

CSE103: Probability and Statistics

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August 8, 2014

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Chapter 1

Introduction

The goal of these notes is to give you a high-level preview of some of the main concepts that you will learn in this course. We will explain these concepts verbally, with very little math. Later on we will give each concept a precise mathematical definition and show you how to use these definitions to solve practical problems. It is my experience that having a rough intuition about concepts makes it easier to absorb the formal math.

1.1 Statistics

One of the fundamental concepts in probability and statistics is that of *sampling*.

Suppose we own a web site and that we make money by placing advertisements on the pages we host. The way web advertisement works, we get paid if a visitor to the page clicks on the advertisement, indicating that she is interested in the product or service that is advertised (or maybe simply that they are bored...). Such an event is called a “click-through” or CT.

For simplicity, let’s consider a single static page, with a single location on the page for presenting the advertisement and just two alternative ads to place in this location, which we will call ad A and ad B. Suppose we don’t have any additional information about the specific visitor.

How can we figure out which is the best advertisement to put on the page?

One thing we can do is this: each time the web page is presented, choose one of the possible ads in an alternating manner (B,A,B,A,B,...) and present the page to the visitor. This is referred to as producing an *impression* of the ad. We then see if the visitor clicks on the advertisement, producing a CT. The fraction of visits to a page that a random visitor clicks on the ad is called the “click through rate” or CTR. If the payment for all ads are equal then the ad with the highest CTR is the best one to put on the page.

This is an example of using *Statistics*. A single page-visit, together with a flag indicating whether or not the ad was clicked is called an *observation* or an *outcome* and the sequence of n independent observations is called a *sample*. Statistics is a set of methods for drawing conclusions from random samples. The process that is generating the observations is called a *Stochastic Process*. The conclusions we draw are stated as properties of this stochastic process. In our case, we conclude that one ad has a higher CTR than the other.

Suppose we have 10,000 impressions for each of the two ads, and suppose we got 200 CTs for ad A 200 and 150 CTs for ad B. It seems reasonable to conclude that ad A is better. However, how confident are we of this conclusions? Are we confident enough to never present ad B again? Or do we need to collect more outcomes for both A and B?

Suppose instead that we collected 1,000,000 impressions and got the 20,000 CTs for A and 10,000 CTs for B. The ratios are the same:

$$\frac{200}{10,000} = \frac{20,000}{1,000,000} = 0.02, \quad \frac{150}{10,000} = \frac{15,000}{1,000,000} = 0.015$$

However, intuitively, when the size of the sample is one million, we are more confident that ad A is indeed the better one. How can we justify this intuition?

To explain and quantify this intuition we use probability theory.

1.2 Probability Theory

Probability theory is a branch of mathematics which is the foundation for statistics. This is similar to the way in which discrete math and the theory of computation are the foundation for writing correct and efficient computer programs.

The theory of computation does not pertain to a specific programming language or computer hardware. Similarly, probability theory does *not* deal with observations of real-world events, that is the job of Statistics. Instead, probability theory uses simplified mathematical models of the underlying stochastic process.

Specifically, in our case, we can model the process generating the click-through observation using two biased coins. An *unbiased coin* is a symmetric coin for which the probability of landing “heads” is equal to the probability of landing “tails”. A *biased coin* is one where these probabilities are different. In our case the coin for ad A has probability p_A of landing “heads” which is equal to the probability that a random visitor will click on the ad. Similarly p_B corresponds to the probability that the coin B lands “heads” which is equal to the probability that a random visitor will click on the ad B. More succinctly, P_A is the CTR of ad A and P_B is the CTR of ad B.

The question that we want to answer is which probability is larger, is $P_A > P_B$ or is the reverse true: $P_B \leq P_A$?

Suppose we are in the first case in which we presented each advertisement 10,000 times and got 200 click-throughs for ad A and 150 for ad B. Clearly, it seems that $P_A > P_B$. But how *confident* can we be that this is indeed the case?

To answer this question we consider two alternative *statistical hypotheses*: the first is that $P_A > P_B$, the second is that $P_A \leq P_B$.

We then find the two settings of P_A and P_B that conform with each hypothesis and give the highest probability for the data. For the hypothesis $P_A > P_B$ we get the highest probability when $P_A = 0.02, P_B = 0.015$. For the alternative hypothesis we use $P_A = 0.0175, P_B = 0.0175$, i.e. we place the two probabilities midway between the two observed rates.¹

We now compute the probability of the observed data corresponding to each of these two settings, which correspond to the two alternative hypotheses. Clearly the probability of the data under the first settings will be higher than the probability of the second, so if we take the ratio of the two probabilities we expect to get a number smaller than 1. The question is, how much smaller than 1?

Computing this ratio is not a trivial matter. You will learn how to do it later in the course. For now, I’ll tell you that when the number of impressions for each ad is 10,000 the ratio is 0.6766, while when the number of impressions is 1,000,000 the ratio is smaller than $10^{-16} = 1/10,000,000,000,000,000$. In other words, in the first case we cannot conclude which ad is better with any degree of confidence, while in the second case we can be pretty sure that the first ad is better.

Note how dramatic is the improvement in confidence, increasing the sample size from 10,000 to 1,000,000 transforms a relative gap of 5% from an insignificant gap to one from which can conclude something almost surely. Keep this very small number 10^{-16} in mind, we will get back to it later in the course.

1.3 Low probability vs. certainty

In computer science we are used to giving absolute guarantees: we expect that hardware and software will give the correct answer each and every time. The whole concept of “debugging” a program is based on the

¹Strictly speaking the mid-point is not the highest probability setting, but the difference is small and we ignore it here.

assumption that every mistake can be traced back to a particular part of the computer code and thereby eliminated.

However, in the real world, many computer errors cannot be reconstructed, explained, or corrected. The more realistic goal is becoming to have computer systems that minimize the number of errors without necessarily correcting all of the bugs.

Certainty is golden, however, in the real world, having a guarantee that some error will occur no more than once every 10^{16} attempts is a very strong guarantee. Increasing n from 1,000,000 to 100,000,000 will reduce the probability to 1 in 10^{64} .

1.4 Average and Mean

The number of observations, or the size of the sample n is of central importance in probability and in statistics. In general, as n increases we reach the “law of large numbers” which tells us that averages converge to the means.

People sometimes use “mean” and “average” interchangeably. However in probability and statistics the difference is very important. Going back to the click-through example above. consider the sequence of presentations of the ad A, each resulting either in a click (1) or in a non-click (0). For example, suppose the sequence is:

0, 0, 0, 1, 0, 0, 0, 0, 1, 1, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, ...

The *average* of the first 5 outcomes is $1/5$. If we compute the average of the first n outcome for $n = 1, 2, 3, \dots$ we get a sequence of *running averages*:

0, 0, 0, $1/3$, $1/4$, $1/5$, $1/6$, $1/7$, $2/8$, $3/9$, $3/10$, $3/11$, ...

As the sequence of outcomes is random, the sequence of averages is also random. By this we mean that if we collected a different sequence of observations from the same source, we are very likely to get a different sequence. In the language of probability, we say that the outcomes and the averages are *random variables*.

The terms: “empirical”, “observational”, “sample”, “random variable” indicate that the quantity we are referring to is likely to change if we repeat the same experiment.

The mean, on the other hand, is *not* a random variable. The mean is a *constant property of the source*, in this case, the mean is equal to P_A, P_B which are the CTRs for ad A and ad B respectively. In fact P_A and P_B are the quantities that determine which ad is more profitable.²

The law of large numbers connects the sequence of running averages and the mean. What the law of large number says (roughly) is that the sequence of averages converges to the mean. In other words, if n is large enough, the difference between the average and the mean is going to be small with high probability.

1.5 Monte-carlo simulations

As I said above, computing the probability flipping a biased coin n times will result in k heads and $n - k$ tails is not trivial and requires some knowledge of probability theory. However, symbolic derivation (also called “closed form solution”) is not the only way to arrive at the answer. There is another way which is called “monte-carlo simulations”.

A monte-carlo simulation is a computer program that simulates the process of generating the outcomes. It uses “pseudo-random number generators” about which we will learn later on. For now it suffices to describe the pseudo-random number generator as a function `random(p)`. Every time `random(p)` is called it returns a bit whose value is 1 with probability p and 0 with probability $1 - p$.

²Other terms that are used to refer to the average are the *empirical mean* or the *sample mean*. These can be easily confused with the regular mean. However, they are random variables, not constants.

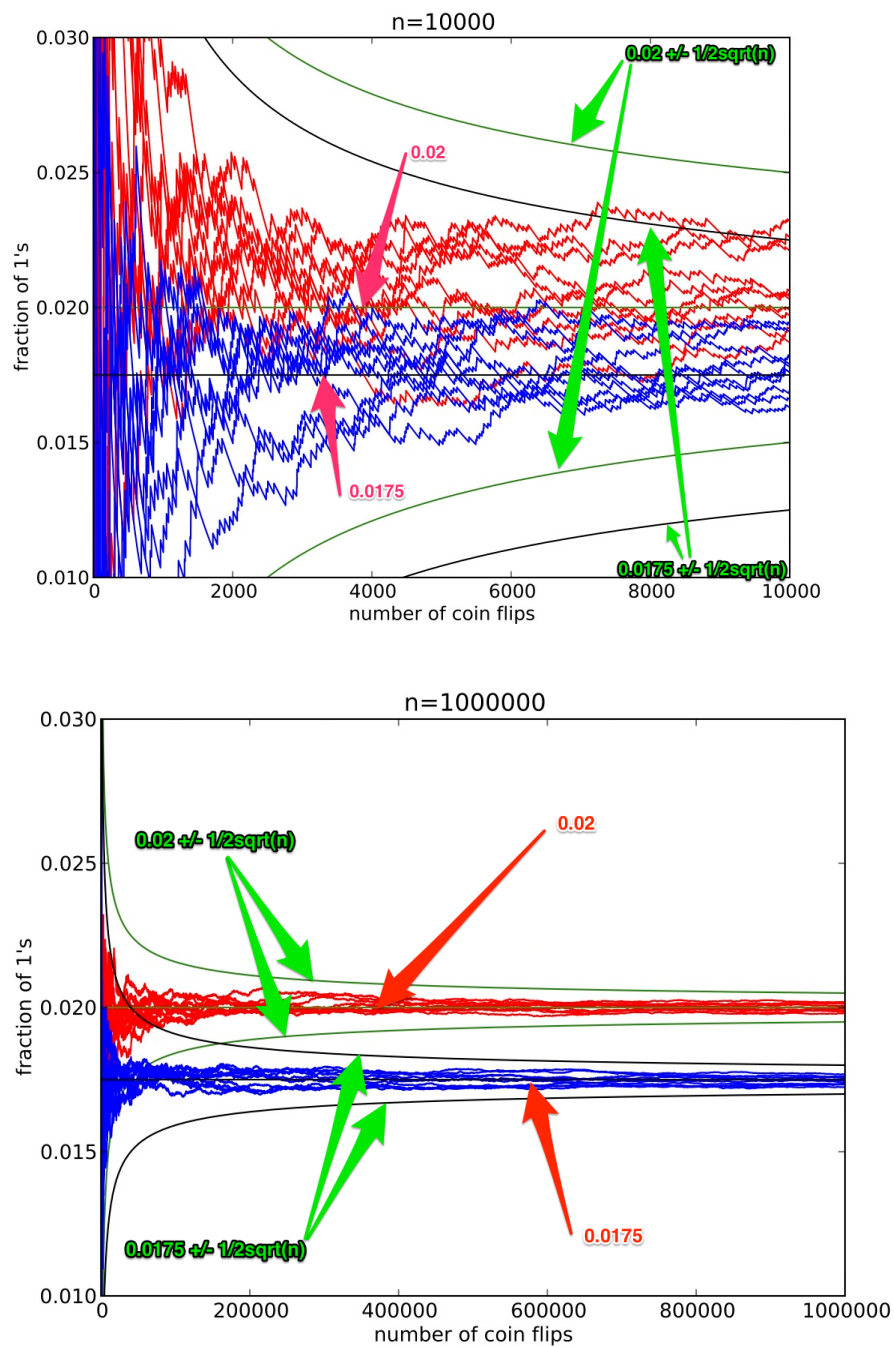


Figure 1.1: Trajectories of running averages of random sequences generated by a biased coin with sides that say “0” and “1”. There are two sets of 10 trajectories. The red trajectories correspond to sequences of random coin flips where the probability of 1 is 0.02. The blue trajectories correspond to sequences of random coin flips where the probability of a 1 is 0.0175

Using a random number generator we can create samples of the type described above, compute running averages of these sample, and plot them, see Figure 1.1.³ These plots demonstrate why there is such a qualitative difference between a sample of size 10,000 and a sample of size 1,000,000. The red trajectories correspond to sequences generated by a coin with bias $P = 0.02$ while the blue trajectories were generated by a coin with bias $P = 0.0175$ (the most likely value for P_A which allows for $P_A \leq P_B$). Looking at the bottom figure, corresponding to $n = 1,000,000$ we see that the sequences all converge to their mean, as is predicted by the law of large numbers. However, if we look at the top figure, where $n = 10,000$, we see that the red trajectories and the blue trajectories are not well separated. The red and the blue lines cross each other many times.

What does this mean for drawing conclusions about whether $P_A > P_B$? The one experiment that we did corresponds to two sequences of length 10,000 one for each ad. In this figure are focusing on the sequence for ad A. We know that this sequence ended up at $k = 200$ when $n = 10,000$. We want to compare the probability that this sequence was generated by a coin with bias $P_A = 0.02$ to the probability that it was generated by a coin with bias $P_A = 0.0175$. What we see from the sample is that the probabilities are comparable. It is hard to say what is the ratio of the probabilities, but if instead of generating 10 trajectories we generated 10,000 trajectories we could probably give an accurate estimate of the ratio.

Compare that situation to the one when $n = 1,000,000$ and you see that now the separation between the two sets of trajectory is perfect. This means that the probability of a blue trajectories having $k = 20,000$ is miniscule.

These graphs give us a useful intuition for the behaviour of running averages of coin flips. We can clearly see the effect of the law of large numbers.

What's more, probability theory tells us that the rate at which the running averages converge to the mean is $O(1/\sqrt{n})$. We demonstrate this in the figures by drawing around the horizontal line representing the means the envelope which represents the rate at which a random sequence is expected to converge to the mean. You can see that there is a nice fit between the random trajectories and the envelope: none of the trajectories escape out of the envelope.

You might think: if I can do a monte-carlo simulation why do I need probability theory? In fact, in many practical problems monte carlo simulations play an important role. However, recall that probability theory tells you that when $n = 1,000,000$ the probability of the hypothesis $P_A = P_B = 0.0175$ is smaller than 10^{-16} . If you wanted to prove this using monte-carlo, you had to generate at least 10^{16} sequences of length 1,000,000, that is a pretty large computer job! Then consider $n = 100,000,000$ which gives rise to a probability of 10^{-64} , and how much resources will it take to do this monte-carlo simulation. On the other hand, using probability theory and a statistical table you can compute these probabilities quite precisely with no computer at all!

1.6 Summary

In this chapter I have introduced you to many new terms without giving you formal definitions. We will define each term in a precise mathematical way in the coming weeks. I hope that this introduction will help you make sense of the math. The math is necessary if you want to compute probabilities, especially small ones, but keeping the applications in mind will help you develop an intuition for what to expect from stochastic processes.

Here is a list of the probability and statistics terms that we touched upon are:

1. Probability Theory
2. Coin flip, biased and unbiased coins.
3. Statistics

³The code is available via GitHub: <https://github.com/yoavfreund/CSE103-code/blob/master/MonteCarlo/monteCarlo.py>

4. Outcome, Sample, sample size.
5. Observational, Empirical.
6. Confidence.
7. Average vs. Mean.
8. Random variable.
9. Monte-carlo simulation.
10. Pseudo-Random number generator.

Chapter 2

Mathematical preliminaries

Probability theory is about sets. In the first lesson you encountered the set of possible outcomes of flipping two coins which contains four elements. If we use H to denote “Heads” and T to denote “Tails” then the set of possible outcomes, also known as the *outcome space* contains four elements: $\{(H, H), (H, T), (T, H), (T, T)\}$. We say that the outcome space is the set of four *tuples*. As the concepts of “set” and “tuple” will be used many times throughout the course, we take some pains to define these concepts and the associated notation, in a somewhat formal mathematical way.

Think of this as learning the syntax and semantics of a new programming language. There is nothing very deep here, it is just a framework through which deeper ideas can be expressed precisely and succinctly.

2.1 Sets

Sets are collections of *elements*. We will mostly consider sets of numbers, but elements can be most anything.

A *set* can be specified by listing its elements within braces, as in

$$\begin{aligned}A &= \{1, 2, 3, 4, 5, 6\} \text{ (the possible outcomes of the roll of a die)} \\B &= \{1, 2, \dots\} \text{ (the positive integers, commonly denoted } \mathbb{Z}^+) \\C &= \{H, T\} \text{ (the possible outcomes of the flip of a coin)}\end{aligned}$$

We say that 5 is an element of A and denote it by $5 \in A$. Sets are *unordered* collections, in other words $\{1, 2, 3, 4, 5, 6\} = \{5, 2, 1, 3, 4, 6\}$. The number of times an element can appear in a set is either 0 or 1, an element cannot appear multiple times in the set (for that there is a different construct called *bags*).

Instead of listing the elements of a set, one can define a set by specifying the precise conditions for an element to be in the set. For example:

$$\begin{aligned}\mathbb{Z}^+ &= \{x : x \text{ is a positive integer}\} \\ \mathbb{R} &= \{x : x \text{ is a real number}\}.\end{aligned}$$

When set S is contained in set T (that is, $x \in S \Rightarrow x \in T$), we write $S \subseteq T$. For instance, $\mathbb{Z}^+ \subseteq \mathbb{R}$. The *empty set* contains no elements and is denoted by $\{\}$ or \emptyset .

Suppose A, B are two sets. The *intersection* of the two sets, denoted $A \cap B$ contains the elements that are in *both* sets. Thus

$$\{1, 2, 3, 4, 5, 6\} \cap \{2, 4, 6, 8, 10\} = \{2, 4, 6\}$$

The *union* of two sets contains those elements that are *either* A or B (or both), thus

$$\{1, 2, 3, 4, 5, 6\} \cup \{2, 4, 6, 8, 10\} = \{1, 2, 3, 4, 5, 6, 8, 10\}$$

2.1.1 Spaces and complements

In probability we call the set of all possible outcomes (for a particular experiment) as *the outcome space* and denote it by Ω . Subsets of Ω are called *events*. The *complement* of an event A is the set of outcomes that are in Ω but not in A . The complement of the set A is denoted A^c . For example, suppose $\Omega = \{1 - 10\}$ then

2.1.2 Tuples, and products of sets

Suppose we toss a coin three times. We can represent the outcome by a 3-tuple like (H, H, T) (where H means heads and T means tails). The set of all such tuples is

$$\{(H, H, H), (H, H, T), (H, T, H), (H, T, T), (T, H, H), (T, H, T), (T, T, H), (T, T, T)\}.$$

It can also be written as $\{H, T\} \times \{H, T\} \times \{H, T\}$, or even more simply, $\{H, T\}^3$.

More generally, if S_1, S_2, \dots, S_k are sets, then $S_1 \times S_2 \times \dots \times S_k$ is the set of all k -tuples in which the first entry is from S_1 , the second entry is from S_2 , and so on. For instance,

$$\begin{aligned}\mathbb{R}^2 &= \{\text{all points in the plane}\} \\ \mathbb{R}^d &= \{\text{all points in } d\text{-dimensional space}\}.\end{aligned}$$

Note that, unlike sets, *order* is significant in tuples. Also note that the same element can appear multiple times in a tuple, but not in a set.

We are often also interested in sets of tuples that cannot be expressed as products of individual sets. For instance, the points in the unit circle in \mathbb{R}^2 are

$$\{(x, y) : x^2 + y^2 \leq 1\},$$

a subset of \mathbb{R}^2 that cannot be written as a product $S_1 \times S_2$.

2.1.3 The size of a set

The *size* of a set A is the number of elements in it and is denoted by $|A|$. Thus $|\{H, T\}| = 2$, $|\emptyset| = 0$ and $|\mathbb{Z}^+| = \infty$.

When S is of the form $S_1 \times \dots \times S_k$, then $|S| = |S_1| \cdot |S_2| \cdot \dots \cdot |S_k|$.

To see an example of this notation, suppose there is a group of n concert-goers, each of whom is selecting a band T-shirt. The available colors are red, yellow, and black. How many possible outcomes are there? Well, let $C = \{\text{red, yellow, black}\}$ be the set of possible colors, and represent each outcome as an n -tuple in which the i th entry is the color of the i th person's T-shirt. Then the possible outcomes are C^n , a set of size $|C|^n = 3^n$.

2.2 Permutations and combinations

Armed with the concepts of sets, tuples and set size we can now tackle some more interesting combinatorial questions.

2.2.1 Sampling with and without replacement when the order matters

Suppose there are four children—Alice, Bill, Christie, and Doug—at an animal shelter, checking out the current pool of n dogs. Each child writes down the name of the dog he or she likes most. How many possible outcomes are there?

We can represent each outcome as a 4-tuple (Alice's choice, Bill's choice, Christie's choice, Doug's choice) in which each entry is the name of a dog. So the number of outcomes is n^4 .

Now suppose that these same children are actually picking out dogs. First Alice chooses a dog to adopt, then Bill chooses a dog to adopt, and so on. How many outcomes are there now?

In this situation, Alice has n choices, but Bill has only $n - 1$ choices, Christie has $n - 2$ choices, and Doug has $n - 3$ choices. So there are $n(n - 1)(n - 2)(n - 3)$ possible outcomes.

The first situation is called *sampling with replacement*: the outcomes are tuples in which the same element (dog) can occur more than once. The number of such k -tuples, chosen from n elements, is n^k . In the example, $k = 4$. The second situation is *sampling without replacement*: the outcomes are tuples in which no element can be repeated. The number of such k -tuples, chosen from n elements, is $n(n - 1)(n - 2) \cdots (n - k + 1)$.

Here's a related question: how many ways are there to order (shuffle) a deck of 52 cards? (Each such ordering is called a *permutation* of the cards.) Well, the result is a 52-tuple, drawn from a set of size 52, in which no card is repeated. Therefore, the number of permutations is $52 \cdot 51 \cdot 50 \cdots 1$, which is called 52 *factorial* and denoted as $52!$. More generally, the number of permutations of n elements is n factorial or $n!$.

Coming back to sampling k out of n elements without replacement, we can write it succinctly as

$$n(n - 1)(n - 2) \cdots (n - k + 1) = \frac{n!}{(n - k)!}$$

2.2.2 When the order doesn't matter

Snow White is off to pick strawberries and asks three of the dwarfs (chosen from the seven: Dopey, Grumpy, Doc, Happy, Bashful, Sneezy, Sleepy) to join her. How many possible groups are there?

In this case, it is misleading to represent an outcome as a 3-tuple, because, for instance, (Dopey, Sleepy, Doc) is a different 3-tuple from (Sleepy, Dopey, Doc) but they represent the same group. So if we count tuples, we would be *over-counting*. Instead, we ought to represent an outcome as a set, {Dopey, Doc, Sleepy}.

So the question becomes: how many different subsets of three dwarfs are there? In general, a set of size n has

$$\binom{n}{k} = \frac{n!}{k!(n - k)!}$$

subsets of size k . So in our example, the answer is $\binom{7}{3} = 35$.

Let's step back and derive the main result: how many subsets of size k does a set of n elements have? We can choose the subset in the following manner: first pick one element from the set, then a second (different) element, then a third (different) element, and so on until we have k distinct elements. This yields a k -tuple (first choice, second choice, etc), and as we saw above (sampling without replacement when the order matters) the number of possible such tuples is $n(n - 1) \cdots (n - k + 1)$. However, we have over-counted because each subset of size k appears multiple times amongst these k -tuples. To be precise, each subset corresponds to exactly $k!$ tuples, depending on the order in which the k elements of the subset are chosen. Thus the number of subsets of size k is

$$\frac{n(n - 1) \cdots (n - k + 1)}{k!} = \frac{n!}{k!(n - k)!}.$$

A second example: how many strings in $\{0, 1\}^{10}$ contain exactly *four* 1s? Well, we need to choose four positions of the ten possibilities in which to place the 1s; that is, we choose a subset of size four from $\{1, 2, \dots, 10\}$. The number of ways to do this is $\binom{10}{4} = 210$.

Let's finish with a more challenging example. You walk into a candy store and notice that there are five types of candy. Your mother allows you to pick exactly three pieces of candy, of whichever type(s) you want. How many ways are there to do this?

You can represent the outcome by 5-tuple (n_1, n_2, \dots, n_5) in which n_i is the number of pieces of the i th type of candy. How many such tuples are there, subject to $n_1 + n_2 + \dots + n_5 = 3$? To answer the question, we'll represent each tuple in a different format, as a sequence of length 7 containing three stars and four bars. For instance, the sequence $|**|||*$ denotes $(0, 2, 0, 0, 1)$ (two candies of type 2 and one candy of type 5): the number of candies of type i is the number of stars between the $(i-1)$ st and i th bars.

So we have rephrased the question thus: how many sequences are there with four bars and three stars? Well, this is a sequence of size 7, and we must pick three of the seven positions at which to place stars. The number of such choices is $\binom{7}{3} = 35$.

2.3 Arithmetic and geometric series

The simplest *arithmetic series* is $1, 2, 3, \dots$. The sum of the first n elements of this series is

$$1 + 2 + \dots + n = \frac{n(n+1)}{2}.$$

Why? suppose that write the sum twice, first going up from 1 to n and then and then going down from n down to 1:

$$(1 + 2 + \dots + (n-1) + n) + (n + (n-1) + \dots + 2 + 1)$$

We can rearrange the sum into a sum of n pairs, the first of which sums the first element in each list, the second sums the second elements in each list etc:

$$(1 + n) + (2 + (n-1)) + (3 + (n-2)) + \dots + (n + 1)$$

It is easy to see that each pair sums to $n+1$ and that there are n pairs, which gives a total of $n(n+1)$. Recalling that we summed two copies of the original sum we get $n(n+1)/2$.

A more general arithmetic series is $a, a+s, a+2s, \dots$ (where a, s are some numbers). The sum of the first n elements of this series is

$$a + (a+s) + \dots + (a + (n-1)s) = an + s(1 + \dots + (n-1)) = an + \frac{sn(n-1)}{2}.$$

One of the most common *geometric series* is $1, 2, 4, 8, \dots$; the sum of the first n elements of this series is

$$1 + 2 + \dots + 2^{n-1} = 2^n - 1.$$

Another common series is $1, \frac{1}{2}, \frac{1}{4}, \dots$, in which the first n terms sum to $2 - (1/2^{n-1})$.

More generally, a geometric series is of the form a, ar, ar^2, ar^3, \dots (where a, r are some numbers), and its first n terms sum to

$$a + ar + \dots + ar^{n-1} = \frac{a(r^n - 1)}{r - 1} = \frac{a(1 - r^n)}{1 - r}.$$

The first form is more useful when $r > 1$, while the second is more useful when $r < 1$.

In the case where $|r| < 1$, we can sum the entire series (with infinitely many terms) to get $a/(1-r)$.

Chapter 3

Probability spaces

3.1 Definition

In order to properly understand a statement like

“the chance of getting a flush in five-card poker is about 0.2% (flush = all five cards are from the same suit)”,

we need to specify the underlying *probability space*. This has two components:

1. A *sample space* or *space of outcomes*.

This is $\Omega = \{\text{all possible five-card hands}\}$.

2. The *probabilities of outcomes* Each outcome is assigned a probability, which is a non-negative real number, such that the sum of the probabilities over all of the outcomes is 1:

$$\sum_{\omega \in \Omega} \Pr(\omega) = 1.$$

In our example, assuming the cards are dealt fairly, all outcomes are equally probable, so

$$\Pr(\omega) = 1/|\Omega| \quad \text{for all } \omega \in \Omega.$$

Events are subsets of Ω , in our example, the event of interest is $A = \{\omega : \omega \text{ is a flush}\}$. This is a subset of Ω ; that is, $A \subset \Omega$. Pictorially we can represent the situation thus:

The outer box is Ω ; every point in it is a particular five-card hand ω . The inner set is A , and the probability that it occurs is

$$\Pr(A) = \sum_{\omega \in A} \Pr(\omega).$$

In general, if Ω is finite, the probability of events is the sum of the probabilities of the outcomes in that event.¹

¹If Ω is continuous then this relationship does not hold and we need to define event probabilities differently. We will get to this a bit later. Till then we will only discuss finite outcome spaces, also referred to as “discrete probability spaces”.

In our example, since all outcomes are equally likely, $\Pr(A) = |A|/|\Omega|$. We now calculate this ratio. The size of Ω is the number of 5 card hands is

$$|\Omega| = \binom{52}{5} = 2,598,960$$

The number of hands that are flush is the number of suits (4) times the number of hands that can be chosen from a single suit:

$$|A| = 4 \times \binom{13}{5} = 5,148$$

Thus the probability of a flush is

$$\frac{5,148}{2,598,960} \approx 0.00198$$

Which, as promised, is approximately 0.2%.

3.2 A first set of canonical examples

1. *Roll a die.* What is the chance of getting a number > 3 ?

Probability space: sample space $\Omega = \{1, 2, 3, 4, 5, 6\}$; probabilities $\Pr(\omega) = 1/6$.

Event of interest: $A = \{4, 5, 6\}$; $\Pr(A) = 1/2$.

2. *Roll three dice.* What is the chance their sum is 3?

The sample space is

$$\begin{aligned} \Omega &= \{(1, 1, 1), (1, 1, 2), \dots, (6, 6, 6)\} \\ &= \{(d_1, d_2, d_3) : 1 \leq d_1, d_2, d_3 \leq 6\} \\ &= \Omega_o \times \Omega_o \times \Omega_o = \Omega_o^3 \quad \text{where } \Omega_o = \{1, 2, 3, 4, 5, 6\}. \end{aligned}$$

The probabilities of outcomes $\omega \in \Omega$ are $\Pr(\omega) = 1/6^3 = 1/216$.

The event of interest is $A = \{(1, 1, 1)\}$ whose probability is $\Pr(A) = 1/216$.

3. *Roll n dice.*

Sample space $\Omega = \Omega_o^n$, where $\Omega_o = \{1, 2, 3, 4, 5, 6\}$. Each outcome $\omega \in \Omega$ has probability $1/|\Omega| = 1/6^n$.

4. *Socks in a drawer.* A drawer contains three blue socks and three red socks. You put your hand in and pick out a random sock. Then you put your hand in again and pick out another random sock. What's the chance the two of them match?

There are several ways to set up the sample space, but one possibility is to have a tuple whose first coordinate is the color of the first sock and whose second coordinate is the color of the second sock. $\Omega = \{B, R\} \times \{B, R\}$. The probabilities of outcomes are

$$\begin{aligned} \Pr((B, B)) &= \frac{3}{6} \cdot \frac{2}{5} = \frac{1}{5} \\ \Pr((B, R)) &= \frac{3}{6} \cdot \frac{3}{5} = \frac{3}{10} \\ \Pr((R, B)) &= \frac{3}{6} \cdot \frac{3}{5} = \frac{3}{10} \\ \Pr((R, R)) &= \frac{3}{6} \cdot \frac{2}{5} = \frac{1}{5} \end{aligned}$$

(Notice that they add up to 1.)

The event of interest is $A = \{(B, B), (R, R)\}$, which has probability $2/5$.

5. *Socks in a drawer, again.* This time the drawer has three blue socks and four red socks.

The sample space Ω is the same, but the probabilities of outcomes are different:

$$\begin{aligned}\Pr((B, B)) &= \frac{3}{7} \cdot \frac{2}{6} = \frac{1}{7} \\ \Pr((B, R)) &= \frac{3}{7} \cdot \frac{4}{6} = \frac{2}{7} \\ \Pr((R, B)) &= \frac{4}{7} \cdot \frac{3}{6} = \frac{2}{7} \\ \Pr((R, R)) &= \frac{4}{7} \cdot \frac{3}{6} = \frac{2}{7}\end{aligned}$$

The event of interest is $A = \{(B, B), (R, R)\}$, which has probability $3/7$.

6. *Shuffling a deck of cards.* You randomly shuffle a deck of 52 cards and lay them out before you.

Here $\Omega = \{\text{all possible orderings of 52 cards}\}$. One way to compute $|\Omega|$ is to reason that there are 52 choices for what the first card in the sequence will be, 51 choices for the second card, 50 choices for the third card, and so on. Therefore

$$|\Omega| = 52 \cdot 51 \cdot 50 \cdots 2 \cdot 1.$$

This expression is called $52!$ (“52 factorial”). It is the number of *permutations* of 52 elements.

3.3 Tossing a fair coin

Suppose you toss a fair coin. The sample space is $\Omega_o = \{H, T\}$ (heads or tails), and each of the two outcomes has probability exactly $1/2$. What is more interesting is to toss the coin multiple times, independently.

3.3.1 Toss a fair coin 10 times

Now the sample space is $\Omega = \Omega_o^{10}$; it includes, for instance, the sequence $(H, T, H, T, H, T, H, T, H, T)$. Since $|\Omega| = 2^{10} = 1024$, each element in Ω has probability exactly $1/1024$.

1. What is the chance that *none* of the coin tosses are heads?

The event of interest is $\{(T, T, T, T, T, T, T, T, T, T)\}$, whose probability is $1/1024$.

2. What is the chance of exactly *one* head?

Now the event is

$$A = \{(H, T, T, T, T, T, T, T, T, T), (T, H, T, T, T, T, T, T, T, T), \dots, (T, T, T, T, T, T, T, T, H, T)\}.$$

Each sequence in A is completely determined by the location of the H within it. There are 10 possible locations; therefore $|A| = 10$, whereupon $\Pr(A) = |A|/|\Omega| = 10/1024$.

3. What is the chance of exactly *nine* heads?

Equivalently, what is the chance of exactly one tail? This is the same calculation as before, $10/1024$.

4. What is the chance of exactly *two* heads?

The sequences of interest are $A = \{\omega \in \Omega : \omega \text{ has exactly 2 heads}\}$. Each such sequence is specified by the locations of its two heads; write these as a pair (i, j) , where $1 \leq i, j \leq 10$ and $i \neq j$. For instance, $(7, 5)$ refers to $(T, T, T, T, H, T, H, T, T, T)$.

The number of such pairs is $10 \cdot 9 = 90$ (10 choices for i , and thereafter just 9 choices for j). But this ends up double-counting sequences, because for instance, the pair $(5, 7)$ also refers to $(T, T, T, T, H, T, H, T, T, T)$. Each sequence in A is counted twice – it corresponds to two pairs – and therefore $|A| = 45$.

Finally, $\Pr(A) = |A|/|\Omega| = 45/1024$.

5. What is the chance of exactly *four* heads?

This time, any sequence in $A = \{\omega : \text{has four heads}\}$ can be written as a 4-tuple (i, j, k, l) , where $1 \leq i, j, k, l \leq 10$ and $i \neq j \neq k \neq l$. For instance, $(7, 2, 4, 9)$ denotes $(T, H, T, H, T, T, H, T, H, T)$. The number of such 4-tuples is $10 \cdot 9 \cdot 8 \cdot 7 = 10!/6!$.

But once again, there is overcounting. $(7, 2, 4, 9)$ refers to the same sequence as $(2, 4, 7, 9)$ and $(2, 7, 9, 4)$ and $(9, 7, 2, 4)$ and many other 4-tuples. How many of them? The number of permutations of the four elements 2, 4, 7, 9, namely $4!$.

Therefore

$$|A| = \frac{10!}{4!6!} = 210$$

and $\Pr(A) = 210/1024$.

6. What is the chance of exactly *six* heads?

This is the same as the chance of four tails, which is identical to the previous calculation.

In the last few calculations, we had to find the number of ways of choosing k positions out of n available slots (for instance, choosing 4 positions out of 10 slots where a H might occur). Generalizing the argument above, the number of ways to do this is

$$\frac{n!}{k!(n-k)!}, \text{ which we write as } \binom{n}{k}$$

(pronounced “ n choose k ”). This is also called a *binomial coefficient*.

3.3.2 Toss a fair coin n times

Now the sample space is $\Omega = \{H, T\}^n$, with each sequence of n outcomes having probability exactly $1/2^n$. Let A_k denote the event that the sequence has k heads.

Notice that the events A_0, A_1, \dots, A_n are *disjoint* (if A_i occurs then A_j cannot occur for $j \neq i$). Moreover,

$$\Omega = A_0 \cup A_1 \cup \dots \cup A_n.$$

Therefore,

$$\sum_{k=0}^n \Pr(A_k) = \Pr(A_0) + \Pr(A_1) + \dots + \Pr(A_n) = 1,$$

or equivalently,

$$\sum_{k=0}^n |A_k| = |A_0| + |A_1| + \dots + |A_n| = |\Omega|.$$

In general, $|A_k|$ is the number of ways of placing k heads in a sequence of size n ; we've seen that this is $\binom{n}{k}$. And since $|\Omega| = 2^n$, the last equality tells us that

$$\sum_{k=0}^n \binom{n}{k} = \binom{n}{0} + \binom{n}{1} + \binom{n}{2} + \cdots + \binom{n}{n} = 2^n.$$

For example, take $n = 5$. Then

$$|A_0| = \binom{5}{0} = 1, |A_1| = \binom{5}{1} = 5, |A_2| = \binom{5}{2} = 10, |A_3| = \binom{5}{3} = 10, |A_4| = \binom{5}{4} = 5, |A_5| = \binom{5}{5} = 1$$

and these add up to $2^5 = 32$.

3.4 A second set of canonical examples

1. *Rooks on a chessboard.* You place 8 rooks at random on a chessboard. What is the chance that they are non-attacking (that is, no rook is attacking another)?

To describe the sample space, number the squares in the chessboard as 1 through 64, and let the configuration of 8 rooks be given by a *set* of eight positions, $\omega \subset \{1, 2, \dots, 64\}$. Thus:

$$\Omega = \{\omega \subset \{1, 2, \dots, 64\} : |\omega| = 8\}.$$

You should check that

$$|\Omega| = \binom{64}{8}$$

and that of these, only $8!$ configurations are non-attacking.

Therefore

$$\Pr(\text{non-attacking configuration}) = \frac{8!56!}{64!}.$$

2. *Five-card poker.* You are dealt five cards at random from a deck of 52 cards. What is the chance of a flush? Of a straight flush? Of exactly one pair?

Let $\Omega = \{\text{all possible 5-card hands}\}$. Then $|\Omega| = \binom{52}{5}$ and each $\omega \in \Omega$ occurs with probability $1/|\Omega|$.

Define three events of interest:

$$\begin{aligned} F &= \text{flush (all five cards of the same suit)} \\ S &= \text{straight flush (same suit and consecutive)} \\ P &= \text{the cards contain a single pair (eg. two 7s)} \end{aligned}$$

Then $|F| = 4 \cdot \binom{13}{5}$ (first choose a suit, then pick 5 cards from that suit), $|S| = 4 \cdot 10$ (first choose a suit, then choose the starting card in the sequence), and $|P| = 13 \cdot \binom{4}{2} \cdot 4^3 \cdot \binom{12}{3}$ (first choose which card occurs in the pair, then choose the two suits for that pair, then choose the suits of the remaining three cards, then choose their values).

3. *Throw a dart at a dartboard.* Suppose for convenience that your dartboard has radius 1, and is centered at the origin. Its bullseye has radius 0.1. You throw a dart at it, which lands at a random location (all positions on the board are equally likely). What is the chance that it lands exactly at the origin? What is the chance that it lands in the bullseye?

This differs from earlier examples in that the sample space is infinite and continuous. It is the set of all possible locations of the dart: any point in the circle. We can represent any such point by its (x, y) coordinates: $\Omega = \{(x, y) : x^2 + y^2 \leq 1\}$.

The chance of landing exactly at the origin is 0, since there are infinitely many places the dart could land. It makes more sense to talk about landing in *regions* $A \subset \Omega$ rather than specific points $\omega \in \Omega$. In general

$$\Pr(A) = \frac{\text{area of } A}{\text{area of } \Omega}$$

and therefore $\Pr(\text{bullseye}) = (0.1)^2 = 0.01$.

4. *Birthday paradox.* A room contains n people. What is the chance that two of them have the same birthday?

The probability space is not properly specified, so we need to make some assumptions. First, we'll assume that the n birthdays are independent (that is, a person's birthday is not influenced by anyone else's birthday). Second, we'll assume that all days are equally likely – that is, the chance of a birthday falling on any particular day is exactly $1/365$ (we're also ignoring the issue of leap years).

Number the people $1, 2, \dots, n$, and number the days of the year $1, 2, \dots, 365$. We will represent the birthdays of the people in the room by an n -tuple $(\omega_1, \dots, \omega_n)$, where $\omega_i \in \{1, 2, \dots, 365\}$ is the birthday of the i th person. Thus $\Omega = \{1, 2, \dots, 365\}^n$ and each $\omega \in \Omega$ has probability exactly $1/365^n$.

The event of interest is

$$A = \{\omega : \omega_i = \omega_j \text{ for some } i \neq j\}.$$

This is a typical situation in which it is easier to analyze the *complement* of A than A itself (that is, it is easier to compute the probability that A *doesn't* occur than the probability that it occurs).

$$A^c = \Omega - A = \{\omega : \omega_1 \neq \omega_2 \neq \dots \neq \omega_n\}.$$

In other words, A^c is the event that everyone's birthday is different. What is the size of A^c ? There are 365 choices for ω_1 , 364 for ω_2 , and so on, whereupon

$$|A^c| = 365 \cdot 364 \cdot 363 \cdots (365 - n + 1) = \frac{365!}{(365 - n)!}.$$

Therefore

$$\Pr(A) = 1 - \Pr(A^c) = 1 - \frac{365!}{(365 - n)!365^n}.$$

This is exactly correct, but it is a little hard to understand intuitively. So let's do the calculation a different way, using an approximation.

A very useful fact is that for small x (positive or negative), $e^x \approx 1 + x$. And in fact, $e^x \geq 1 + x$ no matter what x is. Now let's return to the event A^c .

$$\begin{aligned} \Pr(A^c) &= \Pr(\omega_2 \neq \omega_1) \cdot \Pr(\omega_3 \neq \omega_1, \omega_2) \cdots \Pr(\omega_n \neq \omega_1, \dots, \omega_{n-1}) \\ &= \left(1 - \frac{1}{365}\right) \left(1 - \frac{2}{365}\right) \cdots \left(1 - \frac{n-1}{365}\right) \\ &\leq \exp(-1/365) \cdot \exp(-2/365) \cdots \exp(-(n-1)/365) \quad \text{where } \exp(x) \text{ means } e^x \\ &= \exp\left(-\frac{1}{365} (1 + 2 + \cdots + (n-1))\right) \\ &= \exp\left(-\frac{n(n-1)}{730}\right). \end{aligned}$$

This upper bound is a very good approximation when n is much smaller than 365.

Interestingly, when $n = 23$, we find that $\Pr(A^c) \leq 0.5$, so $\Pr(A) \geq 0.5$. That is, if there are 23 people in the room, chances are that two of them have the same birthday!

5. *Balls in bins.* You have m indistinguishable balls and in front of you is a row of n bins. You place each ball into a bin chosen at random.

Let's write the sample space as $\Omega = \{1, 2, \dots, m\}^n$; in each outcome $\omega = (\omega_1, \dots, \omega_n)$, the value ω_i represents the number of balls in the i th bin.

Here are some interesting tidbits to prove.

- The chance that any particular bin is empty is at most $e^{-m/n}$.
- If $m = 2n \ln n$, the chance that there exists an empty bin is at most $1/n$. To show this, it helps to use the *union bound*: for any events A_1, \dots, A_k ,

$$\Pr(A_1 \cup A_2 \cup \dots \cup A_k) \leq \Pr(A_1) + \Pr(A_2) + \dots + \Pr(A_k).$$

- The chance that no bin has 2 (or more) balls is at most $\exp(-m(m-1)/n)$. How is this related to the birthday paradox?

A lot of different probability spaces are simple cases of balls and bins. For instance, tossing a fair coin m times is like throwing m balls into $n = 2$ bins (call one bin H and the other bin T).

3.5 Tossing a biased coin

Suppose that instead of a fair coin, you have a coin whose probability of coming up heads is $p \in [0, 1]$. The sample space for a single coin toss is $\Omega_o = \{H, T\}$ and the probabilities of the possible outcomes are

$$\Pr(H) = p, \quad \Pr(T) = 1 - p.$$

If you toss this coin n times (sample space $\Omega = \{H, T\}^n$), what is the chance of getting exactly k heads? Well, pick any sequence $\omega \in \Omega$ with k heads. The probability of getting precisely the outcome ω is

$$\Pr(\omega) = p^k(1-p)^{n-k}.$$

Thus the probability of k heads is

$$(\text{number of sequences with } k \text{ heads}) \cdot p^k(1-p)^{n-k} = \binom{n}{k} p^k(1-p)^{n-k}.$$

Sometimes we encode heads and tails numerically:

$$\text{heads} \rightarrow 1, \quad \text{tails} \rightarrow 0.$$

In this case, a single coin flip with bias p has sample space $\{0, 1\}$ and is called a Bernoulli(p) distribution. Suppose n such coins are flipped, and $X_i \in \{0, 1\}$ is the outcome for the i th coin. Then the number of heads is simply

$$X = X_1 + X_2 + \dots + X_n.$$

X has sample space $\{0, 1, \dots, n\}$ and is said to have a Binomial(n, p) distribution.

Chapter 4

Multiple events, conditioning, and independence

4.1 Two or more events on the same sample space

Frequently we end up dealing with multiple events A, B, \dots defined on a single sample space Ω . For instance, Ω might denote the possible outcomes of picking a card from a deck, and the events of interest could include $A = \{\omega : \omega \text{ is a number}\}$, $B = \{\omega : \omega \text{ is a spade}\}$, and so on. Instead of just the single event probabilities $\Pr(A)$ and $\Pr(B)$, we are also interested in probabilities of combinations of events, such as $\Pr(A \cap B)$ and $\Pr(A \cup B)$.

4.1.1 Human intuition about combined event probabilities is fallible

Let's start with Exercise 1.2.25 from the textbook. The famous psychologists Kahneman and Tversky spent a lot of time trying to understand the nature of human rationality and decision making. For instance, do humans think probabilistically? In one experiment, they told subjects the following:

Linda is 31, single, outspoken, and very bright. She majored in philosophy in college. As a student, she was deeply concerned with racial discrimination and other social issues, and participated in anti-nuclear demonstrations.

and then asked them to assess the likelihood of three events:

- (A) Linda is active in the feminist movement.
- (B) Linda is a bank teller.
- (C) Linda is a bank teller who is active in the feminist movement.

A significant majority of respondents deemed A to be the most likely, followed by C , and lastly B . But $\Pr(C) = \Pr(A \cap B) \leq \Pr(B)$! The respondents exhibited what is called a *conjunction fallacy*.

4.1.2 Joint probability tables

One way to write down the probabilities of pairs of events is in a table of all possible outcomes. Let's take another exercise from the textbook, 1.2.15. Here two students, John and Mary, are taking a math course in which the possible grades are A , B , and C . The sample space of possible outcomes can be written as

$\Omega = \{A, B, C\}^2$, where the first coordinate of $\omega \in \Omega$ is John's grade and the second is Mary's grade. We can write down the probabilities of the nine possible outcomes in a 3×3 table:

		Mary		
		<i>A</i>	<i>B</i>	<i>C</i>
John	<i>A</i>	p_{AA}	p_{AB}	p_{AC}
	<i>B</i>	p_{BA}	p_{BB}	p_{BC}
	<i>C</i>	p_{CA}	p_{CB}	p_{CC}

The particular problem (see book) can be solved by writing the evidence in terms of these probabilities and adding and subtracting appropriate events.

4.1.3 The union bound

As another example, suppose that in a city,

60% of people have a car,

20% of people have a bicycle, and

10% of people have a motorcycle.

Anybody who lacks all three ends up walking to work, and nobody walks unless they have to. Based on this data, what fraction of people walk to work?

We don't have enough information to give an exact answer. This is because we don't know about the overlap in ownership of different vehicles: what fraction of the people with cars also have bicycles, and so on. Nonetheless, we can give upper and lower bounds. To get started, consider the experiment of picking a random person in the city, and let Ω be the space of outcomes. We then define the four events of interest: $C = \{\text{owns a car}\}$, $B = \{\text{owns a bicycle}\}$, $M = \{\text{owns a motorcycle}\}$, and $W = \{\text{walks}\}$. Since $W = \Omega - (C \cup B \cup M)$, we need to bound $\Pr(C \cup B \cup M)$.

The least $\Pr(C \cup B \cup M)$ could possibly be is 0.6, which occurs when everyone who has a bicycle or motorcycle also owns a car. The most $\Pr(C \cup B \cup M)$ could be is 0.9, which happens when the sets C, B, M are disjoint. Therefore $0.1 \leq \Pr(W) \leq 0.4$.

Generalizing, we get the extremely useful **union bound**: for any events A_1, A_2, \dots, A_k ,

$$\Pr(A_1 \cup \dots \cup A_k) \leq \Pr(A_1) + \dots + \Pr(A_k).$$

4.2 Conditional probability

You meet a stranger, a random citizen of the United States. What's the chance that he (or, equally likely, she) votes for the Democratic party? Who knows, but it's probably close to 50%.

$$\Omega = \{\text{citizens of the US}\}, \quad E = \{\omega \in \Omega : \text{votes Dem}\}.$$

Now what if you find out a little bit more information: this stranger likes spicy food.

$$F = \{\omega \in \Omega : \text{likes spicy food}\}.$$

How does change the odds? What is $\Pr(E|F)$ ("probability of E given F ")? Again, it's hard to say, but for illustrative purposes here is a (definitely incorrect) set of probabilities:

$$\Pr(E) = 0.5, \quad \Pr(F) = 0.2, \quad \Pr(E \cap F) = 0.15.$$

The Venn diagram for this scenario is

If you stare at it a little bit, you will probably conclude, correctly, that $\Pr(E|F)$ is the chance that a point drawn from the small blob lies inside the large blob, namely $0.15/0.2 = 0.75$. By reasoning this way, you are implicitly using **the formula for conditional probability**

$$\Pr(E|F) = \frac{\Pr(E \cap F)}{\Pr(F)}.$$

We will make heavy use of this and of the equivalent

$$\Pr(E \cap F) = \Pr(E|F)\Pr(F).$$

4.2.1 A few examples

1. *Pregnancy test.* How accurate is a pregnancy test? Here we make up some numbers and compute the relevant conditional probabilities.

The sample space in this case consists of women who use the test; call this Ω . There are two events on this space that we care about: $P = \{\text{actually pregnant}\}$ and $T = \{\text{test says pregnant}\}$. Suppose that the following are determined (warning: these are fabricated!):

$$T \subset P, \quad \Pr(P) = 0.4, \quad \Pr(T) = 0.3.$$

There are two conditional probabilities we'd like to compute.

- What is the chance of pregnancy if the test comes out positive?
Well, since $T \subset P$, we have $\Pr(P|T) = 1.0$. Algebraically, $\Pr(P \cap T) = \Pr(T)$, so $\Pr(P|T) = \Pr(P \cap T)/\Pr(T) = 1.0$.
- What is the chance of pregnancy if the test comes out negative?
Let $T^c = \Omega - T$ be the event that the test is negative. Then $\Pr(T^c) = 1 - \Pr(T) = 0.7$ and $\Pr(P \cap T^c) = \Pr(P) - \Pr(P \cap T) = 0.4 - 0.3 = 0.1$. These are the two probabilities we need.

$$\Pr(P|T^c) = \frac{\Pr(P \cap T^c)}{\Pr(T^c)} = \frac{0.1}{0.7} \approx 0.14.$$

2. *Rolls of a die.* You roll a die twice. What is the probability that the sum of the two rolls is ≥ 10 if:

- The first roll is 6?
We could use the conditional probability formula, but that seems like overkill in so straightforward a situation.

$$\Pr(\text{sum} \geq 10 \mid \text{first} = 6) = \Pr(\text{second} \geq 4) = \frac{1}{2}.$$

- The first roll is ≥ 3 ?
Okay, this is not so trivial anymore. The sample space is $\Omega = \{1, 2, 3, 4, 5, 6\}^2$, with each of the 36 outcomes equally likely.

$$\begin{aligned} \Pr(\text{sum} \geq 10 \mid \text{first} \geq 3) &= \frac{\Pr(\text{sum} \geq 10 \text{ AND first} \geq 3)}{\Pr(\text{first} \geq 3)} \\ &= \frac{\Pr(\{(4, 6), (5, 5), (5, 6), (6, 4), (6, 5), (6, 6)\})}{4/6} = \frac{6/36}{4/6} = \frac{1}{4}. \end{aligned}$$

- The first roll is < 6 ?

$$\begin{aligned}\Pr(\text{sum} \geq 10 \mid \text{first} < 6) &= \frac{\Pr(\text{sum} \geq 10 \text{ AND first} < 6)}{\Pr(\text{first} < 6)} \\ &= \frac{\Pr(\{(5, 5), (5, 6), (4, 6)\})}{5/6} = \frac{3/36}{5/6} = \frac{1}{10}.\end{aligned}$$

3. *To be invisible or to fly?* A few years ago, the question was going round: “which super power would you rather possess: the ability to make yourself invisible or to fly?” It was perhaps an urban legend that men usually wanted to fly while women usually wanted to be invisible; and there was much speculation about the psychological reasons for this. But suppose the following statistics were obtained (warning: these numbers are fabricated!):

$$\Pr(\text{fly}|\text{male}) = 0.8, \quad \Pr(\text{invisible}|\text{female}) = 0.6.$$

Then what is the overall fraction of people who would choose the ability to fly?

This cannot be answered unless it is known what fraction of the population is male and what fraction is female. Suppose it is 60-40. Then

$$\begin{aligned}\Pr(\text{fly}) &= \Pr(\text{fly AND male}) + \Pr(\text{fly AND female}) \\ &= \Pr(\text{fly}|\text{male})\Pr(\text{male}) + \Pr(\text{fly}|\text{female})\Pr(\text{female}) \\ &= (0.8)(0.6) + (0.4)(0.4) = 0.64.\end{aligned}$$

That is, 64% would like to fly.

4.2.2 The summation rule

In the last example, we implicitly used a **summation formula**. Suppose $A_1, \dots, A_k \subset \Omega$ are disjoint events whose union is Ω (that is, exactly one of them will occur). Then for any event $E \subset \Omega$,

$$\Pr(E) = \sum_{i=1}^k \Pr(E \cap A_i) = \sum_{i=1}^k \Pr(E|A_i)\Pr(A_i).$$

(If the A_i are not disjoint, simply replace the first equality with a \leq .) We will often write $\Pr(E \cap A_i)$ as $\Pr(E, A_i)$.

4.3 Tossing a biased coin

Suppose that instead of a fair coin, you have a coin whose probability of coming up heads is $p \in [0, 1]$. The sample space for a single coin toss is $\Omega_o = \{H, T\}$ and the probabilities of the possible outcomes are

$$\Pr(H) = p, \quad \Pr(T) = 1 - p.$$

If you toss this coin n times (sample space $\Omega = \{H, T\}^n$), what is the chance of getting exactly k heads? Well, pick any sequence $\omega \in \Omega$ with k heads. The probability of getting precisely the outcome ω is

$$\Pr(\omega) = p^k(1 - p)^{n-k}.$$

Thus the probability of k heads is

$$(\text{number of sequences with } k \text{ heads}) \cdot p^k(1 - p)^{n-k} = \binom{n}{k} p^k(1 - p)^{n-k}.$$

Sometimes we encode heads and tails numerically:

$$\text{heads} \rightarrow 1, \quad \text{tails} \rightarrow 0.$$

In this case, a single coin flip with bias p has sample space $\{0, 1\}$ and is called a Bernoulli(p) distribution. Suppose n such coins are flipped, and $X_i \in \{0, 1\}$ is the outcome for the i th coin. Then the number of heads is simply

$$X = X_1 + X_2 + \cdots + X_n.$$

X has sample space $\{0, 1, \dots, n\}$ and is said to have a Binomial(n, p) distribution.

4.4 Conditional probability, continued

4.4.1 Another summation rule

There is also a summation rule for conditional probabilities. Suppose A_1, \dots, A_k are disjoint events whose union is Ω ; and let $E, F \subset \Omega$ be any two events. Then

$$\Pr(E|F) = \sum_{i=1}^k \Pr(E \cap A_i|F) = \sum_{i=1}^k \Pr(E|A_i, F) \Pr(A_i|F).$$

(It's just like the regular summation rule, but operating within F rather than Ω .)

4.4.2 Sex bias in graduate admissions

In 1973, the dean of graduate admissions at Berkeley noticed something alarming: a male applicant had a higher chance of being admitted than a female applicant! Specifically,

$$\Pr(\text{admitted}|\text{male}) = 0.44, \quad \Pr(\text{admitted}|\text{female}) = 0.35.$$

This is a significant difference given that the sample space (applicants to graduate programs at Berkeley) was very large, of size 12,763. The dean wondered, which departments were responsible for this bias?

To determine this, data was collected for each of the departments on campus. And it was found that no department (with a few insignificant exceptions) had any bias against females! Specifically, for each department d ,

$$\Pr(\text{admitted}|\text{male}, \text{department} = d) \leq \Pr(\text{admitted}|\text{female}, \text{department} = d).$$

How could this be?

Let's go back to the summation formulas for conditional probabilities.

$$\begin{aligned} \Pr(\text{admit}|\text{male}) &= \sum_d \Pr(\text{admit}|\text{male}, \text{dept} = d) \Pr(\text{dept} = d|\text{male}) \\ \Pr(\text{admit}|\text{female}) &= \sum_d \Pr(\text{admit}|\text{female}, \text{dept} = d) \Pr(\text{dept} = d|\text{female}) \end{aligned}$$

The answer lies in the second term. Some departments (engineering) are easier to get into than others (humanities). Males tended to apply to the easier departments, while females on average applied to the harder departments. So while no individual department had bias, on the whole it looked like women had a lower probability of acceptance.

4.5 Bayes' rule

The following example is taken from *Probabilistic Reasoning in Intelligent Systems* by Judea Pearl:

You wake up in the middle of the night to the shrill sound of your burglar alarm. What is the chance that a burglary attempt has taken place?

The relevant facts are:

- There is a 95% chance that an attempted burglary attempt will trigger the alarm. That is,

$$\Pr(\text{alarm}|\text{burglary}) = 0.95.$$

- There is a 1% chance of a false alarm.

$$\Pr(\text{alarm}|\text{no burglary}) = 0.01.$$

- Based on local crime statistics, there is a one-in-10,000 chance that a house will be burglarized on a given night.

$$\Pr(\text{burglary}) = 10^{-4}.$$

We are interested in the chance of a burglary given that the alarm has sounded. We can use the conditional probability formula for this:

$$\Pr(\text{burglary}|\text{alarm}) = \frac{\Pr(\text{burglary, alarm})}{\Pr(\text{alarm})} = \frac{\Pr(\text{alarm}|\text{burglary})\Pr(\text{burglary})}{\Pr(\text{alarm})}.$$

The one term we don't immediately know is $\Pr(\text{alarm})$. By the summation rule,

$$\Pr(\text{alarm}) = \Pr(\text{alarm}|\text{burglary})\Pr(\text{burglary}) + \Pr(\text{alarm}|\text{no burglary})\Pr(\text{no burglary}).$$

Putting it all together,

$$\Pr(\text{burglary}|\text{alarm}) = \frac{0.95 \times 10^{-4}}{0.95 \times 10^{-4} + 0.01 \times (1 - 10^{-4})} = 0.00941,$$

about 0.94%. Thus our belief in a burglary has risen approximately a hundredfold from its default value of 10^{-4} , on account of the alarm.

It is frequently the case, as in this example, that we wish to update the chances of an event H based on new evidence E . In other words, we wish to know $\Pr(H|E)$. The derivation above implicitly uses the following formula, called **Bayes' rule**:

$$\Pr(H|E) = \frac{\Pr(E|H)\Pr(H)}{\Pr(E)}.$$

As another example, let's look at the Three Prisoner's Paradox, which is actually just a reformulation of the Monty Hall problem. The story goes that there are three prisoners A, B, C in a jail, and one of them is to be declared guilty and executed the following morning. As the night progresses, prisoner A is racked with worry, and calls the prison guard over. He wants to know whether he is the unlucky one. The guard replies, "I am not allowed to tell you whether you will be declared guilty. But I can say that prisoner B will be declared innocent." Prisoner A thinks about this for a little while and then starts worrying even more. Before he asked the question, it seemed like his chances of dying were one-in-three. But after his innocuous question, the chance seems to have risen to one-in-two!

Actually, Prisoner A 's chances are still one in three. The two events of interest are

$$\begin{aligned} G_A &= A \text{ will be declared guilty} \\ I_B &= \text{the guard, when prompted, will declare } B \text{ to be innocent.} \end{aligned}$$

Using the summation rule,

$$\Pr(I_B) = \Pr(I_B|G_A)\Pr(G_A) + \Pr(I_B|G_A^c)\Pr(G_A^c) = \frac{1}{2} \cdot \frac{1}{3} + \frac{1}{2} \cdot \frac{2}{3} = \frac{1}{2}.$$

Therefore, by Bayes' rule,

$$\Pr(G_A|I_B) = \frac{\Pr(I_B|G_A)\Pr(G_A)}{\Pr(I_B)} = \frac{\frac{1}{2} \cdot \frac{1}{3}}{\frac{1}{2}} = \frac{1}{3}.$$

4.6 Independence

Two events are called *independent* if the outcome of one (that is, whether or not it occurs) does not affect the probability that the other will occur. For instance, suppose you flip two fair coins. The outcome of either coin does not influence the other; therefore the two outcomes are independent.

Formally, we say events A and B (defined on some sample space Ω) are independent if

$$\Pr(A \cap B) = \Pr(A)\Pr(B).$$

Can you show that this definition implies the following?

- $\Pr(A|B) = \Pr(A)$.
- $\Pr(B|A) = \Pr(B)$.
- $\Pr(A|B^c) = \Pr(A)$.

In the following examples, are events A and B independent or not?

1. You have two children. $A = \{\text{first child is a boy}\}$, $B = \{\text{second child is a girl}\}$.
2. You throw two dice. $A = \{\text{first is a 6}\}$, $B = \{\text{sum} > 10\}$.
3. You get dealt two cards at random from a deck of 52. $A = \{\text{first is a heart}\}$, $B = \{\text{second is a club}\}$.
4. Same sample space. $A = \{\text{first is a heart}\}$, $B = \{\text{second is a 10}\}$.
5. The three scenarios depicted in these Venn diagrams.

4.6.1 The Monty Hall problem

This probability puzzle is weakly related to a game on an old TV show called *Let's Make a Deal*, and has been renamed after the host of that show. The host brings the game player to a room with three closed doors. One of the doors leads to a treasure chest while the other two doors each lead to a goat. The player picks a door (at random, presumably), hoping for the best. Now something interesting happens. Instead of opening that door, the host opens one of the other two doors to reveal a goat. The player is then allowed to either stick to his original guess, or to switch to the other unopened door. Which should he do?

In surveys, the majority of people feel intuitively that it doesn't make a difference. They reason that there are two unopened doors, and the treasure could be behind either of them, so each has a 50-50 chance of being the lucky door.

The truth is that the only *safe* thing to do is not to switch. We should deviate from this safe choice only if we know something about the Monty Hall's behaviour.

Chapter 5

Random variables, expectation, and variance, I

5.1 Random variables

A *random variable* (r.v.) is defined on a probability space (Ω, \Pr) and is a mapping from Ω to \mathbb{R} .

The value of the random variable is fully determined by the outcome $\omega \in \Omega$. Thus the underlying probability space (probabilities $\Pr(\omega)$) induces a probability distribution over the random variable. Let's look at some examples.

Suppose you roll a fair die. The sample space is $\Omega = \{1, 2, 3, 4, 5, 6\}$, all outcomes being equally likely. On this space we can then define a random variable

$$X = \begin{cases} 1 & \text{if die is } \geq 3 \\ 0 & \text{otherwise} \end{cases}$$

In other words, the outcomes $\omega = 1, 2$ map to $X = 0$, while the outcomes $\omega = 3, 4, 5, 6$ map to $X = 1$. The r.v. X takes on values $\{0, 1\}$, with probabilities $\Pr(X = 0) = 1/3$ and $\Pr(X = 1) = 2/3$.

Or say you roll this same die n times, so that the sample space is $\Omega = \{1, 2, 3, 4, 5, 6\}^n$. Examples of random variables on this larger space are

$$\begin{aligned} X &= \text{the number of 6's rolled,} \\ Y &= \text{the number of 1's seen before the first 6.} \end{aligned}$$

The sample point $\omega = (1, 1, 1, 1, \dots, 1, 6)$, for instance, would map to $X = 1, Y = n - 1$. The variable X takes values in $\{0, 1, 2, \dots, n\}$, with

$$\Pr(X = k) = \binom{n}{k} \left(\frac{1}{6}\right)^k \left(\frac{5}{6}\right)^{n-k}$$

(do you see why?).

As a third example, suppose you throw a dart at a dartboard of radius 1, and that it lands at a random location on the board. Define random variable X to be the distance of the dart from the center of the board. Now X takes values in $[0, 1]$, and for any x in this range, $\Pr(X \leq x) = x^2$.

Henceforth, we'll follow the convention of using capital letters for r.v.'s.

5.2 The mean, or expected value

For a random variable X that takes on a finite set of possible values, the *mean*, or *expected value*, is

$$\mathbb{E}(X) = \sum_x x \Pr(X = x)$$

(where the summation is over all the possible values x that X can have). This is a direct generalization of the notion of *average* (which is typically defined in situations where the outcomes are equally likely). If X is a continuous random variable, then this summation needs to be replaced by an equivalent integral; but we'll get to that later in the course.

Here are some examples.

1. *Coin with bias (heads probability) p .*

Define X to be 1 if the outcome is heads, or 0 if it is tails. Then

$$\mathbb{E}(X) = 0 \cdot \Pr(X = 0) + 1 \cdot \Pr(X = 1) = 0 \cdot (1 - p) + 1 \cdot p = p.$$

Another random variable on this space is X^2 , which also takes on values in $\{0, 1\}$. Notice that $X^2 = X$, and in fact $X^k = X$ for all $k = 1, 2, 3, \dots$! Thus, $\mathbb{E}(X^2) = p$ as well. This simple case shows that in general, $\mathbb{E}(X^2) \neq \mathbb{E}(X)^2$.

2. *Fair die.*

Define X to be the outcome of the roll, so $X \in \{1, 2, 3, 4, 5, 6\}$. Then

$$\mathbb{E}(X) = 1 \cdot \frac{1}{6} + 2 \cdot \frac{1}{6} + 3 \cdot \frac{1}{6} + 4 \cdot \frac{1}{6} + 5 \cdot \frac{1}{6} + 6 \cdot \frac{1}{6} = 3.5.$$

3. *Two dice.*

Let X be their sum, so that $X \in \{2, 3, 4, \dots, 12\}$. We can calculate the probabilities of each possible value of X and tabulate them as follows:

x	2	3	4	5	6	7	8	9	10	11	12
$\Pr(X = x)$	$\frac{1}{36}$	$\frac{2}{36}$	$\frac{3}{36}$	$\frac{4}{36}$	$\frac{5}{36}$	$\frac{6}{36}$	$\frac{5}{36}$	$\frac{4}{36}$	$\frac{3}{36}$	$\frac{2}{36}$	$\frac{1}{36}$

This gives $\mathbb{E}(X) = 7$.

4. *Roll n die; how many sixes appear?*

Let X be the number of 6's. We've already analyzed the distribution of X , so

$$E(X) = \sum_{k=0}^n k \Pr(X = k) = \sum_{k=0}^n k \binom{n}{k} \left(\frac{1}{6}\right)^k \left(\frac{5}{6}\right)^{n-k} = \frac{n}{6}.$$

The last step is somewhat mysterious; just take our word for it, and we'll get back to it later!

5. *Toss a fair coin forever; how many tosses to the first heads?*

Let $X \in \{1, 2, \dots\}$ be the number of tosses until you first see heads. Then

$$\Pr(X = k) = \Pr((T, T, T, \dots, T, H)) = \frac{1}{2^k}.$$

It follows that

$$\mathbb{E}(X) = \sum_{k=1}^{\infty} \frac{k}{2^k} = 2.$$

We saw in class how to do this summation. The technique was based on the formula for the sum of a geometric series: if $|r| < 1$, then

$$a + ar + ar^2 + \cdots = \frac{a}{1-r}.$$

6. *Toss a coin with bias p forever; how many tosses to the first heads?*

Once again, $X \in \{1, 2, \dots\}$, but this time the distribution is different:

$$\Pr(X = k) = \Pr((T, T, T, \dots, T, H)) = (1-p)^{k-1}p.$$

Using the same technique as before, we get $\mathbb{E}(X) = 1/p$.

There's another way to derive this expectation. We always need at least one coin toss. If we're lucky (with probability p), we're done; otherwise (with probability $1-p$), we start again from scratch. Therefore $\mathbb{E}(X) = 1 + (1-p)\mathbb{E}(X)$, so that $\mathbb{E}(X) = 1/p$.

7. *Pascal's wager: does God exist?*

Here was Pascal's take on the issue of God's existence: if you believe there is some chance $p > 0$ (no matter how small) that God exists, then you should behave as if God exists.

Why? Well, let the random variable X denote your amount of suffering.

Suppose you behave as if God exists (that is, you are good). This behavior incurs a significant but finite amount of suffering (you are not able to do some of the things you would like to). Say $X = 10$.

On the other hand, suppose you behave as if God doesn't exist – that is, you do all the things you want to do. If God really doesn't exist, you're fine, and your suffering is $X = 0$. But if God exists, then you go straight to hell and your suffering is $X = \infty$. Thus your *expected* suffering if you behave badly is $\mathbb{E}(X) = 0 \cdot (1-p) + \infty \cdot p = \infty$.

So: to minimize your expected suffering, behave as if God exists!

5.3 Tossing a biased coin

Suppose that instead of a fair coin, you have a coin whose probability of coming up heads is $p \in [0, 1]$. The sample space for a single coin toss is $\Omega_o = \{H, T\}$ and the probabilities of the possible outcomes are

$$\Pr(H) = p, \quad \Pr(T) = 1 - p.$$

If you toss this coin n times (sample space $\Omega = \{H, T\}^n$), what is the chance of getting exactly k heads? Well, pick any sequence $\omega \in \Omega$ with k heads. The probability of getting precisely the outcome ω is

$$\Pr(\omega) = p^k(1-p)^{n-k}.$$

Thus the probability of k heads is

$$(\text{number of sequences with } k \text{ heads}) \cdot p^k(1-p)^{n-k} = \binom{n}{k} p^k(1-p)^{n-k}.$$

Sometimes we encode heads and tails numerically:

$$\text{heads} \rightarrow 1, \quad \text{tails} \rightarrow 0.$$

In this case, a single coin flip with bias p has sample space $\{0, 1\}$ and is called a Bernoulli(p) distribution. Suppose n such coins are flipped, and $X_i \in \{0, 1\}$ is the outcome for the i th coin. Then the number of heads is simply

$$X = X_1 + X_2 + \cdots + X_n.$$

X has sample space $\{0, 1, \dots, n\}$ and is said to have a Binomial(n, p) distribution.

If X and Y are independent random variables, then $\text{var}(X + Y) = \text{var}(X) + \text{var}(Y)$. More generally, if X_1, \dots, X_n are independent, then

$$\text{var}(X_1 + \cdots + X_n) = \text{var}(X_1) + \cdots + \text{var}(X_n).$$

5.3.1 An application to sampling

Suppose you are interested in finding out the fraction of Americans who like sushi. This is some unknown value $p \in [0, 1]$ that you decide to estimate by sampling. To this end, you pick n random people and poll them. Let X_i be 1 if the i th person you ask likes sushi, and 0 if not. Your estimate of p is then

$$Y = \frac{X_1 + \cdots + X_n}{n}.$$

Since $\mathbb{E}(X_i) = p$, it follows by linearity of expectation that

$$\mathbb{E}(Y) = \frac{1}{n} (\mathbb{E}(X_1) + \cdots + \mathbb{E}(X_n)) = p.$$

So Y certainly has the right expected value. But how far does it typically deviate from this expectation? Since the X_i are independent, and since each $\text{var}(X_i) = p(1 - p)$ (recall our earlier coin flip example),

$$\text{var}(Y) = \frac{\text{var}(X_1 + \cdots + X_n)}{n^2} = \frac{\text{var}(X_1) + \cdots + \text{var}(X_n)}{n^2} = \frac{p(1 - p)}{n}.$$

So the standard deviation of Y is $\sqrt{p(1 - p)/n}$: the larger n is, the closer Y stays to the desired value p .

5.4 Linearity of expectation

If you double each value of X , then you also double its average; that is, $\mathbb{E}(2X) = 2\mathbb{E}(X)$. Likewise, if you raise each of its values by 1, you will also increase the average by 1; that is, $\mathbb{E}(X + 1) = \mathbb{E}(X) + 1$. More generally, for any constants a, b ,

$$\mathbb{E}(aX + b) = a\mathbb{E}(X) + b.$$

Another exceptionally useful formula says that the mean value of the sum of variables is simply the sum of their individual means. Formally, for any random variables X, Y ,

$$\mathbb{E}(X + Y) = \mathbb{E}(X) + \mathbb{E}(Y).$$

For example, recall our earlier example about two rolls of a die, in which we let X be the sum of the rolls and derived $\mathbb{E}(X)$ by first computing $\Pr(X = x)$ for all $x \in \{2, 3, \dots, 12\}$. Well, now we can do it much more easily: simply write X_1 for the first roll and X_2 for the second roll, so that $X = X_1 + X_2$. We already know $\mathbb{E}(X_i) = 3.5$, so $\mathbb{E}(X) = 7$.

More generally, for any random variables X_1, X_2, \dots, X_n ,

$$\mathbb{E}(X_1 + \cdots + X_n) = \mathbb{E}(X_1) + \cdots + \mathbb{E}(X_n).$$

Some quick examples:

1. Roll n dice and let X be the number of sixes. What is $\mathbb{E}(X)$?

This time, let X_i be 1 if the i th roll is a six, and 0 otherwise. Thus $\mathbb{E}(X_i) = 1/6$, so $\mathbb{E}(X) = n/6$.

2. Toss n coins of bias p and let X be the number of heads. What is $\mathbb{E}(X)$?

Let X_i be 1 if the i th coin turns up heads, and 0 if it turns up tails. Then $\mathbb{E}(X_i) = p$ and since $X = X_1 + \cdots + X_n$, we have $\mathbb{E}(X) = np$.

3. Toss n coins of bias p ; what is the expected number of times HTH appears in the resulting sequence?

Let X_i be 1 if there is an occurrence of HTH starting at position i (so $1 \leq i \leq n-2$). The total number of such occurrences is $X = X_1 + X_2 + \cdots + X_{n-2}$. Since $\mathbb{E}(X_i) = p^2(1-p)$, we have $\mathbb{E}(X) = (n-2)p^2(1-p)$.

5.4.1 Fixed points of a permutation

The *fixed points* of a permutation are the numbers that remain in their original position. For instance, in the permutation

$$(1, 2, 3, 4, 5, 6) \rightarrow (6, 2, 5, 4, 1, 3)$$

the fixed points are 2 and 4. Let X be the number of fixed points in a random permutation of $(1, 2, \dots, n)$; what is $\mathbb{E}(X)$?

Linearity is very helpful here. Define the random variable X_i to be 1 if i is a fixed point, and 0 otherwise. Then $\mathbb{E}(X_i) = 1/n$. Therefore

$$\mathbb{E}(X) = \mathbb{E}(X_1 + \cdots + X_n) = 1.$$

The expected number of fixed points is 1, regardless of n .

5.4.2 Coupon collector, again

Recall the setting: each cereal box holds one of k action figures (chosen at random), and you want to collect all the figures. What is the expected number of cereal boxes you need to buy?

Suppose you keep buying boxes until you get all the figures. Let X_i be the number of boxes you buy to get from $i-1$ distinct figures to i distinct figures. Therefore $X = X_1 + X_2 + \cdots + X_k$, and of course $X_1 = 1$.

What is $\mathbb{E}(X_i)$? Well, you already have $i-1$ of the figures, so the chance of getting a new figure in a cereal box is $(k - (i-1))/k$. Call this p . Therefore, the expected amount of time you have to wait to get a new figure is $1/p$: just like waiting for a coin with bias p to turn up heads. That is,

$$\mathbb{E}(X_i) = \frac{k}{k-i+1}.$$

Invoking linearity of expectation,

$$\begin{aligned} \mathbb{E}(X) &= \mathbb{E}(X_1) + \cdots + \mathbb{E}(X_k) \\ &= \frac{k}{k} + \frac{k}{k-1} + \frac{k}{k-2} + \cdots + \frac{k}{1} \\ &= k \left(1 + \frac{1}{2} + \cdots + \frac{1}{k} \right) \\ &\approx k \ln k. \end{aligned}$$

This confirms our earlier observations about the coupon collector problem: you need to buy about $k \ln k$ boxes.

5.4.3 Balls in bins, again

Toss m balls in n bins; what is the expected number of *collisions*? Let's make this more precise. For any $1 \leq i < j \leq m$, define the random variable X_{ij} to be 1 if balls i and j land in the same bin, and 0 otherwise. Then the number of collisions is defined to be

$$X = \sum_{1 \leq i < j \leq m} X_{ij}.$$

Since $\mathbb{E}(X_{ij}) = 1/n$ (do you see why?), it follows that the expected number of collisions is

$$\mathbb{E}(X) = \binom{m}{2} \frac{1}{n} = \frac{m(m-1)}{2n}.$$

So if $m < \sqrt{2n}$, the expected number of collisions is < 1 , which means every ball goes into a different bin.

This relates back to the birthday paradox, where m is close to the threshold $\sqrt{2n}$.

5.5 Independent random variables

Random variables X and Y are *independent* if

$$\Pr(X = x, Y = y) = \Pr(X = x)\Pr(Y = y)$$

for all x, y . In words, the joint distribution of (X, Y) factors into the product of the individual distributions. This also implies, for instance, that

$$\Pr(X = x|Y = y) = \Pr(X = x).$$

Which of the following pairs (X, Y) are independent?

1. Pick a random card out of a standard deck. Define X to be 1 if it is a heart; and 0 otherwise. Define Y to be 1 if it is a jack, queen, or king; and 0 otherwise.
2. Toss a fair coin n times, and define X to be the number of heads, and Y to be 1 if the last toss is heads (and 0 otherwise).
3. X and Y take values in $\{-1, 0, 1\}$, and their joint distribution is given by the following table of probabilities.

		Y		
		-1	0	1
X	-1	0.4	0.16	0.24
	0	0.05	0.02	0.03
	1	0.05	0.02	0.03

If X, Y are independent, they satisfy the following useful *product rule*:

$$\mathbb{E}(XY) = \mathbb{E}(X)\mathbb{E}(Y).$$

Another useful fact is that $f(X)$ and $g(Y)$ must also be independent, for any functions f and g .

5.6 Variance

If you need to summarize a probability distribution by a single number, then the mean is a reasonable choice – although often the *median* is better advised (more on this later). But neither the mean nor median captures how *spread out* the distribution is.

Look at the following two distributions:



They both have the same expectation, 100, but one is concentrated near the middle while the other is pretty flat. To distinguish between them, we are interested not just in the mean $\mu = \mathbb{E}(X)$, but also in the typical distance from the mean, $\mathbb{E}(|X - \mu|)$. It turns out to be mathematically convenient to work with the square instead: the *variance* of X is defined to be

$$\text{var}(X) = \mathbb{E}((X - \mu)^2) = \mathbb{E}((X - E(X))^2).$$

In the above example, the distribution on the right has a higher variance than the one on the left.

5.6.1 Properties of the variance

In what follows, take μ to be $\mathbb{E}(X)$.

1. The variance cannot be negative.

Since each individual value $(X - \mu)^2$ is ≥ 0 (since it's squared), the average value $\mathbb{E}((X - \mu)^2)$ must be ≥ 0 as well.

2. $\text{var}(X) = \mathbb{E}(X^2) - \mu^2$.

This is because

$$\begin{aligned} \text{var}(X) &= \mathbb{E}((X - \mu)^2) \\ &= \mathbb{E}(X^2 + \mu^2 - 2\mu X) \\ &= \mathbb{E}(X^2) + \mathbb{E}(\mu^2) + \mathbb{E}(-2\mu X) \quad (\text{linearity}) \\ &= \mathbb{E}(X^2) + \mu^2 - 2\mu\mathbb{E}(X) \\ &= \mathbb{E}(X^2) + \mu^2 - 2\mu^2 = \mathbb{E}(X^2) - \mu^2. \end{aligned}$$

3. For any random variable X , it must be the case that $\mathbb{E}(X^2) \geq (\mathbb{E}(X))^2$.

This is simply because $\text{var}(X) = \mathbb{E}(X^2) - (\mathbb{E}(X))^2 \geq 0$.

4. $\mathbb{E}(|X - \mu|) \leq \sqrt{\text{var}(X)}$.

If you apply the previous property to the random variable $|X - \mu|$ instead of X , you get $\mathbb{E}(|X - \mu|^2) \geq (\mathbb{E}(|X - \mu|))^2$. Therefore, $\mathbb{E}(|X - \mu|) \leq \sqrt{\mathbb{E}(|X - \mu|^2)} = \sqrt{\text{var}(X)}$.

The last property tells us that $\sqrt{\text{var}(X)}$ is a good measure of the typical spread of X : how far it typically lies from its mean. We call this the *standard deviation* of X .

5.6.2 Examples

1. Suppose you toss a coin with bias p , and let X be 1 if the outcome is heads, or 0 if the outcome is tails. Let's look at the distribution of X and of X^2 .

Prob	X	X^2
p	1	1
$1 - p$	0	0

From this table, $\mathbb{E}(X) = p$ and $\mathbb{E}(X^2) = p$. Thus the variance is $\text{var}(X) = \mathbb{E}(X^2) - (\mathbb{E}(X))^2 = p(1 - p)$.

2. Roll a 4-sided die (a tetrahedron) in which each face is equally likely to come up, and let the outcome be $X \in \{1, 2, 3, 4\}$.

We have two formulas for the variance:

$$\begin{aligned}\text{var}(X) &= \mathbb{E}((X - \mu)^2) \\ \text{var}(X) &= \mathbb{E}(X^2) - \mu^2\end{aligned}$$

where $\mu = \mathbb{E}(X)$. Let's try both and make sure we get the same answer. First of all, $\mu = \mathbb{E}(X) = (1 + 2 + 3 + 4)/4 = 2.5$. Now, let's tabulate the distribution of X^2 and $(X - \mu)^2$.

Prob	X	X^2	$(X - \mu)^2$
1/4	1	1	2.25
1/4	2	4	0.25
1/4	3	9	0.25
1/4	4	16	2.25

Reading from this table,

$$\begin{aligned}\mathbb{E}(X^2) &= \frac{1}{4}(1 + 4 + 9 + 16) = 7.5 \\ \mathbb{E}(X - \mu)^2 &= \frac{1}{4}(2.25 + 0.25 + 0.25 + 2.25) = 1.25\end{aligned}$$

The first formula for variance gives $\text{var}(X) = \mathbb{E}(X^2) - \mu^2 = 7.5 - (2.5)^2 = 1.25$. The second formula gives $\text{var}(X) = \mathbb{E}(X^2) - \mu^2 = 7.5 - (2.5)^2 = 1.25$, the same thing.

3. Roll a k -sided die in which each face is equally likely to come up. The outcome is $X \in \{1, 2, \dots, k\}$.
The expected outcome is

$$\mathbb{E}(X) = \frac{1 + 2 + \dots + k}{k} = \frac{\frac{1}{2}k(k+1)}{k} = \frac{k+1}{2},$$

using a special formula for the sum of the first k integers. There's another for the sum of the first k squares, from which

$$\mathbb{E}(X^2) = \frac{1^2 + 2^2 + \dots + k^2}{k} = \frac{\frac{1}{6}k(k+1)(2k+1)}{k} = \frac{(k+1)(2k+1)}{6}.$$

Then

$$\text{var}(X) = \mathbb{E}(X^2) - (\mathbb{E}(X))^2 = \frac{(k+1)(2k+1)}{6} - \frac{(k+1)^2}{4} = \frac{k^2 - 1}{12}.$$

The standard deviation is thus approximately $k/\sqrt{12}$.

4. X is the number of fixed points of a random permutation of $(1, 2, \dots, n)$.

Proceeding as before, let X_i be 1 if i is a fixed point of the permutation, and 0 otherwise. Then $\mathbb{E}(X_i) = 1/n$. For $i \neq j$, the product $X_i X_j$ is 1 only if both i and j are fixed points, which occurs with probability $1/n(n-1)$ (why?). Thus $\mathbb{E}(X_i X_j) = 1/n(n-1)$.

Since X is the sum of the individual X_i , we have $\mathbb{E}(X) = 1$ and

$$\begin{aligned} \mathbb{E}(X^2) &= \mathbb{E}((X_1 + \dots + X_n)^2) \\ &= \mathbb{E}\left(\sum_{i=1}^n X_i^2 + \sum_{i \neq j} X_i X_j\right) \\ &= \sum_i \mathbb{E}(X_i^2) + \sum_{i \neq j} \mathbb{E}(X_i X_j) \\ &= n \cdot \frac{1}{n} + n(n-1) \cdot \frac{1}{n(n-1)} = 2. \end{aligned}$$

Thus $\text{var}(X) = \mathbb{E}(X^2) - (\mathbb{E}(X))^2 = 1$. This means that the number of fixed points has mean 1 and variance 1: in short, it is quite unlikely to be very much larger than 1.

5.6.3 Another property of the variance

Here's a cartoon picture of a well-behaved distribution with mean μ and standard deviation σ (that is, $\mu = \mathbb{E}(X)$ and $\sigma^2 = \text{var}(X)$).

The standard deviation quantifies the *spread* of the distribution whereas the mean specifies its *location*. If you increase all values of X by 10, then the distribution will shift to the right and the mean will increase by 10. But the spread of the distribution – and thus the standard deviation – will remain unchanged.

On the other hand, if you double all values of X , then its distribution becomes twice as wide, and thus its standard deviation σ is doubled. Which means that its variance, which is the square of the standard deviation, gets multiplied by 4.

In summary, for any constants a, b :

$$\text{var}(aX + b) = a^2 \text{var}(X).$$

Contrast this with the mean: $\mathbb{E}(aX + b) = a\mathbb{E}(X) + b$.

5.6.4 Linearity of variance

If X and Y are independent random variables, then $\text{var}(X + Y) = \text{var}(X) + \text{var}(Y)$. More generally, if X_1, \dots, X_n are independent, then

$$\text{var}(X_1 + \dots + X_n) = \text{var}(X_1) + \dots + \text{var}(X_n).$$

In contrast, linearity of expectation ($\mathbb{E}(X + Y) = \mathbb{E}(X) + \mathbb{E}(Y)$) holds even if the random variables are *not* independent.

Chapter 6

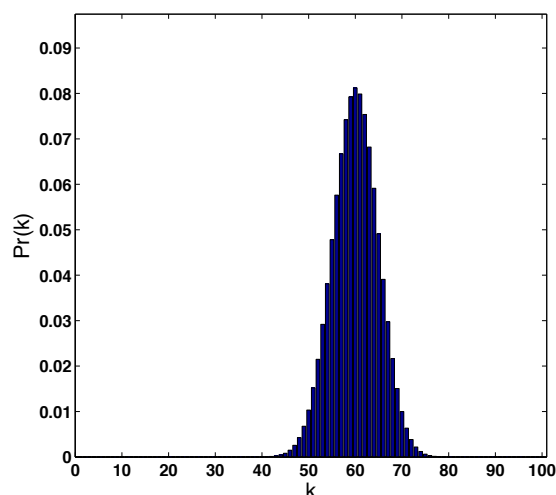
Sampling, hypothesis testing, and the central limit theorem

6.1 The binomial distribution

Let X be the number of heads when a coin of bias p is tossed n times. The distribution of X is so fundamental to probability and statistics that it merits a special name, the *binomial*(n, p) distribution. Here it is, precisely:

$$\begin{aligned}\Sigma &= \{0, 1, \dots, n\} \\ \Pr(X = k) &= \binom{n}{k} p^k (1-p)^{n-k}\end{aligned}$$

The figure below shows the binomial(100, 0.6) distribution.



The key property of this distribution is that it is tightly concentrated around $np = 60$. This is the mean of X , as can be seen by writing it in the form $X = X_1 + \dots + X_n$, where each $X_i \sim B(p)$; in words, X_i is 1 if the i th coin toss comes up heads.

How spread out is the distribution? To quantify this, we need to compute the variance of X . Once again, the representation of X as the sum of X_i 's comes in handy, coupled with the following useful fact.

Fact 1. If Z_1, \dots, Z_n are independent, then $\text{var}(Z_1 + \dots + Z_n) = \text{var}(Z_1) + \dots + \text{var}(Z_n)$.

Each X_i has variance $p(1-p)$, so X has variance $np(1-p)$ and thus standard deviation $\sqrt{np(1-p)}$.

Fact 2. If $X \sim \text{binomial}(n, p)$, then:

$$\begin{aligned}\mathbb{E}(X) &= np \\ \text{var}(X) &= np(1-p) \\ \text{stddev}(X) &= \sqrt{np(1-p)}\end{aligned}$$

There's another very useful fact about the binomial that comes up over and over again: *about 95% of the distribution lies within two standard deviations of the mean.* That is to say,

$$\Pr\left(np - 2\sqrt{np(1-p)} \leq X \leq np + 2\sqrt{np(1-p)}\right) \approx 0.95. \quad (6.1)$$

We'll see how this approximation arises a little later on. As an example of its use, consider the figure shown above for $\text{binomial}(100, 0.6)$. The standard deviation is $\sigma = \sqrt{100(0.6)(0.4)} \approx 5$. And indeed almost all the distribution lies in the range $np \pm 2\sigma = 60 \pm 10$.

The remarkable thing about (6.1) is that although X can potentially take on $n+1$ possible values, it effectively stays within a range of size just $O(\sqrt{n})$; this is miniscule compared to $n+1$ for large n .

6.2 Hypothesis testing

6.2.1 Testing a vaccine

Suppose there is a certain disease that cattle can contract; and that any given cow has a 25% chance of contracting it within the course of a year. A new serum is proposed, and we want to test it to see how well it works. So we choose n cows at random, inject them with the serum, and then keep an eye on them over the next year. Let's say K of them remain healthy.

One possibility is that the serum has no effect whatsoever; call this hypothesis H_0 . If this hypothesis is true, then the chance of infection is exactly the same for the cows that were injected as it is for the cow population at large, and thus $K \sim \text{binomial}(n, 0.75)$.

We hope that the experiment yields a large value of K ; this will provide evidence against hypothesis H_0 . But how large does K need to be? It depends on how much *statistical confidence* we want in our assertion that H_0 is false. A common goal is a *95% confidence level*.

Suppose we have a sample of $n = 100$ cows. The $\text{binomial}(100, 0.75)$ distribution has mean 75 and standard deviation $\sigma = \sqrt{100(0.25)(0.75)} \approx 4.3$. Using equation (6.1), we can deduce that *if H_0 were true*, we would expect (with 95% confidence) a value of K in the range 75 ± 8.6 . If K exceeds this, that is if $K > 83$, then we can reject H_0 with a 95% confidence level.

6.2.2 A blood pressure drug

Suppose a new blood pressure drug is proposed, and to test it, a sample of n patients is selected. Their blood pressure is measured with and without the drug.

Person	B.P. with drug	B.P. without drug
1	x_1	x'_1
2	x_2	x'_2
\vdots	\vdots	\vdots
n	x_n	x'_n

The i th trial is called a success if $x_i < x'_i$; let K be the total number of successes. How should the evidence be evaluated?

Let H_0 be the hypothesis that the drug is useless. Under this hypothesis, $K \sim \text{binomial}(n, 0.5)$. Thus K has expected value $0.5n$ and standard deviation $\sqrt{n(0.5)(0.5)} = 0.5\sqrt{n}$. As we noted above, with 95% confidence, we'd expect K to be within two standard deviations of its mean, that is, $K = 0.5n \pm \sqrt{n}$.

So if K exceeds $0.5n + \sqrt{n}$, we can declare that H_0 is invalidated with 95% confidence, implying that the drug is not entirely useless.

6.3 Sampling

We live in an age where the government and the mass media are continuously polling the public. They wish to know the fraction of people who like sushi, think Obama is doing a good job, support Tiger Woods, think God exists, feel pessimistic about the future, smoke, think the war in Iraq is unnecessary, etc. This constant polling affects decision-making at every level. It advises politicians on what to say and do. It helps companies decide how to most effectively advertise their products. It helps investors decide where to entrust their money. And so on.

In each such case, there is an unknown probability p that is sought: the fraction of people who like sushi, for instance. Determining this fraction exactly would require asking *everyone*, which is prohibitively expensive. So instead a sample of n people is chosen at random, and they are each asked whether they like sushi. Let K be the number of positive responses. Then K has the $\text{binomial}(n, p)$ distribution, with expected value np and variance $np(1-p)$.

An estimate of the fraction of sushi-lovers is K/n . Notice that

$$\begin{aligned}\mathbb{E}\left(\frac{K}{n}\right) &= p \\ \text{var}\left(\frac{K}{n}\right) &= \frac{\text{var}(K)}{n^2} = \frac{p(1-p)}{n} \\ \text{stddev}\left(\frac{K}{n}\right) &= \sqrt{\frac{p(1-p)}{n}}\end{aligned}$$

A standard rule of thumb, given in equation (6.1) is that the estimate K/n will lie within two standard deviations of its expected value with 95% probability. Thus we can assert with 95% confidence that the true fraction of people who like sushi is

$$\frac{K}{n} \pm 2\sqrt{\frac{p(1-p)}{n}}.$$

But this doesn't make sense, since we don't know what p is. A quick fix is to notice that $p(1-p) \leq 1/4$ (the maximization can be done by calculus, for instance), and thus a valid 95% confidence interval is

$$\frac{K}{n} \pm \frac{1}{\sqrt{n}}.$$

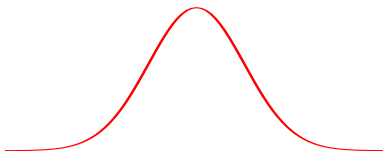
Thus a sample size of 2,500 gives an estimate that is accurate to within $1/\sqrt{n} = 0.02$ (at 95% confidence), whereas a sample size of 10,000 gives an accuracy of 0.01.

What if we want a higher level of confidence, like 99%, or even 99.9%? Equation (6.1) is no longer helpful; we need similar approximations for other confidence levels. It turns out that these are easy to obtain, for any desired confidence level, using the *normal approximation to the binomial distribution*.

read up to here for Wed 11/16

6.4 The normal distribution

You are probably reading these notes in a library or cafeteria. Take a look at the 100 or so people nearest to you. If you were to plot the heights of all the men, it would look kind of like this:

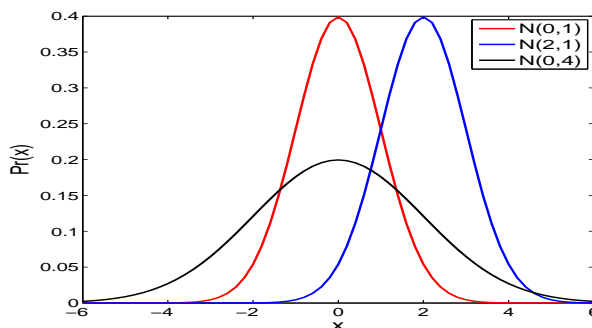


If you were to plot the blood pressure of all the women, it would look much the same. Or if you plotted the velocities of the molecules in the air, once again, same thing. This one distribution is everywhere. For that reason it is called the *normal* distribution.

The normal distribution with mean μ and variance σ^2 is denoted $N(\mu, \sigma^2)$. Unlike most of the examples we've seen so far, it is a *continuous* distribution, a density over the real line. The density at any point x is

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

Don't worry too much about this specific functional form. Instead, let's look at pictures of three different normal distributions.



The red curve (or, if you're reading this in black and white, the tall curve in the middle) is $N(0,1)$: the normal distribution with mean 0 and variance 1. This is sometimes called the *standard normal*. All other normal distributions are simply scaled and translated versions of it. For instance, the blue curve (the one on the right) is $N(2,1)$, which is obtained by shifting the standard normal two units to the right. The black curve (the wide one in the middle), on the other hand, is $N(0,4)$, obtained by scaling the standard normal by a factor of two. Here's a summary of the relationship between different normal distributions.

Fact 3. If $X \sim N(\mu, \sigma^2)$ then $aX + b \sim N(a\mu + b, a^2\sigma^2)$.

6.4.1 Sums of independent random variables

Here's an interesting fact about the normal distribution.

Fact 4. If X, Y are independent, with $X \sim N(\mu_1, \sigma_1^2)$ and $Y \sim N(\mu_2, \sigma_2^2)$, then $X + Y \sim N(\mu_1 + \mu_2, \sigma_1^2 + \sigma_2^2)$.

In words, if a bunch of independent random variables are each normally distributed, and you add them up, the result still has a normal distribution.

In fact, something much more spectacular is true: even if the independent random variables are *not* normally distributed, their sum looks like a normal distribution!

Fact 5 (Central limit theorem). Suppose X_1, \dots, X_n are independent with mean μ and variance σ^2 . Then for sufficiently large n , the distribution of $(X_1 + \dots + X_n)/n$ is approximately $N(\mu, \sigma^2/n)$. Equivalently, the distribution of $X_1 + \dots + X_n$ is approximately $N(n\mu, n\sigma^2)$.

This astonishing fact helps explain why the normal distribution is observed all over the place.

6.4.2 Tails of the normal

In sampling and hypothesis testing, we ultimately end up adding independent random variables; more on this below. Thus the result is well-approximated by the normal distribution, and by analyzing the tails of this distribution, we can get intervals for any desired level of confidence.

Suppose $X \sim N(\mu, \sigma^2)$. If we want a 95% confidence interval, we seek a value of z for which

$$\Pr(\mu - z \leq X \leq \mu + z) = 0.95.$$

The answer, it turns out, is $z = 2\sigma$. If we want a 99% confidence interval, we seek a value of z for which

$$\Pr(\mu - z \leq X \leq \mu + z) = 0.99.$$

In this case, $z = 3\sigma$.

Here is a summary of some key facts about tails of the normal.

Fact 6. If $X \sim N(\mu, \sigma^2)$, then:

- With 66% probability, X lies between $\mu - \sigma$ and $\mu + \sigma$.
- With 95% probability, X lies between $\mu - 2\sigma$ and $\mu + 2\sigma$.
- With 99% probability, X lies between $\mu - 3\sigma$ and $\mu + 3\sigma$.

6.5 Sampling revisited

6.5.1 Polls with yes/no answers

From the population at large n people are chosen at random and are asked a particular question (“Do you approve of the corporate bailouts?”). The goal is to estimate the fraction p of the underlying population that would answer yes. Let's say that K of the sampled people say yes; then $K \sim \text{binomial}(n, p)$, and thus a reasonable estimate of p is K/n .

To analyze the situation further, it helps to approximate the binomial by a normal distribution. Notice that

$$K = X_1 + X_2 + \cdots + X_n$$

where the X_i are independent $B(p)$ random variables (“did the i th person say yes?”). By the central limit theorem,

$$\frac{K}{n} \text{ is distributed like } N\left(p, \frac{p(1-p)}{n}\right).$$

Writing $\sigma = \sqrt{\frac{p(1-p)}{n}} \leq \frac{1}{2\sqrt{n}}$, we can conclude from Fact 6 that the estimate K/n is accurate within

- $\frac{1}{2\sqrt{n}}$ with at least 66% probability.
- $\frac{1}{\sqrt{n}}$ with at least 95% probability.
- $\frac{3}{2\sqrt{n}}$ with at least 99% probability.

And other confidence intervals are also easy to obtain, from standard tables of the normal distribution.

6.5.2 Polls with numeric answers

Many polls demand numeric rather than yes/no answers. How many glasses of wine do you drink daily? What is your salary? How old are you? And so on.

Suppose, for instance, that we wish to assess the overall educational levels (number of years of schooling) of residents of San Diego. If we were to consider *all* San Diegans of age ≥ 25 , this would be a distribution with some unknown mean μ and standard deviation σ . We would like to estimate μ , the average educational level. So we randomly pick n people of age ≥ 25 and ask them how many years they have spent in school. Suppose their answers are X_1, \dots, X_n .

The empirical mean (the mean of the samples) is

$$M = \frac{X_1 + \cdots + X_n}{n}$$

and the empirical standard deviation is

$$S = \sqrt{\frac{(X_1 - M)^2 + \cdots + (X_n - M)^2}{n}}.$$

It is reasonable to use M as an estimate of μ . What kind of confidence interval can we give for it?

This is where the central limit theorem once again comes in. Since the X_i are independent, we can assert that

$$M \text{ is distributed like } N\left(\mu, \frac{\sigma^2}{n}\right).$$

Thus we immediately have the following confidence intervals, from Fact 6.

- With 95% probability, M lies between $\mu - \frac{2\sigma}{\sqrt{n}}$ and $\mu + \frac{2\sigma}{\sqrt{n}}$.
- With 99% probability, M lies between $\mu - \frac{3\sigma}{\sqrt{n}}$ and $\mu + \frac{3\sigma}{\sqrt{n}}$.

Thus, for instance, when using M to estimate μ , we can be 95% certain that it is accurate within $\pm \frac{2\sigma}{\sqrt{n}}$. But wait: we don't know σ . So instead, it is customary to use the empirical standard deviation instead, and to assert that M is accurate within $\pm \frac{2S}{\sqrt{n}}$, with 95% confidence.

Returning to the schooling example, suppose we poll $n = 400$ people, and find that the empirical average and standard deviation are $M = 11.6$ and $S = 4.1$, respectively. Then we can assert with 95% confidence that the average number of years of schooling of San Diegans is

$$11.6 \pm \frac{2 \times 4.1}{\sqrt{400}} = 11.6 \pm 0.41.$$

Chapter 7

Multiple Hypothesis testing, Covariance, Correlation

7.1 The Bonferroni correction

When performing statistical test, we often want to use the same data set to test many different alternative hypotheses. For example, when studying high blood pressure we might want to support or refute the following hypotheses

1. Blood pressure is elevated in patients with high cholesterol.
2. Blood pressure is elevated in older patients.
3. High blood pressure is caused by stress.
4. Blood pressure is elevated in patients that eat too many vegetables.
5. and so on.

Suppose we run a test whose significance is α for each of these hypotheses and find that one of the tests rejects the null hypothesis. Can we say that the significance of this rejection is α ? Clearly, as the number of tests increases, the significance of each test decreases. How can we account for that? It is tempting to think of passing each test as an independent event and calculate the overall significance based on that. However, we don't know whether the tests are independent or not. In fact, the opposite is probably true: older patients tend to also have high cholesterol.

We therefor do the safe thing and use the union bound. Let T_i , $i = 1, \dots, n$ be the event corresponding to test i rejecting the null hypothesis when the null hypothesis is in fact true. Suppose that the p value of each of the n tests is at most α , i.e. $P(T_i) \leq \alpha$.

The union bound tells us that

$$P\left(\bigcup_{i=1}^n T_i\right) \leq \sum_{i=1}^n P(T_i) \leq n\alpha$$

7.2 Catch, mark and release

Statistical techniques are useful for estimating the size of a large population. Suppose for example that we want to count the number of fish in a lake. How would we do that? Instead of trying to catch all the fish, which is both impossible and damaging to the fish population, we perform the following two phase test:

1. We catch fish, mark them with some non-intrusive marker, and release them back to the lake. Suppose we mark m of them with a mark that sticks to the fish but does not hurt it.
2. After we marked the m fish, we wait for them to mix with the other fish and then catch l fish and count how many of these have been marked. We denote the number of marked fish by the random variable Y .

The probability that each fish caught in the second batch is marked is equal to the fraction of all of the fish in the lake that are marked, which is m/n . This means that the random variable Y is a sum of l independent binary random variables each with mean m/n . Therefore the mean of Y is $(lm)/n$. The standard deviation of each of the binary variables is at most $1/2$ (which happens when $m/n = 1/2$). Thus the standard deviation of Y is $\sqrt{l}/2$. Therefore the 95% significance interval for $(lm)/n$ is $[Y - \sqrt{l}, Y + \sqrt{l}]$.

We are interested in estimating n , therefore our estimate is the range.

$$\left[\frac{lm}{Y + \sqrt{l}}, \frac{lm}{Y - \sqrt{l}} \right]$$

Note that if the number of fish in the lake n is large, so that $m/n \approx 1/l$ then there is a good chance we will see no marked fish in the second batch. We might need to mark more and more fish until the chance of catching a marked fish becomes reasonably high.

7.3 Covariance

Two random variables X, Y are independent if and only if for any constants a, b we have:

$$P(X \leq a \text{ and } Y \leq b) = P(X \leq a)P(Y \leq b)$$

If X, Y are restricted to the integers, then they are independent if and only if for any two integers i, j

$$P(X = i \text{ and } Y = j) = P(X = i)P(Y = j) \quad (7.1)$$

Suppose we further restrict X, Y to the integers $1, \dots, 100$. In order to check whether or not X and Y are dependent we need to check $100^2 = 10000$ conditions. Checking for independence of these random variables requires estimating 10,000 joint probabilities, which in turn requires very large samples.

There is an easy to calculate stand-in for dependence, called the *covariance*, which we will now describe. If the covariance is not zero then the two random variables are dependent. However, a covariance of zero between two random variables *does not* imply that they are independent.

The covariance of X and Y is defined as

$$Cov(X, Y) = E[(X - E(X))(Y - E(Y))]$$

Note that $Cov(X, X) = Var(X)$. We can simplify the expression for the covariance as follows:

$$E[(X - E(X))(Y - E(Y))] = E[XY] - E[E(X)Y] - E[XE(Y)] + E[X]E[Y] = E[XY] - E[X]E[Y]$$

We will now show that if X and Y are independent then the covariance is zero. We will show this for integer

valued random variables ¹

$$E[XY] = \sum_{i,j} ijP(X=i \text{ and } Y=j) \quad (7.2)$$

$$= \sum_{i,j} ijP(X=i)P(Y=j) \quad (7.3)$$

$$= \left(\sum_i iP(X=i) \right) \left(\sum_j jP(Y=j) \right) \quad (7.4)$$

$$= E[X]E[Y] \quad (7.5)$$

Equation (7.2) follows from the definition of expectation (i, j vary from $-\infty$ to $+\infty$). Equation (7.3) follows from Equation (7.1). We separate the double summation in Equation (7.3) into a product of two sums to get Equation (7.4), and finally use the definition of expectation to get Equation (7.5). Thus we have shown that when two random variables X, Y are independent, then $E[XY] = E[X]E[Y]$ and thus $Cov(X, Y) = E[XY] - E[X]E[Y] = 0$.

Intuitively, $Cov(X, Y) > 0$ indicates that when X is large Y also tends to be large. When this happens we say that X and Y are *correlated*. If $Cov(X, Y) < 0$ we say that X and Y are *anti-correlated*, and if $Cov(X, Y) = 0$. We say that X and Y are *uncorrelated*.

One problem with the covariance is it's sensitivity to the units in which the random variables are measured, changing the scale changes the covariance. Suppose the sample space corresponds to people and suppose we consider two random variables for each person: H is the height of the person, in inches, and W is the weight of the person, in pounds. We expect the H and W are correlated. However, how should we measure the *degree* of correlation? $Cov(H, W)$ will decrease if we decide to use feet instead of inches because that would decrease each height by a factor of 12 and we get $Cov(H/12, W) = Cov(H, W)/12$. In order to remove the effect of scale we use a normalized version of the covariance, called the correlation coefficient:

$$Corr(X, Y) \doteq \frac{Cov(X, Y)}{\sqrt{Var(X)Var(Y)}}$$

The correlation coefficient is a number in the range $[-1, 1]$. As with the Covariance, if $Corr(X, Y) > 0$ we say that X and Y are *correlated*, if $Corr(X, Y) = 0$ we say that X and Y are *uncorrelated* and if $Corr(X, Y) < 0$ we say that X and Y are *anti-correlated*.

The extreme cases are interesting. If $Corr(X, Y) = 1$ it means that $X = aY$ for some $a > 0$ while if $Corr(X, Y) = -1$, $X = aY$ for some $a < 0$. These and other interesting cases are depicted in Figure 7.1.

An example of correlated random variables are the price of fuel and the price of food. In this case there is a direct cause and effect: fuel prices influence food prices because manufacturing and distributing food requires large amounts of fuel. In general, there might not be a causal relationship between two correlated random variable. For example, consider the sentence: "As ice cream sales increase, the rate of drowning deaths increases sharply. Therefore, ice cream causes drowning.". The factual part of the sentence is that there is a correlation between the random variables corresponding to "ice-cream sales" and "the rate of drowning deaths". However, the correlation does not imply causation. The probable common cause for increases in both ice cream sales and drowning deaths is increases in the number of people that come to the beach. A reminder against making this mistake is the statistical dictum "*Correlation does not imply causation*"

However, correlation *does* imply dependence because, as we show, independence implies that the covariance is zero. The opposite direction does not hold, in other words, zero covariance does not imply that the

¹The extension to continuous random variables is straight forward, but involves some technical issues involving integration that we will not get into here.

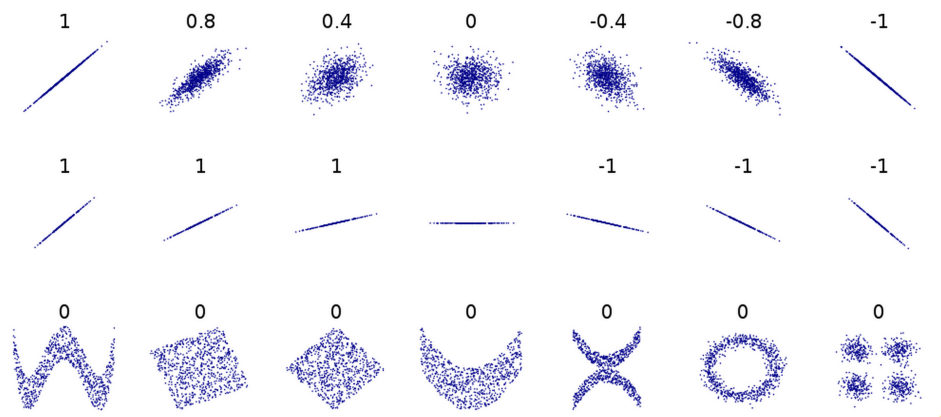


Figure 7.1: Examples of joint distributions and their corresponding correlation coefficients. The distributions are represented by a sample of points drawn IID from the underlying distribution. The number next to each cloud of points is the value of the correlation coefficients corresponding to the distribution. **The top row** shows ellipsoidal distributions with varying levels of correlation. **The middle row** shows distributions that are concentrated on a line of the form $X = aY$, the correlation for these distributions is one of $-1, 0, +1$ depending on the value of a . **The bottom row** shows a variety of distributions where X and Y are uncorrelated. These distributions demonstrate some of the many ways in which uncorrelated random variables can be dependent. (Image taken from Wikipedia:Correlation Coefficients)

two random variables are independent. Here is a simple example, X and Y attain the values $-1, 0, 1$ but only the following four combinations have non-zero probability. Specifically

$$P(X = -1 \wedge Y = 0) = P(X = +1 \wedge Y = 0) = P(X = 0 \wedge Y = -1) = P(X = 0 \wedge Y = +1) = 1/4$$

(where \wedge correspond to “and”). On the one hand, it is easy to see that the covariance is zero, because the expected values of X , Y and XY are all zero. On the other hand, X and Y are not independent because $P(X = 0 \wedge Y = 0) = 0$ while $P(X = 0) = 1/2$ and $P(Y = 0) = 1/2$, and thus $P(X = 0 \wedge Y = 0) \neq P(X = 0)P(Y = 0)$

Chapter 8

Pseudo-randomness

8.1 Randomness and predictability

Consider a sequence of binary random variables: X_1, X_2, \dots, X_n . Where each random variable X_i is equal to 1 or to 0 each with probability $1/2$.

If the random variables are *independent* of each other, then the probability of each of the possible 2^n binary sequences is equal to 2^{-n} . This is the *uniform* distribution over the outcome space.

Suppose that we observe the sequence one bit at a time. Specifically, suppose we observed $X_1 = x_1, X_2 = x_2, \dots, X_i = x_i$ for some $i < n$, can we predict the value of X_{i+1} ? The answer is no, because

$$P(X_{i+1} = x_{i+1} | X_1 = x_1, X_2 = x_2, \dots, X_i = x_i) = \frac{1}{2}$$

In other words, knowing the values of past bits does not provide information about future bits.

Thus independence, uniform distribution and unpredictability are all equivalent.

We say that a random sequence generator is *perfect* if for each $i < n$, X_{i+1} is independent from X_1, \dots, X_i . This is equivalent to saying that for any random variable Y_i that is some function of X_1, \dots, X_i , $P(X_{i+1} = 1 | Y_i = y) = 1/2$. The counter-positive is that if there exists some function of the past bits for which $P(X_{i+1} | Y_i) \neq 1/2$ then the sequence is (slightly) predictable and therefore the source is not a perfect random bits generator.

As we will learn in a little while, sequences of random bits are very useful for computations. Therefore computers need fast random bit generators. Coin flipping is a possibility, but it is too slow for computer applications. There are other physical sources of randomness such as Zener diodes¹ which are much faster than coin flips but suffer from other limitations.

The approach usually taken to generating random bits in a computer is to use a Pseudo-random number generator.

8.2 Pseudo-Randomness

Pseudo-random number generators are computer programs. As such, their output is completely predictable from their input. So in what sense is a pseudo-random number generator random? Let's first define exactly what we mean by a random number generator.

A pseudo-random number generator can be described as a class with three methods: `setState`, `advance`, `generate`, and a shared `state`. The method `setState` receives as input a `seed` and sets `state`

¹For more information on physical random bit generators see

to `seed`. The internal method `advance` updates `seed` using some fixed function $F(\text{State}) \rightarrow \text{state}$. Finally `generate` calls `advance` and then computes one bit as the function of the new state and outputs it as the next random bit.² The typical use pattern of a random number generator is to call `setState` once at initialization and then repeatedly call `generate`.

So, in what sense is a pseudo-random generator actually random? Clearly, if we know the `seed` then we can recreate the sequence of generated numbers exactly, so in that sense the sequence is nothing but random! The key is to argue about a situation in which we don't know the seed.

8.2.1 Predicting a pseudo-random generator

OK, so suppose that we know the code of the generator but we don't know the seed with which it was initialized. We call this generator the "hidden seed" generator or *HS* for short. Can we predict the next bit in this pseudo-random stream?

As we know the code of the generator we know the number of bits used in the seed. We call this number l and observe that there are 2^l different possible seeds. Suppose we instantiate 2^l instances of the pseudo-random algorithm and initialize each with a different seed. We denote the instance with seed i $S(i)$. Our prediction algorithm maintains a set of instances which we call the "pool". We initialize the pool to contain all 2^l instances $S(1), S(2), \dots, S(2^l)$.

As *HS* is also using the same code with some length l seed we know that there is an instance in the pool which predicts the sequence perfectly. Had we know which one it is, we could perfectly simulate *HS*. However, initially we don't have this information. The idea of the algorithm is that each time we make an incorrect prediction the size of the pool will decrease by a factor of two therefor, as we know that there is at least one element in the pool that never makes a mistake. The number of mistakes of the prediction algorithm will be at most l .

In some more detail, suppose the bit sequence generated by *HS* is b_1, b_2, b_3, \dots . After observing b_t and before observing b_{t+1} the prediction algorithm does the following:

1. Remove from the pool all generators that disagree with b_t .
2. Predict b_{t+1} according to the majority of the $t + 1$ 'th bit generated by the instances in the pool.

The analysis is simple: if the prediction algorithm makes a mistake on step 2, then at least half of the instances in the pool made a mistake. These instances will be removed in the following step 1. Therefor the size of the pool is halved each time the prediction algorithm makes a mistake. As the initial size is 2^l and the final pool cannot be empty (because *HS* is an element in the pool) the total number of mistakes is at most l . Thus if we generate a sequence of length, say, l^2 we will easily see that it is not a truly random sequence.

8.2.2 Computationally bounded randomness

In the previous section we showed that, in some sense, pseudo-randomness is no randomness at all. Given enough computational resources you can discriminate between a true random source and a pseudo random source. However, the key word here is *sufficient* computational resources. Think of actually implementing the algorithm described in the previous section for an algorithm that uses a seed of 256 bits, which is a reasonable size seed for a pseudo-random number generator.

We need to maintain a pool of $2^{256} > 10^{25}$ elements, that is a lot of memory space!

So the actual definition of pseudo-random number generator is one such that for most seed values, the generated sequence cannot be distinguished from a truly random sequence using space and time that is polynomial in l .

²In practice, random number generators output several bits each time they are called.

It is worth observing that what we are looking for is a statistical test in the sense that was described in earlier lessons. Specifically we have as a null hypothesis that the sequence corresponds to IID RVs (Identically Distributed and Independent Random Variables) with equal probabilities for 0 and 1. The goal of the test is to reject the null hypothesis. Furthermore, as computer scientists, we want the test to be computationally efficient.

To summarize, pseudo-random number generators generate sequences of bits that cannot be distinguished from truly random sequences by any computationally efficient tests.

8.2.3 Using pseudo-random number generators inside a random algorithm

Randomized algorithms are algorithms that are allowed to flip coins. Based on the assumption that the coins are IID RVs we can calculate the expected running time of the algorithm, or the probability that the algorithm generates a correct output.

But when we actually use the algorithm we use a pseudo-random number generator, which is not the same as a real random sequence. So how do we know that the analysis still works?

Well, suppose for example that the expected running time of the randomized algorithm is much larger when it uses a pseudo-random number generator than when it uses a true random generator. In that case we have found a computationally efficient test for whether or not the sequence is truly random or not - If the running time of the algorithm is much larger than the expected running time (and assume that the variance if the running time is small), then our test would reject the hypothesis that the sequence is truly random.

We assume that our pseudo random number generator is such that no efficiently computable test that can distinguish between the pseudo-random output and a truly random sequence. As a result the running time of our algorithm must be indistinguishable from the running time when using a truly random sequence.

Chapter 9

Randomized algorithms

Randomized algorithms are algorithms that use randomization in order to compute more efficiently. A randomized algorithm is different from a conventional, or deterministic algorithm in that the output that running the algorithm multiple times with the *same input* can result in different traces and in different outputs. The output from a randomized algorithm can be correct only with some non-zero probability. The running time of the algorithm can be short only in expectation.

Programming and debugging randomized algorithms is significantly harder than using deterministic algorithms because errors are harder to reproduce. It is also sometimes hard to convince management to use an algorithm whose behaviour is unpredictable. However, the benefits of using randomized algorithms are often substantial. In some cases, such as Hash tables, the use of randomized algorithms is so common that it is taken for granted.

We will present several randomized algorithms, starting with the simplest one: finding the median.

9.1 Finding percentiles

9.1.1 The mean as a summary statistic

Suppose UCSD tracks this year's graduating class in computer science and finds out everyone's salary ten years down the line. What might these numbers look like? Well, if there are (say) 100 students, the spread might be roughly:

- A few people with zero salary (unemployed)
- A few grad students with salary around 20K
- A few part-timers with salary around 50K
- A whole lot of software engineers with salaries between 100K and 200K

The *mean* salary would then be something like 100K, which UCSD could report with pride in its brochure for prospective students.

Now suppose that one student managed to strike it rich and become a billionaire. Accordingly, take the spread of salaries above and convert one of the 200K salaries to 1000000K. What would be the new mean salary? Answer: at least 10 million dollars! (Do you see why?) If UCSD were to report this number, nobody would take it seriously, despite its being perfectly truthful.

The problem is that the mean is extremely sensitive to *outliers* – it is very easily thrown off by a single number that is unusually small or unusually large. In many circumstances, therefore, the preferred summary

statistic is the *median*, or 50th percentile. For the salary data, for instance, the median would remain unchanged (at around 100K) even if a few people were to become billionaires, or if a few more people were to lose their jobs.

We're also interested in other percentiles – the 25th, 75th, and so on. How can we compute these for a *very large* data set (for instance, a data set giving the salary of everyone in the US)?

9.1.2 Selection

Here the problem, formally.

SELECTION

Input: An array $S[1 \cdots n]$ of n numbers; an integer k between 1 and n

Output: The k th smallest number in the array.

The median corresponds to $k = \lceil n/2 \rceil$, while $k = 1$ retrieves the very smallest element. The p th percentile ($0 \leq p \leq 100$) can be obtained with $k = \lceil pn/100 \rceil$.

The most natural algorithm for this problem is:

Sort S and return $S[k]$

The running time here is dominated by that of sorting, which is $O(n \log n)$. This is pretty good, but we'd like something faster since we often need to compute percentiles of enormous data sets.

9.1.3 A randomized algorithm

Here's a randomized (and recursive) procedure for selection.

For any number v , imagine splitting array S into three categories: elements smaller than v , those equal to v (there might be duplicates), and those greater than v . Call these S_L , S_v , and S_R respectively. For instance, if the array

S :

2	36	5	21	8	13	11	20	5	4	1
---	----	---	----	---	----	----	----	---	---	---

is split on $v = 5$, the three subarrays generated are

S_L :

2	4	1
---	---	---

 S_v :

5	5
---	---

 S_R :

36	21	8	13	11	20
----	----	---	----	----	----

The search can instantly be narrowed down to one of these sublists. If we want, say, the *eighth*-smallest element of S , we know it must be the *third*-smallest element of S_R since $|S_L| + |S_v| = 5$. That is, $\text{SELECTION}(S, 8) = \text{SELECTION}(S_R, 3)$. More generally, by checking k against the sizes of the subarrays, we can quickly determine which of them holds the desired element:

$$\text{SELECTION}(S, k) = \begin{cases} \text{SELECTION}(S_L, k) & \text{if } k \leq |S_L| \\ v & \text{if } |S_L| < k \leq |S_L| + |S_v| \\ \text{SELECTION}(S_R, k - |S_L| - |S_v|) & \text{if } k > |S_L| + |S_v|. \end{cases}$$

The three sublists S_L, S_v, S_R can be computed from S in *linear* time, scanning left-to-right. We then recurse on the appropriate sublist.

The effect of the split is thus to shrink the number of elements from $|S|$ to at most $\max\{|S_L|, |S_R|\}$. How much of an improvement is this, and what is the final running time?

9.1.4 Running time analysis

By how much does a single split reduce the size of the array? Well, this depends on the choice of v .

1. *Worst case.* When v is either the smallest or largest element in the array, the array shrinks by just one element. If we keep getting unlucky in this way, then

$$(\text{time to process array of } n \text{ elements}) = (\text{time to split}) + (\text{time to process array of } n-1 \text{ elements}).$$

Since the time to split is linear, $O(n)$, this works out to a total running time of $n + (n-1) + (n-2) + \dots = O(n^2)$, which is really bad.

Fortunately, this case is unlikely to occur. The probability of consistently picking an element v which is the smallest or largest, is miniscule:

$$\frac{2}{n} \cdot \frac{2}{n-1} \cdot \frac{2}{n-2} \cdots \frac{2}{3} \approx \frac{2^n}{n!}$$

(do you see where this expression comes from?).

2. *Best case.* The best possible case is that v just happens to be the element we are looking for, that is, the k th smallest element in the array. In this case, the running time is $O(n)$, the time for a single split.

This case is also unlikely, but it is certainly a lot more likely than the worst case. In fact, the probability of it occurring is at least $1/n$. (Why? When might it be more than $1/n$?)

Neither the best case nor worst case is a particularly good way to quantify the running time of this algorithm. A more sensible measure is the *expected* running time. Let $T(n)$ be (an upper bound on) the expected time to process an array of n (or fewer) elements. We will now derive an expression for it.

Call a split *lucky* if the resulting S_L and S_R both have size less than $3n/4$; call it *unlucky* otherwise. A split is lucky if v lies somewhere between the 25th and 75th percentile of S , which happens with probability exactly $1/2$.

Therefore,

$$\begin{aligned} T(n) &\leq (\text{time to split}) + (\text{expected time taken to process the larger of } S_L, S_R) \\ &\leq n + \Pr(\text{lucky split})(\text{time for array of size } \leq 3n/4) + \Pr(\text{unlucky split})(\text{time for array of size } n) \\ &\leq n + \frac{1}{2}T(3n/4) + \frac{1}{2}T(n) \end{aligned}$$

Rearranging, we get $T(n) \leq 2n + T(3n/4)$. Expanding it out, and using the formula for the sum of a geometric series, we get

$$T(n) \leq 2n + 2 \cdot \frac{3n}{4} + 2 \cdot \frac{9n}{16} + \dots \leq 2n \left(1 + \frac{3}{4} + \frac{9}{16} + \dots \right) = 8n.$$

Our randomized algorithm for selection has an expected *linear* running time!

9.1.5 A randomized sorting algorithm

There's a very popular algorithm for sorting that operates on similar principles. It's called *quicksort*:

- Given an array $S[1 \cdots n]$, pick an element v from it at random.
- Split S into three pieces:

S_L elements less than v
 S_v elements equal to v
 S_R elements greater than v

- Now return $\text{quicksort}(S_L) \circ S_v \circ \text{quicksort}(S_R)$, where \circ denotes concatenation.

Letting $T(n)$ be the expected running time on an array of n elements, we have

$$\begin{aligned}
 T(n) &= (\text{time to split}) + (\text{expected time to sort } S_L \text{ and } S_R) \\
 &= n + \sum_{i=1}^n \Pr(v \text{ is the } i\text{th smallest element in } S)(T(i-1) + T(n-i)) \\
 &= n + \frac{1}{n} \sum_{i=1}^n (T(i-1) + T(n-i)).
 \end{aligned}$$

This is tricky to solve, but works out to $T(n) = O(n \log n)$.

9.1.6 Two types of randomized algorithms

Our algorithms for finding percentiles and for sorting are guaranteed to return the correct answer. But if you run them multiple times on the same input, their running times will fluctuate, even though the answer will be the same every time. Therefore we are interested in their *expected* running time. We call these *Las Vegas algorithms*.

But in the case of minimum cut we saw another type of algorithm – called a *Monte Carlo algorithm* – that always has the same running time on any given input, but is not guaranteed to return the correct answer. It merely guarantees that it has some probability $p > 0$ of being correct. Therefore, if you run it multiple times on an input, you'll get many different answers, of which roughly a p fraction will be correct. In many cases, it is possible to look through these answers and figure out which one(s) are right.

In a Monte Carlo algorithm, how much does the probability of success increase if you run it multiple times, say k times?

$$\Pr(\text{wrong every time}) = (1 - p)^k \leq e^{-pk}.$$

To make this less than some δ , it is enough to run the algorithm $(1/p) \log(1/\delta)$ times. For instance, to make the failure probability less than 1 in a million, just run the algorithm $20/p$ times (a million is roughly 2^{20}).

9.2 Cumulative distributions and sorting in expected linear time

9.2.1 Cumulative Distribution Functions

Our discussion so far focused on finite event spaces or event spaces that correspond to the integers $0, 1, 2, \dots$ (so-called countable infinite sets). How do we define distributions over the real numbers? That is an *uncountably* infinite set.¹

When defining a distribution over the real it is not enough to assign probabilities to individual points on the real line. Consider the *uniform distribution on the line segment* $[0, 1]$, by which we mean the set $\{x | 0 \leq x \leq 1\}$. We cannot assign each point a probability larger than zero, because that would result in $[0, 1]$ an infinite probability. What we do instead is assign probability to the line segment $0 \leq a < b \leq 1$ the probability $b - a$. Thus for example $P([1/4, 1/3]) = 1/3 - 1/4 = 1/12$.

¹A set A is uncountable if there is no one-to-one mapping from A to the positive integers $1, 2, 3, 4, \dots$. In other words, a set is uncountable if you cannot create a list which includes all of the elements in the set.

More generally, we can define any distribution over the real line using the *Cumulative Distribution Function*:

$$\text{CDF}(a) \doteq P(x \leq a)$$

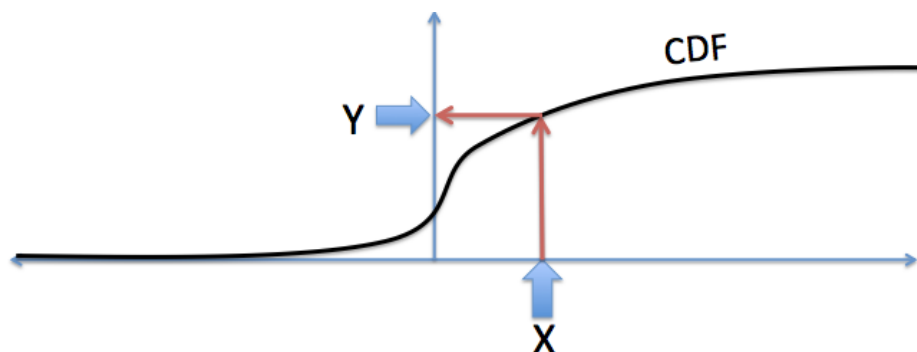


Figure 9.1: This figure depicts an example of mapping a random variable X whose distribution is defined by a CDF (thick black curve) to another random variable Y , whose distribution is uniform in the interval $[0, 1]$. The mapping uses the CDF as a function so that $Y = \text{CDF}(X)$.

As we see in Figure 9.2 the CDF is an increasing function that increases from zero at $-\infty$ to one at $+\infty$. It is easy to see that $P(a < x \leq b) = \text{CDF}(b) - \text{CDF}(a)$.

9.2.2 Examples of distributions on the real line

If the distribution assigns a non-zero probability to some $x = a$ we say that the distribution has a *point mass* at a . In that case the CDF has a jump at a . We denote a point mass distribution concentrated at the point a by $PM(a)$. The distribution $PM(a)$ corresponds to a random variable such that $P(X = a) = 1$.

$$f(x) = \begin{cases} 0.25 & \text{if } -3 \leq x \leq 1 \\ 0 & \text{otherwise} \end{cases}$$

Another important case is when the derivative of the CDF is defined $p(a) = \frac{d}{dx} \big|_{x=a} \text{CDF}(x)$. The function $p(a)$ is called the *probability density*. Note that if $p(a)$ is defined then, regardless of how large $p(a)$ is, $P(x = a) = 0$.

When a distribution over the reals is a density distribution we can calculate the probability of the segment $[a, b]$ using the integral:

$$P(a < x \leq b) = \text{CDF}(b) - \text{CDF}(a) = \int_a^b p(x) dx$$

9.2.3 Worst-case lower bound on sorting

You probably know of some algorithms for sorting n numbers in $O(n \log n)$ time. QuickSort and MergeSort are two such algorithms.

However, did you know that $n \log n$ is a lower bound on *any* sorting algorithm? There is no sorting algorithm that can sort *any* sequence of n elements in time $o(n \log n)$.

The argument is pretty simple. Let us restrict our attention to a sequence of length n that consists of the numbers $1, \dots, n$ appearing in some order, in other words, some permutation of the numbers $1, \dots, n$. As we have shown earlier in the class, there are $n!$ such permutations.

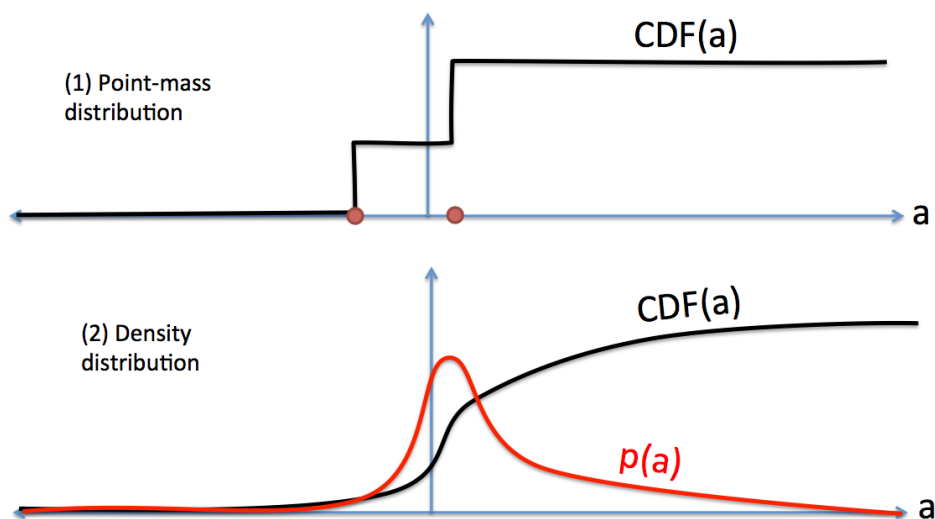
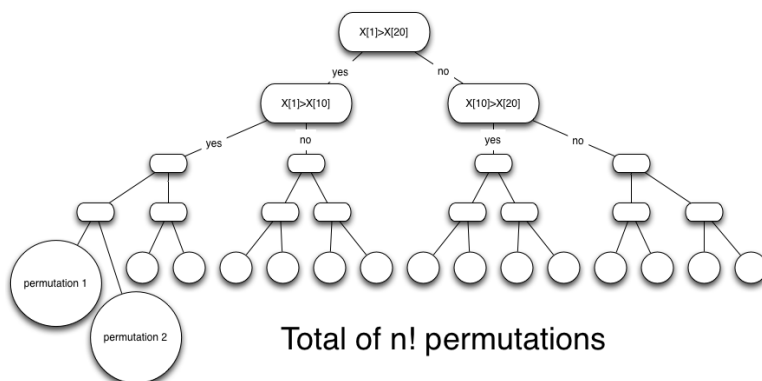


Figure 9.2: The CDFs for two distributions: (1) A point-mass distribution is a distribution that assigns non zero probabilities to two real values (marked by red circles) all sets that do not include at least one of these points have probability zero. The CDF of a point mass distribution is constant every where but at the point masses where it is discontinuous, the size of the discontinuity is the probability of the corresponding point. (2) A density distribution assigns probability zero to any single point. The CDF for such a distribution is a continuous increasing function that has a derivative. This derivative, $p(a)$ is called the *density function* of the distribution. For density distributions the CDF and the density function contain the same information.

An algorithm which sorts each of these sequences must be able to distinguish each one of the $n!$ permutations. Suppose that the algorithm proceeds by comparing pairs of elements in the sequence. Each comparison has two possible outcomes. The result is a binary tree where internal nodes correspond to comparisons and the leaves correspond to permutations.



The depth d of the tree is the worst case number of comparisons done by the algorithm and therefore a lower bound on the worst case running time. A basic fact about binary trees is that the number of leaves is at most 2^d . We therefore have that $n! \leq 2^d$. Taking the natural log of both sides and using the Stirling

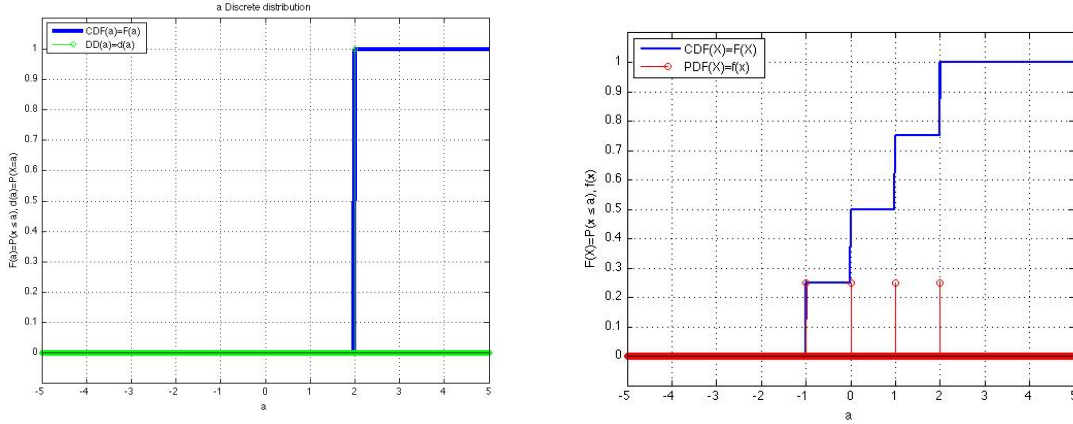


Figure 9.3: **Left:** A discrete distribution concentrated on a single point $P(X = 2) = 1$. We denote this distribution by $PM(2)$. **Right:** A discrete distribution distributed evenly over the four points $-1, 0, 1, 2$. This distribution can be expressed as $(PM(-1) + PM(0) + PM(1) + PM(2))/4$.

approximation of $n!$ (google it!) we find that $d \ln 2 \geq \ln n! \geq (n-1) \ln n$. We have thus found that the worst case running time of any sorting algorithm is $\Omega(n \log n)$.

This shows that the worst case running time is $\Omega(n \log n)$. However, as we shall see, there are sorting algorithms that, under some statistical assumptions, take time $O(n)$ in expectation.

9.2.4 Sorting in expected linear time

Suppose we want to sort an array of numbers $S[1 \dots n]$ that we expect to be distributed uniformly in some range $[\min, \max]$. Here's a *bucket sort* approach:

- Divide $[\min, \max]$ into n equal-sized intervals. These are the *buckets* B_1, B_2, \dots, B_n .
- Now scan array S from left to right, putting each element $S[i]$ in its appropriate bucket.
- Return $\text{sort}(B_1) \circ \text{sort}(B_2) \circ \dots \circ \text{sort}(B_n)$, where “sort” is a standard sorting algorithm (say mergesort).

Notice that there is no randomization in the algorithm. However, we can talk about the expected running time if the elements of S are generated from a uniform distribution over $[\min, \max]$. In that case, each element is equally likely to fall into any of the buckets B_i .

Let N_i be the number of array elements that fall into B_i . Assuming we use a standard sorting procedure for each bucket, we get a total running time of

$$T = N_1 \log N_1 + N_2 \log N_2 + \dots + N_n \log N_n \leq N_1^2 + N_2^2 + \dots + N_n^2.$$

What is $\mathbb{E}(N_i^2)$? The easiest way to compute this is to write N_i as a sum:

$$N_i = X_1 + X_2 + \dots + X_n$$

where X_j is 1 if the array element $S[j]$ falls into bin i , and 0 otherwise. Notice that $X_j^2 = X_j$, and that X_j is independent of $X_{j'}$ whenever $j \neq j'$. Therefore,

$$\begin{aligned}\mathbb{E}(X_j) &= \frac{1}{n} \\ \mathbb{E}(X_j^2) &= \frac{1}{n} \\ \mathbb{E}(X_j X_{j'}) &= \mathbb{E}(X_j) \mathbb{E}(X_{j'}) = \frac{1}{n^2} \quad \text{if } j \neq j'\end{aligned}$$

By linearity of expectation, we then have

$$\begin{aligned}\mathbb{E}(N_i^2) &= \mathbb{E}((X_1 + \dots + X_n)^2) \\ &= \mathbb{E}\left(\sum_j X_j^2 + \sum_{j \neq j'} X_j X_{j'}\right) \\ &= \sum_j \mathbb{E}(X_j^2) + \sum_{j \neq j'} \mathbb{E}(X_j X_{j'}) \\ &= n \cdot \frac{1}{n} + n(n-1) \frac{1}{n^2} \leq 2.\end{aligned}$$

So the expected running time of the sorting algorithm, once again invoking linearity, is

$$\mathbb{E}(T) \leq \mathbb{E}(N_1^2) + \mathbb{E}(N_2^2) + \dots + \mathbb{E}(N_n^2) \leq 2n.$$

It is linear!

9.2.5 Sorting in linear time when the distribution is known

In the previous section we described an algorithm that can sort elements drawn IID from the uniform distribution in expected linear time. In this section we show how to generalize this to sorting elements drawn IID from an arbitrary density function over the reals.

Suppose we use the CDF as a transformation, in other words, map each X to $Y = \text{CDF}(X)$. Y is a new random variable, see figure 9.1. What is the distribution of the random variable Y ? First, it is clear that $0 \leq Y \leq 1$ because that is the range of cumulative distribution function. We need to also assume that the CDF is a *reversible* function. I.e. for any real in the range: $0 < c < 1$ there exists an inverse $b = \text{CDF}^{-1}(c)$ such that $\text{CDF}(b) = c$. A sufficient condition for this to hold is that the distribution over R is defined by a density function.

To understand the distribution of Y , let us calculate the probability that Y is in some range $c < Y < d$, where $0 < c < d < 1$. Using the definition of CDF^{-1} we get

$$P(c \leq Y \leq d) = P(\text{CDF}^{-1}(c) \leq X \leq \text{CDF}^{-1}(d)) = \text{CDF}(\text{CDF}^{-1}(d)) - \text{CDF}(\text{CDF}^{-1}(c)) = d - c \quad (9.1)$$

Where the first equality is justified by the definition of CDF^{-1} , the second by the formula for calculating the probability of a segment using the CDF, and the fourth by the cancellation: $\text{CDF}^{-1}(\text{CDF}(X)) = X$. We find that the distribution of Y is uniform between 0 and 1, under the condition that the CDF is invertible.

It might help to consider a particular CDF as an example. Suppose the CDF of X is $\text{CDF}(x) = \frac{1}{1+e^{-x}}$, this function is invertible and its inverse is $\text{CDF}^{-1}(y) = \ln\left(\frac{1}{y} - 1\right)$. Apply the steps of Equation (9.1) to convince yourself it works.

Recall that we have an efficient algorithm for sorting numbers that are distributed uniformly in some segment $[\min, \max]$. If we know the CDF of the distribution that is generating the numbers we wish to sort, we can map these numbers to the range $[0, 1]$ and then use the method suggested in the first section to sort them in $O(N)$ time.

9.3 Karger's minimum cut algorithm

9.3.1 Clustering via graph cuts

Suppose a mail order company has the resources to prepare two different versions of its catalog, and it wishes to target each version towards a particular sector of its customer base. The data it has is a list of its regular customers, along with their purchase histories. How should this set of customers be partitioned into two coherent groups?

One way to do this is to create a graph with a node for each of the regular customers, and an edge between any two customers whose purchase patterns are similar. The goal is then to divide the nodes into two pieces which have very few edges between them.

More formally, the *minimum cut* of an undirected graph $G = (V, E)$ is a partition of the nodes into two groups V_1 and V_2 (that is, $V = V_1 \cup V_2$ and, $V_1 \cap V_2 = \emptyset$), so that the number of edges between V_1 and V_2 is minimized. In the graph below, for instance, the minimum cut has size two and partitions the nodes into $V_1 = \{a, b, e, f\}$ and $V_2 = \{c, d, g, h\}$.



9.3.2 Karger's algorithm

Here's a randomized algorithm for finding the minimum cut:

- Repeat until just two nodes remain:
 - Pick an edge of G at random and collapse its two endpoints into a single node
- For the two remaining nodes u_1 and u_2 , set $V_1 = \{\text{nodes that went into } u_1\}$ and $V_2 = \{\text{nodes in } u_2\}$

An example is shown in Figure 9.6. Notice how some nodes end up having multiple edges between them.

9.3.3 Analysis

Karger's algorithm returns the minimum cut with a certain probability. To analyze it, let's go through a succession of key facts.

Fact 7. If $\text{degree}(u)$ denotes the number of edges touching node u , then

$$\sum_{u \in V} \text{degree}(u) = 2|E|.$$

To see this, imagine the following experiment: for each node, list all the edges touching it. The number of edges in this list is exactly the left-hand sum. But each edge appears exactly twice in it, once for each endpoint.

Fact 8. If there are n nodes, then the average degree of a node is $2|E|/n$.

This is a straightforward calculation: when you pick a node X at random,

$$\mathbb{E}[\text{degree}(X)] = \sum_{u \in V} \Pr(X = u) \text{degree}(u) = \frac{1}{n} \sum_u \text{degree}(u) = \frac{2|E|}{n}$$

where the last step uses the first Fact.

Fact 9. The size of the minimum cut is at most $2|E|/n$.

Consider the partition of V into two pieces, one containing a single node u , and the other containing the remaining $n - 1$ nodes. The size of this cut is $\text{degree}(u)$. Since this is a valid cut, the minimum cut cannot be bigger than this. In other words, for all nodes u ,

$$(\text{size of minimum cut}) \leq \text{degree}(u).$$

This means that the size of the minimum cut is also \leq the average degree, which we've seen is $2|E|/n$.

Fact 10. If an edge is picked at random, the probability that it lies across the minimum cut is at most $2/n$.

This is because there are $|E|$ edges to choose from, and at most $2|E|/n$ of them are in the minimum cut.

Now we have all the information we need to analyze Karger's algorithm. It returns the right answer *as long as it never picks an edge across the minimum cut*. If it always picks a non-cut edge, then this edge will connect two nodes on the same side of the cut, and so it is okay to collapse them together.

Each time an edge is collapsed, the number of nodes decreases by 1. Therefore,

$$\begin{aligned} \Pr(\text{final cut is the minimum cut}) &= \Pr(\text{first selected edge is not in mincut}) \times \\ &\quad \Pr(\text{second selected edge is not in mincut}) \times \dots \\ &\geq \left(1 - \frac{2}{n}\right) \left(1 - \frac{2}{n-1}\right) \left(1 - \frac{2}{n-2}\right) \dots \left(1 - \frac{2}{4}\right) \left(1 - \frac{2}{3}\right) \\ &= \frac{n-2}{n} \cdot \frac{n-3}{n-1} \cdot \frac{n-4}{n-2} \dots \frac{2}{4} \cdot \frac{1}{3} \\ &= \frac{2}{n(n-1)}. \end{aligned}$$

The last equation comes from noticing that almost every numerator cancels with the denominator two fractions down the line.

Karger's algorithm succeeds with probability $p \geq 2/n^2$. Therefore, it should be run $\Omega(n^2)$ times, after which the smallest cut found should be chosen.

Those who are familiar with minimum spanning tree algorithms might be curious to hear that another way to implement Karger's algorithm is the following:

- Assign each edge a random weight
- Run Kruskal's algorithm to get the minimum spanning tree
- Break the largest edge in the tree to get the two clusters

(Do you see why?) Over the decades, the running time of Kruskal's algorithm has been thoroughly optimized via special data structures. Now this same technology can be put to work for cuts!

9.4 Hashing

In many situations, such as a dictionary application, we need to store a vast collection of items in such a way that we can look up any item instantaneously. The way to do this is by *hashing*.

9.4.1 The hashing framework

Suppose you have a large collection of items x_1, \dots, x_n that you want to store (for instance, all English words), where these items are drawn from some set \mathbb{U} (for instance, the set of all conceivable words). The requirements are:

1. The total storage space used should be $O(n)$.
2. Given a query $q \in \mathbb{U}$, it should be possible to *very rapidly* determine whether q is one of the stored items x_i .

9.4.2 A simple solution using randomization

1. Pick a completely random function $h : \mathbb{U} \rightarrow \{1, 2, \dots, n\}$.

This is the *hash function*.

2. Create a table T of size n , each of whose entries is a pointer to a linked list, initialized to null.
3. Store each x_i in the linked list at $T[h(x_i)]$.

We say x_i *hashes to* location $h(x_i)$.

4. Given a query q , look through the linked list at $T[h(q)]$ to see if it's there.

Here's a picture of the data structure.

The storage used is $O(n)$. What about the query time?

9.4.3 Average query time

Suppose query q is picked at random, so that it is equally likely to hash to any of the locations $1, 2, \dots, n$. What is the expected query time?

$$\begin{aligned}
 \text{Expected query time} &= \sum_{i=1}^n \Pr(q \text{ hashes to location } i) \cdot (\text{length of list at } T[i]) \\
 &= \frac{1}{n} \sum_i (\text{length of list at } T[i]) \\
 &= \frac{1}{n} \cdot n = 1
 \end{aligned}$$

So the average query time is constant!

9.4.4 Worst case query time, and a balls-in-bins problem

What is the worst case query time; that is, what is the length of the longest linked list in T ? Equivalently, when you throw n balls in n bins, what is the size of the largest bin? We'll see that with very high probability, no bin gets $\geq \log n$ balls.

For any bin i , let E_i be the event that it gets $\geq \log n$ balls.

$$\Pr(E_i) \leq \binom{n}{\log n} \left(\frac{1}{n}\right)^{\log n}.$$

(Do you see why?)

To upper bound this probability we use the inequality (see cheat sheet) that

$$\binom{n}{k} \leq \left(\frac{ne}{k}\right)^k$$

Applying this inequality we get:

$$\binom{n}{\log n} \left(\frac{1}{n}\right)^{\log n} \leq \left(\frac{ne}{n \log n}\right)^{\log n} = \left(\frac{e}{\log n}\right)^{\log n} = \frac{n^{\log e}}{(\log n)^{\log n}} \leq \frac{1}{n^2}$$

Where the last inequality can be shown by moving the n from the left to the right and taking $1/x$ and then log of both sides:

$$(\log n)(\log \log n) \geq (2 + \log e) \log n$$

Which holds when $n > 2000$

Having shown that $\Pr(E_i) \leq 1/n^2$, it follows that

$$\Pr(\text{some bin gets } \geq \log n \text{ balls}) = \Pr(E_1 \cup E_2 \cup \dots \cup E_n) \leq \Pr(E_1) + \dots + \Pr(E_n) \leq \frac{1}{n}.$$

For instance, if you throw a million balls into a million bins, then the chance that there is a bin with ≥ 20 balls is at most 1 in a million.

Getting back to hashing, this means that the worst case query time is (with high probability) $O(\log n)$.

9.4.5 The power of two choices

Here's a variant on the balls and bins setup. As usual, you have before you a row of n bins, along with a collection of n identical balls. But now, when throwing each ball, *you pick two bins at random and you put the ball in whichever of them is less full.*

It turns out, using an analysis that is too complicated to get into here, that under this small change, the maximum bin size will be just $O(\log \log n)$ instead of $O(\log n)$.

This inspires an alternative hashing scheme:

1. Pick *two* completely random functions $h_1, h_2 : \mathbb{U} \rightarrow \{1, 2, \dots, n\}$.
2. Create a table T of size n , each of whose entries is a pointer to a linked list, initialized to null.
3. For each x_i , store it in either the linked list at $T[h_1(x_i)]$ or $T[h_2(x_i)]$, whichever is shorter.
4. Given a query q , look through *both* the linked list at $T[h_1(q)]$ and at $T[h_2(q)]$ to see if it's there.

The storage requirement is still $O(n)$, the average query time is still $O(1)$, but now the worst case query time drops to $O(\log \log n)$.

9.5 Information retrieval

When you go to Google and enter a query, like

`what are treatment options for pneumonia`

or

`new song by radiohead`

you immediately get back a list of highly suitable pages. It's as if the search engine were instantaneously able to look through the tens of billions of pages on the web and find the relevant ones. How does it pull this off? The answer is, by a combination of clever preprocessing, statistics, hashing, and clustering.

In fact, these basic techniques apply not just to web search but to any system for *information retrieval*: answering unstructured queries about a large collection of documents.

9.5.1 Preprocessing

There are at five crucial preprocessing steps for a search engine.

1. Give each webpage a *reliability score*.

Most of the “information” on the web is grossly unreliable: spam, ignorant ravings, unfounded conjectures, and idle gossip. But we'll see (a bit later in the course) that it is possible to assess the reliability or authoritativeness of individual webpages — by analyzing the statistics of linkage patterns.

2. Ignore *near-duplicates* of webpages.

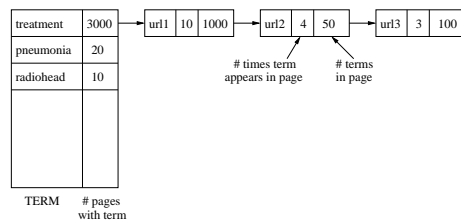
More on this very shortly.

3. Discover the set of *terms*.

A *term* is an individual word, or a sequence of words that should be considered together, such as **Katy Perry** or **Rage Against the Machine**. Terms can be discovered by analyzing co-occurrence patterns. If a sequence of k words keeps occurring together, they should be designated a term.

4. Create the *postings list*.

This is a hash table in which each term is associated with a linked list of the pages containing it.



Each linked list is arranged in decreasing order of “priority” (some notion that takes into account reliability scores), and is usually truncated at a certain point.

5. Compute *term frequencies*.

How common is each term?

9.5.2 Answering a query

The first step in answering a query is to order query terms by importance. The important terms are those that are uncommon. For instance, in

what are treatment options for pneumonia

the most important term is **pneumonia**, since this is the least common. Next comes **treatment**, and then **options**. The remaining words are so common that they can be ignored.

The next step is to look at the postings list, and get all pages containing the important query term(s). Then, assign each a score based on:

- the reliability of that page
- which of the important query terms it contains
- the number of times each query term appears on that page, divided by the length of the page

This yields an ordered list of webpages, starting with the “most relevant”. But the list will typically contain way too many pages. So they need to be clustered, and the user can then be presented with one representative page from each cluster, with the option to select “more like this”.

For instance, pages about Rome might be clustered into categories based on whether they refer to:

- Ancient Rome
- Modern Rome
- The TV series “Rome”
- and so on.

9.6 Detecting near-duplicates

Near-duplication is pervasive in the web: there are large numbers of distinct URLs which have exactly the same content but differ only in unimportant details like headers and footers. The user of a search engine would not be pleased if the answer to his query was a set of 10 near-identical pages! In order to remove this redundancy, we need to define a notion of *similarity* between documents.

9.6.1 The similarity between two documents

For any document—call it d —let the set of all words in d be denoted $C(d)$. For two documents d and d' , we will measure their similarity by the function

$$S(d, d') = \frac{|C(d) \cap C(d')|}{|C(d) \cup C(d')|}.$$

If the two documents are truly identical, $S(d, d') = 1$. If they are almost-identical, $S(d, d')$ will be close to 1. And if they are completely different, with no words in common, then $S(d, d')$ will be zero. We’ll consider d and d' to be near-duplicates if $S(d, d')$ is sufficiently close to 1.

Now, imagine a search engine that is going through a list of documents or webpages, and wants to eliminate near-duplicates. Here’s an algorithm it could use:

- $\mathcal{D} = \emptyset$ (set of documents, initially empty)
- for each document d that appears:
 - if $S(d, d')$ is significantly smaller than 1 for all d' in \mathcal{D} : add d to \mathcal{D}

The final set of documents \mathcal{D} will contain no near-duplicates. This is good, but the algorithm is very slow. Suppose for the sake of simplicity that there are n documents in total, each of length L . Then computing the similarity between two documents takes $O(L)$ time, and the algorithm is $O(n^2L)$. This quadratic dependence on n is prohibitive in web-scale applications, where n could easily be in the billions or tens of billions.

To get a faster algorithm, we once again resort to hashing.

9.6.2 An algorithm based on random permutations

We will encode each document by a single number. Here's how.

- Pick any encoding of words as numbers: for instance, any word is in any case stored as a binary number in the computer, and we can just use that number. Let $e(w)$ be the encoding of word w . Suppose these encodings are in the range $1, \dots, M$.
- Let σ be a *random permutation* of $(1, 2, \dots, M)$. Thus for each i , $\sigma(i)$ is a number in the range 1 to M , and all the $\sigma(i)$ are different.
- Hash each document d to the single number

$$f(d) = \min\{\sigma(e(w)) : w \in d\}.$$

That is, first think of all the words in the document as numbers, then apply the random permutation to each of these numbers (to get a different set of numbers), and finally pick the smallest of these resulting numbers. It is important that the same permutation σ is used for *all* the documents.

We will use the single number $f(d)$ in place of the entire document d ! The rationale for doing this is captured in the following lemma, which says that near-duplicate documents are likely to be hashed to the same value.

Lemma 11. *Let d, d' be any two documents. If σ is a random permutation, then*

$$\Pr(f(d) = f(d')) = S(d, d').$$

Proof. For any word w , we will call $\sigma(e(w))$ its *value*.

Now, $f(d)$ and $f(d')$ will be equal if and only if the word in d with the smallest value is the same as the word in d' with the smallest value. This is the same as saying that the smallest value among words in $d \cup d'$ lies in $d \cap d'$. The probability of this is exactly

$$\frac{\# \text{ words in } d \cap d'}{\# \text{ words in } d \cup d'} = S(d, d').$$

Reason: σ is a random permutation, so each word in $d \cup d'$ is equally likely to be the one with the smallest value. \square

Here's the revised algorithm.

- Create a boolean array `seen`[1... M], initialized to `false`
- $\mathcal{D} = \emptyset$ (set of documents, initially empty)
- for each document d that appears:
 - if not `seen`[$f(d)$]: add d to \mathcal{D} and set `seen`[$f(d)$] = `true`

This time, the running time is $O(nL)$, just linear in n .

In practice, this algorithm is run not with the words in each document but with all sequences of k words (called “ k -shingles”). For instance, the document

the quick brown fox jumped over the lazy dog

has the following 3-shingles: the quick brown, quick brown fox, brown fox jumped, fox jumped over, jumped over the, over the lazy, the lazy dog.

9.7 Bloom Filters

In some situations we are given a very long string, say billions of characters long, and we want to find all words that appear more than one time. A reasonably efficient way of doing that is to create a large hash table, keyed by words which stores the *count* for each observed word. This gives us a linear time algorithm in the length of the input.

However, in many cases the number of different words that appear in the input is very large but most of them occur only once (mis-spellings, people's names etc). This single-occurrence words or *singletons* place a large demand on the computer memory while containing no useful information.²

What we need is a *filter*. This filter will receive as input the stream of words, one word at a time. For each word it will answer the question “did this word appear earlier in the stream?”. If this is the first time the word appears, then it is *filtered out* or ignored. If the word has appeared earlier then it is *filtered in* or passed on to the hash table holding the counters. We would like to find a method which uses much less memory than would be used by the hash table. **Bloom filters** provide an elegant solution to this problem, but with a slight caveat: while no word that appears more than once will be mistakenly filtered out, the method does allow a small fraction of the singletons to be filtered in.

We now describe Bloom filters. Initially, two integer parameters k, m are chosen (how to choose it will be described a little later). We then choose and fix k different hash functions h_1, h_2, \dots, h_k that map words to integers in the range $1, \dots, l$. We also allocate a bit vector $B[\cdot]$ of length m where all bits are initialized to zero.

The filter operates as follows. Given a word w , it computes the k numbers $h_1(w), h_2(w), \dots, h_k(w)$ and uses them as indices into the bit vector B . If all of the k bits $B[h_1(w)], B[h_2(w)], \dots, B[h_k(w)]$ are equal to 1 then we declare that word w did appear earlier in the stream and therefore w is filtered *in*. If any of the k bits is not 1 then the word w is filtered *out* and not counted and the k bits in B are set to 1.

We now want to analyze the probability that the Bloom filter makes a mistake. There are two types of mistakes: filtering out a word that appeared previously and filtering in a word that did not appear previously. We consider each error type in turn:

- **Filtering out a word that appeared previously** (false negative) This can never happen. If the word w appeared in the past then the bits $B[h_1(w)], B[h_2(w)], \dots, B[h_k(w)]$ have been set to 1. As the algorithm never resets bits to zero, these bits must still be all 1 when we encounter w for the second, third, ... time. As a result w will not be filtered out. The Bloom filter does not make false negative mistakes.
- **Filtering in a word that did not previously appear** (false positive) This can happen. The k bits that are checked might have been set to 1 as a result of observing other words. However, we will now show that the probability of this event is small (provided k and m are set appropriately. Note also that the cost of a false positive mistake is small - it means that the algorithm will unnecessarily store a singleton word in the hash table. The result is a waste of memory space but not an actual error.

We now analyze the probability of making a false positive mistake, i.e. incorrectly declaring that a new word appeared earlier in the sequence. Let n be the number of different elements (words) that we inserted into the filter before we test the new word. We assume that each hash function $h_j(w)$ is a number chosen uniformly at random from the range $1 \leq i \leq m$. Consider a particular location j in the bitvector B , which is one of the k locations that the new word w is mapped to. We want to compute the probability that this

²Distributions where a significant fraction of the items (words) in a random sample appear only once, are called Zipf distributions. Zipf distributions are prevalent whenever a very large and under-utilized set of labels is used. This includes words, URLs, IP addresses etc. You can think of Zipf distributions as lying in the mid-point between discrete distributions (over a finite set) and density distributions. In the first case we expect *all* values to appear many times in a large enough sample, while in the second case we don't expect to see *any* value more than once.

bit is *not* set to one. The probability that one of the k hash functions, operating on one of the previous n words, does *not* set the bit to one is

$$1 - \frac{1}{m}$$

Thus the probability that none of the k hash functions, operating on any of the n words sets the j th bit to one is

$$\left(1 - \frac{1}{m}\right)^{kn}$$

Thus the probability that the j th bit is set to one is

$$1 - \left(1 - \frac{1}{m}\right)^{kn}$$

Finally, the new word will be identified as new only if all of the k locations in B to which it is hashed have been set to one. As these locations are independent, we get that the probability of making a false positive mistake is

$$\left(1 - \left(1 - \frac{1}{m}\right)^{kn}\right)^k = \left(1 - \left(\left(1 - \frac{1}{m}\right)^m\right)^{kn/m}\right)^k \approx \left(1 - e^{-kn/m}\right)^k$$

Note that the only way that m and n enter the equation is through the ratio m/n . We call the ratio $r = m/n$ the *redundancy* of the bitmap, because it defines the number of bits that are associated with each word. And we can rewrite the (approximate) probability of a false positives as

$$\left(1 - e^{-k/r}\right)^k$$

The number of hash functions k that approximately minimizes the probability is (remember that k is an integer)

$$k \approx r \ln 2 \approx 0.7r \tag{9.2}$$

which gives the false positive probability of

$$p = \left(1 - e^{-\ln 2}\right)^k = (1/2)^k \approx (0.6185)^r.$$

The required redundancy for a desired false positive probability p (assuming the optimal value of k is used) can be computed by taking the \ln of the two side in the last expression

$$\ln p = -r(\ln 2)^2. \tag{9.3}$$

Recalling that $r = m/n$ we get that the length of the bit vector is

$$m = -\frac{n \ln p}{(\ln 2)^2}.$$

To gain some intuition about these results, lets compare the performance for the optimal $k \approx m/n$ defined in Equation (9.2) with the performance for $k = 1$. The case $k = 1$ is very intuitive, each word is mapped to a single bit and if this bit is one, then the algorithm concludes that the word has been seen before. As the length of the bit vector B is m and the number of different words already observed is n then n of the m bits in B are set. The result is that the probability of making a false positive mistake is $p = n/m$. If we had a perfect hashing function, that maps each word to a different bit, we would be able to use a table with no redundancy, i.e. $r = 1$. As we showed above when $k = 1$, $p = 1/r$.

Consider now using the optimal setting for k as defined in Equation (9.2). In this case we have from Equation (9.3) that:

$$p = \exp\left(-\frac{m}{n}(\ln 2)^2\right) \leq \exp\left(-0.48\frac{m}{n}\right) = \exp(-0.48r)$$

We find that in both cases the probability of a false positive is a function of the redundancy, however, while for $k = 1$, p decreases like $1/r$ for the optimal value of k it decreases much faster, like e^{-r} . Thus with the same size bit vector we get a much smaller probability of error.

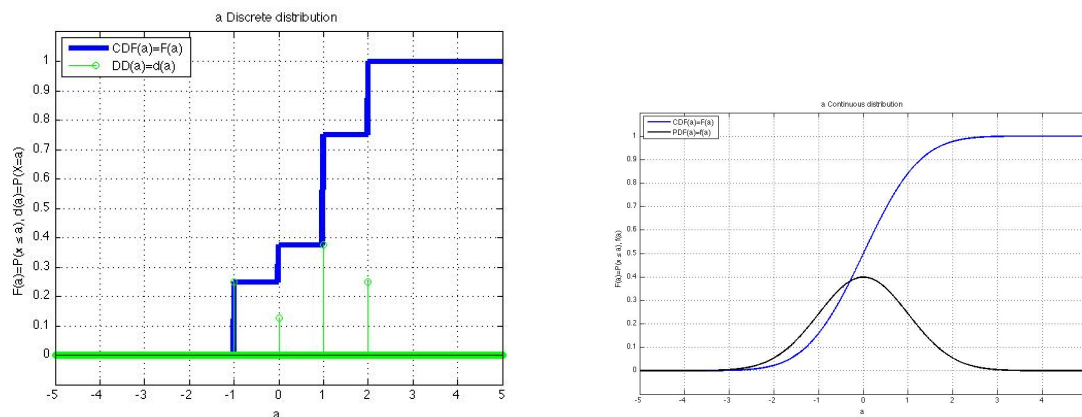


Figure 9.4: **Left:** A non-uniform discrete distribution. This distribution can be expressed as $(1/4)PM(-1) + (1/8)PM(0) + (5/8)PM(1) + (1/4)PM(2)$. **Right:** The normal distribution with mean 0 and variance 1, denoted $\mathcal{N}(0, 1)$. This is a density distribution and its density function is $f(x) = \frac{1}{\sqrt{2\pi}} \exp(-x^2/2)$.

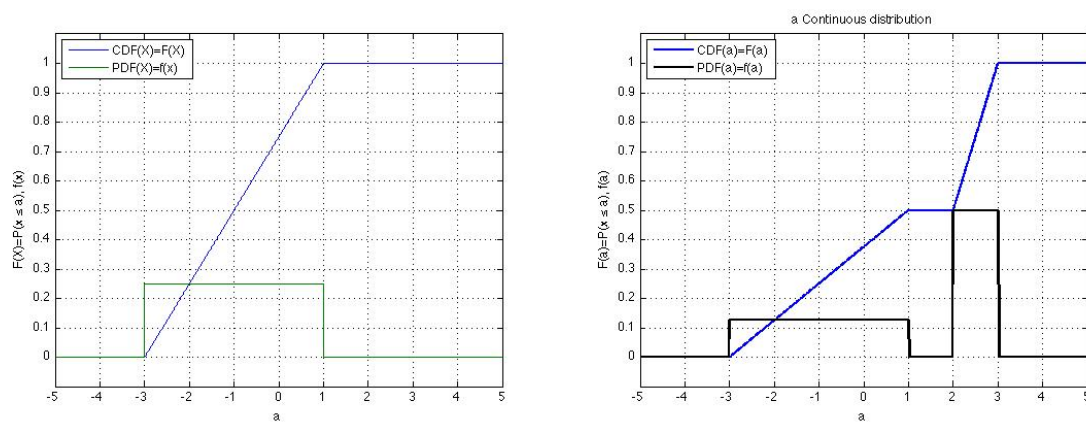


Figure 9.5: **Left:** A uniform distribution between -3 and 1 . We denote this distribution by $U(-3, 1)$. **Right:** A mixture of two uniform distributions: $(U(-3, 1) + U(2, 3))/2$.

14 edges to choose from
Pick $b - f$ (probability $1/14$)



13 edges to choose from
Pick $g - h$ (probability $1/13$)



12 edges to choose from
Pick $d - gh$ (probability $1/6$)



10 edges to choose from
Pick $a - e$ (probability $1/10$)



9 edges to choose from
Pick $ab - ef$ (probability $4/9$)

