimation of multinomial probabilities, the MLE also turns out to be the relative-frequency estimate. Figure 4.2 visualizes an example of this. The MLE is also an intuitive and unbiased estimator for the means of normal and Poisson distributions.

Likelihood as function of data or model parameters?

In Equation (4.2) I defined the likelihood as a function first and foremost of the parameters of one's model. I did so as

4.3.2 Limitations of the MLE: variance

As intuitive and general-purpose as it may be, the MLE has several important limitations, hence there is more to statistics than maximum-likelihood. Although the MLE for multinomial distributions is unbiased, its variance is problematic for estimating parameters that determine probabilities of events with low expected counts. This can be a major problem

[2]The expression $\arg\max_x f(x)$ is defined as "the value of x that yields the maximum value for the expression $f(x)$." It can be read as "arg-max over x of $f(x)$."

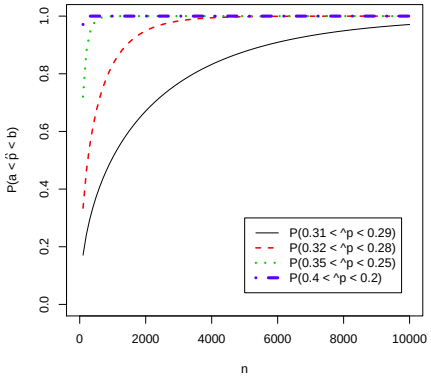


Figure 4.1: Consistency of relative frequency estimation. Plot indicates the probability with which the relative-frequency estimate $\hat{\pi}$ for binomial distribution with parameter $\pi = 0.3$ lies in narrow ranges around the true parameter value as a function of sample size n.

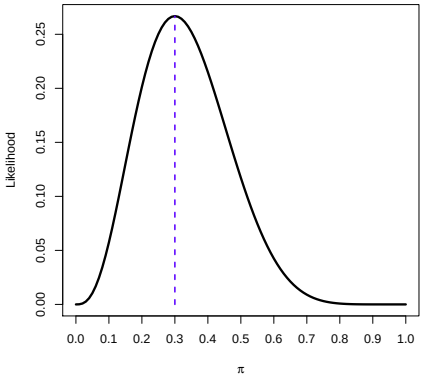


Figure 4.2: The likelihood function for the binomial parameter π for observed data where $n = 10$ and $m = 3$. The MLE is the RFE for the binomial distribution. Note that this graph is *not* a probability density and the area under the curve is much less than 1.

even when the sample size is very large. For example, WORD N-GRAM PROBABILITIES—the probability distribution over the next word in a text given the previous $n-1$ words of context—are of major interest today not only in applied settings such as speech recognition but also in the context of theoretical questions regarding language production, comprehension, and acquisition (e.g., Gahl, 2008; Saffran et al., 1996b; 2-gram probabilities are sometimes called TRANSITIONAL PROBABILITIES). N-gram probability models are simply collections of large multinomial distributions (one distribution per context). Yet even for extremely high-frequency preceding contexts, such as the word sequence *near the*, there will be many possible next words that are improbable yet not impossible (for example, *reportedly*). Any word that does not appear in the observed data in that context will be assigned a conditional probability of zero by the MLE. In a typical n-gram model there will be many, many such words—the problem of DATA SPARSITY. This means that the MLE is a terrible means of prediction for n-gram word models, because if *any* unseen word continuation appears in a new dataset, the MLE will assign zero likelihood to the *entire dataset*. For this reason, there is a substantial literature on learning high-quality n-gram models, all of which can in a sense be viewed as managing the variance of estimators for these models while keeping the bias reasonably low (see Chen and Goodman, 1998 for a classic survey).

4.3.3 Limitations of the MLE: bias

In addition to these problems with variance, the MLE is biased for some types of model parameters. Imagine a linguist interested in inferring the original time of introduction of a

novel linguistic expression currently in use today, such as the increasingly familiar phrase *the boss of me*, as in:[3]

(3) "You're too cheeky," said Astor, sticking out his tongue. "You're not the boss of me." (Tool, 1949, cited in *Language Log* by Benjamin Zimmer, 18 October 2007)

The only direct evidence for such expressions is, of course, attestations in written or recorded spoken language. Suppose that the linguist had collected 60 attestations of the expression, the oldest of which was recored 120 years ago.

From a probabilistic point of view, this problem involves choosing a probabilistic model whose generated observations are n attestation dates $\boldsymbol{y}$ of the linguistic expression, and one of whose parameters is the earliest time at which the expression is coined, or t_0. When the problem is framed this way, the linguist's problem is to devise a procedure for constructing a parameter estimate $\hat{t}_0$ from observations. For expository purposes, let us oversimplify and use the uniform distribution as a model of how attestation dates are generated.[4] Since the innovation is still in use today (time t_{now}), the parameters of the uniform distribution are $[t_0, t_{now}]$ and the only parameter that needs to be estimated is t_{now}. Let us arrange our attestation dates in chronological order so that the earliest date is y_1.

What is the maximum-likelihood estimate $\hat{t}_0$? For a given choice of t_0, a given date y_i either falls in the interval $[t_0, t_{now}]$ or it does not. From the definition of the uniform distribution (Section 2.7.1) we have:

$$P(y_i|t_0, t_{now}) = \begin{cases} \frac{1}{t_{now}-t_0} & t_0 \leq y_i \leq t_{now} \\ 0 & \text{otherwise} \end{cases} \tag{4.4}$$

Due to independence, the likelihood for the interval boundaries is $\text{Lik}(t_0) = \prod_i P(y_i|t_0, t_{now})$. This means that for any choice of interval boundaries, if at least one date lies before t_0, the entire likelihood is zero! Hence the likelihood is non-zero only for interval boundaries containing all dates. For such boundaries, the likelihood is

$$\text{Lik}(t_0) = \prod_{i=1}^{n} \frac{1}{t_{now} - t_0} \tag{4.5}$$

$$= \frac{1}{(t_{now} - t_0)^n} \tag{4.6}$$

This likelihood grows larger as $t_{now} - t_0$ grows smaller, so it will be maximized when the interval length $t_{now} - t_0$ is as short as possible—namely, when t_0 is set to the earliest attested

[3]This phrase has been the topic of intermittent discussion on the *Language Log* blog since 2007.

[4]This is a dramatic oversimplification, as it is well known that linguistic innovations prominent enough for us to notice today often followed an S-shaped trajectory of usage frequency (Bailey, 1973; Cavall-Sforza and Feldman, 1981; Kroch, 1989; Wang and Minett, 2005). However, the general issue of bias in maximum-likelihood estimation present in the oversimplified uniform-distribution model here also carries over to more complex models of the diffusion of linguistic innovations.

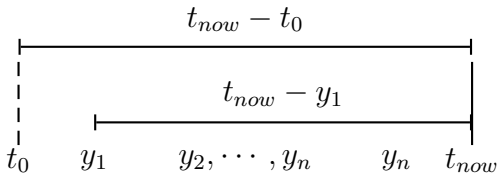


Figure 4.3: The bias of the MLE for uniform distributions

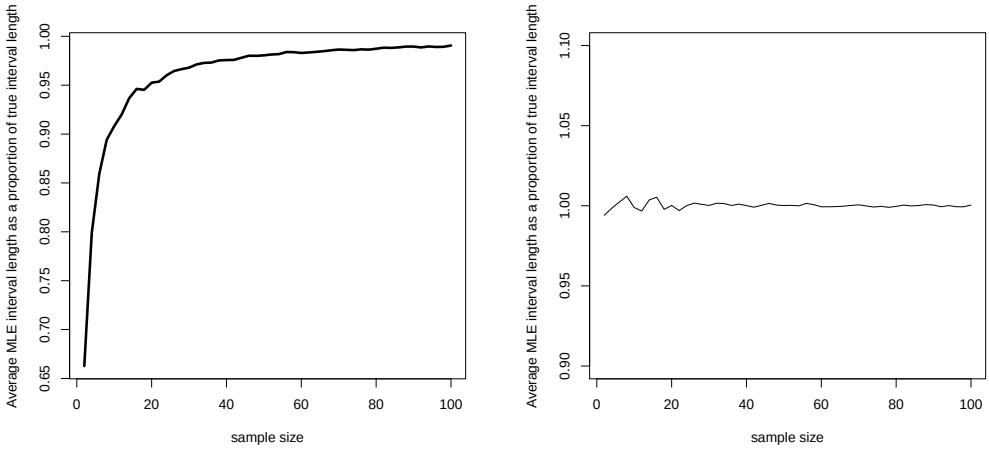


Figure 4.4: Bias of the MLE (left) and the bias-corrected estimator (right), shown numerically using 500 simulations for each value of n.

date y_1. This fact is illustrated in Figure 4.3: the tighter the posited interval between t_0 and t_{now}, the greater the resulting likelihood.

You probably have the intuition that this estimate of the contact interval duration is conservative: certainly the novel form appeared in English no later than t_0, but it seems rather unlikely that the first use in the language was also the first attested use![5] This intuition is correct, and its mathematical realization is that the MLE for interval boundaries of a uniform distribution is biased. Figure 4.4 visualizes this bias in terms of average interval length (over a number of samples) as a function of sample size.

For any finite sample size, the MLE is biased to underestimate true interval length, although this bias decreases as sample size increases (as well it should, because the MLE is a consistent estimator). Fortunately, the size of the MLE's bias can be quantified analytically: the expected ML-estimated interval size is $\frac{n}{n+1}$ times the true interval size.Therefore, if we adjust the MLE by multiplying it by $\frac{n+1}{n}$, we arrive at an unbiased estimator for interval length. The correctness of this adjustment is confirmed by the right-hand plot in Figure 4.4. In the case of our historical linguist with three recovered documents, we achieve the estimate

[5]The intuition may be different if the first attested use was by an author who is known to have introduced a large number of novel expressions into the language which subsequently gained in popularity. This type of situation would point to a need for a more sophisticated probabilistic model of innovation, diffusion, and attestation.

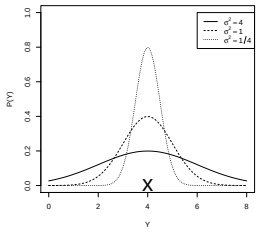


Figure 4.5: Bias in the MLE for σ of a normal distribution.

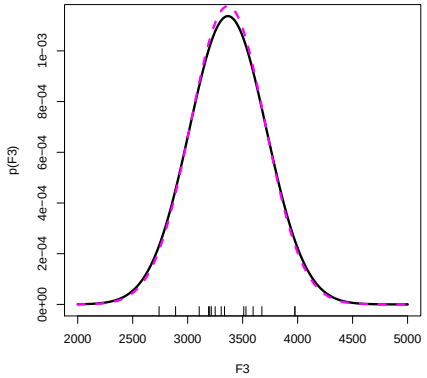


Figure 4.6: Point estimation of a normal distribution. The maximum-likelihood estimate is the dotted magenta line; the bias-adjusted estimate is solid black.

$$\hat{t}_0 = 120 \times \frac{61}{60} = 122 \text{ years ago}$$

Furthermore, there is a degree of intuitiveness about the behavior of the adjustment in extreme cases: if $N = 1$, the adjustment would be infinite, which makes sense: one cannot estimate the size of an unconstrained interval from a single observation.

Another famous example of bias in the MLE is in estimating the variance of a normal distribution. The MLEs for mean and variance of a normal distribution as estimated from a set of N observations $\boldsymbol{y}$ are as follows:

$$\hat{\mu}_{MLE} = \frac{1}{N}\sum_i y_i \qquad \text{(i.e. the sample mean)} \tag{4.7}$$

$$\hat{\sigma}^2_{MLE} = \frac{1}{N}\sum_i (y_i - \hat{\mu})^2 \qquad \text{(i.e. the sample variance divided by } N\text{)} \tag{4.8}$$

While it turns out that $\hat{\mu}_{MLE}$ is unbiased, $\hat{\sigma}^2_{MLE}$ is biased for reasons similar to those given for interval size in the uniform distribution. You can see this graphically by imagining the MLE for a single observation, as in Figure 4.5. As $\hat{\sigma}^2$ shrinks, the likelihood of the observation will continue to rise, so that the MLE will push the estimated variance to be arbitrarily small. This is a type of OVERFITTING (see Section 2.11.5).

It turns out that the this bias can be eliminated by adjusting the MLE by the factor $\frac{N}{N-1}$. This adjusted estimate of σ^2 is called S^2:

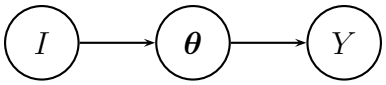


Figure 4.7: The structure of a simple Bayesian model. Observable data Y and prior beliefs I are conditionally independent given the model parameters.

$$S^2 = \frac{N}{N-1}\hat{\sigma}^2_{MLE} \tag{4.9}$$

$$= \frac{1}{N-1}\sum_i (y_i - \hat{\mu})^2 \tag{4.10}$$

This is the most frequently used estimate of the underlying variance of a normal distribution from a sample. In `R`, for example, the function `var()`, which is used to obtain sample variance, computes S^2 rather than $\hat{\sigma}_{MLE}$. An example of estimating normal densities is shown in Figure 4.6, using F3 formants from 15 native English-speaking children on the vowel [æ]. The MLE density estimate is a slightly narrower curve than the bias-adjusted estimate.

4.4 Bayesian parameter estimation and density estimation

In frequentist statistics as we have discussed thus far, one uses observed data to construct a point estimate for each model parameter. The MLE and bias-adjusted version of the MLE are examples of this. In Bayesian statistics, on the other hand, parameter estimation involves placing a *probability distribution* over model parameters. In fact, there is no conceptual difference between parameter estimation (inferences about $\boldsymbol{\theta}$) and prediction or density estimation (inferences about future $\boldsymbol{y}$) in Bayesian statistics.

4.4.1 Anatomy of inference in a simple Bayesian model

A simple Bayesian model has three components. Observable data are generated as random variables $\boldsymbol{y}$ in some model from a model family with parameters $\boldsymbol{\theta}$. Prior to observing a particular set of data, however, we already have beliefs/expectations about the possible model parameters $\boldsymbol{\theta}$; we call these beliefs I. These beliefs affect $\boldsymbol{y}$ only through the mediation of the model parameters—that is, $\boldsymbol{y}$ and I are *conditionally independent* given $\boldsymbol{\theta}$ (see Section 2.4.2). This situation is illustrated in Figure 6.1, which has a formal interpretation as a graphical model (Appendix C).

In the Bayesian framework, both parameter estimation and density estimation simply involve the application of Bayes' rule (Equation (2.5)). For example, parameter estimation means calculating the probability distribution over $\boldsymbol{\theta}$ given observed data $\boldsymbol{y}$ and our prior beliefs I. We can use Bayes rule to write this distribution as follows:

$$P(\boldsymbol{\theta}|\boldsymbol{y}, I) = \frac{P(\boldsymbol{y}|\theta, I)P(\theta|I)}{P(\boldsymbol{y}|I)} \tag{4.11}$$

$$= \frac{\overbrace{P(\boldsymbol{y}|\boldsymbol{\theta})}^{\text{Likelihood for } \boldsymbol{\theta}} \quad \overbrace{P(\boldsymbol{\theta}|I)}^{\text{Prior over } \boldsymbol{\theta}}}{\underbrace{P(\boldsymbol{y}|I)}_{\text{Likelihood marginalized over } \boldsymbol{\theta}}} \qquad \text{(because } \boldsymbol{y} \perp I \mid \boldsymbol{\theta}) \tag{4.12}$$

The numerator in Equation (4.12) is composed of two quantities. The first term, $P(\boldsymbol{y}|\boldsymbol{\theta})$, should be familiar from Section 2.11.5: it is the likelihood of the parameters $\boldsymbol{\theta}$ for the data $\boldsymbol{y}$. As in much of frequentist statistics, the likelihood plays a central role in parameter estimation in Bayesian statistics. However, there is also a second term, $P(\boldsymbol{\theta}|I)$, the PRIOR DISTRIBUTION over $\boldsymbol{\theta}$ given only I. The complete quantity (4.12) is the POSTERIOR DISTRIBUTION over $\boldsymbol{\theta}$. It is important to realize that the terms "prior" and "posterior" in no way imply any temporal ordering on the realization of different events. The only thing that $P(\boldsymbol{\theta}|I)$ is "prior" to is the incorporation of the particular dataset $\boldsymbol{y}$ into inferences about $\boldsymbol{\theta}$. I can in principle incorporate all sorts of knowledge, including other data sources, scientific intuitions, or—in the context of language acquisition—innate biases. Finally, the denominator is simply the MARGINAL LIKELIHOOD $P(\boldsymbol{y}|I) = \int_{\boldsymbol{\theta}} P(\boldsymbol{y}|\boldsymbol{\theta})P(\boldsymbol{\theta}|I)\, d\boldsymbol{\theta}$ (it is the model parameters $\boldsymbol{\theta}$ that are being marginalized over; see Section 3.2). The data likelihood is often the most difficult term to calculate, but in many cases its calculation can be ignored or circumvented because we can accomplish everything we need by computing posterior distributions up to a normalizing constant (Section 2.8; we will see an new example of this in the next section).

Since Bayesian inference involves placing probability distributions on model parameters, it becomes useful to work with probability distributions that are specialized for this purpose. Before we move on to our first simple example of Bayesian parameter and density estimation, we'll now introduce one of the simplest (and most easily interpretable) such probability distributions: the beta distribution.

4.4.2 The beta distribution

The BETA DISTRIBUTION is important in Bayesian statistics involving binomial distributions. It has two parameters α_1, α_2 and is defined as follows:

$$P(\pi|\alpha_1, \alpha_2) = \frac{1}{B(\alpha_1, \alpha_2)} \pi^{\alpha_1 - 1}(1-\pi)^{\alpha_2 - 1} \qquad (0 \leq \pi \leq 1, \alpha_1 > 0, \alpha_2 > 0) \tag{4.13}$$

where the BETA FUNCTION $B(\alpha_1, \alpha_2)$ (Section B.1) serves as a normalizing constant:

$$B(\alpha_1, \alpha_2) = \int_0^1 \pi^{\alpha_1 - 1}(1-\pi)^{\alpha_2 - 1}\, d\pi \tag{4.14}$$

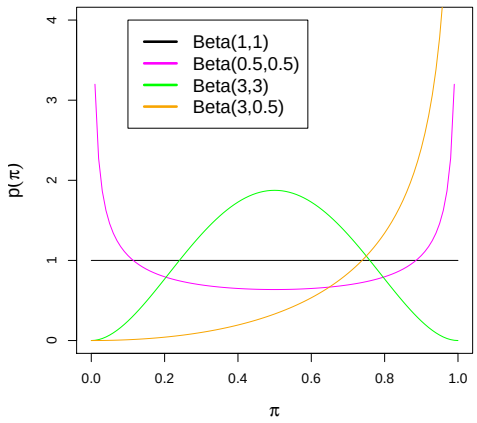


Figure 4.8: Beta distributions

Figure 4.8 gives a few examples of beta densities for different parameter choices. The beta distribution has a mean of $\frac{\alpha_1}{\alpha_1+\alpha_2}$ and mode (when both $\alpha_1, \alpha_2 > 1$) of $\frac{\alpha_1-1}{\alpha_1+\alpha_2-2}$. Note that a uniform distribution on $[0, 1]$ results when $\alpha_1 = \alpha_2 = 1$.

Beta distributions and beta functions are very often useful when dealing with Bayesian inference on binomially-distributed data. One often finds oneself in the situation of knowing that some random variable X is distributed such that $P(X) \propto \pi^a(1-\pi)^b$, but not knowing the normalization constant. If and when you find yourself in this situation, recognize that X must be beta-distributed, which allows you to determine the normalization constant immediately. Additionally, whenever one is confronted with an integral of the form $\int_0^1 \pi^a(1-\pi)^b \, d\pi$ (as in Section 5.2.1), recognize that it is a beta function, which will allow you to compute the integral very easily.

4.4.3 Simple example of Bayesian estimation with the binomial distribution

Historically, one of the major reasons that Bayesian inference has been avoided is that it can be computationally intensive under many circumstances. The rapid improvements in available computing power over the past few decades are, however, helping overcome this obstacle, and Bayesian techniques are becoming more widespread both in practical statistical applications and in theoretical approaches to modeling human cognition. We will see examples of more computationally intensive techniques later in the book, but to give the flavor of the Bayesian approach, let us revisit the example of our native American English speaker and her quest for an estimator for π, the probability of the passive voice, which turns out to be analyzable without much computation at all.

We have already established that transitive sentences in the new variety can be modeled using a binomial distribution where the parameter π characterizes the probability that a

given transitive sentence will be in the passive voice. For Bayesian statistics, we must first specify the beliefs I that characterize the prior distribution $P(\boldsymbol{\theta}|I)$ to be held before any data from the new English variety is incorporated. In principle, we could use any proper probability distribution on the interval $[0, 1]$ for this purpose, but here we will use the beta distribution (Section 4.4.2). In our case, specifying prior knowledge I amounts to choosing beta distribution parameters α_1 and α_2.

Once we have determined the prior distribution, we are in a position to use a set of observations $\boldsymbol{y}$ to do parameter estimation. Suppose that the observations $\boldsymbol{y}$ that our speaker has observed are comprised of n total transitive sentences, m of which are passivized. Let us simply instantiate Equation (4.12) for our particular problem:

$$P(\pi|\boldsymbol{y}, \alpha_1, \alpha_2) = \frac{P(\boldsymbol{y}|\pi)P(\pi|\alpha_1, \alpha_2)}{P(\boldsymbol{y}|\alpha_1, \alpha_2)} \tag{4.15}$$

The first thing to notice here is that the denominator, $P(\boldsymbol{y}|\alpha_1, \alpha_2)$, is not a function of π. That means that it is a normalizing constant (Section 2.8). As noted in Section 4.4, we can often do everything we need without computing the normalizing constant, here we ignore the denominator by re-expressing Equation (4.15) in terms of proportionality:

$$P(\pi|\boldsymbol{y}, \alpha_1, \alpha_2) \propto P(\boldsymbol{y}|\pi)P(\pi|\alpha_1, \alpha_2)$$

From what we know about the binomial distribution, the likelihood is $P(\boldsymbol{y}|\pi) = \binom{n}{m}\pi^m(1-\pi)^{n-m}$, and from what we know about the beta distribution, the prior is $P(\pi|\alpha_1, \alpha_2) = \frac{1}{B(\alpha_1,\alpha_2)}\pi^{\alpha_1-1}(1-\pi)^{\alpha_2-1}$. Neither $\binom{n}{m}$ nor $B(\alpha_1, \alpha_2)$ is a function of π, so we can also ignore them, giving us

$$\begin{aligned} P(\pi|\boldsymbol{y}, \alpha_1, \alpha_2) &\propto \overbrace{\pi^m(1-\pi)^{n-m}}^{\text{Likelihood}}\overbrace{\pi^{\alpha_1-1}(1-\pi)^{\alpha_2-1}}^{\text{Prior}} \\ &\propto \pi^{m+\alpha_1-1}(1-\pi)^{n-m+\alpha_2-1} \end{aligned} \tag{4.16}$$

Now we can crucially notice that the posterior distribution on π itself has the form of a beta distribution (Equation (4.13)), with parameters $\alpha_1 + m$ and $\alpha_2 + n - m$. This fact that the posterior has the same functional form as the prior is called CONJUGACY; the beta distribution is said to be CONJUGATE TO the binomial distribution. Due to conjugacy, we can circumvent the work of directly calculating the normalizing constant for Equation (4.16), and recover it from what we know about beta distributions. This gives us a normalizing constant of $B(\alpha_1 + m, \alpha_2 + n - m)$.

Now let us see how our American English speaker might apply Bayesian inference to estimating the probability of passivization in the new English variety. A reasonable prior distribution might involve assuming that the new variety could be somewhat like American English. Approximately 8% of spoken American English sentences with simple transitive

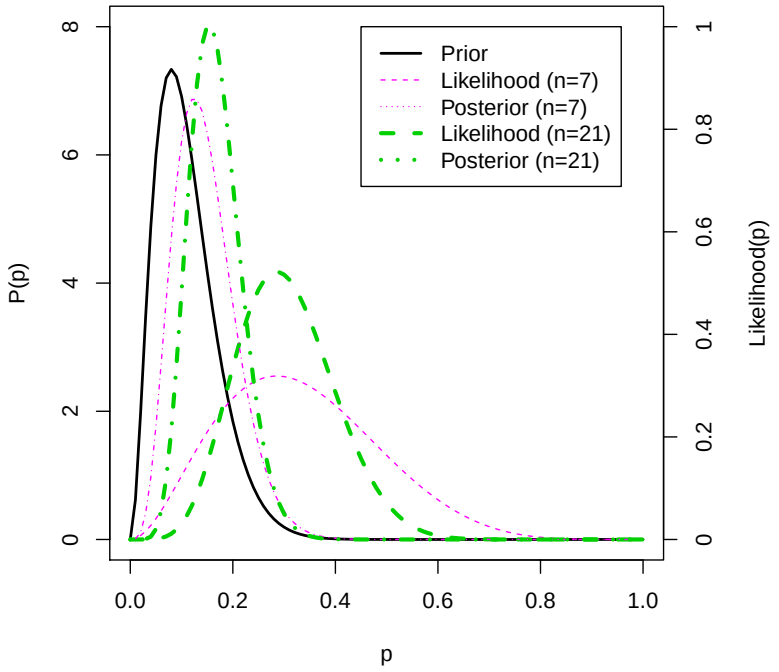


Figure 4.9: Prior, likelihood, and posterior distributions over π. Note that the likelihood has been rescaled to the scale of the prior and posterior; the original scale of the likelihood is shown on the axis on the right.

verbs are passives (Roland et al., 2007), hence our speaker might choose α_1 and α_2 such that the mode of $P(\pi|\alpha_1, \alpha_2)$ is near 0.08. A beta distribution has a mode if $\alpha_1, \alpha_2 > 1$, in which case the mode is $\frac{\alpha_1 - 1}{\alpha_1 + \alpha_2 - 2}$, so a reasonable choice might be $\alpha_1 = 3, \alpha_2 = 24$, which puts the mode of the prior distribution at $\frac{2}{25} = 0.08$.[6] Now suppose that our speaker is exposed to $n = 7$ transitive verbs in the new variety, and two are passivized ($m = 2$). The posterior distribution will then be beta-distributed with $\alpha_1 = 3 + 2 = 5, \alpha_2 = 24 + 5 = 29$. Figure 4.9 shows the prior distribution, likelihood, and posterior distribution for this case, and also for the case where the speaker has been exposed to three times as much data in similar proportions ($n = 21, m = 6$). In the $n = 7$, because the speaker has seen relatively little data, the prior distribution is considerably more peaked than the likelihood, and the posterior distribution is fairly close to the prior. However, as our speaker sees more and more data, the likelihood becomes increasingly peaked, and will eventually dominate in the behavior of the posterior (See Exercise to be included with this chapter).

In many cases it is useful to summarize the posterior distribution into a point estimate of the model parameters. Two commonly used such point estimates are the *mode* (which

[6] Compare with Section 4.3.1—the binomial likelihood function has the same shape as a beta distribution!

we covered a moment ago) and the *mean*. For our example, the posterior mode is $\frac{4}{32}$, or 0.125. Selecting the mode of the posterior distribution goes by the name of MAXIMUM A POSTERIORI (MAP) estimation. The mean of a beta distribution is $\frac{\alpha_1}{\alpha_1+\alpha_2}$, so our POSTERIOR MEAN is $\frac{5}{34}$, or about 0.15. There are no particular deep mathematical principles motivating the superiority of the mode over the mean or vice versa, although the mean should generally be avoided in cases where the posterior distribution is multimodal. The most "principled" approach to Bayesian parameter estimation is in fact *not* to choose a point estimate for model parameters after observing data, but rather to make use of the entire posterior distribution in further statistical inference.

Bayesian density estimation

The role played in density estimation by parameter estimation up to this point has been as follows: an estimator is applied to observed data to obtain an estimate for model parameters $\hat{\boldsymbol{\theta}}$, and the resulting probabilistic model determines a set of predictions for future data, namely the distribution $P(Y|\hat{\boldsymbol{\theta}})$. If we use Bayesian inference to form a posterior distribution on $\boldsymbol{\theta}$ and then summarize that distribution into a point estimate, we can use that point estimate in exactly the same way. In this sense, using a given prior distribution together with the MAP or posterior mean can be thought of as simply one more estimator. In fact, this view creates a deep connection between Bayesian inference and maximum-likelihood estimation: maximum-likelihood estimation (Equation (4.3)) is simply Bayesian MAP estimation when the prior distribution $P(\boldsymbol{\theta}|I)$ (Equation (4.11)) is taken to be uniform over all values of $\boldsymbol{\theta}$.

However, in the purest Bayesian view, it is undesirable to summarize our beliefs about model parameters into a point estimate, because this discards information. In Figure 4.9, for example, the two likelihoods are peaked at the same place, but the $n = 21$ likelihood is more peaked than the $n = 7$ likelihood. This translates into more peakedness and therefore more certainty in the posterior; this certainty is not reflected in the MLE or even in the MAP estimate. Pure Bayesian density estimation involves *marginalization* (Section 3.2) over the model parameters, a process which automatically incorporates this degree of certainty. That is, we estimate a density over new observations $\boldsymbol{y}_{new}$ as:

$$P(\boldsymbol{y}_{new}|\boldsymbol{y}, I) = \int_{\boldsymbol{\theta}} P(\boldsymbol{y}_{new}|\boldsymbol{\theta}) P(\boldsymbol{\theta}|\boldsymbol{y}, I)\, d\boldsymbol{\theta} \tag{4.17}$$

where $P(\boldsymbol{\theta}|\boldsymbol{y}, I)$ is familiar from Equation (4.12).

Suppose, for example, that after hearing her n examples from the new English dialect, our speaker wanted to predict the number of passives r she would hear after the next k trials. We would have:

$$P(r|k, I, \boldsymbol{y}) = \int_0^1 P(r|k, \pi) P(\pi|\boldsymbol{y}, I)\, d\pi$$

This expression can be reduced to

$$P(r|k, I, \boldsymbol{y}) = \binom{k}{r} \frac{\prod_{i=0}^{r-1}(\alpha_1 + m + i) \prod_{i=0}^{k-r-1}(\alpha_2 + n - m + i)}{\prod_{i=0}^{k-1}(\alpha_1 + \alpha_2 + n + i)} \tag{4.18}$$

$$= \binom{k}{r} \frac{B(\alpha_1 + m + r, \alpha_2 + n - m + k - r)}{B(\alpha_1 + m, \alpha_2 + n - m)} \tag{4.19}$$

which is an instance of what is known as the BETA-BINOMIAL MODEL. The expression may seem formidable, but experimenting with specific values for k and r reveals that it is simpler than it may seem. For a single trial ($k = 1$), for example, this expression reduces to $P(r = 1|k, I, \boldsymbol{y}) = \frac{\alpha_1 + m}{\alpha_1 + \alpha_2 + n}$, which is exactly what would be obtained by using the posterior mean. For two trials ($k = 2$), we would have $P(r = 1|k, I, \boldsymbol{y}) = 2\frac{(\alpha_1 + m)(\alpha_2 + n - m)}{(\alpha_1 + \alpha_2 + n)(\alpha_1 + \alpha_2 + n + 1)}$, which is slightly less than what would be obtained by using the posterior mean.[7] This probability mass lost from the $r = 1$ outcome is redistributed into the more extreme $r = 0$ and $r = 2$ outcomes. For $k > 1$ trials in general, the beta-binomial model leads to density estimates of greater variance—also called DISPERSION in the modeling context—than for the binomial model using posterior mean. This is illustrated in Figure 4.10. The reason for this greater dispersion is that different future trials are only conditionally independent given a fixed choice of the binomial parameter π. Because there is residual uncertainty about this parameter, successes on different future trials are positively correlated in the Bayesian prediction despite the fact that they are conditionally independent given the underlying model parameter (see also Section 2.4.2 and Exercise 2.2). This is an important property of a wide variety of models which involve marginalization over intermediate variables (in this case the binomial parameter); we will return to this in Chapter 8 and later in the book.

4.5 Computing approximate Bayesian inferences with sampling techniques

In the example of Bayesian inference given in Section 4.4.3, we were able to express both (i) the posterior probability over the binomial parameter π, and (ii) the probability distribution over new observations as the CLOSED-FORM expressions[8] shown in Equations (4.16)

[7] With the posterior mean, the term $(\alpha_1 + \alpha_2 + n + 1)$ in the denominator would be replaced by another instance of $(\alpha_1 + \alpha_2 + n)$, giving us

$$P(r = 1|k, \hat{\pi}) = \frac{(\alpha_1 + m)(\alpha_2 + n - m)}{(\alpha_1 + \alpha_2 + n)^2} \tag{4.20}$$

[8] A closed-form expression is one that can be written exactly as a combination of a finite number of "well-known" functions (such as polynomials, logarithms, exponentials, and so forth).

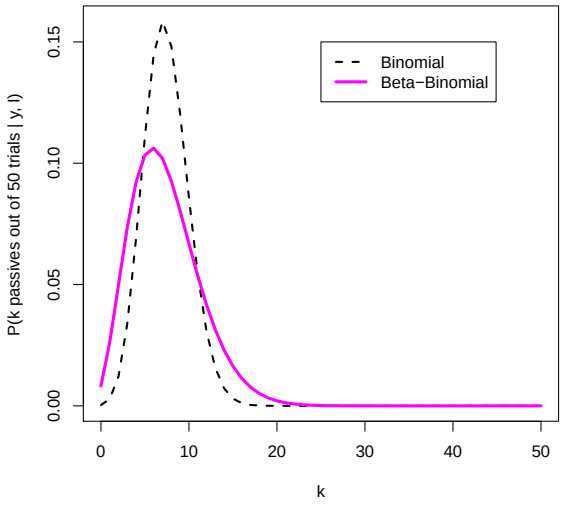


Figure 4.10: The beta-binomial model has greater dispersion than the binomial model. Results shown for $\alpha_1 + m = 5$, $\alpha_2 + n - m = 29$.

and (4.20) respectively. We were able to do this due to the CONJUGACY of the beta distribution to the binomial distribution. However, it will sometimes be the case that we want to perform Bayesian inferences but don't have conjugate distributions to work with. As a simple example, let us turn back to a case of inferring the ordering preference of an English binomial, such as {*radio, television*}. The words in this particular binomial differ in length (quantified as, for example, number of syllables), and numerous authors have suggested that a short-before-long metrical constraint is one determinant of ordering preferences for English binomials (Cooper and Ross, 1975; Pinker and Birdsong, 1979, inter alia). Our prior knowledge therefore inclines us to expect a preference for the ordering *radio and television* (abbreviated as `r`) more strongly than a preference for the ordering *television and radio* (`t`), but we may be relatively agnostic as to the particular strength of the ordering preference. A natural probabilistic model here would be the binomial distribution with success parameter π, and a natural prior might be one which is uniform within each of the ranges $0 \leq \pi \leq 0.5$ and $0.5 < \pi < 1$, but twice as large in the latter range as in the former range. This would be the following prior:

$$p(\pi = x) = \begin{cases} \frac{2}{3} & 0 \leq x \leq 0.5 \\ \frac{4}{3} & 0.5 < x \leq 1 \\ 0 & \text{otherwise} \end{cases} \tag{4.21}$$

which is a step function, illustrated in Figure 4.11a.

In such cases, there are typically no closed-form expressions for the posterior or predictive distributions given arbitrary observed data $\boldsymbol{y}$. However, these distributions can very

often be approximated using general-purpose SAMPLING-BASED approaches. Under these approaches, samples (in principle independent of one another) can be drawn over quantities that are unknown in the model. These samples can then be used in combination with density estimation techniques such as those from Chapter **??** to approximate any probability density of interest. Chapter **??** provides a brief theoretical and practical introduction to sampling techniques; here, we introduce the steps involved in sampling-based approaches as needed.

For example, suppose we obtain data $\boldsymbol{y}$ consisting of ten binomial tokens—five of `r` and five of `t`—and are interested in approximating the following distributions:

1. The posterior distribution over the success parameter π;

2. The posterior predictive distribution over the observed ordering of an eleventh token;

3. The posterior predictive distribution over the number of `r` orderings seen in ten more tokens.

We can use `BUGS`, a highly flexible language for describing and sampling from structured probabilistic models, to sample from these distributions. `BUGS` uses GIBBS SAMPLING, a Markov-chain Monte Carlo technique (Chapter **??**), to produce samples from the posterior distributions of interest to us (such as $P(\pi|\boldsymbol{y}, I)$ or $P(\boldsymbol{y}_{new}|\boldsymbol{y}, I)$). Here is one way to describe our model in `BUGS`:

```
model {
      /* the model */
      for(i in 1:length(response)) { response[i] ~ dbern(p) }
      /* the prior */
      pA ~ dunif(0,0.5)
      pB ~ dunif(0.5,1)
      i ~ dbern(2/3)
      p <- (1 - i) * pA + i * pB
      /* predictions */
      prediction1 ~ dbern(p)
      prediction2 ~ dbin(p, 10) /* dbin() is for binomial distribution */
}
```

The first line,

```
      for(i in 1:length(response)) { response[i] ~ dbern(p) }
```

says that each observation is the outcome of a Bernoulli random variable with success parameter `p`.
The next part,

```
pA ~ dunif(0,0.5)
pB ~ dunif(0.5,1)
i ~ dbern(2/3)
p <- (1 - i) * pA + i * pB
```

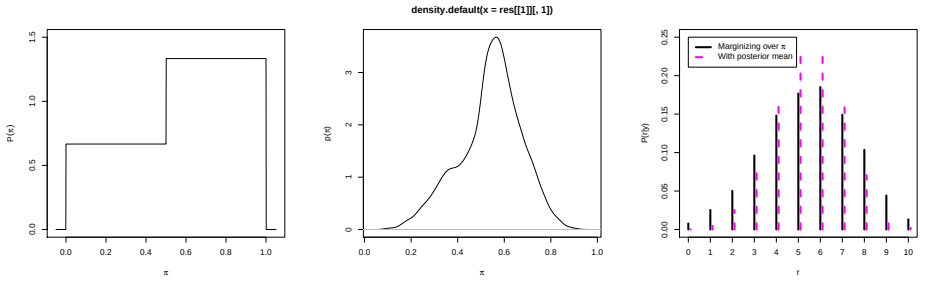
is a way of encoding the step-function prior of Equation (4.21). The first two lines say that there are two random variables, `pA` and `pB`, drawn from uniform distributions on $[0, 0.5]$ and $[0.5, 1]$ respectively. The next two lines say that the success parameter `p` is equal to `pA` $\frac{2}{3}$ of the time, and is equal to `pB` otherwise. These four lines together encode the prior of Equation (4.21).

Finally, the last two lines say that there are two more random variables parameterized by `p`: a single token (`prediction1`) and the number of `r` outcomes in ten more tokens (`prediction2`).

There are several incarnations of `BUGS`, but here we focus on a newer incarnation, `JAGS`, that is open-source and cross-platform. `JAGS` can interface with R through the R library `rjags`.[9] Below is a demonstration of how we can use `BUGS` through R to estimate the posteriors above with samples.

```
> ls()
> rm(i,p)
> set.seed(45)
> # first, set up observed data
> response <- c(rep(1,5),rep(0,5))
> # now compile the BUGS model
> m <- jags.model("../jags_examples/asymm_binomial_prior/asymm_binomial_prior.bug",dat
> # initial period of running the model to get it converged
> update(m,1000)
> # Now get samples
> res <- coda.samples(m, c("p","prediction1","prediction2"), thin = 20, n.iter=5000)
> # posterior predictions not completely consistent due to sampling noise
> print(apply(res[[1]],2,mean))
> posterior.mean <- apply(res[[1]],2,mean)

> plot(density(res[[1]][,1]),xlab=expression(pi),ylab=expression(paste("p(",pi,")")))

> # plot posterior predictive distribution 2
> preds2 <- table(res[[1]][,3])
> plot(preds2/sum(preds2),type='h',xlab="r",ylab="P(r|y)",lwd=4,ylim=c(0,0.25))
> posterior.mean.predicted.freqs <- dbinom(0:10,10,posterior.mean[1])
> x <- 0:10 + 0.1
> arrows(x, 0, x, posterior.mean.predicted.freqs,length=0,lty=2,lwd=4,col="magenta")
> legend(0,0.25,c(expression(paste("Marginizing over ",pi)),"With posterior mean"),lty
```

[9] `JAGS` can be obtained freely at `http://calvin.iarc.fr/~martyn/software/jags/`, and `rjags` at `http://cran.r-project.org/web/packages/rjags/index.html`.



(a) Prior over π

(b) Posterior over π

(c) Posterior predictive distribution for $N = 10$, marginalizing over π versus using posterior mean

Figure 4.11: A non-conjugate prior for the binomial distribution: prior distribution, posterior over π, and predictive distribution for next 10 outcomes

Two important notes on the use of sampling: first, immediately after compiling we specify a "burn-in" period of 1000 iterations to bring the Markov chain to a "steady state" with:[10]

```
update(m,1000)
```

Second, there can be AUTOCORRELATION in the Markov chain: samples near to one another in time are non-independent of one another.[11] In order to minimize the bias in the estimated probability density, we'd like to minimize this autocorrelation. We can do this by sub-sampling or "thinning" the Markov chain, in this case taking only one out of every 20 samples from the chain as specified by the argument `thin = 20` to `coda.samples()`. This reduces the autocorrelation to a minimal level. We can get a sense of how bad the autocorrelation is by taking an unthinned sample and computing the autocorrelation at a number of time lags:

```
> m <- jags.model("../jags_examples/asymm_binomial_prior/asymm_binomial_prior.bug",dat
> # initial period of running the model to get it converged
> update(m,1000)
> res <- coda.samples(m, c("p","prediction1","prediction2"), thin = 1, n.iter=5000)
> autocorr(res,lags=c(1,5,10,20,50))
```

We see that the autocorrelation is quite problematic for an unthinned chain (lag 1), but it is much better at higher lags. Thinning the chain by taking every twentieth sample is more than sufficient to bring the autocorrelation down

[10] For any given model there is no guarantee how many iterations are needed, but most of the models covered in this book are simple enough that on the order of thousands of iterations is enough.

[11] The autocorrelation of a sequence $\vec{x}$ for a time lag τ is simply the covariance between elements in the sequence that are τ steps apart, or $\text{Cov}(x_i, x_{i+\tau})$.

Notably, the posterior distribution shown in Figure 4.11a looks quite different from a beta distribution. Once again the greater dispersion of Bayesian prediction marginalizing over π, as compared with the predictions derived from the posterior mean, is evident in Figure 4.11c.

Finally, we'll illustrate one more example of simple Bayesian estimation, this time of a normal distribution for the F3 formant of the vowel [æ], based on speaker means of 15 child native speakers of English from Peterson and Barney (1952). Since the normal distribution has two parameters—the mean μ and variance σ^2—we must use a slightly more complex prior of the form $P(\mu, \sigma^2)$. We will assume that these parameters are independent of one another in the prior—that is, $P(\mu, \sigma^2) = P(\mu)P(\sigma^2)$. For our prior, we choose NON-INFORMATIVE distributions (ones that give similar probability to broad ranges of the model parameters). In particular, we choose uniform distributions over μ and $\log \sigma$ over the ranges $[0, 10^5]$ and $[-100, 100]$ respectively.:[12] This gives us the model:

$$\begin{aligned} \boldsymbol{y} &\sim \mathcal{N}(\mu, \sigma^2) \\ \mu &\sim \mathcal{U}(0, 10^5) \\ \log \sigma &\sim \mathcal{U}(-100, 100) \end{aligned}$$

where $\sim$ means "is distributed as".

Here is the model in BUGS:

```
var predictions[M]
model {
      /* the model */
      for(i in 1:length(response)) { response[i] ~ dnorm(mu,tau) }
      /* the prior */
      mu ~ dunif(0,100000) # based on F3 means for other vowels
      log.sigma ~ dunif(-100,100)
      sigma <- exp(log.sigma)
      tau <- 1/(sigma^2)
      /* predictions */
      for(i in 1:M) { predictions[i] ~ dnorm(mu,tau) }
}
```

The first line,

```
var predictions[M]
```

states that the `predictions` variable will be a numeric array of length `M` (with M to be specified from `R`). `BUGS` parameterizes the normal distribution differently than we have, using a precision parameter $\tau \stackrel{\text{def}}{=} \frac{1}{\sigma^2}$. The next line,

[12] See Gelman et al. (2004, Appendix C) for the relative merits of different choices of how to place a prior on σ^2.

```
for(i in 1:length(response)) { response[i] ~ dnorm(mu,tau) }
```

simply expresses that observations $\boldsymbol{y}$ are drawn from a normal distribution parameterized by μ and τ. The mean μ is straightforwardly parameterized with a uniform distribution over a wide range. When we set the prior over τ we do so in three stages, first saying that $\log \sigma$ is uniformly distributed:

```
log.sigma ~ dunif(-100,100)
```

and transforming from $\log \sigma$ to σ and then to τ:

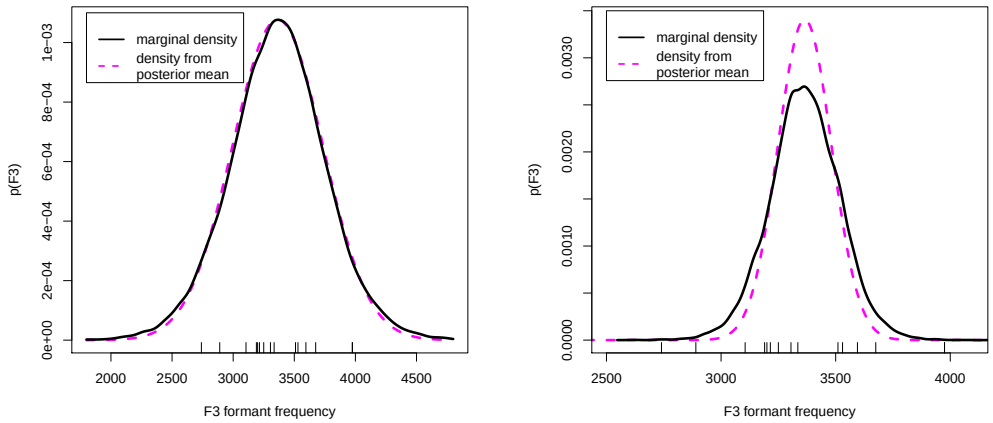
```
sigma <- exp(log.sigma)
tau <- 1/(sigma^2)
```

From R, we can compile the model and draw samples as before:

```
> pb <- read.table("../data/peterson_barney_data/pb.txt",header=T)
> pb.means <- with(pb,aggregate(data.frame(F0,F1,F2,F3), by=list(Type,Sex,Speaker,Vowe
> names(pb.means) <- c("Type","Sex","Speaker","Vowel","IPA",names(pb.means)[6:9])
> set.seed(18)
> response <- subset(pb.means,Vowel=="ae" & Type=="c")[["F3"]]
> M <- 10 # number of predictions to make
> m <- jags.model("../jags_examples/child_f3_formant/child_f3_formant.bug",data=list("
> update(m,1000)
> res <- coda.samples(m, c("mu","sigma","predictions"),n.iter=20000,thin=1)
```

and extract the relevant statistics and plot the outcome as follows:

```
> # compute posterior mean and standard deviation
> mu.mean <- mean(res[[1]][,1])
> sigma.mean <- mean(res[[1]][,12])
> # plot Bayesian density estimate
> from <- 1800
> to <- 4800
> x <- seq(from,to,by=1)
> plot(x,dnorm(x,mu.mean,sigma.mean),col="magenta",lwd=3,lty=2,type="l",xlim=c(from,to
> lines(density(res[[1]][,2],from=from,to=to),lwd=3)
> rug(response)
> legend(from,0.0011,c("marginal density","density from\nposterior mean"),lty=c(1,2),l
> # plot density estimate over mean observed in 10 more observations
> from <- 2500
> to <- 4100
> plot(x,dnorm(x,mu.mean,sigma.mean/sqrt(M)),type="l",lty=2,col="magenta",lwd=3,xlim=c
> lines(density(apply(res[[1]][,2:11],1,mean,from=from,to=to)),lwd=3) # using samples
> rug(response)
> legend(from,0.0035,c("marginal density","density from\nposterior mean"),lty=c(1,2),l
```



(a) Estimated density

(b) Density estimate over mean of ten new observations

Figure 4.12: Bayesian inference for normal distribution

The resulting density estimate for a single future observation is shown in Figure 4.12a. This is almost the same as the result obtained from using the posterior mean. However, the density estimate for the mean obtained in ten future observations, shown in Figure 4.12b, is rather different: once again it has greater dispersion than the estimate obtained using the posterior mean.[13]

The ability to specify model structures like this, drawing from a variety of distributions, and to compute approximate posterior densities with general-purpose tools, gives tremendous modeling flexibility. The only real limits are conceptual—coming up with probabilistic models that are appropriate for a given type of data—and computational—time and memory.

4.6 Further reading

Gelman et al. (2004) is probably the best reference for practical details and advice in Bayesian parameter estimation and prediction.

4.7 Exercises

Exercise 4.1

[13]The density on the mean of ten future observations under the posterior mean μ and σ^2 is given by expressing the mean as a linear combination of ten independent identically distributed normal random variables (Section 3.3).

Confirm using simulations that the variance of relative-frequency estimation of π for binomially distributed data really is $\frac{\pi(1-\pi)}{n}$: for all possible combinations of $\pi \in \{0.1, 0.2, 0.5\}, n \in \{10, 100, 1000\}$, randomly generate 1000 datasets and estimate $\hat{\pi}$ using relative frequency estimation. Plot the observed variance against the variance predicted in Equation 4.1.

Exercise 4.2: Maximum-likelihood estimation for the geometric distribution

You encountered the geometric distribution in Chapter 3, which models the generation of sequence lengths as the repeated flipping of a weighted coin until a single success is achieved. Its lone parameter is the success parameter π. Suppose that you have a set of observed sequence lengths $\boldsymbol{y} = y_1, \ldots, y_n$. Since a sequence of length k corresponds to $k-1$ "failures" and one "success", the total number of "failures" in $\boldsymbol{y}$ is $\sum_i (y_i - 1)$ and the total number of "successes" is n.

1. From analogy to the binomial distribution, guess the maximum-likelihood estimate of π.

2. Is your guess of the maximum-likelihood estimate biased? You're welcome to answer this question either through mathematical analysis or through computational simulation (i.e. choose a value of π, repeatedly generate sets of geometrically-distributed sequences using your choice of π, and quantify the discrepancy between the average estimate $\hat{\pi}$ and the true value).

3. Use your estimator to find best-fit distributions for token-frequency and type-frequency distributions of word length in syllables as found in the file `brown-counts-lengths-nsyll` (parsed Brown corpus; see Exercise 3.7).

Exercise 4.3

We covered Bayesian parameter estimation for the binomial distribution where the prior distribution on the binomial success parameter π was of the form

$$P(\pi) \propto \pi^a (1-\pi)^b$$

Plot the shape of this prior for a variety of choices of a and b. What determines the mode of the distribution (i.e., the value of π where the curve's maximum lies) and its degree of peakedness? What do a and b together represent?

Exercise 4.4: "Ignorance" priors

A uniform prior distribution on the binomial parameter, $P(\pi) = 1$, is often called the "ignorance" distribution. But what is the ignorance of? Suppose we have

$$X \sim Binom(n, \pi).$$

The beta-binomial distribution over X (i.e., marginalizing over π) is $P(X = k) = \int_0^1 \binom{n}{k} \pi^n (1-\pi)^{n-k}\, d\pi$. What does this integral evaluate to (as a function of n and k) when the prior distribution on π is uniform? (Bayes, 1763; Stigler, 1986)

Exercise 4.5: Binomial and beta-binomial predictive distributions

Three native English speakers start studying a new language together. This language has flexible word order, so that sometimes the subject of the sentence can precede the verb (SV), and sometimes it can follow the verb (VS). Of the first three utterances of the new language they are taught, one is VS and the other two are SV.

Speaker A abandons her English-language preconceptions and uses the method of maximum likelihood to estimate the probability that an utterance will be SV. Speakers B and C carry over some preconceptions from English; they draw inferences regarding the SV/VS word order frequency in the language according to a beta-distributed prior, with $\alpha_1 = 8$ and $\alpha_2 = 1$ (here, SV word order counts as a "success"), which is then combined with the three utterances they've been exposed to thus far. Speaker B uses maximum a-posterior (MAP) probability to estimate the probability that an utterance will be SV. Speaker C is fully Bayesian and retains a full posterior distribution on the probability that an utterance will be SV.

It turns out that the first three utterances of the new language were uncharacteristic; of the next twenty-four utterances our speakers hear, sixteen of them are VS. Which of our three speakers was best prepared for this eventuality, as judged by the predictive distribution placed by the speaker on the word order outcomes of these twenty-four utterances? Which of our speakers was worst prepared? Why?

Exercise 4.6: Fitting the constituent-order model.

Review the constituent-order model of Section 2.8 and the word-order-frequency data of Table 2.2.

- Consider a heuristic method for choosing the model's parameters: set γ_1 to the relative frequency with which S precedes O, γ_2 to the relative frequency with which S precedes V, and γ_3 to the relative frequency with which V precedes O. Compute the probability distribution it places over word orders.

- Implement the likelihood function for the constituent-order model and use convex optimization software of your choice to find the maximum-likelihood estimate of $\gamma_1, \gamma_2, \gamma_3$ for Table 2.2. (In `R`, for example, the `optim()` function, using the default Nelder-Mead algorithm, will do fine.) What category probabilities does the ML-estimated model predict? How does the heuristic-method fit compare? Explain what you see.

Exercise 4.7: What level of autocorrelation is acceptable in a Markov chain?

How do you know when a given level of autocorrelation in a thinned Markov chain is acceptably low? One way of thinking about this problem is to realize that a sequence of independent samples is generally going to have *some* non-zero autocorrelation, by pure

chance. The longer such a sequence, however, the lower the autocorrelation is likely to be. (Why?) Simulate a number of such sequences of length $N = 100$, drawn from a uniform distribution, and compute the 97.5% quantile autocorrelation coefficient—that is, the value r such that 97.5% of the generated sequences have correlation coefficient smaller than this value. Now repeat this process for a number of different lengths N, and plot this threshold r as a function of N.

Exercise 4.8: Autocorrelation of Markov-chain samples from `BUGS`.

Explore the autocorrelation of the samples obtained in the two models of Section 4.5, varying how densely you subsample the Markov chain by varying the thinning interval (specified by the `thin` argument of `coda.samples()`). Plot the average (over 20 runs) autocorrelation on each model parameter as a function of the thinning interval. For each model, how sparsely do you need to subsample the chain in order to effectively eliminate the autocorrelation? **Hint:** in `R`, you can compute the autocorrelation of a vector `x` with:

```
> cor(x[-1],x[-length(x)])
```

Chapter 5

Confidence Intervals and Hypothesis Testing

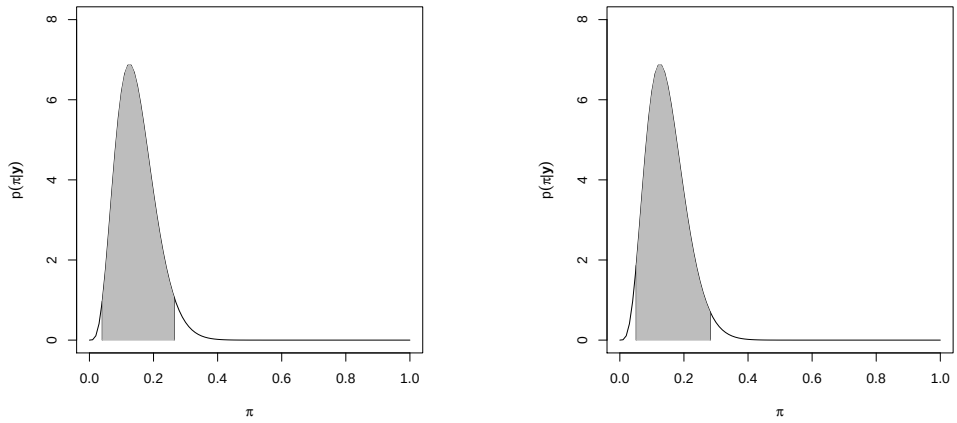
Although Chapter 4 introduced the theoretical framework for estimating the parameters of a model, it was very much situated in the context of prediction: the focus of statistical inference is on inferring the kinds of additional data that are likely to be generated by a model, on the basis of an existing set of observations. In much of scientific inquiry, however, we wish to use data to make inferences about models themselves: what plausible range can be inferred for a parameter or set of parameters within a model, or which of multiple models a given set of data most strongly supports. These are the problems of CONFIDENCE INTERVALS and HYPOTHESIS TESTING respectively. This chapter covers the fundamentals of Bayesian and frequentist approaches to these problems.

5.1 Bayesian confidence intervals

Recall from Section 4.4 that Bayesian parameter estimation simply involves placing a posterior probability distribution over the parameters θ of a model, on the basis of Bayes rule:

$$P(\theta|\boldsymbol{y}) = \frac{P(\boldsymbol{y}|\theta)P(\theta)}{P(\boldsymbol{y})} \tag{5.1}$$

In Bayesian inference, a CONFIDENCE INTERVAL over a single model parameter ϕ is simply a contiguous interval $[\phi_1, \phi_2]$ that contains a specified proportion of the posterior probability mass over ϕ. The proportion of probability mass contained in the confidence interval can be chosen depending on whether one wants a narrower or wider interval. The tightness of the interval (in frequentist as well as Bayesian statistics) is denoted by a value α that expresses the amount of probability mass *excluded* from the interval—so that $(1-\alpha)\%$ of the probability mass is within the interval. The interpretation of a $(1-\alpha)\%$ confidence interval $[\phi_1, \phi_2]$ is that **the probability that the model parameter ϕ resides in $[\phi_1, \phi_2]$ is $(1-\alpha)$.**



(a) 95% HPD confidence interval (b) Symmetric 95% confidence interval

Figure 5.1: HPD and symmetric Bayesian confidence intervals for a posterior distributed as $Beta(5, 29)$

Of course, there is always more than one way of choosing the bounds of the interval $[\phi_1, \phi_2]$ to enclose $(1-\alpha)\%$ of the posterior mass. There are two main conventions for determining how to choose interval boundaries:

- Choose the *shortest* possible interval enclosing $(1-\alpha)\%$ of the posterior mass. This is called a HIGHEST POSTERIOR DENSITY (HPD) confidence interval.
- Choose interval boundaries such that an *equal amount of probability mass* is contained on either side of the interval. That is, choose $[\phi_1, \phi_2]$ such that $P(\phi < \phi_1|\boldsymbol{y}) = P(\phi > \phi_2|\boldsymbol{y}) = \frac{\alpha}{2}$. This is called a SYMMETRIC confidence interval.

Let us return, for example, to our American English speaker of Chapter 4, assuming that she models speaker choice in passivization as a binomial random variable (with passive voice being "success") with parameter π over which she has a Beta prior distribution with parameters $(3, 24)$, and observes five active and two passive clauses. The posterior over π has distribution $Beta(5, 29)$. Figure 5.1 shows HPD and symmetric 95% confidence intervals over π, shaded in gray, for this posterior distribution. The posterior is quite asymmetric, and for the HPD interval there is more probability mass to the right of the interval than there is to the left. The intervals themselves are, of course, qualitatively quite similar.

5.2 Bayesian hypothesis testing

In all types of statistics, hypothesis testing involves entertaining multiple candidate generative models of how observed data has been generated. The hypothesis test involves an

assessment of which model is most strongly warranted by the data. Bayesian hypothesis testing in particular works just like any other type of Bayesian inference. Suppose that we have a collection of hypotheses $H_1, \ldots, H_n$. Informally, a hypothesis can range over diverse ideas such as "this coin is fair", "the animacy of the agent of a clause affects the tendency of speakers to use the passive voice", "females have higher average F1 vowel formants than males regardless of the specific vowel", or "a word's frequency has no effect on naming latency". Formally, each hypothesis should specify a model that determines a probability distribution over possible observations $\boldsymbol{y}$. Furthermore, we need a prior probability over the collection of hypotheses, $P(H_i)$. Once we have observed some data $\boldsymbol{y}$, we use Bayes' rule (Section 2.4.1) to calculate the posterior probability distribution over hypotheses:

$$P(H_i|\boldsymbol{y}) = \frac{P(\boldsymbol{y}|H_i)P(H_i)}{P(\boldsymbol{y})} \tag{5.2}$$

where $P(\boldsymbol{y})$ marginalizes (Section 3.2) over the hypotheses:

$$P(\boldsymbol{y}) = \sum_{j=1}^{n} P(\boldsymbol{y}|H_j)P(H_j) \tag{5.3}$$

As an example, let us return once more to the case of English binomials, such as *salt and pepper*. A number of constraints have been hypothesized to play a role in determining binomial ordering preferences; as an example, one hypothesized constraint is that ordered binomials of the form *A and B* should be disfavored when *B* has ultimate-syllable stress (*Bstr; Bolinger, 1962; Müller, 1997). For example, *pepper and salt* violates this constraint against ultimate-syllable stress, but its alternate *salt and pepper* does not. We can construct a simple probabilistic model of the role of *Bstr in binomial ordering preferences by assuming that every time an English binomial is produced that could potentially violate *Bstr, the binomial is produced in the satisfying order *B and A* ordering with probability π, otherwise it is produced in the violating ordering *A and B*.[1] If we observe n such English binomials, then the distribution over the number of satisfactions of *Bstr observed is (appropriately enough) the binomial distribution with parameters π and n.

Let us now entertain two hypotheses about the possible role of *Bstr in determining binomial ordering preferences. In the first hypothesis, H_1, *Bstr plays no role, hence orderings *A and B* and *B and A* are equally probable; we call this the "no-preference" hypothesis. Therefore in H_1 the binomial parameter π is 0.5. In Bayesian inference, we need to assign probability distributions to choices for model parameters, so we state H_1 as:

$$H_1 : P(\pi|H_1) = \begin{cases} 1 & \pi = 0.5 \\ 0 & \pi \neq 0.5 \end{cases}$$

[1] For now we ignore the role of multiple overlapping constraints in jointly determining ordering preferences, as well as the fact that specific binomials may have idiosyncratic ordering preferences above and beyond their constituent constraints. The tools to deal with these factors are introduced in Chapters 6 and 8 respectively.

The probability above is a PRIOR PROBABILITY on the binomial parameter π.

In our second hypothesis H_2, *BSTR *does* affect binomial ordering preferences (the "preference" hypothesis). For this hypothesis we must place a non-trivial probability distribution on π. Keep in mind have arbitrarily associated the "success" outcome with satisfaction of *BSTR. Suppose that we consider only two possibilities in H_2: that the preference is either $\frac{2}{3}$ for *A and B* or $\frac{2}{3}$ for outcome *B and A*, and let these two preferences be equally likely in H_2. This gives us:

$$H_2 : P(\pi|H_2) = \begin{cases} 0.5 & \pi = \frac{1}{3} \\ 0.5 & \pi = \frac{2}{3} \end{cases} \tag{5.4}$$

In order to complete the Bayesian inference of Equation (5.2), we need prior probabilities on the hypotheses themselves, $P(H_1)$ and $P(H_2)$. If we had strong beliefs one way or another about the binomial's ordering preference (e.g., from prior experience with other English binomials, or with experience with a semantically equivalent binomial in other languages), we might set one of these prior probabilities close to 1. For these purposes, we will use $P(H_1) = P(H_2) = 0.5$.

Now suppose we collect a dataset $\boldsymbol{y}$ of six English binomials in which two orderings violate *BSTR from a corpus:

Binomial	Constraint status (S: *BSTR satisfied, V: *BSTR violated)
salt and pepper	S
build and operate	S
follow and understand	V
harass and punish	S
ungallant and untrue	V
bold and entertaining	S

Do these data favor H_1 or H_2?

We answer this question by completing Equation (5.2). We have:

$$P(H_1) = 0.5$$

$$P(\boldsymbol{y}|H_1) = \binom{6}{4} \pi^4(1-\pi)^2 \qquad = \binom{6}{4} \left(\frac{1}{2}\right)^4 \left(\frac{1}{2}\right)^2 = 0.23$$

Now to complete the calculation of $P(\boldsymbol{y})$ in Equation (5.3), we need $P(\boldsymbol{y}|H_2)$. To get this, we need to marginalize over the possible values of π, just as we are marginalizing over H to get the probability of the data. We have:

$$
\begin{aligned}
P\left(\boldsymbol{y}|H_2\right) &= \sum_i P\left(\boldsymbol{y}|\pi_i\right) P\left(\pi_i|H_2\right) \\
&= P\left(\boldsymbol{y}|\pi = \frac{1}{3}\right) P\left(\pi = \frac{1}{3}|H_2\right) + \quad P\left(\boldsymbol{y}|\pi = \frac{2}{3}\right) P\left(\pi = \frac{2}{3}|H_2\right) \\
&= \binom{6}{4}\left(\frac{1}{3}\right)^4\left(\frac{2}{3}\right)^2 \times 0.5 + \binom{6}{4}\left(\frac{2}{3}\right)^4\left(\frac{1}{3}\right)^2 \times 0.5 \\
&= 0.21
\end{aligned}
$$

thus

$$
\begin{aligned}
P(\boldsymbol{y}) &= \overbrace{0.23}^{P(\boldsymbol{y}|H_1)} \times \overbrace{0.5}^{P(H_1)} + \overbrace{0.21}^{P(\boldsymbol{y}|H_2)} \times \overbrace{0.5}^{P(H_2)} && (5.5) \\
&= 0.22 && (5.6)
\end{aligned}
$$

And we have

$$
\begin{aligned}
P(H_1|\boldsymbol{y}) &= \frac{0.23 \times 0.5}{0.22} && (5.7) \\
&= 0.53 && (5.8)
\end{aligned}
$$

Note that even though the maximum-likelihood estimate of $\hat{\pi}$ from the data we observed is exactly one of the two possible values of π under H_2, our data in fact support the "preference" hypothesis H_1 – it went from prior probability $P(H_1) = 0.5$ up to posterior probability $P(H_1|\boldsymbol{y}) = 0.53$. See also Exercise 5.3.

5.2.1 More complex hypotheses

We might also want to consider more complex hypotheses than H_2 above as the "preference" hypothesis. For example, we might think all possible values of π in $[0, 1]$ are equally probable *a priori*:

$$H_3 : P(\pi|H_3) = 1 \quad 0 \leq \pi \leq 1$$

(In Hypothesis 3, the probability distribution over π is continuous, not discrete, so H_3 is still a proper probability distribution.) Let us discard H_2 and now compare H_1 against H_3.

Let us compare H_3 against H_1 for the same data. To do so, we need to calculate the likelihood $P(\boldsymbol{y}|H_3)$, and to do this, we need to marginalize over π:

Since π can take on a continuous range of values under H_3, this marginalization takes the form of an integral:

$$P(\boldsymbol{y}|H_3) = \int_\pi P(\boldsymbol{y}|\pi)P(\pi|H_3)\,d\pi = \int_0^1 \overbrace{\binom{6}{4}\pi^4(1-\pi)^2}^{P(\boldsymbol{y}|\pi)} \overbrace{1}^{P(\pi|H_3)}\,d\pi$$

We use the critical trick of recognizing this integral as a beta function (Section 4.4.2), which gives us:

$$= \binom{6}{4} B(5,3) = 0.14$$

If we plug this result back in, we find that

$$\begin{aligned} P(H_1|\boldsymbol{y}) &= \frac{\overbrace{0.23}^{P(\boldsymbol{y}|H_1)} \times \overbrace{0.5}^{P(H_1)}}{\underbrace{0.23}_{P(\boldsymbol{y}|H_1)} \times \underbrace{0.5}_{P(H_1)} + \underbrace{0.14}_{P(\boldsymbol{y}|H_3)} \times \underbrace{0.5}_{P(H_3)}} \\ &= 0.62 \end{aligned}$$

So H_3 fares even worse than H_2 against the no-preference hypothesis H_1. Correspondingly, we would find that H_2 is favored over H_3.

5.2.2 Bayes factor

Sometimes we do not have strong feelings about the prior probabilities $P(H_i)$. Nevertheless, we can quantify how much evidence a given dataset provides for one hypothesis over another. We can express the relative preference between H and H' in the face of data $\boldsymbol{y}$ in terms of the PRIOR ODDS of H versus H' combined with the LIKELIHOOD RATIO between the two hypotheses. This combination gives us the POSTERIOR ODDS:

$$\overbrace{\frac{P(H|\boldsymbol{y})}{P(H'|\boldsymbol{y})}}^{\text{Posterior odds}} = \overbrace{\frac{P(\boldsymbol{y}|H)}{P(\boldsymbol{y}|H')}}^{\text{Likelihood ratio}} \overbrace{\frac{P(H)}{P(H')}}^{\text{Prior odds}}$$

The contribution of the data $\boldsymbol{y}$ to the posterior odds is simply the likelihood ratio:

$$\frac{P(\boldsymbol{y}|H)}{P(\boldsymbol{y}|H')} \tag{5.9}$$

which is also called the BAYES FACTOR between H and H'. A Bayes factor above 1 indicates support for H over H'; a Bayes factor below 1 indicates support for H' over H. For example, the Bayes factors for H_1 versus H_2 and H_1 versus H_3 in the preceding examples

$$\frac{P(\boldsymbol{y}|H_1)}{P(\boldsymbol{y}|H_2)} = \frac{0.23}{0.21} \qquad \frac{P(\boldsymbol{y}|H_1)}{P(\boldsymbol{y}|H_3)} = \frac{0.23}{0.14}$$
$$= 1.14 \qquad = 1.64$$

indicating weak support for H_1 in both cases.

5.2.3 Example: Learning contextual contingencies in sequences

One of the key tasks of a language learner is to determine which cues to attend to in learning distributional facts of the language in their environment (Saffran et al., 1996a; Aslin et al., 1998; Swingley, 2005; Goldwater et al., 2007). In many cases, this problem of cue relevance can be framed in terms of hypothesis testing or model selection.

As a simplified example, consider a length-21 sequence of syllables:

`da ta da ta ta da da da da da ta ta ta da ta ta ta da da da da`

Let us entertain two hypotheses. The first hypothesis H_1, is that the probability of an `da` is independent of the context. The second hypothesis, H_2, is that the probability of an `da` is dependent on the preceding token. The learner's problem is to choose between these hypotheses—that is, to decide whether immediately preceding context is relevant in estimating the probability distribution over what the next phoneme will be. How should the above data influence the learner's choice? (Before proceeding, you might want to take a moment to examine the sequence carefully and answer this question on the basis of your own intuition.)

We can make these hypotheses precise in terms of the parameters that each entails. H_1 involves only one binomial parameter $P(\texttt{da})$, which we will denote as π. H_2 involves three binomial parameters:

1. $P(\texttt{da}|\emptyset)$ (the probability that the sequence will start with `da`), which we will denote as $\pi_\emptyset$;
2. $P(\texttt{da}|\texttt{da})$ (the probability that an `da` will appear after an `da`), which we will denote as $\pi_{\texttt{da}}$;
3. $P(\texttt{da}|\texttt{ta})$ (the probability that an `da` will appear after an `ta`), which we will denote as $\pi_{\texttt{ta}}$.

(For expository purposes we will assume that the probability distribution over the number of syllables in the utterance is the same under both H_1 and H_2 and hence plays no role in the Bayes factor.) Let us assume that H_1 and H_2 are equally likely; we will be concerned with the Bayes factor between the two hypotheses. We will put a uniform prior distribution on all model parameters—recall that this can be expressed as a beta density with parameters $\alpha_1 = \alpha_2 = 1$ (Section 4.4.2).

There are 21 observations, 12 of which are `da` and 9 of which are `ta`. The likelihood of H_1 is therefore simply

$$\begin{aligned}\int_0^1 \pi^{12}(1-\pi)^9\, d\pi &= B(13,10)\\ &= 1.55 \times 10^{-7}\end{aligned}$$

once again recognizing the integral as a beta function (see Section 4.4.2).

To calculate the likelihood of H_2 it helps to lay out the 21 events as a table of conditioning contexts and outcomes:

	Outcome	
Context	`da`	`ta`
$\emptyset$	1	0
`da`	7	4
`ta`	4	5

The likelihood of H_2 is therefore

$$\begin{aligned}\int_0^1 \pi_\emptyset^1\, d\pi_\emptyset \int_0^1 \pi_{\texttt{da}}^7(1-\pi_{\texttt{da}})^4\, d\pi_{\texttt{da}} \int_0^1 \pi_{\texttt{ta}}^4(1-\pi_{\texttt{ta}})^5\, d\pi_{\texttt{ta}} &= B(2,1)B(8,5)B(5,6)\\ &= 1 \times 10^{-7}\end{aligned}$$

This dataset provides some support for the simpler hypothesis of statistical independence—the Bayes factor is 1.55 in favor of H_1.

5.2.4 Phoneme discrimination as hypothesis testing

In order to distinguish spoken words such as *bat* and *pat* out of context, a listener must rely on acoustic cues to discriminate the sequence of phonemes that is being uttered. One particularly well-studied case of phoneme discrimination is of voicing in stop consonants. A variety of cues are available to identify voicing; here we focus on the well-studied cue of *voice onset time* (VOT)—the duration between the sound made by the burst of air when the stop is released and the onset of voicing in the subsequent segment. In English, VOT is shorter for so-called "voiced" stops (e.g., /b/,/d/,/g/) and longer for so-called "voiceless" stops (e.g., /p/,/t/,/k/), particularly word-initially, and native speakers have been shown to be sensitive to VOT in phonemic and lexical judgments (Liberman et al., 1957).

Within a probabilistic framework, phoneme categorization is well-suited to analysis as a Bayesian hypothesis test. For purposes of illustration, we dramatically simplify the problem by focusing on two-way discrimination between the voiced/voiceless stop pair /b/ and /p/. In order to determine the phoneme-discrimination inferences of a Bayesian listener, we must specify the acoustic representations that describe spoken realizations x of any phoneme,

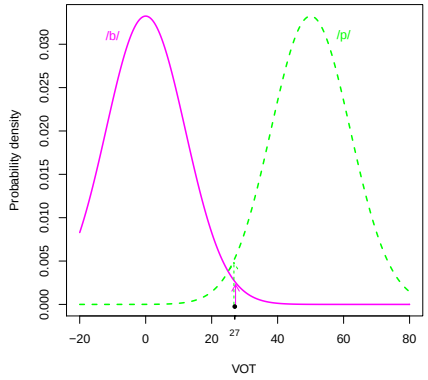


Figure 5.2: Likelihood functions for /b/–/p/ phoneme categorizations, with $\mu_{\text{b}} = 0, \mu_{\text{p}} = 50, \sigma_{\text{b}} = \sigma_{\text{p}} = 12$. For the input $x = 27$, the likelihoods favor /p/.

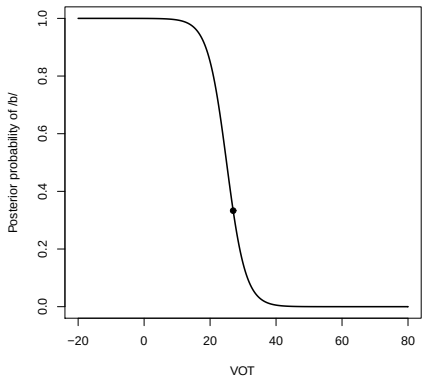


Figure 5.3: Posterior probability curve for Bayesian phoneme discrimination as a function of VOT

the conditional distributions over acoustic representations, $P_{\text{b}}(x)$ and $P_{\text{p}}(x)$ for /b/ and /p/ respectively (the likelihood functions), and the prior distribution over /b/ versus /p/. We further simplify the problem by characterizing any acoustic representation x as a single real-valued number representing the VOT, and the likelihood functions for /b/ and /p/ as normal density functions (Section 2.10) with means $\mu_{\text{b}}, \mu_{\text{p}}$ and standard deviations $\sigma_{\text{b}}, \sigma_{\text{p}}$ respectively.

Figure 5.2 illustrates the likelihood functions for the choices $\mu_{\text{b}} = 0, \mu_{\text{p}} = 50, \sigma_{\text{b}} = \sigma_{\text{p}} = 12$. Intuitively, the phoneme that is more likely to be realized with VOT in the vicinity of a given input is a better choice for the input, and the greater the discrepancy in the likelihoods the stronger the categorization preference. An input with non-negligible likelihood for each phoneme is close to the "categorization boundary", but may still have a preference. These intuitions are formally realized in Bayes' Rule:

$$P(/\text{b}/|x) = \frac{P(x|/\text{b}/)P(/\text{b}/)}{P(x)} \tag{5.10}$$

and since we are considering only two alternatives, the marginal likelihood is simply the weighted sum of the likelihoods under the two phonemes: $P(x) = P(x|/\text{b}/)P(/\text{b}/) + P(x|/\text{p}/)P(/\text{p}/)$. If we plug in the normal probability density function we get

$$P(/\text{b}/|x) = \frac{\frac{1}{\sqrt{2\pi\sigma_{\text{b}}^2}} \exp\left[-\frac{(x-\mu_{\text{b}})^2}{2\sigma_{\text{b}}^2}\right] P(/\text{b}/)}{\frac{1}{\sqrt{2\pi\sigma_{\text{b}}^2}} \exp\left[-\frac{(x-\mu_{\text{b}})^2}{2\sigma_{\text{b}}^2}\right] P(/\text{b}/) + \frac{1}{\sqrt{2\pi\sigma_{\text{p}}^2}} \exp\left[-\frac{(x-\mu_{\text{p}})^2}{2\sigma_{\text{p}}^2}\right] P(/\text{p}/)} \tag{5.11}$$

In the special case where $\sigma_{\text{b}} = \sigma_{\text{p}} = \sigma$ we can simplify this considerably by cancelling the

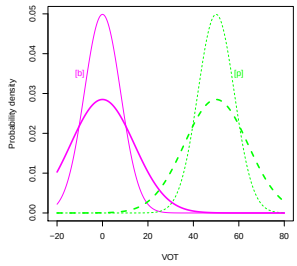


Figure 5.4: Clayards et al. (2008)'s manipulation of VOT variance for /b/–/p/ categories

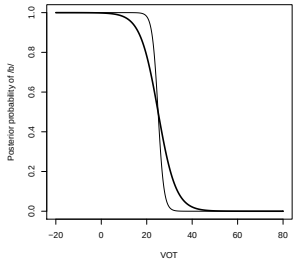


Figure 5.5: Ideal posterior distributions for narrow and wide variances

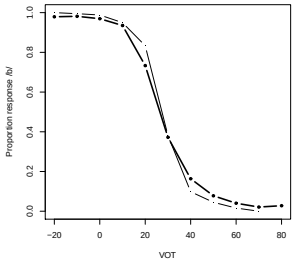


Figure 5.6: Response rates observed by Clayards et al. (2008)

constants and multiplying through by $\exp\left[\frac{(x-\mu_{\text{b}})^2}{2\sigma_{\text{b}}^2}\right]$:

$$P(/\text{b}/|x) = \frac{P(/\text{b}/)}{P(/\text{b}/) + \exp\left[\frac{(x-\mu_{\text{b}})^2-(x-\mu_{\text{p}})^2}{2\sigma^2}\right] P(/\text{p}/)} \tag{5.12}$$

Since $e^0 = 1$, when $(x-\mu_{\text{b}})^2 = (x-\mu_{\text{p}})^2$ the input is "on the category boundary" and the posterior probabilities of each phoneme are unchanged from the prior. When x is closer to μ_{b}, $(x-\mu_{\text{b}})^2 - (x-\mu_{\text{p}})^2 > 0$ and /b/ is favored; and vice versa when x is closer to μ_{p}. Figure 5.3 illustrates the phoneme categorization curve for the likelihood parameters chosen for this example and the prior $P(/\text{b}/) = P(/\text{p}/) = 0.5$.

This account makes clear, testable predictions about the dependence on the parameters of the VOT distribution for each sound category on the response profile. Clayards et al. (2008), for example, conducted an experiment in which native English speakers were exposed repeatedly to words with initial stops on a /b/–/p/ continuum such that either sound category would form a word (*beach–peach*, *beak–peak*, *bes–peas*). The distribution of the /b/–/p/ continuum used in the experiment was bimodal, approximating two overlapping Gaussian distributions (Section 2.10); high-variance distributions (156ms^2) were used for some experimental participants and low-variance distribution (64ms^2) for others (Figure 5.4). If these speakers were to learn the true underlying distributions to which they were exposed and use them to draw ideal Bayesian inferences about which word they heard on a given trial, then the posterior distribution as a function of VOT would be as in Figure 5.5: note that low-variance Gaussians would induce a steeper response curve than high-variance Gaussians. The actual response rates are given in Figure 5.6; although the discrepancy between the low- and high-variance conditions is smaller than predicted by ideal inference, suggesting that learning may have been incomplete, the results of Clayards et al. confirm human response curves are indeed steeper when category variances are lower, as predicted by principles of Bayesian inference.

5.3 Frequentist confidence intervals

We now move on to frequentist confidence intervals and hypothesis testing, which have been developed from a different philosophical standpoint. To a frequentist, it does not make sense to say that "the true parameter θ lies between these points x and y with probability p^*." The parameter θ is a real property of the population from which the sample was obtained and is either in between x and y, or it is not. Remember, to a frequentist, the notion of probability as reasonable belief is not admitted! Under this perspective, the Bayesian definition of a confidence interval—while intuitively appealing to many—is incoherent.

Instead, the frequentist uses more indirect means of quantifying their certainty about the estimate of θ. The issue is phrased thus: imagine that I were to repeat the same experiment—drawing a sample from my population—many times, and each time I repeated the experiment I constructed an interval I on the basis of my sample according to a fixed procedure `Proc`. Suppose it were the case that $1 - p$ percent of the intervals I thus constructed actually contained θ. Then for any given sample S, the interval I constructed by `Proc` is a $(1 - p)\%$ confidence interval for θ.

If you think that this seems like convoluted logic, well, you are not alone. **Frequentist confidence intervals are one of the most widely misunderstood constructs in statistics.** The Bayesian view is more intuitive to most people. Under some circumstances, there is a happy coincidence where Bayesian and frequentist confidence intervals look the same and you are free to misinterpret the latter as the former. In general, however, they do *not* necessarily look the same, and you need to be careful to interpret each correctly.

Here's an example, where we will explain the STANDARD ERROR OF THE MEAN. Suppose that we obtain a sample of n observations from a normal distribution $N(\mu, \sigma^2)$. It turns out that the following quantity follows the t_{n-1} distribution (Section B.5):

$$\frac{\hat{\mu} - \mu}{\sqrt{S^2/n}} \sim t_{n-1} \tag{5.13}$$

where

$$\hat{\mu} = \frac{1}{n} \sum_i X_i \qquad \text{[maximum-likelihood estimate of the mean]}$$

$$S^2 = \frac{1}{n-1} \sum_i (X_i - \hat{\mu})^2 \qquad \text{[unbiased estimate of } \sigma^2\text{; Section 4.3.3]}$$

Let us denote the quantile function for the t_{n-1} distribution as $Q_{t_{n-1}}$. We want to choose a symmetric interval $[-a, a]$ containing $(1 - \alpha)$ of the probability mass of t_{n-1}. Since the t distribution is symmetric around 0, if we set $a = \sqrt{S^2/n}\, Q_{t_{n-1}}(1 - \alpha/2)$, we will have

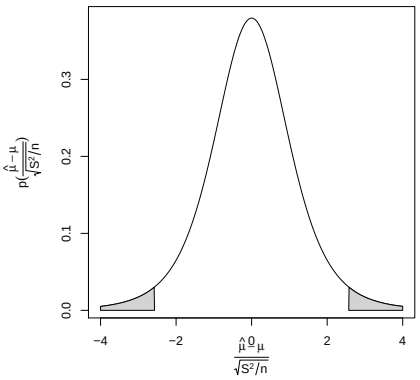


Figure 5.7: Visualizing confidence intervals with the t distribution

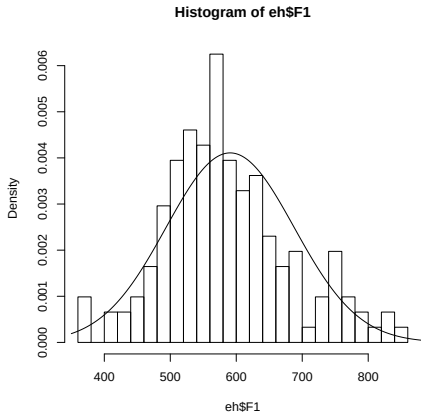


Figure 5.8: Distribution of F1 formant for [ɛ]

$$P(\hat{\mu} - \mu < -a) = \frac{\alpha}{2} \tag{5.14}$$
$$P(\hat{\mu} - \mu > a) = \frac{\alpha}{2}$$

Figure 5.7 illustrates this for $\alpha = 0.05$ (a 95% confidence interval). Most of the time, the "standardized" difference between $\hat{\mu}$ and μ is small and falls in the unshaded area. But 5% of the time, this standardized difference will fall in the shaded area—that is, the confidence interval won't contain μ.

Note that the quantity $S/\sqrt{n}$ is called the the STANDARD ERROR OF THE MEAN or simply the STANDARD ERROR. Note that this is different from the standard deviation of the sample, but related! (How?) When the number of observations n is large, the t distribution looks approximately normal, and as a rule of thumb, the symmetric 95% tail region of the normal distribution is about 2 standard errors away from the mean.

Another example: let's look at the data from a classic study of the English vowel space (Peterson and Barney, 1952). The distribution of the F1 formant for the vowel ɛ is roughly normal (see Figure 5.8). The 95% confidence interval can be calculated by looking at the quantity $S/\sqrt{n}\ Q_{t_{151}}(0.975) = 15.6$. This is half the length of the confidence interval; the confidence interval should be centered around the sample mean $\hat{\mu} = 590.7$. Therefore our 95% confidence interval for the mean F1 is $[575.1, 606.3]$.

5.4 Frequentist hypothesis testing

In most of science, including areas such as psycholinguistics and phonetics, statistical inference is most often seen in the form of hypothesis testing within the NEYMAN-PEARSON PARADIGM. This paradigm involves formulating two hypotheses, the NULL HYPOTHESIS H_0

and a more general ALTERNATIVE HYPOTHESIS H_A (sometimes denoted H_1). We then design a *decision procedure* which involves collecting some data $\boldsymbol{y}$ and computing a statistic $T(\boldsymbol{y})$, or just T for short. Before collecting the data $\boldsymbol{y}$, $T(\boldsymbol{y})$ is a random variable, though we do not know its distribution because we do not know whether H_0 is true. At this point we divide the range of possible values of T into an ACCEPTANCE REGION and a REJECTION REGION. Once we collect the data, we accept the null hypothesis H_0 if T falls into the acceptance region, and reject H_0 if T falls into the rejection region.

Now, T is a random variable that will have one distribution under H_0, and another distribution under H_A. Let us denote the probability mass in the rejection region under H_0 as α, and the mass in the same region under H_A as $1-\beta$. There are four logically possible combinations of the truth value of H_0 and our decision once we have collected $\boldsymbol{y}$:

(1)

		Our decision	
		Accept H_0	Reject H_0
H_0 is...	True	Correct decision (prob. $1-\alpha$)	Type I error (prob. α)
	False	Type II error (prob. β)	Correct decision (prob. $1-\beta$)

The probabilities in each row of I sum to 1, since they represent the conditional probability of our decision given the truth/falsity of H_0.

As you can see in I, there are two sets of circumstances under which we have done the right thing:

1. The null hypothesis is true, and we accept it (probability $1-\alpha$).
2. The null hypothesis is false, and we reject it (probability $1-\beta$).

This leaves us with two sets of circumstances under which we have made an error:

1. The null hypothesis is true, but we reject it (probability α). This by convention is called a TYPE I ERROR.
2. The null hypothesis is false, but we accept it (probability β). This by convention is called a TYPE II ERROR.

For example, suppose that a psycholinguist uses a simple visual world paradigm to examine the time course of word recognition. She presents to participants a display on which a desk is depicted on the left, and a duck is depicted on the right. Participants start with their gaze on the center of the screen, and their eye movements are recorded as they hear the word "duck". The question at issue is whether participants' eye gaze fall reliably more often on the duck than on the desk in the window $200-250$ milliseconds after the onset of "duck", and the researcher devises a simple rule of thumb that if there are more than twice as many fixations on the duck than on the chair within this window, the null hypothesis will be rejected. Her experimental results involve 21% fixations on the duck and 9% fixations on the chair, so she rejects the null hypothesis. However, she later finds out that her computer was miscalibrated by 300 milliseconds and the participants had not even heard the onset of

the word by the end of the relevant window. The researcher had committed a Type I error. (In this type of scenario, a Type I error is often called a FALSE POSITIVE, and a Type II error is often called a FALSE NEGATIVE.)

The probability α of Type I error is referred to as the SIGNIFICANCE LEVEL of the hypothesis test. In the Neyman-Pearson paradigm, T is always chosen such that its (asymptotic) distribution can be computed. The probability $1 - \beta$ of *not* committing Type II error is called the POWER of the hypothesis test. There is always a trade-off between significance level and power, but the goal is to use decision procedures that have the highest possible power for a given significance level. To calculate β and thus the power, however, we need to know the true model, so determining the optimality of a decision procedure with respect to power can be tricky.

Now we'll move on to a concrete example of hypothesis testing in which we deploy some probability theory.

5.4.1 Hypothesis testing: binomial ordering preference

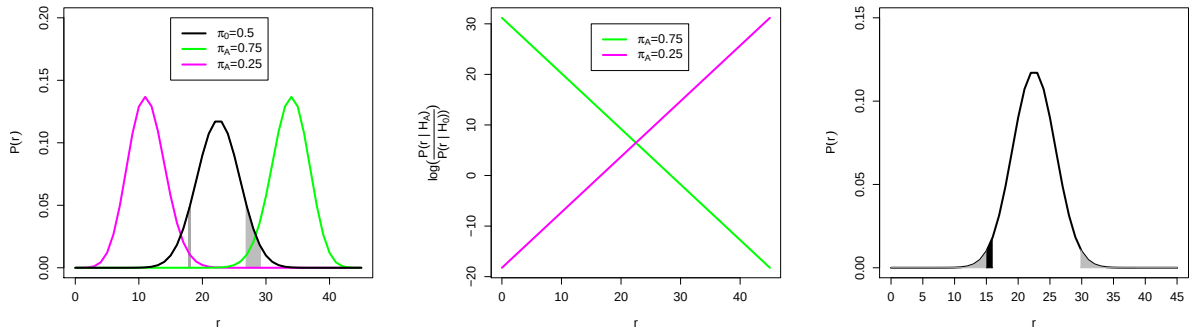
One of the simplest cases of hypothesis testing—and one that is often useful in the study of language—is the BINOMIAL TEST, which we illustrate here.

You decide to investigate the role of ultimate-syllable stress avoidance in English binomial ordering preferences by collecting from the British National Corpus 45 tokens of binomials in which *BSTR could be violated. As the test statistic T you simply choose the number of successes r in these 45 tokens. Therefore the distribution of T under the no-preference null hypothesis $H_0 : \pi = 0.5$ is simply the distribution on the number of successes r for a binomial distribution with parameters $n = 45, \pi = 0.5$. The most general natural alternative hypothesis H_A of "preference" would be that the binomial has some arbitrary preference

$$H_A : 0 \leq \pi \leq 1 \tag{5.15}$$

Unlike the case with Bayesian hypothesis testing, we do not put a probability distribution on π under H_A. We complete our decision procedure by partitioning the possible values of T into acceptance and rejection regions. To achieve a significance level α we must choose a partitioning such that the rejection region contains probability mass of no more than α under the null hypothesis. There are many such partitions that achieve this. For example, the probability of achieving 18 successes in 45 trials is just under 5%; so is the probability of achieving at least 27 successes but not more than 29 successes. The black line in Figure 5.9a shows the probability density function for H_0, and each of the gray areas corresponds to one of these rejection regions.

However, the principle of maximizing statistical power helps us out here. Recall that when H_A is true, the power of the hypothesis test, $1-\beta$, is the probability that $T(\boldsymbol{y})$ will fall in our rejection region. The significance level α that we want to achieve, however, constrains how large our rejection region can be. To maximize the power, it therefore makes sense to choose as the rejection region that part of the range of T assigned lowest probability by H_0



(a) Probability densities over r for H_0 and two instantiations of H_A

(b) The log-ratio of probability densities under H_0 and two instantiations of H_A

(c) Standard (maximum-power) two-tailed and one-tailed rejection regions

Figure 5.9: The trade-off between significance level and power

and highest probability by H_A. Let us denote the probability mass functions for T under H_0 and H_A as $P_0(T)$ and $P_A(T)$ respectively. Figure 5.9b illustrates the tradeoff by plotting the log-ratio $\log \frac{P_A(T)}{P_0(T)}$ under two example instantiations of H_A: $\pi_A = 0.25$ and $\pi_A = 0.75$. The larger this ratio for a given possible outcome t of T, the more power is obtained by inclusion of t in the rejection region. When $\pi_A < 0.5$, the most power is obtained by filling the rejection region with the largest possible values of T. Likewise, when $\pi_A > 0.5$, the most power is obtained by filling the rejection region with the smallest possible values of T.[2] Since our H_A entertains all possible values of π, we obtain maximal power by splitting our rejection region into two symmetric halves, one on the left periphery and the other on the right periphery. In Figure 5.9c, the gray shaded area represents the largest such split region that contains less than 5% of the probability mass under H_0 (actually $\alpha = 0.0357$). If our 45 tokens do not result in at least 16 and at most 29 successes, we will reject H_0 in favor of H_A under this decision rule. This type of rule is called a TWO-TAILED TEST because the rejection region is split equally in the two tails of the distribution of T under H_0.

Another common type of alternative hypothesis would be that is a tendency to *satisfy* *BSTR. This alternative hypothesis would naturally be formulated as $H'_A : 0.5 < \pi \leq 1$. This case corresponds to the green line in Figure 5.9b; in this case we get the most power by putting our rejection region entirely on the left. The largest possible such rejection region for our example consists of the lefthand gray region plus the black region in Figure 5.9c ($\alpha = 0.0362$). This is called a ONE-TAILED TEST. The common principle which derived the form of the one-tailed and two-tailed tests alike is the idea that *one should choose the rejection region that maximizes the power of the hypothesis test if H_A is true.*

Finally, a common approach in science is not simply to choose a significance level α

[2] Although it is beyond the scope of this text to demonstrate it, this principle of maximizing statistical power leads to the same rule for constructing a rejection region regardless of the precise values entertained for π under H_A, so long as values both above and below 0.5 are entertained.

in advance and then report whether H_0 is accepted or rejected, but rather to report the lowest value of α for which H_0 would be rejected. This is what is known as the p-VALUE of the hypothesis test. For example, if our 45 tokens resulted in 14 successes and we conducted a two-tailed test, we would compute twice the cumulative distribution function of Binom(45,0.5) at 14, which would give us an outcome of $p = 0.016$.

5.4.2 Quantifying strength of association in categorical variables

There are many situations in quantitative linguistic analysis where you will be interested in the possibility of association between two categorical variables. In this case, you will often want to represent your data as a contingency table. A 2×2 contingency table has the following form:

$$\begin{array}{cc|cc|c} & & \multicolumn{2}{c|}{Y} & \\ & & y_1 & y_2 & \\ \hline X & x_1 & n_{11} & n_{12} & n_{1*} \\ & x_2 & n_{21} & n_{22} & n_{2*} \\ \hline & & n_{*1} & n_{*2} & n_{**} \end{array} \tag{5.16}$$

where the n_{i*} are the marginal totals for different values of x_i across values of Y, the n_{*j} are the marginal totals for different values of y_j across values of X, and n_{**} is the grand total number of observations.

We'll illustrate the use of contingency tables with an example of quantitative syntax: the study of coordination. In traditional generative grammar, rules licensing coordination had the general form

NP $\rightarrow$ NP Conj NP

or even

X $\rightarrow$ X Conj X

encoding the intuition that many things could be coordinated with each other, but at some level every coordination should be a "combination of like categories", a constraint referred to as CONJOIN LIKES (Chomsky, 1965). However, this approach turned out to be of limited success in a categorical context, as demonstrated by clear violations of like-category constraints such as II below (Sag et al., 1985; Peterson, 1986):

(2) Pat is *a Republican* and *proud of it* (coordination of noun phrase with adjective phrase)

However, the preference for coordination to be between like categories is certainly strong as a *statistical tendency* (Levy, 2002). This in turn raises the question of whether the preference for coordinated constituents to be similar to one another extends to a level more fine grained than gross category structure (Levy, 2002; Dubey et al., 2008). Consider, for example, the following four coordinate noun phrases (NPs):

Example		NP1	NP2
1.	The girl and the boy	noPP	noPP
2.	[The girl from Quebec] and the boy	hasPP	noPP
3.	The girl and [the boy from Ottawa]	noPP	hasPP
4.	The girl from Quebec and the boy from Ottawa	hasPP	hasPP

Versions 1 and 4 are *parallel* in the sense that both NP conjuncts have prepositional-phrase (PP) postmodifiers; versions 2 and 3 are non-parallel. If Conjoin Likes holds at the level of NP-internal PP postmodification as a violable preference, then we might expect coordinate NPs of types 1 and 4 to be more common than would "otherwise be expected"—a notion that can be made precise through the use of contingency tables.

For example, here are patterns of PP modifications in two-NP coordinations of this type from the parsed Brown and Switchboard corpora of English, expressed as 2×2 contingency tables:

(3)

Brown		NP2 hasPP	NP2 noPP	
NP1	hasPP	95	52	147
	noPP	174	946	1120
		269	998	1267

Switchboard		NP2 hasPP	NP2 noPP	
NP1	hasPP	78	76	154
	noPP	325	1230	1555
		403	1306	1709

From the table you can see that in both corpora, NP1 is more likely to have a PP postmodifier when NP2 has one, and NP2 is more likely to have a PP postmodifier when NP1 has one. But we would like to go beyond that and *quantify* the strenght of the association between PP presence in NP1 on NP2. We would also like to *test for significance* of the association.

Quantifying association: odds ratios

In Section 3.3 we already saw one method of quantifying the strength of association between two binary categorical variables: COVARIANCE or CORRELATION. Another popular way way of quantifying the predictive power of a binary variable X on another binary variable Y is with the ODDS RATIO. To introduce this concept, we first introduce the overall ODDS ω^Y of y_1 versus y_2:

$$\omega^Y \stackrel{\text{def}}{=} \frac{n_{*1}}{n_{*2}} \tag{5.17}$$

Likewise, the odds ω^X of x_1 versus x_2 are $\frac{n_{1*}}{n_{2*}}$. For example, in our Brown corpus examples we have $\omega^Y = \frac{147}{1120} = 0.13$ and $\omega^X = \frac{269}{998} = 0.27$.

We further define the odds for Y if $X = x_1$ as ω_1^Y and so forth, giving us:

$$\omega_1^Y \stackrel{\text{def}}{=} \frac{n_{11}}{n_{12}} \quad \omega_2^Y \stackrel{\text{def}}{=} \frac{n_{21}}{n_{22}} \qquad\qquad \omega_1^X \stackrel{\text{def}}{=} \frac{n_{11}}{n_{21}} \quad \omega_2^X \stackrel{\text{def}}{=} \frac{n_{12}}{n_{22}}$$

If the odds of Y for $X = x_2$ are greater than the odds of Y for $X = x_1$, then the outcome of $X = x_2$ **increases** the chances of $Y = y_1$. We can express the effect of the outcome of X on the odds of Y by the **odds ratio** (which turns out to be symmetric between X, Y):

$$\mathcal{OR} \stackrel{\text{def}}{=} \frac{\omega_1^Y}{\omega_2^Y} = \frac{\omega_1^X}{\omega_2^X} = \frac{n_{11}n_{22}}{n_{12}n_{21}}$$

An odds ratio $\mathcal{OR} = 1$ indicates no association between the variables. For the Brown and Switchboard parallelism examples:

$$\mathcal{OR}_{Brown} = \frac{95\times946}{52\times174} = 9.93 \quad \mathcal{OR}_{Swbd} = \frac{78\times1230}{325\times76} = 3.88$$

So the presence of PPs in left and right conjunct NPs seems more strongly interconnected for the Brown (written) corpus than for the Switchboard (spoken). Intuitively, this difference might be interpreted as parallelism of PP presence/absence in NPs being an aspect of stylization that is stronger in written than in spoken language.

5.4.3 Testing significance of association in categorical variables

In frequentist statistics there are several ways to test the significance of the association between variables in a two-way contingency table. Although you may not be used to thinking about these tests as the comparison of two hypotheses in form of statistical models, they are!

Fisher's exact test

Fisher's exact test applies to 2×2 contingency tables such as (5.16). It takes as H_0 the model in which all *marginal totals* are fixed, but that the individual cell totals are not—alternatively stated, that the individual outcomes of X and Y are independent. **This means that under H_0, the true underlying odds ratio $\mathcal{OR}$ is 1.** H_A is the model that the individual outcomes of X and Y are not independent. With Fisher's exact test, the test statistic T is the odds ratio $\mathcal{OR}$, which follows the HYPERGEOMETRIC DISTRIBUTION under the null hypothesis (Section B.3).

An advantage of this test is that it computes the *exact* p-value (that is, the smallest α for which H_0 would be rejected). Because of this, Fisher's exact test can be used even for very small datasets. In contrast, many of the tests we cover elsewhere in this book (including the chi-squared and likelihood-ratio tests later in this section) compute p-values that are only asymptotically correct, and are unreliable for small datasets. As an example, consider the small hypothetical parallelism dataset given in IV below:

(4)

			NP2 hasPP	NP2 noPP	
NP1	hasPP		3	14	26
	noPP		22	61	83
			34	75	109

The odds ratio is 2.36, and Fisher's exact test gives a p-value of 0.07. If we were to see twice the data in the exact same proportions, the odds ratio would stay the same, but the significance of Fisher's exact test for non-independence would increase.

Chi-squared test

This is probably the best-known contingency-table test. It is very general and can be applied to arbitrary N-cell tables, if you have a model with k parameters that predicts expected values E_{ij} for all cells. For the chi-squared test, the test statistic is Pearson's X^2:

$$X^2 = \sum_{ij} \frac{[n_{ij} - E_{ij}]^2}{E_{ij}} \tag{5.18}$$

In the chi-squared test, H_A is the model that each cell in the table has its own parameter p_i in one big multinomial distribution. When the expected counts in each cell are large enough (the generally agreed lower bound is ≥ 5), the X^2 statistic is approximately distributed as a chi-squared (χ^2) random variable with $N - k - 1$ degrees of freedom (Section B.4). The χ^2 distribution is asymmetric and the rejection region is always placed in the right tail of the distribution (see Section B.4), so we can calculate the p-value by subtracting from one the value of the cumulative distribution function for the observed X^2 test statistic.

The most common way of using Pearson's chi-squared test is to test for the independence of two factors in a two-way contingency table. Take a $k \times l$ two-way table of the form:

	y_1	y_2	$\cdots$	y_l	
x_1	n_{11}	n_{12}	$\cdots$	n_{1l}	n_{1*}
x_2	n_{21}	n_{22}	$\cdots$	n_{2l}	n_{2*}
	$\vdots$	$\vdots$	$\ddots$	$\vdots$	$\vdots$
x_l	n_{k1}	n_{k2}	$\cdots$	n_{kl}	n_{k*}
	n_{*1}	n_{*2}	$\cdots$	n_{*l}	n

Our null hypothesis is that the x_i and y_i are independently distributed from one another. By the definition of probabilistic independence, that means that H_0 is:

$$P(x_i, y_j) = P(x_i)P(y_j)$$

In the chi-squared test we use the relative-frequency (and hence maximum-likelihood; Section 4.3.1) estimates of the marginal probability that an observation will fall in each row or

column: $\hat{P}(x_i) = \frac{n_{i*}}{n}$ and $\hat{P}(y_j) = \frac{n_{*j}}{n}$. This gives us the formula for the expected counts in Equation (5.18):

$$E_{ij} = nP(x_i)P(y_j)$$

Example: For the Brown corpus data in III, we have

$$P(x_1) = \frac{147}{1267} = 0.1160 \qquad P(y_1) = \frac{269}{1267} = 0.2123 \tag{5.19}$$

$$P(x_2) = \frac{1120}{1267} = 0.8840 \qquad P(y_2) = \frac{998}{1267} = 0.7877 \tag{5.20}$$

giving us

$$E_{11} = 31.2 \quad E_{12} = 115.8 \qquad E_{21} = 237.8 \quad E_{21} = 882.2 \tag{5.21}$$

Comparing with III, we get

$$X^2 = \frac{(95-31.2)^2}{31.2} + \frac{(52-115.8)^2}{115.8} + \frac{(174-237.8)^2}{237.8} + \frac{(946-882.2)^2}{882.2} \tag{5.22}$$

$$= 187.3445 \tag{5.23}$$

We had 2 parameters in our model of independence, and there are 4 cells, so X^2 is distributed as χ^2_1 (since $4-2-1=1$). The cumulative distribution function of χ^2_1 at 187.3 is essentially 1, so the p-value is vanishingly small; by any standards, the null hypothesis can be confidently rejected.

Example with larger data table:

	NP PP	NP NP	NP other
gave	17	79	34
paid	14	4	9
passed	4	1	16

It is worth emphasizing, however, that the chi-squared test is not reliable when expected counts in some cells are very small. For the low-count table in IV, for example, the chi-squared test yields a significance level of $p = 0.038$. Fisher's exact test is the gold standard here, revealing that the chi-squared test is too aggressive in this case.

5.4.4 Likelihood ratio test

With this test, the statistic you calculate for your data $\boldsymbol{y}$ is the LIKELIHOOD RATIO

$$\Lambda^* = \frac{\max \text{Lik}_{H_0}(\boldsymbol{y})}{\max \text{Lik}_{H_A}(\boldsymbol{y})} \tag{5.24}$$

—that is, the ratio of the data likelihood under the MLE in H_0 to the data likelihood under the MLE in H_A. This requires that you explicitly formulate H_0 and H_A, since you need to find the MLEs and the corresponding likelihoods. The quantity

$$G^2 \stackrel{\text{def}}{=} -2 \log \Lambda^* \tag{5.25}$$

is sometimes called the DEVIANCE, and it is approximately chi-squared distributed (Section B.4) with degrees of freedom equal to the difference in the number of free parameters in H_A and H_0. (This test is also unreliable when expected cell counts are low, as in < 5.)

The likelihood-ratio test gives similar results to the chi-squared for contingency tables, but is more flexible because it allows the comparison of arbitrary nested models. We will see the likelihood-ratio test used repeatedly in later chapters.

Example: For the Brown corpus data above, let H_0 be the model of independence between NP1 and NP2 with respective success parameters π_1 and π_2, and H_A be the model of full non-independence, in which each complete outcome $\langle x_i, y_j \rangle$ can have its own probability π_{ij} (this is sometimes called the SATURATED MODEL). We use maximum likelihood to fit each model, giving us for H_0:

$$\pi_1 = 0.116 \qquad\qquad \pi_2 = 0.212$$

and for H_A:

$$\pi_{11} = 0.075 \quad \pi_{12} = 0.041 \qquad\qquad \pi_{21} = 0.137 \quad \pi_{22} = 0.747$$

We calculate G^2 as follows:

$$\begin{aligned}
-2 \log \Lambda^* &= -2 \log \frac{(\pi_1 \pi_2)^{95} (\pi_1 (1-\pi_2))^{52} ((1-\pi_1)\pi_2)^{174} ((1-\pi_1)(1-\pi_2))^{946}}{\pi_{11}^{95} \pi_{12}^{52} \pi_{21}^{174} \pi_{22}^{946}} \\
&= -2 \left[95 \log(\pi_1 \pi_2) + 52 \log(\pi_1 (1-\pi_2)) + 174 \log((1-\pi_1)\pi_2) + 946 \log((1-\pi_1)(1-\pi_2)) \right. \\
&\quad \left. -95\pi_{11} - 52\pi_{12} - 174\pi_{21} - 946\pi_{22} \right] \\
&= 151.6
\end{aligned}$$

H_0 has two free parameters, and H_A has three free parameters, so G^2 should be approximately distributed as χ^2_1. Once again, the cumulative distribution function of χ^2_1 at 151.6 is essentially 1, so the p-value of our hypothesis test is vanishingly small.

5.5 Exercises

Exercise 5.1

Would the Bayesian hypothesis-testing results of Section 5.2 be changed at all if we did not consider the data as summarized by the number of successes and failures, and instead used the likelihood of the specific sequence `HHTHTH` instead? Why?

Exercise 5.2

For Section 5.2, compute the posterior probabilities of H_1, H_2, and H_3 in a situation where all three hypotheses are entertained with prior probabilities $P(H_1) = P(H_2) = P(H_3) = \frac{1}{3}$.

Exercise 5.3

Recompute the Bayesian hypothesis tests, computing both posterior probabilities and Bayes Factors, of Section 5.2 (H_1 vs. H_2 and H_1 vs. H_3) for the same data replicated twice – that is, the observations `SSVSVSSSVSVS`. Are the preferred hypotheses the same as for the original computations in Section 5.2? What about for the data replicated three times?

Exercise 5.4: Phoneme discrimination for Gaussians of unequal variance and prior probabilities.

1. Plot the optimal-response phoneme discrimination curve for the /b/–/p/ VOT contrast when the VOT of each category is realized as a Gaussian and the Gaussians have equal variances $\sigma_{\text{b}} = 12$, different means $\mu_{\text{b}} = 0, \mu_{\text{p}} = 50$, and different prior probabilities: $P(/b/) = 0.25, P(/p/) = 0.75$. How does this curve look compared with that in Figure **??**?

2. Plot the optimal-response phoneme discrimination curve for the /b/–/p/ VOT contrast when the Gaussians have equal prior probabilities but both unequal means and unequal variances: $\mu_{\text{b}} = 0, \mu_{\text{p}} = 50, \sigma_{\text{b}} = 8, \sigma_{\text{p}} = 14$.

3. Propose an experiment along the lines of Clayards et al. (2008) testing the ability of listeners to learn category-specific variances and prior probabilities and use them in phoneme discrimination.

4. It is in fact the case that naturalistic VOTs in English have larger variance /p/ than for /b/ [**TODO: get reference for this**]. For part 2 of this question, check what the model predicts as VOT extends to very large negative values (e.g., -200ms). There is some counter-intuitive behavior: what is it? What does this counter-intuitive behavior tell us about the limitations of the model we've been using?

Exercise 5.5

Use simulation to check that the theoretical confidence interval based on the t distribution for normally distributed data in Section 5.3 really works.

Exercise 5.6

For a given choice of α, is the procedure denoted in Equation (5.14) the only frequentist confidence interval that can be constructed for μ for normally distributed data?

Exercise 5.7: Hypothesis testing: philosophy.

You surreptitiously observe an obsessed linguist compulsively searching a corpus for binomials of the form *pepper and salt* (`P`) or *salt and pepper* (`S`). He collects twenty examples, obtaining the sequence

```
SPSSSPSPSSSSPPSSSSSP
```

1. The linguist's research assistant tells you that the experiment was to obtain twenty examples and record the number of `P`'s obtained. Can you reject the no-preference null hypothesis H_0 at the $\alpha = 0.05$ level?

2. The next day, the linguist tells you in class that she purposely misled the research assistant, and the actual experiment was to collect tokens from the corpus until six `P` examples were obtained and then stop. Does this new information affect the p-value with which you can reject the null hypothesis?

3. The linguist writes up her research results and sends them to a prestigious journal. The editor sends this article to two Bayesian reviewers. Both reviewers argue that this mode of hypothesis testing is ridiculous, and that a Bayesian hypothesis test should be made. Reviewer A suggests that the null hypothesis H_0 of $\pi = 0.5$ should be compared with the alternative hypothesis H_1 of $\pi = 0.25$, and the two hypotheses should be given equal prior probability.

   (a) What is the posterior probability of H_0 given the binomials data? Does the criteria by which the scientist decided how many binomials to collect affect the conclusions of a Bayesian hypothesis test? **Hint:** if $\frac{P(H_0|\vec{x})}{P(H_1|\vec{x})} = a$, then

   $$P(H_0|\vec{x}) = \frac{a}{1+a}$$

   because $P(H_0|\vec{x}) = 1 - P(H_1|\vec{x})$.

   (b) Reviewer B suggests that H_1 should be $\pi = 0.4$ instead. What is the posterior probability of H_0 under this Bayesian comparison?

Exercise 5.8: Bayesian confidence intervals.

The `binom.bayes()` function in the `binom` package permits the calculation of Bayesian confidence intervals over π for various numbers of successes x, total trials n, and a and b (specified as `prior.shape1` and `prior.shape2` respectively—but `prior.shape1`=$a-1$ and `prior.shape2`=$b-1$). Install the `binom` package with the command

```
install.packages("binom")
```

and then use the `binom.bayes()` function to plot the size of a 95% confidence interval on π as a function of the total number of trials n, ranging from 10 to 10000 (in multiples of 10), where 70% of the trials are always successes. (Hold a and b constant, as values of your choice.)

Exercise 5.9: Contextual dependency in phoneme sequences.

1. Reproduce the Bayesian hypothesis test of Section 5.2.3 for uniform priors with the following sequences, computing $P(H_1|\boldsymbol{y})$ for each sequence. One of the three sequences was generated from a context-independent distribution, whereas the other two were generated from context-dependent distributions. Which one is most strongly indicated by the Bayesian hypothesis test to be generated from the context-independent distribution?

   (a) A B A B B B B B A B B B A A A B B B B B B

   (b) B A B B A B A B A A B A B A B B A A B A B

   (c) B B B B A A A A B B B B B A A A A B B B B

2. Although we put uniform priors on all success parameters in Section 5.2.3, in the contextual-dependence model it makes more sense to have a SPARSE prior—that is, one that favors strong preferences for some phonemes over others after each type of context. A sparse beta prior is one for which at least one α_i parameter is low (< 1). Revise the model so that the prior on $\pi_\emptyset$ remains uniform, but that π_A and π_B have symmetric $\langle \alpha, \alpha \rangle$ priors (and give both π_A and π_B the same prior). Plot the posterior probabilities $P(H_1|\boldsymbol{y})$ for sequences (i-iii) as a function of α for $0 < \alpha \leq 1$. What is the value of α for which the context-independent sequence is most strongly differentiated from the context-dependent sequences (i.e. the differences in $P(H_1|\boldsymbol{y})$ between sequence pairs are greatest)?

Exercise 5.10: Phoneme categorization.

1. Plot the Bayesian phoneme discrimination curve for /b/–/p/ discrimination with $\mu_\text{b} = 0, \mu_\text{p} = 50, \sigma_\text{b} = 5, \sigma_\text{p} = 10$.

2. Write out the general formula for Bayesian phoneme discrimination when VOTs in the two categories are normally distributed with unequal variances. Use algebra to simplify it into the form $P(/\text{b}/|x) = \frac{1}{1+\ldots}$. Interpret the formula you obtained.

Exercise 5.11

Frequentist confidence intervals.

In this problem you'll be calculating some frequentist confidence intervals to get a firmer sense of exactly what they are.

1. The `english` dataset in `languageR` has lexical-decision and naming reaction times (`RTlexdec` and `RTnaming` respectively) for 2197 English words. Plot histograms of the mean RT of each item. Calculate 95% frequentist confidence intervals for lexical-decision and naming times respectively, as described in Lecture 7, Section 2. Which experimental method gives tighter confidence intervals on mean RT?

2. The `t.test()` function, when applied to a set of data, returns a list whose component `conf.int` is the upper and lower bounds of a 95% confidence interval:

```
> x <- rnorm(100,2)
> t.test(x)$conf.int

[1] 1.850809 2.241884
attr(,"conf.level")
[1] 0.95
```

   Show that the procedure used in Section 5.3 gives the same results as using `t.test()` for the confidence intervals for the English lexical decision and naming datasets.

3. Not all confidence intervals generated from an "experiment" are the same size. For "experiments" consisting of 10 observations drawn from a standard normal distribution, use `R` to calculate a histogram of lengths of 95% confidence intervals on the mean. What is the shape of the distribution of confidence interval lengths? For this problem, feel free to use `t.test()` to calculate confidence intervals.

Exercise 5.12: Comparing two samples.

In class we covered confidence intervals and the one-sample t-test. This approach allows us to test whether a dataset drawn from a(n approximately) normally distributed population departs significantly from has a particular mean. More frequently, however, we are interested in comparing two datasets $\boldsymbol{x}$ and $\boldsymbol{y}$ of sizes $n_{\boldsymbol{x}}$ and $n_{\boldsymbol{y}}$ respectively, and inferring whether or not they are drawn from the same population. For this purpose, the TWO-SAMPLE t-TEST is appropriate.[3]

1. **Statistical power.** Suppose you have two populations and you can collect n total observations from the two populations. Intuitively, how should you distribute your observations among the two populations to achieve the greatest STATISTICAL POWER in a test that the two populations follow the same distribution?

[3]For completeness, the statistic that is t-distributed for the two-sample test is:

$$\frac{\bar{\boldsymbol{y}} - \bar{\boldsymbol{x}}}{\sqrt{\sigma^2\left(\frac{1}{n_{\boldsymbol{x}}} + \frac{1}{n_{\boldsymbol{y}}}\right)}}$$

where $\bar{\boldsymbol{x}}$ and $\bar{\boldsymbol{y}}$ are the sample means; in general, the variance σ^2 is unknown and is estimated as $\hat{\sigma}^2 = \frac{\sum_i (x_i - \bar{\boldsymbol{x}})^2 + \sum_i (y_i - \bar{\boldsymbol{y}})^2}{N-2}$ where $N = n_{\boldsymbol{x}} + n_{\boldsymbol{y}}$.

2. Check your intuitions. Let $n = 40$ and consider all possible values of $n_{\boldsymbol{x}}$ and $n_{\boldsymbol{y}}$ (note that $n_{\boldsymbol{y}} = n - n_{\boldsymbol{x}}$). For each possible value, run 1000 experiments where the two populations are $X \sim \mathcal{N}(0, 1)$ and $Y \sim \mathcal{N}(1, 1)$. Plot the power of the two-sample t-test at the $\alpha = 0.05$ level as a function of $n_{\boldsymbol{x}}$.

3. **Paired t-tests.** Sometimes a dataset can be naturally thought of as consisting of pairs of measurements. For example, if a phonetician measured voice onset time for the syllables [ba] and [bo] for many different speakers, the data could be grouped into a matrix of the form

	Syllable	
Speaker	[ba]	[bo]
1	x_{11}	x_{12}
2	x_{21}	x_{22}
	$\vdots$	

If we wanted to test whether the voice onset times for [ba] and [bo] came from the same distribution, we could simply perform a two-sample t-test on the data in column 1 versus the data in column 2.

On the other hand, this doesn't take into account the systematic differences in voice-onset time that may hold across speakers. What we might really want to do is test whether the *differences* between x_{i1} and x_{i2} are clustered around zero—which would indicate that the two data vectors probably do come from the same population—or around some non-zero number. This comparison is called a PAIRED t-TEST.

The file `spillover_word_rts` contains the average reading time (in milliseconds) of the second "spillover" word after a critical manipulation in self-paced reading experiment, for 52 sentence pairs of the form:

> The children went outside to **play** early in the afternoon. (Expected)
> The children went outside to **chat** early in the afternoon. (Unexpected)

In a separate sentence completion study, 90% of participants completed the sentence

> The children went outside to __

with the word *play*, making this the Expected condition. In these examples, the word whose reading time (RT) is measured would be *in*, as it appears two words after the critical word (in bold).

(a) Use paired and unpaired t-tests to test the hypothesis that mean reading times at the second spillover word differ significantly in the Expected and Unexpected conditions. Which test leads to a higher significance value?

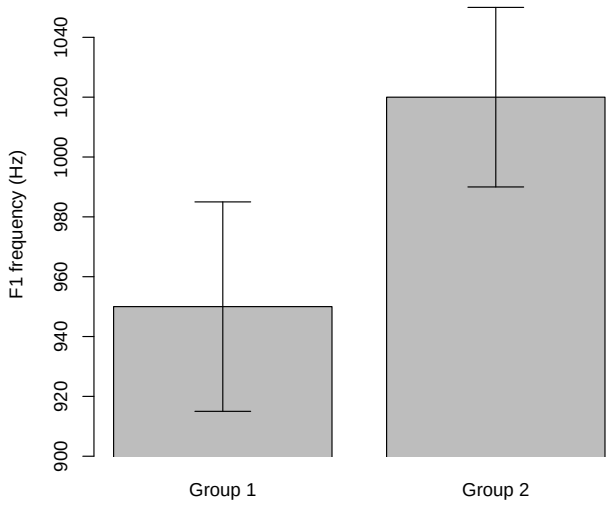


Figure 5.10: A bar plot with non-overlapping standard error bars

(b) Calculate the correlation between the RTs for the unexpected and expected conditions of each item. Intuitively, should higher correlations lead to an increase or drop in statistical power for the paired test over the unpaired test? Why?

Exercise 5.13: Non-overlapping standard errors.$^{\heartsuit}$

You and your colleague measure the F1 formant frequency in pronunciation of the vowel [a] for two groups of 50 native speakers of English, one measurement for each speaker. The means and standard errors of these measurements are shown in Figure 5.10. Your colleague states, "we can be fairly confident in inferring that the two groups have significantly different mean F1 formant frequencies. As a rule of thumb, when you have a reasonably large number of measurements in each group and the standard error bars between the two groups are non-overlapping, we can reject the null hypothesis that the group means are the same at the $p < 0.05$ level." Is your colleague's rule of thumb correct?

Exercise 5.14: Log odds ratio versus correlation.

Are (log) odds ratios any different from correlation coefficients? Plot the relationship between log odds ratio and correlation coefficient for a number of different 2×2 contingency tables. (If you want to take a sampling-based approach to exploring the space of possible contingency tables, you might use the Dirichlet distribution—see Section B.8—to randomly generate sets of cell probabilities).

Exercise 5.15: Contingency tables.

1. Bresnan et al. (2007) conducted a detailed analysis of the dative alternation, as in the example below:

   The actress gave **the toys** *to the children*. (Prepositional Object, PO)
   The actress gave *the children* **the toys**. (Double Object, DO)

   The analysis was based on data obtained from the parsed Switchboard corpus (Godfrey et al., 1992).[4] Irrespective of which alternate was used, it turns out that there are correlations among the properties of the theme (**the toys**) and the recipient (*the children*).

   Definiteness and animacy are often found to be correlated. Look at the relationship between animacy and definiteness of (1) the theme, and (2) the recipient within this dataset, constructing contingency tables and calculating the odds ratios in each case. For which semantic role are definiteness and animacy more strongly associated? Why do you think this might be the case? (Note that organizations, animals, intelligent machines, and vehicles were considered animate for this coding scheme (Zaenen et al., 2004)).

2. The language Warlpiri, one of the best-studied Australian Aboriginal languages, is characterized by extremely free word order and heavy use of morphological cues as to the grammatical function played by each word in the clause (i.e. case marking). Below, for example, the *ergative* case marking (ERG) on the first word of the sentence identifies it as the subject of the sentence:

   Ngarrka- ngku ka wawirri panti- rni. (Hale, 1983)
   man ERG AUX kangaroo spear NONPAST

   "The man is spearing the kangaroo".

   In some dialects of Warlpiri, however, using the ergative case is not obligatory. Note that there would be a semantic ambiguity if the case marking were eliminated from the first word, because neither *man* nor *kangaroo* would have case marking to indicate its grammatical relationship to the verb *spear*. O'Shannessy (2009) carried out a study of word order and case marking variation in sentences with transitive main clauses and overt subjects ("A" arguments in the terminology of Dixon, 1979) in elicited story descriptions by Warlpiri speakers. Her dataset includes annotation of speaker age, whether the transitive subject was animate, whether the transitive subject had ergative case marking, whether the sentence had an animate object (Dixon's "O" argument), whether that object was realized overtly, and whether the word order of the sentence was subject-initial.[5]

[4] The dataset can be found in R's `languageR` package; there it is a data frame named `dative`.
[5] O'Shannessy's dataset can be found in R's `languageR` package under the name `warlpiri`.

(a) Does *subject animacy* have a significant association (at the $\alpha = 0.05$ level) with ergative case marking? What about *word order* (whether the subject was sentence-initial)?

(b) Which of the following variables have an effect on whether subject animacy and word order have a significant association with use of ergative case marking? (For each of the below variables, split the dataset in two and do a statistical test of association on each half.)

overtness of object
age group

Chapter 6

Generalized Linear Models

In Chapters 2 and 4 we studied how to estimate simple probability densities over a single random variable—that is, densities of the form $P(Y)$. In this chapter we move on to the problem of estimating *conditional* densities—that is, densities of the form $P(Y|X)$. Logically speaking, it would be possible to deal with this problem simply by assuming that Y may have an arbitrarily different distribution for each possible value of X, and to use techniques we've covered already to estimate a different density $P(Y|X = x_i)$ for each possible value x_i of X. However, this approach would miss the fact that X may have a *systematic* effect on Y; missing this fact when it is true would make it much more difficult to estimate the conditional distribution. Here, we cover a popular family of conditional probability distributions known as GENERALIZED LINEAR MODELS. These models can be used for a wide range of data types and have attractive computational properties.

6.1 The form of the generalized linear model

Suppose we are interested in modeling the distribution of Y conditional on a number of random variables $X_1, \ldots, X_n$. Generalized linear models are a framework for modeling this type of conditional distribution $P(Y|X_1, \ldots, X_n)$ subject to four key assumptions:

1. The influences of the $\{X_i\}$ variables on Y can be summarized into an intermediate form, the LINEAR PREDICTOR η;
2. η is a linear combination of the $\{X_i\}$;
3. There is a smooth, invertible function l mapping η to the expected value μ of Y;
4. The distribution $P(Y = y; \mu)$ of Y around μ is a member of a certain class of noise functions and is not otherwise sensitive to the X_i variables.[1]

Assumptions 1 through 3 can be expressed by the following two equations:

[1]The class of allowable noise functions is described in Section **??**.

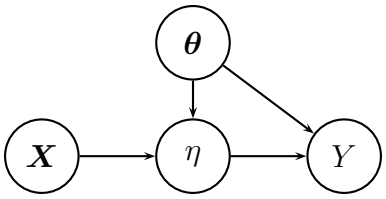


Figure 6.1: A graphical depiction of the generalized linear model. The influence of the conditioning variables $\boldsymbol{X}$ on the response Y is completely mediated by the linear predictor η.

$$\eta = \alpha + \beta_1 X_1 + \cdots + \beta_n X_n \qquad \text{(linear predictor)} \tag{6.1}$$

$$\eta = l(\mu) \qquad \text{(link function)} \tag{6.2}$$

Assumption 4 implies conditional independence of Y from the $\{X_i\}$ variables given η.

Various choices of $l(\mu)$ and $P(Y = y; \mu)$ give us different classes of models appropriate for different types of data. In all cases, we can estimate the parameters of the models using any of likelihood-based techniques discussed in Chapter 4. We cover three common classes of such models in this chapter: linear models, logit (logistic) models, and log-linear models.

6.2 Linear models and linear regression

We can obtain the classic LINEAR MODEL by chooosing the identity link function

$$\eta = l(\mu) = \mu$$

and a noise function that adds noise

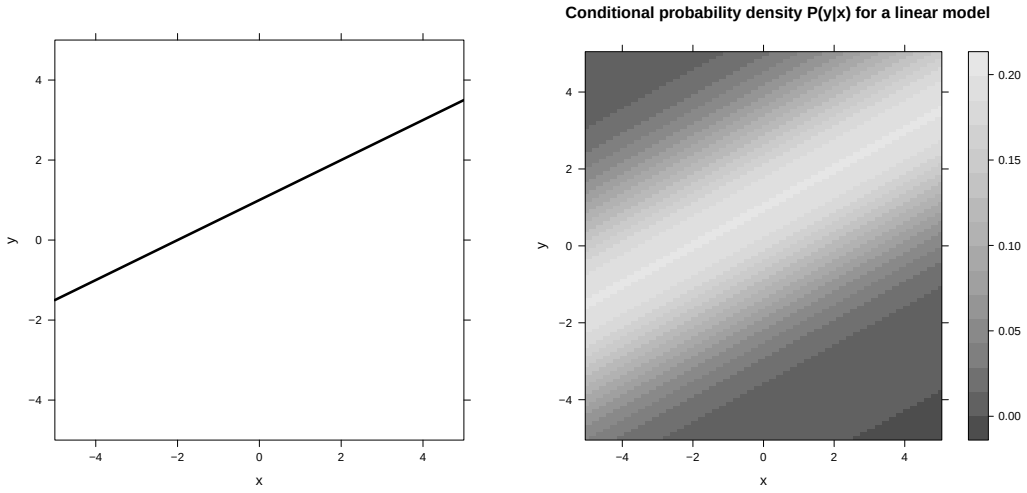
$$\epsilon \sim N(0, \sigma^2)$$

to the mean μ. Substituting these in to Equations (6.1) and 6.2, we can write Y directly as a function of $\{X_i\}$ as follows:

$$Y = \overbrace{\alpha + \beta_1 X_1 + \cdots + \beta_n X_n}^{\text{Predicted Mean}} + \overbrace{\epsilon}^{\text{Noise}\sim N(0,\sigma^2)} \tag{6.3}$$

We can also write this whole thing in more compressed form as $Y \sim N(\alpha \sum_i \beta_i X_i, \sigma^2)$.

To gain intuitions for how this model places a conditional probability density on Y, we can visualize this probability density for a single independent variable X, as in Figure 6.2—lighter means more probable. Each vertical slice of constant $X = x$ represents a conditional



(a) Predicted outcome

(b) Probability density

Figure 6.2: A plot of the probability density on the outcome of the Y random variable given the X random variable; in this case we have $\eta = \frac{1}{2}X$ and $\sigma^2 = 4$.

distribution $P(Y|x)$. If you imagine a vertical line extending through the plot at $X = 0$, you will see that the plot along this line is lightest in color at $Y = -1 = \alpha$. This is the point at which ϵ takes its most probable value, 0. For this reason, α is also called the INTERCEPT parameter of the model, and the β_i are called the SLOPE parameters.

6.2.1 Fitting a linear model

The process of estimating the parameters α and β_i of a linear model on the basis of some data (also called FITTING the model to the data) is called LINEAR REGRESSION. There are many techniques for parameter estimation in linear regression; here we will cover the method of maximum likelihood and also Bayesian linear regression.

Maximum-likelihood linear regression

Before we talk about exactly what the maximum-likelihood estimate looks like, we'll introduce some useful terminology. Suppose that we have chosen model parameters $\hat{\alpha}$ and $\{\hat{\beta}_i\}$. This means that for each point $\langle x_j, y_j \rangle$ in our dataset $\boldsymbol{y}$, we can construct a PREDICTED VALUE for $\hat{y}_j$ as follows:

$$\hat{y}_j = \hat{\alpha} + \hat{\beta}_1 x_{j1} + \ldots \hat{\beta}_n x_{jn}$$

where x_{ji} is the value of the i-th predictor variable for the j-th data point. This predicted value is both the expectated value and the modal value of Y_j due to the Gaussian-noise assumption of linear regression. We define the RESIDUAL of the j-th data point simply as

$$y_j - \hat{y}_j$$

—that is, the amount by which our model's prediction missed the observed value.

It turns out that for linear models with a normally-distributed error term ϵ, the log-likelihood of the model parameters with respect to $\boldsymbol{y}$ is proportional to the sum of the squared residuals. This means that the maximum-likelihood estimate of the parameters is also the estimate that minimizes the the sum of the squared residuals. You will often see description of regression models being fit using LEAST-SQUARES estimation. Whenever you see this, recognize that this is equivalent to maximum-likelihood estimation under the assumption that residual error is normally-distributed.

6.2.2 Fitting a linear model: case study

The dataset `english` contains reaction times for lexical decision and naming of isolated English words, as well as written frequencies for those words. Reaction times are measured in milliseconds, and word frequencies are measured in appearances in a 17.9-million word written corpus. (All these variables are recorded in log-space) It is well-established that words of high textual frequency are generally responded to more quickly than words of low textual frequency. Let us consider a linear model in which reaction time RT depends on the log-frequency, F, of the word:

$$RT = \alpha + \beta_F F + \epsilon \tag{6.4}$$

troduction to tion 11.1

This linear model corresponds to a FORMULA in `R`, which can be specified in either of the following ways:

```
RT ~ F
RT ~ 1 + F
```

The `1` in the latter formula refers to the intercept of the model; the presence of an intercept is implicit in the first formula.

The result of the linear regression is an intercept $\alpha = 843.58$ and a slope $\beta_F = -29.76$. The `WrittenFrequency` variable is in natural log-space, so the slope can be interpreted as saying that if two words differ in frequency by a factor of $e \approx 2.718$, then on average the more frequent word will be recognized as a word of English 26.97 milliseconds faster than the less frequent word. The intercept, 843.58, is the predicted reaction time for a word whose log-frequency is 0—that is, a word occurring only once in the corpus.

6.2.3 Conceptual underpinnings of best linear fit

Let us now break down how the model goes about fitting data in a simple example.

Suppose we have only three observations of log-frequency/RT pairs:

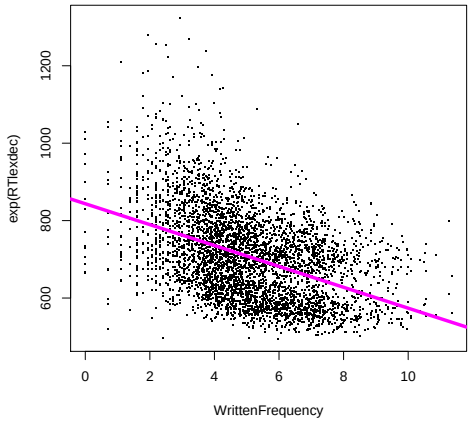


Figure 6.3: Lexical decision reaction times as a function of word frequency

$$\langle 4, 800 \rangle$$
$$\langle 6, 775 \rangle$$
$$\langle 8, 700 \rangle$$

Let use consider four possible parameter estimates for these data points. Three estimates will draw a line through two of the points and miss the third; the last estimate will draw a line that misses but is reasonably close to all the points.

First consider the solid black line, which has intercept 910 and slope -25. It predicts the following values, missing all three points:

x	$\hat{y}$	Residual $(\hat{y} - y)$
4	810	-10
6	760	15
8	710	-10

and the sum of its squared residuals is 425. Each of the other three lines has only one non-zero residual, but that residual is much larger, and in all three case, the sum of squared residuals is larger than for the solid black line. This means that the likelihood of the parameter values $\alpha = 910, \beta_F = -25$ is higher than the likelihood of the parameters corresponding to any of the other lines.

What is the MLE for α, β_F with respect to these three data points, and what are the residuals for the MLE?

Results of a linear fit (almost every statistical software package supports linear regression) indicate that the MLE is $\alpha = 908\frac{1}{3}, \beta = -25$. Thus the MLE has the same slope as the solid

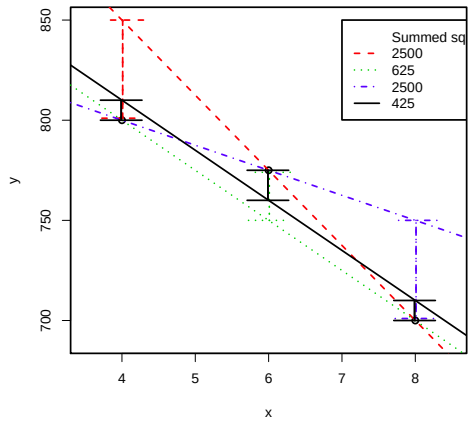


Figure 6.4: Linear regression with three points

black line in Figure 6.4, but the intercept is slightly lower. The sum of squared residuals is slightly better too.

Take-home point: for linear regression, getting everything wrong by a little bit is better than getting a few things wrong by a lot.

6.3 Handling multiple predictors

In many cases, we are interested in simultaneously investigating the linear influence of two or more predictor variables on a single response. We'll discuss two methods of doing this: RESIDUALIZING and MULTIPLE LINEAR REGRESSION.

As a case study, consider naming reaction times from the `english` dataset, and now imagine that we're interested in the influence of orthographic neighbors. (An orthographic neighbor of a word w is one that shares most of its letters with w; for example, *cat* has several orthographic neighbors including *mat* and *rat*.) The `english` dataset summarizes this information in the `Ncount` variable, which measures ORTHOGRAPHIC NEIGHBORHOOD DENSITY as (I believe) the number of maximally close orthographic neighbors that the word has. How can we investigate the role of orthographic neighborhood while simultaneously taking into account the role of word frequency?

6.3.1 Residualizing

One approach would be a two-step process: first, construct a linear regression with frequency as the predictor and RT as the response. (This is commonly called "regressing RT against frequency".) Second, construct a new linear regression with neighborhood density as the predictor the *residuals from the first regression* as the response. The transformation of a raw RT into the residual from a linear regression is called RESIDUALIZATION. Figure 6.5):

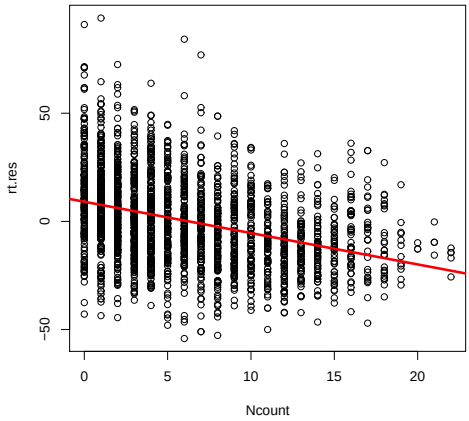


Figure 6.5: Plot of frequency-residualized word naming times and linear regression against neighborhood density

```
> english.young <- subset(english,AgeSubject=="young")
> attach(english.young)
> rt.freq.lm <- lm(exp(RTnaming) ~ WrittenFrequency)
> rt.freq.lm

Call:
lm(formula = exp(RTnaming) ~ WrittenFrequency)

Coefficients:
     (Intercept)  WrittenFrequency
         486.506            -3.307

> rt.res <- resid(rt.freq.lm)
> rt.ncount.lm <- lm(rt.res ~ Ncount)
> plot(Ncount, rt.res)
> abline(rt.ncount.lm,col=2,lwd=3)
> detach()
> rt.ncount.lm

Call:
lm(formula = rt.res ~ Ncount)

Coefficients:
(Intercept)       Ncount
      9.080       -1.449
```

Even after linear effects of frequency have been accounted for by removing them from the RT measure, neighborhood density still has some effect – words with higher neighborhood density are named more quickly.

6.3.2 Multiple linear regression

The alternative is to build a single linear model with more than one predictor. A linear model predicting naming reaction time on the basis of both frequency F and neighborhood density D would look like this:

$$RT = \alpha + \beta_F F + \beta_D D + \epsilon$$

and the corresponding `R` formula would be either of the following:

```
RT ~ F + D
RT ~ 1 + F + D
```

Plugging this in gives us the following results:

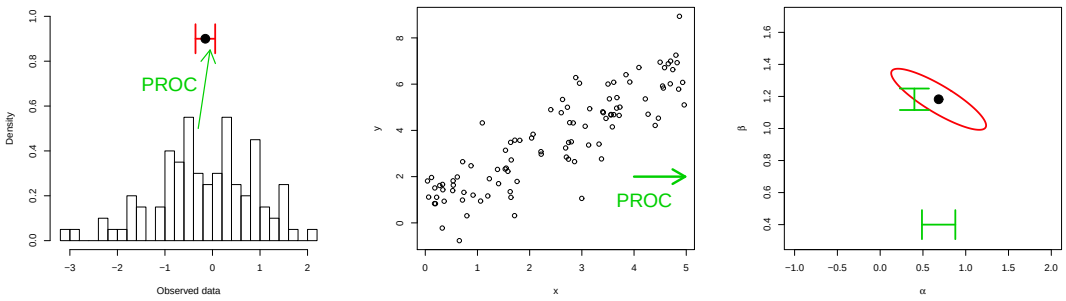
```
> rt.both.lm <- lm(exp(RTnaming) ~ WrittenFrequency + Ncount, data=english.young)
> rt.both.lm

Call:
lm(formula = exp(RTnaming) ~ WrittenFrequency + Ncount, data = english.young)

Coefficients:
     (Intercept)  WrittenFrequency            Ncount
         493.638            -2.899            -1.465
```

Note that the results are qualitatively similar but quantitatively different than for the residualization approach: larger effect sizes have been estimated for both `WrittenFrequency` and `Ncount`.

6.4 Confidence intervals and hypothesis testing for linear regression

Just as there was a close connection between hypothesis testing with the one-sample t-test and a confidence interval for the mean of a sample, there is a close connection between hypothesis testing and confidence intervals for the parameters of a linear model. We'll start by explaining the confidence interval as the fundamental idea, and see how this leads to hypothesis tests.

Figure 6.6 illustrates the procedures by which confidence intervals are constructed for a sample mean (one parameter) and for the intercept and slope of a linear regression with one



(a) Sample mean (b) Data (c) Confidence region

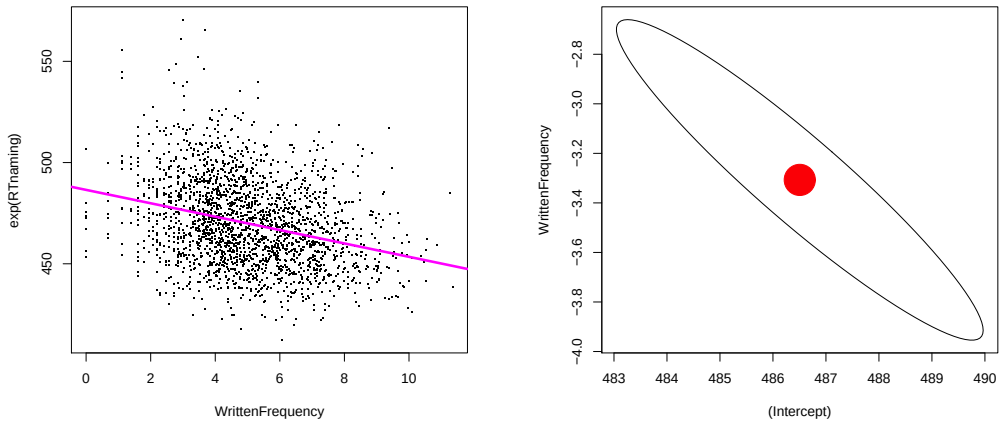
Figure 6.6: The confidence-region construction procedure for (a) sample means and (b-c) parameters of a linear model. The black dots are the maximum-likelihood estimates, around which the confidence regions are centered.

predictor. In both cases, a dataset $\boldsymbol{y}$ is obtained, and a fixed procedure is used to construct boundaries of a CONFIDENCE REGION from $\boldsymbol{y}$. In the case of the sample mean, the "region" is in one-dimensional space so it is an interval. In the case of a linear regression model, the region is in two-dimensional space, and looks like an ellipse. The size and shape of the ellipse are determined by the VARIANCE-COVARIANCE MATRIX of the linear predictors, and are determined using the fact that the joint distribution of the estimated model parameters is multivariate-normal distributed (Section 3.5). If we collapse the ellipse down to only one dimension (corresponding to one of the linear model's parameters), we have a confidence interval on that parameter; this one-dimensional confidence interval is t distributed with $N - k$ degrees of freedom (Section B.5), where N is the number of observations and k is the number of parameters in the linear model.[2]

We illustrate this in Figure 6.7 for the linear regression model of frequency against word naming latency.The model is quite certain about the parameter estimates; however, note that there is a correlation between the parameter estimates. According to the analysis, if we reran this regression many times by repeatedly drawing data from the same population and estimating parameters, whenever the resulting intercept (i.e., average predicted RT for the rarest class of word) is higher, the facilitative effect of written frequency would tend to be larger, and vice versa. This is intuitively sensible because the most important thing for the regression is where it passes through the centroid of the data; so that if the intercept drops a bit, the slope has to rise to compensate.

Perhaps a more interesting example is looking at the confidence region obtained for the parameters of two predictors. In the literature on word recognition, for example, there has been some discussion over whether word frequency or word familiarity drives variability in average word-recognition time (or whether both have independent effects). Because

[2]Formally this corresponds to marginalizing over the estimates of the other parameters that you're collapsing over.



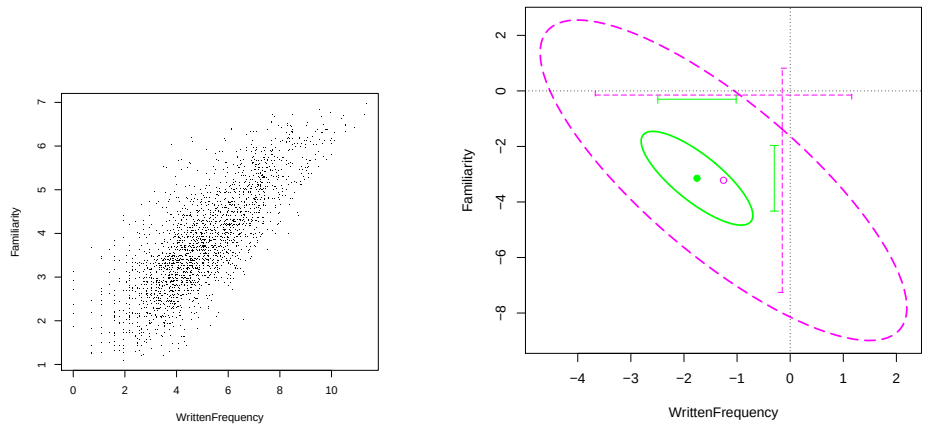
(a) Data and best linear fit

(b) Confidence ellipse

Figure 6.7: Confidence ellipse for parameters of regression of word naming latency against written frequency

subjective ratings of word familiarity are strongly correlated with word frequency, it is empirically difficult to disentangle the two. Figure 6.8a shows a scatterplot of word familiarity against word frequency ratings for 2,197 English nouns and verbs (Spieler and Balota, 1997; Balota and Spieler, 1998); the empirical correlation is 0.79. The naming study carried out by Spieler and Balota (1997) was very large, and they obtained naming times for each of these words from 31 undergraduate native English speakers. A multiple linear regression analysis with frequency and familiarity as predictors puts 95% confidence intervals for their slopes in the linear model at [-2.49,-1.02] and [-4.33,-1.96] respectively. Hence we can conclude that each of frequency and familiarity contribute independently in determining naming time (insofar as the measurements of frequency and familiarity themselves are accurately measured).

However, this was a very large study, and one might reasonably ask what conclusions one could draw from a much smaller study. The same multiple linear regression based on a random subsample of 200 of the words from Spieler and Balota's study gives us confidence intervals for the effects of word frequency and familiarity on naming time of [-3.67,1.16] and [-7.26,0.82]. With this smaller dataset, we cannot confidently conclude that either predictor is independently a determinant of naming time. Yet this negative result conceals an important conclusion that we can still draw. Figure 6.8 plots confidence *regions* for the two model parameters, as well as confidence intervals for each individual parameter, in models of the full dataset (solid green lines) and the reduced, 200-word dataset (dashed magenta lines). Although the reduced-dataset confidence region shows that we cannot be confident that either parameter is negative (i.e. that it has a facilitatory effect on naming time), we can be quite confident that it is not the case that *both* parameters are non-negative: the ellipse does not come close to encompassing the origin. That is, we can be confident that *some combination* of word frequency and familiarity has a reliable influence on naming time. We



(a) Scatterplot of word frequency & familiarity rating

(b) Confidence region for influence on word naming time

Figure 6.8: Confidence region on written word frequency and word familiarity for full dataset of Spieler and Balota (1997), and reduced subset of 200 items

return to this point in Section 6.5.2 when we cover how to compare models differing by more than one parameter through the F test.

6.5 Hypothesis testing in multiple linear regression

An extremely common use of linear models is in testing hypotheses regarding whether one or more predictor variables have a reliable influence on a continuously-distributed response. Examples of such use in the study of language might include but are not limited to:

- Does a word's frequency reliably influence how rapidly it is recognized, spoken, or read?
- Are words of different parts of speech recognized, spoken, or read at different rates above and beyond the effects of word frequency (and perhaps other properties such as word length)?
- Does the violation of a given syntactic constraint affect a native speaker's rating of the felicity of sentences with the violation (as compared to sentences without the violation)?
- Does the context in which a sound is uttered reliably influence one of its phonetic properties (such as voice-onset time for stops, or format frequency for vowels)?

All of these questions may be addressed within the Neyman-Pearson paradigm frequentist hypothesis-testing paradigm introduced in Section 5.4. Recall that the Neyman-Pearson paradigm involves specifying a null hypothesis H_0 and determining whether to reject it in

favor of a more general and complex hypothesis H_A. In many cases, we are interested in comparing whether a more complex linear regression is justified by the data over a simpler regression. Under these circumstances, we can take the simpler model M_0 as the null hypothesis, and the more complex model M_A as the alternative hypothesis. There are two statistical tests that you will generally encounter for this purpose: one based on the t statistic (which we already saw in Section 5.3) and another, the F test, which is based on what is called the F statistic. However, the former is effectively a special case of the latter, so here we'll look at how to use the F statistic for hypothesis testing with linear models; then we'll briefly cover the use of the t statistic for hypothesis testing as well.

6.5.1 Decomposition of variance

The F test takes advantage of a beautiful property of linear models to compare M_0 and M_A: the DECOMPOSITION OF VARIANCE. Recall that the VARIANCE of a sample is simply the sum of the square deviations from the mean:

$$\text{Var}(\boldsymbol{y}) = \sum_j (y_j - \bar{y})^2 \tag{6.5}$$

where $\bar{y}$ is the mean of the sample $\boldsymbol{y}$. For any model M that predicts values $\hat{y}_j$ for the data, the RESIDUAL VARIANCE or RESIDUAL SUM OF SQUARES of M is quantified in exactly the same way:

$$RSS_M(\boldsymbol{y}) = \sum_j (y_j - \hat{y}_j)^2 \tag{6.6}$$

A beautiful and extraordinarily useful property of linear models is that the sample variance can be split apart, or DECOMPOSED, into (a) the component that is explained by M, and (b) the component that remains unexplained by M. This can be written as follows (see Exercise 6.5):

$$\text{Var}(\boldsymbol{y}) = \overbrace{\sum_j (y_j - \hat{y}_j)^2}^{\text{explained by } M} + \overbrace{\sum_j (\hat{y}_j - \bar{y})^2}^{RSS_M(\boldsymbol{y}),\text{unexplained}} \tag{6.7}$$

Furthermore, if two models are nested (i.e., one is a special case of the other), then the variance can be futher subdivided among those two models. Figure 6.9 shows the partitioning of variance for two nested models.

6.5.2 Comparing linear models: the F test statistic

The F test is widely used for comparison of linear models, and forms the foundation for many analytic techniques including the analysis of variance (ANOVA).

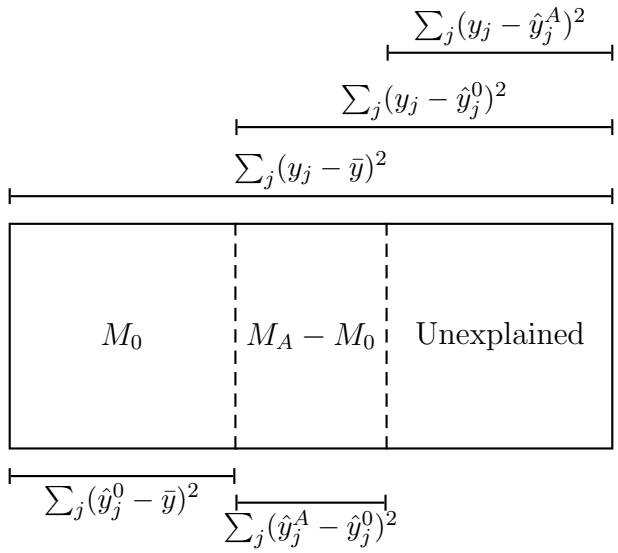


Figure 6.9: The partitioning of residual variance in linear models. Symbols in the box denote the variance explained by each model; the sums outside the box quantify the variance in each combination of sub-boxes.

Recall that our starting assumption in this section was that we had two linear models: a more general model M_A, and a special case M_0—that is, for any instance of M_0 we can achieve an instance of M_A with the same distribution over Y by setting the parameters appropriately. In this situation we say that M_0 is NESTED inside M_A. Once we have found maximum-likelihood estimates of M_0 and M_A, let us denote their predicted values for the j-th observation as $\hat{y}_j^0$ and $\hat{y}_j^A$ respectively. The sample variance unexplained by M_0 and M_A respectively is

$$\sum_j (\hat{y}_j - \hat{y}_j^0)^2 \ (M_0) \tag{6.8}$$

$$\sum_j (\hat{y}_j - \hat{y}_j^A)^2 (M_A) \tag{6.9}$$

so the additional variance explained by M_A above and beyond M_0 is

$$\sum_j (\hat{y}_j - \hat{y}_j^A)^2 - \sum_j (\hat{y}_j - \hat{y}_j^0)^2 = \sum_j (\hat{y}_j^A - \hat{y}_j^0)^2 \tag{6.10}$$

Let us suppose that M_0 has k_0 parameters, M_A has k_A parameters, and we have n observations. It turns out that the quantities in Equations (6.8), (6.9), and (6.10) are distributed proportional to χ^2 random variables with $n - k_0$, $n - k_A$, and $k_A - k_0$ degrees of freedom respectively (Section B.4). These quantities are also independent of one another; and, crucially, *if M_0 is the true model then the proportionality constants for Equations (6.9) and (6.10) are the same.*

These facts form the basis for a frequentist test of the null hypothesis $H_0 : M_0$ is correct, based on the F STATISTIC, defined below:

$$F = \frac{\sum_j (\hat{y}_j^A - \hat{y}_j^0)^2/(k_A - k_0)}{\sum_j (y_j - \hat{y}_j^A)^2/(n - k_A)} \tag{6.11}$$

Under H_0, the F statistic follows the F distribution (Section B.6)—which is parameterized by *two* degrees of freedom—with $(k_A - k_0, n - k_A)$ degrees of freedom. This follows from the fact that under H_0, we have

$$\sum_j (\hat{y}_j^A - \hat{y}_j^0)^2/(k_A - k_0) \sim C\chi^2_{k_A - k_0}; \qquad \sum_j (\hat{y}_j - \hat{y}_j^A)^2/(n - k_A) \sim C\chi^2_{n-k_A}$$

for some proportionality constant C; when the ratio of the two is taken, the two Cs cancel, leaving us with an F-distributed random variable.

Because of the decomposition of variance, the F statistic can also be written as follows:

$$F = \frac{\left[\sum_j (y_j - \hat{y}_j^0)^2 - \sum_j (y_j - \hat{y}_j^A)^2\right]/(k_A - k_0)}{\left[\sum_j (y_j - \hat{y}_j^A)^2\right]/(n - k_A)}$$

which underscores that the F statistic compares the amount of regularity in the observed data explained by M_A beyond that explained by M_0 (the numerator) with the amount of regularity unexplained by M_A (the denominator). The numerator and denominator are often called MEAN SQUARES.

Because of the decomposition of variance, the F test can be given a straightforward geometric interpretation. Take a look at the labels on the boxes in Figure 6.9 and convince yourself that the sums in the numerator and the denominator of the F statistic correspond respectively to the boxes $M_A - M_0$ and Unexplained. Thus, using the F statistic for hypothesis testing is often referred to as evaluation of the RATIO OF MEAN SQUARES.

Because of its importance for frequentist statistical inference in linear models, the F distribution has been worked out in detail and is accessible in most statistical software packages.

6.5.3 Model comparison: case study

We can bring the F test to bear in our investigation of the relative contributions of word frequency and familiarity on word naming latency; we will focus on analysis of the reduced 200-item dataset. First let us consider a test in which the null hypothesis H_0 is that only word frequency has a reliable effect, and the alternative hypothesis H_A is that both word frequency (or "Freq" for short) and familiarity ("Fam") have reliable effects. H_0 corresponds

to the model $RT \sim \mathcal{N}(\alpha + \beta_{\text{Freq}}\text{Freq}, \sigma^2)$; H_A corresponds to the model $RT \sim \mathcal{N}(\alpha + \beta_{\text{Freq}}\text{Freq} + \beta_{\text{Fam}}\text{Fam}, \sigma^2)$. After obtaining maximum-likelihood fits of both models, we can compute the residual sums of squares $\sum_j (\hat{y}_j - y_j)^2$ for each model; these turn out to be 76824.28 for M_0 and 75871.58 for M_A. M_0 has two parameters, M_A has three, and we have 200 observations; hence $k_A - k_0 = 1$ and $N - k_A = 197$. The F statistic for our hypothesis test is thus

$$\begin{aligned} F &= \frac{[76824.28 - 75871.58]/1}{[75871.58]/197} \\ &= 2.47 \end{aligned}$$

with (1,197) degrees of freedom. Consulting the cumulative distribution function for the F statistic we obtain a p-value of 0.12.

We can also apply the F test for comparisons of models differing in multiple parameters, however. For example, let M_0' be a model in which neither word frequency nor familiarity has an effect on naming time. The residual variance in this model is the entire sample variance, or 82270.49. For a comparison between M_0' and M_A we obtain an F statistic of

$$\begin{aligned} F &= \frac{[82270.49 - 75871.58]/2}{[75871.58]/197} \\ &= 8.31 \end{aligned}$$

with (2,197) degrees of freedom. The corresponding p-value is 0.00034, indicating that our data are extremely unlikely under M_0' and that M_A is far preferable. Thus, although we could not adjudicate between word frequency and familiarity with this smaller dataset, we could say confidently that *some combination of the two* has a reliable effect on word naming time.

Another widely used test for the null hypothesis that within a k-parameter model, a *single* parameter β_i is 0. This hypothesis can be tested through a t-test where the t statistic is the ratio of the parameter estimate, $\hat{\beta}_i$ to the standard error of the estimate, $\text{SE}(\hat{\beta}_i)$. For a dataset with N observations, this t-test has $N-k$ degrees of freedom. However, a F statistic with (1,m) has the same distribution as the square of a t statistic with m degrees of freedom. For this reason, the t-test for linear models can be seen as a special case of the more general F test; the latter can be applied to compare nested linear models differing in any number of parameters.

6.6 Analysis of Variance

Recall that we just covered linear models, which are conditional probability distributions of the form

$$P(Y|X) = \alpha + \beta_1 X_1 + \beta_2 X_2 + \cdots + \beta_n X_n + \epsilon \tag{6.12}$$

where $\epsilon \sim \mathcal{N}(0, \sigma^2)$. We saw how this paradigm can be put to use for modeling the predictive relationship of continuous variables, such as word frequency, familiarity, and neighborhood density, on reaction times in word recognition experiments.

In many cases, however, the predictors of interest are not continuous. For example, for the `english` dataset in `languageR` we might be interested in how naming times are influenced by the type of the initial phoneme of the word. This information is coded by the `Frication` variable of the dataset, and has the following categories:

`burst`	the word starts with a burst consonant
`frication`	the word starts with a fricative consonant
`long`	the word starts with a long vowel
`short`	the word starts with a short vowel

It is not obvious how these categories might be meaningfully arranged on the real number line. Rather, we would simply like to investigate the possibility that the mean naming time differs as a function of initial phoneme type.

The most widespread technique used to investigate this type of question is the ANALYSIS OF VARIANCE (often abbreviated ANOVA). Although many books go into painstaking detail covering different instances of ANOVA, you can gain a firm foundational understanding of the core part of the method by thinking of it as a special case of multiple linear regression.

6.6.1 Dummy variables

Let us take the example above, where `Frication` is a categorical predictor. Categorical predictors are often called FACTORS, and the values they take are often called LEVELS. (This is also the nomenclature used in `R`.) In order to allow for the possibility that each level of the factor could have arbitrarily different effects on mean naming latency, we can create DUMMY PREDICTOR VARIABLES, one per level of the factor:

Level of `Frication`	X_1	X_2	X_3	X_4
`burst`	1	0	0	0
`frication`	0	1	0	0
`long`	0	0	1	0
`short`	0	0	0	1

(Variables such as these which are 0 unless a special condition holds, in which case they are 1, are often referred to as INDICATOR VARIABLES). We then construct a standard linear model with predictors X_1 through X_4:

$$Y = \alpha + \beta_1 X_1 + \beta_2 X_2 + \beta_3 X_3 + \beta_4 X_4 + \epsilon \tag{6.13}$$

When we combine the dummy predictor variables with the linear model in (9.7), we get the following equations for each level of `Frication`:

Level of `Frication`	Linear model
`burst`	$Y = \alpha + \beta_1 + \epsilon$
`frication`	$Y = \alpha + \beta_2 + \epsilon$
`long`	$Y = \alpha + \beta_3 + \epsilon$
`short`	$Y = \alpha + \beta_4 + \epsilon$

This linear model thus allows us to code a different predicted mean (and most-likely predicted value) for each level of the predictor, by choosing different values of α and β_i.

However, it should be clear from the table above that only four distinct means can be predicted in this linear model—one for each level of `Frication`. We don't need five parameters (one for α and four for the β_i) to encode four means; one of the parameters is redundant. This is problematic when fitting the model because it means that there is no unique maximum-likelihood estimate.[3] To eliminate this redundancy, we arbitrarily choose one level of the factor as the BASELINE level, and we don't introduce a dummy predictor for the baseline level. If we choose `burst` as the baseline level,[4] then we can eliminate X_4, and make X_1, X_2, X_3 dummy indicator variables for `frication`, `long`, and `short` respectively, giving us the linear model

$$Y = \alpha + \beta_1 X_1 + \beta_2 X_2 + \beta_3 X_3 + \epsilon \tag{6.14}$$

where predicted means for the four classes are as follows:[5]

Level of `Frication`	Predicted mean
`burst`	α
`frication`	$\alpha + \beta_1$
`long`	$\alpha + \beta_2$
`short`	$\alpha + \beta_3$

6.6.2 Analysis of variance as model comparison

Now that we have completed the discussion of using dummy variables to construct a linear model with categorical predictors (i.e., factors), we shall move on to discussing what analysis

[3] For example, if $\alpha = 0, \beta_1 = \beta_2 = \beta_3 = \beta_4 = 1$ is a maximum-likelihood estimate, then $\alpha = 1, \beta_1 = \beta_2 = \beta_3 = \beta_4 = 0$ is as well because it encodes exactly the same model.

[4] By default, `R` chooses the first level of a factor as the baseline, and the first level of a factor is whatever level comes first alphabetically unless you specified otherwise when the factor was constructed—see the `levels` argument of the function `factor()` in the documentation.

[5] This choice of coding for the dummy variables is technically known as the choice of CONTRAST MATRIX. The choice of contrast matrix described here is referred to as the TREATMENT contrast matrix, or `contr.treatment` in `R`.

of variance actually *does*. Consider that we now have two possible models of how word-initial frication affects naming time. We have the model of Equation (6.14) above, in which each class of frication predicts a different mean naming time, with noise around the mean distributed the same way for each class. We might also consider a simpler model in which frication has no effect on naming time. Such a model looks as follows:

$$Y = \alpha + \epsilon \tag{6.15}$$

Now look again at Figure 6.9 and think of the simpler model of Equation (6.15) as M_0, and the more complex model of Equation (6.14) as M_A. (Actually, the M_0 explains *no* variance in this case because it just encodes the mean.) Because ANOVA is just a comparison of linear models, we can perform a hypothesis test between M_0 and M_A by constructing an F statistic from the ratio of the amount of variance contained in the boxes $M_A - M_0$ and Unexplained. The simpler model has one parameter and the more complex model has four, so we use Equation (6.11) with $k_0 = 1, k_A = 4$ to construct the F statistic. The MLE of the single parameter for M_0 (aside from the residual noise variance) is the sample mean $\hat{\alpha} = 470$, and the sum of squared residuals in this model is 1032186. For M_A with the dummy variable coding we've used, the MLEs are $\hat{\alpha} = 471$, $\hat{\beta}_1 = 6$, $\hat{\beta}_2 = -4$, and $\hat{\beta}_3 = -16$; the sum of squared residuals is 872627. Thus the F statistic for this model comparison is

$$\begin{aligned} F(3, 2280) &= \frac{(1032186 - 872627)/3}{872627/2280} \\ &= 138.97 \end{aligned}$$

This F statistic corresponds to a p-value of 1.09×10^{-82}, yielding exceedingly clear evidence that the type of initial segment in a word affects its average naming latency.

6.6.3 Testing for interactions

The `english` dataset includes average naming latencies not only for college-age speakers but also for speakers age 60 and over. This degree of age difference turns out to have a huge effect on naming latency (Figure 6.10):

```
histogram(~ RTnaming | AgeSubject, english)
```

Clearly, college-age speakers are faster at naming words than speakers over age 60. We may be interested in including this information in our model. In Lecture 10 we already saw how to include both variables in a multiple regression model. Here we will investigate an additional possibility: that different levels of frication may have different effects on mean naming latency depending on speaker age. For example, we might think that fricatives, which our linear model above indicates are the hardest class of word onsets, might be even harder for elderly speakers than they are for the young. When these types of inter-predictor contingencies are included in a statistical model they are called INTERACTIONS.

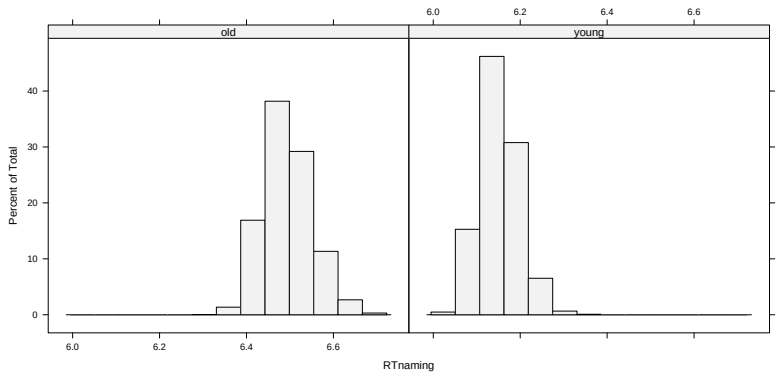


Figure 6.10: Histogram of naming latencies for young (ages $\sim$ 22.6) versus old (ages $>$ 60 speakers)

It is instructive to look explicitly at the linear model that results from introducing interactions between multiple categorical predictors. We will take `old` as the baseline value of speaker age, and leave `burst` as the baseline value of frication. This means that the "baseline" predictor set involves an old-group speaker naming a burst-initial word, and the intercept α will express the predicted mean latency for this combination. There are seven other logically possible combinations of age and frication; thus our full model will have to have seven dummy indicator variables, each with its own parameter. There are many ways to set up these dummy variables; we'll cover perhaps the most straightforward way. In addition to $X_{\{1,2,3\}}$ for the non-baseline levels of frication, we add a new variable X_4 for the non-baseline levels of speaker age (`young`). This set of dummy variables allows us to encode all eight possible groups, but it doesn't allow us to estimate separate parameters for all these groups. To do this, we need to add three more dummy variables, one for each of the non-baseline frication levels when coupled with the non-baseline age level. This gives us the following complete set of codings:

Frication	Age	X_1	X_2	X_3	X_4	X_5	X_6	X_7
burst	old	0	0	0	0	0	0	0
frication	old	1	0	0	0	0	0	0
long	old	0	1	0	0	0	0	0
short	old	0	0	1	0	0	0	0
burst	young	0	0	0	1	0	0	0
frication	young	1	0	0	1	1	0	0
long	young	0	1	0	1	0	1	0
short	young	0	0	1	1	0	0	1

We can test this full model against a strictly ADDITIVE model that allows for effects of both age and initial phoneme class, but not for interactions—that is, one with only $X_{\{1,2,3,4\}}$. It is critical to realize that the additive model is a *constrained* model: five parameters (α and β_1 through β_4) cannot be used to encode eight arbitrary condition means within the

linear framework. The best this M_0 can do—the predicted condition means in its MLE—are compared with the true condition means below:

	Predicted in M_0		Actual (and predicted in M_A)		
	Young	Older		Young	Older
Burst	662.23	470.23	Burst	661.27	471.19
Fricative	670.62	478.61	Fricative	671.76	477.48
Long vowel	653.09	461.09	Long vowel	647.25	466.93
Short vowel	647.32	455.32	Short vowel	647.72	454.92

The predicted per-category means in M_0 can be recovered from the MLE parameter estimates:

$$\hat{\alpha} = 662.23 \quad \hat{\beta}_1 = 8.39 \quad \hat{\beta}_2 = -9.14 \quad \hat{\beta}_3 = -14.91 \quad \hat{\beta}_4 = -192$$

Recovering the predicted means in M_0 from these parameter estimates is left as an exercise for the reader.

When the MLEs of M_0 and M_A are compared using the F-test, we find that our F-statistic turns out to be $F(3, 4560) = 2.69$, or $p = 0.0449$. Hence we also have some evidence that initial segment type has different effects on average naming times for younger and for older speakers—though this evidence is far less conclusive than that for differences across initial-segment type among younger speakers.

6.6.4 Repeated Measures ANOVA and Error Stratification

In the foregoing sections we have covered situations where all of the systematicity across observations can be summarized as deriving from predictors whose effects on the response are systematic and deterministic; all stochastic, idiosyncratic effects have been assumed to occur on level of the individual measurement of the response. In our analysis of average response times for recognition of English words, for example, we considered systematic effects of word frequency, familiarity, neighborhood density, and (in the case of word naming times) initial segment.

Yet it is a rare case in the study of language when there are no potential idiosyncratic effects that are incidental to the true interest of the researcher, yet affect entire *groups* of observations, rather than individual observations. As an example, Alexopolou and Keller (2007) elicited quantitative subjective ratings of sentence acceptability in a study of pronoun resumption, embedding depth, and syntactic islands. One part of one of their experiments involved investigating whether there might be an interaction between embedding and the presence of a resumptive pronoun on sentence acceptability even in cases which are not syntactic islands (Ross, 1967). That is, among the four syntactic frames below, (1-b) should be much less acceptable than (1-a), but (1-d) should not be so much less acceptable than (1-c).

(1) a. Who will we fire __? [UNEMBEDDED, −RESUMPTION]

b. Who will we evict him? [UNEMBEDDED, +RESUMPTION]
c. Who does Lucy claim we will punish __? [EMBEDDED, −RESUMPTION]
d. Who does Emily claim we will arrest him? [EMBEDDED, +RESUMPTION]

As is no doubt evident to the reader, even if we were to find that such a pattern holds for average acceptability ratings of these four sentences, a skeptic could reasonably object that the pattern might well result from the choice of words—the LEXICALIZATIONS—used to fill in the four syntactic templates. For example, *evict* is the least frequent of the four critical verbs above, and it is reasonable to imagine that sentences with less frequent words might tend to be rated as less acceptable.

Hence we want to ensure that our results *generalize* across the specific choice of lexicalizations used in this particular set of four sentences. One way of achieving this would be to prepare $k > 1$ instances of syntactic frame, choosing a separate lexicalization randomly for each of the k instances of each frame ($4k$ lexicalizations total). We might reasonably assume that the effects of choice of lexicalization on acceptability are normally distributed. Following our previous examples, we could use the following dummy-variable encodings:

	X_1	X_2	X_3
[UNEMBEDDED, −RESUMPTION]	0	0	0
[UNEMBEDDED, +RESUMPTION]	1	0	0
[EMBEDDED, −RESUMPTION]	0	1	0
[EMBEDDED, +RESUMPTION]	1	1	1

If ϵ_L is the stochastic effect of the choice of lexicalization and ϵ_E is the normally-distributed error associated with measuring the acceptability of a lexicalized frame, we get the following linear model:

$$Y = \alpha + \beta_1 X_1 + \beta_2 X_2 + \beta_3 X_3 + \epsilon_L + \epsilon_E$$

Typically, we can think of speaker-level stochastic effects and measurement-level stochastic effects as independent of one another; hence, because the sum of two independent normal random variables is itself normally distributed (Section 3.5.1), we can just combine these two stochastic components of this equation:

$$Y = \alpha + \beta_1 X_1 + \beta_2 X_2 + \beta_3 X_3 + \epsilon$$

so we have a completely standard linear model. We could conduct hypothesis tests for this model in the same way as we have done previously in this chapter. For example, we could test the significance of an interaction between embedding and resumption—formally a comparison between a null-hypothesis model M_0 in which $\beta_3 = 0$ and an alternative model M_A with unconstrained β_3—by partitioning variance as in Table 6.1 and conducting an F

test comparing the variance explained by adding β_3 to the model with the residual variance left unexplained by M_A.

By choosing a different set of lexicalizations for each syntactic frame, however, we have introduced additional noise into our measurements that will only increase the difficulty of drawing reliable inferences regarding the effects of embedding, resumption, and their potential interaction. It turns out that we can in general do much better, by using the *same* lexicalizations for each syntactic frame. This is in fact what Alexopolou and Keller did, contrasting a total of nine sentence cohorts of the following types:

(2)
a. (i) Who will we fire __? [UNEMBEDDED, −RESUMPTION]
   (ii) Who will we fire him? [UNEMBEDDED, +RESUMPTION]
   (iii) Who does Mary claim we will fire __? [EMBEDDED, −RESUMPTION]
   (iv) Who does Mary claim we will fire him? [EMBEDDED, +RESUMPTION]

b. (i) Who will we evict __? [UNEMBEDDED, −RESUMPTION]
   (ii) Who will we evict him? [UNEMBEDDED, +RESUMPTION]
   (iii) Who does Elizabeth claim we will evict __? [EMBEDDED, −RESUMPTION]
   (iv) Who does Elizabeth claim we will evict him? [EMBEDDED, +RESUMPTION]

c. ...

Each cohort corresponds to a single lexicalization; in experimental studies such as these the more generic term is ITEM is often used instead of lexicalization. This experimental design is often called WITHIN-ITEMS because the manipulation of ultimate interest—the choice of syntactic frame, or the CONDITION—is conducted for each individual item. Analysis of within-items designs using ANOVA is one type of what is called a REPEATED-MEASURES ANOVA, so named because multiple measurements are made for each of the items. The set of observations obtained for a single item thus constitute a CLUSTER that we hypothesize may have idiosyncratic properties that systematically affect the response variable, and which need to be taken into account when we draw statistical inferences regarding the generative process which gave rise to our data. For this reason, repeated-measures ANOVA is an analytic technique for what are known as HIERARCHICAL MODELS. Hierarchical models are themselves an extremely rich topic, and we take them up in Chapter 8 in full detail. There is also, however, a body of analytic techniques which uses the partitioning of variance and F tests to analyze certain classes of hierarchical models using repeated-measures ANOVA. Because these techniques are extremely widespread in many literatures in the study of language and because these techniques do not require the full toolset for dealing with hierarchical models in general, we cover the repeated-measures ANOVA here. The reader is strongly encouraged, however, to compare the repeated-measure ANOVA with the analytic techniques introduced in Chapter 8, which ultimately offer greater overall flexibility and depth of analysis.

Simple random-intercepts repeated-measures ANOVA

Exactly how to conduct repeated-measures ANOVA depends on the precise nature of the idiosyncratic cluster-level properties assumed. In our current example, the simplest scenario

would be if each item (lexicalization) contributed the same fixed amount to average perceived acceptability regardless of the condition (syntactic frame) in which the lexicalization appeared. If we call the contribution of item i to acceptability a_i, then our model becomes

$$Y = \alpha + \beta_1 X_1 + \beta_2 X_2 + \beta_3 X_3 + a_i + \epsilon$$

We may consider the a_i themselves to be stochastic: most canonically, they may be normally distributed around 0 with some unknown variance. Happily, the stochasticity in this model does not affect how we go about assessing the systematic effects—β_1 through β_3—of ultimate interest to us. We can partition the variance exactly as before.

6.6.5 Condition-specific random effects and error stratification

More generally, however, we might consider the possibility that idiosyncratic cluster-level properties themselves *interact* with the manipulations we intend to carry out. In our case of embedding and resumption, for example, it could be the case that some of the verbs we choose might be particularly unnatural embedded in a complement clause, particularly natural with an overt resumptive-pronoun object, and/or particularly sensitive to specific combinations of embedding and resumptivity. Such a more general model would thus say that

$$Y = \alpha + \beta_1 X_1 + \beta_2 X_2 + \beta_3 X_3 + a_i + b_{i1} X_1 + b_{i2} X_2 + b_{i3} X_3 + \epsilon$$

where $\langle a_i, b_{1i}, b_{2i}, b_{3i} \rangle$ are jointly multivariate-normal with mean zero and some unknown covariance matrix Σ. [6]

With this richer structure of idiosyncratic cluster-level properties, it turns out that we *cannot* partition the variance as straightforwardly as depicted in Figure **??** and draw reliable inferences in hypothesis tests about β_1, β_2, and β_3. It is instructive to step through the precise reason for this. Suppose that we were to test for the presence of an interaction between resumption and embedding—that is, to test the null hypothesis $M_0 : \beta_3 = 0$ against the alternative, more general M_A. Even if M_0 is correct, in general the fit of M_A will account for more variance than M_0 simply because M_A is a more expressive model. As in all cases, the amount of variance that M_A fails to explain will depend on the amount of noise at the level of specific observations (the variance of ϵ). But if M_0 is true, the variance explained by M_A beyond M_0 will depend not only the amount of observation-level noise but also on the

[6] Technically, the F-tests covered in this chapter for repeated-measures ANOVA is fully appropriate only when the covariance matrix Σ is such that all differences between pairs of cluster-specific properties have equal variance: technically, for all $x, y \in \{a, b_1, \ldots, b_n\}$, $\sigma_x^2 + \sigma_y^2 - 2\sigma_{xy}$ is constant. This condition is known as SPHERICITY. Violation of sphericity can lead to anti-conservativity of F-tests; remedies include corrections for this anti-conservativity [**insert references**] as well as adopting hierarchical-model analyses of the type introduced in Chapter 8.

amount and nature of cluster-level noise—that is, the variance of b_{i3} and its correlation with a_i, b_{i1}, and b_{i2}. Exercise 6.7 asks you to demonstrate this effect through simulations.

Fortunately, there *does* turn out to be a way to test hypotheses in the face of such a rich structure of (normally-distributed) cluster-level properties: the STRATIFICATION OF VARIANCE. [**TODO: summary of how to determine what comparisons to make**]

As a first example, let us simply examine the simple effect of adding a level of embedding to object-extracted cases without resumptive pronouns: Example (1-c) versus (1-c). In these cases, according to our dummy variable scheme we have $X_1 = X_3 = 0$, giving us the simplified linear equation:

$$Y = \alpha + \beta_2 X_2 + a_i b_{i2} X_2 + \epsilon \tag{6.16}$$

Figure 6.11 demonstrates the stratification of variance. Although everything except the box labeled "Residual Error" is part of the complete model of Equation (6.16), our F-test for the presence of a significant effect of embedding will pit the variance explained by embedding against the variance explained by idiosyncratic subject sensitivities to embedding condition.

Here is code that demonstrates the execution of the repeated-measures ANOVA:

```
> set.seed(2)
> library(mvtnorm)
> n <- 20
> m <- 20
> beta <- c(0.6,0.2) ## beta[1] corresponds to the intercept; beta[2] corresponds to t
> Sigma.b <- matrix(c(0.3,0,0,0.3),2,2) ## in this case, condition-specific speaker se
> sigma.e <- 0.3
> df.1 <- expand.grid(embedding=factor(c("Unembedded","Embedded")),lexicalization=fact
> df <- df.1
> for(i in 1:(n-1))
+   df <- rbind(df,df.1)
> B <- rmvnorm(m,mean=c(0,0),sigma=Sigma.b)
> df$y <- with(df,beta[embedding] + B[cbind(lexicalization,(as.numeric(embedding)))] +
> m <- aov(y ~ embedding + Error(lexicalization/embedding),df)
```

Alexopolou & Keller 2007 data

```
> library(lme4)
```

6.6.6 Case study: two-way analysis of variance for self-paced reading

Here we cover a slightly more complex case study: a TWO-WAY (so named because we examine possible effects of two predictors and their potential interaction) ANOVA of word-by-word READING TIMES (RTs) in a moving-window self-paced reading experiment conducted

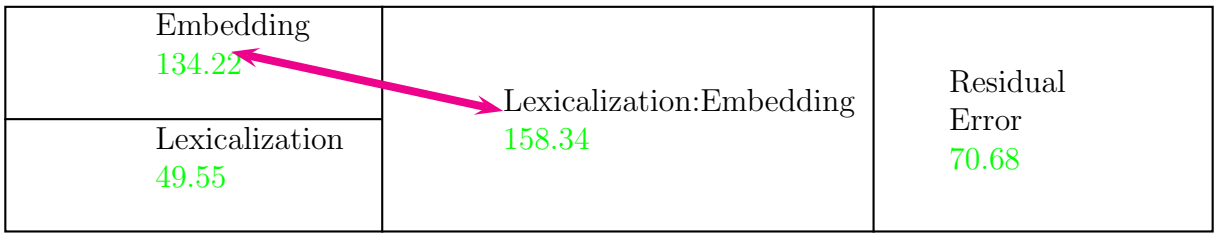


Figure 6.11: Stratification of variance in a simple repeated-measures ANOVA.

by Rohde et al. (2011).[7] In addition to the pure mathematical treatment of the ANOVA, we also cover some preliminary aspects of data analysis. The question under investigation was whether certain kinds of verbs (*implicit causality* (IC) *verbs*) such as "detest", which intuitively demand some sort of explanation, can affect readers' online syntactic attachment preferences.

(3) a. John **detests** the children of the musician who **is** generally arrogant and rude (IC,LOW)
b. John **detests** the children of the musician who **are** generally arrogant and rude (IC,HIGH)
c. John **babysits** the children of the musician who **is** generally arrogant and rude (NONIC,LOW)
d. John **babysits** the children of the musician who **are** generally arrogant and rude (NONIC,HIGH)

We hypothesized that the use of an IC verb should facilitate reading of high-attached RCs, which are generally found in English to be harder to read than low-attached RCs

[7] Moving-window self-paced reading involves presenting sentences one word or group of words at a time, masking previously presented material as new material is revealed, e.g.:

```
-----------.
The -------.
--- cat ---.
------- sat.
```

Participants control the pace at which they read through the material by pressing a button to reveal each new chunk of input; the time between consecutive button presses constitutes the reading time on the pertinent chunk of input.

(Cuetos and Mitchell, 1988). The reasoning here is that the IC verbs demand an explanation, and one way of encoding that explanation linguistically is through a relative clause. In these cases, the most plausible type of explanation will involve a clause in which the object of the IC verb plays a role, so an RC modifying the IC verb's object should become more expected. This stronger expectation may facilitate processing when such an RC is seen (Levy, 2008).

The stimuli for the experiment consist of 20 quadruplets of sentences of the sort above. Such a quadruplet is called an EXPERIMENTAL ITEM in the language of experimental psychology. The four different variants of each item are called the CONDITIONS. Since a participant who sees one of the sentences in a given item is liable to be strongly influenced in her reading of another sentence in the item, the convention is only to show each item once to a given participant. To achieve balance, each participant will be shown five items in each condition.

	Item					
Participant	1	2	3	4	5	...
1	IC,HIGH	NONIC,HIGH	IC,LOW	NONIC,LOW	IC,HIGH	...
2	NONIC,LOW	IC,HIGH	NONIC,HIGH	IC,LOW	NONIC,LOW	...
3	IC,LOW	NONIC,LOW	IC,HIGH	NONIC,HIGH	IC,LOW	...
4	NONIC,HIGH	IC,LOW	NONIC,LOW	IC,HIGH	NONIC,HIGH	...
5	IC,HIGH	NONIC,HIGH	IC,LOW	NONIC,LOW	IC,HIGH	...
⋮	⋮	⋮	⋮	⋮	⋮	⋱

The experimental data will be analyzed for effects of verb type and attachment level, and more crucially for an *interaction* between these two effects. For this reason, we plan to conduct a two-way ANOVA.

In self-paced reading, the observable effect of difficulty at a given word often shows up a word or two downstream, particularly when the word itself is quite short as in this case (short words are often read very quickly, perhaps because the preliminary cue of word length suggests that linguistic analysis of the input will be easy, inducing the reader to initiate the motor activity that will move him/her on to the next word before the difficulty of the linguistic analysis is noticed). Here we focus on the first word after the disambiguator—*generally* in III—often called the first SPILLOVER REGION.

Figure 6.12 provides scatterplots and kernel density estimates (Section 2.11.2) of RT distributions observed in each condition at this point in the sentence. The kernel density estimates make it exceedingly clear that these RTs are far from normally distributed: they are severely right-skewed. ANOVA—in particular repeated-measures ANOVA as we have here—is robust to this type of departure from normality: the non-normality will not lead to anti-conservative inferences in frequentist hypothesis tests. However, the presence of a non-negligible proportion of extremely high values means that the variance of the error is very high, which leads to a poor signal-to-noise ratio; this is a common problem when analyzing data derived from distributions heavier-tailed than the normal distribution. One common means of remedying this issue is adopting some standardized criterion for identifying some observations as OUTLIERS and excluding them from analysis. The practices and reasoning behind outlier removal will vary by data type. In self-paced reading, for example, one rationale for outlier removal is that processes unrelated to sentence comprehension can affect

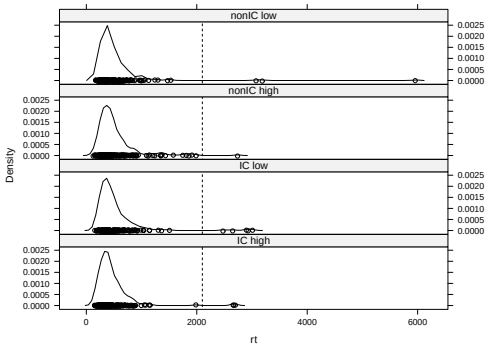


Figure 6.12: Density plots for reading times at the first spillover region for the experiment of Rohde et al. (2011)

recorded reaction times (e.g., the participant sneezes and takes a few seconds to recover); these processes will presumably be independent of the experimental manipulation itself, so if data that were probably generated by these processes can be identified and removed without biasing the outcome of data analysis, it can improve signal-to-noise ratio.

Here we'll adopt a relatively simple approach to outlier removal: binning all our observations, we determine an upper threshold of $\bar{\boldsymbol{y}} + 4\sqrt{S^2}$ where $\bar{\boldsymbol{y}}$ is the sample mean and S^2 is the unbiased estimate of the sample variance (Section 4.3.3). That threshold is plotted in Figure 6.12 as a dotted line; and any observations above that threshold are simply discarded. Note that 12 of the 933 total observations are discarded this way, or 1.3% of the total; consultation of the normal cumulative density function reveals that only 0.0032% would be expected if the data were truly normally distributed.

The comparisons to make

In this experiment, two factors characterize each stimulus: a particular individual reads a particular item that appears with particular *verbtype* (implicit-causality—IC—or non-implicit-causality) and *attachment* level of the relative clause (high or low) manipulations. `verb` and `attachment` have two levels each, so if we had m participants and n items we would in principle need at least $2 \times 2 \times m \times n$ observations to consider a full linear model with interactions of all possible types. However, because each subject saw each item only once, we only have $m \times n$ observations. Therefore it is not possible to construct the full model.

For many years dating back to Clark (1973), the standard ANOVA analysis in this situation has been to construct two separate analyses: one in which the , and one for items. In the analysis over subjects, we take as our individual data points the *mean* value of all the observations in each cell of Subject × Verb × Attachment—that is, we AGGREGATE, or average, across items. Correspondingly, in the analysis over items, we aggregate across subjects. We can use the function `aggregate()` to perform this averaging:

`aggregate()`

`with()`

```
sp.1.subj <- with(spillover.1.to.analyze,aggregate(list(rt=rt),
```

		Subject					
Verb	Attachment	1	2	3	4	5	...
IC	High	280.7	396.1	561.2	339.8	546.1	...
	Low	256.3	457.8	547.3	408.9	594.1	...
nonIC	High	340.9	507.8	786.7	369.8	453.0	...
	Low	823.7	311.4	590.4	838.3	298.9	...

Table 6.1: Repeated-measures (within-subjects) view of item-aggregated data for subjects ANOVA

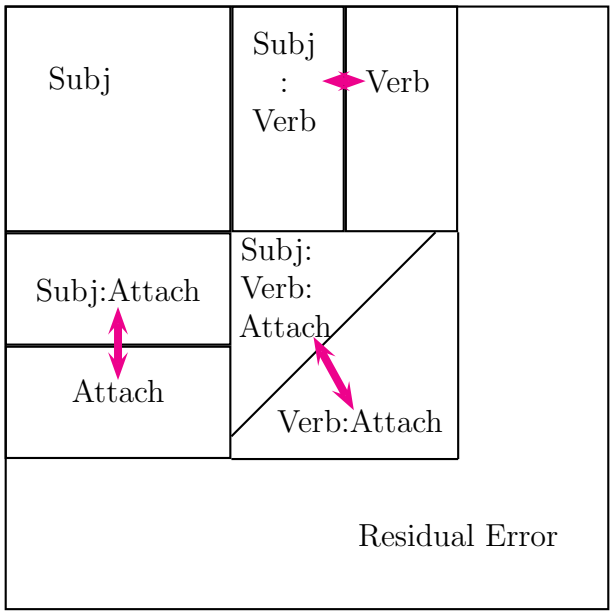


Figure 6.13: The picture for this 2×2 ANOVA, where Verb and Attachment are the fixed effects of interest, and subjects are a random factor

```
  list(subj=subj,verb=verb,attachment=attachment),mean))
sp.1.item <- with(spillover.1.to.analyze,aggregate(list(rt=rt),
  list(item=item,verb=verb,attachment=attachment),mean))
```

The view of the resulting data for the analysis over subjects can be seen in Table 6.1. This setup is called a WITHIN-SUBJECTS or REPEATED-MEASURES design because each subject participates in each condition—or, in another manner of speaking, we take multiple measurements for each subject. Designs in which, for some predictor factor, each subject participates in only one condition are called BETWEEN-SUBJECTS designs.

The way we partition the variance for this type of analysis can be seen in Figure 6.13. Because we have averaged things out so we only have one observation per Subject/Verb/Attachment combination, there will be no variation in the Residual Error box. Each test for an effect of a predictor sets of interest (`verb`, `attachment`, and `verb:attachment`) is performed by comparing the variance explained by the predictor set P with the variance associated with

arbitrary random interactions between the subject and P. This is equivalent to performing a model comparison between the following two linear models, where i range over the subjects and j over the conditions in P:

$$rt_{ij} = \alpha + B_i \text{Subj}_\text{i} + \epsilon_{ij} \qquad \text{(null hypothesis)} \tag{6.17}$$

$$rt_{ij} = \alpha + B_i \text{Subj}_\text{i} + \beta_j P_j + \epsilon_{ij} \qquad \text{(alternative hypothesis)} \tag{6.18}$$

$$\tag{6.19}$$

There is an added wrinkle here, which is that the B_i are not technically free parameters but rather are themselves assumed to be random and normally distributed. However, this difference does not really affect the picture here. (In a couple of weeks, when we get to mixed-effects models, this difference will become more prominent and we'll learn how to handle it in a cleaner and more unified way.)

Fortunately, `aov()` is smart enough to know to perform all these model comparisons in the appropriate way, by use of the `Error()` specification in your model formula. This is done as follows, for subjects:

```
> summary(aov(rt ~ verb * attachment
    + Error(subj/(verb *attachment)), sp.1.subj))

Error: subj
          Df  Sum Sq Mean Sq F value Pr(>F)
Residuals 54 4063007   75241

Error: subj:verb
          Df Sum Sq Mean Sq F value  Pr(>F)
verb       1  48720   48720  7.0754 0.01027 *
Residuals 54 371834    6886
---
Signif. codes:  0 `***' 0.001 `**' 0.01 `*' 0.05 `.' 0.1 ` ' 1

Error: subj:attachment
           Df Sum Sq Mean Sq F value Pr(>F)
attachment  1    327     327  0.0406  0.841
Residuals  54 434232    8041

Error: subj:verb:attachment
                Df Sum Sq Mean Sq F value  Pr(>F)
verb:attachment  1  93759   93759  6.8528 0.01146 *
Residuals       54 738819   13682
---
Signif. codes:  0 `***' 0.001 `**' 0.01 `*' 0.05 `.' 0.1 ` ' 1
```

and for items:

```
> summary(aov(rt ~ verb * attachment
    + Error(item/(verb *attachment)), sp.1.item))

Error: item
          Df Sum Sq Mean Sq F value Pr(>F)
Residuals 19 203631   10717

Error: item:verb
          Df Sum Sq Mean Sq F value Pr(>F)
verb       1  21181   21181  3.5482  0.075 .
Residuals 19 113419    5969
---
Signif. codes:  0 `***' 0.001 `**' 0.01 `*' 0.05 `.' 0.1 ` ' 1

Error: item:attachment
           Df Sum Sq Mean Sq F value Pr(>F)
attachment  1    721     721   0.093 0.7637
Residuals  19 147299    7753

Error: item:verb:attachment
                Df Sum Sq Mean Sq F value  Pr(>F)
verb:attachment  1  38211   38211  5.4335 0.03092 *
Residuals       19 133615    7032
---
Signif. codes:  0 `***' 0.001 `**' 0.01 `*' 0.05 `.' 0.1 ` ' 1
```

Fortunately, the by-subjects and by-items analysis yield largely similar results: they both point towards (a) a significant main effect of verb type; and (b) more interestingly, a significant interaction between verb type and attachment level. To interpret these, we need to look at the means of each condition. It is conventional in psychological experimentation to show the condition means from the aggregated data for the by-subjects analysis:

```
> with(sp.1.subj,tapply(rt,list(verb),mean))
      IC    nonIC
452.2940 482.0567
> with(sp.1.subj,tapply(rt,list(verb,attachment),mean))
          high      low
IC    430.4316 474.1565
nonIC 501.4824 462.6309
```

The first spillover region was read more quickly in the implicit-causality verb condition than in the non-IC verb condition. The interaction was a CROSSOVER INTERACTION: in the high

attachment conditions, the first spillover region was read more quickly for IC verbs than for non-IC verbs; but for the low attachment conditions, reading was faster for non-IC verbs than for IC verbs.

We interpreted this result to indicate that IC verbs do indeed facilitate processing of high-attaching RCs, to the extent that this becomes the preferred attachment level.

6.7 Other generalized linear models

Recall that we've looked at linear models, which specify a conditional probability density $P(Y|X)$ of the form

$$Y = \alpha + \beta_1 X_1 + \cdots + \beta_n X_n + \epsilon \tag{6.20}$$

Linear models thus assume that the only stochastic part of the data is the normally-distributed noise ϵ around the predicted mean. Yet many—probably most—types of data do not meet this assumption at all. These include:

- Continuous data in which noise is not normally distributed;
- Categorical data, where the outcome is one of a number of discrete classes;
- Count data, in which the outcome is restricted to non-negative integers.

By choosing different link and noise functions, you can help ensure that your statistical model is as faithful a reflection of possible of the major patterns in the data you are interested in representing. In the remainder of this chapter, we look at two other major classes of GLM: LOGIT and LOG-LINEAR models.

6.7.1 Logit models

Suppose we want a GLM that models binomially distributed data from n trials. We will use a slightly different formulation of the binomial distribution from what that of Chapter 2: instead of viewing the response as the number of successful trials r, we view the response as the *proportion* of successful trials $\frac{r}{n}$; call this Y. The mean proportion for binomial distribution is simply the success parameter π; hence, π is also the predicted mean μ of our GLM. This gives us enough information to specify precisely the resulting model (from now on we replace μ with π for simplicity):

$$P(Y = y; \pi) = \binom{n}{yn} \pi^{ny} (1-\pi)^{n(1-y)} \qquad \text{(or equivalently, replace } \mu \text{ with } \pi\text{)} \tag{6.21}$$

which is just the binomial distribution from back in Equation 3.8.

This is the second part of designing a GLM: choosing the distribution over Y, given the mean μ (Equation 6.1). Having done this means that we have placed ourselves in the BINOMIAL GLM FAMILY. The other part of specifying our GLM is choosing a relationship between the linear predictor η and the mean μ. Unlike the case with the classical linear model, the identity link function is not a possibility, because η can potentially be any real number, whereas the mean proportion μ of successes can only vary between 0 and 1. There are many link functions that can be chosen to make this mapping valid, but here we will use the most popular link function, the LOGIT transform:[8]

$$\log \frac{\pi}{1-\pi} = \eta \tag{6.22}$$

or equivalently the INVERSE LOGIT transform:

$$\pi = \frac{e^{\eta}}{1+e^{\eta}} \tag{6.23}$$

Figure 6.14 shows the relationship between η and π induced by the logit transform

When we insert the full form of the linear predictor from Equation (6.1) back in, we arrive at the final formula for logit models:

$$\pi = \frac{e^{\alpha+\beta_1 X_1+\cdots+\beta_n X_n}}{1+e^{\alpha+\beta_1 X_1+\cdots+\beta_n X_n}} \tag{6.24}$$

Fitting a logit model is also called LOGISTIC REGRESSION.

6.7.2 Fitting a simple logistic regression model

The most common criterion by which a logistic regression model for a dataset is fitted is exactly the way that we chose the parameter estimates for a linear regression model: the method of maximum likelihood. That is, we choose the parameter estimates that give our dataset the highest likelihood.

We will give a simple example using the `dative` dataset. The response variable here is whether the recipient was realized as an NP (i.e., the double-object construction) or as a PP (i.e., the prepositional object construction). This corresponds to the `RealizationOfRecipient` variable in the dataset. There are several options in `R` for fitting basic logistic regression models, including `glm()` in the `stats` package and `lrm()` in the `Design` package. In this case we will use `lrm()`. We will start with a simple study of the effect of recipient pronominality on the dative alternation. Before fitting a model, we examine a contingency table of the outcomes of the two factors:

[8] Two other popular link functions for binomial GLMs are the PROBIT link and the COMPLEMENTARY LOG-LOG link. See Venables and Ripley (2002, Chapter 7) for more details.

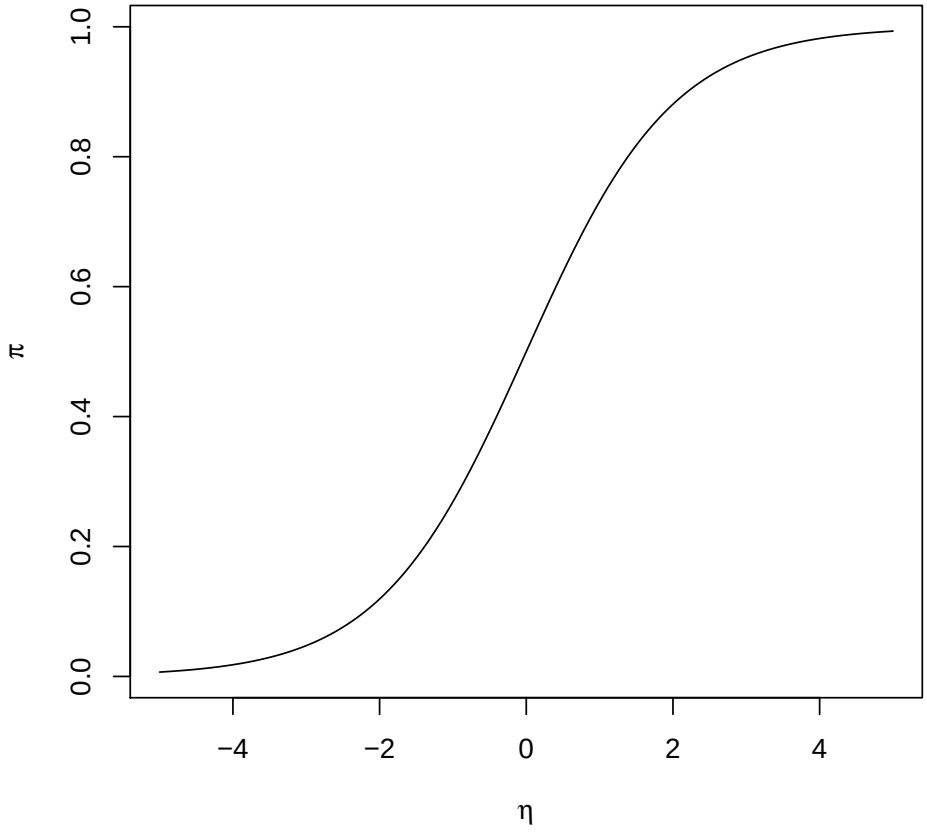


Figure 6.14: The logit transform

```
> library(languageR)
> xtabs(~ PronomOfRec + RealizationOfRecipient,dative)

               RealizationOfRecipient
PronomOfRec       NP   PP
  nonpronominal  600  629
  pronominal    1814  220
```

So sentences with nonpronominal recipients are realized roughly equally often with DO and PO constructions; but sentences with pronominal recipients are recognized nearly 90% of the time with the DO construction. We expect our model to be able to encode these findings.

It is now time to construct the model. To be totally explicit, we will choose ourselves which realization of the recipient counts as a "success" and which counts as a "failure" (although `lrm()` will silently make its own decision if given a factor as a response). In addition,

our predictor variable is a factor, so we need to use dummy-variable encoding; we will satisfice with the R default of taking the alphabetically first factor level, nonpronominal, as the baseline level.

```
> library(rms)
> response <- ifelse(dative$RealizationOfRecipient=="PP",
+                    1,0) # code PO realization as success, DO as failure
> lrm(response ~ PronomOfRec, dative)
```

The thing to pay attention to for now is the estimated coefficients for the intercept and the dummy indicator variable for a pronominal recipient. We can use these coefficients to determine the values of the linear predictor η and the predicted mean success rate p using Equations (6.1) and (6.24):

$$\eta_{--} = 0.0472 + (-2.1569) \times 0 \quad = 0.0472 \quad \text{(non-pronominal receipient)} \tag{6.25}$$

$$\eta_{+} = 0.0472 + (-2.1569) \times 1 \quad = -2.1097 \quad \text{(pronominal recipient)} \tag{6.26}$$

$$p_{\text{nonpron}} = \frac{e^{0.0472}}{1 + e^{0.0472}} \quad = 0.512 \tag{6.27}$$

$$p_{\text{pron}} = \frac{e^{-2.1097}}{1 + e^{-2.1097}} \quad = 0.108 \tag{6.28}$$

When we check these predicted probabilities of PO realization for nonpronominal and pronominal recipients, we see that they are equal to the proportions seen in the corresponding rows of the cross-tabulation we calculated above: $\frac{629}{629+600} = 0.518$ and $\frac{220}{220+1814} = 0.108$. This is exactly the expected behavior, because (a) we have two parameters in our model, α and β_1, which is enough to encode an arbitrary predicted mean for each of the cells in our current representation of the dataset; and (b) as we have seen before (Section 4.3.1), the maximum-likelihood estimate for a binomial distribution is the relative-frequency estimate—that is, the observed proportion of successes.

6.7.3 Multiple logistic regression

Just as we were able to perform multiple linear regression for a linear model with multiple predictors, we can perform multiple logistic regression. Suppose that we want to take into account pronominality of both recipient and theme. First we conduct a complete cross-tabulation and get proportions of PO realization for each combination of pronominality status:

```
> tab <- xtabs(~ RealizationOfRecipient + PronomOfRec + PronomOfTheme, dative)
> tab

, , PronomOfTheme = nonpronominal
```

```
                        PronomOfRec
RealizationOfRecipient nonpronominal pronominal
                    NP           583       1676
                    PP           512         71

, , PronomOfTheme = pronominal

                        PronomOfRec
RealizationOfRecipient nonpronominal pronominal
                    NP            17        138
                    PP           117        149
```

```
> apply(tab,c(2,3),function(x) x[2] / sum(x))

               PronomOfTheme
PronomOfRec     nonpronominal pronominal
  nonpronominal     0.4675799  0.8731343
  pronominal        0.0406411  0.5191638
```

Pronominality of the theme consistently increases the probability of PO realization; pronominality of the recipient consistently increases the probability of DO realization.

We can construct a logit model with independent effects of theme and recipient pronominality as follows:

```
> library(rms)
> dative.lrm <- lrm(response ~ PronomOfRec + PronomOfTheme, dative)
> dative.lrm
```

And once again, we can calculate the predicted mean success rates for each of the four combinations of predictor variables:

Recipient	Theme	η	$\hat{p}$
nonpron	nonpron	-0.1644	0.459
pron	nonpron	-3.0314	0.046
nonpron	pron	2.8125	0.943
pron	pron	-0.0545	0.486

In this case, note the predicted proportions of success are not the same as the observed proportions in each of the four cells. This is sensible – we cannot fit four arbitrary means with only three parameters. If we added in an interactive term, we would be able to fit four arbitrary means, and the resulting predicted proportions would be the observed proportions for the four different cells.

6.7.4 Transforming predictor variables

TODO

Predictor	Coefficient	Factor Weight	Multiplicative effect on odds
Intercept	-0.1644	0.4590	0.8484
Pronominal Recipient	-2.8670	0.0538	0.0569
Pronominal Theme	2.9769	0.9515	19.627

Table 6.2: Logistic regression coefficients and corresponding factor weights for each predictor variable in the `dative` dataset.

6.7.5 Multiplicativity of the odds

Let us consider the case of a dative construction in which both the recipient and theme are encoded with pronouns. In this situation, both the dummy indicator variables (indicating that the theme and recipient are pronouns) have a value of 1, and thus the linear predictor consists of the sum of three terms. From Equation (6.22), we can take the exponent of both sides and write

$$\frac{p}{1-p} = e^{\alpha+\beta_1+\beta_2} \tag{6.29}$$

$$= e^{\alpha} e^{\beta_1} e^{\beta_2} \tag{6.30}$$

The ratio $\frac{p}{1-p}$ is the ODDS OF SUCCESS, and in logit models the effect of any predictor variable on the response variable is multiplicative in the odds of success. If a predictor has coefficent β in a logit model, then a unit of that predictor has a multiplicative effect of e^{β} on the odds of success.

Unlike the raw coefficient β, the quantity e^{β} is not linearly symmetric—it falls in the range $(0, \infty)$. However, we can also perform the full REVERSE LOGIT TRANSFORM of Equation (6.23), mapping β to $\frac{e^{\beta}}{1+e^{\beta}}$ which ranges between zero and 1, and is linearly symmetric around 0.5. The use of logistic regression with the reverse logit transform has been used in quantitative sociolinguistics since Cedergren and Sankoff (1974) (see also Sankoff and Labov, 1979), and is still in widespread use in that field. In quantitative sociolinguistics, the use of logistic regression is often called VARBRUL (variable rule) analysis, and the parameter estimates are reported in the reverse logit transform, typically being called FACTOR WEIGHTS.

Tables 6.2 and 6.3 show the relationship between the components of the linear predictor, the components of the multiplicative odds, and the resulting predictions for each possible combination of our predictor variables.

6.8 Confidence intervals and model comparison in logit models

We'll close our introduction to logistic regression with discussion of confidence intervals and model comparison.

Recip.	Theme	Linear Predictor	Multiplicative odds	P(PO)
–pron	–pron	-0.16	0.8484	0.46
+pron	–pron	$-0.16 - 2.87 = -3.03$	$0.85 \times 0.06 = 0.049$	0.046
–pron	+pron	$-0.16 + 2.98 = 2.81$	$0.85 \times 19.6 = 16.7$	0.94
+pron	+pron	$-0.16 - 2.87 + 2.98 = -0.05$	$0.85 \times 0.06 \times 19.63 = 0.947$	0.49

Table 6.3: Linear predictor, multiplicative odds, and predicted values for each combination of recipient and theme pronominality in the `dative` dataset. In each case, the linear predictor is the log of the multiplicative odds.

6.8.1 Frequentist Confidence intervals for logit models

When there are a relatively large number of observations in comparison with the number of parameters estimated, the standardized deviation of the MLE for a logit model parameter θ is approximately normally distributed:

$$\frac{\hat{\theta} - \theta}{\text{StdErr}(\hat{\theta})} \sim \mathcal{N}(0,1) \quad \text{(approximately)} \tag{6.31}$$

This is called the Wald statistic[9]. This is very similar to the case where we used the t statistic for confidence intervals in classic linear regression (Section 6.4; remember that once the t distribution has a fair number of degrees of freedom, it basically looks like a standard normal distribution). If we look again at the output of the logit model we fitted in the previous section, we see the standard error, which allows us to construct confidence intervals on our model parameters.

```
                          Coef    S.E.    Wald Z P
Intercept                 -0.1644 0.05999  -2.74 0.0061
PronomOfRec=pronominal    -2.8670 0.12278 -23.35 0.0000
PronomOfTheme=pronominal   2.9769 0.15069  19.75 0.0000
```

Following the exact same logic as in Section 6.4, we find that the 95% confidence interval for each parameter β_i is bounded below by $\hat{\beta}_i - 1.96SE(\hat{\beta}_i)$, and bounded below by $\hat{\beta}_i + 1.96SE(\hat{\beta}_i)$. This gives us the following bounds:

```
a  -0.1673002  0.2762782
b1 -3.1076138 -2.6263766
b2  2.6815861  3.2722645
```

The Wald statistic can also be used for a frequentist test on the null hypothesis that an individual model parameter is 0. This is the source of the p-values given for the model parameters above.

[9] It is also sometimes called the Wald Z statistic, because of the convention that standard normal variables are often denoted with a Z, and the Wald statistic is distributed approximately as a standard normal.

6.8.2 Bayesian confidence intervals for logit models

In order to construct a Bayesian confidence interval for a logit model, we need to choose prior distributions on the weights α and $\{\beta_i\}$ that go into the linear predictor (Equation (6.1)), and then use sampling-based techniques (Section 4.5). As a simple example, let us take the multiple logistic regression of Section 6.7.3. The model has three parameters; we will express agnosticism about likely parameter values by using a diffuse prior. Specifically, we choose a normally-distributed prior with large variance for each parameter:

$$\begin{aligned}\alpha &\sim \mathcal{N}(0, 10000)\\ \beta_1 &\sim \mathcal{N}(0, 10000)\\ \beta_2 &\sim \mathcal{N}(0, 10000)\end{aligned}$$

With sampling we can recover 95% HPD confidence intervals (Section 5.1) for the parameters:

```
a  -0.1951817  0.2278135
b1 -3.1047508 -2.6440788
b2  2.7211833  3.2962744
```

There is large agreement between the frequentist and Bayesian confidence intervals in this case. A different choice of prior would change the HPD confidence intervals, but we have a lot of data relative to the complexity of the model we're trying to estimate, so the data dominates the prior in our case.

6.8.3 Model comparison

Just as in the analysis of variance, we are often interested in conducting tests of the hypothesis that introducing *several* model parameters simultaneously leads to a better overall model. In this case, we cannot simply use a single Wald statistic for hypothesis testing. Instead, the most common approach is to use the LIKELIHOOD-RATIO TEST, first introduced in Section 5.4.4. To review, the quantity

$$G^2 = 2\left[\log \text{Lik}_{M_1}(\boldsymbol{y}) - \log \text{Lik}_{M_0}(\boldsymbol{y})\right] \tag{6.32}$$

is approximately distributed as a χ^2_k random variable, where k is the difference in the number of free parameters between M_1 and M_0.

As an example of using the likelihood ratio test, we will hypothesize a model in which pronominality of theme and recipient both still have additive effects but that these effects may vary depending on the modality (spoken versus written) of the dataset. We fit this model and our modality-independent model using `glm()`, and use `anova()` to calculate the likelihood ratio:

```
> m.0 <- glm(response ~ PronomOfRec + PronomOfTheme,dative,family="binomial")
> m.A <- glm(response ~ PronomOfRec*Modality + PronomOfTheme*Modality,dative,family="b
> anova(m.0,m.A)
```

We can look up the p-value of this deviance result in the χ^2_3 distribution:

```
> 1-pchisq(9.07,3)

[1] 0.02837453
```

Thus there is some evidence that we should reject a model that doesn't include modality-specific effects of recipient and theme pronominality.

6.8.4 Dealing with symmetric outcomes

In the study of language, there are some types of categorical outcomes that are symmetrical in a way that can make it difficult to see how to properly assign values to explanatory variables. Consider, for example, the study of word order in the coordination of like categories. Suppose we are interested in the joint effect of word frequency and word length on ordering preferences in word pairs conjoined by *and* (called, appropriately enough, BINOMIALS), and our observation is the phrase *evasive and shifty*. The word *evasive* is longer (has more syllables) than *shifty*, but it is less frequent as well. How do we characterize these independent variables, and do we call the outcome a "success" or a "failure"?

Fortunately, we can address this problem by noticing that the central issue is really not whether *evasive and shifty* is a success or failure; the central issue is, rather, the pattern of how the explanatory variables are aligned with observed orderings. We now cover an example of how to deal with this problem taken from Benor and Levy (2006), a corpus study of English binomials. We will restrict ourselves to word pairs occurring exactly once in Benor and Levy's dataset, and look at the effects of perceptual markedness, weight (in terms of number of syllables), and word frequency. The covariates in the model are thus comparative properties—for example, whether one of the words denotes a property that is more perceptually salient, or which of the words is more frequent (also *chanted*). We can code each property P_i as a quantitative variable X_i by arbitrarily choosing an alignment direction for the property, and giving the binomial a positive value for the X_i if P_i is aligned with the binomial, a negative value of equal magnitude if P_i is aligned against the binomial, and zero if P_i is inactive. The logit response variable now serves as a dummy variable—it is always a "success". For perceptual markedness, word length, and word frequency we choose the following alignments:

- Perceptual markedness is positive if the first word in the binomial is more perceptually salient than the last word;
- Word length (in number of syllables) is positive if the last word has more syllables than the first word;

- Word frequency is positive if the first word is more frequent than the last word.

These aligned properties can be thought of as SOFT (or GRADIENT) CONSTRAINTS in the sense of Optimality Theory and similar frameworks, with statistical model fitting as a principled means of investigating whether the constraints tend not to be violated, and how strong such a tendency may be. A few such observations in the dataset thus coded are:

Word.Pair	Percept	Freq	Syl	Response
chanted and chortled	1	1	0	1
real and vibrant	0	-1	-1	1
evasive and shifty	0	1	-1	1

Note that *chanted and chortled* has a perceptual markedness value of 1, since chortling is a quieter action; *vibrant and real* has a response of 0 since it is observed in the opposite ordering; and the `Syl` covariate value for *evasive and shifty* is -1 because *evasive* has more syllables than *shifty*.

It would be nonsensical to use an intercept when fitting a model to this dataset: setting the intercept arbitrarily high, and the other model parameters to zero, would be the best fit. If, however, we remove the intercept from the model, the model expresses the tendency of each covariate to align with the binomial ordering:

```
> dat <- read.table("../data/binomials_data/single_count_binomials.txt",header=T,fill=
> summary(glm(Response ~ Percept + Syl + Freq - 1, dat,family="binomial"))$coef

         Estimate Std. Error  z value    Pr(>|z|)
Percept 1.1771339  0.5158658 2.281861 0.022497563
Syl     0.4926385  0.1554392 3.169332 0.001527896
Freq    0.3660976  0.1238079 2.956981 0.003106676
```

All three constraints have positive coefficients, indicating significant alignment with binomial ordering: the constraints do indeed tend not to be violated. It's worth noting that even though perceptual markedness is estimated to be the strongest of the three constraints (largest coefficient), its standard error is also the largest: this is because the constraint is active (non-zero) least often in the dataset.

6.9 Log-linear and multinomial logit models

A class of GLM very closely related to logit models is LOG-LINEAR MODELS. Log-linear models choose the log as the link function:

$$l(\mu) = \log \mu = \eta \qquad\qquad \mu = e^{\eta} \tag{6.33}$$

and the Poisson distribution, which ranges over non-negative integers, as the noise function:

$$P(Y = y; \mu) = e^{-\mu}\frac{\mu^y}{y!} \quad (y = 0, 1, \dots) \tag{6.34}$$

When used to model count data, this type of GLM is often called a POISSON MODEL or POISSON REGRESSION.

In linguistics, the log-linear model is most often used to model probability distributions over multi-class outcomes. Suppose that for there are M classes of possible outcomes, each with its own linear predictor η_i and random variable Y_i. If we conditionalize on the total count of all classes being 1, then the only available count outcomes for each class are 0 and 1, with probabilities:

$$P(Y_i = 1; \mu_i = e^{\eta_i}) = e^{\mu_i}e_i^{\eta} \qquad P(Y_i = 0; \mu_i = e^{\eta_i}) = e^{\mu_i} \tag{6.35}$$

and the joint probability of the single observation falling into class i is

$$\begin{aligned} P(Y_i = 1, \{Y_{j\neq i}\} = 0) &= \frac{e^{\mu_i}e_i^{\eta}\prod_{j\neq i}e^{\mu_j}}{\sum_{i'}e^{\mu_{i'}}e_{i'}^{\eta}\prod_{j\neq i'}e^{\mu_j}} \\ &= \frac{e_i^{\eta}\prod_j e^{\mu_j}}{\sum_{i'}e_{i'}^{\eta}\prod_j e^{\mu_j}} \\ &= \frac{e_i^{\eta}\prod_j e^{\mu_j}}{\prod_j e^{\mu_j}\sum_{i'}e_{i'}^{\eta}} \\ P(Y_i = 1, \{Y_{j\neq i}\} = 0) &= \frac{e_i^{\eta}}{\sum_{i'}e_{i'}^{\eta}} \end{aligned} \tag{6.36}$$

When we are thinking of a log-linear model as defining the probability distribution over which class each observation falls into, it is often useful to define the class-specific success probabilities $\pi_i \stackrel{\text{def}}{=} P(Y_i = 1, \{Y_{j\neq i}\} = 0)$. This allows us to think of a log-linear model as using a MULTINOMIAL noise distribution (Section 3.4.1).

Expressive subsumption of (multinomial) logit models by log-linear models*

Basic logit models are used to specify probability distributions over outcomes in two classes (the "failure" class 0 and the "success" class 1). Log-linear models can be used to specify probability distributions over outcomes in any number of classes. For a two-class log-linear model, the success probability for class 1 is (Equation (6.24)):

$$\pi_1 = \frac{e^{\alpha_1+\beta_{1,1}X_1+\cdots+\beta_{1,n}X_n}}{e^{\alpha_0+\beta_{0,1}X_1+\cdots+\beta_{0,n}X_n} + e^{\alpha_1+\beta_{1,1}X_1+\cdots+\beta_{1,n}X_n}} \tag{6.37}$$

$$\tag{6.38}$$

If we divide both the numerator and denominator by $e^{\alpha_0+\beta_{0,1}X_1+\cdots+\beta_{0,n}X_n}$, we get

$$\pi_1 = \frac{e^{(\alpha_1-\alpha_0)+(\beta_{1,1}-\beta_{0,1})X_1+\cdots+(\beta_{1,n}-\beta_{0,n})X_n}}{1+e^{(\alpha_1-\alpha_0)+(\beta_{1,1}-\beta_{0,1})X_1+\cdots+(\beta_{1,n}-\beta_{0,n})X_n}} \tag{6.39}$$

This is significant because the model now has exactly the same form as the logit model (Equation (6.24), except that we have parameters of the form $(\alpha_1-\alpha_0)$ and $(\beta_{1,i}-\beta_{0,i})$ rather than α and β_i respectively. This means that log-linear models EXPRESSIVELY SUBSUME logit models: any logit model can also be expressed by some log-linear model. Because of this, when maximum-likelihood estimation is used to fit a logit model and a log-linear model with the same set of variables, the resulting models will determine the same probability distribution over class proportions. There are only three differences:

1. The log-linear model can also predict the total number of observations.
2. The logit model has fewer parameters.
3. When techniques other than MLE (e.g., Bayesian inference marginalizing over model parameters) are used, the models will generally yield different predictive distributions.

6.10 Log-linear models of phonotactics

We introduce the framework of LOG-LINEAR or MAXIMUM-ENTROPY models by turning to the linguistic problem of phonotactics. A speaker's PHONOTACTIC KNOWLEDGE is their knowledge of what logically possible sound sequences constitute legitimate potential lexical items in her language. In the probabilistic setting, phonotactic knowledge can be expressed as a probability distribution over possible sound sequences. A good probabilistic model of phonotactics assigns low probability to sequences that are not possible lexical items in the language, and higher probability to sequences that are possible lexical items. A categorical characterization of sound sequences as being either impossible or possible in the language could be identified with respective assignment of zero or non-zero probability in the model. The classic example of such a distinction is that whereas native English speakers judge the non-word *blick* [blɪk] to be a possible word of English, they judge the non-word *bnick* [bnɪk] not to be a possible word of English. [citations here] However, probabilistic phonotactic models have the further advantage of being able to make *gradient* distinctions between forms that that are "more" or "less" appropriate as possible lexical items.

Construct a probabilistic phonotactic model entails putting a probability distribution over the possible sound sequences of the language. There are many approaches that could be taken to this problem; here we examine two different approaches in the context of modeling one of the best-studied problems in phonotactics: constrants on of English *word onsets*—the consonant sequences with which words begin. For simplicity, we restrict discussion here to onsets consisting of exactly two segments drawn from a subset of the inventory of English consonants, namely [f], [v], [s], [z], [sh], [p], [b], [t], [d], [l], and [r]. Table 6.4 presents a list

of the two-segment word onsets which can be constructed from these segments and which are found in the Carnegie Mellon Pronouncing Dictionary of English (Weide, 1998). Of the 121 logically possible onsets, only 30 are found. They are highly disparate in frequency, and most of the rarest (including everything on the right-hand side of the table except for [sf] as in *sphere*) are found only in loan words. In the study of phonotactics; there is some question as to exactly what counts as an "attested" sequence in the lexicon; for present purposes, I will refer to the twelve most frequent onsets plus [sf] as *unambiguously attested*.

We begin the problem of estimating a probability distribution over English two-segment onsets using simple tools from Chapters 2 and 4: multinomial models and relative frequency estimation. Let us explicitly represent the sequence structure of an English onset x_1x_2 as a $\#_L x_1 x_2 \#_R$, where $\#_L$ represents the left edge of the onset and $\#_R$ represents the right edge of the onset. Every two-segment onset can be thought of as a linearly ordered joint event comprised of the left edge, the first segment, the second segment, and the right edge. We can use the chain rule to represent this joint event as a product of conditional probabilities:

$$P(\#_L x_1 x_2 \#_R) = P(\#_L)P(x_1|\#_L)P(x_2|\#_L x_1)P(\#_R|\#_L x_1 x_2) \tag{6.40}$$

The left edge is obligatory, so that $P(\#_L) = 1$; and since we are restricting our attention to two-segment onsets, the right edge is also obligatory when it occurs, so that $P(\#_R|\#_L x_1 x_2) = 1$. We can thus rewrite Equation 6.40 as

$$P(\#_L x_1 x_2 \#_R) = P(x_1|\#_L)P(x_2|\#_L x_1) \tag{6.41}$$

We consider three possible methods for estimating this probability distribution from our data:

1. Treat each complete onset $\#_L x_1 x_2 \#_R$ as a single outcome in a multinomial model, with 121 possible outcomes; the problem then becomes estimating the parameters of this single multinomial from our data. As described in Chapter XXX, the maximum likelihood estimate for multinomials is also the relative frequency estimate, so the probability assigned to an onset in this model is directly proportional to the onset's frequency of occurrence.

   With this model it is also useful to note that for any segment x, if the event y immediately preceding it is not the left edge $\#_L$, then y itself is preceded by $\#_L$. This means that $P(x_2|\#_L x_1) = P(x_2|x_1)$. This allows us to rewrite Equation **??**:

   $$P(\#_L x_1 x_2 \#_R) = P(x_1|\#_L)P(x_2|x_1) \tag{6.42}$$

   Hence this model can also be thought of as a *bigram* model in which the probability of an event is, given the immediately preceding event, conditionally independent on everything earlier in the sequence. Note here that if we have N possible segments, we must fit $N + 1$ multinomial distributions.

2. We can introduce the strong independence assumption that the probability of a segment is entirely independent of its context: $P(x_i|x_{1\ldots i-1}) = P(x_i)$. This is a *unigram* model, giving

$$P(\#_L x_1 x_2 \#_R) = P(x_1)P(x_2) \tag{6.43}$$

   Here we need to fit only one multinomial distribution.

3. We can introduce the somewhat weaker independence assumption that the probability of a segment depends on whether it is the first or second segment in the onset, but not on what other segments occur in the onset.

$$P(\#_L x_1 x_2 \#_R) = P(x_1|\#_L)P(x_2|\#_L\_) \tag{6.44}$$

   where _ indicates the presence of *any* segment. We might call this a *positional unigram* model to emphasize the position-dependence. This model requires that we fit two multinomial distributions.

Columns 3–5 of Table 6.4 show estimated probabilities for attested onsets in these three models. Major differences among the models are immediately apparent. Among unambiguously attested onsets, [st] is much more probable in the bigram model than in either unigram model; [tr] and [sf] are much more probable in the unigram model than in the other two models; and [sp] is much less probable in the positional unigram model (see also Exercise 6.12).

A substantive claim about the nature of phonotactic knowledge put forth by researchers including Hayes and Wilson (2007) as well as XXX is that probabilistic models which do a good job accounting for the distribution of segment sequences in the lexicon should also be able to accurately predict native-speaker judgments of the acceptability of "nonce" words (sequences that are not actually words) such as *blick* and *bnick* as potential words of the language. Challenges for this approach become apparent when one examines existing datasets of native-speaker nonce-word judgments. For example, Scholes (1966) conducted a study of English onsets in nonce-word positions and uncovered regularities which seem challenging for the multinomial models we considered above. Among other results, Scholes found the following differences between onsets in the frequency with which nonce words containing them were judged acceptable:

(4) [br] > [vr] > [sr], [ml] > [sf] > [zl], [fs] > [zv]

The fact that the unattested onset [ml] leads to greater acceptability than the unambiguously attested onset [sf] clearly indicates that English phonotactic knowledge involves *some* sorts of generalization beyond the raw contents of the lexicon; hence the bigram model of Table 6.4 is

Segment	Freq	P_{unigram}	P_{unipos}	P_{bigram}	Segment	Freq	P_{unigram}	P_{unipos}	P_{bigram}
st	1784	0.0817	0.0498	0.1755	vl	15	0.0011	0.0006	0.0015
br	1500	0.1122	0.112	0.1476	vr	14	0.003	0.0016	0.0014
pr	1494	0.1405	0.1044	0.147	sf	12	0.0395	0.0003	0.0012
tr	1093	0.1555	0.0599	0.1075	sr	10	0.1553	0.154	0.001
fr	819	0.0751	0.0745	0.0806	zl	9	0.0003	0.0003	0.0009
sp	674	0.0738	0.0188	0.0663	zb	4	0.0003	0.0	0.0004
bl	593	0.0428	0.0427	0.0583	sht	4	0.0067	0.0041	0.0004
fl	572	0.0286	0.0284	0.0563	dv	3	0.0002	0.0001	0.0003
pl	458	0.0535	0.0398	0.0451	zv	2	0.0	0.0	0.0002
dr	441	0.0239	0.0239	0.0434	tv	2	0.0016	0.0003	0.0002
sl	379	0.0592	0.0587	0.0373	dz	2	0.0001	0.0	0.0002
shr	155	0.0128	0.0128	0.0152	tl	1	0.0593	0.0228	0.0001
shl	79	0.0049	0.0049	0.0078	shv	1	0.0001	0.0001	0.0001
ts	23	0.0817	0.0003	0.0023	sb	1	0.059	0.0001	0.0001
sv	19	0.0016	0.0008	0.0019	fs	1	0.0395	0.0003	0.0001

Table 6.4: The attested two-segment onsets of English, based on the segments [f], [v], [s], [z], [sh], [p], [b], [t], [d], [l], and [r], sorted by onset frequency. Probabilities are relative frequency estimates, rounded to 4 decimal places.

unacceptable. At the same time, however, [br] is clearly preferred to [sr], indicating that both unigram models are too simplistic. One might consider a mixture model which interpolates between bigram and unigram models. The difficulty with this approach, however, is that no simple mixture is obvious that would achieve the preferences necessary. The preference of [sr] over [sf] would seem to indicate that unigrams should receive considerable weighting; but the preference of [vr] over [sr] would be undermined by heavy unigram weighting.

To motivate our next development, let us consider specifically the mystery of the relative acceptability of [vr] and [sr] among onsets that are not unambiguously attested. A key piece of information we have not yet considered is the phonological substructure of the segments in question. There are many ways of representing phonological substructure, but one straightforward approach for consonants is a representation that decomposes each segment into three PHONOLOGICAL FEATURES: its PLACE of articulation, MANNER of articulation, and VOICING [refs]. The value of each of these features for each consonant used in our current example can be found in Table 6.5. The set of segments picked out by some conjunction of phonological features or their exclusion is often called a NATURAL CLASS. For example, among the consonants currently under consideration, the phonological feature [+labial] picks out the natural class {[p],[b]}; the feature [-stop] picks out {[s],[z],[f],[v],[sh],[r],[l]}; the phonological feature conjunction [+labiodental,-voiced] picks out the natural class {[f]}; and so forth.

6.10.1 Log-linear models

With multinomial models, it is not obvious how one might take advantage of the featural decomposition of segments in constructing a probability distribution over the discrete

Place	Labial [p],[b]	Labiodental [f],[v]	Alveolar [s],[z],[t],[d],[r],[l]	Alveopalatal [sh]	Velar [k],[g]
Manner	Stop [p],[b],[t],[d],[k],[g]	Fricative [s],[z],[f],[v],[sh]	Liquid [r],[l]		
Voicing	Voiced [b],[d],[g],[v],[z],[r],[l]	Unvoiced [p],[t],[k],[f],[s],[sh]			

Table 6.5: Simple phonological decomposition of the consonants used in Table 6.4

set of possible phoneme sequences. We now turn to a modeling framework that allows such decompositions to be taken into account in modeling such discrete random variables: the framework of LOG-LINEAR models. In this framework, which is intimately related to the logistic-regression models covered previously (see Section XXX), the goal is once again modeling conditional probability distributions of the form $P(Y|X)$, where Y ranges over a countable set of response *classes* $\{y_i\}$. Unlike the cases covered previously in this chapter, however, the log-linear framework is relatively agnostic to the representation of X itself. What is crucial, however, is the presence of a finite set of FEATURE FUNCTIONS $f_j(X, Y)$, each of which maps every possible paired instance of X and Y to a real number. Taken in aggregate, the feature functions map each possible response class y_i to a FEATURE VECTOR $\langle f_1(x, y_i), f_2(x, y_i), \ldots, f_n(x, y_i)\rangle$. Finally, each feature function f_j has a corresponding parameter λ_j. Given a collection of feature functions, corresponding parameter values, and a value x for the conditioning random variable X, the conditional probability of each class y_i is defined to be:

$$P(Y = y_i|X = x) = \frac{1}{Z} \exp\left[\sum_j \lambda_j f_j(x, y_i)\right] \tag{6.45}$$

where Z is a normalizing term ensuring that the probability distribution is proper.

In order to translate our phonotactic learning problem into the log-linear framework, we must identify what serves as the conditioning variable X, the response Y, and what the feature functions f_i are. Since we are putting a probability distribution over logically possible English onsets, the response must be which onset found in a (possible) lexical item. The feature functions should correspond to the phonological features identified earlier.[10] Finally, since we are only trying to fit a single probability distribution over possible English onsets that is not dependent on any other information, whatever we take the conditioning variable X to be, our feature functions will not depend on it; so we can simplify our problem somewhat so that it involves fitting the distribution $P(Y)$ using feature functions $f_j(Y)$ with

[10]Note that the term *feature* is being used in two different here: on the one hand, as part of a decomposition of individual phonological segments, on the other hand as a function that will apply to entire onsets and which is associated with a parameter in the log-linear model. Although phonological features could be used directly as features in the log-linear model, the space of possible log-linear model features is much richer than this.

parameters λ_j (also called FEATURE WEIGHTS), with the functional form of the probability distribution as follows:

$$P(Y = y_i) = \frac{1}{Z} \exp\left[\sum_j \lambda_j f_j(y_i)\right] \tag{6.46}$$

Simple log-linear models of English onsets

What remains is for us to choose the feature functions for our phonotactic model. This choice of feature functions determines what generalizations can be directly encoded in our model. As a first, highly oversimplified model, we will construct exactly one feature function for each natural class specifiable by a single phonological feature of *manner* or *voicing*. This feature function will return the number of segments in that natural class contained in the onset. That is,

$$f_j(y_i) = \begin{cases} 2 & \text{if both segments in onset } i \text{ belong to the } j\text{-th natural class;} \\ 1 & \text{if only one segment in onset } i \text{ belongs to the } j\text{-th natural class;} \\ 0 & \text{if neither segment in onset } i \text{ belongs to the } j\text{-th natural class.} \end{cases} \tag{6.47}$$

There are four manner/voicing phonological features for our segment inventory; each can be negated, giving eight natural classes.[11] Each onset is thus mapped to an eight-dimensional feature vector. In the onset [sr], for example we would have the following counts:

Natural class	Matching segments in [sr]	Natural class	Matching segments in [sr]
[+stop]	0	[-stop]	2
[+fric]	1	[-fric]	1
[+liquid]	1	[-liquid]	1
[+voiced]	1	[-voiced]	1

so that the feature vector for [sr] in this model would be $\langle 0, 2, 1, 1, 1, 1, 1, 1\rangle$.

What remains is for us to fit the parameter values $\lambda_1, \ldots, \lambda_8$ corresponding to each of these features. For a simple model like this, in which there are relatively few parameters (eight) for many outcome classes (121) and many observations (10,164), maximum likelihood estimation is generally quite reliable. We find the following maximum-likelihood estimates four our eight feature weights:

[+stop]	-0.0712	[-stop]	0.0928
[+fric]	-0.5472	[-fric]	0.5012
[+liquid]	0.5837	[-liquid]	-0.6679
[+voiced]	-0.4713	[-voiced]	0.7404

[11] We omit the phonological feature of unvoicedness because, since voicing here is a binary distinction, [+unvoiced] would be equivalent to [-voiced].

Onset	Freq	P_{M_1}	P_{M_2}	P_{M_3A}	P_{M_3B}	Onset	Freq	P_{M_1}	P_{M_2}	P_{M_3A}	P_{M_3B}
st	1784	0.0097	0.1122	0.1753	0.1587	vl	15	0.0035	0.0007	0.0013	0.0018
br	1500	0.0086	0.1487	0.1473	0.1415	vr	14	0.0035	0.0018	0.0014	0.0034
pr	1494	0.0287	0.1379	0.1468	0.1442	sf	12	0.004	0.0003	0.0009	0.001
tr	1093	0.0287	0.0791	0.1075	0.1033	sr	10	0.0119	0.0915	0.0014	0.0155
fr	819	0.0119	0.0443	0.0802	0.0726	zl	9	0.0035	0.0004	0.0009	0.0017
sp	674	0.0097	0.0423	0.066	0.056	zb	4	0.0009	0.0001	0.0001	0.0001
bl	593	0.0086	0.0567	0.0582	0.0541	sht	4	0.0097	0.0093	0.0003	0.0039
fl	572	0.0119	0.0169	0.0561	0.0454	dv	3	0.0009	0.0001	0.0001	0.0001
pl	458	0.0287	0.0526	0.045	0.046	zv	2	0.0004	0	0.0001	0
dr	441	0.0086	0.0317	0.0432	0.0391	tv	2	0.0029	0.0001	0.0001	0.0002
sl	379	0.0119	0.0349	0.0374	0.0359	dz	2	0.0009	0	0	0.0001
shr	155	0.0119	0.0076	0.0153	0.0143	tl	1	0.0287	0.0301	0.0006	0.0106
shl	79	0.0119	0.0029	0.0077	0.0067	shv	1	0.0012	0.0001	0	0
ts	23	0.0097	0.0005	0.0017	0.0002	sb	1	0.0029	0.0002	0.0002	0.0016
sv	19	0.0012	0.0011	0.0017	0.0002	fs	1	0.004	0.0003	0.0001	0.0005

Table 6.6: Probabilities estimated from four log-linear models for attested English onsets consisting of pairs from the segment inventory [f], [v], [s], [z], [sh], [p], [b], [t], [d], [l].

Similar to the case in logistic regression, positive feature weights indicates preference for onsets with large values for the feature in question, and negative feature weights indicate dispreference for such onsets. The model has learned that stops are slightly dispreferred to non-stops; fricatives and liquids are strongly preferred to non-fricatives and non-liquids; and unvoiced consonants are strongly preferred to voiced consonants. A sharper view, however, of the generalizations made by the model can be seen in Table 6.6, which shows the probabilities placed by this model on attested onsets. Although there are some things that seem to be correct about this model's generalizations—for example, none of the unambiguously attested onsets are given probability below 0.004—the model makes far too few distinctions, leading to problems such as the assignment of high probability to [tl], and the assignment of identical probabilities to [ts] and [st]. This failure should have been expected, however, given that our feature functions failed to encode any positional information, or to distinguish at all between certain segments, such as [t] and [p].

We address some of these concerns by moving on to a more complex model, which allows the following generalizations as feature functions:

- Preferences for particular segments to occur in position 1;
- Preferences for particular segments to occur in position 2;
- Preferences for particular bigrams of natural classes specifiable by a single phonological feature of either manner or voicing.

The first two types of features give the log-linear model the same generalizational power as the positional unigram model we covered earlier. The third type of feature, however,

goes beyond the positional unigram model, and allows the model to make use of abstract phonological features in generalizing over possible lexical items. Formally speaking, we have one feature function for each segment in position 1, one feature function for each segment in position 2, and one feature function for each possible pairing of single-feature natural classes. This gives us twenty-two possible single-segment feature functions and 8*8=64 possible bigram feature functions, for a total of 86. We will let each serve as an INDICATOR FUNCTION mapping those onsets it correctly describes to the value 1, and all other onsets to the value 0:

$$f_j(y_i) = \begin{cases} 1 & \text{if the } j\text{-th feature describes } y_i; \\ 0 & \text{otherwise.} \end{cases} \tag{6.48}$$

As a concrete example of how these feature functions would be applied, let us again consider the onset [sr]. It satisfies the following descriptions:

- [s] is in position 1 (we represent this feature as `s.`, with `.` indicating that anything can appear in position 2)
- [r] is in position 2 (we represent this feature as `.r`)
- [-liquid][+voice]
- All pairwise combinations of [-liquid],[-stop],[+fric],[-voice] in position 1 with [+liquid],[-stop],[-fric],[+voice] in position (16 combinations in total)

Thus the feature vector for [sr] would have eighteen entries of 1 and 68 entries of 0. Using the method of maximum likelihood to estimate values for the 86 parameters of the model, we find that the features with strongest absolute preferences and dispreferences are as follows:

[-voice][-voice]	5.62962436676025390625
.v	3.64033722877502441406
[-liquid][-stop]	2.91994524002075195312
[-voice][-stop]	2.36018443107604980469
s.	1.81566941738128662109
[-liquid][+liquid]	1.72637474536895751953
.t	1.68454444408416748047
[-stop][-liquid]	1.56158518791198730469
...	
.b	-1.03666257858276367188
z.	-1.07121777534484863281
[-liquid][-liquid]	-1.20901763439178466797
[-stop][+fric]	-1.24043428897857666016
.f	-1.30032265186309814453
[-stop][-stop]	-1.85031402111053466797
.d	-1.97170710563659667969
.sh	-3.09503102302551269531

Brief inspection indicates that most of the model's strongest preferences involve generalization on natural class cooccurences: preference for onsets to involve pairs of unvoiced segments, dispreference for pairs matching in manner of articulation, and so forth. In addition, some strong segment-specific positional dispreferences are also found, such as the preference for initial [s] and dispreference for initial [sh]. Caution is required, however, in interpreting individual feature weights too simplistically—for example, it is clear from the lexicon of English that [sh] is dispreferred even more strongly in the second position than in the first position, yet second-position [sh] feature does not appear in the list of most strongly dispreferred features. The reason for this is that several other features—including the four with the largest negative weights—strongly penalize second-position [sh] already. As with linear and logistic regression models, the proper interpretation of a feature weight is what effect a change in the associated feature value would have, *if all other feature values were kept constant.*

The other way of inspecting the generalizations made by the model is by looking at the predictive distribution on the response variable itself, as seen in Table 6.6. This model has a number of clear advantages over our simplest model: it is relatively successful at giving unambiguously attested onsets higher probability than attested onsets, but at the same time gives [sr] higher probability than many other onsets, including some that are unambiguously attested. However, it also has some weaknesses: for example, the probability for [sf] has dropped below many onsets that are not unambiguously attested, such as [vl].

Overparameterization and regularization

At some level, we might want to allow our model to have specific sensitivity to the frequency of *every* possible onset, so that each instance of a given onset x_1x_2 contributes directly and idiosyncratically to the probability of other words with that onset; but at the same time, we clearly want our model to generalize to onsets that do not occur in the English lexicon as well. Within the maximum-likelihood log-linear framework we have developed thus far, these two requirements are in conflict with one another, for the following reason. In order to allow the model sensitivity to the frequency of specific onsets, we would want to introduce one feature function for each possible onsets, giving us 121 feature functions and thus 121 parameters to estimate. However, this parameterization allows the encoding of *any* probability distribution over the 121 possible response classes. As we saw in Chapter 4, the maximum-likelihood estimate for a multinomial distribution is just the relative-frequency estimate. Hence a maximum-likelihood log-linear model with onset-specific feature functions would simply memorize the relative frequencies of the onsets. Since adding more natural class-based features to the model can only *increase* its expressivity, no ML-estimated model with these 121 features will generalize beyond relative frequencies.

It *is* possible, however, to learn both onset-specific knoweldge and natural-class-level generalizations simultaneously within the log-linear framework, however, by moving away from maximum-likelihood point estimation and instead adopting a Bayesian framework. Recall that in the Bayesian approach, the posterior probability of the model parameters λ is proportional to the likelihood of the data under λ times the prior probability of λ, which in our

case works out to:

$$P(\lambda|Y) = P(Y|\lambda)P(\lambda) \tag{6.49}$$

$$= \left[\prod_i \frac{1}{Z} \exp\left[\sum_j \lambda_j f_j(y_i)\right]\right] P(\lambda) \tag{6.50}$$

with Z a normalizing factor dependent on λ. The next step is to choose a prior distribution over the model parameters, $P(\lambda)$. In principle, any prior could be used; in practice, a popular choice is a multivariate *Gaussian* prior distribution (Section 3.5) with center μ and covariance matrix Σ, so that the prior probability of an N-dimensional parameter vector λ is

$$P(\lambda) = \frac{1}{\sqrt{(2\pi|\boldsymbol{\Sigma}|)^N}} \exp\left[\frac{(\lambda-\mu)^{\mathrm{T}}\boldsymbol{\Sigma}^{-1}(\lambda-\mu)}{2}\right] \tag{6.51}$$

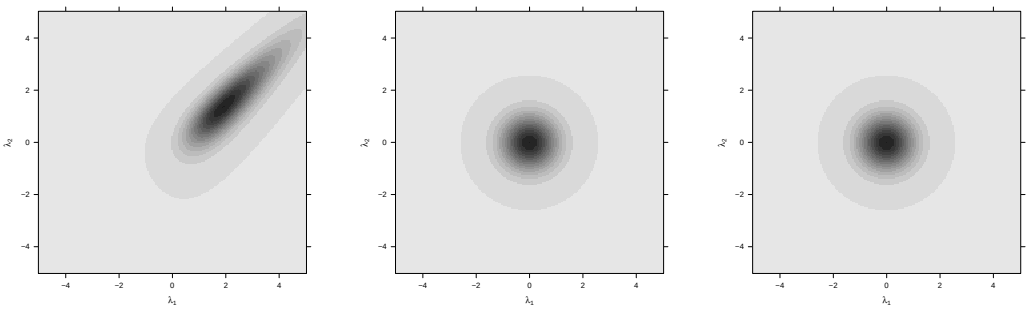
This choice of prior is popular for three reasons: (i) it has an intuitive interpretation as encoding a bias toward the parameter vector μ that is weak in the vicinity of μ but grows rapidly stronger with increasing distance from μ; (ii) for log-linear models, the posterior distribution over λ remains convex with a Gaussian prior; and (iii) Gaussian priors have been found to work well in allowing fine-grained learning while avoiding overfitting with log-linear models. The simplest choice of prior is one in which with mean $\mu = 0$ and a diagonal covariance matrix whose nonzero entries are all the same value: $\Sigma = \begin{pmatrix} \sigma^2 & \dots & 0 \\ \vdots & \ddots & \vdots \\ 0 & \dots & \sigma^2 \end{pmatrix}$. Multivariate Gaussian distributions like this are often called SPHERICAL, because surfaces of equal probability are (hyper-)spheres. With a spherical Gaussian prior, the posterior distribution can be written as follows:

$$P(\lambda|Y) \propto P(Y|\lambda)P(\lambda) \tag{6.52}$$

$$= \left[\prod_i \frac{1}{Z} \exp\left[\sum_j \lambda_j f_j(y_i)\right]\right] \exp\left[\sum_j \frac{-\lambda_j^2}{2\sigma^2}\right] \tag{6.53}$$

If we shift to log space we get

$$\log P(\lambda|Y) \propto \overbrace{\sum_i \left[\log \frac{1}{Z} + \sum_j \lambda_j f_j(y_i)\right]}^{\text{Log-likelihood}} - \overbrace{\left[\sum_j \frac{\lambda_j^2}{2\sigma^2}\right]}^{\text{Negative log-prior probability}} \tag{6.54}$$



(a) Likelihood (b) Prior (c) Posterior

Figure 6.15: A multivariate Gaussian prior ($\mu = 0, \sigma = 1$) for a simple log-linear model with three possible response classes and two indicator features functions: f_1 associated with class 1 and f_2 associated with class 2. First panel is model likelihood for class 1–3 frequencies of 7, 4, and 1 respectively; second panel is the prior distribution; third panel is the posterior distribution.

Note that the log-posterior probability falls off quadratically with the sum of the feature weights. For this reason, a Gaussian prior is sometimes called a QUADRATIC prior.

The effect of a Gaussian prior of this form can be seen in Figure 6.15: the prior penalizes deviations from its mode of 0 (a symmetric model in which all outcomes are equally likely), so that the posterior mode falls in between the MLE and the prior mode.

Let us now turn back to our study of English onsets, ready to apply our Bayesian log-linear model. We are now in a position to deploy a richer set of feature functions: on top of the positional single-segment and paired natural-class features we included in the previous model, we add paired-segment and positional single-natural-class features. This gives us an inventory of 223 total feature functions; the feature-vector representation for the onset [sr], for example, would now have the paired-segment feature `sr`, as well as the positional single-natural-class features [-stop]., [+fric]., [-liquid]., [-voiced]., .[-stop], .[-fric], .[+liquid], and .[+voiced].

As is always the case with Bayesian inference, we have a number of choices as to handle the problems of parameter estimation and prediction. Unlike the case with multinomial models, however, there are no readily available analytic techniques for dealing with Bayesian log-linear models, and sampling techniques can be quite computationally intensive. A popular approach is to use maximum a-posteriori (MAP) estimation to find the set of feature weights with (near-)maximum posterior probability, and to approximate Bayesian prediction by using these MAP parameter estimates. In our problem, using a symmetric Gaussian prior centered around $\mathbf{0}$ with standard deviation $\sigma = 1$, the features with largest and smallest weights in the MAP estimate are as follows:

st	3.24827671051025390625
sp	2.78049993515014648438
fl	2.51510095596313476562
ts	2.09755825996398925781
s.	1.87449419498443603516
[-voice][-voice]	1.80559206008911132812
fr	1.80392193794250488281
.v	1.72066390514373779297
...	
[-stop][+fric] -0.67749273777008056641	
[+voice][-voice] -0.70867472887039184570	
.d	-1.00191879272460937500
shp	-1.00633215904235839844
ss	-1.12540340423583984375
fp	-1.57261526584625244141
.sh	-1.64139485359191894531
zr	-1.65136361122131347656
ft	-1.85411751270294189453
dl	-2.24138593673706054688
tl	-3.16438293457031250000
sr	-4.12058639526367187500

Comparison with the previous model indicates important overall similarities, but it is clear that the new features are also being used by the model, perhaps most notably in encoding idiosyncratic preferences for [st] and dispreferences for [sr] and [sh]. The predictive distribution of this model, M_{3A}, can be found in Table 6.6. As expected, there is more probability mass on unambiguously attested onsets in this model than in either previous model, since this model is able to directly encode idiosyncratic preferences for specific onsets. Additionally, much of the apparent weakness of M_2 has been partly remedied—for example, the probability of [sr] has dropped below all the other unambiguously attested sequences except for [sf] while the lower probability of [vr] has stayed about the same.

Strength of the prior and generalization in log-linear models

What is the effect of increasing the strength of the prior distribution, as encoded by decreasing the standard deviation σ of the spherical multivariate Gaussian? There are two key effects we'll cover here consideration. The first effect is an overall tendency for the posterior to look more like the prior, a straightforward and intuitive consequence of the fact that in Bayesian inference, prior and likelihood stand on equal ground in determining posterior beliefs. There is a second, more subtle effect that merits attention, however, and which becomes clear from careful inspection of Equation 6.54. Consider the contribution of an individual feature weight λ_j to the posterior probability of the complete parameter vector λ. The choice of λ_j contributes directly to the log-likelihood once for *every* observation for which the corresponding

feature is implicated, but contributes to the prior log-probability only once regardless of how many observations in which the corresponding feature is implicated. This fact leads has an important consequence: a stronger prior penalizes feature weights more heavily the *sparser* the corresponding feature—that is, the less often that feature is unambiguously implicated in the data.

We can illustrate this consequence by re-fitting our previous log-linear phonotactic model using a much stronger prior: a spherical Gaussian distribution with standard deviation $\sigma = 0.01$. The resulting probability distribution over attested onsets is shown in Table 6.6 as model M_{3B}. Compared with M_{3A} (which had $\sigma = 1$), there is an overall shift of probability mass away from unambiguously attested onsets; this is the first effect described above. However, the remaining onsets do *not* all undergo similar increases in probability: the onsets [sr] and [tl], for example, undergo very large increases, whereas onsets such as [vl] and [zb] stay about the same. The reason for this is as follows. The more general features—natural-class and segment unigrams and natural-class bigrams—favor [sr] and [tl]: in our data, [s] and [t] are common as the first segment of two-segment onsets, [r] and [l] are common as the second segment of two-segment onsets, and [-voiced][+liquid] is a common natural-class bigram. The burden of fitting the low empirical frequency of [sr] and [tl] falls on the most specific features—segment bigrams—but large weights for specific features are disfavored by the strong prior, so that the resulting predictive probabilities of these onsets rises. In contrast, [vl] and [zb] are not favored by the more general features, so that their predictive probability does not rise appreciably with this moderate increase in prior strength.

A word of caution

Finally, a word of caution is necessary in the practical use of MAP estimation techniques with overparameterized log-linear models: even using Bayesian techniques so that the MAP estimate is well-defined, the posterior distribution can be *very* flat in the vicinity of its optimum, which can make it difficult to be sure how close the obtained solution may be to the true optimum. In these cases, one would do well to impose stringent convergence criteria on whatever optimization algorithm is used to search for the MAP estimate.

Log-linear distributions are maximum-entropy distributions

mention the term maxent, and point out that log-linear models satisfy the maxent property

6.10.2 Translating between logit models and log-linear models

Although we have demonstrated in Section 6.9 that log-linear models expressively subsume logit models, translating between the two can be require some care. We go through a brief example here.

SAY MORE

Gabe's needs doing example.

```
> dat <- read.table("../data/needs_doing_data/needs.txt",header=T)
> dat$Response <- ifelse(dat$Response=="ing",1,0)
> dat$Anim1 <- factor(ifelse(dat$Anim=="abst","abst","conc"))
> model.logit <- glm(Response ~ Anim1 + sqrt(Dep.Length), data=dat, family=binomial)
> # data processing to get data in format for log-linear/Poisson model
> dat.for.loglin <- with(dat,as.data.frame(as.table(tapply(Response, list(Anim1=Anim1,
> names(dat.for.loglin)[4] <- "x"
> dat.for.loglin$DL <- dat.for.loglin$Dep.Length
> dat.for.loglin$Dep.Length <- as.numeric(as.character(dat.for.loglin$DL))
> dat.for.loglin$Response <- as.numeric(as.character(dat.for.loglin$Response))
> dat.for.loglin$x <- sapply(dat.for.loglin$x, function(x) ifelse(is.na(x), 0, x))
> model.loglin <- glm(x ~ Anim1*DL + Response + Response:(Anim1 + sqrt(Dep.Length)),da
> summary(model.loglin)$coef[c(32,62,63),]

                            Estimate Std. Error   z value     Pr(>|z|)
Response                  -0.2950173 0.11070848 -2.664812 7.703144e-03
Anim1conc:Response         1.3333414 0.14315638  9.313880 1.232457e-20
Response:sqrt(Dep.Length) -0.6048434 0.06369311 -9.496215 2.176582e-21

> summary(model.logit)$coef

                   Estimate Std. Error   z value     Pr(>|z|)
(Intercept)      -0.2950173 0.11070848 -2.664812 7.703141e-03
Anim1conc         1.3333414 0.14315636  9.313881 1.232446e-20
sqrt(Dep.Length) -0.6048434 0.06369308 -9.496218 2.176519e-21
```

What we see here is that the "effect of the response variable category" in the log-linear model corresponds to the intercept in the logit model; and the interactions of response with animacy and dependency length in the log-linear model correspond to the animacy and dependency length effects in the logit model. Of course, the logit model is far more efficient to fit; it involved only three parameters, whereas the log-linear model required sixty-three.

WHAT ABOUT MODELS WHERE WE HAVE NO BASELINE CLASS BUT ALSO DON'T NEED ALL THOSE EXTRA PARAMETERS TO MODEL THE COUNTS?

...

6.11 Guide to different kinds of log-linear models

Because we have covered several types of log-linear models in this chapter, it is useful to take a moment to carefully consider the relationship among them. A diagram making these relationships explicit is given in Figure 6.16. This section briefly describes these relationships. For brevity, we have used dot-product notation instead of summation notation: model parameters and feature-function outcomes are both denoted with vectors $\boldsymbol{\lambda}$ and $\boldsymbol{f}(x, y_i)$, so

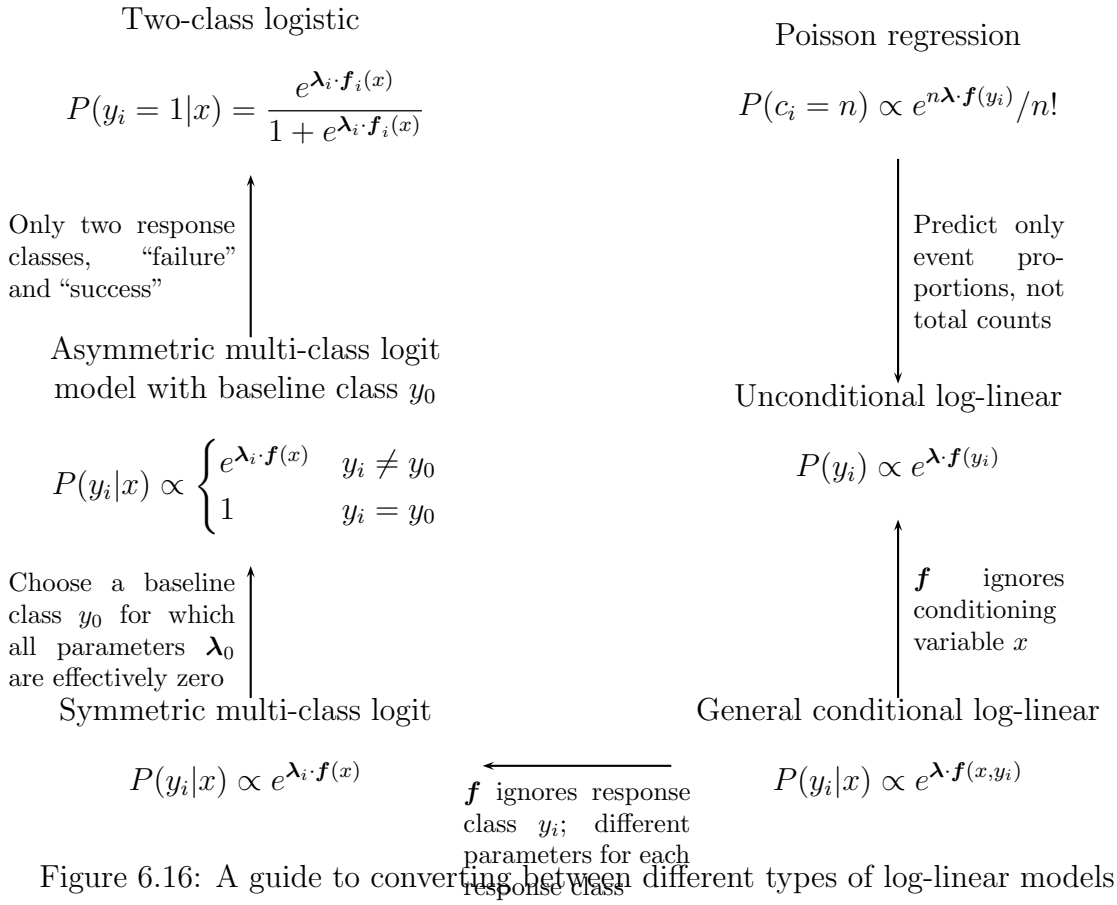


Figure 6.16: A guide to converting between different types of log-linear models

that the weighted sums $\sum_j \lambda_j f_j(x, y_i)$ we have seen previously can be succinctly expressed as dot products $\boldsymbol{\lambda} \cdot \boldsymbol{f}(x, y_i)$.

In the bottom-right corner of Figure 6.16 is the general conditional log-linear model we covered in Section XXX. In this model, there is a collection of feature functions f_j each of which maps an input x paired with a response class y_i to a real number. Each feature function f_j has an associated parameter weight λ_j. In the general conditional log-linear model, no further constraints are placed on the nature of these feature functions.

It is a common modeling decision, however, to assume that there should effectively be a single set of feature functions shared identically by all possible response classes. As an example, consider the problem of relativizer choice for non-subject extracted relative clauses with animate head nouns, such as in *the actress __ you mentioned*. In modeling this problem with conditional distributions P(Relativizer|Context), one might consider three possible response classes: *that*, *who(m)*, and relativizer omission. To examine the effect of frequency of the head noun (here, *actress*), we might want to come up with a single numerical encoding (say, log of Brown-corpus frequency) which is associated with a different feature function for each response class. Thus we would have three feature functions $f_{1,2,3}$, each of which is defined as follows:

$$f_j(x, y_i) = \begin{cases} \text{Log head-noun frequency} & j = i \\ 0 & \text{otherwise} \end{cases}$$

An equivalent approach, however, would be to say that there is only one feature function f_1 which always returns log head-noun frequency, but has a different parameter λ_{1i} for each response class. Taking this approach moves us to the lower-left corner of Figure 6.16: symmetric multi-class logistic regression. This category of model is more restrictive than the general conditional log-linear model: the latter can express probability distributions unavailable to the former, by using feature functions that are active for more than one response class, or by using feature functions active for one response class which have no matching feature function for another response class.

Some readers may have noticed that the symmetric multi-class logit model has more parameters than it needs. Let us identify one of the N response classes y_0 as the BASELINE CLASS. Then for an input x, we can the probability of any outcome y_i is as follows:

$$P(y_i|x) = \frac{e^{\boldsymbol{\lambda}_i \boldsymbol{f}(x)}}{e^{\boldsymbol{\lambda}_0 \boldsymbol{f}(x)} + e^{\boldsymbol{\lambda}_1 \boldsymbol{f}(x)} + \cdots + e^{\boldsymbol{\lambda}_N \boldsymbol{f}(x)}} \tag{6.55}$$

Let us now divide both the top and bottom of this fraction by $e^{\boldsymbol{\lambda}_0 \boldsymbol{f}(x)}$:

$$P(y_i|x) = \frac{e^{\boldsymbol{\lambda}_i \boldsymbol{f}(x)} \frac{1}{e^{\boldsymbol{\lambda}_0 \boldsymbol{f}(x)}}}{\left[e^{\boldsymbol{\lambda}_0 \boldsymbol{f}(x)} + e^{\boldsymbol{\lambda}_1 \boldsymbol{f}(x)} + \cdots + e^{\boldsymbol{\lambda}_N \boldsymbol{f}(x)}\right] \frac{1}{e^{\boldsymbol{\lambda}_0 \boldsymbol{f}(x)}}} \tag{6.56}$$

$$= \frac{e^{[\boldsymbol{\lambda}_i - \boldsymbol{\lambda}_0] \boldsymbol{f}(x)}}{e^{[\boldsymbol{\lambda}_0 - \boldsymbol{\lambda}_0] \boldsymbol{f}(x)} + e^{[\boldsymbol{\lambda}_1 - \boldsymbol{\lambda}_0] \boldsymbol{f}(x)} + \cdots + e^{[\boldsymbol{\lambda}_N - \boldsymbol{\lambda}_0] \boldsymbol{f}(x)}} \tag{6.57}$$

But $\boldsymbol{\lambda}_i - \boldsymbol{\lambda}_0 = \mathbf{0}$, so $e^{[\boldsymbol{\lambda}_0 - \boldsymbol{\lambda}_0] \boldsymbol{f}(x)} = 1$. If we now define $\boldsymbol{\lambda}'_i \equiv \boldsymbol{\lambda}_i - \boldsymbol{\lambda}_0$, we have:

$$P(y_i|x) = \frac{e^{\boldsymbol{\lambda}'_i \boldsymbol{f}(x)}}{1 + e^{\boldsymbol{\lambda}'_1 \boldsymbol{f}(x)} + \cdots + e^{\boldsymbol{\lambda}'_N \boldsymbol{f}(x)}} \tag{6.58}$$

This is a new expression of the same model, but with fewer parameters. Expressing things in this way leads us to the middle-left model in Figure 6.16. This is an *asymmetric* multiclass logit model in that we had to distinguish one class as the "baseline", but it is just as expressive as the symmetric multiclass logit model: any probability distribution that can be represented with one can be represented with the other. Therefore, any predictive inferences made using maximum-likelihood estimation techniques will be the same for the two approaches. Other techniques—such as Bayesian MAP parameter estimation or Bayesian prediction while "integrating out"—may lead to different results, however, due to the sensitivity of the prior to the structure of model parameterization.

Cases of this model where there are only two possible outcome classes are traditional *two-class* logit models (top left corner of Figure 6.16), which we covered in detail in Section

XXX. This is the type of log-linear model that the majority of readers are likely to have encountered first.

Returning to the general conditional log-linear case in the bottom-right corner of Figure 6.16, another option is to omit any sensitivity of feature functions to the input x. This is equivalent to throwing out the conditioning-variable part of the model altogether, and is sensible in cases such as our modeling of phonotactic knowledge (Section XXX), where simply wanted to infer a single probability distribution over English two-segment onsets. This decision takes us to the middle-right cell in Figure 6.16, UNCONDITIONAL log-linear models.

Finally, the unconditional log-linear model that we have here is closely related to another type of generalized linear model: POISSON REGRESSION. The key difference between unconditional log-linear models as we have described them here and Poisson regression is as follows: whereas our models have placed multinomial distributions over a set of possible response classes, the goal of Poisson regression is to put a probability distribution over *counts of observed events* in each possible response class. The two models are intimately related: if we take a fitted Poisson-regression model and use it to compute the joint probability distribution over counts in response class subject to the constraint that the total count of all response classes is 1, we get the same probability distribution that would be obtained using an unconditional log-linear model with the same parameters (Exercise 6.18). Although Poisson regression is popular in statistical modeling in general, we have not covered it here; it does turn up in some work on language modeling the frequencies of event counts in large corpora (e.g., Baayen, 2001).

6.12 Feed-forward neural networks

XXX

6.13 Further reading

There are many places to go for reading more about generalized linear models and logistic regression in particular. The classic comprehensive reference on generalized linear models is McCullagh and Nelder (1989). For GLMs on categorical data, Agresti (2002) and the more introductory Agresti (2007) are highly recommended. For more information specific to the use of GLMs and logistic regression in `R`, Venables and Ripley (2002, Section 7), Harrell (2001, Chapters 10–12), and Maindonald and Braun (2007, Section 8.2) are all good places to look.

Scheffé (1959) and Bock (1975) are comprehensive references for traditional ANOVA (including repeated-measures).

6.14 Notes and references

There are many good implementations of log-linear/maximum-entropy models publicly available; one that is simple to use from the command line, flexible, and fast is MegaM (Daumé and Marcu, 2006).

- Mention L_1 prior in addition to L_2 prior.

6.15 Exercises

Exercise 6.1: Linear regression

1. The `elp` dataset contains naming-time and lexical-decision time data by college-age native speakers for 2197 English words from a datset collected by Balota and Spieler (1998), along with a number of properties of each word. (This dataset is a slightly cleaned-up version of the `english` dataset provided by the `languageR` package; Baayen, 2008.) Use linear regression to assess the relationship between reaction time NEIGHBORHOOD DENSITY (defined as the number of words of English differing from the target word by only a single-letter edit). Is higher neighborhood density associated with faster or slower reaction times? Introduce written word (log-)frequency as a control variable. Does the direction of the neighborhood-density effect change? Is it a reliable effect (that is, what is its level of statistical significance)? Finally, is there an interaction between neighborhood density and word frequency in their effects on reaction time?

   Carry out this analysis for both word-naming and lexical-decision recognition times. In both cases, write a careful interpretation of your findings, describing not only what you found but what it might imply regarding how word recognition works. Construct visualizations of the main effects, and also of any interactions you find. If you find any qualitative differences in the way that the two predictors (and their interaction) affect reaction times, describe them carefully, and speculate why these differences might exist.

2. The dataset `nonwordsLexdec` presents average reaction times for 39 *non-word* letter sequences of English in a primed lexical decision experiment by Bicknell et al. (2010). The prime preceding the non-word always *was* a word, so trials were of the form *dish–kess*, *otter–peme*, and so forth. The dataset also contains neighborhood densities for each of the non-words, and word log-frequencies for the primes. Use linear regression to assess the relationship between neighborhood density and lexical-decision reaction time, controlling for prime log-frequency. Is the relationship between neighborhood density and reaction time the same as for the `english` dataset? Is the relationship reliable? Why do you see the results you see?

Exercise 6.2: Linear regression

The `durationsGe` dataset has as dependent variable the length of the Dutch prefix *ge-* in seconds. Use linear regression to investigate which of the following predictors have significant effects on prefix length:

- Word frequency
- Speaker sex
- Speech rate

Make sure to account for the possibility of interactions between the predictors. In addition, for word frequency and speech rate, use data visualization and `loess()` to get an intuition for whether to transform the predictors before putting them in the regression. (**Hint:** to get rid of rows in a data frame with NA's in them, the function `is.na()` is useful.)

Exercise 6.3: Analysis of variance

We talked about the idea of using a log-transformation on response variables such as reaction times to make them look more normal and hence be more faithful to the assumptions of linear models. Now suppose you are conducting a two-way ANOVA and are interested in the possibility of an interaction between the two factors. Your data are reaction times and look more normal when log-transformed. What are the potential consequences of log-transforming your response variable for investigating whether there is an interaction between your two predictors of interest? **Hint:** try constructing a set of four condition means for a two-by-two that reflect an additive pattern, and then look at the pattern when you take the log of each cell.

Exercise 6.4: Linear regression

Compare the residualization and multiple linear regression approaches. Imagine an underlying model of reading time of words in sentences in which the negative logs of raw word frequency (F_{log}) and contextual predictability (P_{log}) both play a role in determining the average reading time (RT, measured in milliseconds) of a given word. Take as the model of average reading time

$$\begin{aligned} RT &= 300 - 50F_{log} - 10P_{log} + \epsilon \\ \epsilon &\sim \mathcal{N}(0, 40) \end{aligned}$$

and suppose that F_{log} and P_{log} are generated from a multivariate normal distribution centered at $(-4, -4)$ with variance-covariance matrix $\left(\begin{smallmatrix} 0.7 & 0.5 \\ 0.5 & 1.2 \end{smallmatrix}\right)$. In this case where predictability and frequency are positively correlated, is your intuition that residualization or multiple linear regression will have greater statistical power in detecting the effect of predictability? (That is, on average which approach will yield a higher proportion of successful detections of a significance effect of predictability?) Test your intuitions by comparing residualization versus multiple linear regression approaches for detecting the effect of P_{log}. Generate 1000 sample datasets, each of size 200. Which approach has more statistical power in detecting the effect

of predictability? **Hint:** You can automatically extract a p-value from the t-statistic for a regression model parameter by looking at the fourth component of the `summary()` of an `lm` object (the result of `summary()` is a list), which is an array. For example:

```
> lexdec.lm <- lm(RT ~ Frequency, lexdec)
> summary(lexdec.lm)[[4]]
               Estimate  Std. Error    t value     Pr(>|t|)
(Intercept)  6.58877844 0.022295932 295.514824 0.000000e+00
Frequency   -0.04287181 0.004532505  -9.458744 1.026564e-20
> summary(lexdec.lm)[[4]][2,4]
[1] 1.026564e-20
```

Exercise 6.5: Decomposition of variance

Prove Equation 6.7.

Exercise 6.6: F tests and t statistics

With a randomly-selected 200-sample subset of the Spieler and Balota (1997) dataset, replicate the model comparisons reported in Section 6.5.2 and XXX

Exercise 6.7: Repeated measures and stratification of error

In English, the best-studied phonetic property distinguishing unvoiced stops ([p],[t],[k]) from voiced stops ([b],[d],[g]) is VOICE ONSET TIME (VOT): the time (typically measured in milliseconds) between (a) the acoustic burst corresponding to release of the stoppage of airflow in the vocal tract and (b) the onset of vibration of the vocal folds in the following sound (Liberman et al., 1958; Lisker and Abramson, 1967). Among other manipulations and measurements, Cho and Keating (2009) measured VOT for the first [t] in the invented name "Tebabet" (intended pronunciation [tɛbəbɛt]) in utterance-initial versus utterance-medial position, when the name was stressed:

(5) a. **Tebabet** fed them [Utterance-initial]
b. One deaf **Tebabet** [Utterance-medial]

Multiple native English speakers participated in this study, and Cho and Keating recorded several utterances of each sentence for each speaker. Hence this experiment involves a *repeated-measures* design. If we assume that different speakers may have individual idiosyncracies for the utterance-initial versus utterance-medial contrast, then we get the linear model

$$Y = \alpha + \beta X + a_i + b_i X + \epsilon$$

where X is the contrast between utterance-initial and utterance-medial position; a_i and b_i are the idiosyncracies of speaker i, distributed multivariate-normal around 0 with covariance matrix Σ; and ϵ is utterance-specific noise, also normally distributed around 0 with variance σ_2.

1. Demonstrate that applying a traditional (not repeated-measures) ANOVA according to Figure 6.9 for a repeated-measures study, in which we test a null-hypothesis model $M_0 : \beta = 0$ against an alternative-hypothesis model M_A with unconstrained β by comparing the variance explained by M_A over M_0 with the residual variance unexplained by M_A, will in general lead to anti-conservative inference. That is: assume $\beta = 0$; choose values of α, Σ, and σ^2, the number of speakers $m > 1$ and utterances per speaker $n > 1$; randomly generate N datasets using this model; analyze each dataset using a non-repeated-measures procedure; and report the proportion of models in which the null hypothesis would be rejected by the criterion $p < 0.05$.

2. Now demonstrate that the stratification-of-error procedure introduced in Section 6.6.5 avoids anti-conservative inference, through repeated generation of simulated data as in the first part of this problem.

Exercise 6.8: Outlier removal

Does outlier removal of the type introduced in Section 6.6.6 lead to anti-conservative inferences regarding differences between experimental conditions? Use simulations and/or mathematical analysis to support your claim. What if the criteria for outlier removal are determined separately for each experimental condition, instead of uniformly across conditions as done in Section 6.6.6?

Exercise 6.9: Analysis of variance.

Perform by-subjects and by-items repeated-measures ANOVA analyses of the second spillover region (`RC_VERB+2`) the Rohde et al. (2011) self-paced reading dataset. Try the results both with and without applying outlier removal; a typical outlier-removal criterion would be to discard observations more than either three or four standard deviations above the mean, with "mean" and "standard deviation" determined using only observations from the specific region being analyzed. How, if at all, does outlier removal change the results? Why do you think this is the case?

Exercise 6.10: The t-test versus Bayesian model comparison

Consider data that is generated from two normal distributions, with means $\mu_1 = 1$ and $\mu_2 = 2.5$, and with common noise $\sigma_\epsilon = 5$. Let's look at the power of the frequentist t-test versus a Bayesian model comparison in choosing between hypotheses H_0 in which the two distributions have the same mean, versus H_1 in which the two distributions have different means. Assume that our observations Y consist of 250 points from each distribution. For the Bayesian model comparison, use the specifications

$$\begin{aligned} \mu_1 &\sim \mathcal{N}(0, \sigma_\mu) \\ \mu_2 - \mu_1 &\sim \mathcal{N}(0, \sigma_\mu) \\ \sigma_\epsilon &\sim \mathcal{U}(1, 100) \end{aligned}$$

and the prior distribution $P(H_0) = P(H_1) = 1/2$. Using JAGS or similar sampling-based Bayesian inference software, plot the proportion of trials in which the posterior proability of H_0 is less then 0.05: $P(H_0|Y) < 0.05$, as a function of σ_μ. Explain the pattern you see in intuitive terms.

Exercise 6.11: Logistic regression

In analyzing the `dative` dataset [Section 6.7] we found in a logit model with linear predictor

```
RealizationOfRecipient ~ PronomOfRec + PronomOfTheme
```

that pronominality of recipient and theme had similar-sized but opposite effects (in logit space) on the probability of use of the prepositional-object construction. We tentatively interpreted this result as consistent with the idea that there is a general "pronouns like to be shifted left" constraint that operates with equal strength on recipients and themes.

1. The model above (call it M_1) has three free parameters. Define a new predictor variable that (a) is a function of the two variables `PronomOfRec` and `PronomOfTheme`; and (b) allows us to simplify the model above into a new model with only two free parameters.

2. Fit the model (call it M_2) to the `dative` dataset. How do the resulting parameter estimates compare to those of M_1?

3. Your new model M_2 should be nested inside M_1 (that is, it should be a special case of M_1). Explain this nesting—specifically, explain what special conditions imposed on M_1 result in equivalence to M_2. This nesting makes it possible to conduct a likelihood-ratio test between M_1 and M_2. Do this and report the p-value for the test. Does M_2 oversimplify the data compared with M_1?

Exercise 6.12

Use your knowledge of the English lexicon to explain why, in Table 6.4, [ts] and [sr] are so much more probable in the unigram model than in the other models, [st] is so much more probable in the bigram model than in the other models, and [tr] is so much less probable in the positional unigram model than in the other models.

Exercise 6.13

In Section **??**, the log-linear model of English onsets didn't include any conditioning information X. What conditioning information X might you include in a richer model of English onset phonotactics?

Exercise 6.14

Of the phonotactic models introduced in Section 6.10, which is the best predictive model with respect to the distribution of English onsets (as opposed to prediction of native speaker

non-word acceptability judgments)? Assess the cross-validated log-likelihood achieved by each model using ten-fold cross-validation.

Exercise 6.15

Consider the following frequency counts for the part of speech of the first word in each sentence of the parsed Brown corpus:

(Pro)noun	9192
Verb	904
Coordinator	1199
Number	237
(Pre-)Determiner	3427
Adverb	1846
Preposition or Complementizer	2418
wh-word	658
Adjective	433

Using a log-linear model with exactly one indicator feature function for each part of speech, demonstrate for yourself that the maximum-likelihood predictive distribution is simply the relative frequency estimate. Then introduce a Gaussian prior to your model. Plot the KL divergence from the MAP-estimated predictive distribution to the maximum-likelihood distribution as a function of the standard deviation of the prior.

Exercise 6.16

How would you obtain confidence regions for parameter estimates in a Bayesian log-linear model? After reading Appendix **??**, define and implement a Metropolis algorithm for sampling from the posterior distribution of a log-linear model with a Gaussian prior on the parameter estimates. Use this algorithm to generate confidence intervals for the feature weights in the models of Section 6.10.1. Which feature weights does the model have the most certainty about, and how should these features be interpreted? [HINT: you will save a lot of time if you use standard gradient-descent software to find the MAP-estimated feature weights and use these weights to initialize your sampling algorithm.]

Exercise 6.17

The file `word_suffixes` contains frequency counts from CELEX (Baayen et al., 1995) for all suffixes of English word lemmas constructible from 17 English phonemes which are of length 2 or less.

- Define a small set of feature functions (no more than in the neighborhood of 20) on the basis of generalizations you see in the data and write a script to automatically extract the outputs of these feature functions for each form in the frequency database.

- Fit a maximum-likelihood log-linear model from this output. Inspect the feature weights and the predictive distribution. What conclusions can you draw from the results?

- Introduce a Gaussian prior and fit a new log-linear model using MAP estimation. How do the feature weighs and the predictive distribution change?
- Based on any limitations you may see from the results of your first model, add new feature functions, refit the model, and discuss the changes you see between the simpler and more complex models.

Exercise 6.18

Use Bayes' Rule to show that when a fitted Poisson distribution with parameters $\boldsymbol{\lambda}$ is used to compute the probability distribution over counts in each response class subject to the constraint that the total count over all response classes is equal to 1, the resulting distribution is equivalent to that obtained by an unconditional log-linear model with the same parameters (see Figure 6.16).

Exercise 6.19: Symmetric versus baseline-class log-linear models and priors on the weights

Consider a simple model of the dative alternation, where the response variable Y is whether the recipient precedes or follows the theme, and the only predictor variable X is whether the recipient is pronominal. If we treat this as a symmetric, two-class problem we define the classes y_1 as recipient-first and y_2 as theme-first;

```
> ### part 3: no prior penalty on intercept, but penalty on all else
> library(rms)
> dat <- data.frame(x=rep(c("pro","pro","notPro","notPro"),c(8,2,2,8)),y=rep(c("NP","P
> m <- lrm(y~x,dat,penalty=1)
> predict(m,dat,type="fitted")

        1         2         3         4         5         6         7         8
0.2896893 0.2896893 0.2896893 0.2896893 0.2896893 0.2896893 0.2896893 0.2896893
        9        10        11        12        13        14        15        16
0.2896893 0.2896893 0.7103107 0.7103107 0.7103107 0.7103107 0.7103107 0.7103107
       17        18        19        20
0.7103107 0.7103107 0.7103107 0.7103107
```

Exercise 6.20: Interactions in a linear model

In the English Lexicon Project, data were collected from both younger participants (22.6± 5 y.o.) and older participants (73.4 ± 3 y.o.). For the word naming data you have availalbe from this project, analyze the effect of subject age (as a categorical variable: young vs. old) and its possible interaction with age of acquisition. Do younger participants name words faster or slower overall than older participants do? What is the effect of a word's age of acquisition on its naming latency? Is this effect any different for younger participants than for older participants? If so, how? If you see a significant difference, speculate on why the difference you see might exist.

Chapter 7

Interlude chapter (no content yet)

Chapter 8

Hierarchical Models

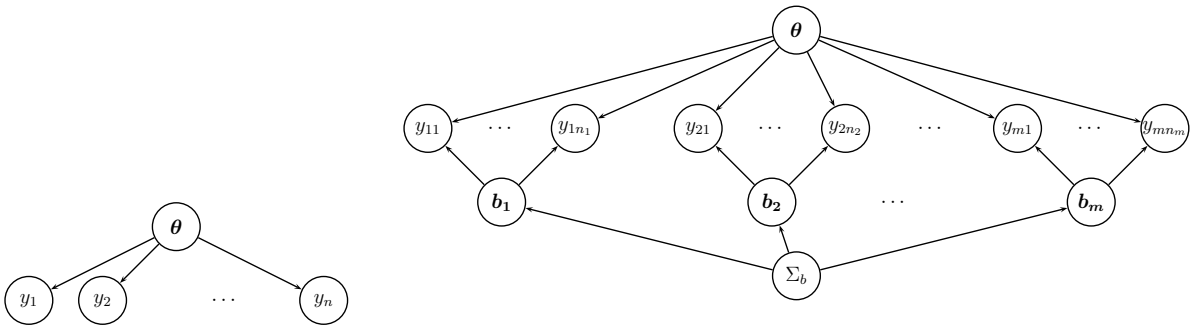
In the (generalized) linear models we've looked at so far, we've assumed that the observations are independent of each other given the predictor variables. However, there are many situations in which that type of independence does not hold. One major type of situation violating these independence assumptions is CLUSTER-LEVEL ATTRIBUTES: when observations belong to different clusters and each cluster has its own properties (different response mean, different sensitivity to each predictor). We'll now cover HIERARCHICAL (also called MULTI-LEVEL and, in some cases MIXED-EFFECTS) models, which are designed to handle this type of mutual dependence among datapoints. Common instances in which hierarchical models can be used include:

- Observations related to linguistic behavior are clustered at the level of the speaker, and speaker-specific attributes might include different baseline reading rates, differential sensitive to construction difficulty, or preference for one construction over another;

- Different sentences or even words may have idiosyncratic differences in their ease of understanding or production, and while we may not be able to model these differences, we may be able model the fact that there is incidental variation at the sentence or word level;

- Education-related observations (e.g., vocabulary size) of students have multiple levels of clustering: multiple measurements may be taken from a given student, multiple students may be observed from a class taught by a given teacher, multiple teachers may teach at the same school, multiple schools may be in the same city, and so forth.

This chapter introduces hierarchical models, building on the mathematical tools you have acquired throughout the book. This chapter makes considerably heavier use of Bayesian-style thinking and techniques than the previous chapter; this would be a good time to review marginalization (Section 3.2), Bayesian prediction and parameter estimation (Section 4.4), approximate posterior inference (Section 4.5), and confidence intervals (Chapter 5).



(a) A non-hierarchical model

(b) A simple hierarchical model, in which observations are grouped into m clusters

Figure 8.1: Non-hierarchical and hierarchical models

8.1 Introduction

The core idea behind the hierarchical model is illustrated in Figure 8.1. Figure 8.1a depicts the type of probabilistic model that we have spent most of our time with thus far: a model family has parameters $\boldsymbol{\theta}$, which determine a probability distribution over outcomes, and a set of observations $\boldsymbol{y}$ arises as a collection of independent draws from this distribution. Figure 8.1b illustrates the simplest type of hierarchical model: observations fall into a number of CLUSTERS, and the distribution over outcomes is determined jointly by (i) parameters $\boldsymbol{\theta}$ shared across clusters, and (ii) parameters $\boldsymbol{b}$ which are shared among observations within a cluster, but may be different across clusters. Crucially, there is a second probability distribution, parameterized by $\Sigma_{\boldsymbol{b}}$, over the cluster-specific parameters $\boldsymbol{b}$ themselves. In Figure 8.1b, there are m clusters, and for each cluster i there have been n_i observations $y_{i1}, \ldots, y_{in_i}$ made. All else being equal, we can expect that observations within a single cluster will tend to look more like each other than like observations in other clusters.

Let us consider a simple case in which the distribution from which the observations y_{ij} are drawn is characterized by just a few parameters—for example, they may be normally distributed, in which case the parameters are the mean and the variance. One natural type of clustering would be for each cluster to have its own mean μ_i but for all the clusters to have the same variance σ_y^2. In the terminology of Figure 8.1b, we would classify the μ_i as cluster-specific parameters (in the $\boldsymbol{b}$ nodes) and the variance σ_y^2 as a shared parameter (in the $\boldsymbol{\theta}$ node). In order to complete this probabilistic model, we would need to specify the distribution over the cluster-specific μ_i. We might make this distribution normal as well, which requires two parameters of its own: a global mean μ and variance $\sigma_{\boldsymbol{b}}^2$ (these would live in the Σ_b node). We can write this specification compactly as follows:

$$\begin{aligned} \mu_i &\sim \mathcal{N}(\mu, \sigma_b^2) \\ y_{ij} &\sim \mathcal{N}(\mu_i, \sigma_y^2) \end{aligned} \tag{8.1}$$

Equivalently, we could consider the cluster-specific parameters to be *deviations* from the

overall mean μ. In this approach, we would consider μ as a shared $\boldsymbol{\theta}$ parameter, and the mean of the deviations would be 0. We can compactly specify this version of the model as:

$$\begin{aligned} b_i &\sim \mathcal{N}(0, \sigma_b^2) \\ \mu_i &= \mu + b_i \\ y_{ij} &\sim \mathcal{N}(\mu_i, \sigma_y^2) \end{aligned} \tag{8.2}$$

The specifications in Equations 8.1 and 8.2 describe exactly the same family of probabilistic models. The advantage of the former specification is that it is more compact. The advantage of the latter specification is that the cluster-specific parameters are more directly interpretable as deviations "above" or "below" the overall average μ. In addition, the latter specification leads to a nice connection with our discussion of linear models in Section 6.2. We can describe the same model as follows:

$$y_{ij} = \mu + \underbrace{b_i}_{\sim\mathcal{N}(0,\sigma_b^2)} + \underbrace{\epsilon_{ij}}_{\sim\mathcal{N}(0,\sigma_y^2)} \tag{8.3}$$

That is, an individual observation y_{ij} is the sum of the overall mean μ, a normally-distributed cluster-level deviation b_i, and a normally-distributed observation-level deviation ϵ_{ij}.

Let us now consider a concrete example with slightly greater complexity. Suppose that a phonetician is interested in studying the distribution of the pronunciation of the vowel [ɑ], recruits six native speakers of American English, and records each speaker once a week for fifteen weeks. In each case, the phonetician computes and records the F1 and F2 formants of the pronounced syllable. Now, no two recordings will be exactly alike, but different individuals will tend to pronounce the syllable in different ways—that is, there is both within-individual and between-individual variation in F1 formant from recording to recording. Let us assume that inter-speaker (cluster-level) variation and inter-trial (observation-level) variation are both multivariate-normal. If we denote the ⟨F1,F2⟩ value for the jth recording of speaker i as y_{ij}, then we could write our model as follows:

$$\begin{aligned} b_i &\sim \mathcal{N}(\mathbf{0}, \Sigma_b) \\ \mu_i &= \mu + b_i \\ y_{ij} &\sim \mathcal{N}(\mu_i, \Sigma_y) \end{aligned} \tag{8.4}$$

where $\mathbf{0}$ is the vector $\langle 0, 0\rangle$.

The only difference between the models in Equations 8.2 and 8.4 is that whereas the former is univariate, the latter is multivariate: b_i is distributed around zero according to some covariance matrix Σ_b, and the y_{ij} are distributed around μ_i according to another covariance matrix Σ_y. Both the univariate and multivariate models (Equations 8.2 and 8.4) have precisely the structure of Figure 8.1b, with μ and Σ_y being the shared parameters θ. For the

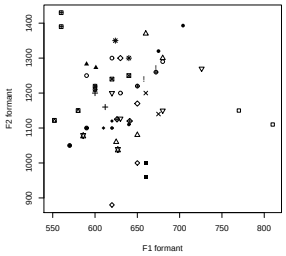


Figure 8.2: Empirically observed male adult speaker means for first and second formants of [ɑ]

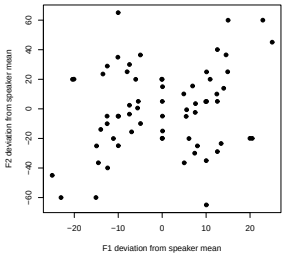


Figure 8.3: Empirically observed deviations from speaker means

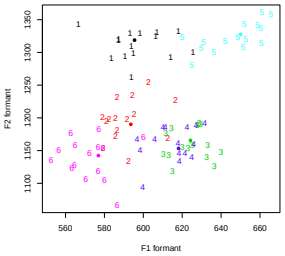


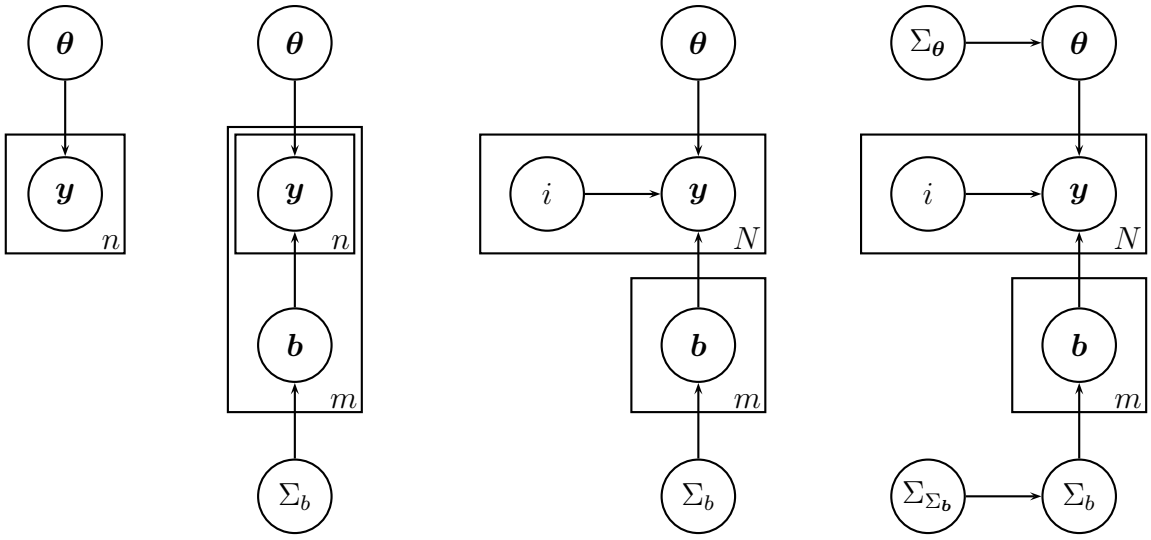
Figure 8.4: Simulated formant data for six speakers. Speaker-specific means $\mu + b_i$ are given as filled circles.

moment, to estimate the model parameters we use the simple expedient of using the sample mean and covariance of speaker-averages of adult-male data due to Peterson and Barney (1952) (shown in Figure 8.2) to estimate μ, and Σ_b, and the covariance of deviations from speaker means (shown in Figure 8.3) to estimate Σ_y. Figure 8.4 gives sample data generated from this model. The individual speakers correspond to clusters of trial-level observations. Note how there is considerable intra-cluster variation but the variation between clusters is at least as large.

8.2 Parameter estimation in hierarchical models

The previous section outlines what is essentially the complete probabilistic theory of hierarchical models. However, the problems of statistical inference within hierarchical models require more discussion. Before we dive into these issues, however, it is worthwhile to introduce a more succinct graphical representation of hierarchical models than that used in Figure 8.1b. Figure 8.5a is a representation of non-hierarchical models, as in Figure 8.1a, where the individual observations y_i have been collapsed into a single node $\boldsymbol{y}$. The box labeled "n" surrounding the $\boldsymbol{y}$ node indicates that n independent events are generated at this node; the labeled box is called a PLATE. Likewise, Figure 8.5b is a representation of the class of simple hierarchical models shown in Figure 8.1b, with both individual observations y_{ij} and class-specific parameters $\boldsymbol{b_i}$ compressed into single nodes. The outer plate indicates that m independent events are generated at the $\boldsymbol{b}$ node; the inner plate (embedded in the outer plate) indicates that for the i-th of these m events, n_i sub-events are generated. Each sub-event has a "cluster identity" label—the node labeled i, which allows us to track which cluster each observation falls into—and the nodes $\boldsymbol{b}$, $\boldsymbol{\theta}$, and i jointly determine the distribution over the outcome at the $\boldsymbol{y}$ node for this sub-event.

In light of this picture, let us consider the problem of parameter estimation for a case such as the formant measurements of the previous section. We know our observations $\boldsymbol{y}$, and we also know the cluster identity variable i—that is, which individual produced each



(a) The non-hierarchical model of Figure 8.1a

(b) The simple hierarchical model of Figure 8.1b

(c) Alternative representation for Figure 8.5b, with cluster identities explicit

(d) The model of Figure 8.1b with priors over $\boldsymbol{\theta}$ and $\boldsymbol{\Sigma_b}$

Figure 8.5: A more succinct representation of the models in Figure 8.1

observation. We do not know the shared model parameters $\boldsymbol{\theta}$ the parameters $\Sigma_{\boldsymbol{b}}$ governing cross-speaker variability, or the speaker-specific variations $\boldsymbol{b_i}$ themselves. Upon reflection, however, it should become clear that the primary goal of the study is to learn $\boldsymbol{\theta}$ and $\Sigma_{\boldsymbol{b}}$, not $\boldsymbol{b_i}$. Yet the $\boldsymbol{b_i}$ stand in the way of estimating $\Sigma_{\boldsymbol{b}}$. It might seem like a good idea to first construct point estimates of $\boldsymbol{b_i}$ and then use these estimates directly to estimate $\Sigma_{\boldsymbol{b}}$, but this approach throws away valuable information (our uncertainty about the true values of the $\boldsymbol{b_i}$, which we should take into account). How can we make inferences about our parameters of interest in a principled way?

The answer is actually quite simple: whatever technique of parameter estimation we choose, we should *marginalize* over the cluster-specific $\boldsymbol{b_i}$. This leads us to two basic approaches to parameter estimation for hierarchical models:

1. Construct point estimates of model parameters ($\widehat{\Sigma_{\boldsymbol{b}}}$ and/or $\widehat{\boldsymbol{\theta}}$) using the principle of maximum likelihood. There are actually two different maximum-likelihood approaches that have widespread currency. The first is to simultaneously choose $\widehat{\Sigma_{\boldsymbol{b}}}$ and $\widehat{\boldsymbol{\theta}}$ to maximize the likelihood, marginal over $\boldsymbol{b}$:

$$\text{Lik}(\Sigma_{\boldsymbol{b}}, \boldsymbol{\theta}; \boldsymbol{y}) = \int_{\boldsymbol{b}} P(\boldsymbol{y}|\boldsymbol{\theta}, \boldsymbol{b}, i) P(\boldsymbol{b}|\Sigma_{\boldsymbol{b}}) \, \mathrm{d}b \tag{8.5}$$

   We will follow common practice in simply calling this approach "Maximum Likelihood" (ML) estimation. The second approach, called Restricted Maximum Likelihood (REML), is perhaps most easily understood as placing an (improper) uniform distribution over the shared model parameters $\boldsymbol{\theta}$ and marginalizing over them (Harville, 1974),

so that we select only $\widehat{\Sigma_{\boldsymbol{b}}}$ according to the likelihood

$$\text{Lik}(\Sigma_{\boldsymbol{b}}; \boldsymbol{y}) = \int_{\boldsymbol{b},\boldsymbol{\theta}} P(\boldsymbol{y}|\boldsymbol{\theta}, \boldsymbol{b}, i) P(\boldsymbol{b}|\Sigma_{\boldsymbol{b}}) \, \mathrm{d}\boldsymbol{b} \, \mathrm{d}\boldsymbol{\theta} \tag{8.6}$$

On the REML approach, the parameters $\boldsymbol{\theta}$ are of secondary interest, but one would estimate them as

$$\arg\max_{\boldsymbol{\theta}} P(\boldsymbol{y}|\boldsymbol{\theta}, \widehat{\Sigma_{\boldsymbol{b}}}_{REML}, i) = \int_{\boldsymbol{b}} P(\boldsymbol{y}|\boldsymbol{\theta}, \boldsymbol{b}, i) P(\boldsymbol{b}|\widehat{\Sigma_{\boldsymbol{b}}}_{REML}) \, \mathrm{d}\boldsymbol{b}$$

For practical purposes, maximum-likelihood and restricted maximum-likelihood estimation often give results that are quite similar to one another when there are relatively few free parameters in $\boldsymbol{\theta}$ compared with the number in $\boldsymbol{b}$ (Dempster et al., 1981). We will return to the ML/REML distinction in Section 8.3.2.

2. Use Bayesian inference: introduce prior distributions over $\boldsymbol{\theta}$ and $\Sigma_{\boldsymbol{b}}$, and compute the (approximate) posterior distribution over $\boldsymbol{\theta}$ and $\Sigma_{\boldsymbol{b}}$. Since the introduction of priors means that $\boldsymbol{\theta}$ and $\Sigma_{\boldsymbol{b}}$ are themselves drawn from some distribution, this is actually a shift to a slightly more complex hierarchical model, shown in Figure 8.5d. $\Sigma_{\boldsymbol{\theta}}$ and $\Sigma_{\Sigma_{\boldsymbol{b}}}$, chosen by the researcher, parameterize the priors over $\boldsymbol{\theta}$ and $\Sigma_{\boldsymbol{b}}$ respectively. Via Bayes' rule, the posterior distributions of interest can be written as follows:

$$P(\Sigma_{\boldsymbol{b}}, \boldsymbol{\theta}|\boldsymbol{y}) \propto \int_{\boldsymbol{b}} P(\boldsymbol{y}|\boldsymbol{\theta}, \boldsymbol{b}) P(\boldsymbol{b}|\Sigma_{\boldsymbol{b}}, i) P(\boldsymbol{\theta}|\Sigma_{\boldsymbol{\theta}}) P(\Sigma_{\boldsymbol{b}}|\Sigma_{\Sigma_{\boldsymbol{b}}}) \, \mathrm{d}b \tag{8.7}$$

Note that the posterior distribution looks very similar to the unnormalized likelihood of Equation (8.5) above. The only difference is, as always, the presence of the prior probability $P(\boldsymbol{\theta}|\Sigma_{\boldsymbol{\theta}})P(\Sigma_{\boldsymbol{b}}|\Sigma_{\Sigma_{\boldsymbol{b}}})$ in the posterior distribution. It's worth recalling at this point that if the prior distribution is chosen to be uniform, then the maximum-likelihood estimate is also the Bayesian maximum a-posteriori (MAP) estimate.

We'll now illustrate each of these approaches with reference to actual formant data from recordings of adult male American speakers' pronunciations of [ɑ] by Peterson and Barney (1952). The F1 data are plotted in Figure 8.6.

8.2.1 Point estimation based on maximum likelihood

We illustrate the point estimation approach by treating the F1 and F2 formats separately.[1] For each of the formants, we assume the model of Equation (8.2): that the speaker-specific deviations from the grand mean are normally distributed, and that trial-specific deviations are also normally distributed. We reiterate that there are three parameters to be estimated

[1]The R package lme4 is the state of the art in likelihood-based point estimation for a wide variety of hierarchical models, and we use it here.

in each model: the overall mean μ, the inter-speaker variance $\Sigma_{\boldsymbol{b}}$, and the intra-speaker, inter-trial variance $\Sigma_{\boldsymbol{y}}$. The maximum-likelihood estimates for these parameters can be seen in the output of each model fit:

	F1	F2
μ	630.6	1191.9
$\sigma_{\boldsymbol{b}}$	43.1	100.8
$\sigma_{\boldsymbol{y}}$	16.9	40.1

In this case, there is considerably more inter-speaker variation than intra-speaker variation. Eyeballing Figure 8.6 and comparing it with the parameter estimates above, we can see that the overall mean μ is right at the grand mean of all the observations (this has to occur because the dataset is balanced in terms of cluster size), and that nearly all of the observations lie within two cluster-level standard deviations (i.e. $\sigma_{\boldsymbol{b}}$) of the grand mean.

Conditional estimates of cluster-specific parameters

In the point-estimation approach, we have focused on the parameters of interest—$\boldsymbol{\theta}$ and $\Sigma_{\boldsymbol{b}}$—while maintaining our ignorance about $\boldsymbol{b}$ by marginalizing over it. Nevertheless, in many cases we may be interested in recovering information about $\boldsymbol{b}$ from our model. For example, although the ultimate point of the phonetic study above was to estimate inter-speaker and intra-speaker variation in the pronunciation of [ɑ], we might also be peripherally interested in making inferences about the average pronunciation behavior of the specific individuals who participated in our study. Formally, the point estimates of $\boldsymbol{\theta}$ and $\Sigma_{\boldsymbol{b}}$ determine a conditional probability distribution over $\boldsymbol{b}$. The mode of this distribution is called the BEST LINEAR UNBIASED PREDICTOR (BLUP) $\widehat{\boldsymbol{b}}$:

$$\widehat{\boldsymbol{b}} \stackrel{\text{def}}{=} \arg\max_{\boldsymbol{b}} P(\boldsymbol{b}|\widehat{\boldsymbol{\theta}}, \widehat{\Sigma_{\boldsymbol{b}}}, \boldsymbol{y})$$

The F1 BLUPs for speakers in the current example are plotted as magenta circles in Figure 8.7.

Shrinkage

Another way of estimating speaker-specific averages would simply be to take mean recorded F1 frequency for each speaker. But these two approaches lead to different inferences. Figure 8.7 shows the deviation of each speaker's mean recorded F1 frequency from the grand mean as black squares; recall that the conditional estimate $\widehat{\boldsymbol{b}}$ are magenta circles. Notice that the conditional modes are systematically closer to zero than the means of the raw trials; this effect is more dramatic for speakers with larger deviations. This happens because the finite variance of $\boldsymbol{b}$ in the hierarchical model penalizes large deviations from the grand mean μ. This effect is called SHRINKAGE and is ubiquitous in hierarchical models.

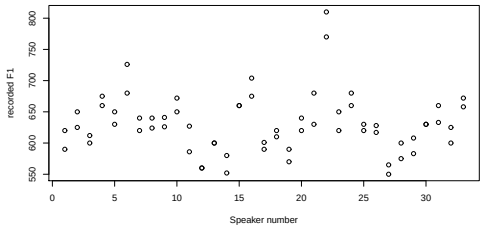


Figure 8.6: Observed F1 measurements by speaker

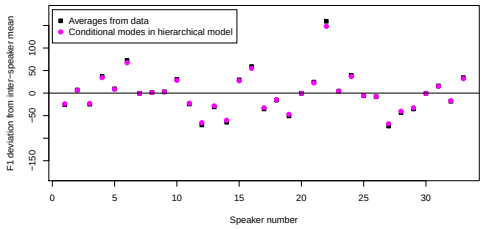


Figure 8.7: Conditional estimates of speaker-specific mean F1 frequencies, and shrinkage

8.2.2 Bayesian posterior inference in hierarchical models

We can compare the point estimates (with standard errors) that we obtained in Section 8.2.1 with posterior estimates obtained using Bayesian inference. We specify the hierarchical model as follows:

$$\begin{aligned}
\mu &\sim \mathcal{N}(0, 10^5) \\
\log \sigma_{\boldsymbol{b}} &\sim \mathcal{U}(-100, 100) \\
\log \sigma_{\boldsymbol{y}} &\sim \mathcal{U}(-100, 100) \\
b_i &\sim \mathcal{N}(0, \sigma^2_{\boldsymbol{b}}) \\
\mu_i &= \mu + b_i \\
y_{ij} &\sim \mathcal{N}(\mu_i, \sigma^2_{\boldsymbol{y}})
\end{aligned} \tag{8.8}$$

This is exactly the same model as in Equation 8.2, with the addition of three extra lines at the top specifying prior distributions over the overall mean μ, inter-speaker variability $\sigma_{\boldsymbol{b}}$, and intra-speaker variability $\sigma_{\boldsymbol{y}}$. There are two important points regarding this model specification. The first is that we are using a normal distribution with very large variance as a prior on the grand mean μ. The normal distribution is conjugate (Section 4.4.3) to the mean of a normal distribution, which has computational advantages; the large variance means that the prior is relatively uninformative, placing little constraint on our inferences about likely values of μ. The second point is how we are defining the priors on the variance parameters $\sigma_{\boldsymbol{b}}$ and $\sigma_{\boldsymbol{y}}$. Although the inverse chi-squared distribution (Section B.4) is conjugate to the variance parameter of a normal distribution, this distribution does not lend itself well to an uninformative specification. As described earlier in Section 4.5, placing a uniform distribution over the log of the standard deviation allows our prior to be uninformative in a "scale-free" sense.[2]

Using the sampling techniques described in Section 4.5, we can obtain approximate highest-posterior density confidence intervals and conditional modes (the latter being ap-

[2]Good discussion of practical choices for priors on variance parameters can be found in Gelman et al. (2004, Appendix C).

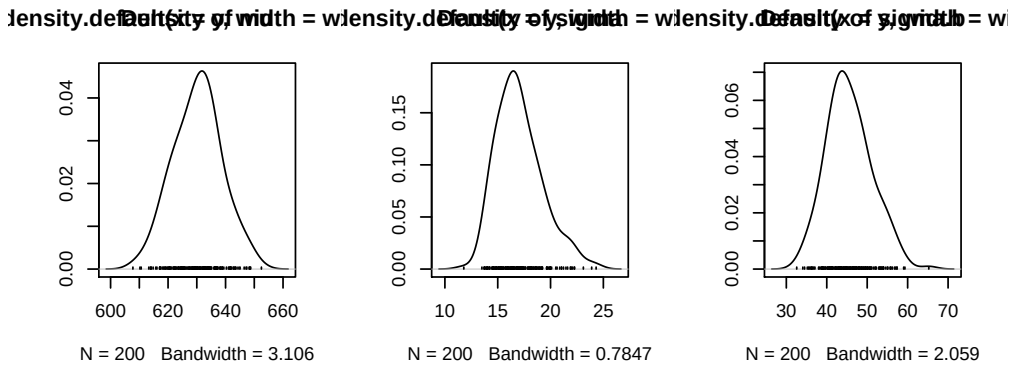


Figure 8.8: Output of MCMC sampling on hierarchical model parameters

proximated by a very narrow HPD interval), and plot estimates of the posterior (Figure 8.8). For F1 formants, these 95% HPD intervals and posterior modes are:

	lower bound	upper bound	posterior mode
μ	615.7	648.7	629.4
$\sigma_{\boldsymbol{b}}$	36	57.4	43.3
$\sigma_{\boldsymbol{y}}$	13.8	21.9	16.4

The posterior simulations are in broad agreement with the point estimates and standard errors obtained in Section 8.2.1. We leave obtaining similar results for F2 as Exercise 8.4.

8.2.3 Multivariate responses

One shortcoming of the analysis of the previous two sections is that F1 and F2 formants were analyzed separately. Correlations between F1 and F2 frequency are captured at neither the inter-speaker nor the intra-speaker level. However, there is a hint of such a correlation in the Figure 8.3. This raises the question of whether such a correlation is reliable at either level. We can address this question directly within a hierarchical model by using bivariate representations of $\boldsymbol{y}$ and $\boldsymbol{b}$. We'll illustrate this type of analysis in a Bayesian framework. The model specification looks similar to the univariate case given in Equation 8.8, but we are using different prior distributions because our normal distributions of interest are multivariate (even though they are still written as $\mathcal{N}$):

$$
\begin{aligned}
b_i &\sim \mathcal{N}(\mathbf{0}, \Sigma_{\boldsymbol{b}}) \\
\mu_i &= \mu + b_i \\
y_{ij} &\sim \mathcal{N}(\mu_i, \Sigma_{\boldsymbol{y}}) \\
\mu &\sim \mathcal{N}\left(\mathbf{0}, \left[\begin{smallmatrix} 10^5 & 0 \\ 0 & 10^5 \end{smallmatrix}\right]\right) \\
\Sigma_{\boldsymbol{b}} &\sim \mathcal{IW}\left(\left[\begin{smallmatrix} 10^5 & 0 \\ 0 & 10^5 \end{smallmatrix}\right], 2\right) \\
\Sigma_{\boldsymbol{y}} &\sim \mathcal{IW}\left(\left[\begin{smallmatrix} 10^5 & 0 \\ 0 & 10^5 \end{smallmatrix}\right], 2\right)
\end{aligned}
$$

The symbol $\mathcal{IW}$ stands for the inverse Wishart distribution, which is a widely-used prior distribution for covariance matrices; the large diagonal entries in the matrix parameterizing it signal uninformativity, and the zero off-diagonal entries signal that there is no particular prior expectation towards correlation between F1 and F2 deviations. The inverse Wishart distribution is described more completely in Section B.7.

There are eight distinct parameters in our model over which we would like to make inferences: two μ parameters, three $\Sigma_{\boldsymbol{b}}$ parameters, and three $\Sigma_{\boldsymbol{y}}$ parameters (recall from Section 3.5 that $\Sigma_{\boldsymbol{b}}$ and $\Sigma_{\boldsymbol{y}}$ have the form $\left[\begin{smallmatrix} \sigma_{11} & \sigma_{12} \\ \sigma_{21} & \sigma_{22} \end{smallmatrix}\right]$ but that $\sigma_{12} = \sigma_{21}$). Using BUGS once more we obtain the following 95% HPD confidence intervals from the posterior distribution:

	lower bound	higher bound	posterior mode
μ	$\langle 612.4, 1148.8 \rangle$	$\langle 641.8, 1226.3 \rangle$	$\langle 628.4, 1190.7 \rangle$
$\Sigma_{\boldsymbol{b}}$	$\begin{bmatrix} 34.4 & -0.43 \\ -0.43 & 75.8 \end{bmatrix}$	$\begin{bmatrix} 54.8 & 0.3 \\ 0.3 & 133.4 \end{bmatrix}$	$\begin{bmatrix} 42.5 & -0.03 \\ -0.03 & 98.8 \end{bmatrix}$
$\Sigma_{\boldsymbol{y}}$	$\begin{bmatrix} 13.6 & -0.06 \\ -0.06 & 31.5 \end{bmatrix}$	$\begin{bmatrix} 22.4 & 0.53 \\ 0.53 & 52.5 \end{bmatrix}$	$\begin{bmatrix} 17.1 & 0.29 \\ 0.29 & 39.7 \end{bmatrix}$

Of particular interest are the inferences about correlations between F1 and F2 formants, which are the most compelling reason to do multivariate analysis in the first place. In the above analysis, the posterior mode suggests a negative F1-F2 correlation at the inter-speaker level, but positive correlation at the intra-speaker level. However, the confidence intervals on these correlations show that this suggestion is far from conclusive.

It is instructive to compare this analysis to a more straightforward analysis of F1-F2 correlation in which inter-speaker correlation is estimated by calculating speaker means and computing a correlation coefficient on these means, and intra-speaker correlation is estimated obtained by simply subtracting out the speaker-specific mean from each observation and then calculating a correlation coefficient on the resulting residuals. For inter-speaker variation, it gives an empirical correlation coefficient of $r = -0.01$, with a 95% confidence interval of $[-0.35, 0.34]$; for intra-speaker variation, it gives an empirical correlation coefficient of $r = 0.24$, with a 95% confidence interval of $[-0.002, 0.46]$.[3] Although this approach also leads to the conclusion that there is no reliable F1-F2 correlation at either the inter-speaker

[3]This confidence interval is derived by using the transform $z = \frac{1}{2} \log \frac{1+r}{1-r}$; the resulting z is approximately normally distributed (Cohen et al., 2003, p. 45), and so a confidence interval based on the normal distribution can be calculated as described in Section 5.3.

or intra-speaker level, these confidence intervals indicate considerably more certainty in the true correlation than the Bayesian HPD intervals suggest, and the p-value for correlation at the intra-speaker level is very close to significant at 0.052. A key point here is that this latter approach based on empirical speaker means doesn't take into account the uncertainty about true speaker means, and thus leads to conclusions about inter-speaker variation of greater certainty than may be warranted. The Bayesian HPD interval takes this uncertainty into account, and is thus more agnostic about the true correlation.

8.3 Hierarchical linear models

Now we'll move on from hierarchical models of the form in Equation 8.3 to conditional models. Thus we'll be estimating distributions of the form

$$P(Y|X,i) \tag{8.9}$$

where X are the covariates (there can be many of them) and i are the cluster identities. Figure 8.9 illustrates this type of model. The only change from Figure 8.5b is the addition of the covariates X as a separate node in the graph. Once again, the primary targets of inference are typically $\boldsymbol{\theta}$ and Σ, and we'd want to marginalize over $\boldsymbol{b}$ in making our inferences about them.

We'll start with a study of hierarchical linear models. Assume that we have covariates $X_1, \ldots, X_M$ on which we want to condition Y. We can express the j-th outcome in the i-th cluster as

$$y_{ij} = \alpha + b_{i0} + (\beta_1 + b_{i1})X_1 + \cdots + (\beta_M + b_{iM})X_M + \epsilon \tag{8.10}$$

where ϵ is, as before, normally distributed. This equation means that every cluster i has a cluster-specific intercept $\alpha + b_{i0}$ and a slope parameter $\beta_k + b_{ik}$ that determines the contribution of covariate X_k to the mean outcome. In the notation of Figure 8.9, the parameters α and $\{\beta_k\}$, along with the variability $\sigma_{\boldsymbol{y}}$ governing ϵ, are $\boldsymbol{\theta}$ parameters, shared across clusters, whereas the b_{ik} parameters are specific to cluster i. Figure 8.10 shows a slightly more nuanced picture illustrating how the predicted mean mediates the influence of covariates and cluster identity on the outcome; here, only α and $\{\beta_k\}$ are $\boldsymbol{\beta}$ parameters. Equation 8.10 describes the most general case, where all predictors have both shared parameters and cluster-specific parameters. However, the models can be constrained such that some predictors have only shared parameters and some others have only cluster-specific parameters.

8.3.1 Fitting and drawing inferences from a hierarchical linear model: practice

We'll illustrate the utility of hierarchical linear models with a simple instance in which the covariates are categorical. Stanford (2008) investigated variability in the low lexical tone

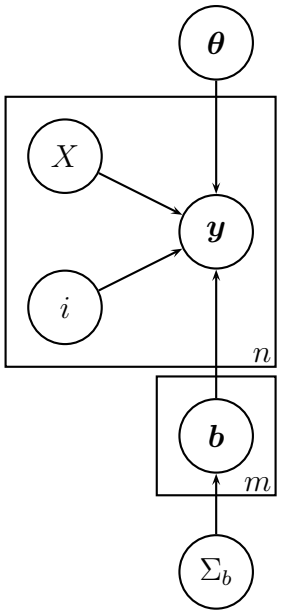


Figure 8.9: A conditional hierarchical model for probability distributions of the form $P(Y|X,i)$

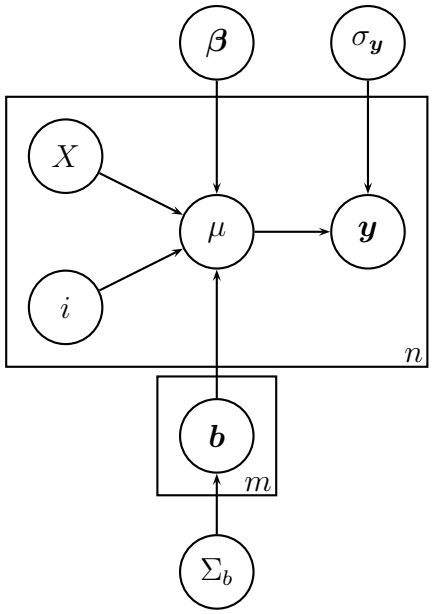
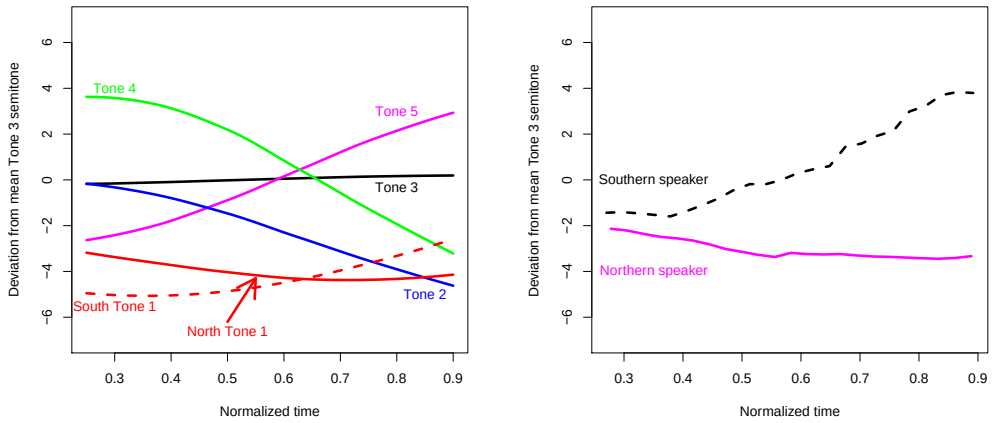


Figure 8.10: A structure more specific to hierarchical linear models, where the influence of cluster identity i and covariates X on the outcome y is only on the predicted mean μ. The shared parameters $\boldsymbol{\theta}$ from Figure 8.9 are explicitly represented here as $\boldsymbol{\beta}$ and $\sigma_{\boldsymbol{y}}$.

contour of Sui, a minority language in Southwest China. The Sui practice clan exogamy: a wife and husband must originate from different clans, and the wife immigrates to the husband's village. Both Northern and Southern Sui clan dialects have six tones, but they have different low-tone (Tone 1) pitch contours. Figure 8.11 illustrates the mean contours for five of the six Sui tones, along with sample tone contours taken from individual recordings of one southern Sui and one northern Sui speaker (who lived in their home village). According to Stanford (2008), the difference in this tone contour is audible but subtle, and the Sui do not mention it as a hallmark of the tone differences between northern and southern clan dialects. Stanford investigated two questions:

1. whether this tone contour can be reliably measured; and
2. whether immigrant Sui speakers adopt the lexical tone contour of their husband's clan, or keep their original tone contour.

We begin with question 1. Stanford observed that in tone 1, from the temporal midway point of each tone to the end, the mean tone contour is fairly straight, but it tends to rise for Southern speakers whereas it stays flat for Northern speakers (Figure 8.11a). Therefore one difference between northern and southern tone 1 contour may be characterizable by the *slope*



(a) Mean Sui tone contours

(b) Two specific trial Sui tone 1 contours for the word *jun*

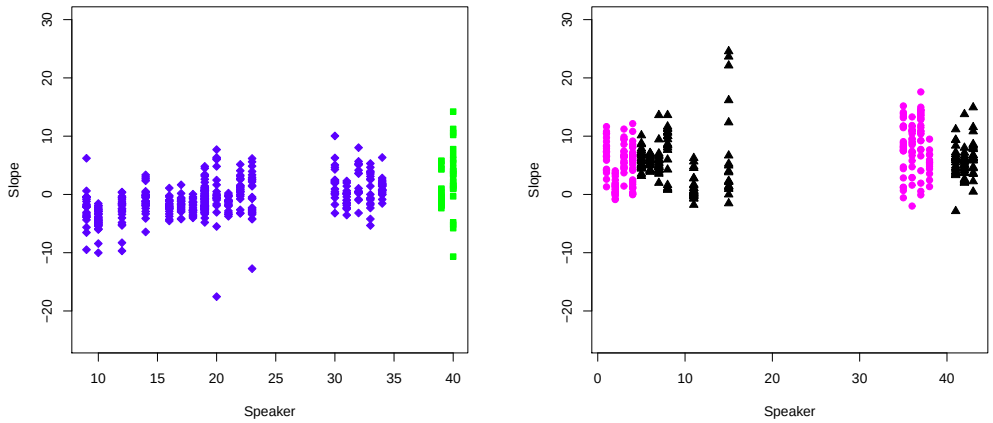
Figure 8.11: Sui tone contours

(in the sense of linear regression) of the tone contour in this part of the syllable. Figure 8.12 plots the distribution of tone contour slopes for each individual trial for Northern-origin and Southern-origin speakers. There is an apparent trend for Northern speakers to have lower slopes. However, there is also an apparent trend for different speakers of each origin to have idiosyncratically different slopes. We could deal with this nesting structure through analysis of variance with speaker as a random factor (Section 6.6), but the data are unbalanced, which is not ideal for analysis of variance. Lack of balance presents no fundamental difficulty for a hierarchical linear model, however.

In our first model of this dataset we include (i) effects on all observations of speaker origin, northward migration, and southward migration; (ii) speaker-specific idiosyncracies in average tone contour; and, of course, (iii) trial-level variability in tone contour. This linear model is thus specified as follows:

$$y_{ij} = \alpha + \beta_1 SO + \beta_2 MN + \beta_3 MS + \underbrace{b_i}_{\sim\mathcal{N}(0,\sigma_b^2)} + \underbrace{\epsilon_{ij}}_{\sim\mathcal{N}(0,\sigma_y^2)} \tag{8.11}$$

where SO is speaker origin (valued 1 for southern origin and 0 for northern origin), MN is migration north and MS migration south (each 1 if the speaker has migrated in that direction, 0 otherwise), and $\boldsymbol{b}$ is a normally-distributed speaker-level slope deviation distributed as $\mathcal{N}(0, \sigma_{\boldsymbol{b}})$. The data to which the model is fitted are shown in Figure 8.12. A maximum-likelihood fit of the parameters for this model is given in Table 8.1. For the shared model parameters (what are often called the "fixed effects" in the "mixed-effects" parlance), considering for the moment only the parameter estimates (and ignoring the standard errors and t statistics) we see that in the maximum-likelihood fit southern origin and northward migration are associated with more sharply upward-sloping tone contour, as visualized in



(a) Northern-origin slope distribution (b) Southern-origin slope distribution

Figure 8.12: Distribution of slopes for speakers originating northern and southern clans. Southward and northward migrants are plotted in green squares and magenta circles respectively.

Figure 8.11, and southward migration is associated with slightly more downward-sloping tone contour. As far as the parameter $\sigma_{\boldsymbol{b}}$ governing inter-speaker variability is concerned, note that its MLE is slightly larger than that of trial-level variability $\sigma_{\boldsymbol{y}}$ and that both these standard deviations are less than half the size of the effect of speaker origin, suggesting that while inter-speaker variability is considerable, the difference between northern-origin and southern-origin speakers is large even compared to this.

8.3.2 Hypothesis testing in hierarchical linear models

Of course, it would also be desirable to measure our certainty in the presence of the effects we just described from reading off the maximum-likelihood estimates in Table 8.1. We begin with the question of how can we assess the contribution of inter-speaker variability in this model. In a frequentist paradigm this can be done via model comparison between models fitted with and without inter-speaker variability, using the likelihood ratio test (Section 5.4.4). REML-fitted likelihoods are generally considered preferable to ML-fitted likelihoods for this purpose (e.g., Morrell, 1998), but in general the p-values obtained by the likelihood-ratio test for models differing in the number of parameters governing inter-cluster variability ("random-effects" structure, or $\Sigma_{\boldsymbol{b}}$) are CONSERVATIVE (Stram and Lee, 1994; Pinheiro and Bates, 2000; Baayen et al., 2008), meaning that the true p-value will generally be smaller (i.e. more significant) than the p-value obtained by consulting the χ^2 distribution. Conservativity is good in the sense that an obtained significant p-value can be trusted, but dangerous in the sense that a large (i.e. insignificant) p-value is not necessarily grounds to exclude inter-cluster variability from the model. Whether it is a better idea to err

	$\hat{\beta}_{ML}$	$SE(\hat{\beta}_{ML})$	t_{ML}	$\hat{\beta}_{REML}$	$SE(\hat{\beta}_{REML})$	t_{REML}
$\sigma_{\boldsymbol{b}}$	3.35			3.81		
$\sigma_{\boldsymbol{y}}$	3.07			3.07		
Intercept	-0.72	0.47	-1.53	-0.72	0.5	-1.44
SO	7.21	0.83	8.67	7.21	0.88	8.17
MN	2.38	1.44	1.65	2.38	1.53	1.56
MS	-0.82	0.94	-0.87	-0.82	1	-0.82

Table 8.1: Shared parameter estimates ($\hat{\beta}$), standard errors ($SE(\hat{\beta})$), and t statistics (defined as $\frac{\hat{\beta}}{SE(\hat{\beta})}$) for the Sui tone model defined in Equation (8.11). Note that standard errors are not appropriate for estimates of $\sigma_{\boldsymbol{b}}$ or $\sigma_{\boldsymbol{y}}$, as these are not normally distributed.

on the side of including or excluding parameters for inter-cluster variability when in doubt will depend on the precise goals of one's modeling, and we will have more to say about it in Section XXX.

To illustrate this type of hypothesis test on cluster-level parameters, we construct a "null hypothesis" version of our original Sui tone model from Equation (8.11) differing only in the absence of idiosyncratic speaker-level variability $\boldsymbol{b}$:

$$y_{ij} = \alpha + \beta_1 SO + \beta_2 MN + \beta_3 MS + \underbrace{\epsilon_{ij}}_{\sim\mathcal{N}(0,\sigma_y^2)} \tag{8.12}$$

and we can call this new model M_0 and the original model M_1. The log-likelihood of the REML fit of M_0 turns out to be -2403.8 whereas the log-likelihood for M_1 is -2306.2. Consulting twice the difference of these log-likelihoods against the χ^2_1 distribution, we find that the improvement of M_1 over M_0 is extremely unlikely under M_0 ($p \ll 0.001$). Broadly consistent with the visual picture in Figure 8.12 and with the results in Table 8.1, there is extremely strong evidence that speakers vary idiosyncratically in their average tone 1 contours, above and beyond the other sources of cross-speaker variability in the model (origin and migration).

We now move to the question of hypothesis testing involving shared model parameters ("fixed effects" structure, or θ). Perhaps surprisingly, how to test for significance of an effect of a shared model parameter is a matter of some current controversy. In principle, one could use the likelihood ratio test to compare a more complex model with a simpler model. However, it has been argued that the likelihood ratio test will lead to ANTI-CONSERVATIVE p-values (i.e. the true p-value is less significant than the p-value obtained by consulting the χ^2 distribution) for comparison of models with the same cluster-level parameters but different shared parameters (Pinheiro and Bates, 2000, pp. 87–92).[4] This leaves two approaches currently in vogue. On the first approach, a single model is fitted with the method of maximum

[4]As a caveat, it is not clear to this author that the anti-conservativity involved is appreciable unless the number of total parameters in the model is quite large relative to the number of observations, which quite often is *not* the case for linguistic datasets.

likelihood, and for the shared parameter of interest, the parameter estimate and its standard error are used to obtain a p-value based on the t statistic, just as in standard linear regression (Section 6.4; for testing multiple parameters simultaneously, an F-test is used). This approach itself carries a degree of controversy involving how many degrees of freedom the relevant t distribution should be assumed to have. As a rule of thumb, however, if there are many more observations than model parameters, the t distribution is generally taken to be approximated by the standard normal distribution (see also Section B.5). This is illustrated in Table 8.1, which gives the MLEs, standard errors, and resulting t statistics for our four parameters of interest. Recall that the standard normal distribution has just over 95% of its probability mass in the interval [-2,2] (e.g., Section 5.3), so that finding $|t| > 2$ is roughly a $p < 0.05$ result. Thus we conclude from the ML fit.

The second approach currently in vogue is to use Bayesian inference and bypass the classical hypothesis testing paradigm altogether. Instead, one can estimate a Bayesian confidence region (Section 5.1) on the shared parameters θ, by sampling from the posterior distribution over $\boldsymbol{\theta}$ using Markov Chain Monte Carlo (MCMC) sampling as discussed in Section 4.5, earlier in this chapter, and in Appendix **??**. Here we illustrate this approach by sampling from the posterior in Figure 8.10 over $P(\boldsymbol{\beta}|\boldsymbol{y}, \widehat{\Sigma_{\boldsymbol{b}}}, \widehat{\sigma_{\boldsymbol{y}}})$, performed by the `lme4` package and giving us the following 95% HPD confidence intervals and posterior modes:

	lower bound	upper bound	posterior mode
α	-1.56	0.17	-1.32
SO	5.72	8.58	7.45
MN	-0.06	5.05	2.46
MS	-2.36	1.06	-0.89

On the Bayesian interpretation, we can be over 95% certain that the true parameter estimate for the effect of being from the south (with respect to the reference level of clan origin, the north) is positive. It has recently become popular in the psycholinguistics literature to call the largest value q such that $1 - \frac{q}{2}$ of the posterior probability mass on a parameter θ lies on one side of zero a "MCMC-based p-value" for θ (Baayen, 2008). Although this value q is certainly a useful heuristic for assessing the strength of the evidence supporting a meaningful role for θ in the model, it is also worth keeping in mind that this value q is NOT a p-value in the traditional Neyman-Pearson paradigm sense of the term.

Simultaneous assessment of significance of multiple parameters

We now turn to another question: whether migration into a new clan has a reliable effect on tone 1 slope. If it did, then the theoretically sensible prediction would be that migration of a southern-origin woman to the north should tend to lower the slope, and migration of a northern woman to the south should tend to raise the slope. To test this possibility, we can consult model M_1, whose parameters associated with variables MN and MS encode this effect. Looking at Table 8.1, we see that both coefficients associated with migration are consistent with the theoretical prediction. There is considerable uncertainty about each parameter (as indicated by the t-value), but what we would really like to do is to assess the overall explanatory benefit accrued by introducing them together. The conceptually simplest

way to do this is to use the F statistic from model comparison between M_1 and a simpler model M_0' in which effects of MN and MS are absent. Computing an F-test between these two models we obtain an F statistic of 1.743. In order to evaluate statistical significance, we need to choose which F distribution should serve as the reference distribution, but as noted earlier, there is some controversy as to how many degrees of freedom to use in the *denominator* for such an F statistic. However, we can play the devil's advocate momentarily and ask how much evidence would exist for an effect of migration in the most optimistic interpretation. The maximum degrees of freedom for the F statistic denominator is the number of observations minus the number of parameters in the full model, or 887. The cumulative distribution function for $F_{2,887}$ at 1.743 is 0.824, hence the best-case p-value is 0.176, and the overall effect is thus marginal at best.

8.3.3 Heteroscedasticity across clusters

One noteworthy thing about Figure 8.12 is that some speakers clearly have more inter-trial variability than others (compare, for example, speakers 15 and 11). This presence of inter-cluster differences in residual variability is called HETEROSCEDASTICITY. (The lack of heteroscedasticity—when residual intra-cluster variability is the same for all clusters—is called HOMOSCEDASTICITY.) Although the differences are not particularly severe in this case, we can still investigate whether they affect our inferences by incorporating them into our model. Conceptually speaking, this is a minor change to the structure of the model as depicted in Figure 8.9: the residual variance σ_y moves from being a shared θ parameter to being a cluster-specific $\boldsymbol{b}$ parameter. We present a Bayesian analysis (once again because methods for point-estimation are not readily available), with the following model:

$$\begin{aligned}
\alpha, \beta_{\{1,2,3\}} &\sim \mathcal{N}(0, 10^5) \\
\mu_i &= \alpha + \beta_1 SO + \beta_2 MN + \beta_3 MS + b_i \\
b_i &\sim \mathcal{N}(0, \sigma_b) \\
y_{ij} &\sim \mathcal{N}(\mu_i, \sigma_{\boldsymbol{y},i}) \\
\log \sigma_b &\sim \mathcal{U}(-100, 100) \\
\log \sigma_{\boldsymbol{y},i} &\sim \mathcal{U}(-100, 100)
\end{aligned}$$

Approximate 95% HPD confidence intervals and posterior modes obtained from sampling look as follows:

	lower bound	upper bound	posterior mode
α	-1.68	-0.12	-1.04
SO	5.82	8.65	6.78
MN	-2.81	0.95	-1.41
MS	-1.09	4.92	2.88

Comparing these results with the point-estimate results obtained in the previous section, we see that failing to account for heteroscedasticity doesn't qualitatively change the conclusions

of the model: there is still a strong association of clan origin with tone 1 slope, and there are no reliable effects of migration. Once again, similar inferences from multiple model specifications should strengthen your confidence in the conclusions obtained.

8.3.4 Multiple clusters per observation

One of the most exciting new developments in hierarchical modeling has been improvement in the computational treatment of cases where there are multiple classes of cluster to which each observation belongs. Consider the typical psycholinguistics experiment in speech perception or language comprehension, where each observation is derived from a particular participant reading or listening to a particular experimental stimulus which appears in a certain form. For example, the self-paced reading experiment of Rohde et al. (2011), described in Section 6.6.6 involved 58 subjects each reading 20 sentences (ITEMS), where each sentence could appear in any of four possible forms. The sample sentence is repeated below:

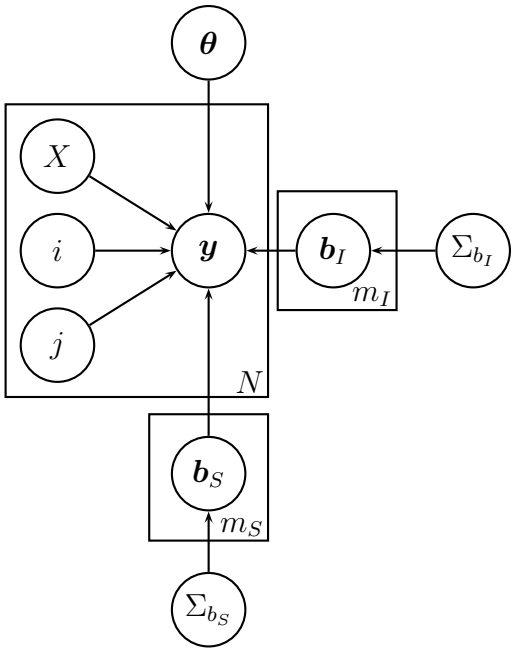
(1) John {detests/babysits} the children of the musician who {is/are} generally arrogant and rude.

where there are two experimentally manipulated predictors: the type of verb used (implicit causality (IC) or non-IC), and the level of relative-clause attachment (high or low). This corresponds to a more complex hierarchical model structure, shown in Figure 8.13. In this figure, there are two cluster identity nodes i and j; the subject-specific effects for the i-th subject are denoted by $\boldsymbol{b}_{S,i}$, and the item-specific effects for the j-th item are denoted by $\boldsymbol{b}_{I,j}$. This type of model is conceptually no different than the simpler hierarchical models we have dealt with so far. We illustrate by replicating the analysis of variance performed in Section 6.6.6 using a hierarchical linear model. Because the interaction between RC attachment level and verb type is of major interest to us, it is critical to us that we use an appropriate contrast coding (Section **??**), using predictors V to represent verb type, with values 0.5 and -0.5 for IC and non-IC verb types, and A to represent attachment level, with values 0.5 and -0.5 for high and low attachment. We will allow different subject- and item-specific effects for each of the four possible conditions C. The hierarchical model can be compactly written as follows:

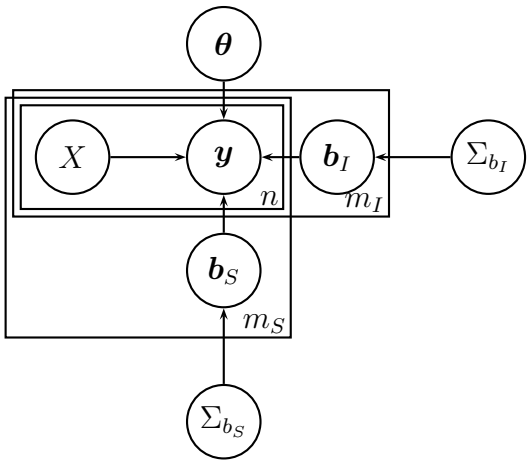
$$\begin{aligned}
\boldsymbol{b}_{S,i} &\sim \mathcal{N}(\mathbf{0}, \Sigma_{\boldsymbol{b}_S}) \\
\boldsymbol{b}_{I,j} &\sim \mathcal{N}(\mathbf{0}, \Sigma_{\boldsymbol{b}_I}) \\
\mu_{ij} &= \alpha + \beta_V V + \beta_A A + \beta_{VA} VA + \boldsymbol{b}_{S,i} C + \boldsymbol{b}_{I,j} C \\
y_{ijk} &\sim \mathcal{N}(\mu_{ij}, \sigma_{\boldsymbol{y}})
\end{aligned} \tag{8.13}$$

We'll start by using point estimation of the model parameters using (unrestricted) maximum likelihood. There is a considerable amount of detail in the resulting model so we present the complete printed representation of the fitted model from `R`:

```
Linear mixed model fit by maximum likelihood
Formula: rt ~ V * A + ((C - 1) | subj) + ((C - 1) | item)
```



(a) Crossed-clustering graphical model in which cluster identities are explicitly represented



(b) Crossed-clustering graphical model in which plates are overlapping/nested and cluster identity variables are implicit

Figure 8.13: A conditional hierarchical model for probability distributions of the form $P(Y|X,i,j)$, with observations cross-classified into two classes of clusters. The two graphical models are equivalent; in Figure 8.13a plates are non-overlapping and cluster identity variables are explicitly represented, whereas in Figure 8.13b cluster plates are overlapping, the observation plate is nested in both, and cluster identity variables are implicit

```
   Data: d
   AIC   BIC logLik deviance REMLdev
 12527 12648  -6239    12477   12446
Random effects:
 Groups   Name        Variance Std.Dev. Corr
 subj     CIC high    11971.19 109.413
          CIC low     18983.98 137.782  0.909
          CnonIC high 23272.40 152.553  0.883 0.998
          CnonIC low  16473.41 128.349  0.988 0.963 0.946
 item     CIC high      657.90  25.650
          CIC low       563.35  23.735  1.000
          CnonIC high  6062.73  77.864  0.271 0.271
          CnonIC low   3873.88  62.241  0.991 0.991 0.399
 Residual             38502.59 196.221
Number of obs: 919, groups: subj, 55; item, 20
```

$$\Sigma_{\boldsymbol{b}_S} = \begin{bmatrix} 109.41 & 0.91 & 0.88 & 0.99 \\ 0.91 & 137.78 & 1 & 0.96 \\ 0.88 & 1 & 152.55 & 0.95 \\ 0.99 & 0.96 & 0.95 & 128.35 \end{bmatrix} \qquad \Sigma_{\boldsymbol{b}_I} = \begin{bmatrix} 25.65 & 1 & 0.27 & 0.99 \\ 1 & 23.73 & 0.27 & 0.99 \\ 0.27 & 0.27 & 77.86 & 0.4 \\ 0.99 & 0.99 & 0.4 & 62.24 \end{bmatrix}$$

Parameter	Associated Predictor	$\hat{\beta}_{ML}$	$SE[\hat{\beta}]_{ML}$	t_{ML}
α	Intercept	470.48	20.6	22.84
β_V	Verb type (Implicit Causality=0.5, not=-0.5)	-33.71	16.78	-2.01
β_A	Relative clause (RC) attachment (high=0.5, not=-0.5)	-0.42	15.69	-0.03
β_{VA}	Verb type/RC attachment interaction	-85.31	35	-2.44

Table 8.2: Cross-classified cluster (experimental participant and item) hierarchical linear model for Rohde et al. (2011) self-paced reading study. For ease of interpretation, $\Sigma_{\boldsymbol{b}_S}$ and $\Sigma_{\boldsymbol{b}_I}$ are presented with standard deviations on the diagonal entries and correlation coefficients on the non-diagonal entries.

```
Fixed effects:
            Estimate Std. Error t value
(Intercept) 470.4823    20.6029  22.836
V           -33.7094    16.7787  -2.009
A            -0.4173    15.6899  -0.027
V:A         -85.3055    34.9994  -2.437
```

The negative estimates for β_V and β_A indicate that the IC-verb and high-attachment conditions respectively are associated with faster reading time at this region, though the effect of attachment level is very small. VA is positive in the IC/high and non-IC/low conditions, so the negative estimate for β_{VA} indicates that reading times at this region are faster in these two conditions.

We now turn to assessment of statistical significance. Once again resorting to our rule of thumb that with many more observations than estimated parameters (13 versus 919 in our case), the t statistic is distributed approximately as the standard normal, we see that the hierarchical analysis leads us to the same conclusions as the ANOVA of Section 6.6.6: there is a reliable interaction between verb type and RC attachment level in reading times at the first spillover region (*generally* in Example I). Importantly, this result is now obtained from a single hypothesis test rather than from separate by-subjects and by-items tests as has been the tradition in psycholinguistics for the past three decades.[5]

[5]Single hypothesis tests can also be done with separate by-subjects and by-items ANOVAs using the *min-F* test introduced by Clark (1973), this test is quite conservative and in practice is very rarely used.

Interpreting model parameter estimates

The ability to do a single hypothesis test when observations belong to multiple cross-cutting clusters is an advantage of the hierarchical analysis approach. However, where the hierarchical approach really shines is in obtaining a single model that can be inspected, interpreted, and used. From the subject-level variance parameters, we can see that there is much more intersubjective variation in reading speed for each condition (the subject-intercept standard deviations range from 111 to 154) than there is inter-item variability (standard deviations between 26 and 81). The residual trial-level variability is larger than both the subject- and item-level variability put together. Beyond this, however, there is something else worth noticing. The correlations between subject-level parameters for each condition are extremely high. That is, when a subject reads slowly in one condition, he or she reads slowly in *all* conditions. The correlations between item-level parameters are also high, except that there is much lower correlation between the implicit-causality, high-attachment condition and the rest of the conditions. This result could be illuminating if item-level parameter estimates were extracted and compared with the experimental materials themselves.

Turning to the shared parameters ("fixed effects"), we see that there is an overall 34-millisecond speed advantage for the implicit-causality verbs at this point, but no real overall effect of attachment level. Above and beyond these main effects, there is a large (85-ms) advantage for high-attaching RCs after IC verbs over low-attaching RCs after non-IC verbs. These estimates comport fairly well with those derived from the per-condition means obtained in Section 6.6.6, but the estimates obtained here put inter-subject and inter-item variation on equal footing, and are obtained automatically as part of the model-fitting process.

Fully Bayesian analysis

We can try a similar analysis using fully Bayesian techniques rather than the point estimate. We'll present a slightly simpler model in which the speaker- and item-specific variations do not depend on condition; this simpler type of model is often called a model with *random subject- and item-specific intercepts* in the literature. A Bayesian version of the more complex model of the previous section is left to the reader (see Exercise 8.8). Here is the model specification:

$$
\begin{aligned}
\alpha, \beta_{\{1,2,3\}} &\sim \mathcal{N}(0, 10^5) \\
\log \sigma_{b_S} &\sim \mathcal{U}(-100, 100) \\
\log \sigma_{b_I} &\sim \mathcal{U}(-100, 100) \\
\log \sigma_{b_y} &\sim \mathcal{U}(-100, 100) \\
b_{S,i} &\sim \mathcal{N}(0, \sigma_{b_S}) \\
b_{I,j} &\sim \mathcal{N}(0, \sigma_{b_I}) \\
\mu_{ij} &= \alpha + \beta_1 V + \beta_2 A + \beta_3 VA + b_{S,i} + b_{I,j} \\
y_{ijk} &\sim \mathcal{N}(\mu_{ij}, \sigma_y)
\end{aligned}
$$

Note the close resemblance to the previous model specification in Equation 8.13; the two differences are the addition of the top four lines representing priors over the shared parameters α and $\beta_{\{1,2,3\}}$, and the simplified $b_{S,i}$ and $b_{I,j}$ since we only have subject- and item-specific intercepts now.

Sampling from the posterior gives us the following 95% HPD confidence intervals and posterior modes for the effects of V, A, and the interaction VA:

	lower bound	upper bound	posterior mode
V	-56.87	-1.43	-41.75
A	-26.34	23.79	-5.69
VA	-136.52	-20.65	-96.3

Once again, there is broad agreement between the point estimates obtained earlier in this section and the Bayesian HPD confidence intervals. Most notably, there is (a) strong evidence of an overall trend toward faster reading in this region for the IC verbs; and (b) even stronger evidence for an interaction between IC verb type and attachment level. One should believe an apparent trend in the data more strongly if the same trend is confirmed across multiple statistical analyses, as is the case here.

8.4 Hierarchical generalized linear models

We now shift from linear models to the broader case of generalized linear models, focusing on logit models since they (along with linear models) are the most widely used GLM in the study of language. We move from generalized linear models (GLMs) to hierarchical GLMs by adding a stochastic component to the linear predictor (c.f. Equation 6.1):

$$
\eta = \alpha + (\beta_1 + b_{i1})X_1 + \cdots + (\beta_n + b_{in})X_n \tag{8.14}
$$

and assume that the cluster-specific parameters $\boldsymbol{b}$ themselves follow some distribution parameterized by $\Sigma_{\boldsymbol{b}}$.

We then follow the rest of the strategy laid out in Section 6.1 for constructing a GLM: choosing a link function $\eta = l(\mu)$, and then choosing a function for noise around μ.

8.4.1 Hierarchical logit models

In a hierarchical logit model, we simply embed the stochastic linear predictor in the binomial error function (recall that in this case, the predicted mean μ corresponds to the binomial parameter π):

$$P(y;\mu) = \binom{n}{yn}\mu^{yn}(1-\mu)^{(1-y)n} \qquad \text{(Binomial error distribution)} \tag{8.15}$$

$$\log\frac{\mu}{1-\mu} = \eta \qquad \text{(Logit link)} \tag{8.16}$$

$$\mu = \frac{e^{\eta}}{1+e^{\eta}} \qquad \text{(Inverse logit function)} \tag{8.17}$$

8.4.2 Fitting and interpreting hierarchical logit models

As with hierarchical linear models, the likelihood function for a multi-level logit model must marginalize over the cluster-level parameters $\boldsymbol{b}$ (Equation 8.5). We can take either the maximum-likelihood approach or a Bayesian approach. Unlike the case with hierarchical linear models, however, the likelihood of the data $P(\boldsymbol{y}|\theta,\Sigma_{\boldsymbol{b}})$ (marginalizing over cluster-level parameters $\boldsymbol{b}$) cannot be evaluated exactly and thus the MLE must be approximated (Bates, 2007, Section 9). The tool of choice for approximate maximum-likelihood estimation is once again the `lme4` package in `R`.[6]

8.4.3 An example

We return to the dataset of Bresnan et al. (2007), illustrated by the alternation

(2) Susan gave *toys* **to the children**. (PP realization of recipient)

(3) Susan gave **the children** *toys*. (NP realization of recipient)

To illustrate the approach, we construct a model with the length, animacy, discourse accessibility, pronominality, and definiteness of both the recipient and theme arguments as predictors, and with verb as a random effect. We use log-transformed length predictors (see Section 6.7.4 for discussion).

Defining the model

We arbitrarily denote length, animacy, discourse status, pronominality, and definiteness of the theme with the variables L_T, A_T, S_T, P_T, D_T respectively, and those properties of the

[6] The recommended approximations to maximum likelihood are Laplacian approximation (see, e.g., Robert and Casella (2004, Section 3.4)) and adaptive Gaussian quadrature; the former is available in `lme4` and the recommended default, but the latter isn't (yet).

	$\hat{\beta}$	$SE(\hat{\beta})$	z
$\sigma_{\boldsymbol{b}}$	2.33		
Intercept	2.32	0.66 3.51	
log Recipient Length	1.31	0.15	8.64
log Theme Length	-1.17	0.11	-10.97
Recipient Animacy	2.14	0.25	8.43
Theme Animacy	-0.92	0.5	-1.85
Recipient Discourse Status	1.33	0.21	6.44
Theme Discourse Status	-1.76	0.27	-6.49
Recipient Pronominality	-1.54	0.23	-6.71
Theme Pronominality	2.2	0.26	8.37
Recipient Definiteness	0.8	0.2	3.97
Theme Definiteness	-1.09	0.2	-5.49

Figure 8.14: Point estimate for a hierarchical logit model of the dative alternation

recipient as L_R, A_R, S_R, P_R, D_R.[7] We can now write our hierarchical model as follows:

$$\begin{aligned}
b_i &\sim N(0, \sigma_b) \\
\eta_i &= \alpha + \beta_{L_T} L_T + \beta_{A_T} A_T + \beta_{S_T} S_T + \beta_{P_T} P_T + \beta_{D_T} D_T \\
&\quad + \beta_{L_R} L_R + \beta_{A_R} A_R + \beta_{S_R} S_R + \beta_{P_R} P_R + \beta_{D_R} D_R + b_i \\
\pi_i &= \frac{e_i^\eta}{1 + e_i^\eta} \\
y_{ij} &\sim Binom(1, \pi_i)
\end{aligned} \tag{8.18}$$

(Note that we could equally specify the last line as a Bernoulli distribution: $y_{ij} \sim Bern(\pi)$.) We arbitrarily consider prepositional-object (PO) realization of the recipient as the "successful" outcome (with which positive contributions to the linear predictor η will be associated). Approximate maximum-likelihood estimation gives us the following parameter estimates: The fixed-effect coefficients, standard errors, and Wald z-values can be interpreted as normal in a logistic regression (Section 6.7.1). It is important to note that there is considerable variance in verb-specific preferences for PO versus DO realizations. The scale of the random effect is that of the linear predictor, and if we consult the logistic curve we can see that a standard deviation of 2.33 means that it would be quite typical for the magnitude of this random effect to be the difference between a PO response probability of 0.1 and 0.5.

We now turn our attention to the shared model parameters. The following properties are associated with PO outcomes:

[7] To simplify model interpretation, I have reduced the tripartite distinction of Bresnan et al. of discourse status as `given`, `accessible`, and `new` into a binary distinction of `given` versus `new`, with `accessible` being lumped together with `new`.

- Longer recipients
- Inanimate recipients
- Discourse-new recipients
- Non-pronominal recipients
- Indefinite recipients

- Shorter themes
- Animate themes
- Discourse-old themes
- Pronominal themes
- Definite themes

There is a clear trend here: those properties of the theme that favor PO outcomes are the reverse of those properties that favor DO outcomes. This raises the linguistically interesting possibility that there is a unified set of principles that applies to word ordering preferences in the English postverbal domain and which is sensitive to high-level properties of constituents such as length, discourse status, and so forth, but *not* to specific combinations of these properties with the grammatical functions of the constituents. This possibility is followed up on in Exercise 8.10.

Inferences on cluster-specific parameters

Because of this considerable variance of the effect of verb, it is worth considering the inferences that we can make regarding verb-specific contributions to the linear predictor. One way of doing this would be to look at the conditional modes of the distribution on verb-specific effects $\boldsymbol{b}$, that is to say the BLUPs (Section 8.2.1). There is a disadvantage to this approach, however: there is no easy way to assess our degree of confidence in the conditional modes. Another option is to use a fully Bayesian approach and plot posterior modes (of $P(\boldsymbol{b}|y, \Sigma_{\sigma_b}, \Sigma_\theta)$, which is different from the BLUPs) along with confidence intervals. This is the approach taken in Figure 8.15, using uniform priors on all the shared parameters as well as on $\log \sigma_{\boldsymbol{b}}$. On the labels axis, each verb is followed by its SUPPORT: the number of instances in which it appears in the `dative` dataset. For most verbs, we do not have enough information to tell whether it truly has a preference (within the model specification) toward one realization or the other. However, we do have reliable inferences some verbs: for the most part, those with large support and/or with posterior modes far from 0.[8] We can see that *tell*, *teach*, *charge*, and *show* are strongly biased toward the double-object construction, whereas *loan*, *bring*, *sell*, and *take* are biased toward the prepositional-object construction.

These results are theoretically interesting because the dative alternation has been at the crux of a multifaceted debate that includes:

- whether the alternation is meaning-invariant;
- if it is not meaning-invariant, whether the alternants are best handled via constructional or lexicalist models;

[8] This is not the whole story, however: comparing *deny* with *promise*, the former has both larger support and a more extreme posterior mode, but it is the latter that has an HPD confidence interval that is closer to not including 0.

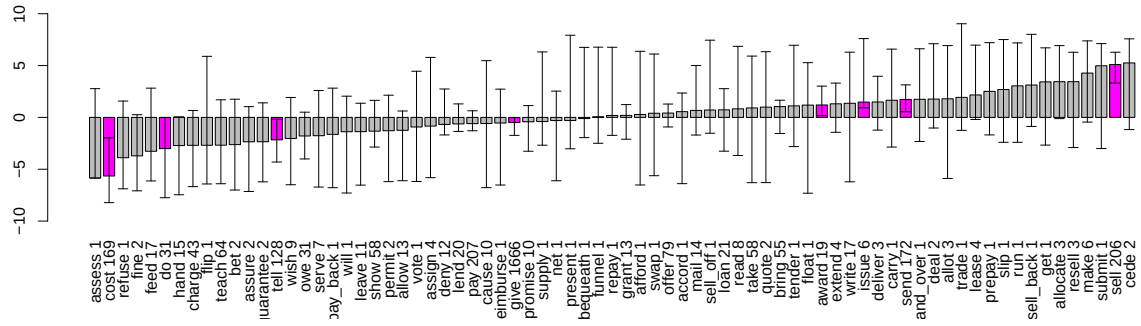


Figure 8.15: Verb-specific preferences in analysis of the `dative` dataset. 95% HPD confidence intervals are plotted on each preference. Verbs for which the 95% HPD interval is entirely on one side of the origin have their bars plotted in magenta.

- whether verb-specific preferences observable in terms of raw frequency truly have their locus at the verb, or can be explained away by other properties of the individual clauses at issue.

Because verb-specific preferences in this model play such a strong role despite the fact that many other factors are controlled for, we are on better footing to reject the alternative raised by the third bullet above that verb-specific preferences can be entirely explained away by other properties of the individual clauses. Of course, it is always possible that there are other explanatory factors correlated with verb identity that will completely explain away verb-specific preferences; but this is the nature of any type of scientific explanation. (This is also a situation where controlled, designed experiments can play an important role by eliminating the correlations between predictors.)

8.4.4 Model comparison & hypothesis testing

The framework for hypothesis testing in hierarchical generalized linear models is similar overall to that for hierarchical linear models as described in Section 8.3.2. For model comparisons involving the same shared-parameter structure but nested cluster-specific parameter structures, likelihood-ratio tests are conservative. For the assessment of the significance of a single shared parameter estimate $\hat{\beta}_i$ against the null hypothesis that $\beta_i = 0$, the Wald z-statistic (Section 6.8.1), which is approximately standard-normal distributed under the null hypothesis, can be used. In Figure 8.14, for example, the z-statistic for log of recipient length is $\frac{1.31}{0.15} = 8.64$, which is extremely unlikely under the null hypothesis.

To simultaneously assess the significance of the contribution of more than one shared parameter to a model, a likelihood-ratio test is most appropriate. Once again, however, in hierarchical models this test may be anti-conservative, as described in Section 8.3.2, so caution should be used in interpreting apparently significant results. As an example of how this test can be useful, however, let us consider an alternative model of the dative alternation in

which the tripartite discourse status of recipients and themes into given, accessible, and new (Collins, 1995). This difference introduces two new parameters into the model. Twice the difference in the log-likelihoods of the original and the updated model is 3.93; the cumulative distribution function for χ^2_2 at this point is 0.86, giving us a best-case p-value of 0.14, so we can safely state that we don't have sufficient evidence to adopt the tripartite distinction over the bipartite given/new distinction used earlier.

8.4.5 Assessing the overall performance of a hierarchical logit model

We conclude the chapter with a brief discussion of assessing overall performance of hierarchical logit models. As with any probabilistic model, the data likelihood is an essential measure of model quality, and different candidate models can be compared by assessing the likelihood they assign to a dataset. Cross-validated or held-out likelihood can be used to alleviate concerns about overfitting (Section 2.11.5). It is also useful to visualize the model's performance by plotting predictions against empirical data. When assessing the fit of a model whose response is continuous, a plot of the residuals is always useful. This is not a sensible strategy for assessing the fit of a model whose response is categorical. Something that is often done instead is to plot *predicted probability* against *observed proportion* for some binning of the data. This is shown in Figure 8.16 for 20 evenly-spaced bins on the x-axis, with the point representing each bin of size proportionate to the number of observations summarized in that point. There is a substantial amount of information in this plot: the model is quite certain about the expected outcome for most observations, and the worst-outlying bins are between predicted probability of 0.7 and 0.8, but contain relatively little data. Producing this visualization could be followed up by examining those examples to see if they contain any important patterns not captured in the model. Probability-proportion plots can also be constructed using cross-validation (Exercise 8.13).

8.5 Further Reading

Hierarchical models are an area of tremendous activity in statistics and artificial intelligence. There is good theoretical coverage (and some examples) of hierarchical generalized linear models in Agresti (2002, Chapter 12). Pinheiro and Bates (2000) is an important book on theory and practice for linear and non-linear hierarchical models from the frequentist perspective. There is also a bit of `R`-specific coverage in Venables and Ripley (2002, Section 10.4) which is useful to read as a set of applied examples, but the code they present uses penalized quasi-likelihood estimation and this is outdated by `lme4`. A more recent and comprehensive text for hierarchical regression models is Gelman and Hill (2007), which focuses the Bayesian perspective but is practically oriented, and includes coverage of both `lme4` and `BUGS`. At the time of writing, this is probably the single best place to turn to when learning the practicalities of working with hierarchical models for the analysis of complex datasets.

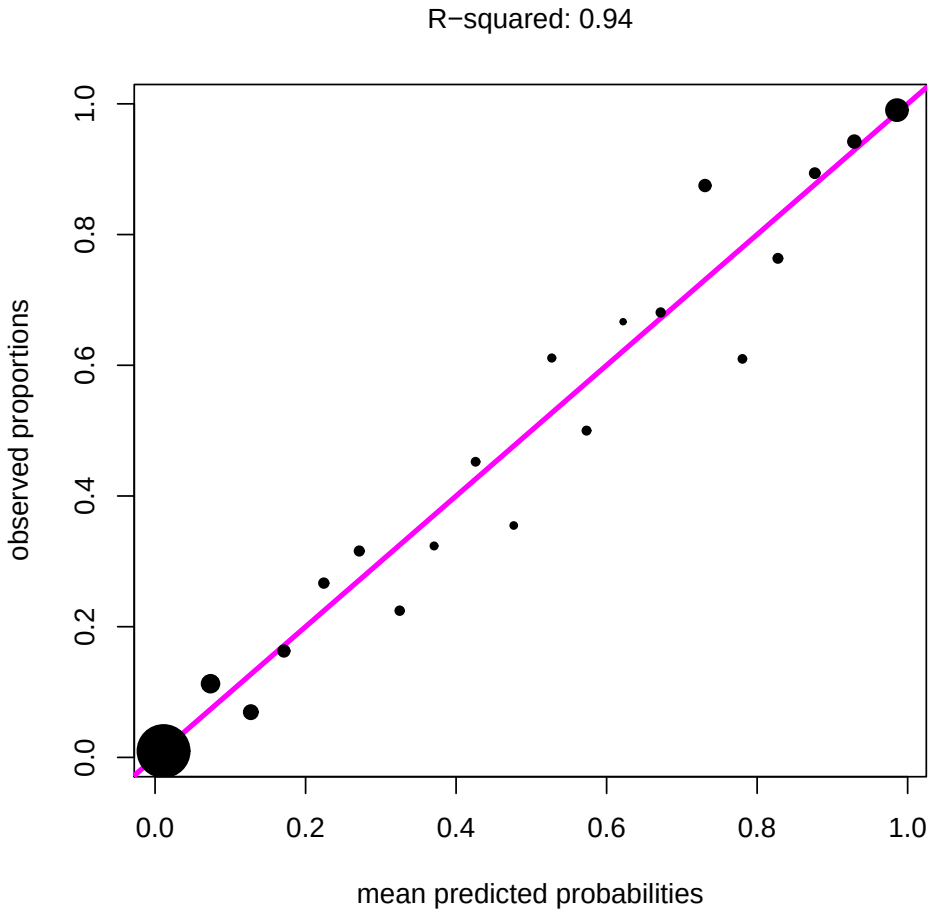


Figure 8.16: The fit between predicted probabilities and observed proportions for each 5% of predicted probability for our model

8.6 Exercises

Exercise 8.1: Defining a hierarchical model

The F1 formant levels of children's vowels from Peterson & Barney's dataset tend not to be normally distributed, but are often right-skewed (Figure 8.17). Define a hierarchical probabilistic model of F1 formant values for the vowel [a] in which the speaker-specific variation component b_i are log-normally distributed—that is, if $\log b_i = x_i$, then the x_i are normally distributed with some mean and standard deviation. Write the hierarchical model in the style of Equation 8.2. Choose parameters for your model by hand that generate data that looks qualitatively like that of Figure 8.17.

Exercise 8.2: Restricted maximum likelihood and testing "fixed effects"

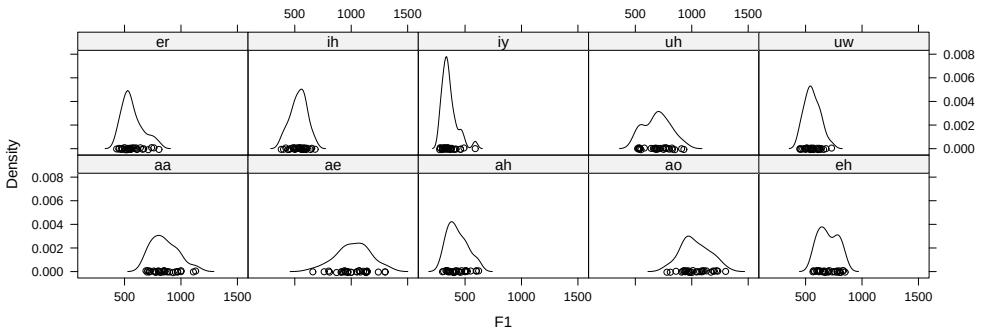


Figure 8.17: Density plots of children's F1 formant recordings from Peterson & Barney

In Section 8.3.2 I stated that one should not use ordinary (unrestricted) maximum likelihood, not REML, in frequentist test on models differing in what is often called "fixed-effects" structure (i.e., models differing only in the shared parameters $\boldsymbol{\theta}$). Can you think of any reasons why REML comparisons would not be a good idea for this purpose?

Exercise 8.3: Shrinkage

Consider the simple point estimate hierarchical model of [ɑ] first-formant (F1) data from Peterson and Barney (1952) obtained in Section 8.2.1. In this model, calculate the joint log-likelihood of $\widehat{\boldsymbol{b}}$ and $\boldsymbol{y}$—that is, of speaker-specific averages and trial-specific observations—using as $\widehat{\boldsymbol{b}}$ (i) the average recorded F1 frequency for each speaker, and (ii) the conditional modes, or BLUPs, obtained from the hierarchical model. Is the joint log-likelihood higher in (i) or (ii)?

Exercise 8.4

Replicate the posterior inference procedure in Section 8.2.2 for F2 formant frequencies from Peterson and Barney (1952).

Exercise 8.5: Priors on $\sigma_{\boldsymbol{y}}$

In Section 8.2.2, we used a prior that was locally uniform on the log of the variance parameter $\sigma_{\boldsymbol{y}}$. Another alternative would be to use a prior that was locally uniform on $\sigma_{\boldsymbol{y}}$ itself. Check to see how much of a difference, if any, this alternative would have on posterior inference over μ and $\Sigma_{\boldsymbol{b}}$. (You probably will want to do several simulations for each type of model to get a sense of how much variation there is over samples in each case.

Exercise 8.6: Hierarchical Bayesian linear models

Use `R` and `BUGS` together to replicate the analysis of Section 8.3.2, but with homoscedastic intra-cluster variation. Do the Bayesian confidence intervals on effects of northward migration, southward migration, and clan origin look similar to those obtained using point estimation?

Exercise 8.7: Hypothesis testing for random effects

Using the method of maximum likelihood via `lmer()`, together with the likelihood-ratio test, conduct a hypothesis test for the implicit-causality data of Section 8.3.4 on whether subject- and item-specific effects of experimental condition (as opposed to just subject- and item-specific intercepts) significantly improve the likelihood of a hierarchical model. That is, build a model where the only cluster-specific parameters are by-subject and by-item intercepts, and compare its log-likelihood to the full model in which all experimental conditions interact. What are your conclusions?

Exercise 8.8: Hierarchical Bayesian linear models with crossed effects

Replicate the fully Bayesian analysis presented in Section 8.3.4, but with condition-specific inter-subject and inter-item variation. Write down the complete model specification, implement it with JAGS, and compare the resulting inferences about model parameters with those from the point-estimate analysis and from the simpler Bayesian model. Be sure to consider both inferences about shared parameters and about the parameters governing cross-cluster variation!

Exercise 8.9: Transforms of quantitative predictors in mixed-effect models

Re-run the `dative.glmm` regression from Section 8.4.3, but use raw constituent lengths rather than log-transformed lengths. Compute cross-validated likelihoods (Section 2.11.5) to compare the performance of this model and of the original model? Which approach yields higher log-likelihood?

Exercise 8.10: Simplifying a model based on linguistic principles and model comparison

Define a simpler version of the model in Section 8.4.3 in which the effects of each of constituent length, animacy, discourse status, pronominality, and definiteness must be equal and opposite for recipients versus themes. Fit the model using approximate maximum-likelihood estimation, and compare it to the original model using the likelihood ratio test. Can you safely conclude that the effects of these factors truly are equal and opposite? (**Hint:** the easiest way to construct the simpler model is to define new quantitative predictors that express the summed influence of the property from both recipient and theme; see Exercise 6.11. Also keep in mind that the likelihood-ratio test can be anti-conservative for shared ("fixed-effect") parameters in hierarchical models.)

Exercise 8.11: Mixed-effects logit models and magnitudes of parameter estimates

Unlike with mixed-effects linear models, accounting for a cluster-level variable in a mixed-effects logit model can systematically change the magnitude of the parameter estimates for fixed effects. (**Warning:** this may be a pretty hard problem.)

1. Re-run the `dative.glmm` regression from Section 8.4.3 as a standard logistic regression model, completely omitting the random effect of verb, but replacing it with a fixed effect of the verb's Semantic Class). Do the magnitudes of most of the fixed-effect coefficients (intercept excluded) increase or decrease? Can you think of any reason why this would happen?

2. Test your intuitions by constructing a simple population with two clusters (call the factor `Cluster` with levels `C1,C2`) and a single two-level fixed effect (call the factor `Treatment` with levels `A,B`). Assume the underlying model involves the following linear predictor:

$$\eta = -1 + 2X + bZ$$

where X is a dummy indicator variable that is active when treatment level is `B`, Z is the cluster variable, and b is 1 for cluster 1 and -1 for cluster 2. Generate a dataset consisting of the following cell counts:

	C1	C2
A	250	250
B	250	250

using a logit model, and fit (1) a standard logistic regression with only `Treatment` as a fixed effect, and (2) a mixed-effects logistic regression. How does the estimation of the fixed effect change between models (1) and (2)?

3. Repeat your controlled experiment from (b) above, except this time use linear models (classic and mixed-effects) where the noise has standard deviation 1. Does the same change in the estimated effect of `Treatment` occur as in the logit model?

Exercise 8.12: Different priors on verb-specific effects

1. Use kernel density estimation to estimate the posterior density of the BLUPs for verbs in the dative alternation from the hierarchical logit model of Section 8.4.3. Plot this estimated density, and overlay on it a normal density with mean 0 and standard deviation $\hat{\sigma}_{\boldsymbol{b}}$. Do the BLUPs look like they follow this normal distribution? Choose another distribution for $\boldsymbol{b}$ in this model and implement it in BUGS. (Be forewarned that this is conceptually relatively simple but computationally rather intensive; loading the model and sampling from the posterior are likely to take several minutes or hours even on a new processor.) Plot the posterior inferences on $\boldsymbol{b}$ as in Figure 8.15 and compare them to the results of the original model. Are the results considerably different?

Exercise 8.13: Cross-validated likelihood and probability-proportion plot

Reconstruct Figure 8.16 using ten-fold cross-validation to obtain predicted probabilities. Does the resulting fit look better? Worse? Also compare the cross-validated likelihood to the original model's likelihood. Does the model seem substantially overfit?

Chapter 9

Dimensionality Reduction and Latent Variable Models

9.1 Gaussian mixture models

As a case study to motivate our first latent-variables model, we consider the problem of how infants learn the phonological categories of their native language. There is ample evidence that phonological-category learning involves a combination of both innate bias and experience. There are some phonetic distinctions which cannot be reliably identified by adult native speakers of languages that lack them (e.g., alveolar [d] versus retroflex [ɖ] for English speakers, or [r] versus [l] for Japanese speakers; Werker and Tees, 1984; Kuhl et al., 2006, inter alia), suggesting the power of innate bias. Likewise, it has more recently become clear that there are some phonetic distinctions which cannot be reliably identified by younger infants but which can be reliably identified not only by adult native speakers of languages which possess the distinction but also by older infants being raised in those language environments (e.g., syllable-initial [n] versus [ŋ] in Filipino language environments; citealpnarayan-etal: Explicit models of phonological category learning could potentially be of considerable value in gaining insight into how such learning takes place across languages.

An appreciation for some of the challenges inherent in the phonological category learning problem can be appreciated by considering inter-speaker variation in the realization of different categories. Figure 9.1 presents sample data drawn from multivariate Gaussian approximations of the realization of the vowels [i], [ɪ], [e], [ɛ] (as in *beet*, *bit*, *bait*, and *bet* respectively), for two native Canadian English speakers, plotted by their F1 and F2 formants as well as vowel durations respectively. To minimize gross inter-speaker variation, each dimension has been standardized according to the speaker's overall distributions in these three dimensions. Two difficulties stand out in this graph. First, whereas the first speaker has clear separation among the four vowels, the separation for the second speaker is much less clear; it is really essential to take F1 into account even to separate [ɛ] from the other three vowels, and the separation among the remaining three vowels is poor. Second, the distinctions among the vowels are not entirely robust across speakers: for example, whereas for the

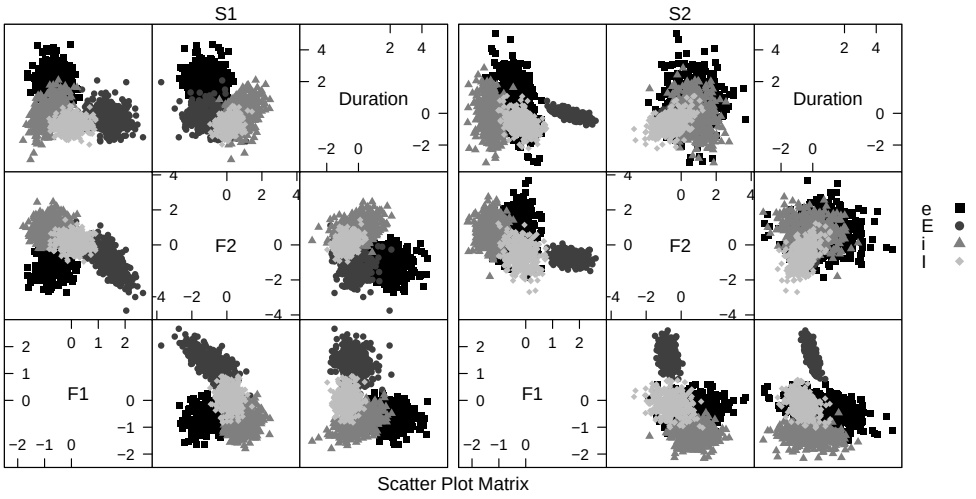


Figure 9.1: F1 frequency, F2 frequency, and duration of vowels [i],[ɪ],[e],[ɛ] for two speakers of English. Each of the three variables is standardized for each speaker.

first speaker [e] tends to have lower F2 than [ɪ], for the second speaker it is [ɪ] that tends to have lower F2 than [e]. Figure 9.2 shows samples from all four vowels mixed across nineteen speakers of English.

We will formalize the learning problem faced by the infant as follows: given a set of observations in a multidimensional phonetic space, draw inferences about (i) the proper grouping of the observations into categories; and (ii) the underlying abstract representations of those categories (e.g., what new observations drawn from each category are likely to look like). Every possible grouping of observations $\boldsymbol{y}$ into categories represents a PARTITION Π of the observations $\boldsymbol{y}$; let us denote the parameters determining the categories' underlying representations as $\boldsymbol{\theta}$. In probabilistic terms, our learning problem is to infer the probability distribution

$$P(\Pi, \boldsymbol{\theta}|\boldsymbol{y}) \tag{9.1}$$

from which we could recover the two marginal probability distributions of interest:

$$P(\Pi|\boldsymbol{y}) \qquad \text{(the distribution over partitions given the data; and)} \tag{9.2}$$

$$P(\boldsymbol{\theta}|\boldsymbol{y}) \qquad \text{(the distribution over category properties given the data.)} \tag{9.3}$$

To complete the formalization of the learning problem, we need to specify the representations $\boldsymbol{\theta}$ of the underlying categories, as well as a method for inferring the two probability distributions above. For the present problem, we will assume that each phonological category consists of a multivariate Gaussian distribution in the three-dimensional space of F1 frequency, F2 frequency, and vowel duration; hence the representations are the means $\boldsymbol{\mu}$ and covariance matrices $\boldsymbol{\Sigma}$ of multivariate normal distributions (see Section 3.5). This specifica-

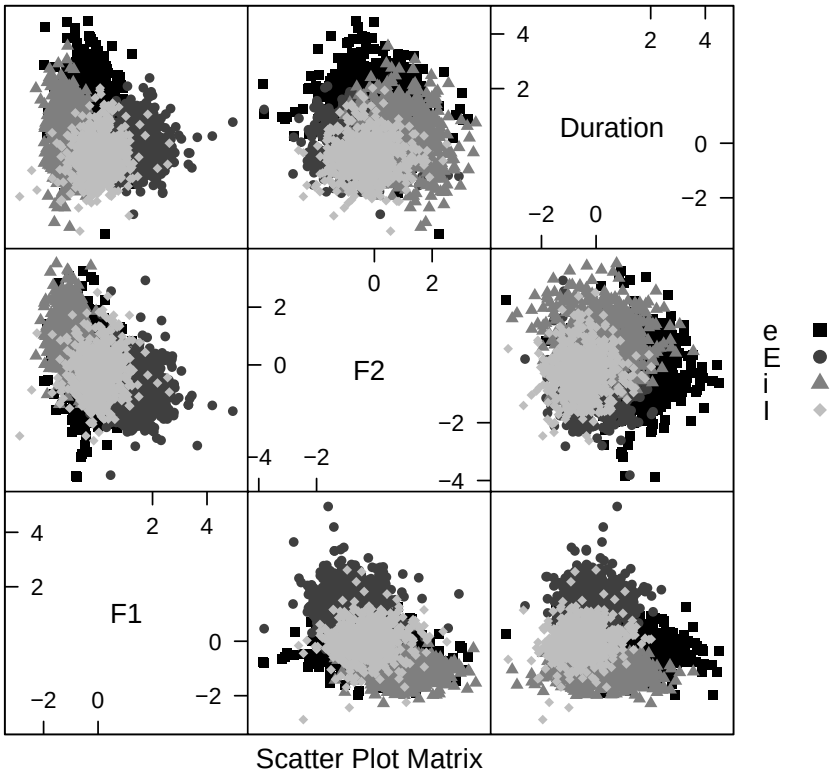


Figure 9.2: F1 frequency, F2 frequency, and duration of vowels [i],[ɪ],[e],[ɛ], mixed from 19 speakers of English.

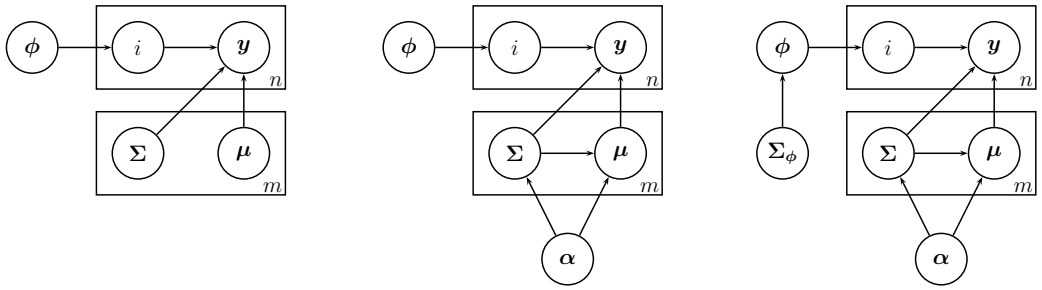
tion of category representations gives us the beginning of a generative model of our observations: each observation is drawn independently from the Gaussian distribution associated with one underlying category.

Thus far, the model is formally identical to the models examined in Chapter 6, where the category i to which each observation belongs could be treated as a categorical predictor variable, and our model specification is of the conditional probability distribution $P(Y|i)$. The crucial difference, however, is that in the present setting, the category identity of each observation is unknown—it is a LATENT VARIABLE which needs to be inferred. This means that the current specification is incomplete: it does not give us a probability distribution over possible observations in phonetic space. To complete the generative model, we need to specify the multinomial probabilities $\boldsymbol{\phi}$ that an observation will be drawn from each underlying category. This gives us the following generative model:

$$i \sim \text{Multinom}(\boldsymbol{\phi}) \tag{9.4}$$

$$y \sim \mathcal{N}(\mu_i, \Sigma_i) \tag{9.5}$$

In the probabilistic setting, the complete underlying properties to be inferred are thus



(a) Simple model

(b) Bayesian model priors over category parameters

(c) Learning category probabilities as well

Figure 9.3: Graphical model for simple mixture of Gaussians

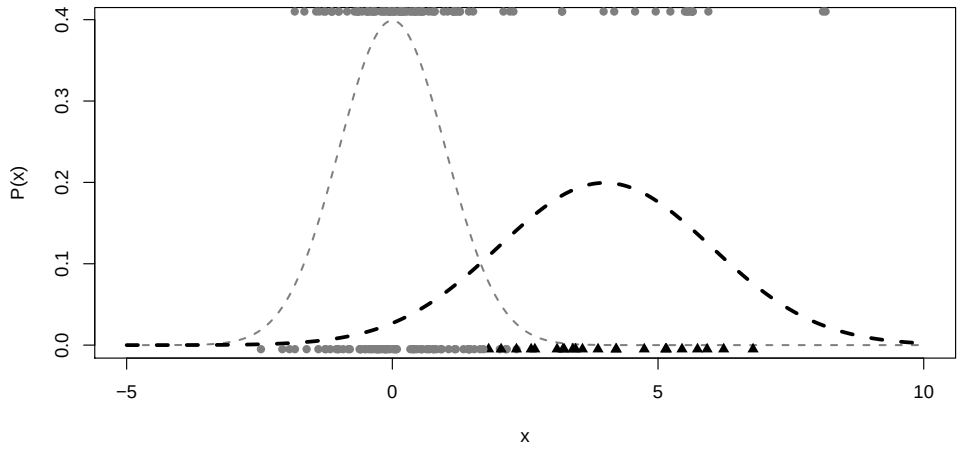


Figure 9.4: The generative mixture of Gaussians in one dimension. Model parameters are: $\phi_1 = 0.35, \mu_1 = 0, \sigma_1 = 1, \mu_2 = 4, \sigma_2 = 2$.

$\boldsymbol{\theta} = \langle \boldsymbol{\phi}, \boldsymbol{\mu}, \boldsymbol{\Sigma} \rangle$. This model is known as a MIXTURE OF GAUSSIANS, since the observations are drawn from some mixture of individually Gaussian distributions. An illustration of this generative model in one dimension is given in Figure 9.4, with the Gaussian mixture components drawn above the observations. At the bottom of the graph is one sample from this Gaussian mixture in which the underlying categories are distinguished; at the top of the graph is another sample in which the underlying categories are not distinguished. The relatively simple supervised problem would be to infer the means and variances of the Gaussian mixture components from the category-distinguished sample at the bottom of the graph; the much harder unsupervised problem is to infer these means and variances—and potentially the number of mixture components!—from the category-undistinguished sample at the top of the graph. The graphical model corresponding to this unsupervised learning problem is given in Figure 9.3a.

9.1.1 Inference for Gaussian mixture models

Let us temporarily set aside the problem of inferring the number of underlying categories and treat it as solved (we will return to this problem in Chapter **??**). Even so, we are faced with a challenging problem. If there are n observations and m categories, then there are m^n logically possible partitions, and it turns out that there is no way to get around this exponentially large number of partitions to find exact solutions for the two probabilities of interest, given in Equations (9.2) and (9.3). Furthermore, it isn't even possible to try obtaining a point estimate of Equation (9.3) through hill-climbing on a continuous surface, as we did with (for example) log-linear models in Chapter 6, because the partitions are discrete.

Additionally, there is a subtle but important property of the mixture-of-Gaussians problem that makes pure maximum-likelihood techniques deeply problematic. Consider a partition in which one category contains exactly one observation (in the case of Figure 9.4, for example, for the sample on the top of the graph let the rightmost point belong to one category, and let all other points belong to the other category). Now let the mean of that category be the observation itself. As the variance of that category approaches zero, the likelihood of that observation from that category approaches infinity (this is a case of the bias in the maximum-likelihood estimate of the variance, which we saw in Section 4.3.2). Therefore, any "maximum-likelihood" solution to this problem will involve categories which are centered around single observations and which have zero variance.[1]

This, therefore, is a very clear case where we need to inject prior knowledge in order to learn anything meaningful about category inventories at all. At a minimum, it is essential that this prior knowledge enforces the constraint that category variances approaching zero are forbidden. This requirement makes the Bayesian framework especially appealing: the constraint on category variances can be formalized by letting the prior probability of each category's parameters go to zero as the category variance itself goes to zero. Within the Bayesian framework, we can use sampling techniques to approximate the posterior distributions of interest in Equations (9.2) and (9.3).

A first Gaussian mixture model

We begin by simplifying the problem in assuming that category probabilities $\boldsymbol{\phi}$ are known and equal: $\phi_1 = \phi_2 = \phi_3 = \phi_4 = \frac{1}{4}$. These category probabilities serve as a uniform prior distribution over partitions. However, we still need to put priors over the individual category means $\boldsymbol{\mu}$ and covariances $\boldsymbol{\Sigma}$ in order to draw inferences about them. As always, there are many choices here; for convenience, we choose priors that are widely used for Bayesian learning of normal distributions with unknown mean and variance. This prior is specified in two parts, $P(\boldsymbol{\Sigma})$ and $P(\boldsymbol{\mu}|\boldsymbol{\Sigma})$:

[1] Purely likelihood-based methods for Gaussian mixture models, such as methods using the Expectation-Maximization (EM) algorithm, are indeed often seen, but they only yield non-trivial solutions (ones in which more than one cluster has at least two observations) by getting trapped in local optima.

$$\Sigma_i \sim \mathcal{IW}(\Sigma_0, \nu)$$
$$\mu_i | \boldsymbol{\Sigma} \sim \mathcal{N}(\mu_0, \Sigma_i / A)$$

where A is a scaling parameter and, as in Chapter 8, $\mathcal{IW}$ signifies the inverse Wishart distribution (Appendix B). This formulation may seem complex at first glance, but it is actually fairly straightforward. The first line states that the prior distribution on the covariance matrix is centered around some matrix Σ_0 which is treated as if it had been estimated from ν samples. The second line states that the prior distribution on the mean is normal and centered around μ_0, with covariance matrix proportional (by some factor $1/A$) to the covariance matrix Σ_i for observations. Placing dependence of the prior for the mean on the prior for the covariance matrix may seem counter-intuitive, but there are two good reasons to do it. First, this prior is conjugate to the likelihood of observed data within the cluster.[2] Second, according to this prior, any indication that there is low variability across observations (Σ_i small) is also an indication that we can estimate the mean with relatively high certainty (Σ_i / A small). This is exactly the way that the variance and mean are related in inferences from observed data: when observed data are broadly distributed, we estimate the variance to be large and have low certainty about the mean, but observed data are tightly distributed, we estimate the variance to be small and have high certainty about the mean.

Figure 9.5 is a visualization of this conjugate joint prior distribution over Σ and μ for univariate data (so that Σ can be represented as a scalar, σ). Note that this distribution drops off rapidly to zero near $\sigma = 0$.

Sampling from the posterior distribution

With this setup, it is straightforward to use Gibbs sampling (a type of Markov-chain Monte Carlo technique; see Section XXX) to draw samples from the joint posterior distribution $P(\Pi, \boldsymbol{\theta} | \boldsymbol{y})$, and to use these samples as the basis for any inferences we wish to make. Gibbs sampling here can be taken as alternating between sampling of a partition given model parameters from $P(\Pi | \boldsymbol{\theta}, \boldsymbol{y})$ and sampling of model parameters given a partition from $P(\boldsymbol{\theta} | \Pi, \boldsymbol{y})$. Because observations are conditionally independent of one another given model parameters (see Figure 9.3b), sampling a partition simply involves sampling a category i for each instance y_j conditioned on model parameters from $P(i | y_j, \boldsymbol{\theta})$, which can be rewritten using Bayes' rule as

$$P(i | y_j, \boldsymbol{\theta}) = \frac{P(y_j | i, \boldsymbol{\theta})}{\sum_i P(y_j | i, \boldsymbol{\theta})} \tag{9.6}$$

In our case, computing the numerator and each term of the sum in the denominator simply involves looking up the appropriate normal probability density. As regards $P(\boldsymbol{\theta} | \Pi, \boldsymbol{y})$, since the prior is conjugate to the likelihood of the observations given the partition, we can sample

[2] ***Reference Gelman et al. for better treatment of this conjugacy.

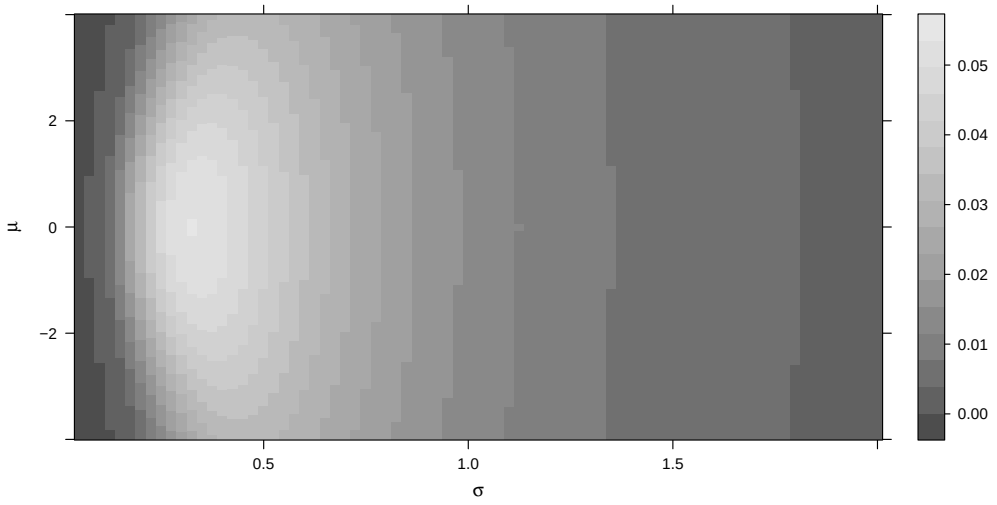


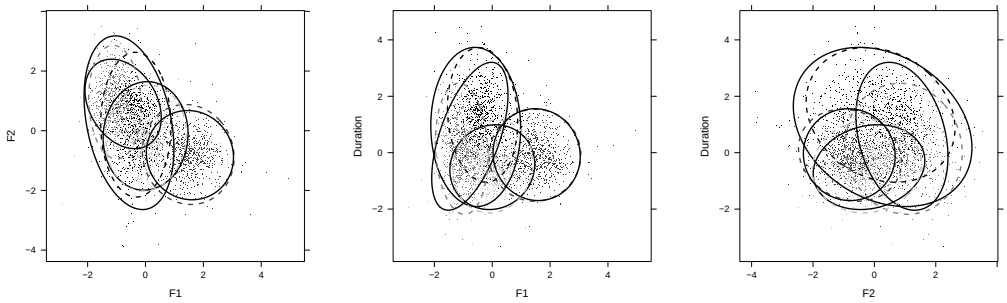
Figure 9.5: The joint distribution over component variances and means for a 1-dimensional Gaussian mixture model

the model parameters easily, first drawing a covariance matrix and then drawing a mean given the covariance matrix.

Evaluating samples from the posterior density on partitions and category parameters

Each Gibbs sample contains an estimate of both the model parameters and of the partition. The question now arises of how to use these samples, and how to assess the overall quality of the posterior distribution. In terms of assessing model parameters, it is not really appropriate in principle to average across samples because our problem is PERMUTATION INVARIANT in the categories: if we took one set of model parameters $\boldsymbol{\theta}$ fit and then permuted the category labels to get another set of parameters $\boldsymbol{\theta}'$, there would no reason to prefer one or the other. For this reason, it is common simply to get a sense of the posterior distribution over model parameters by inspecting a single sample (or by inspecting a small number of samples individually). In Figure 9.6, we have taken the last of 1000 samples and plotted its characteristic ellipses alongside the "true" characteristic ellipses for the four categories' Gaussian distributions (to be precise, the bias-corrected maximum-likelihood estimated Gaussians based on true category membership of our observations). Overall, the unsupervised model has done quite a good job of finding categories that turn out to match the underlying categories fairly well.

We now turn to evaluating the the quality of the partitions themselves. This task is made a bit tricky by the fact that there are no deep principles available to map categories learned by our model to "true" categories given in the data. That is, suppose that we draw a sample partition from the model which puts observations y_1, y_2, and y_3 in category 1, and observa-



(a) F1 and F2 (b) F1 versus Duration (c) F2 versus Duration

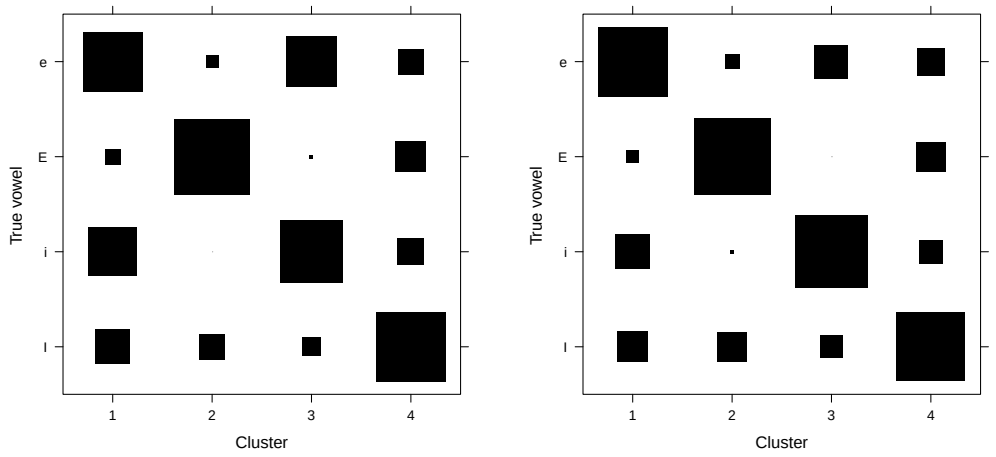
Figure 9.6: Categories inferred through unsupervised learning (solid lines) compared with the categories estimated from the same data with known categories via bias-corrected maximum likelihood (dotted lines)

tions y_4 and y_5 in category 2; but that underlyingly, y_1 and y_2 are instances of the vowel [i], and y_3, y_4, and y_5 are instances of the vowel [ɪ]. How accurate is the partition? A common approach is to choose the MAPPING from model categories to true categories that maximizes the proportion of correctly assigned observations, and use this proportion as a measure of model performance; in our toy example, we would assign category 1 to [i] and category 2 to [ɪ], and assess model performance at 80%. This approach has the disadvantage that the number of possible mappings increases exponentially with the number of true and learned categories, and greedy algorithms must be used to approximate the best mapping. Additionally, the mapping approach can become both conceptually and practically problematic when the number of latent categories is not equal to the number of true categories.[3]

Here we cover two other methods of assessing model performance in assignment of categories to partitions. The first method is purely visual: for a single sample partition, we construct a CONFUSION TABLE between true and guessed categories. Such a confusion table is in Figure 9.7a. In this table, each column is a model category and each row is a true vowel. The size of the square in each cell indicates the proportion of the guessed category that actually belongs to the true category. In this case, the model has some trouble distinguishing [i] from [e], but otherwise does a good job in distinguishing among the vowels. The corresponding confusion table for a supervised version of the model can be seen in Figure 9.7b; it is very clean.

The last method we cover here is assessing how well the model performs on average at the decision of whether two randomly drawn observations fall in the same category. This method is free of the matching-accuracy measure's need for a greedy cluster-assignment

[3]For example, one has to choose whether to impose a one-to-one constraint on the mapping between latent and true categories. When there are fewer true categories than there are latent categories, imposing a one-to-one constraint penalizes the model for making use of its full category inventory. On the other hand, if a one-to-one constraint is not imposed, then in the logical extreme case when the model has as many categories as it has observations, it is guaranteed to be assessed perfect accuracy!



(a) Unsupervised model (b) Supervised model

Figure 9.7: Confusion tables in the four-vowel unsupervised learning model.

algorithm, but has similar problems to matching accuracy when the number of categories in the model is not equal to the number of true categories. Like the matching-accuracy measure and unlike the confusion-matrix approach, the same-category measure can take advantage of averaging across multiple samples. In our case, drawing 1000 observation pairs without replacement from our dataset and averaging over every tenth sample from among the final 100 samples gives us a same-category measure of 0.752. The same measure can be applied to the supervised model, with a performance here of 0.852. In our case, a baseline measure using random-category assignment would have performance of $0.75^2 + 0.25^2 = 0.625$: there is a 75% chance that the observations willl be randomly drawn from different categories and the random category-assigner will assign different categories, and a 25% chance that the observations will be randomly drawn from the same category and the random assigner will assign the same category. Thus we can see that by this measure that the unsupervised learning model has learned enough to discriminate with accuracy far greater than chance whether two observations belong to the same category, but (unsurprisingly) has not reached the performance of the supervised learner.

9.1.2 Learning mixture probabilities

The simulation we set up was made artificially easy by the equal representation of all four vowels in our learning data, together with our hard prior constraint that category probabilities ϕ_i be identical. In real learning scenarios, underlying categories occur with different frequencies—for example, [ɪ] occurs more frequently in spoken American English than the other vowels here [add ref]. In principle, one might suppose that these category frequencies might not be learned initially; once the categories themselves have been learned and become accurately identifiable in the linguistic input, their frequencies can be estimated rel-

atively trivially. On the other hand, it is also possible that categories and their frequencies are learned simultaneously—indeed, this approach might facilitate learning of the categories themselves.

In our current framework, this approach would entail that inferences about the multinomial category probabilities $\boldsymbol{\phi}$ are drawn together with inferences about possible partitions Π and category structure parameters $\boldsymbol{\theta}$. It is straightforward to accommodate this additional aspect of inference within the Bayesian framework, putting a prior on $\boldsymbol{\phi}$, as in Figure 9.3c. A natural prior to use is the Dirichlet distribution, as it is conjugate to the multinomial (Sections XXX and B.8):

$$\boldsymbol{\phi} \sim \mathcal{D}(\boldsymbol{\Sigma}_{\boldsymbol{\phi}})$$

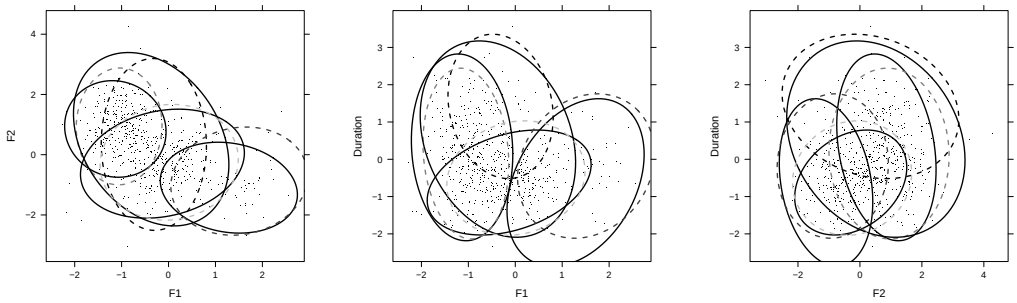
This combines with the other probability distributions we have used earlier:

$$\begin{aligned} \Sigma_i &\sim \mathcal{IW}(\Sigma_0, \nu) \\ \mu_i | \boldsymbol{\Sigma} &\sim \mathcal{N}(\mu_0, \Sigma_i / A) \\ i &\sim \text{Multinom}(\boldsymbol{\phi}) \\ y &\sim \mathcal{N}(\mu_i, \Sigma_i) \end{aligned}$$

to form our complete model. As discussed [elsewhere], the Dirichlet parameters $\boldsymbol{\Sigma}_{\boldsymbol{\phi}}$ are a vector of "pseudocounts", with larger total summed pseudocounts indicating higher confidence in the underlying probability. For our four-category Dirichlet prior, we use $\boldsymbol{\Sigma}_{\boldsymbol{\phi}} = \langle 4, 4, 4, 4 \rangle$, giving us a prior on category probabilities biased toward but not enforcing a uniform distribution. As before, we can use Gibbs sampling to draw from the posterior distribution over category probabilities; this is easy because of the conjugacy of the Dirichlet distribution to the multinomial distribution, which gives us an analytic form for $P(\boldsymbol{\phi} | \boldsymbol{\Sigma}_{\boldsymbol{\phi}}, \Pi)$.

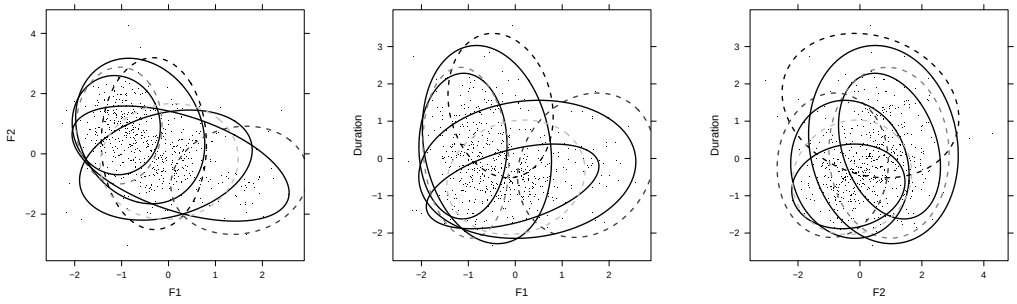
We evaluate the performance of this model by changing the probability of each vowel based loosely the frequencies in American English, but exaggerating the skew across vowels to emphasize the consequences for learning. We assign [e] a probability of 0.04, [ɛ] a probability of 0.05, [i] a probability of a probability of 0.29, and [ɪ] a probability of 0.62 respectively. The inability to learn category frequencies becomes an especially prominent issue with smaller samples (see Exercise **??** for more on this), so we give only 30 per speaker, distributed according to the probabilities just given. Results from the final of 1000 Gibbs samples are plotted in Figure 9.8. The learning problem has become much more difficult, due both to the smaller amount of data provided and to the less-constrained model space. Nevertheless, there are clear signs that the model has learned the qualitative structure of the four vowel categories.

These results can be contrasted with those obtained when our previous model—in which $\boldsymbol{\phi}_i$ were constrained to be equiprobable—is applied to these same data. The results from the final of 1000 Gibbs samples are shown in Figure 9.9. This model has also made some progress in the learning of category structure; there is a crucial difference, however, in that there is



(a) F1 and F2 (b) F1 and Duration (c) F2 and Duration

Figure 9.8: Learning category probabilities too.



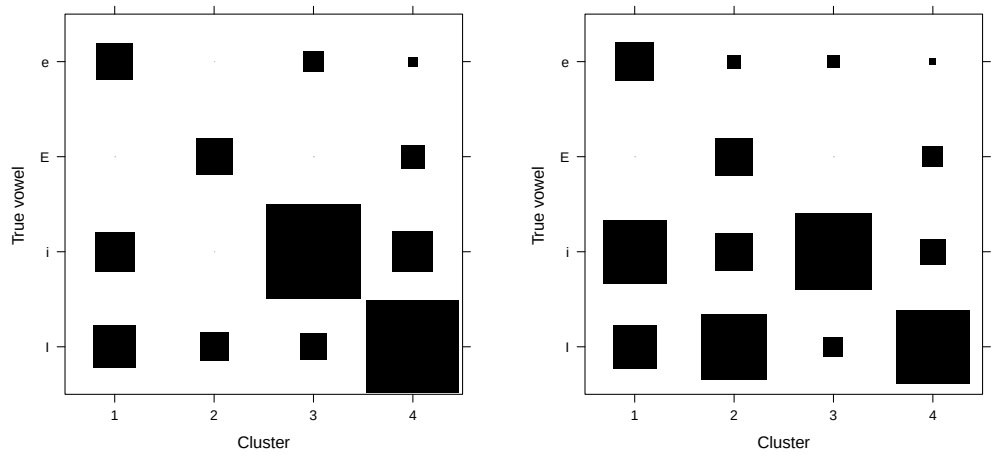
(a) F1 and F2 (b) F1 and Duration (c) F2 and Duration

Figure 9.9: Inferences in the skewed category-frequency case without the ability to learn category probability.

much heavier overlap across categories in the F1 and F2 dimensions. The difference in the results of the two models becomes more apparent when confusion matrices are constructed, as in Figure 9.10. The category-frequency learner clearly has trouble distinguishing between [e] and [i], but it has succeeded in learning a three-way distinction between [e]/[i], [ɛ], and [ɪ], and it has learned that [ɪ] is the most frequent category. The fixed-category-frequency learner, on the other hand, has not as clearly learned the difference between [ɛ] and [ɪ], and underlying [ɪ] observations are scattered widely across its four latent categories. ***Same-different performance: catfreqlearn: 0.627; fixed: 0.625

9.2 Latent Dirichlet Allocation and Topic Models

Another prominent dimension of language where the acquisition of latent structure is widely considered to be of great importance is *word meaning*. The sheer rate of word learning in native speakers is staggering: current estimates are that American native English speakers know an average of 40–100,000 words by age 17, and are thus learning new words at a rate



(a) With learning of category frequencies (b) Without learning of category frequencies

Figure 9.10: Confusion matrices in the skewed category-frequency case with and without the ability to learn category frequencies

of somewhere around ten a day (Nagy and Anderson, 1984; Landauer, 1986; Bloom, 2001). Researchers such as Landauer and Dumais (1997) have argued that most of the learning of word meanings must be implicit, since there is relatively little explicit instruction about the meanings of new words in classrooms, children's and young adults' reading materials, or in daily conversational interaction. The strong implication is that native speakers are able to construct sufficiently constraining representations of the possible meanings that an unknown word may have on the basis of the context (both linguistic and extra-linguistic) in which it appears to greatly facilitate learning of the unknown word's meaning. Investigation into the nature of these constraining representations of context has been an area of considerable interest in linguistics, cognitive science, and natural language processing.

One of the most extensively developed lines of research in this area has treated the representation of linguistic context with the use of VECTOR SPACES. On the most straightforward interpretation of this approach, linguistic meaning can be thought of as a continuous multidimensional semantic space populated by words meanings, each of which can be represented by a real-valued vector. The implications for how word learning could be facilitated by such representations are clear: if the learner is ultimately exposed to N words but the underlying vector space is of dimension $T \ll N$, the majority of the learning task may simply be learning the underlying vector space, which could be accomplished by exposure to a much smaller number of words N' on the order of T; after learning the vector space, fitting in the meanings of the remaining $N - N'$ words would be a much easier task.

Although it seems fairly clear that vector spaces are far from adequate as a complete model of word meaning—they leave unaddressed important qualitative facets of lexical semantics such as argument structure, aspect, distinctions between different types of antonymy, scalarity of adjectives, and so forth—they have proven quite popular as a research tool, in

no small part because formal methods for inferring vector-space meaning representations have been able to draw upon well-developed statistical techniques. Here, we cover two of the leading approaches to learning vector-space representations of word meaning: LATENT SEMANTIC ANALYSIS (LSA; Landauer and Dumais, 1997) and LATENT DIRICHLET ALLOCATION (LDA, also known as TOPICS MODELS; Blei et al., 2003; Griffiths and Steyvers, 2004; Griffiths et al., 2007). Viewed from the framework we have been pursuing in this textbook, LSA can be seen as a pure likelihood-based model based on assumptions of underlying normally distributed observations; LDA as most commonly practiced can be seen as a Bayesian model based on assumptions of multinomial-distributed observations. Both can be seen as instances of DIMENSIONALITY-REDUCTION techniques, where a lossless representation of the distribution of N word types across D documents is compressed down to a lossy representation in $T \ll N$ dimensions of word meaning. We cover LSA in Section XXX; here we cover LDA.

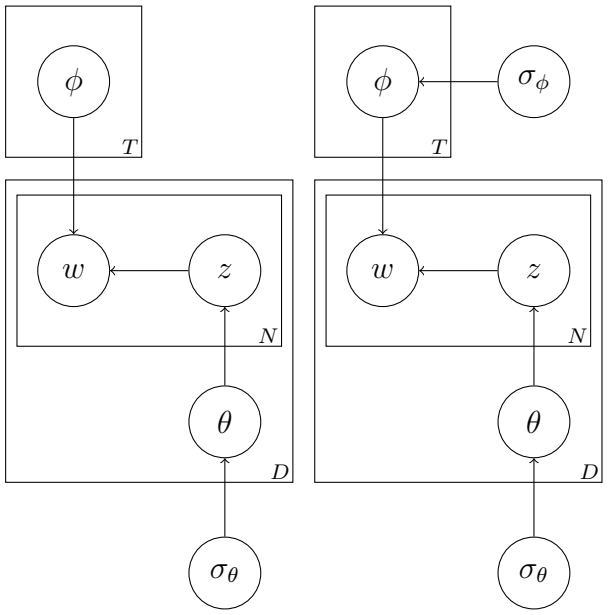
9.2.1 Formal specification

Formally, an LDA model involves the following components:

- A fixed vocabulary V of words;
- A set of T topics;
- For the i-th topic z_i, a multinomial distribution with parameters ϕ_i over all words in the vocabulary;
- For each document d, a multinomial distribution with parameters θ_d over the topics—this distribution can be called the TOPIC MIXTURE for d;
- A distribution over topic mixtures, generally taken to be a Dirichlet distribution with parameters σ_θ;
- Some distribution ζ over the number of words contained in a document.

The generative process for each document d is as follows: first, the number of words in d is drawn from ζ. Then, each word is generated by first sampling a topic z_j from θ_d, and then sampling a word w_j from ϕ_j. This process is used independently for each document. LDA as a graphical model is shown in Figure 9.11a. In the notation we've been using for specifying the individual component probability distributions in the graphical model, we have

$$\begin{aligned} \theta &\sim \mathcal{D}(\sigma_\theta) \\ z_i|\theta &\sim \text{Multinom}(\theta) \\ w_i|z_i, \phi &\sim \text{Multinom}(\phi_i) \end{aligned}$$



(a) Basic LDA (b) LDA with words-multinomial prior

Figure 9.11: Latent Dirichlet Allocation as a generative model of words in documents

At this point, careful comparison with Figure **??** is worthwhile. LDA is a hierarchical model in which the individual observations (words) are grouped into clusters (documents), and each cluster has specific properties that are drawn from some overall distribution governing inter-cluster variability. Additionally, in LDA, as with hierarchical models in Figure **??**, some parameters are shared across all clusters. The key difference in the structure of an LDA model as compared with the hierarchical models covered in Chapter 8 is that in LDA, the influence of the document-specific parameters θ is mediated completely through the assignment of topic identity for each word. That is, document-specific properties θ are conditionally independent of word identity given topic identity and the topic-specific word distributions ϕ. In the hierarchical models of Chapter 8, in contrast, cluster-specific properties directly affected the probability distribution on the response.

4

- state distr's used for LDA
- comment on what's done and what else might be considered

9.2.2 An LDA example

[4]The tradition within the topic models literature is to use a slightly different nomenclature for cluster parameters and distribution on cluster identities, but we'll stick with the current nomenclature for consistency.

```
We live in a dog eat dog world
The dog was chasing the cat
It was raining cat s and dog s
The cat and the dog were both on the mat
On Sunday the moon will pass before the sun
It is more dangerous to study the sun than it is to study the moon
```

Figure 9.12: A small synthetic corpus for use in inspecting LDA results. Note that for expository purposes, *cats* and *dogs* have been separated out into their constituent morphemes

Figure 9.12 depicts a small, artificial six-"document" corpus constructed for purposes of illustrating the behavior of LDA, and describing how to inspect the results of a model run. The salient feature of this dataset will be immediately obvious upon inspection: the words *dog* and *cat* have very strong co-occurrence within a given document, as do the words *sun* and *moon*. Thus a question of interest will be whether LDA can pick up on these associations by placing *dog* and *cat* in one topic and *sun* and *moon* in another. Another question of interest is what is done with the remaining words, which have varying degrees of correlation of co-occurrence with the four words listed above.

To fully define a Bayesian LDA model for this dataset we must: (i) pick a number of topics T, (ii) pick a prior over document-specific topic multinomials σ_θ, and (iii) pick a prior over topic-specific word multinomials σ_ϕ. We choose the following values:

$$\begin{aligned} T &= 2 \\ \sigma_\theta &= \langle 1, 1 \rangle \\ \sigma_\phi &= \langle 0.1, 0.1 \rangle \end{aligned}$$

Here we defer the question of discovery of number of topics for later discussion and simply assume there to be two topics. As we will describe in greater detail later on, it is important for σ_ϕ to be a *sparse* distribution, but there is a bit more flexibility in the choice of σ_θ.

Given a set of observed documents D with words $\boldsymbol{w}$, the exact posterior distributions on any subset of document-specific topic distributions θ, topic-specific word distributions ϕ, and on topic assignments $\boldsymbol{z}$ are intractable. However, there are a number of methods that have been developed to approximate and/or draw samples from the posterior distribution. For example, Griffiths and Steyvers (2004) developed a Gibbs sampling Markov technique to sample over the topic assignments $\boldsymbol{z}$, marginalizing over θ and ϕ. A topic assignment for our example is illustrated in Figure 9.13, with all the words in one topic rendered in lowercase and all the words in the other topic in CAPITALS. Here we see intuitive behavior from the model: it grouped all instances of *cat* and *dog* into a single topic, and all instances of *sun* and *moon* into a single topic. Note, however, that the topic assignments for the other words in the dataset are much more heterogeneous. In general, the prior distributions one chooses will have a powerful impact on the clusterings discovered in LDA. In the example thus far, we placed a uniform distribution on document-specific topic multinomials, and the sample

```
WE LIVE in a DOG eat DOG world
THE DOG WAS CHASING THE CAT
IT WAS RAINING CAT S AND DOG S
the CAT AND the DOG WERE both on the mat
on sunday the moon WILL pass before the sun
it is more dangerous to study the sun than it
```

Figure 9.13: Results of a topic model run with $T = 2$, $\sigma_\phi = \langle 0.1, 0.1 \rangle$, and $\sigma_\theta = \langle 1, 1 \rangle$

```
we live in a dog eat dog world
the dog was chasing the cat
it was raining cat s and dog s
the cat and the dog were both on the mat
ON SUNDAY THE MOON WILL PASS BEFORE THE SUN
IT IS MORE DANGEROUS TO STUDY THE SUN THAN IT
```

Figure 9.14: Results of a topic model run with a sparser document-topic prior: $T = 2$, $\sigma_\phi = \langle 0.1, 0.1 \rangle$, and $\sigma_\theta = \langle 0.01, 0.01 \rangle$

reflects use of both relatively uniform distributions (documents 1 and 4) and more skewed distributions (documents 2, 3, 5, and 6). If we change the prior to favor more skewed topic multinomials—say $\sigma_\theta = \langle 0.01, 0.01 \rangle$, closer to requiring "one topic per document"—we see that the model is guided by the *cat/dog*↔*sun/moon* structure of the dataset to cluster the documents (Figure 9.14).

Although the precise quantitative results of LDA applied to a corpus depend on the choice of prior, there are some broad qualitative generalizations that can be made regarding the type of clusterings of words into topics. One way of illustrating these generalizations is to consider the probability that two word tokens are assigned the same topic.

[TODO: add results of LDA with more topics on larger-scale document collection]

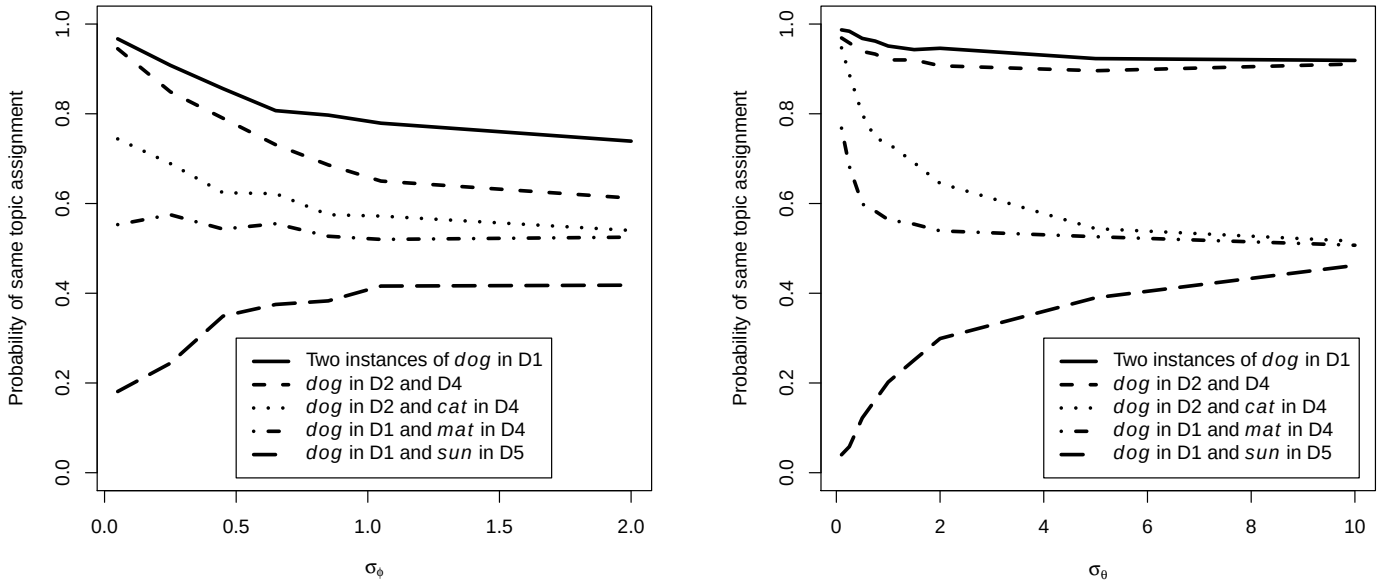
The posterior on topic-word and document-topic multinomials

Based on a sample of topic assignments $\boldsymbol{z}$ from the posterior distribution $P(\boldsymbol{z}|\boldsymbol{w}, \sigma_\theta, \sigma_\phi)$, one can approximate the document-specific topic distributions and topic-specific word distributions by treating the sampled topic assignments as observed. Let us suppose that $\sigma_\theta = \langle \alpha_1, \alpha_2, \ldots, \alpha_T \rangle$ and $\sigma_\phi = \langle \beta_1, \beta_2, \ldots, \beta_V \rangle$. Due to Dirichlet-multinomial conjugacy, if document i has N_i words of which m_j are assigned to topic j, we have

$$P(\theta|\boldsymbol{w}, \sigma_\theta, \sigma_\phi) \approx \mathcal{D}(\alpha_1 + m_1, \alpha_2 + m_2, \ldots, \alpha_T + m_T) \tag{9.7}$$

and if m_{jk} instances of word k are assigned to topic j, we have

$$P(\phi_j|\boldsymbol{w}, \sigma_\theta, \sigma_\phi) \approx \mathcal{D}(\beta_1 + m_{j1}, \beta_2 + m_{j2}, \ldots, \beta_V + m_{jT}). \tag{9.8}$$



(a) Varying σ_ϕ with $\sigma_\theta = 1$

(b) Varying σ_θ with σ_ϕ=0.1

Figure 9.15: The probability that two word tokens will be grouped into the same topic as a function of σ_ϕ and σ_θ

(See also Exercises **??** and **??**.)

9.2.3 Collapsed Gibbs Sampling

The techniques available for inspecting the posterior distribution over partitions (topic assignments) (z), document-specific topic mixtures (θ), and topic-specific word distributions (ϕ) in Latent Dirichlet Allocation provide a particularly clear example of how efficiencies in Bayesian inference for relatively complex graphical models can sometimes be found with appropriate choices of prior distribution. Consulting Figure 9.11b, we see that nodes in the graph which are either observed or set by researchers are σ_ϕ, σ_θ, and w. In a typical Gibbs sampling approach, we would alternate between sampling values at the ϕ, θ, and z nodes from the appropriate conditional probability distributions. Due to the use of Dirichlet distributions as priors and their conjugacy to the multinomial, all the distributions in question for the LDA Gibbs sampler turn out to be either multinomial or Dirichlet, this approach is perfectly feasible.

However, it turns out to be possible to do even better than this. Let us imagine that we know topics for all the words in our dataset except for the jth word of the ith document, which we can call w_{ij}. We can denote this set of topic assignments as $\boldsymbol{z}_{-ij}$. The distribution on the topic for that word, z_{ij}, conditional on $\boldsymbol{z}_{-ij}$ can be written using Bayes' rule as follows:

$$P(z_{ij}|\boldsymbol{w}, \boldsymbol{z}_{-ij}, \sigma_\theta, \sigma_\phi) = \frac{P(w_{ij}|\boldsymbol{z}, \boldsymbol{w}_{-ij}, \sigma_\theta, \sigma_\phi)P(z_{ij}|\boldsymbol{w}_{-ij}, \boldsymbol{z}_{-ij}, \sigma_\theta, \sigma_\phi)}{P(w_{ij}|\boldsymbol{z}_{-ij}, \boldsymbol{w}_{-ij}, \sigma_\theta, \sigma_\phi)} \tag{9.9}$$

Let us ignore the denominator (which is just a normalizing constant) and focus on the numerator. Inspecting Figure 9.11b, we can see that the first term (the likelihood of w_{ij} given its topic assignment z_{ij}) is conditionally independent of θ and σ_θ, since the only connection between these nodes and w_{ij} is strictly downstream in the graph and goes through z_{ij}, which is being conditioned on (see Chapter C). However, w_{ij} is *not* independent of ϕ, which we do not know. In this case, we need to marginalize:

$$P(w_{ij}|\boldsymbol{z}, \boldsymbol{w}_{-ij}, \sigma_\phi) = \int_\phi P(w_{ij}|\boldsymbol{z}, \boldsymbol{w}_{-ij}, \phi)P(\phi|\boldsymbol{z}, \sigma_\phi, \boldsymbol{w}_{-ij})\, d\phi \tag{9.10}$$

Recall that ϕ is a set of multinomial parameters—one multinomial for each topic. Since we are concerned only with the probability of a word generated from topic z_{ij}, we can ignore all the multinomial parameters except for those associated with this topic. Now, there are only two sources of information regarding these multinomial parameters: (i) the prior, and (ii) the words that have been observed to be emitted from topic z_{ij}. This prior is Dirichlet and the likelihood is multinomial, so that the predictive distribution over w_{ij} is a DIRICHLET-MULTINOMIAL model (Section B.8; compare with the beta-binomial model introduced in Section 4.4.2). For each word in the lexicon w, let the prior parameter for this word be denoted as $\sigma_\phi(w)$ and the number of observations of w to which topic z_{ij} has been assigned in the current sample as $c(w)$. The Dirichlet-multinomial model gives a simple analytic form for the marginal probability of w_{ij}:

$$P(w_{ij}|\boldsymbol{z}, \boldsymbol{w}_{-ij}, \sigma_\phi) = \frac{\sigma_\phi(w) + c(w)}{\sum_{w'} \sigma_\phi(w') + c(w')}$$

That is, we can *marginalize* over the parameters ϕ instead of sampling from them.

If we look at the second term of the numerator in Equation (9.9), we can see that it can also be expressed as a marginalization over document-specific multinomial parameters θ, with several conditioning variables being irrelevant:

$$P(z_{ij}|\boldsymbol{w}_{-ij}, \boldsymbol{z}_{-ij}, \sigma_\theta, \sigma_\phi) = \int_\theta P(z_{ij}|\theta)P(\theta|\boldsymbol{z}_{-ij}, \sigma_\theta)\, d\theta$$

In the same way as before, the first term in this integral—the likelihood—is multinomial, and the second term—the prior—is Dirichlet, giving us a Dirichlet-multinomial predictive distribution. If for each topic z we denote its prior parameter as $\sigma_\theta(z)$ and the number of words within document i that in the current sample have been assigned to z as $c_i(z)$, this predictive distribution has a simple form:

$$P(z_{ij}|\boldsymbol{w}_{-ij}, \boldsymbol{z}_{-ij}, \sigma_\theta, \sigma_\phi) = \frac{\sigma_\theta(w) + c_i(w)}{\sum_{z'} \sigma_\theta(z') + c_i(z')}$$

Combining the two expressions we get

$$P(w_{ij}|\boldsymbol{z}, \boldsymbol{w}_{-ij}, \sigma_\phi) \propto \frac{(\sigma_\phi(w) + c(w))\,(\sigma_\theta(w) + c_i(w))}{(\sum_{w'} \sigma_\phi(w') + c(w'))\,(\sum_{z'} \sigma_\theta(z') + c_i(z'))}$$

which eliminates the need to sample any multinomial parameters whatsoever. This technique of marginalizing over some latent variables in a Gibbs sampler is known as the COLLAPSED GIBBS SAMPLER, because the samples collapse (marginalize) over some of the nodes in the graphical model. The collapsed Gibbs sampler is generally more efficient than the corresponding uncollapsed Gibbs sampler (Liu, 1994)

9.3 Further Reading

There is an enormous literature on Gaussian mixture modeling in many fields; within language it has seen the most use in automated speech recognition Jurafsky and Martin (2008, Chapter 9). Specific applications to problems of language acquisition include Vallabha et al. (2007) and Feldman et al. (2009).

Topics models were introduced by (Blei et al., 2003; see also Griffiths and Steyvers, 2004) and have seen widespread applications and variants since then.

Appendix A

Mathematics notation and review

This appendix gives brief coverage of the mathematical notation and concepts that you'll encounter in this book. In the space of a few pages it is of course impossible to do justice to topics such as integration and matrix algebra. Readers interested in strengthening their fundamentals in these areas are encouraged to consult XXX [calculus] and Healy (2000).

A.1 Sets ($\{\}, \cup, \cap, \emptyset$)

The notation $\{a, b, c\}$ should be read as "the set containing the elements a, b, and c". With sets, it's sometimes a convention that lower-case letters are used as names for elements, and upper-case letters as names for sets, though this is a weak convention (after all, sets can contain anything—even other sets!).

$A \cup B$ is read as "the union of A and B", and its value is the set containing exactly those elements that are present in A, in B, or in both.

$A \cap B$ is read as "the intersection of A and B", and its value is the set containing only those elements present in both A and B.

$\emptyset$, or equivalently $\{\}$, denotes the empty set—the set containing nothing. Note that $\{\emptyset\}$ isn't the empty set—it's the set containing only the empty set, and since it contains something, it isn't empty!

[introduce set complementation if necessary]

A.1.1 Countability of sets

[briefly describe]

A.2 Summation ($\sum$)

Many times we'll want to express a complex sum of systematically related parts, such as $1 + \frac{1}{2} + \frac{1}{3} + \frac{1}{4} + \frac{1}{5}$ or $x_1 + x_2 + x_3 + x_4 + x_5$, more compactly. We use SUMMATION notation for this:

$$\sum_{i=1}^{5} \frac{1}{i} = 1 + \frac{1}{2} + \frac{1}{3} + \frac{1}{4} + \frac{1}{5} \qquad \sum_{i=1}^{5} x_i = x_1 + x_2 + x_3 + x_4 + x_5$$

In these cases, i is sometimes called an INDEX VARIABLE, linking the RANGE of the sum (1 to 5 in both of these cases) to its contents. Sums can be nested:

$$\sum_{i=1}^{2}\sum_{j=1}^{2} x_{ij} = x_{11} + x_{12} + x_{21} + x_{22} \qquad \sum_{i=1}^{3}\sum_{j=1}^{i} x_{ij} = x_{11} + x_{21} + x_{22} + x_{31} + x_{32} + x_{33}$$

Sums can also be infinite:

$$\sum_{i=1}^{\infty} \frac{1}{i^2} = \frac{1}{1^2} + \frac{1}{2^2} + \frac{1}{3^2} + \dots$$

Frequently, the range of the sum can be understood from context, and will be left out; or we want to be vague about the precise range of the sum. For example, suppose that there are n variables, x_1 through x_n. In order to say that the sum of all n variables is equal to 1, we might simply write

$$\sum_{i} x_i = 1$$

A.3 Product of a sequence ($\prod$)

Just as we often want to express a complex sum of systematically related parts, we often want to express a product of systematically related parts as well. We use PRODUCT notation to do this:

$$\prod_{i=1}^{5} \frac{1}{i} = 1 \times \frac{1}{2} \times \frac{1}{3} \times \frac{1}{4} \times \frac{1}{5} \qquad \prod_{i=1}^{5} x_i = x_1 x_2 x_3 x_4 x_5$$

Usage of product notation is completely analogous to summation notation as described in Section A.2.

A.4 "Cases" notation ($\{$)

Some types of equations, especially those describing probability functions, are often best expressed in the form of one or more conditional statements. As an example, consider a six-sided die that is weighted such that when it is rolled, 50% of the time the outcome is

a six, with the other five outcomes all being equally likely (i.e. 10% each). If we define a discrete random variable X representing the outcome of a roll of this die, then the clearest way of specifying the probability mass function for X is by splitting up the real numbers into three groups, such that all numbers in a given group are equally probable: (a) 6 has probability 0.5; (b) 1, 2, 3, 4, and 5 each have probability 0.1; (c) all other numbers have probability zero. Groupings of this type are often expressed using "cases" notation in an equation, with each of the cases expressed on a different row:

$$P(X = x) = \begin{cases} 0.5 & x = 6 \\ 0.1 & x \in \{1, 2, 3, 4, 5\} \\ 0 & \text{otherwise} \end{cases}$$

A.5 Logarithms and exponents

The log in base b of a number x is expressed as $log_b x$; when no base is given, as in $log x$, the base should be assumed to be the mathematical constant e. The expression $exp[x]$ is equivalent to the expression e^x. Among other things, logarithms are useful in probability theory because they allow one to translate between sums and products: $\sum_i \log x_i = \log \prod_i x_i$. Derivatives of logarithmic and exponential functions are as follows:

$$\frac{d}{dx} \log_b x = \frac{1}{x \log b}$$

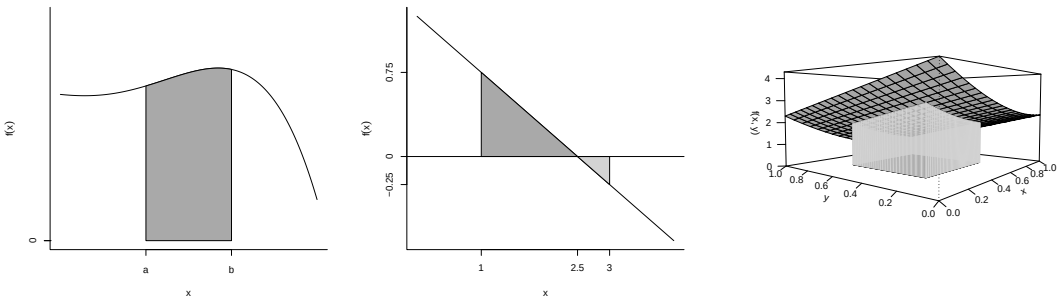
$$\frac{d}{dx} y^x = y^x \log y$$

A.6 Integration ($\int$)

Sums are always over countable (finite or countably infinite) sets. The analogue over a continuum is INTEGRATION. Correspondingly, you need to know a bit about integration in order to understand continuous random variables. In particular, a basic grasp of integration is essential to understanding how Bayesian statistical inference works.

One simple view of integration is as computing "area under the curve". In the case of integrating a function f over some range $[a, b]$ of a one-dimensional variable x in which $f(x) > 0$, this view is literally correct. Imagine plotting the curve $f(x)$ against x, extending straight lines from points a and b on the x-axis up to the curve, and then laying the plot down on a table. The area on the table enclosed on four sides by the curve, the x-axis, and the two additional straight lines is the integral

$$\int_a^b f(x) \, \mathrm{d}x$$



(a) (b) (c)

Figure A.1: Integration

This is depicted graphically in Figure A.1a.

The situation is perhaps slightly less intuitive, but really no more complicated, when $f(x)$ crosses the x-axis. In this case, area under the x-axis counts as "negative" area. An example is given in Figure A.1b; the function here is $f(x) = \frac{1}{2}(2.5 - x)$. Since the area of a triangle with height h and length l is $\frac{lh}{2}$, we can compute the integral in this case by subtracting the area of the smaller triangle from the larger triangle:

$$\int_1^3 f(x)\,\mathrm{d}x = \frac{1.5 \times 0.75}{2} - \frac{0.5 \times 0.25}{2} = 0.5$$

Integration also generalizes to multiple dimensions. For instance, the integral of a function f over an area in two dimensions x and y, where $f(x, y) > 0$, can be thought of as the volume enclosed by projecting the area's boundary from the x, y plane up to the $f(x, y)$ surface. A specific example is depicted in Figure A.1c, where the area in this case is the square bounded by 1/4 and 3/4 in both the x and y directions.

$$\int_{\frac{1}{4}}^{\frac{3}{4}} \int_{\frac{1}{4}}^{\frac{3}{4}} f(x, y)\,\mathrm{d}x\,\mathrm{d}y$$

An integral can also be over the *entire* range of a variable or set of variables. For instance, one would write an integral over the entire range of x as $\int_{-\infty}^{\infty} f(x)\,\mathrm{d}x$. Finally, in this book and in the literature on probabilistic inference you will see the abbreviated notation $\int_\theta f(\theta)\,\mathrm{d}\theta$, where θ is typically an ensemble (collection) of variables. In this book, the proper interpretation of this notation is as the integral over the entire range of all variables in the ensemble θ.

A.6.1 Analytic integration tricks

Computing an integral ANALYTICALLY means finding an exact form for the value of the integral. There are entire books devoted to analytic integration, but for the contents of this book you'll get pretty far with just a few tricks.

1. **Multiplication by constants.** The integral of a function times a constant C is the product of the constant and the integral of the function:

$$\int_a^b Cf(x)\,\mathrm{d}x = C\int_a^b f(x)\,\mathrm{d}x$$

2. **Sum rule.** The integral of a sum is the sum of the integrals of the parts:

$$\int_a^b [f(x)+g(x)]\,\mathrm{d}x = \int_a^b f(x)\,\mathrm{d}x + \int_a^b g(x)\,\mathrm{d}x$$

3. **Expressing one integral as the difference between two other integrals:** For $c < a, b$,

$$\int_a^b f(x)\,\mathrm{d}x = \int_c^b f(x)\,\mathrm{d}x - \int_c^a f(x)\,\mathrm{d}x$$

   This is an extremely important technique when asking whether the outcome of a continuous random variable falls within a range [a,b], because it allows you to answer this question in terms of cumulative distribution functions (Section 2.6); in these cases you'll choose $c = -\infty$.

4. **Polynomials.** For any $n \neq -1$:

$$\int_a^b x^n\,\mathrm{d}x = \frac{1}{n+1}(b^{n+1} - a^{n+1})$$

   And the special case for $n = -1$ is:

$$\int_a^b x^{-1}\,\mathrm{d}x = \log b - \log a$$

   Note that this generalization holds for $n = 0$, so that integration of a constant is easy:

$$\int_a^b C\,\mathrm{d}x = C(b-a)$$

5. **Normalizing constants.** If the function inside an integral looks the same as the probability density function for a known probability distribution, then its value is related to normalizing constant of the probability distribution. [Examples: normal distribution; beta distribution; others?] For example, consider the integral

$$\int_{-\infty}^{\infty} \exp\left[-\frac{x^2}{18}\right] \mathrm{d}x$$

This may look hopelessly complicated, but by comparison with Equation 2.21 in Section 2.10 you will see that it looks just like the probability density function of a normally distributed random variable with mean $\mu = 0$ and variance $\sigma^2 = 9$, except that it doesn't have the normalizing constant $\frac{1}{\sqrt{2\pi\sigma^2}}$. In order to determine the value of this integral, we can start by noting that any probability density function integrates to 1:

$$\int_{-\infty}^{\infty} \frac{1}{\sqrt{2\pi\sigma^2}} \exp\left[-\frac{(x-\mu)^2}{2\sigma^2}\right] \mathrm{d}x = 1$$

Substituting in $\mu = 0, \sigma^2 = 9$ we get

$$\int_{-\infty}^{\infty} \frac{1}{\sqrt{18\pi}} \exp\left[-\frac{x^2}{18}\right] \mathrm{d}x = 1$$

By the rule of multiplication by constants we get

$$\frac{1}{\sqrt{18\pi}} \int_{-\infty}^{\infty} \exp\left[-\frac{x^2}{18}\right] \mathrm{d}x = 1$$

or equivalently

$$\int_{-\infty}^{\infty} \exp\left[-\frac{x^2}{18}\right] \mathrm{d}x = \sqrt{18\pi}$$

giving us the solution to the original problem.

A.6.2 Numeric integration

The alternative to analytic integration is NUMERIC integration, which means approximating the value of an integral by explicit numeric computation. There are many ways to do this—one common way is by breaking up the range of integration into many small pieces, approximating the size of each piece, and summing the approximate sizes. A graphical

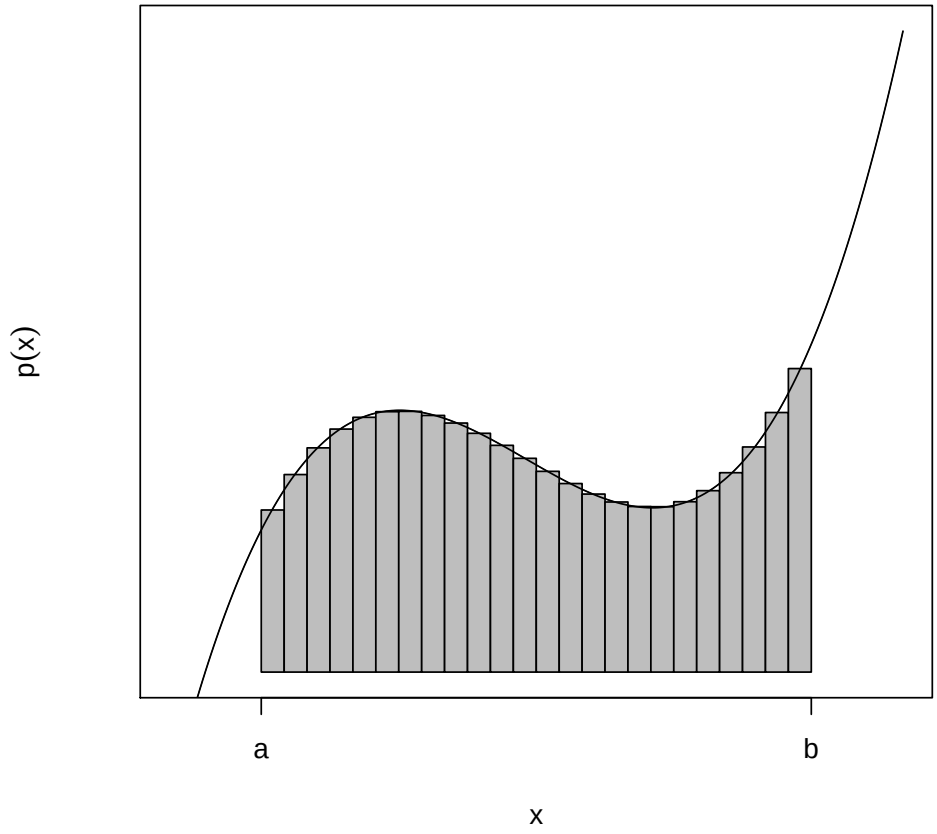


Figure A.2: Numeric integration

example of how this might be done is shown in Figure A.2, where each piece of the area under the curve is approximated as a rectangle whose height is the average of the distances from the x-axis to the curve at the left and right edges of the rectangle. There are many techniques for numeric integration, and we shall have occasional use for some of them in this book.

A.7 Precedence ($\prec$)

The $\prec$ operator is used occasionally in this book to denote LINEAR PRECEDENCE. In the syntax of English, for example, the information that "a verb phrase (VP) can consist of a verb (V) followed by a noun phrase (NP) object" is most often written as:

$$\text{V} \rightarrow \text{V NP}$$

This statement combines two pieces of information: (1) a VP can be comprised of a V and an NP; and (2) in the VP, the V should precede the NP. In a syntactic tradition stemming from Generalized Phrase Structure Grammar (Gazdar et al., 1985), these pieces of information can be separated:

$$(1)\text{V} \rightarrow \text{V, NP} \qquad\qquad (2)\text{V} \prec \text{NP}$$

where V,NP means "the unordered set of categories V and NP", and V $\prec$ NP reads as "V precedes NP".

A.8 Combinatorics ($\binom{n}{r}$)

The notation $\binom{n}{r}$ is read as "n choose r" and is defined as the number of possible ways of selecting r elements from a larger collection of n elements, allowing each element to be chosen a maximum of once and ignoring order of selection. The following equality holds generally:

$$\binom{n}{r} = \frac{n!}{r!(n-r)!} \tag{A.1}$$

The solution to the closely related problem of creating m classes from n elements by selecting r_i for the i-th class and discarding the leftover elements is written as $\binom{n}{r_1 \ldots r_m}$ and its value is

$$\binom{n}{r_1 \ldots r_m} = \frac{n!}{r_1! \ldots r_m!} \tag{A.2}$$

Terms of this form appear in this book in the binomial and multinomial probability mass functions, and as normalizing constant for the beta and Dirichlet distributions.

A.9 Basic matrix algebra

There are a number of situations in probabilistic modeling—many of which are covered in this book—where the computations needing to be performed can be simplified, both conceptually and notationally, by casting them in terms of MATRIX operations. A matrix $\boldsymbol{X}$ of dimensions $m \times n$ is a set of mn entries arranged rectangularly into m rows and n columns, with its entries indexed as x_{ij}:

$$\boldsymbol{X} = \begin{bmatrix} x_{11} & x_{12} & \dots & x_{1n} \\ x_{21} & x_{21} & \dots & x_{2n} \\ \vdots & \vdots & \ddots & \vdots \\ x_{m1} & x_{m1} & \dots & x_{mn} \end{bmatrix}$$

For example, the matrix $\boldsymbol{A} = \begin{bmatrix} 3 & 4 & -1 \\ 0 & -2 & 2 \end{bmatrix}$ has values $a_{11} = 3$, $a_{12} = 4$, $a_{13} = -1$, $a_{21} = 0$, $a_{22} = -2$, and $a_{23} = 2$. For a matrix $\boldsymbol{X}$, the entry x_{ij} is often called the i, j-th entry of $\boldsymbol{X}$.

If a matrix has the same number of rows and columns, it is often called a SQUARE matrix. Square matrices are often divided into the DIAGONAL entries $\{x_{ii}\}$ and the OFF-DIAGONAL entries $\{x_{ij}\}$ where $i \neq j$. A matrix of dimension $m \times 1$—that is, a single-column matrix—is often called a VECTOR.

Symmetric matrices: a square matrix $\boldsymbol{A}$ is SYMMETRIC if $\boldsymbol{A}^T = \boldsymbol{A}$. For example, the matrix

$$\begin{bmatrix} 10 & -1 & 4 \\ -1 & 3 & 2 \\ 4 & 2 & 5 \end{bmatrix}$$

is symmetric. You will generally encounter symmetric matrices in this book as variance-covariance matrices (e.g., of the multivariate normal distribution, Section 3.5). Note that a symmetric $n \times n$ matrix has $\frac{n(n+1)}{2}$ "free" entries—one can choose the entries on and above the diagonal, but the entries below the diagonal are fully determined by the entries above it.

Diagonal and Identity matrices: For a square matrix $\boldsymbol{X}$, the entries x_{ii}—that is, when the column and row numbers are the same—are called the DIAGONAL entries. A square matrix whose non-diagonal entries are all zero is called a DIAGONAL MATRIX. A diagonal matrix of size $n \times n$ whose diagonal entries are all 1 is called the size-n IDENTITY matrix. Hence $\boldsymbol{A}$ below is a diagonal matrix, and $\boldsymbol{B}$ below is the size-3 identity matrix.

$$\boldsymbol{A} = \begin{bmatrix} 3 & 0 & 0 \\ 0 & -2 & 0 \\ 0 & 0 & 1 \end{bmatrix} \qquad \boldsymbol{B} = \begin{bmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{bmatrix}$$

The $n \times n$ identity matrix is sometimes notated as $\boldsymbol{I}_n$; when the dimension is clear from context, sometimes the simpler notation $\boldsymbol{I}$ is used.

Transposition: For any matrix $\boldsymbol{X}$ of dimension $m \times n$, the TRANSPOSE of $\boldsymbol{X}$, or $\boldsymbol{X}^{\mathrm{T}}$, is an $n \times m$-dimensional matrix such that the i, j-th entry of $\boldsymbol{X}^{\mathrm{T}}$ is the j, i-th entry of $\boldsymbol{X}$. For the matrix $\boldsymbol{A}$ above, for example, we have

$$\boldsymbol{A}^{\mathrm{T}} = \begin{bmatrix} 3 & 0 \\ 4 & -2 \\ -1 & 2 \end{bmatrix} \tag{A.3}$$

Addition: Matrices of like dimension can be added. If $\boldsymbol{X}$ and $\boldsymbol{Y}$ are both $m \times n$ matrices, then $\boldsymbol{X} + \boldsymbol{Y}$ is the $m \times n$ matrix whose i, j-th entry is $x_{ij} + y_{ij}$. For example,

$$\begin{bmatrix} 3 & 0 \\ 4 & -2 \\ -1 & 2 \end{bmatrix} + \begin{bmatrix} -1 & -1 \\ 0 & 2 \\ 5 & 5 \end{bmatrix} = \begin{bmatrix} 2 & -1 \\ 4 & 0 \\ 4 & 7 \end{bmatrix} \tag{A.4}$$

Multiplication: If $\boldsymbol{X}$ is an $l \times m$ matrix and $\boldsymbol{Y}$ is an $m \times n$ matrix, then $\boldsymbol{X}$ and $\boldsymbol{Y}$ can be multiplied together; the resulting matrix $\boldsymbol{XY}$ is an $l \times m$ matrix. If $\boldsymbol{Z} = \boldsymbol{XY}$, the i, j-th entry of $\boldsymbol{Z}$ is:

$$z_{ij} = \sum_{k=1}^{m} x_{ik} y_{kj}$$

For example, if $\boldsymbol{A} = \begin{bmatrix} 1 & 2 \\ -1 & 0 \\ 3 & 1 \end{bmatrix}$ and $\boldsymbol{B} = \begin{bmatrix} 3 & 4 & -1 & 6 \\ 0 & -5 & 2 & -2 \end{bmatrix}$, we have

$$\begin{aligned} \boldsymbol{AB} &= \begin{bmatrix} 1 \times 3 + 2 \times 0 & 1 \times 4 + 2 \times (-5) & 1 \times (-1) + 2 \times 2 & 1 \times 6 + 2 \times (-2) \\ (-1) \times 3 + 0 \times 0 & (-1) \times 4 + 0 \times (-5) & (-1) \times (-1) + 0 \times 2 & (-1) \times 6 + 0 \times (-2) \\ 3 \times 3 + 1 \times 0 & 3 \times 4 + 1 \times (-5) & 3 \times (-1) + 1 \times 2 & 3 \times 6 + 1 \times (-2) \end{bmatrix} \\ &= \begin{bmatrix} 3 & -6 & 3 & 2 \\ -3 & -4 & 1 & -6 \\ 9 & 7 & -1 & 16 \end{bmatrix} \end{aligned}$$

Unlike multiplication of scalars, matrix multiplication is **not** commutative—that is, it is not generally the case that $\boldsymbol{XY} = \boldsymbol{YX}$. In fact, being able to form the matrix product $\boldsymbol{XY}$ does not even guarantee that we can do the multiplication in the opposite order and form the matrix product $\boldsymbol{YX}$; the dimensions may not be right. (Such is the case for matrices A and B in our example.)

Determinants. For a square matrix $\boldsymbol{X}$, the DETERMINANT $|\boldsymbol{X}|$ is a measure of the matrix's "size". In this book, determinants appear in coverage of the multivariate normal distribution (Section 3.5); the normalizing constant of the multivariate normal density includes the determinant of the covariance matrix. (The univariate normal density, introduced in Section 2.10, is a special case; there, it is simply the variance of the distribution that appears in the normalizing constant.) For small matrices, there are simple techniques for calculating determinants: as an example, the determinant of a 2×2 matrix $\boldsymbol{A} = \begin{bmatrix} a & b \\ c & d \end{bmatrix}$ is $|\boldsymbol{A}| = ad - bc$. For larger matrices, computing determinants requires more general and complex techniques, which can be found in books on linear algebra such as Healy (2000).

Matrix Inversion. The INVERSE or RECIPROCAL of an $n \times n$ square matrix $\boldsymbol{X}$, denoted $\boldsymbol{X}^{-1}$, is the $n \times n$ matrix such that $\boldsymbol{X}\boldsymbol{X}^{-1} = \boldsymbol{I}_n$. As with scalars, the inverse of the inverse

of a matrix $\boldsymbol{X}$ is simply $\boldsymbol{X}$. However, not all matrices have inverses (just like the scalar 0 has no inverse).

For example, the following pair of matrices are inverses of each other:

$$\boldsymbol{A} = \begin{bmatrix} 2 & 1 \\ 1 & 2 \end{bmatrix} \qquad \boldsymbol{A}^{-1} = \begin{bmatrix} \frac{2}{3} & -\frac{1}{3} \\ -\frac{1}{3} & \frac{2}{3} \end{bmatrix}$$

A.9.1 Algebraic properties of matrix operations

Associativity, Commutativity, and Distributivity

Consider matrices $\boldsymbol{A}$, $\boldsymbol{B}$, and $\boldsymbol{C}$. Matrix multiplication is associative ($\boldsymbol{A}(\boldsymbol{BC}) = (\boldsymbol{AB})\boldsymbol{C}$) and distributive over addition ($\boldsymbol{A}(\boldsymbol{B}+\boldsymbol{C}) = (\boldsymbol{A}+\boldsymbol{B})\boldsymbol{C}$), but not commutative: even if the multiplication is possible in both orderings (that is, if $\boldsymbol{B}$ and $\boldsymbol{A}$ are both square matrices with the same dimensions), in general $\boldsymbol{AB} \neq \boldsymbol{BA}$.

Transposition, inversion and determinants of matrix products.

- The transpose of a matrix product is the product of each matrix's transpose, in reverse order: $(\boldsymbol{AB})^T = \boldsymbol{B}^T\boldsymbol{A}^T$.
- Likewise, the inverse of a matrix product is the product of each matrix's inverse, in reverse order: $(\boldsymbol{AB})^{-1} = \boldsymbol{B}^{-1}\boldsymbol{A}^{-1}$.
- The determinant of a matrix product is the product of the determinants:

$$|\boldsymbol{AB}| = |\boldsymbol{A}|\,|\boldsymbol{B}|$$

- Because of this, the determinant of the inverse of a matrix is the reciprocal of the matrix's determinant:

$$\left|\boldsymbol{A}^{-1}\right| = \frac{1}{|\boldsymbol{A}|}$$

A.10 Miscellaneous notation

- $\propto$: You'll often see $f(x) \propto g(x)$ for some functions f and g of x. This is to be read as "$f(x)$ is proportional to $g(x)$", or "$f(x)$ is equal to $g(x)$ to within some constant". Typically it's used when $f(x)$ is intended to be a probability, and $g(x)$ is a function that obeys the first two axioms of probability theory, but is improper. This situation obtains quite often when, for example, conducting Bayesian inference.

Appendix B

More probability distributions and related mathematical constructs

This chapter covers probability distributions and related mathematical constructs that are referenced elsewhere in the book but aren't covered in detail. One of the best places for more detailed information about these and many other important probability distributions is Wikipedia.

B.1 The gamma and beta functions

The GAMMA FUNCTION $\Gamma(x)$, defined for $x > 0$, can be thought of as a generalization of the factorial $x!$. It is defined as

$$\Gamma(x) = \int_0^\infty u^{x-1} e^{-u}\, du$$

and is available as a function in most statistical software packages such as `R`. The behavior of the gamma function is simpler than its form may suggest: $\Gamma(1) = 1$, and if $x > 1$, $\Gamma(x) = (x-1)\Gamma(x-1)$. This means that if x is a positive integer, then $\Gamma(x) = (x-1)!$.

The BETA FUNCTION $B(\alpha_1, \alpha_2)$ is defined as a combination of gamma functions:

$$B(\alpha_1, \alpha_2) \stackrel{\text{def}}{=} \frac{\Gamma(\alpha 1)\Gamma(\alpha 2)}{\Gamma(\alpha 1 + \alpha 2)}$$

The beta function comes up as a normalizing constant for beta distributions (Section 4.4.2). It's often useful to recognize the following identity:

$$B(\alpha_1, \alpha_2) = \int_0^1 x^{\alpha_1 - 1}(1-x)^{\alpha_2 - 1}\, dx$$

B.2 The Poisson distribution

The POISSON DISTRIBUTION is a generalization of the binomial distribution in which the number of trials n grows arbitrarily large while the mean number of successes πn is held constant. It is traditional to write the mean number of successes as λ; the Poisson probability density function is

$$P(y;\lambda) = e^{\lambda}\frac{\lambda^y}{y!} \quad (y = 0, 1, \dots) \tag{B.1}$$

The Gamma distribution is conjugate for the Poisson parameter λ, hence it is common to use a Gamma prior on λ in Bayesian inference.

B.3 The hypergeometric distribution

One way of thinking of the binomial distribution is as n repeated draws from a bag with M marbles, πM of which are black and the rest of which are white; each outcome is recorded and the drawn marble is replaced in the bag, and at the end the total number of black marbles is the outcome k. This picture is often called SAMPLING WITH REPLACEMENT. The HYPERGEOMETRIC distribution is similar to this conception of the binomial distribution except that the marbles are not replaced after drawn—this is SAMPLING WITHOUT REPLACEMENT. The hypergeometric distribution has three parameters: the number of marbles M, the number of black marbles m, and the number of draws n; the probability mass function on the number of "successes" X (black marbles drawn) is

$$P(X = r) = \frac{\binom{m}{r}\binom{M-m}{n-r}}{\binom{M}{m}}$$

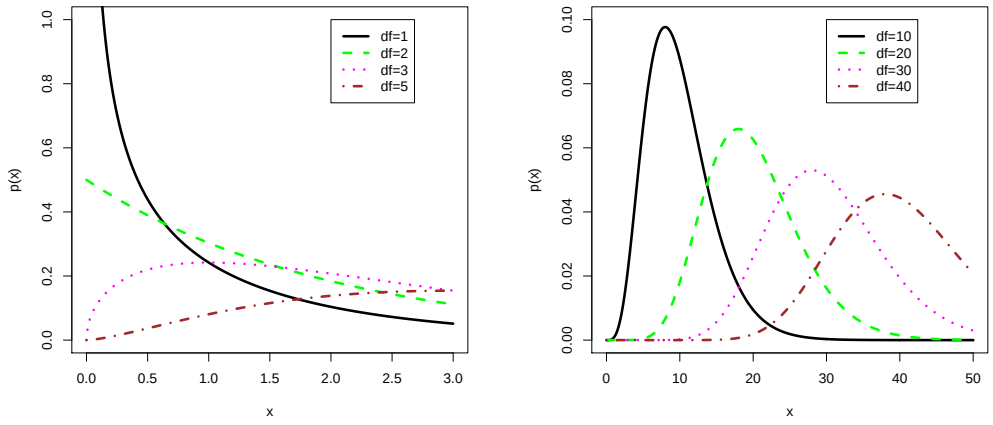
In this book, the hypergeometric distribution comes up in discussion of Fisher's exact test (Section 5.4.3).

B.4 The chi-square distribution

Suppose that we have a standard normal random variable Z—that is, $Z \sim N(0, 1)$. The distribution that the quantity Z^2 follows is called the CHI-SQUARE DISTRIBUTION with ONE DEGREE OF FREEDOM. This distribution is typically denoted as χ^2_1.

If we have k independent random variables $U_1, \dots, U_k$ such that each $U_i \sim \chi^2_1$, then the distribution of $U = U_1 + \cdots + U_k$ is the chi-squared with k degrees of freedom. This is denoted as $U \sim \chi^2_k$. The expectation of U is k and its variance is $2k$.

Figure B.1 illustrates the probability density functions for χ^2 distributions with various degrees of freedom. The χ^2_1 distribution grows asyptotically as x approaches 0, and χ^2_2 decreases monotonically, but all other χ^2_k distributions have a mode for some positive $x < k$.



(a) df≤10 (b) df≥10

Figure B.1: The χ^2 distribution with various degrees of freedom

As k grows large, more and more of the probability mass becomes located relatively close to $x = k$.

The key place where χ^2 variables arise is as the distribution of variance of a normal distribution. If we sample n points from $\mathcal{N}(\mu, \sigma^2)$ (once again: that's a normal distribution with mean μ and variance σ^2), then the quantity

$$\frac{1}{\sigma^2} \sum_{i=1}^{n} (x_i - \hat{\mu})^2$$

is distributed as χ^2_{n-1}.

If U is distributed as χ^2_k, then the distribution of the quantity $1/U$ is called the INVERSE CHI-SQUARE DISTRIBUTION with k degrees of freedom. The inverse chi-square distribution is used in Bayesian inference as a conjugate prior (Section 4.4.3) for the variance of the normal distribution.

B.5 The t-distribution

Suppose once again that we have a standard normal random variable $Z \sim N(0, 1)$, and also that we have a chi-squared random variable U with k degrees of freedom. The distribution of the quantity

$$\frac{Z}{\sqrt{U/k}} \tag{B.2}$$

is called the t-DISTRIBUTION WITH k DEGREES OF FREEDOM. It has expectation 0, and as long as $k > 2$ its variance is $\frac{k}{k-2}$ (it has infinite variance if $k \leq 2$).

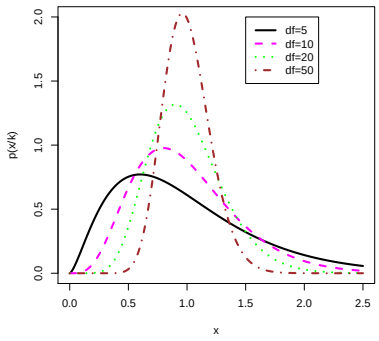


Figure B.2: The χ^2 distribution, normalized by degrees of freedom

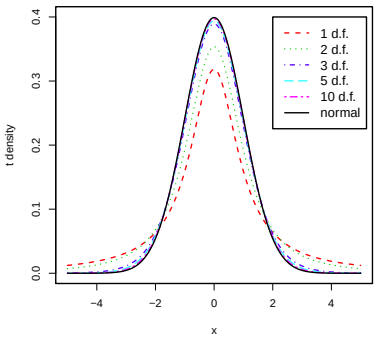


Figure B.3: The t distribution

Figure B.3 shows the probability density functions for t distributions with varying degrees of freedom, together with the standard normal distribution for reference. The t distribution is *heavier-tailed* than the normal distribution, but even with 10 degrees of freedom the t distribution is already very close to the standard normal. As the degrees of freedom grow, the t distribution converges to the standard normal; intuitively, this is because χ^2_k becomes more and more centered around k, so the quantity U/k in Equation B.2 converges to 1.

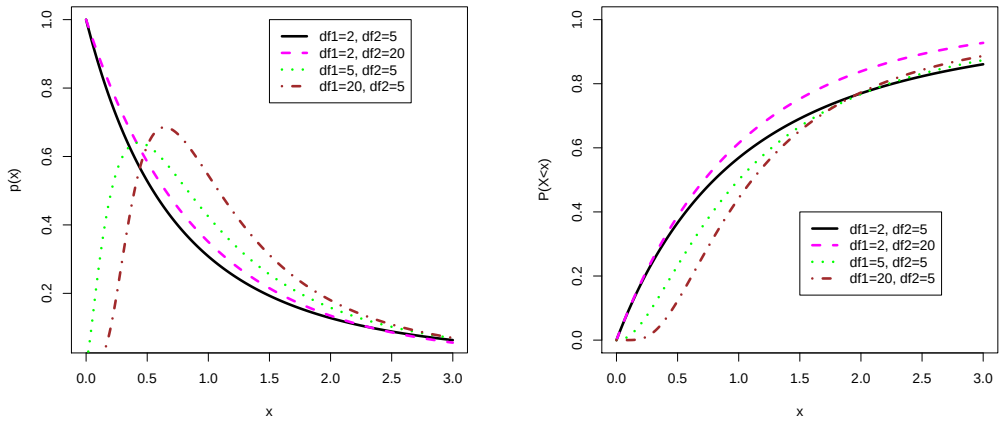
B.6 The F distribution

The F distribution, named after Ronald A. Fisher, one of the founders of the frequentist school of statistical analysis, is the distribution of the normalized ratio of two independent normalized χ^2 random variables. More formally, if $U \sim \chi^2_{k_1}$ and $V \sim \chi^2_{k_2}$, we have

$$F_{k_1,k_2} \sim \frac{U/k_1}{V/k_2} \tag{B.3}$$

Here are a few things to note about the F distribution:

- The F distribution comes up mainly in frequentist hypothesis testing for linear models (Section 6.5).
- As k_1 and k_2 grow, all the probability mass in the F distribution converges to $x = 1$. Because the variance of a sample is distributed as a χ^2 random variable, the ratio of variances in linear models (as in Figure 6.9) can be compared to the F distribution.
- Consider the case where $k_1 = 1$. Since U is then the square of a standard normal random variable, a random variable with distribution F_{1,k_2} has the same distribution as the square of a random variable with distribution t_{k_2} (compare Equation (B.2)).



(a) Density functions

(b) Cumulative distribution functions

Figure B.4: Density and cumulative distribution functions for the F distribution

It is useful to play a bit with the F distribution to see what it looks like. Figure B.4 gives sample density and cumulative distribution functions for several choices of the degrees of freedom. In general, the cumulative distribution is more interesting and pertinent than the probability density function (unless you have an anomalously low F statistic).

B.7 The Wishart distribution

Recall that the χ^2 distribution is used to place probability distributions over the inverse variance of a normal distribution (or of a sample from a normally-distributed population). The WISHART DISTRIBUTION is a multi-dimensional generalization of the χ^2 distribution; it generates inverse covariance matrices. Suppose that we have k independent observations from an $n \leq k$-dimensional multivariate normal distribution that itself has mean zero and covariance matrix Σ. Each observation $\boldsymbol{z}_i$ can be written as $\langle z_{i1}, \ldots, z_{in} \rangle$. If we write the matrix

$$\boldsymbol{Z} = \begin{bmatrix} z_{11} & z_{12} & \cdots & z_{1n} \\ z_{21} & z_{22} & \cdots & z_{2n} \\ \vdots & \vdots & \ddots & \vdots \\ z_{2n} & z_{2n} & \cdots & z_{kn} \end{bmatrix}$$

then the matrix $\boldsymbol{X} = \boldsymbol{Z}^{\mathrm{T}}\boldsymbol{Z}$ follows a Wishart distribution with k degrees of freedom and scale matrix Σ.

If $\boldsymbol{X}$ is Wishart-distributed, then its inverse $\boldsymbol{X}^{-1}$ is said to be INVERSE WISHART-DISTRIBUTED. The inverse Wishart distribution is used in Bayesian inference as the con-

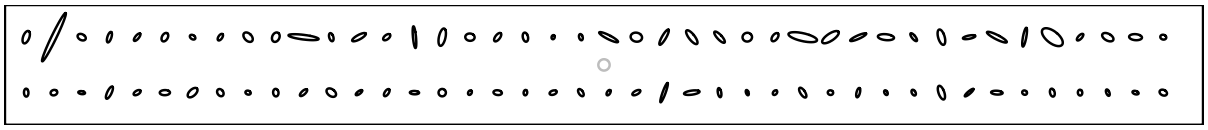


Figure B.5: Covariance-matrix samples from the two-dimensional inverse Wishart distribution with $\Sigma = \left(\begin{smallmatrix} 1 & 0 \\ 0 & 1 \end{smallmatrix}\right)$ and $k = 2$ (top row) or $k = 5$ (bottom row), represented by their characteristic ellipses. The unit circle appears in gray in the center of the figure for reference.

jugate prior (Section 4.4.3) for the covariance matrix of a multivariate normal distribution. Figure B.5 illustrates the inverse Wishart distribution for different degrees of freedom. Note that the variability in the covariance structure are more extreme when there are fewer degrees of freedom.

B.8 The Dirichlet distribution

The DIRICHLET DISTRIBUTION is a generalization of the beta distribution (Section 4.4.2). Beta distributions are probability distributions over the success parameter π of a binomial distribution; the binomial distribution has two possible outcome classes. Dirichlet distributions are probability distributions over the parameters $\pi_1, \ldots, \pi_k$ of a k-class multinomial distribution (Section 3.4.1; recall that π_k is not a true model parameter as it is fully determined by $\pi_1, \ldots, \pi_{k-1}$). The Dirichlet distribution is characterized by parameters $\alpha_1, \ldots, \alpha_k$, and $\mathcal{D}(\pi_1, \ldots, \pi_k)$ is defined as

$$\mathcal{D}(\pi_1, \ldots, \pi_k) \stackrel{\text{def}}{=} \frac{1}{Z} \pi_1^{\alpha_1 - 1} \pi_2^{\alpha_2 - 1} \ldots \pi_k^{\alpha_k - 1}$$

where the normalizing constant Z is

$$Z = \frac{\Gamma(\alpha_1)\Gamma(\alpha_2)\ldots\Gamma(\alpha_k)}{\Gamma(\alpha_1 + \alpha_2 + \cdots + \alpha_k)}$$

By comparing with the beta function and beta distribution as defined in Sections 4.4.2 and B.1, it will be apparent that the beta distribution is a Dirichlet distribution in which $k = 2$. Just as there is a beta-binomial distribution giving the probability of obtaining y successes out of N draws from a binomial distribution drawn from a beta distribution, there is a DIRICHLET-MULTINOMIAL distribution that gives the probability of obtaining $y_1, \ldots, y_k$ outcomes in each of the k response classes respectively when taking N draws from a multinomial drawn from a Dirichlet distribution with parameters $\alpha_1, \ldots, \alpha_k$. If we define $\alpha = \sum_{i=1}^{k} \alpha_i$, then the predictive distribution is (Leonard, 1977):

$$P(y_1, \ldots, y_k) = \int_\pi P(y_1, \ldots, y_k|\pi) P(\pi|\alpha_{1\ldots k})\, d\pi = \frac{\prod_{i=1}^{k} \binom{\alpha_i + y_i - 1}{\alpha_i}}{\binom{\alpha + N - 1}{\alpha}}$$

The special case of this predictive distribution is when we draw a multinomial distribution from the Dirichlet, and then draw one sample X from that multinomial distribution. The probability that that sample X has outcome class i is given by the value

$$P(X = i|\alpha_{1\ldots k}) = \frac{\alpha_i}{\alpha}$$

This is often convenient for using Gibbs sampling to draw samples from the posterior distribution in Bayesian models which use Dirichlet priors over multinomial distributions. An example of this usage is given in Section **??**.

The Dirichlet distribution has the following useful property. For any k-class Dirichlet distribution with parameters $\alpha_1, \ldots, \alpha_k$, suppose we partition the k outcome classes into a smaller, new set of $k' < k$ classes, with the j-th new class consisting of outcome classes $c_{j1}, \ldots, c_{jM_j}$. The resulting distribution over the new set of k' outcome classes is *also* Dirichlet-distributed, with parameters $\alpha_j = \sum_{i=1}^{M_j} \alpha_{ij}$. [see also Dirichlet process in Section XXX; and give example here?]

B.9 The beta-binomial distribution

We saw the beta-binomial distribution before in Section 4.4.3. If there is a binomial distribution with unknown success parameter π and we put a beta prior with parameters α_1, α_2 over π, then the marginal distribution on a sample of size n from the binomial distribution is beta-binomial, with form

$$P(m|\alpha_1, \alpha_2, m) = \binom{n}{m} \qquad\qquad = \binom{k}{r} \frac{B(\alpha_1 + m, \alpha_2 + m - n)}{B(\alpha_1, \alpha_2)}$$

Appendix C

The language of directed acyclic graphical models

Beginning with Chapter 8, this book makes considerable use of the formalism of DIRECTED ACYCLIC GRAPHICAL MODELS, or BAYESIAN NETWORKS (Bayes nets). In a few pages we cannot to do justice to the diversity of work within this formalism, but this appendix introduces the formalism and a few critical accompanying concepts.

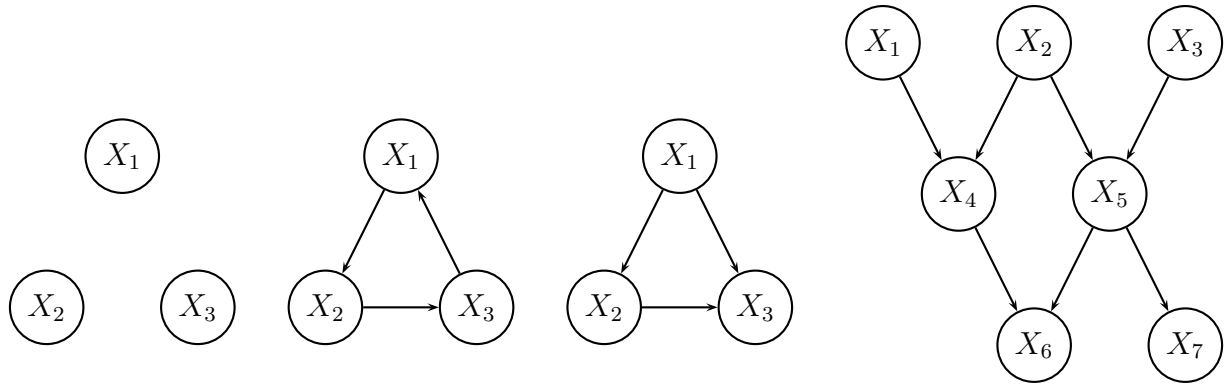
In the general case, graphical models are a set of formalisms for compactly expressing different types of conditional independence relationships between an ENSEMBLE of random variables. A graphical model on an ensemble $X_1, \ldots, X_n$ is literally a graph with one node for each random variable X_i, and in which each node may or may not be connected to each other node. The class of *directed* graphical models is those graphical models in which all the inter-node connections have a direction, indicated visually by an arrowhead. The class of directed *acyclic* graphical models, or DAGs (or Bayes nets), is those directed graphical models with no cycles—that is, one can never start at a node X_i and, by traverse edges in the direction of the arrows, get back to X_i. DAGs are the only type of graphical model that you'll see in this book. Figure C.1 shows examples of several different types of graphical models.

C.1 Directed graphical models and their interpretation

The structure of a given DAG encodes what conditional independencies hold among the variables in the ensemble $X_1, \ldots, X_n$. First a bit of nomenclature. The PARENTS of a node X_i are the nodes that are pointing directly to it—in Figure C.1d, for example, the parents of X_5 are X_3 and X_4. The ANCESTORS of a node are all the nodes that can be reached from the node by traveling "upstream" on edges in the direction opposite to the arrows—in Figure C.1d, for example, all other nodes are ancestors of X_5, but X_4 has no ancestors.

The set of connections between nodes in a DAG has a formal semantic interpretation whose simplest statement is as follows:

> Any node X_i is conditionally independent of its non-descendents given its parents.



(a) A graphical model with no dependencies

(b) A directed cyclic graphical model

(c) A directed acyclic graphical model (DAG)

(d) A more complex DAG

Figure C.1: Different classes of graphical models

In Figure C.1d, for instance, we have that:

$$X_6 \perp \{X_1, X_2, X_3, X_7\} \mid \{X_4, X_5\}$$

An important proviso is that—recalling from Chapter 2—conditional independencies can disappear with the accrual of new knowledge. In particular, two nodes are *not* conditionally independent of one another given a common descendent. So in Figure C.1d, for example, X_4 has many conditional independencies given only its parents:

$$X_4 \perp \{X_3, X_5, X_7\} \mid \{X_1, X_2\}$$

but two of them go away when its child X_6 is also given:

$$\begin{aligned} X_4 \not\perp X_3 \mid \{X_1, X_2, X_6\} \\ X_4 \not\perp X_5 \mid \{X_1, X_2, X_6\} \\ X_4 \perp X_7 \mid \{X_1, X_2, X_6\} \end{aligned}$$

A more complete statement of conditional independence in DAGs is given in Section C.2.

This statement of conditional independence simplifies the factorization of the joint probability distribution into smaller components. For example, we could simply use the chain rule (Section 2.4) to write the joint probability distribution for Figure C.1d as follows:

$$P(X_{1\ldots7}) = P(X_7|X_{1\ldots6})P(X_6|X_{1\ldots5})P(X_5|X_{1\ldots4})P(X_4|X_{1\ldots3})P(X_3|X_1, X_2)P(X_2|X_1)P(X_1)$$

but we can use the following conditional independencies, which can be read off the connectivity in the graph, to simplify this:

$$\begin{aligned} P(X_7|X_{1\ldots6}) &= P(X_7|X_5) \\ P(X_6|X_{1\ldots5}) &= P(X_5|X_4, X_5) \\ P(X_5|X_{1\ldots4}) &= P(X_5|X_3) \\ P(X_4|X_{1\ldots3}) &= P(X_4|X_1, X_2) \\ P(X_3|X_1, X_2) &= P(X_3) \\ P(X_2|X_1) &= P(X_1) \end{aligned} \tag{C.1}$$

giving us the following expression for the joint probability distribution

$$P(X_{1\ldots7}) = P(X_7|X_5)P(X_6|X_5, X_4)P(X_5|X_3)P(X_4|X_1, X_2)P(X_3)P(X_2)P(X_1)$$

which is much simpler. These minimal conditional probability distributions seen in (C.1) are the components whose form needs to be specified in order to give a complete probabilistic model of a given domain.

[say something about proper indexing of variables?]

When conducting statistical inference in DAGs, it is often the case that we observe the more "downstream" variables and need to infer some of the more "upstream" variables. The catch is that the conditional probability distributions in the DAG are specified in terms of downstream variables given upstream variables. Conducting inference upstream, then, requires Bayesian inference (the reason that DAGs are often called "Bayes nets"). As an example, in Figure C.1d suppose that we observe (or choose via prior knowledge) all variables except X_4. To draw inferences about X_4, we'd use Bayes rule, targeting the downstream variable X_6 for Bayesian inversion:

$$P(X_4|X_1, X_2, X_3, X_5, X_6, X_7) = \frac{P(X_6|X_{1\ldots5}, X_7)P(X_4|X_{1\ldots3}, X_5, X_7)}{P(X_6|X_{1\ldots3}, X_5, X_7)}$$

We can now apply the conditional independencies in the graph to simplify all the numerator of the right-hand side:

$$= \frac{P(X_6|X_4, X_5)P(X_4|X_1, X_2)}{P(X_6|X_{1\ldots3}, X_5, X_7)}$$

If we wanted to compute the denominator of Equation C.2, we'd need to do it by marginalizing over all possible values x_4 that can be taken by X_4:

$$= \frac{P(X_6|X_4, X_5)P(X_4|X_1, X_2)}{\sum_{x_4} P(X_6|X_{1\ldots5}, X_7)P(X_4|X_{1\ldots3}, X_5, X_7)}$$

Applying the conditional independencies of the graph to the explicit marginalization reveals that X_3 and X_7 can be ignored:

$$= \frac{P(X_6|X_4, X_5)P(X_4|X_1, X_2)}{\sum_{x_4} P(X_6|X_4, X_5)P(X_4|X_1, X_2)}$$

If we now drop the explicit marginalization, we obtain the simplest characterization of Bayesian inference on X_4 available for this graph:

$$P(X_4|X_1, X_2, X_3, X_5, X_6, X_7) = \frac{P(X_6|X_4, X_5)P(X_4|X_1, X_2)}{P(X_6|X_1, X_2, X_5)} \tag{C.2}$$

C.2 Conditional independence in DAGS: d-separation†

We have already briefly described the intuitive picture for when conditional independence holds in a DAG: given its parents, a node is conditionally independent of all of its non-descendents. However, we also saw that such conditional independencies can be broken when more information is conditioned on. In this section, we give the comprehensive criterion by which conditional independence can be assessed in any DAG. This criterion is known as D-SEPARATION (Pearl, 1988, Section 3.3).

Consider two disjoint subsets A and B of nodes in a DAG. A PATH between A and B is simply a sequence of edges that, when taken together, connects some node in A with some node in B (note that this definition doesn't require that the arrows along the path all point in the same direction). Any node on a given path is said to have CONVERGING ARROWS if two edges on the path connect to it and point to it. A node on the path is said to have NON-CONVERGING ARROWS if two edges on the path connect to it, but at least one does not point to it. (Note that the starting and ending nodes on the path are each connected to by only one edge on the path, so are not said to have either converging or non-converging arrows.)

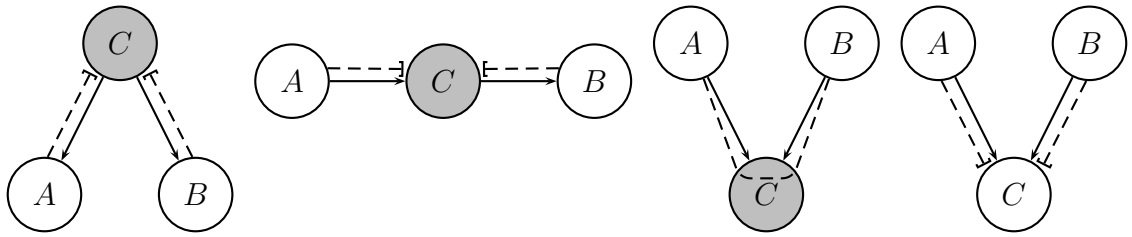
Now consider a third subset C of nodes in the DAG, disjoint from both A and B. C is said to d-separate A and B if for every path between A and B, one of the following two properties holds:

1. there is some node on the path with converging arrows which *is not* in C; or

2. there is some node on the path whose arrows do not converge and which *is* in C.

If C d-separates A and B, then A and B must be conditionally independent given C. If C does not d-separate A and B, then A and B are not in general conditionally independent.

Figure C.2 illustrates the canonical cases of d-separation and of failure of d-separation. In Figures C.2a, we have d-separation: C is on the path between A and B, and it does not have converging arrows. Therefore if C is known, then A and B become conditionally independent:



(a) Common-cause d-separation

(b) Intervening d-separation

(c) Explaining away: no d-separation

(d) D-separation in the absence of knowledge of C

Figure C.2: Examples of d-separation and of failure of d-separation. C blocks the path between A and B in Figures C.2a, C.2b, and C.2d, but not in Figure C.2c.

$A \perp B \mid C$.[1] This configuration is sometimes called "common cause" d-separation: if A and B are the outcomes of two tosses of a possibly unfair coin, then knowing the coin's weighting (C) renders the tosses independent.

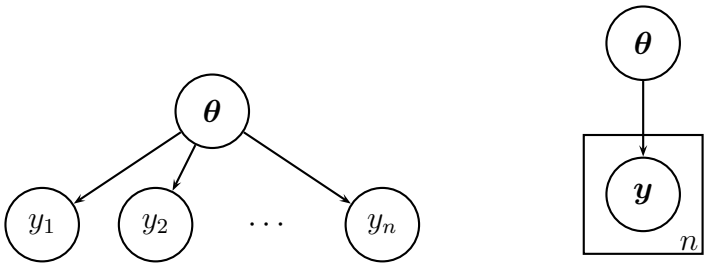
The same holds of Figure C.2b: C is on the path between A and B, and doesn't have converging arrows, so $A \perp B \mid C$. This configuration is often known as "indirect cause": if I know my mother's genome (C), then the respective contents of my genome (B) and my mother's mother's genome (A) become conditionally independent.

In Figures C.2c and C.2d, on the other hand, C is on the path between A and B but it has converging arrows. Therefore C does not d-separate A and B, so $A \not\perp B \mid C$ (Figure C.2c. This configuration is often known as "common effect": a signal (C) indicating whether the tosses of two fair coins (A and B) came up on the same side renders the two tosses conditionally dependent. However, *not* having seen this signal leaves the two tosses independent. In the language of graphical models, d-separation, and conditional independence, we have $A \perp B \mid \emptyset$ (Figure C.2d).

C.3 Plate notation

Since graphical models for structured datasets can get quite complex when the full set of variables, including observations, latent classes, and model parameters, is written out explicitly, it is common to use "plate" notation to succinctly express repetitive structure in the model. The semantics of "plate" notation are simply that any part of a graphical model on a plate with subscript n should be interpreted as being repeated n times, with all the dependencies between nodes external to the plate and nodes internal to the plate preserved and no dependencies between elements on different replicates of the plate. Figure C.3 gives

[1] Technically, since d-separation is a property holding among *sets* of nodes, we should write $\{A\} \perp \{B\} \mid \{C\}$; but for simplicity we drop the braces as a slight abuse of notation when a set consists of exactly one node.



(a) "Flat" model with no hierarchical structure (b)

Figure C.3: Equivalent directed graphical models in plate and no-plate notation

two examples of equivalent models in plate notation and "unfolded" into a plate-free format. Note in particular that in Figure C.3b in the "unfolded" version the variables XXX_i and $YYY_{i'}$ are not connected for $i \neq i'$ [**TODO!**]. Further examples of equivalent non-plate and non-plate models can be found early in Chapter 8.

C.4 Further reading

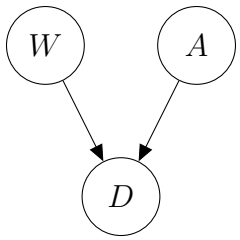
Directed graphical models are an area of considerable research activity. For further reading, some key sources are Pearl (1988, 2000); Jordan (1998); Russell and Norvig (2003, Chapter 14); Bishop (2006, Chapter 8).

Exercise C.1: Conditional independencies in Bayes nets

In each case, state the conditions (what sets of nodes must and/or must not be known) under which the specified node sets will be conditionally independent from one another. If the node sets are always independent or can never be independent, say so.

Example:

W	is the word intended to be spoken a hard word?
A	was the speaker's attention distracted?
D	was a disfluency uttered?

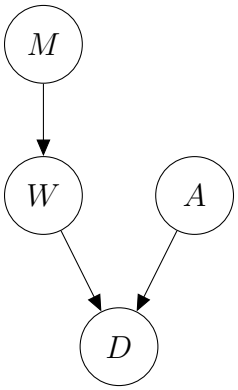


- $\{W\}$ and $\{A\}$ are conditionally independent if and only if D is unknown.
- $\{W\}$ and $\{D\}$ are never conditionally independent.

Examples to solve:

1. A variant of the disfluency model we saw earlier:

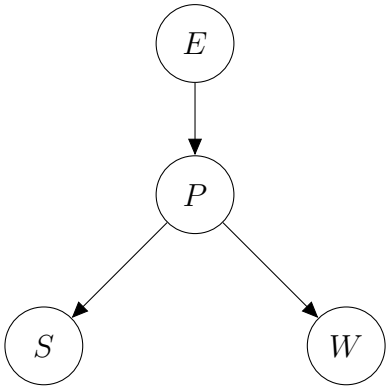
   M intended meaning to be conveyed
   W is the word intended to be spoken a hard word?
   A was the speaker's attention distracted?
   D was a disfluency uttered?



   (a) $\{W\}$ and $\{A\}$
   (b) $\{M\}$ and $\{D\}$
   (c) $\{M\}$ and $\{A\}$
   (d) $\{D\}$ and $\{A\}$

2. The relationship between a child's linguistic environment, his/her true linguistic abilities/proficiency, and measures of his/her proficiency in separate spoken and written tests

   E a child's linguistic environment
   P the child's linguistic proficiency (number of words known, etc.)
   S the child's performance on a spoken language proficiency test
   W the child's performance on a written language proficiency test



(a) $\{S\}$ and $\{W\}$

(b) $\{E\}$ and $\{P\}$

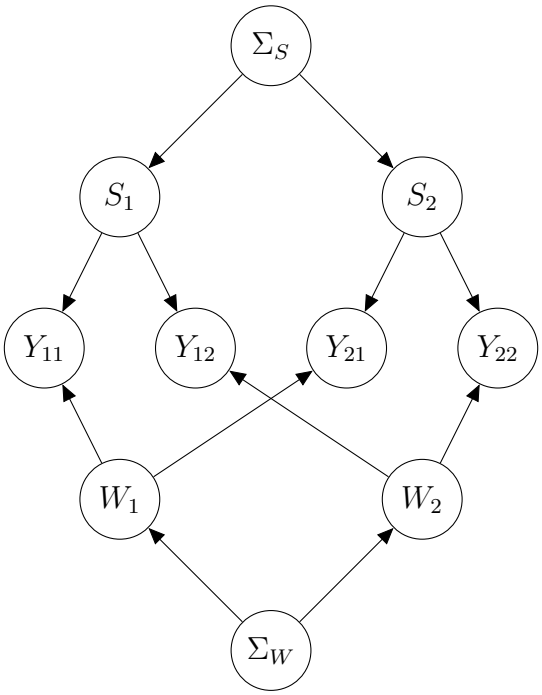
(c) $\{E\}$ and $\{S\}$

(d) $\{E, P\}$ and $\{S\}$

(e) $\{E$,$P\}$ and $\{S$,$W\}$

3. Speakers' familiarities (quantified, say, on a scale of 1 to 10) with different words

S_i	the i-th speaker's general vocabulary size
W_j	the j-th word's general difficulty/rarity
Σ_S	the variability in vocabulary sizes across speakers
Σ_W	the variability in difficulties/rarities across words
Y_{ij}	the i-th speaker's familiarity with the j-th word



- $\{\Sigma_S\}$ and $\{\Sigma_W\}$
- $\{Y_{11}\}$ and $\{Y_{22}\}$
- $\{Y_{11}\}$ and $\{Y_{12}\}$
- $\{Y_{11}\}$ and $\{S_2\}$
- $\{W_1\}$ and $\{S_1\}$, supposing that you know Y_{21}
- $\{W_1\}$ and $\{S_1\}$, supposing that you know Y_{22}

Appendix D

Dummy chapter

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