Chapter 7
Probability

Consider trying to drive through an unfamiliar city. Even if we are able to plan a route from our starting location to our destination, navigation can fail on two counts: sometimes we don't know where we are on a map, and sometimes, due to traffic or road work or bad driving, we fail to execute a turn we had intended to take.

In such situations, we have some information about where we are: we can make observations of our local surroundings, which give us useful information; and we know what actions we have taken and the consequences those are likely to have on our location. So, the question is: how can we take information from a sequence of actions and local observations and integrate it into some sort of estimate of where we are? What form should that estimate take?

We'll consider a probabilistic approach to answering this question. We'll assume that, as you navigate, you maintain a *belief state* which contains your best information about what state you're in, which is represented as a probability distribution over all possible states. So, it might say that you're sure you're somewhere in Boston, and you're pretty sure it's Storrow drive, but you don't know whether you're past the Mass Ave bridge or not (of course, it will specify this all much more precisely).

We'll start by defining probability distributions on simple and complex spaces, and develop a set of methods for defining and manipulating them. Then, we'll formulate problems like the navigation problem discussed above as *state estimation* problems in *stochastic state machines*. Finally, we'll develop an algorithm for estimating the unobservable state of system, based on observations of its outputs.

7.1 State spaces

We have been using state machines to model systems and how they change over time. The *state* of a system is a description of the aspects of the system that allow us to predict its behavior over time. We have seen systems with finite and infinite state spaces:

- A basic enumeration of states, such as `('closed', 'closing', 'open', 'opening')` for an elevator controller, we will call an *atomic* finite state space. The states are atomic because they don't have any further detailed structure.
- A state space that is described using more than one variable, such as a counter for seconds that goes from 0 to 59 and a counter for minutes that goes from 0 to 59 can be described as having two *state variables*: seconds and minutes. We would say that this state space is *factored*: a state is actually described by a value of each of the two variables.
- A state space described by a single integer is a countably infinite atomic state space.
- A state space described by a real number is uncountably infinite, but still atomic.

- A state space described by more than one integer or real number (or a combination of continuous and discrete state variables) is a factored state space.

In this chapter, we will concentrate on factored, finite state spaces, and see how to represent and manipulate probability distributions on them.

7.2 Probability distributions on atomic state spaces

Probability theory is a calculus that allows us to assign numerical assessments of uncertainty to possible events, and then do calculations with them in a way that preserves their meaning. (A similar system that you might be more familiar with is algebra: you start with some facts that you know, and the axioms of algebra allow you to make certain manipulations of your equations that you know will preserve their truth).

The typical informal interpretation of probability statements is that they are long-term frequencies: to say "the probability that this coin will come up heads when flipped is 0.5" is to say that, in the long run, the proportion of flips that come up heads will be 0.5. This is known as the *frequentist interpretation* of probability. But then, what does it mean to say "there is a 0.7 probability that it will rain somewhere in Boston sometime on April 29, 2017"? How can we repeat that process a lot of times, when there will only be one April 29, 2017? Another way to interpret probabilities is that they are measures of a person's (or robot's) *degree of belief* in the statement. This is sometimes referred to as the *Bayesian interpretation*. In either interpretation, the formal calculus is the same.

So, studying and applying the axioms of probability will help us make true statements about long-run frequencies and make consistent statements about our beliefs by deriving sensible consequences from initial assumptions.

We will restrict our attention to discrete sample spaces[1], so we'll let U be the *universe* or sample space, which is a set of *atomic events*. An atomic event is just a state: an outcome or a way the world could be. It might be a die roll, or whether the robot is in a particular room, for example. Exactly one (no more, no less) event in the sample space is guaranteed to occur; we'll say that the atomic events are "mutually exclusive" (no two can happen at once) and "collectively exhaustive" (one of them is guaranteed to happen).

Example 8.1

- The sample space for a coin flip might be `H, T`, standing for heads and tails.
- The sample space for a sequence of three coin flips might be `HHH, HHT, HTH, HTT, THH, THT, TTH, TTT`: all possible sequences of three heads or tails.
- The sample space for a robot navigating in a city might be the set of intersections in the city.
- The sample space for a randomly generated document might be all strings of fewer than 1000 words drawn from a particular dictionary.

[1] In probability, it is typical to talk about a 'sample space' rather than a 'state space,' but they both come to the same thing: a space of possible situations.

An *event* is a subset of U; it will contain zero or more atomic events.

Example 8.2

- An event in the three-coin-flip space might be that there are at least two heads: $\{HHH, HHT, HTH, THH\}$.
- An event in the robot navigation problem might be that the robot is within one mile of MIT.
- An event in the document domain might be that the document contains, in sequence, the words '6.01' and 'rules'.

A probability measure $\Pr$ is a mapping from events to numbers that satisfy the following axioms:

$$\begin{aligned} \Pr(U) &= 1 \\ \Pr(\{\}) &= 0 \\ \Pr(E_1 \cup E_2) &= \Pr(E_1) + \Pr(E_2) - \Pr(E_1 \cap E_2) \end{aligned}$$

Or, in English:

- The probability that something will happen is 1.
- The probability that nothing will happen is 0.
- The probability that an atomic event in the set E_1 or an atomic event in the set E_2 will happen is the probability that an atomic event of E_1 will happen plus the probability that n atomic event of E_2 will happen, minus the probability that an atomic event that is in both E_1 and E_2 will happen (because those events effectively got counted twice in the sum of $\Pr(E_1)$ and $\Pr(E_2)$).

Armed with these axioms, we are prepared to do anything that can be done with discrete probability!

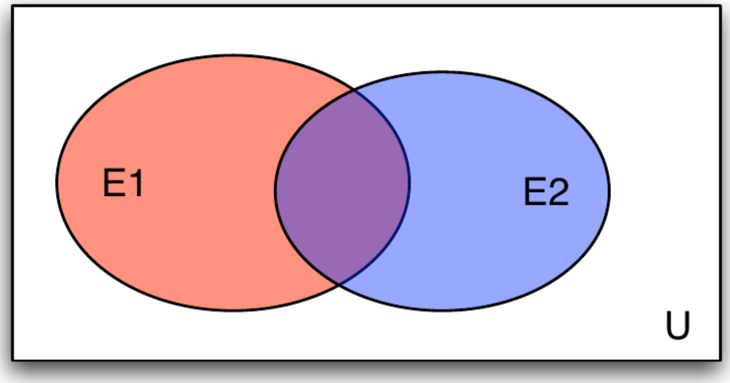
Conditional probability

One of the most important operations in probabilistic reasoning is incorporating evidence into our models. So, we might wonder what the probability of an event is *given* or *conditioned on* some other relevant information we have received. For example, we might want to know the probability of getting a die roll greater than 3, if we already know that the die roll will be odd.

We will write conditional probabilities as $\Pr(E_1 \mid E_2)$, pronounced "the probability of E_1 given E_2 ", where E_1 and E_2 are events (subset of the atomic sample space). The formal definition of conditional probability is this:

$$\Pr(E_1 \mid E_2) = \frac{\Pr(E_1 \cap E_2)}{\Pr(E_2)} \quad .$$

In the figure below, E_1 is the red ellipse, E_2 is the blue ellipse, and $E_1 \cap E_2$ is the purple intersection. When we condition on E_2 , we restrict our attention entirely to the blue ellipse, and ask what percentage of the blue ellipse is also in the red ellipse. This is the same as asking for the ratio of the purple intersection to the whole blue ellipse.



Example 8.3 What is the conditional probability of getting a die roll greater than 3, given that it will be odd? The probability of a die roll greater than 3 (in a fair six-sided die) is $1/2$. But if we know the roll will be odd, then we have to consider ratio of the probabilities of two events: that the die roll will be odd and greater than three, and that the die roll will be odd. This is $1/6$ divided by $1/2$, which is $1/3$. So, learning that the die roll will be odd decreases our belief that it will be greater than three.

7.3 Random variables

Just as some state spaces are naturally described in their factored form (it's easier to say that there are 10 coins, each of which can be heads or tails, than to enumerate all 2^{10} possible sequences), we often want to describe probability distributions over one or more variables. We will call a probability distribution that is described over one dimension of a state space a *random variable*.

A discrete random variable is a discrete set of values, $v_1 \ldots v_n$, and a mapping of those values to probabilities $p_1 \ldots p_n$ such that $p_i \in [0, 1]$ and $\sum_i p_i = 1$. So, for instance, the random variable associated with flipping a somewhat biased coin might be $\{\mathit{heads} : 0.6, \mathit{tails} : 0.4\}$. We will speak of random variables having distributions: so, for example, two flips of the same biased coin are actually two different random variables, but they have the same distribution.

In a world that is appropriately described with multiple random variables, the atomic event space is the *Cartesian product* of the value spaces of the variables. So, for example, consider two random variables, C for *cavity* and A for *toothache*. If they can each take on the values T or F (for *true* and *false*), then the universe is pairs of values, one for each variable:

$$C \times A = \{(T, T), (T, F), (F, T), (F, F)\} \quad .$$

We will systematically use the following notation when working with random variables:

- A : capital letters stand for random variables;
- a : small letters stand for possible values of random variables; so a is an element of the domain (possible set of values) of random variable A ;
- $A = a$: an equality statement with a random variable in it is an event: in this case, the event that random variable A has value a

Some non-atomic events in a universe described by random variables A and C might be $C = c$ (which includes atomic events with all possible values of A), or $C = A$ (which includes all atomic events consisting of pairs of the same value).

Joint distribution

The *joint distribution* of a set of random variables is a function from elements of the product space to probability values that sum to 1 over the whole space. So, we would say that $(C = c, A = a)$ (with a comma connecting the equalities), which is short for $(C = c$ *and* $A = a)$ is an atomic event in the joint distribution of C, A .

In most of our examples, we'll consider joint distributions of two random variables, but all of the ideas extend to joint distributions over any finite number of variables: if there are n random variables, then the domain of the joint distribution is all n -tuples of values, one drawn from the domain of each of the component random variables. We will write $\Pr(A, B, \ldots, N)$ to stand for an entire joint distribution over two or more variables.

Conditional distribution

In Section 8.2 we gave the basic definition of conditional probabilities, in terms of events on atomic subspaces. Sometimes, it will be useful to define conditional probabilities directly. A *conditional probability distribution*, written $\Pr(A \mid B)$, where A and B are random variables (we can generalize this so that they are groups of random variables), is a function from values, b , of B , to probability distributions on A . We can think of it this way:

$$\Pr(A \mid B) = \lambda b. \Pr(A \mid B = b)$$

Here, we are using λ in the same way that it is used in Python: to say that this is a function that takes a value b as an argument, and returns a distribution over A .

Example 8.4 Conditional distributions are often used to model the efficacy of medical tests. Consider two random variables: D , which has value *disease* if someone has a disease and value *nodisease* otherwise; and T , which has value *positive* if the test comes out positive and value *negative* otherwise. We can characterize the efficacy of the test by specifying $\Pr(T \mid D)$, that is, a conditional distribution on the test results given whether a person has the disease. We might specify it as:

$$\Pr(T \mid D) = \begin{cases} \text{positive} : 0.99, \text{negative} : 0.01, & \text{if } D = \text{disease} \\ \text{positive} : 0.001, \text{negative} : 0.999, & \text{if } D = \text{nodisease} \end{cases}$$

7.3.1 Python representations of distributions

We can represent distributions in Python in a number of ways. We'll use a simple discrete distribution class, called `DDist`, which stores its entries in a dictionary, where the elements of the sample space are the keys and their probabilities are the values.

```
class DDist:
    def __init__(self, dictionary):
        self.d = dictionary
```

The primary method of the `DDist` class is `prob`, which takes as an argument an element of the domain of this distribution and returns the probability associated with it. If the element is not present in the dictionary, we return 0. This feature allows us to represent distributions over large sets efficiently, as long as they are sparse, in the sense of not having too many non-zero entries.

```
    def prob(self, elt):
        if elt in self.d:
            return self.d[elt]
        else:
            return 0
```

(The expression `elt in self.d` is a nicer way to say `self.d.has_key(elt)`. That is a call to a built-in method of the Python dictionary class, which returns `True` if the dictionary contains the key `elt` and `False` otherwise.)

It is useful to know the `support` of the distribution, which is a list of elements that have non-zero probability. Just in case there are some zero-probability elements stored explicitly in the dictionary, we filter to be sure they do not get returned.

```
    def support(self):
        return [k for k in self.d.keys() if self.prob(k) > 0]
```

If we want to use the probability distribution to make a simulation, or to do something like shuffle or deal cards, it's useful to be able to `draw` from it. This method returns an element from the sample space of the distribution, selected at random according to the specified distribution.

```
    def draw(self):
        r = random.random()
        sum = 0.0
        for val in self.support():
            sum += self.prob(val)
            if r < sum:
                return val
```

We can represent a joint distribution on two random variables simply as a `DDist` on pairs of their values. So, for example, this distribution

```
dist.DDist({(0, 0) : 0.5, (0, 1): 0.2, (1, 0): 0.1, (1, 1): 0.2})
```

can be seen as the joint distribution on two random variables, each of which can take on values 0 or 1. (Remember that expressions like `key1 :  v1, key2 :  v2` create a new dictionary).

Finally, we will represent conditional distributions as Python procedures, from values of the conditioning variable to distributions on the conditioned variable. This distribution

$$\mathsf{Pr}(\mathsf{T} \mid \mathsf{D}) = \begin{cases} \text{positive : } 0.99, \text{negative : } 0.01, & \text{if } \mathrm{D} = \text{disease} \\ \text{positive : } 0.001, \text{negative : } 0.999, \text{if } \mathrm{D} = \text{nodisease} \\ \end{cases}$$

would be represented in Python as

```
def TgivenD(D):
    if D == 'disease':
        return dist.DDist({'positive' : 0.99, 'negative' : 0.01})
    elif D == 'nodisease':
        return dist.DDist({'positive' : 0.001, 'negative' : 0.999})
    else:
        raise Exception, 'invalid value for D'
```

To find a value for $\Pr(T = negative \mid D = disease)$, we would evaluate this Python expression:

```
>>> TgivenD('disease').prob('negative')
```

7.4 Operations on random variables

Now that we can talk about random variables, that is, distributions over their sets of values, we can follow the PCAP principle to define a systematic way of combining them to make new distributions. In this section, we will define important basic operations.

7.4.1 Constructing a joint distribution

A convenient way to construct a joint distribution is as a product of factors. We can specify a joint distribution on C and A by the product of a distribution $\Pr(A)$ and a conditional distribution $\Pr(C \mid A)$ by computing the individual elements of the joint, for every pair of values a in the domain of A and c in the domain of C :

$$\Pr(C = c, A = a) = \Pr(C = c)\Pr(A = a \mid C = c)$$

It is also true that

$$\Pr(C = c, A = a) = \Pr(A = a)\Pr(C = c \mid A = a)$$

Exercise 8.1 Use the definition of conditional probability to verify that the above formulas are correct.

In the domain where the random variable C stands for whether a person has a cavity and A for whether they have a toothache, we might know:

- The probability of a randomly chosen patient having a cavity:
$$\Pr(C) = \{T : 0.15, F : 0.85\}$$
- The conditional probability of someone having a toothache given that they have a cavity:
$$\Pr(A \mid C) = \begin{cases} \{T : 0.333, F : 0.667\}, \text{if } C = T \\ \{T : 0.0588, F : 0.9412\}, \text{if } C = F \\ \end{cases}$$

Then we could construct the following table representing the joint distribution:

		C	
		T	F
A	T	0.05	0.05
	F	0.1	0.8

The numbers in the table make up the joint probability distribution. They are assignments of probability values to atomic events, which are complete specifications of the values of all of the random variables. For example, $\Pr(C = T, A = F) = 0.1$; that is, the probability of the atomic event that random variable C has value T and random variable A has value F is 0.1 . Other events can be made up of the union of these primitive events, and specified by the assignments of values to only some of the variables. So, for instance, the event $A = T$ is really a set of primitive events: $\{(A = T, C = F), (A = T, C = T)\}$, which means that

$$\Pr(A = T) = \Pr(A = T, C = T) + \Pr(A = T, C = F) \quad ,$$

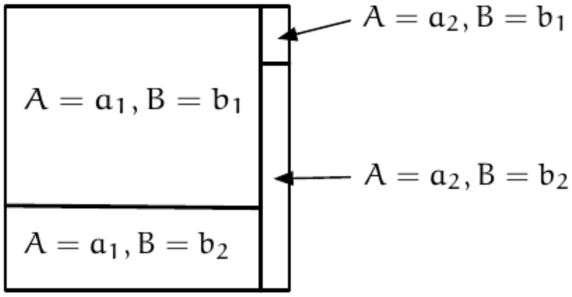
which is just the sum of the row in the table.

$$\Pr(T \mid D) = \begin{cases} \text{positive} : 0.99, \text{negative} : 0.01, & \text{if } D = \text{disease} \\ \text{positive} : 0.001, \text{negative} : 0.999, & \text{if } D = \text{nodisease} \\ \end{cases}$$

Here is another example of forming a joint distribution. Imagine that we are given the following distributions:

$\Pr(A) = \{a_1 : 0.9, a_2 : 0.1\}$ <br /> $\Pr(B \mid A) = \begin{cases} b_1 : 0.7, b_2 : 0.3, & \text{if } A = a_1 \\ b_1 : 0.2, b_2 : 0.8, & \text{if } A = a_2 \\ \end{cases}$

You can visualize the joint distribution spatially, like this:



The sample space is divided vertically according to the distribution $\Pr(A)$, and then, for each value of A , it is divided horizontally according to the distribution $\Pr(B \mid A = a)$. This joint distribution is represented numerically by the table:

		A	
		a_1	a_2
B	b_1	0.63	0.02
	b_2	0.27	0.08

We can also think of this joint distribution as just another regular distribution on a larger state space:

$$\Pr(A, B) = \{(a_1, b_1) : 0.63, (a_1, b_2) : 0.27, (a_2, b1) : 0.02, (a_2, b_2) : 0.08\}$$

More generally, we can construct a joint distribution on an arbitrary number of random variables, $\Pr(V_1, \dots, V_n)$, as follows:

$$\begin{aligned}\Pr(V_1 = v_1, \dots, V_n = v_n) = &\Pr(V_1 = v_1 \mid V_2 = v_2, \dots, V_n = v_n)\\ &\cdot \Pr(V_2 = v_2 \mid V_3 = v_3, \dots, V_n = v_n)\\ &\dots\\ &\cdot \Pr(V_{n-1} = v_{n-1} \mid V_n = v_n)\\ &\cdot \Pr(V_n = v_n)\end{aligned}$$

This can be done with the variables in any order.

7.4.2 Marginalization

A *marginal distribution* over any individual random variable can be obtained from the joint distribution by summing over all assignments to the other random variables in the joint distribution. In two dimensional tables, this means summing the rows or the columns:

$$\Pr(A = a) = \sum_b \Pr(A = a, B = b)$$

Example 8.6 In our example with toothaches and cavities, we can compute the marginal distributions:

$$\begin{aligned}\Pr(A) &= \{T : 0.1, F : 0.9\}\\ \Pr(C) &= \{T : 0.15, F : 0.85\}\end{aligned}$$

Although you can compute the marginal distributions from the joint distribution, **you cannot in general compute the joint distribution from the marginal distributions!!** In the **very special case** when two random variables A and B do not influence one another, we say that they are *independent*, which is mathematically defined as

$$\Pr(A = a, B = b) = \Pr(A = a) \Pr(B = b) \quad .$$

If we only knew the marginals of toothaches and cavities, and assumed they were independent, we would find that $\Pr(C = T, A = T) = 0.015$, which is much less than the value in our joint distribution. This is because, although cavity and toothache are relatively rare events, they are highly dependent.

7.4.3 Conditioning

One more important operation on a joint distribution is *conditioning*. It is fundamentally the same operation as computing a conditional probability, but when the conditioning event (on the right hand side of the bar) is that a random variable has a particular value, then we get a nice simplification. So, for example, if we wanted to condition our joint toothache/cavity distribution on the event $A = T$, we could write $\Pr(C, A \mid A = T)$. But since the value for A is already made explicit in the conditioning event, we typically write this as $\Pr(C \mid A = T)$. It is obtained by:

- Finding the row (or column) of the joint distribution corresponding to the conditioning event. In our example, it would be the row for $A = T$, which consists of $\Pr(A = T, C = T)$ and $\Pr(A = T, C = F)$.
- Dividing each of the numbers in that row (or column) by the probability of the conditioning event, which is the marginal probability of that row (or column). In our example, we would divide 0.05 by 0.1 to get
$$\Pr(C \mid A = T) = \{T : 0.5, F : 0.5\}$$

So, in this example, although a cavity is relatively unlikely, it becomes much more likely conditioned on knowing that the person has a toothache.

We have described conditioning in the case that our distribution is only over two variables, but it applies to joint distributions over any number of variables. You just have to think of selecting the entries whose value for the specified random variable equals the specified value, and then renormalizing their probabilities so they sum to 1.

7.4.4 Bayesian reasoning

Frequently, for medical diagnosis or characterizing the quality of a sensor, it's easiest to measure conditional probabilities of the form $\Pr(\mathit{Symptom} \mid \mathit{Disease})$, indicating what proportion of diseased patients have a particular symptom. (These numbers are often more useful, because they tend to be the same everywhere, even though the proportion of the population that has disease may differ.) But in these cases, when a patient comes in and demonstrates some actual symptom s , we really want to know $\Pr(\mathit{Disease} \mid \mathit{Symptom} = s)$. We can compute that if we also know a *prior* or *base rate* distribution, $\Pr(\mathit{Disease})$. The computation can be done in two steps, using operations we already know:

- Form the joint distribution: $\Pr(\mathit{Disease}, \mathit{Symptom})$
- Condition on the event $\mathit{Symptom} = s$, which means selecting the row (or column) of the joint distribution corresponding to $\mathit{Symptom} = s$ and dividing through by $\Pr(\mathit{Symptom} = s)$.

So, given an actual observation of symptoms s , we can determine a conditional distribution over $\mathit{Disease}$, by computing for every value of d ,

$$\Pr(\mathit{Disease} = d \mid \mathit{Symptom} = s) = \frac{\Pr(\mathit{Symptom}=s|\mathit{Disease}=d) \Pr(\mathit{Disease}=d)}{\Pr(\mathit{Symptom}=s)} .$$

The formula, when written this way, is called *Bayes' Rule*, after Rev. Thomas Bayes who first formulated this solution to the 'inverse probability problem,' in the 18th century.

Multiple pieces of evidence

With Bayes' rule, we have seen how to update a probability distribution $P(A)$ based on receiving some evidence $E = e$ to get a new distribution $P(A \mid E = e)$. Now, what happens if we get yet another piece of evidence $F = f$?

If the two pieces of evidence are *conditionally independent given* A , that is, that $P(F \mid A, E) = P(F \mid A)$ and $P(E \mid A, F) = P(E \mid A)$then we can incorporate the evidence sequentially. That is, we can:

- Use Bayes' rule to incorporate the first piece of evidence to get $P(A \mid E = e)$; then
- Use Bayes' rule again, with $P(A \mid E = e)$ as the starting distribution on A to incorporate the second piece of evidence and get $P(A \mid E = e, F = f)$.

And the totally cool thing is that it doesn't matter what order we do this in! We'll get the same result.

First, let's derive a small generalization of Bayes' rule, which applies when we are conditioning on more than one variable.

$$P(A \mid E, F) = \frac{P(E|A,F)P(A|F)}{P(E|F)}$$

which, when E and F are conditionally independent given A is

$$P(A \mid E, F) = \frac{P(E|A)P(A|F)}{P(E|F)}$$

So, now, let's think about updating a distribution on some random variable of interest A , given two pieces of evidence: $E = e$ and $F = f$. (It might be that we're modeling our information about a disease someone has (A) given the results of two tests ($E = e$ and $F = f$). We can start by applying the rule we derived above:

$$P(A \mid E = e, F = f) = \frac{P(E=e|A)P(A|F=f)}{P(E=e|F=f)}$$

And now, we can take the term $P(A \mid F = f)$ and apply Bayes' rule to it, inside this formula, to get

$$P(A \mid E = e, F = f) = \frac{P(E=e|A)P(F=f|A)P(A)}{P(E=e|F=f)P(F=f)}$$

This is looking pretty promising. We assume we know how evidence variables E and F depend on A , and we certainly have the prior $P(A)$. So we just have to play around with the denominator a little, to get

$$P(A \mid E = e, F = f) = \frac{P(E=e|A)P(F=f|A)P(A)}{P(F=f|E=e)P(E=e)}$$

Now, we can gather up the terms slightly differently to reveal a sequential update structure:

$$P(A \mid E = e, F = f) = \frac{P(E=e|A)P(A)}{P(E=e)} \cdot \frac{P(F=f|A)}{P(F=f|E=e)}$$

Clearly, the first factor in the right-hand side is the Bayes update of $P(A)$ based on evidence $E = e$. The second factor takes that distribution, and does another Bayesian update, this time based on the evidence that $F = f$. The second denominator might cause some confusion. We can think about the denominators in two ways: a careful way and a relaxed way.

The careful way is to remember that $P(E = e) = \sum_a P(E = e \mid A = a)P(A = a)$, which we can easily compute as the sum of the numerator terms of the first factor for all values of a . And, similarly,

$$P(F = f \mid E = e) = \sum_a P(F = f \mid E = e, A = a)P(A = a \mid E = e)$$

which can be rewritten as

$$P(F = f \mid E = e) = \sum_a P(F = f \mid A = a)P(E = e \mid A = a)P(A = a)/P(E = e)$$

The cool thing to note is that this is just the sum of products of the the numerator terms, once we cancel $P(E = e)$.

The relaxed way is to note that neither denominator term depends on the particular value of a we are interested in: from the perspective of making a distribution over A , these are just constants, and we can pick them to make it so that the distribution sums to 1. This all boils down to normalizing the distribution after each evidence update.

So, we can see that to compute $P(A \mid E = e, F = f)$ we just need to compute $P(A \mid E = e)$ using Bayes rule, then take that distribution, and apply Bayes rule again to get.

Check Yourself 1. Convince yourself that if we did the updates in the other, first based on $F = f$ and then based on $E = e$, we would get the same result.

Example 8.7

Write a method of `DDist` called `multiBayes` that assumes `self` is a representation of some distribution $P(A)$, and takes as an argument a list of n pairs, each of which has the form $(P(E_i \mid A), e_i)$, representing several pieces of evidence, and returns a distribution representing $P(A \mid E_1 = e_1, \ldots, E_n = e_n)$.
This is sometimes called *recursive Bayesian updating*. For fun, do it recursively!
Verify that if you change the order of presentation of evidence that the resulting distribution is the same.

7.4.5 Total probability

Another common pattern of reasoning is sometimes known as *the law of total probability*. What if we have our basic distributions specified in an inconvenient form: we know, for example, $\Pr(A)$ and $\Pr(B \mid A)$, but what we really care about is $\Pr(B)$? We can form the joint distribution over A and B , and then marginalize it by summing over values of A . To compute one entry of the resulting distribution on B , we would do:

$$\Pr(B = b) = \sum_a \Pr(B = b \mid A = a) \Pr(A = a)$$

but it's easier to think about as an operation on the whole distributions.

7.4.6 Python operations on distributions

We can implement the operations described in this section as operations on `DDist` instances.

Constructing a joint distribution

We start by defining a procedure that takes a distribution $\Pr(A)$, named `PA`, and a conditional distribution $\Pr(B \mid A)$, named `PBgA`, and returns a joint distribution $\Pr(A, B)$, represented as a Python `dist.DDist` instance. It must be the case that the domain of A in `PA` is the same as in `PBgA`. It creates a new instance of `dist.DDist` with entries `(a, b)` for all `a` with support in `PA` and `b` with support in `PB`. The Python expression `PA.prob(a)` corresponds to $\Pr(A = a)$; `PBgA` is a conditional probability distribution, so `PBgA(a)` is the distribution $\Pr(B \mid A = a)$ on B , and `PBgA(a).prob(b)` is $\Pr(B = b \mid A = a)$.

So, for example, we can re-do our joint distribution on A and B as:

```
PA = dist.DDist({’a1’ : 0.9, ’a2’ : 0.1})
def PBgA(a):
    if a == ’a1’:
        return dist.DDist({’b1’ : 0.7, ’b2’ : 0.3})
    else:
        return dist.DDist({’b1’ : 0.2, ’b2’ : 0.8})
>>> PAB = JDist(PA, PBgA)
>>> PAB
DDist((a1, b2): 0.270000, (a1, b1): 0.630000, (a2, b2): 0.080000, (a2, b1): 0.020000)
```

We have constructed a new joint distribution. We leave the implementation as an exercise.

Marginalization

Now, we can add a method to the `DDist` class to marginalize out a variable. It is only appropriately applied to instances of `DDist` whose domain is pairs or tuples of values (corresponding to a joint distribution). It takes, as input, the index of the variable that we want to *marginalize out*.

It can be implemented using two utility procedures: `removeElt` takes a list and an index and returns a new list that is a *copy* of the first list with the element at the specified index removed; `incrDictEntry` takes a dictionary, a key, and a numeric increment and adds the increment to the value of the key, adding the key if it was not previously in the dictionary.

```
def removeElt(items, i):
    result = items[:i] + items[i+1:]
    if len(result) == 1:
        return result[0]
    else:
        return result
def incrDictEntry(d, k, v):
    if d.has_key(k):
        d[k] += v
    else:
        d[k] = v
```

Now, we can understand `marginalizeOut` as making a new dictionary, with entries that have the variable at the specified index removed; the probability associated with each of these entries is the sum of the old entries that agree on the remaining indices. So, for example, we could take the joint distribution, `PAB`, that we defined above, and marginalize out the variable A (by specifying index 0) or B (by specifying index 1):

```
>>> PAB.marginalizeOut(0)
DDist(b1: 0.650000, b2: 0.350000)
>>> PAB.marginalizeOut(1)
DDist(a1: 0.900000, a2: 0.100000)
```

Conditioning

We can also add a `conditionOnVar` method to `DDist` which, like `marginalizeOut`, should only be applied to joint distributions. It takes as input an index of the value to be conditioned on, and a value for that variable, and returns a `DDist` on the remaining variables. It operates in three steps:

- Collect all of the value-tuples in the joint distribution that have the specified value at the specified index. This is the new universe of values, over which we will construct a distribution.
- Compute the sum of the probabilities of those elements.
- Create a new distribution by removing the elements at the specified index (they are redundant at this point, since they are all equal) and dividing the probability values by the sum of the probability mass in this set. The result is guaranteed to be a distribution in the sense that the probability values properly sum to 1.

Now, we can compute, for example, the distribution on A, given that $B = b_1$:

```
>>> PAB.conditionOnVar(1, 'b1')
DDist(a1: 0.969231, a2: 0.030769)
```

Note that this is *not* a conditional distribution, because it is not a function from values of B to distributions on A. At this point, it is simply a distribution on A.

Exercise 8.2 Define a method `condDist(self, index)` of the `DDist` class that makes a new conditional probability distribution. Remember that a conditional distribution is *not a distribution*. It is a function that takes as input a value of the random variable we are conditioning on, and returns, as a result a probability distribution over the other variable(s).
So, this method takes an index (of the variable we are conditioning on) and returns a conditional probability distribution of the other variables in the joint distribution, given the variable at the specified index.

Answer:

```
def condDist(self, index):
return lambda val: self.conditionOnVar(index, val)
```

Bayesian Evidence

The operation of updating a distribution on a random variable A, given evidence in the form of the value b of a random variable B, can be implemented as a procedure that takes as arguments the prior distribution $\Pr(A)$, named `PA`, a conditional distribution $\Pr(B \mid A)$, named `PBgA`, and the actual evidence b, named `b`. It starts by constructing the joint distribution $\Pr(A, B)$ with `JDist`. Then, remembering that the order of the variables in the joint distribution is `(A, B)`, it conditions on the variable with index 1 (that is, B) having value `b`, and returns the resulting distribution over A.

So, for example, given a prior distribution on the prevalence of disease in the population

```
pDis = dist.DDist({True: 0.001, False: 0.999})
```

and the conditional distribution of test results given disease:

```
def pTestGivenDis(disease):
    if disease:
        return dist.DDist({True: 0.99, False: 0.01})
    else:
        return dist.DDist({True: 0.001, False: 0.999})
```

we can determine the probability that someone has the disease if the test is positive:

```
>>> dist.bayesEvidence(pDis, pTestGivenDis, True)
DDist(False: 0.502262, True: 0.497738)
```

Exercise 8.3 Does the result above surprise you? What happens if the prevalence of disease in the population is one in a million? One in ten?

Total Probability

Finally, we can implement the law of total probability straightforwardly in Python. Given a distribution $\Pr(A)$, called `PA`, and $\Pr(B \mid A)$, called `PBgA`, we compute $\Pr(B)$. We do this by constructing the joint distribution and then marginalizing out A (which is the variable with index 0).

To compute the probability distribution of test results in the example above, we can do:

```
>>> dist.totalProbability(pDis, pTestGivenDis)
DDist(False: 0.998011, True: 0.001989)
```

7.5 Modeling with distributions

When we have a small number of discrete states, it is relatively easy to specify probability distributions. But, as domains become more complex, we will need to develop another PCAP system, just for constructing distributions. In this section, we'll describe a collection of relatively standard primitive distributions, and a method, called a *mixture distribution* for combining them, and show how they can be implemented in Python.

7.5.1 Primitives

Delta

Sometimes we'd like to construct a distribution with all of the probability mass on a single element. Here's a handy way to create *delta* distributions, with a probability spike on a single element:

```
def deltaDist(v):
    return DDist({v:1.0})
```

Uniform

Another common distribution is the *uniform* distribution. On a discrete set of size n , it assigns probability $1/n$ to each of the elements:

```
def uniformDist(elts):
    p = 1.0 / len(elts)
    return DDist(dict([(e, p) for e in elts]))
```

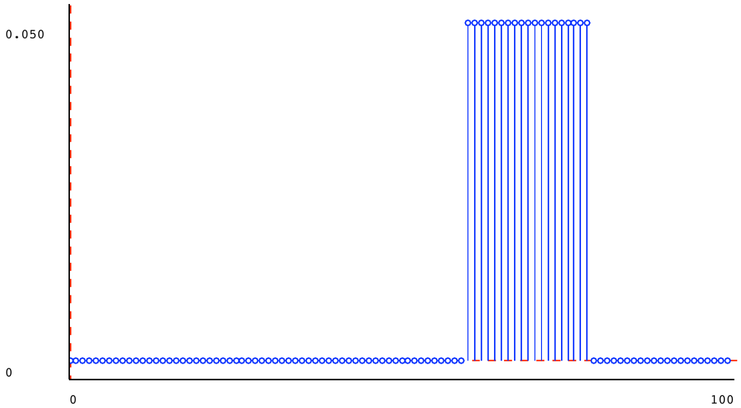
Square

There are some distributions that are particularly valuable in numeric spaces. Since we are only dealing with discrete distributions, we will consider distributions on the integers.

One useful distribution on the integers is a *square distribution*. It is defined by parameters *lo* and *hi*, and assigns probability

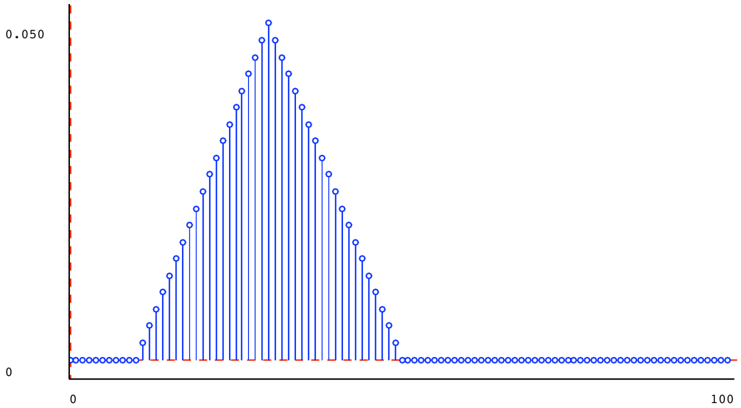
$$p = \frac{1}{hi - lo}$$

to all integers from lo to $hi - 1$. Here is a square distribution (from 60 to 80):



Because it is non-zero on 20 values, those values have probability 0.05 .

Another useful distribution is a *triangle distribution*. It is defined by parameters *peak* and *halfWidth*. It defines a shape that has its maximum value at index *peak*, and has linearly decreasing values at each of $halfWidth - 1$ points on either side of the peak. The values at the indices are scaled so that they sum to 1. Here is a triangular distribution with peak 30 and half-width 20.



7.5.2 Mixture distribution

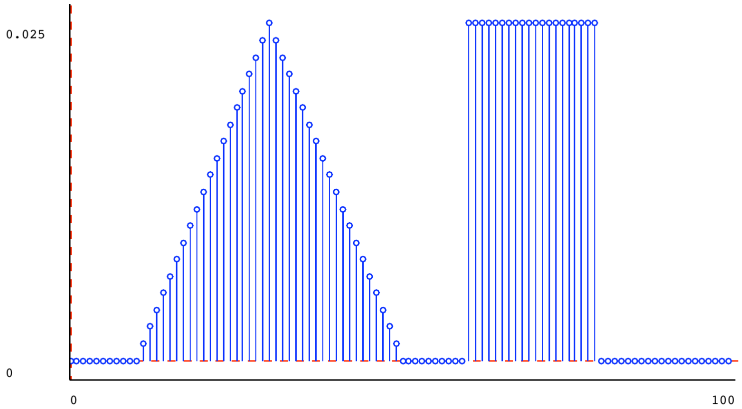
We can combine distributions by *mixing* them. To create a mixture distribution, we specify two distributions, d_1 and d_2 and a *mixing parameter* p , with $0 \leqslant p \leqslant 1$. The intuition is that, to draw an element from a mixture distribution, first we first flip a coin that comes up heads with probability p . If it is heads, then we make a random draw from d_1 and return that; otherwise we make a random draw from d_2 and return it. Another way to see it is that, if we think of a random variable D_1 having distribution d_1 and another random variable D_2 having distribution d_2 , then

$$\Pr_{mix}(x) = p \Pr(D_1 = x) + (1 - p) \Pr(D_2 = x)$$

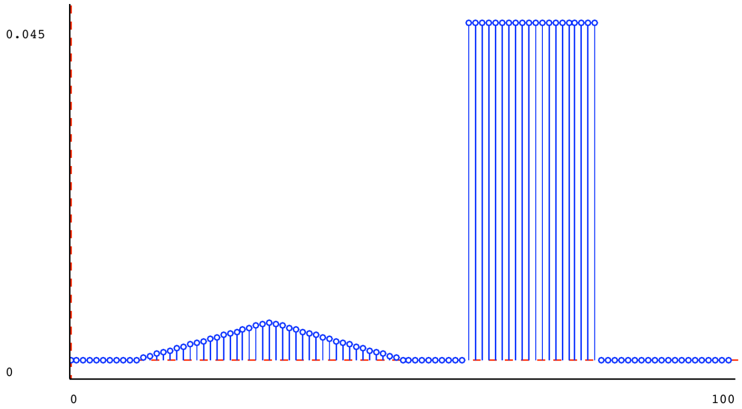
that is, the probability of an element x under the mixture distribution is p times its probability under distribution d_1 plus $1 - p$ times its probability under distribution d_2 .

Exercise 8.4 Convince yourself that if both d_1 and d_2 are proper probability distributions, in that they sum to 1 over their domains, then any mixture of them will also be a proper probability distribution.

We can make a mixture of the square and triangle distributions shown above, with mixture parameter 0.5:



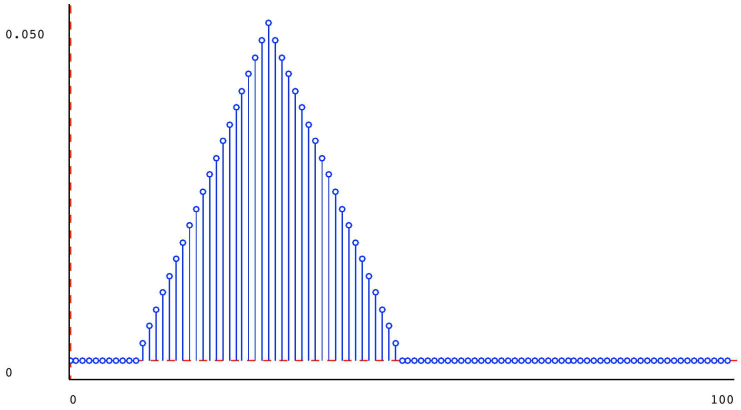
Here it is, with mixture parameter 0.9, where the square is d_1 and the triangle is d_2 :



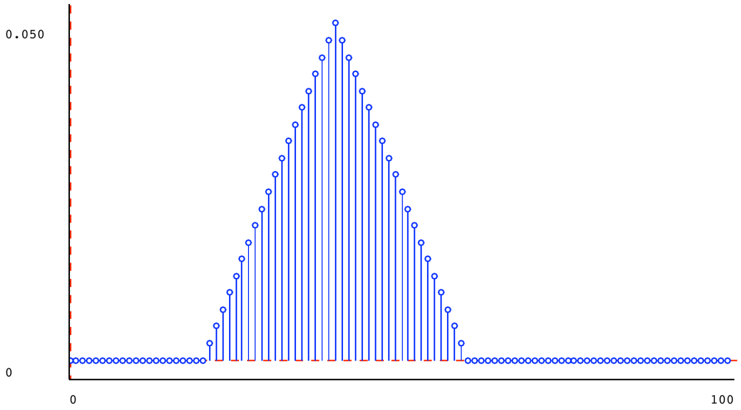
To implement a mixture distributions, we have two choices. One would be to go through the supports of both component distributions and create a new explicit `DDist`. Below, we have taken the 'lazy' approach, similar to the way we handled signal composition. We define a new class that stores the two component distributions and the mixture parameter, and computes the appropriate probabilities as necessary.

Here are some example mixture distributions, created in Python and plotted below.

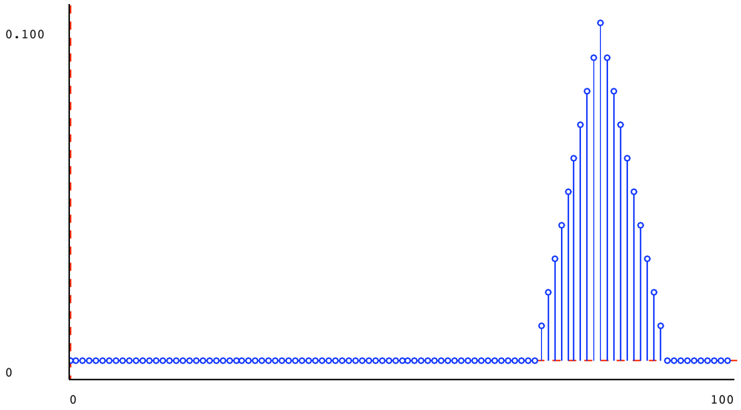
```
t1 = dist.triangleDist(30, 20)
t2 = dist.triangleDist(40, 20)
t3 = dist.triangleDist(80, 10)
s1 = dist.squareDist(0, 100)
s2 = dist.squareDist(60, 80)
m1 = dist.mixture(t1, t2, 0.5)
m2 = dist.mixture(s1, s2, 0.95)
m3 = dist.mixture(t1, t3, 0.5)
m4 = dist.mixture(t1, t3, 0.9)
m5 = dist.mixture(m2, m4, 0.5)
```



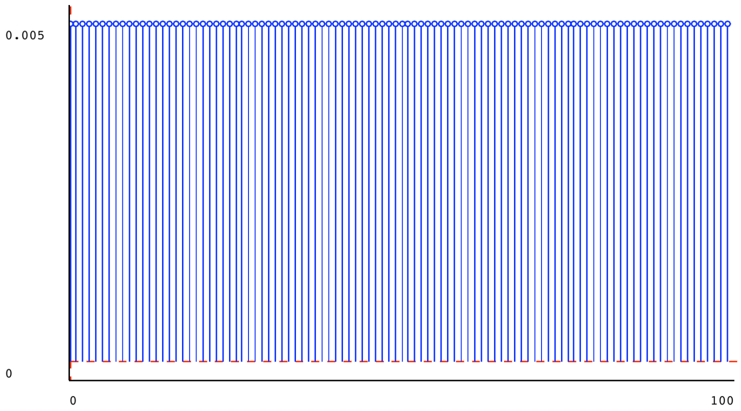
t1



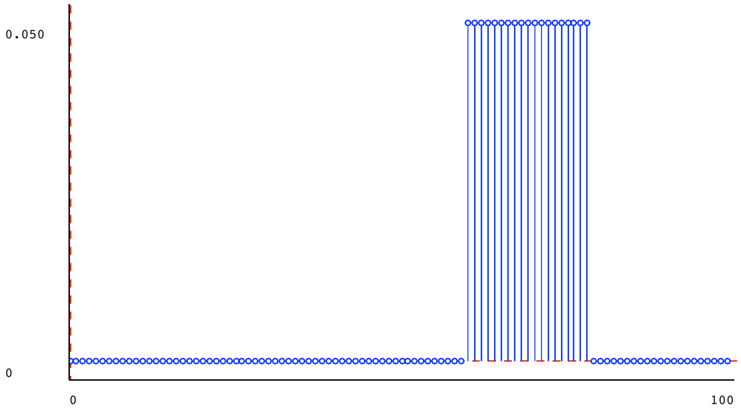
t2



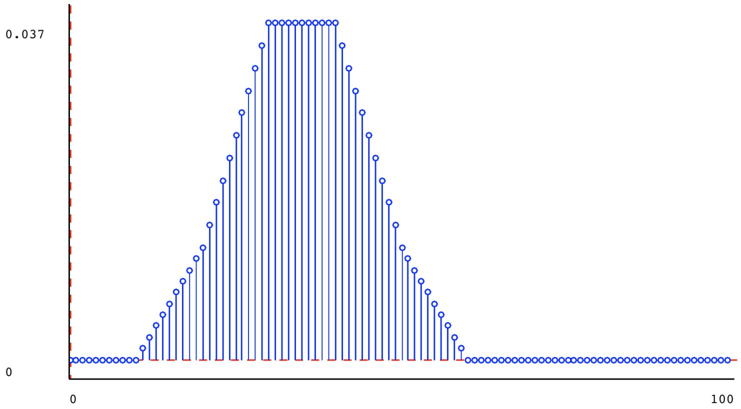
t3



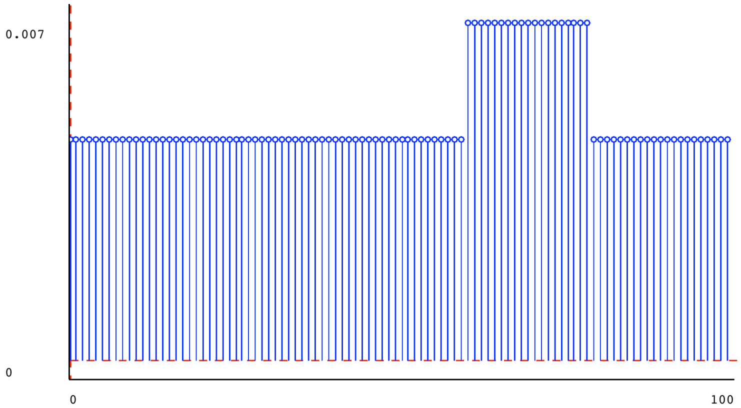
s1



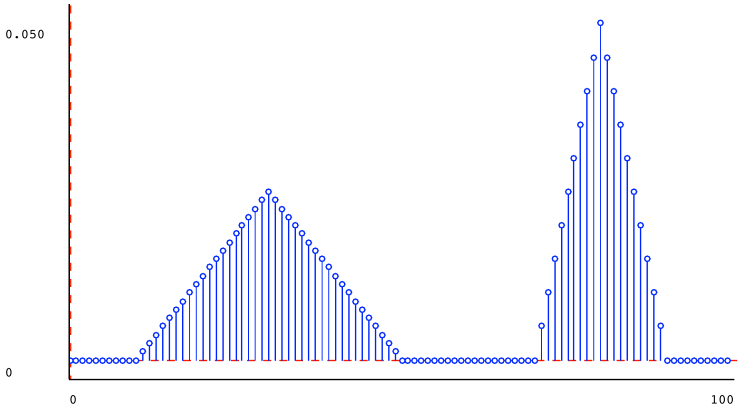
s2



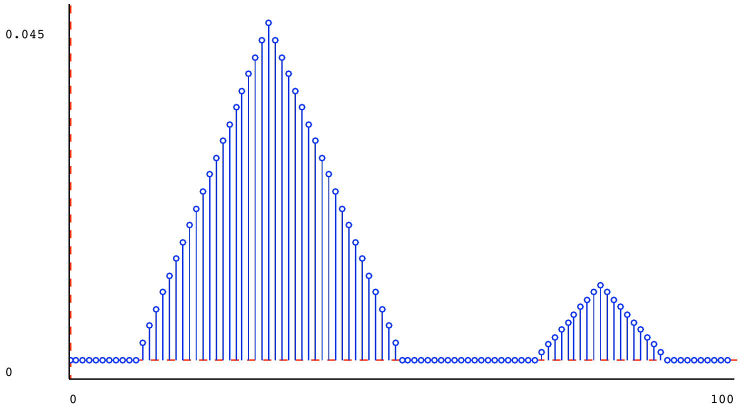
m1



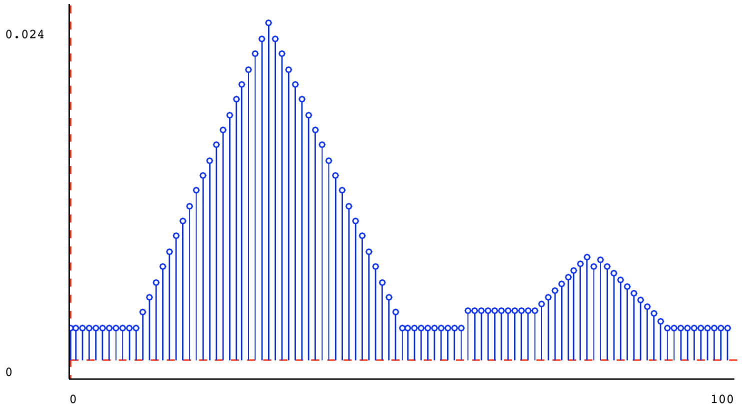
m2



m3



m4



m5

7.6 Stochastic state machines

As we saw earlier, a state machine is a model of some process that changes over time. LTI systems are one kind of state machine, in which the state is some vector of previous inputs and outputs, and the output at each step is a linear function of the input and the values in the state. LTI systems are *infinite state*: the possible internal states are vectors of real numbers, and it is generally not the case that they will ever revisit a state. We also looked at *finite state machines*, in which we could characterize the transition function and output function using simple tables.

In this section, we will consider state machines that have a finite number of possible states, but are more interesting in that they don't behave deterministically. Instead of the next state being determined from the previous state and input by looking them up in a table, the next state will be *drawn from a probability distribution* that depends on the previous state and input. The output generated by the machine will be drawn from a probaiblity distriution, as well. The general case is pretty complicated, so we will work up to it in stages.

7.6.1 Markov chains

We'll start by thinking just about state transitions, and not worry about inputs or outputs (if you want to, you can think of the case where the output is equal to the state of the machine, and where the next state depends only on the previous state, and not on the input). A finite state machine whose next state depends probabilistically on the previous state is called a *Markov chain*.

Mathematically, we can specify a Markov chain with three components:

- **States** $\mathcal{S}$
- **Initial state distribution** $\Pr(S_0)$
- **Transition distribution** $\Pr(S_{t+1} \mid S_t)$. Because the process is time-invariant, this is the same for all t .

There is a finite set of possible states $\mathcal{S}$. We will use random variables S_t to stand for the state of the system at time t ; these random variables can have values in $\mathcal{S}$.

The initial state, S_0 , is a random variable: we don't even (necessarily) know where we will start! We specify a distribution over the starting state with $\Pr(S_0)$.

Then, to specify how the state changes over time, we have to specify a conditional probability distribution $\Pr(S_{t+1} \mid S_t)$. Given a state at some time step t , called S_t , it specifies a distribution over the state at the next time step, S_{t+1} . Markov chains are *time invariant*: that is, although the state may change over time, the probability distribution governing these changes stays constant.

Furthermore their state transitions are *Markov*: that is, the state at time $t + 1$ is conditionally independent of all previous states, given the state at time t . Another way to say that is: the state at time t is all you need to make the best possible prediction of the state at time $t + 1$; knowing any or all of the states before that won't help you make a better prediction.

As a very simple example, let's consider a copy machine: we'll model it in terms of two possible internal states: *good* and *bad*. Here is a specification of it.

- **States:** $\{\mathrm{good}, \mathrm{bad}\}$
- **Initial state distribution:**

$$\Pr(S_0) = \{\mathrm{good} : 0.9, \mathrm{bad} : 0.1\}$$

- **Transition distribution:**

$$\Pr(S_{t+1} \mid S_t) = \begin{cases} \{\mathrm{good} : 0.7, \mathrm{bad} : 0.3\} \mathrm{if} S_t = \mathrm{good} \\ \{\mathrm{good} : 0.1, \mathrm{bad} : 0.9\} \mathrm{if} S_t = \mathrm{bad} \end{cases}$$

It will initially start out in the state *good* (meaning that it is basically functioning well) with reasonably high probability (0.9). But, its state may change on every time step. For concreteness, let's assume that a "time step" for this process occurs every time we use the machine to make a copy.

Remember that the transition distribution is a conditional probability distribution, and that a conditional distribution is actually a function from values of the variable that is being conditioned on (in this case, S_t) to distributions over the variable on the left (in this case, S_{t+1}). This particular transition distribution says that, if the machine was in a *good* state at time t , then with probability 0.7 it will stay good, and with probability 0.3 , it will transition to the *bad* state at time $t+1$. (That's a pretty terrible machine!). If it is in a *bad* state at time t , then with probability 0.1 it miraculously becomes good, and with probability 0.9 it stays bad at time $t + 1$.

Python representation

We can represent these basic distributions in Python using the `DDist` class that we have already developed. First, we have the initial state distribution, which is quite straightforward:

```
initialStateDistribution = dist.DDist({'good': 0.9, 'bad': 0.1})
```

The transition distribution is a conditional probability distribution:

```
def transitionDistribution(oldState):
    if oldState == 'good':
        return dist.DDist({'good' : 0.7, 'bad' : 0.3})
    else:
        return dist.DDist({'good' : 0.1, 'bad' : 0.9})
```

Finally, we can define a new class, called `MarkovChain`.

```
class MarkovChain:
    def __init__(self, startDistribution, transitionDistribution)
        self.startDistribution = startDistribution
        self.transitionDistribution = transitionDistribution
```

Now, we can define our copy machine:

```
copyMachine = MarkovChain(initialStateDistribution, transitionDistribution)
```

Questions about Markov chains

There are a number of interesting questions we can ask about a Markov chain. Let's explore how to answer them with the probability theory we know.

Probability of a sequence

One might be interested in the question, how likely is it that the system will go through some particular sequence of states $s_0, s_1, \ldots, s_T$. That is, we're interested in

$$\Pr(S_0 = s_0, S_1 = s_1, \ldots, S_T = s_T)$$

We can use the operation of conditioning to rewrite this as:

$$\Pr(S_T = s_T \mid S_{T-1} = s_{T-1}, \ldots, S_0 = s_0) \cdot \Pr(S_{T-1} = s_{T-1} \mid S_{T-2} = s_{T-2} \ldots, S_0 = s_0) \cdot \\ \ldots \cdot \Pr(S_1 = s_1 \mid S_0 = s_0) \cdot \Pr(S_0 = s_0)$$

That's still pretty ugly. But, because of the Markov property, we can simplify it to:

$$\Pr(S_T = s_T \mid S_{T-1} = s_{T-1}) \cdot \Pr(S_{T-1} = s_{T-1} \mid S_{T-2} = s_{T-2}) \cdot \ldots \cdot \Pr(S_1 = s_1 \mid S_0 = s_0) \cdot \Pr(S_0 = s_0)$$

which, if we're feeling fancy, we can finally write as:

$$\Pr(S_0 = s_0, S_1 = s_1, \ldots, S_T = s_T) = \Pr(S_0 = s_0) \prod_{t=0}^{T-1} \Pr(S_{t+1} = s_{t+1} \mid S_t = s_t)$$

Example 8.9

What is the probability that our copy machine is good for three copies, when we take it out of the box? That is, what is

$$\Pr(S_0 = \text{good}, S_1 = \text{good}, S_2 = \text{good})$$

We can use the definition above to get:

$$\Pr(S_2 = \text{good} \mid S_1 = \text{good}) \cdot \Pr(S_1 = \textit{good} \mid S_0 = \text{good}) \Pr(S_0 = \text{good})$$

All those probabilities are given in the initial distribution and the transition distribution. So, we have

$$\Pr(S_0 = \text{good}, S_1 = \text{good}, S_2 = \text{good}) = 0.7 \cdot 0.7 \cdot 0.9$$

Example 8.10 What is the probability that machine will start out bad at time 0, be bad at times 1 and 2, and then miraculously start to work when we bring it back to Best Buy at time 3?

Distribution at time t

Rather than asking about a particular trajectory through the state space, we might want to know, more generally, how likely the machine is to be in some state at a particular time (without caring so much about how it got there). That is, we could be interested in:

$$\Pr(S_T = s_T)$$

This problem seems like it might be tricky, but we can apply some tools from the previous section. Mostly we will be interested in the law of total probability. We can write

$$\Pr(S_T = s_T) = \sum_{s_0,\ldots,s_{T-1}} \Pr(S_0 = s_0, S_1 = s_1, \ldots, S_T = s_T)$$

That says that, in order to think about the probability that the state of the system at time T is s_T , we have to marginalize over all possible sequences states that end in s_T . Yikes!! If T is very big, then that's a lot of sequences.

Luckily, the Markov property comes to the rescue. To determine the distribution over states at time T , it is sufficient to know the distribution at the previous time step. We can exploit that property to develop a more efficient algorithm.

Let's start by thinking about the state distribution at time 0. That's easy. It's just the starting distribution $\Pr(S_0)$, which we know.

Now, how do we get the distribution over the state at time 1? We can make the joint on S_0 and S_1 and then marginalize out S_0 .

$$\Pr(S_1 = s_1) = \sum_{s_0} \Pr(S_0 = s_0, S_1 = s_1) = \sum_{s_0} \Pr(S_1 = s_1 \mid S_0 = s_0) \Pr(S_0 = s_0)$$

We even have a compact way of thinking of this as the law of total probability. This should now suggest a way of proceeding in general:

$$\Pr(S_{t+1} = s_{t+1}) = \sum_{s_t} \Pr(S_t = s_t, S_{t+1} = s_{t+1}) = \sum_{s_t} \Pr(S_{t+1} = s_{t+1} \mid S_t = s_t) \Pr(S_t = s_t)$$

This is a kind of *dynamic programming* algorithm: it makes use of intermediate results (the occupation disributions at earlier time steps) to efficiently calculate a final result, without enumerating all possible state sequences.

Example 13 What is the running time of your algorithm in a domain with n states as a function of t?

Limiting distribution

For some distributions, if we let t approach ∞ , the occupation distribution at time t converges to some fixed distribution. We can call this the *stationary* or *limiting* distribution. The exact condition under which such a distribution exists is a little bit complicated, but we can definitely guarantee that it exists if $\Pr(S_{t+1} = s_i \mid S_t = s_j) > 0$ for all s_i, s_j : that is, if every state has a non-zero chance of transitioning to every other state.

Let's call the limiting distribution $\Pr(S_\infty)$. It will have the property that:

$$\Pr(S_\infty = s') = \sum_s \Pr(S_{t+1} = s' \mid S_t = s) \Pr(S_\infty = s)$$

That is, that applying the transition distribution to the limiting distribution just gets you the limiting distribution back again.

You can find a limiting distribution by solving a set of linear equations. We'll just do it by example, for the copy machine Markov chain:

$$\Pr(S_\infty = \mathrm{good}) = \Pr(S_{t+1} = \mathrm{good} \mid S_t = \mathrm{good}) \Pr(S_\infty = \mathrm{good}) + \Pr(S_{t+1} = \mathrm{good} \mid S_t = \mathrm{bad}) \Pr(S_\infty = \mathrm{bad})$$
$$\Pr(S_\infty = \mathrm{bad}) = \Pr(S_{t+1} = \mathrm{bad} \mid S_t = \mathrm{good}) \Pr(S_\infty = \mathrm{good}) + \Pr(S_{t+1} = \mathrm{bad} \mid S_t = \mathrm{bad}) \Pr(S_\infty = \mathrm{bad})$$

We can use shorter names for the variables: g for $\Pr(S_\infty = \mathrm{good}$ and b for $\Pr(S_\infty = \mathrm{bad})$, and plug in numbers to get a simple system of equations:

$$\begin{aligned} g &= 0.7g + 0.1b \\ b &= 0.3g + 0.9b \\ b + g &= 1 \end{aligned}$$

We add the last one because we are looking for a probability distribution, so our values have to sum to 1. The result in this case is $b = 0.25, g = 0.75$.

7.6.2 Hidden Markov models

A *hidden Markov model* (HMM) is a Markov chain in which we are not allowed to observe the state.

Now we can return to the application of primary interest: there is a system moving through some sequence of states over time, but instead of getting to see the states, we only get to make a sequence of observations of the system, where the observations give partial, noisy information about the actual underlying state. The question is: what can we infer about the current state of the system give the history of observations we have made?

Let's return to our copy machine: since we don't get to see inside the machine, we can only make observations of the copies it generates; they can either be *perfect*, *smudged*, or *all black*.

In an HMM, we extend a Markov chaing by thinking also about the observation at each step. So, we'll use random variables random variables $O_0, O_1, \ldots$ to model the observation at each time step.

Our problem will be to compute a probability distribution over the state at some time $t + 1$ given the past history of observations $o_0 \ldots, o_t$; that is, to compute

$$\Pr(S_{t+1} \mid O_0 = o_0 \ldots, O_t = o_t) \quad .$$

Along with the Markov assumption, we will assume that the state at time t is sufficient to determine the probability distribution over the observation at time t , and that the distribution governing the observations is constant.

So, in order to specify our model of how this system works, we need to provide three probability distributions:

- **Initial state distribution:**
$$\Pr(S_0) \quad .$$
- **State transition model:**
$$\Pr(S_{t+1} \mid S_t) \quad ,$$
- **Observation model:** This is often also called the *sensor model*. It is described by the conditional probability distribution
$$\Pr(O_t \mid S_t) \quad ,$$
which specifies for each possible state of the system, s , a distribution over the observations that will be obtained when the system is in that state.

7.6.3 Copy machine example

To make an HMM model for our copy machine example, we just need to add an observation distribution:

- **Observation distribution:** $\Pr(O_t \mid S_t) = \begin{cases} \{\mathrm{perfect} : 0.8, \mathrm{smudged} : 0.1, \mathrm{black} : 0.1\} \text{if } S_t = \mathrm{good} \\ \{\mathrm{perfect} : 0.1, \mathrm{smudged} : 0.7, \mathrm{black} : 0.2\} \text{if } S_t = \mathrm{bad} \end{cases}$

7.7 State estimation

Now, given the model of the way a system changes over time, and how its outputs reflect its internal state, we can do *state estimation*. The problem of state estimation is to take a sequence of observations, and determine the sequence of hidden states of the system. Of course, we won't be able to determine that sequence exactly, but we can derive some useful probability distributions.

We will concentrate on the problem of *filtering* or *sequential state estimation*, in which we imagine sitting and watching the stream of observations go by, and we are required, on each step, to produce a state estimate, in the form

$$\Pr(S_{t+1} \mid O_0 = o_0, \ldots, O_t = o_t)$$

We will develop a procedure for doing this by working through a few steps of the example with the copy machine, and then present it more generally.

7.7.1 Our first copy

Let's assume we get a brand new copy machine in the mail, and we think it is probably (0.9) good, but we're not entirely sure. We print out a page, and it looks perfect. Yay! Now, what do we believe about the state of the machine? We'd like to compute

$$\Pr(S_1 \mid O_0 = \mathrm{perfect}) \quad .$$

We'll do this in two steps. First, we'll consider what information we have gained about the machine's state at time 0 from the observation, and then we'll consider what state it might have transitioned to on step 1.

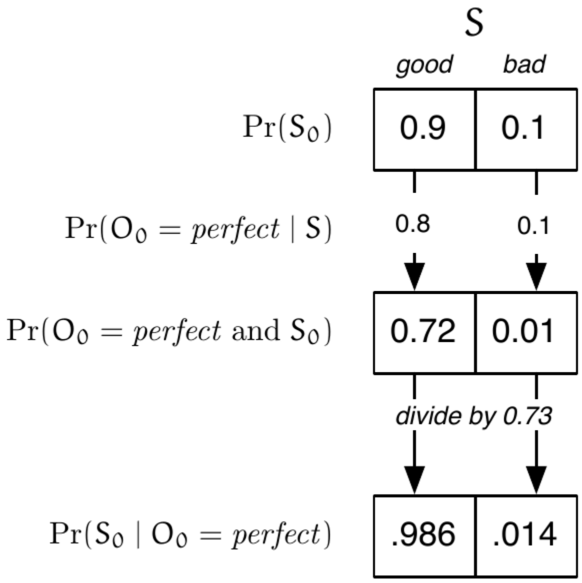
What information do we gain from knowing that the machine's first copy was perfect? We can use Bayesian reasoning to form the joint distribution between the state and observations in general, and then condition on the observation we actual received. The joint distribution has the form

		O		
		perfect	*smudged*	*black*
S	*good*	0.72	0.09	0.09
	bad	0.01	0.07	0.02

Now, conditioning on the actual observation, $O_0 = \mathtt{perfect}$, we extract the column corresponding to the observation, $\{0.72, 0.01\}$, and divide by the sum, 0.73 , to get the distribution

$$\mathrm{Pr}(S_0 \mid O_0 = \mathtt{perfect}) = \{\mathtt{good} : 0.986, \mathtt{bad} : 0.014\}$$

Here is a schematic version of this update rule, which is a good way to think about computing it by hand. Rather than creating the whole joint distribution and then conditioning by selecting out a single column, we just create the column we know we're going to need (based on the observation we got):


S
good
bad
$\mathrm{Pr}(S_0)$
0.9
0.1
$\mathrm{Pr}(O_0 = \mathit{perfect} \mid S)$
0.8
0.1
$\mathrm{Pr}(O_0 = \mathit{perfect}\text{ and }S_0)$
0.72
0.01
divide by 0.73
$\mathrm{Pr}(S_0 \mid O_0 = \mathit{perfect})$
.986
.014

Because we will use it in later calculations, we will define B'_0 as an abbreviation:

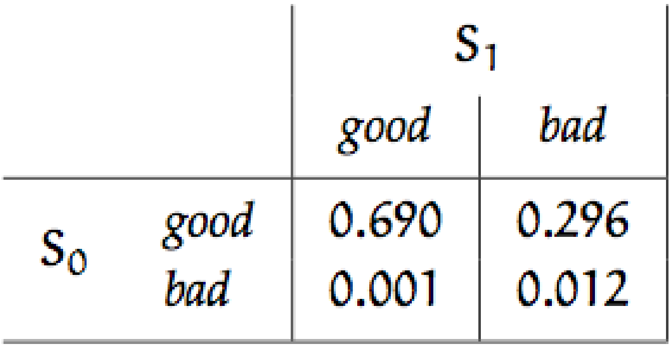
$$B'_0 = \mathrm{Pr}(S_0 \mid O_0 = \mathtt{perfect}) \quad ;$$

that is, our belief that the system is in state s on the 0th step, after having taken the actual observation o_0 into account. This update strategy computes $B'_0(s)$ for all s , which we'll need in order to do further calculations.

Now, we can think about the consequences of the passage of one step of time. We'd like to compute $\mathrm{Pr}(S_1 \mid O_0 = \mathtt{perfect})$. Note that we are not yet thinking about the observation we'll get on step 1; just what we know about the machine on step 1 having observed a perfect copy at step 0.

What matters is the probability of making transitions between states at time 0 and states at time 1. We can make this relationship clear by constructing the joint probability distribution on S_0 and

S_1 (it is actually conditioned on $O_0 = \mathrm{perfect}$). So, $\Pr(S_0, S_1 \mid O_0 = \mathrm{perfect})$ can be constructed from $\Pr(S_0 \mid O_0 = \mathrm{perfect})$ (which, it is important to remember, is a distribution on S_0) and $\Pr(S_1 \mid S_0)$, which is our transition model:



		S_1	
		good	*bad*
S_0	*good*	0.690	0.296
	bad	0.001	0.012

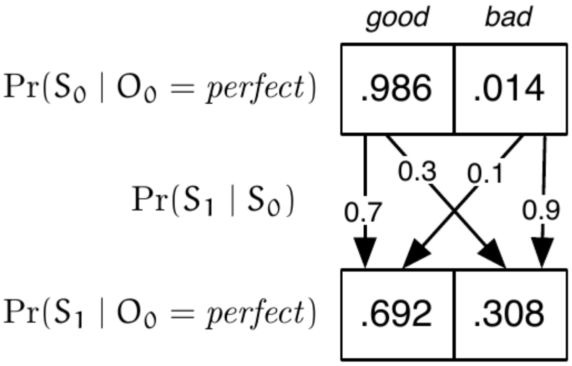
Now, we have never really known the value of S_0 for sure, and we can never really know it; we'd like to concentrate all of our information in a representation of our knowledge about S_1 . We can do that by computing the marginal distribution on S_1 from this joint. Summing up the columns, we get

$$\Pr(S_1 \mid O_0 = \mathrm{perfect}) = \{\mathrm{good} : 0.692, \mathrm{bad} : 0.308\}$$

This is an application of the law of total probability.

We'll give this distribution, $\Pr(S_1 \mid O_0 = \mathrm{perfect})$, that is, everything we know about the machine after the first observation and transition, the abbreviation B_1 .

Here is a schematic version of the transition update:

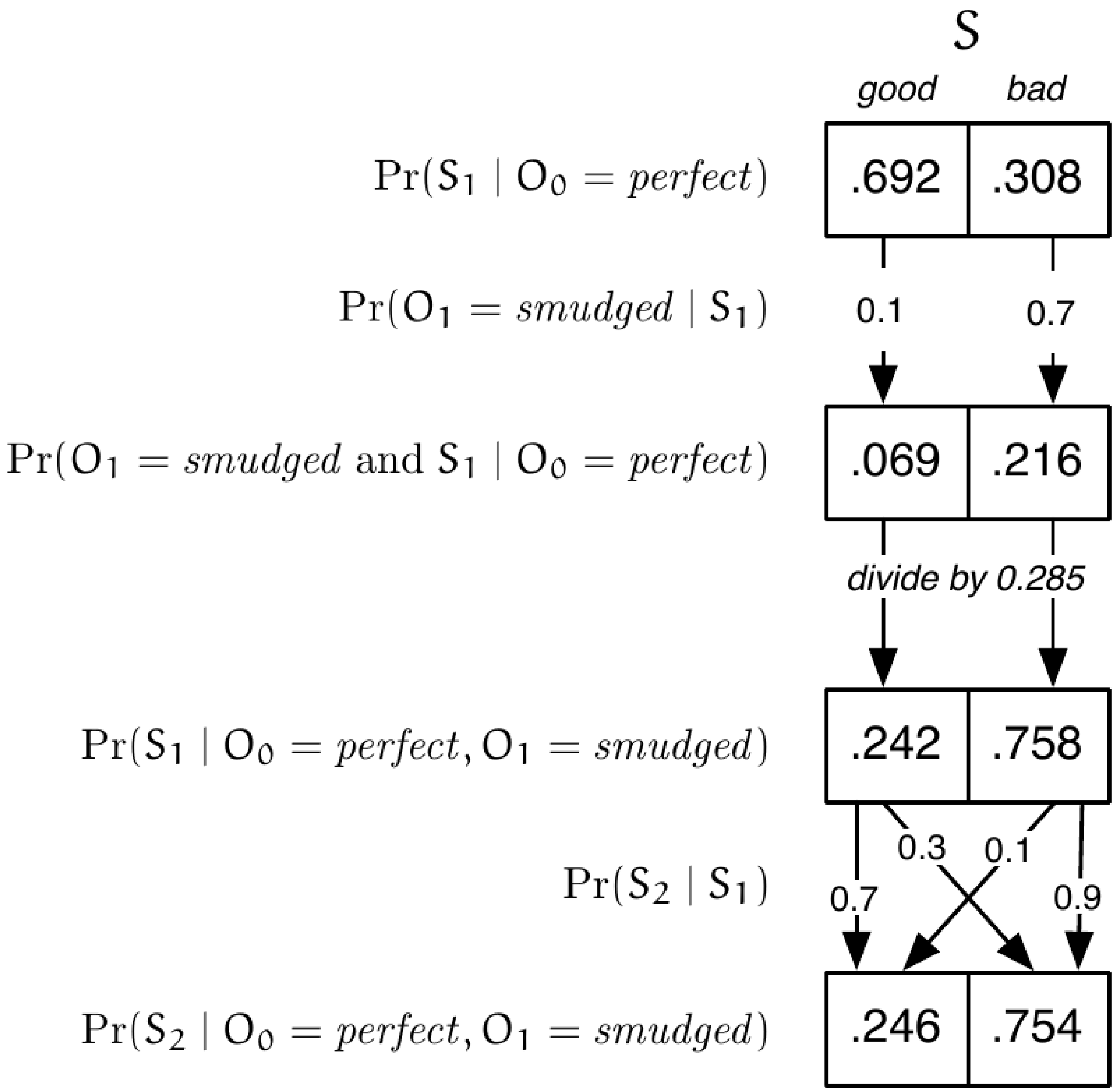


You can see that there are two ways the copier could be in a good state at time 1: because it was in a good state at time 0 (probability 0.986) and made a transition to a good state at time 1 (probability 0.7) or because it was in a bad state at time 0 (probability 0.014) and made a transition to a good state at time 1 (probability 0.1). So, the resulting probability of being in a good state is $0.986 \cdot 0.7 + 0.014 \cdot 0.1 = 0.692$. The reasoning for ending in a bad state is the same.

7.7.2 Our second copy

Now, let's imagine we print another page, and it's smudged. We want to compute $\Pr(S_2 \mid O_0 = \mathrm{perfect}, O_1 = \mathrm{smudged})$. This can be computed in two stages as before. We start with B_1 , which already has the information that $O_0 = \mathrm{perfect}$ incorporated into it. Our job will be to fold in the information that $O_1 = \mathrm{smudged}$, and then the passage of another step of time.

- Construct a joint distribution from B_1 and $\Pr(O_1 \mid S_1)$, and condition on $O_1 = smudged$ to get B_1' . This is a Bayesian reasoning step.
- Construct a joint distribution from B_1' and $\Pr(S_2 \mid S_1)$ and marginalize out S_1 to get B_2 . This is a law-of-total-probability step.


S
good
bad
$\Pr(S_1 \mid O_0 = perfect)$
.692
.308
$\Pr(O_1 = smudged \mid S_1)$
0.1
0.7
$\Pr(O_1 = smudged \text{ and } S_1 \mid O_0 = perfect)$
.069
.216
divide by 0.285
$\Pr(S_1 \mid O_0 = perfect, O_1 = smudged)$
.242
.758
$\Pr(S_2 \mid S_1)$
0.3
0.1
0.7
0.9
$\Pr(S_2 \mid O_0 = perfect, O_1 = smudged)$
.246
.754

Ow. Now we're pretty sure our copy machine is no good. Planned obsolescence strikes again!

7.8 General state estimation

Now we'll write out the state-update procedure for HMMs in general. As a reminder, here are the random variables involved:

- State at each time $S_0, \ldots, S_T$
- Observation at each time $O_0, \ldots, O_T$

Here are the components of the model:

- **Initial distribution** $\Pr(S_0)$
- **Observation distribution** $\Pr(O_t \mid S_t)$. Because the process is time-invariant, this is the same for all t .
- **Transition distribution** $\Pr(S_{t+1} \mid S_t)$. Because the process is time-invariant, this is the same for all t . Think of i as selecting a particular conditional transition distribution to be used in the update.

Now, here is the update procedure. Assume that we have a *belief state* at time t , corresponding to $\Pr(S_t \mid O_{0..t-1} = o_{0..t-1})$. Then we proceed in two steps:

- **Observation update, given** o_t :

$$\Pr(S_t \mid O_{0..t} = o_{0..t}) \\ = \frac{\Pr(O_t{=}o_t|S_t)\Pr(S_t|O_{0..t-1}{=}o_{0..t-1})}{\Pr(O_t{=}o_t|O_{0..t-1}{=}o_{0..t-1})}$$

- **Transition update, given** i_t :

$$\Pr(S_{t+1} \mid O_{0..t} = o_{0..t}) \\ = \sum_r \Pr(S_{t+1} \mid S_t = r)\Pr(S_t = r \mid O_{0..t} = o_{0..t})$$

A very important thing to see about these definitions is that they enable us to build what is known as a *recursive* state estimator. (Unfortunately, this is a different use of the term "recursive" than we're used to from programming languages). If we define our belief at time t ,

$$B_t = \Pr(S_t \mid O_{0..t-1} = o_{0..t-1})$$

and our belief after making the observation update to be

$$B'_t = \Pr(S_t \mid O_{0..t} = o_{0..t}) \quad ,$$

then after each observation and transition, we can update our belief state, to get a new B_t . Then, we can forget the particular observation we had, and just use the B_t and o_t to compute B_{t+1} . This is justified because the observations are conditionally independent given the state, and so this is like the example we saw earlier of using Bayes' rule to incorporate multiple pieces of evidence sequentially.

Algorithmically, we can run a loop of the form:

- **Condition on actual observation** $O_t = o_t$ **.**

$$B'(s) = \frac{\Pr(O_t{=}o_t|S_t{=}s)B(s)}{\sum_r \Pr(O_t{=}o_t|S_t{=}r)B(r)}$$

- **Make transition.**

$$B(s) = \sum_r \Pr(S_{t+1} = s \mid S_t = r)B'(r)$$

where B is initialized to be our initial belief about the state of the system.