Hypothesis and Inference

It is the mark of a truly intelligent person to be moved by statistics.
—George Bernard Shaw

What will we do with all this statistics and probability theory? The *science* part of data science frequently involves forming and testing *hypotheses* about our data and the processes that generate it.

Statistical Hypothesis Testing

Often, as data scientists, we'll want to test whether a certain hypothesis is likely to be true. For our purposes, hypotheses are assertions like "this coin is fair" or "data scientists prefer Python to R" or "people are more likely to navigate away from the page without ever reading the content if we pop up an irritating interstitial advertisement with a tiny, hard-to-find close button" that can be translated into statistics about data. Under various assumptions, those statistics can be thought of as observations of random variables from known distributions, which allows us to make statements about how likely those assumptions are to hold.

In the classical setup, we have a *null hypothesis*, H_0, that represents some default position, and some alternative hypothesis, H_1, that we'd like to compare it with. We use statistics to decide whether we can reject H_0 as false or not. This will probably make more sense with an example.

Example: Flipping a Coin

Imagine we have a coin and we want to test whether it's fair. We'll make the assumption that the coin has some probability p of landing heads, and so our null hypothesis

is that the coin is fair—that is, that $p = 0.5$. We'll test this against the alternative hypothesis $p \neq 0.5$.

In particular, our test will involve flipping the coin some number, n, times and counting the number of heads, X. Each coin flip is a Bernoulli trial, which means that X is a Binomial(n,p) random variable, which (as we saw in Chapter 6) we can approximate using the normal distribution:

```python
from typing import Tuple
import math

def normal_approximation_to_binomial(n: int, p: float) -> Tuple[float, float]:
    """Returns mu and sigma corresponding to a Binomial(n, p)"""
    mu = p * n
    sigma = math.sqrt(p * (1 - p) * n)
    return mu, sigma
```

Whenever a random variable follows a normal distribution, we can use `normal_cdf` to figure out the probability that its realized value lies within or outside a particular interval:

```python
from scratch.probability import normal_cdf

# The normal cdf _is_ the probability the variable is below a threshold
normal_probability_below = normal_cdf

# It's above the threshold if it's not below the threshold
def normal_probability_above(lo: float,
                             mu: float = 0,
                             sigma: float = 1) -> float:
    """The probability that an N(mu, sigma) is greater than lo."""
    return 1 - normal_cdf(lo, mu, sigma)

# It's between if it's less than hi, but not less than lo
def normal_probability_between(lo: float,
                               hi: float,
                               mu: float = 0,
                               sigma: float = 1) -> float:
    """The probability that an N(mu, sigma) is between lo and hi."""
    return normal_cdf(hi, mu, sigma) - normal_cdf(lo, mu, sigma)

# It's outside if it's not between
def normal_probability_outside(lo: float,
                               hi: float,
                               mu: float = 0,
                               sigma: float = 1) -> float:
    """The probability that an N(mu, sigma) is not between lo and hi."""
    return 1 - normal_probability_between(lo, hi, mu, sigma)
```

We can also do the reverse—find either the nontail region or the (symmetric) interval around the mean that accounts for a certain level of likelihood. For example, if we want to find an interval centered at the mean and containing 60% probability, then

we find the cutoffs where the upper and lower tails each contain 20% of the probability (leaving 60%):

```python
from scratch.probability import inverse_normal_cdf

def normal_upper_bound(probability: float,
                       mu: float = 0,
                       sigma: float = 1) -> float:
    """Returns the z for which P(Z <= z) = probability"""
    return inverse_normal_cdf(probability, mu, sigma)

def normal_lower_bound(probability: float,
                       mu: float = 0,
                       sigma: float = 1) -> float:
    """Returns the z for which P(Z >= z) = probability"""
    return inverse_normal_cdf(1 - probability, mu, sigma)

def normal_two_sided_bounds(probability: float,
                            mu: float = 0,
                            sigma: float = 1) -> Tuple[float, float]:
    """
    Returns the symmetric (about the mean) bounds
    that contain the specified probability
    """
    tail_probability = (1 - probability) / 2

    # upper bound should have tail_probability above it
    upper_bound = normal_lower_bound(tail_probability, mu, sigma)

    # lower bound should have tail_probability below it
    lower_bound = normal_upper_bound(tail_probability, mu, sigma)

    return lower_bound, upper_bound
```

In particular, let's say that we choose to flip the coin $n = 1,000$ times. If our hypothesis of fairness is true, X should be distributed approximately normally with mean 500 and standard deviation 15.8:

```python
mu_0, sigma_0 = normal_approximation_to_binomial(1000, 0.5)
```

We need to make a decision about *significance*—how willing we are to make a *type 1 error* ("false positive"), in which we reject H_0 even though it's true. For reasons lost to the annals of history, this willingness is often set at 5% or 1%. Let's choose 5%.

Consider the test that rejects H_0 if X falls outside the bounds given by:

```python
# (469, 531)
lower_bound, upper_bound = normal_two_sided_bounds(0.95, mu_0, sigma_0)
```

Assuming p really equals 0.5 (i.e., H_0 is true), there is just a 5% chance we observe an X that lies outside this interval, which is the exact significance we wanted. Said differ-

ently, if H_0 is true, then, approximately 19 times out of 20, this test will give the correct result.

We are also often interested in the *power* of a test, which is the probability of not making a *type 2 error* ("false negative"), in which we fail to reject H_0 even though it's false. In order to measure this, we have to specify what exactly H_0 being false *means*. (Knowing merely that p is *not* 0.5 doesn't give us a ton of information about the distribution of X.) In particular, let's check what happens if p is really 0.55, so that the coin is slightly biased toward heads.

In that case, we can calculate the power of the test with:

```
# 95% bounds based on assumption p is 0.5
lo, hi = normal_two_sided_bounds(0.95, mu_0, sigma_0)

# actual mu and sigma based on p = 0.55
mu_1, sigma_1 = normal_approximation_to_binomial(1000, 0.55)

# a type 2 error means we fail to reject the null hypothesis,
# which will happen when X is still in our original interval
type_2_probability = normal_probability_between(lo, hi, mu_1, sigma_1)
power = 1 - type_2_probability       # 0.887
```

Imagine instead that our null hypothesis was that the coin is not biased toward heads, or that $p \leq 0.5$. In that case we want a *one-sided test* that rejects the null hypothesis when X is much larger than 500 but not when X is smaller than 500. So, a 5% significance test involves using `normal_probability_below` to find the cutoff below which 95% of the probability lies:

```
hi = normal_upper_bound(0.95, mu_0, sigma_0)
# is 526 (< 531, since we need more probability in the upper tail)

type_2_probability = normal_probability_below(hi, mu_1, sigma_1)
power = 1 - type_2_probability       # 0.936
```

This is a more powerful test, since it no longer rejects H_0 when X is below 469 (which is very unlikely to happen if H_1 is true) and instead rejects H_0 when X is between 526 and 531 (which is somewhat likely to happen if H_1 is true).

p-Values

An alternative way of thinking about the preceding test involves *p-values*. Instead of choosing bounds based on some probability cutoff, we compute the probability—assuming H_0 is true—that we would see a value at least as extreme as the one we actually observed.

For our two-sided test of whether the coin is fair, we compute:

```
def two_sided_p_value(x: float, mu: float = 0, sigma: float = 1) -> float:
    """
    How likely are we to see a value at least as extreme as x (in either
    direction) if our values are from an N(mu, sigma)?
    """
    if x >= mu:
        # x is greater than the mean, so the tail is everything greater than x
        return 2 * normal_probability_above(x, mu, sigma)
    else:
        # x is less than the mean, so the tail is everything less than x
        return 2 * normal_probability_below(x, mu, sigma)
```

If we were to see 530 heads, we would compute:

```
two_sided_p_value(529.5, mu_0, sigma_0)    # 0.062
```

Why did we use a value of 529.5 rather than using 530? This is what's called a *continuity correction*. It reflects the fact that nor mal_probability_between(529.5, 530.5, mu_0, sigma_0) is a better estimate of the probability of seeing 530 heads than nor mal_probability_between(530, 531, mu_0, sigma_0) is.

Correspondingly, normal_probability_above(529.5, mu_0, sigma_0) is a better estimate of the probability of seeing at least 530 heads. You may have noticed that we also used this in the code that produced Figure 6-4.

One way to convince yourself that this is a sensible estimate is with a simulation:

```
import random

extreme_value_count = 0
for _ in range(1000):
    num_heads = sum(1 if random.random() < 0.5 else 0     # Count # of heads
                    for _ in range(1000))                 # in 1000 flips,
    if num_heads >= 530 or num_heads <= 470:              # and count how often
        extreme_value_count += 1                          # the # is 'extreme'

# p-value was 0.062 => ~62 extreme values out of 1000
assert 59 < extreme_value_count < 65, f"{extreme_value_count}"
```

Since the *p*-value is greater than our 5% significance, we don't reject the null. If we instead saw 532 heads, the *p*-value would be:

```
two_sided_p_value(531.5, mu_0, sigma_0)    # 0.0463
```

which is smaller than the 5% significance, which means we would reject the null. It's the exact same test as before. It's just a different way of approaching the statistics.

Similarly, we would have:

```
upper_p_value = normal_probability_above
lower_p_value = normal_probability_below
```

For our one-sided test, if we saw 525 heads we would compute:

```
upper_p_value(524.5, mu_0, sigma_0) # 0.061
```

which means we wouldn't reject the null. If we saw 527 heads, the computation would be:

```
upper_p_value(526.5, mu_0, sigma_0) # 0.047
```

and we would reject the null.

> Make sure your data is roughly normally distributed before using `normal_probability_above` to compute *p*-values. The annals of bad data science are filled with examples of people opining that the chance of some observed event occurring at random is one in a million, when what they really mean is "the chance, assuming the data is distributed normally," which is fairly meaningless if the data isn't.
>
> There are various statistical tests for normality, but even plotting the data is a good start.

Confidence Intervals

We've been testing hypotheses about the value of the heads probability *p*, which is a *parameter* of the unknown "heads" distribution. When this is the case, a third approach is to construct a *confidence interval* around the observed value of the parameter.

For example, we can estimate the probability of the unfair coin by looking at the average value of the Bernoulli variables corresponding to each flip—1 if heads, 0 if tails. If we observe 525 heads out of 1,000 flips, then we estimate *p* equals 0.525.

How *confident* can we be about this estimate? Well, if we knew the exact value of *p*, the central limit theorem (recall "The Central Limit Theorem" on page 80) tells us that the average of those Bernoulli variables should be approximately normal, with mean *p* and standard deviation:

```
math.sqrt(p * (1 - p) / 1000)
```

Here we don't know *p*, so instead we use our estimate:

```
p_hat = 525 / 1000
mu = p_hat
sigma = math.sqrt(p_hat * (1 - p_hat) / 1000)   # 0.0158
```

This is not entirely justified, but people seem to do it anyway. Using the normal approximation, we conclude that we are "95% confident" that the following interval contains the true parameter *p*:

```
normal_two_sided_bounds(0.95, mu, sigma)        # [0.4940, 0.5560]
```

This is a statement about the *interval*, not about *p*. You should understand it as the assertion that if you were to repeat the experiment many times, 95% of the time the "true" parameter (which is the same every time) would lie within the observed confidence interval (which might be different every time).

In particular, we do not conclude that the coin is unfair, since 0.5 falls within our confidence interval.

If instead we'd seen 540 heads, then we'd have:

```
p_hat = 540 / 1000
mu = p_hat
sigma = math.sqrt(p_hat * (1 - p_hat) / 1000) # 0.0158
normal_two_sided_bounds(0.95, mu, sigma) # [0.5091, 0.5709]
```

Here, "fair coin" doesn't lie in the confidence interval. (The "fair coin" hypothesis doesn't pass a test that you'd expect it to pass 95% of the time if it were true.)

p-Hacking

A procedure that erroneously rejects the null hypothesis only 5% of the time will—by definition—5% of the time erroneously reject the null hypothesis:

```python
from typing import List

def run_experiment() -> List[bool]:
    """Flips a fair coin 1000 times, True = heads, False = tails"""
    return [random.random() < 0.5 for _ in range(1000)]

def reject_fairness(experiment: List[bool]) -> bool:
    """Using the 5% significance levels"""
    num_heads = len([flip for flip in experiment if flip])
    return num_heads < 469 or num_heads > 531

random.seed(0)
experiments = [run_experiment() for _ in range(1000)]
num_rejections = len([experiment
                      for experiment in experiments
                      if reject_fairness(experiment)])

assert num_rejections == 46
```

What this means is that if you're setting out to find "significant" results, you usually can. Test enough hypotheses against your dataset, and one of them will almost certainly appear significant. Remove the right outliers, and you can probably get your *p*-value below 0.05. (We did something vaguely similar in "Correlation" on page 64; did you notice?)

This is sometimes called *p-hacking* and is in some ways a consequence of the "inference from *p*-values framework." A good article criticizing this approach is "The Earth Is Round", by Jacob Cohen.

If you want to do good *science*, you should determine your hypotheses before looking at the data, you should clean your data without the hypotheses in mind, and you should keep in mind that *p*-values are not substitutes for common sense. (An alternative approach is discussed in "Bayesian Inference" on page 91.)

Example: Running an A/B Test

One of your primary responsibilities at DataSciencester is experience optimization, which is a euphemism for trying to get people to click on advertisements. One of your advertisers has developed a new energy drink targeted at data scientists, and the VP of Advertisements wants your help choosing between advertisement A ("tastes great!") and advertisement B ("less bias!").

Being a *scientist*, you decide to run an *experiment* by randomly showing site visitors one of the two advertisements and tracking how many people click on each one.

If 990 out of 1,000 A-viewers click their ad, while only 10 out of 1,000 B-viewers click their ad, you can be pretty confident that A is the better ad. But what if the differences are not so stark? Here's where you'd use statistical inference.

Let's say that N_A people see ad A, and that n_A of them click it. We can think of each ad view as a Bernoulli trial where p_A is the probability that someone clicks ad A. Then (if N_A is large, which it is here) we know that n_A/N_A is approximately a normal random variable with mean p_A and standard deviation $\sigma_A = \sqrt{p_A(1 - p_A)/N_A}$.

Similarly, n_B/N_B is approximately a normal random variable with mean p_B and standard deviation $\sigma_B = \sqrt{p_B(1 - p_B)/N_B}$. We can express this in code as:

```python
def estimated_parameters(N: int, n: int) -> Tuple[float, float]:
    p = n / N
    sigma = math.sqrt(p * (1 - p) / N)
    return p, sigma
```

If we assume those two normals are independent (which seems reasonable, since the individual Bernoulli trials ought to be), then their difference should also be normal with mean $p_B - p_A$ and standard deviation $\sqrt{\sigma_A^2 + \sigma_B^2}$.

This is sort of cheating. The math only works out exactly like this if you *know* the standard deviations. Here we're estimating them from the data, which means that we really should be using a *t*-distribution. But for large enough datasets, it's close enough that it doesn't make much of a difference.

This means we can test the *null hypothesis* that p_A and p_B are the same (that is, that $p_A - p_B$ is 0) by using the statistic:

```python
def a_b_test_statistic(N_A: int, n_A: int, N_B: int, n_B: int) -> float:
    p_A, sigma_A = estimated_parameters(N_A, n_A)
    p_B, sigma_B = estimated_parameters(N_B, n_B)
    return (p_B - p_A) / math.sqrt(sigma_A ** 2 + sigma_B ** 2)
```

which should approximately be a standard normal.

For example, if "tastes great" gets 200 clicks out of 1,000 views and "less bias" gets 180 clicks out of 1,000 views, the statistic equals:

```python
z = a_b_test_statistic(1000, 200, 1000, 180)    # -1.14
```

The probability of seeing such a large difference if the means were actually equal would be:

```python
two_sided_p_value(z)                            # 0.254
```

which is large enough that we can't conclude there's much of a difference. On the other hand, if "less bias" only got 150 clicks, we'd have:

```python
z = a_b_test_statistic(1000, 200, 1000, 150)    # -2.94
two_sided_p_value(z)                            # 0.003
```

which means there's only a 0.003 probability we'd see such a large difference if the ads were equally effective.

Bayesian Inference

The procedures we've looked at have involved making probability statements about our *tests*: e.g., "There's only a 3% chance you'd observe such an extreme statistic if our null hypothesis were true."

An alternative approach to inference involves treating the unknown parameters themselves as random variables. The analyst (that's you) starts with a *prior distribution* for the parameters and then uses the observed data and Bayes's theorem to get an updated *posterior distribution* for the parameters. Rather than making probability judgments about the tests, you make probability judgments about the parameters.

For example, when the unknown parameter is a probability (as in our coin-flipping example), we often use a prior from the *Beta distribution*, which puts all its probability between 0 and 1:

```python
def B(alpha: float, beta: float) -> float:
    """A normalizing constant so that the total probability is 1"""
    return math.gamma(alpha) * math.gamma(beta) / math.gamma(alpha + beta)

def beta_pdf(x: float, alpha: float, beta: float) -> float:
    if x <= 0 or x >= 1:          # no weight outside of [0, 1]
        return 0
    return x ** (alpha - 1) * (1 - x) ** (beta - 1) / B(alpha, beta)
```

Generally speaking, this distribution centers its weight at:

```
alpha / (alpha + beta)
```

and the larger `alpha` and `beta` are, the "tighter" the distribution is.

For example, if `alpha` and `beta` are both 1, it's just the uniform distribution (centered at 0.5, very dispersed). If `alpha` is much larger than `beta`, most of the weight is near 1. And if `alpha` is much smaller than `beta`, most of the weight is near 0. Figure 7-1 shows several different Beta distributions.
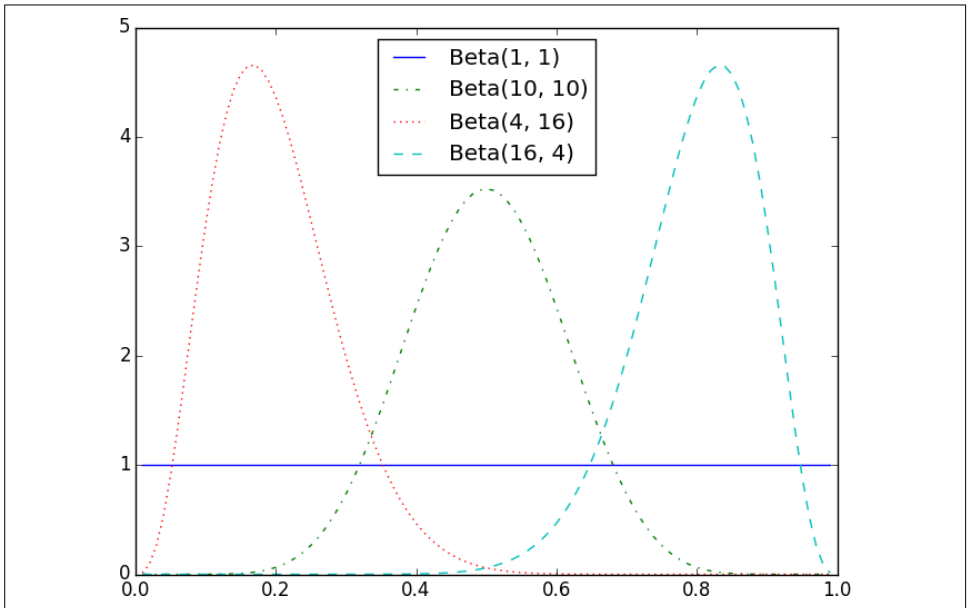

Figure 7-1. Example Beta distributions

Say we assume a prior distribution on *p*. Maybe we don't want to take a stand on whether the coin is fair, and we choose `alpha` and `beta` to both equal 1. Or maybe we have a strong belief that the coin lands heads 55% of the time, and we choose `alpha` equals 55, `beta` equals 45.

Then we flip our coin a bunch of times and see *h* heads and *t* tails. Bayes's theorem (and some mathematics too tedious for us to go through here) tells us that the poste-

rior distribution for p is again a Beta distribution, but with parameters `alpha + h` and `beta + t`.

It is no coincidence that the posterior distribution was again a Beta distribution. The number of heads is given by a Binomial distribution, and the Beta is the *conjugate prior* to the Binomial distribution. This means that whenever you update a Beta prior using observations from the corresponding binomial, you will get back a Beta posterior.

Let's say you flip the coin 10 times and see only 3 heads. If you started with the uniform prior (in some sense refusing to take a stand about the coin's fairness), your posterior distribution would be a Beta(4, 8), centered around 0.33. Since you considered all probabilities equally likely, your best guess is close to the observed probability.

If you started with a Beta(20, 20) (expressing a belief that the coin was roughly fair), your posterior distribution would be a Beta(23, 27), centered around 0.46, indicating a revised belief that maybe the coin is slightly biased toward tails.

And if you started with a Beta(30, 10) (expressing a belief that the coin was biased to flip 75% heads), your posterior distribution would be a Beta(33, 17), centered around 0.66. In that case you'd still believe in a heads bias, but less strongly than you did initially. These three different posteriors are plotted in Figure 7-2.
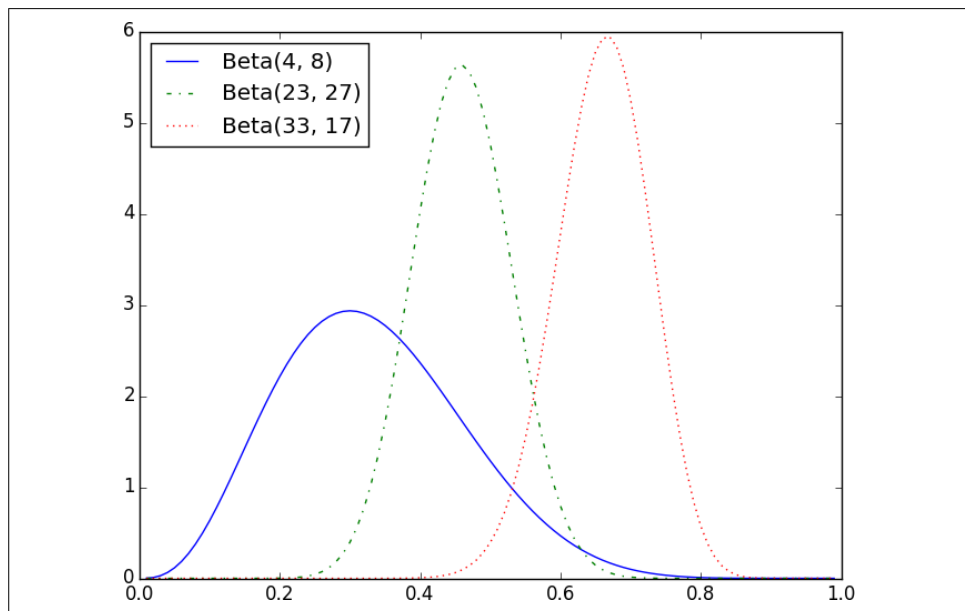

Figure 7-2. Posteriors arising from different priors

If you flipped the coin more and more times, the prior would matter less and less until eventually you'd have (nearly) the same posterior distribution no matter which prior you started with.

For example, no matter how biased you initially thought the coin was, it would be hard to maintain that belief after seeing 1,000 heads out of 2,000 flips (unless you are a lunatic who picks something like a Beta(1000000,1) prior).

What's interesting is that this allows us to make probability statements about hypotheses: "Based on the prior and the observed data, there is only a 5% likelihood the coin's heads probability is between 49% and 51%." This is philosophically very different from a statement like "If the coin were fair, we would expect to observe data so extreme only 5% of the time."

Using Bayesian inference to test hypotheses is considered somewhat controversial—in part because the mathematics can get somewhat complicated, and in part because of the subjective nature of choosing a prior. We won't use it any further in this book, but it's good to know about.

For Further Exploration

- We've barely scratched the surface of what you should know about statistical inference. The books recommended at the end of Chapter 5 go into a lot more detail.
- Coursera offers a Data Analysis and Statistical Inference course that covers many of these topics.