STAT340 Lecture 06: Estimation part 1

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Introduction

These notes will discuss the problem of *estimation*.

Estimation refers to the task of giving a value or range of values that are a "good guess" about some quantity out there in the world. This quantity could be a parameter of a model, or a number or quantity out there in the world.

We've already seen an example of estimation problems this semester: we've used Monte Carlo methods many times so far to *estimate* the probability of an event. We've also discussed the problem of estimating numbers like the average human height. We'll delve more into these and related problems this week and next.

Learning objectives

After this lesson, you will be able to

- Explain the statistical task of estimation and give examples of real-world estimation problems.
- Define the concept of a *statistic* and explain how and why we view a statistic as a random quantity.
- Explain the difference between an estimate and an estimator.
- Use the law of large numbers to explain why larger sample sizes are generally preferable when performing estimation.

Statistical Estimation I

The goal of estimation is to determine the value of a quantity. Often we identify this quantity with a parameter in a model.

Example: Human heights

Let's think back to our human height example from our first lecture. Recall that our goal was to determine the average human height, μ.

We said that it was infeasible to measure the height of every human, but we could measure the heights $X_1, X_2, \ldots, X_n$ of a few thousand humans and report the mean of that sample (the "sample mean"),

$$\hat{\mu} = \bar{X} = \frac{1}{n}\sum_{i=1}^{n} X_i,$$

hat notation

$\hat{\mu}$: "estimate of" μ

where n is the number of humans in our sample.

Statistical Estimation II

Thus, we might report the value of $\hat{\mu}$ (say, 172.1 cm) and state that "We estimate the average human height to be 172.1 cm."

This value $\hat{\mu}$ is called a *point estimate*. We make our "best guess" as to the true value of μ.

Statistical Estimation III

Facts from probability theory (specifically, the law of large numbers, which we'll talk about soon) state that this sample mean $\hat{\mu}$ is close to the true population mean μ.

But how close is close?

In addition to our estimate $\hat{\mu}$, we would like to have some kind of notion of how certain we are in our estimate.

Said another way, if we say that "we estimate the average human height to be 172.1 cm", we might also be willing to say that 172.3 cm or 171.8 cm are also reasonable estimates.

This week, we'll talk primarily about point estimates, but we're also building the groundwork needed to talk about confidence intervals next week.

Example: Universal Widgets of Madison I

The Universal Widgets of Madison (UW-Madison) company manufactures widgets

Unfortunately, not all widgets produced by the machine are functional. A widget is functional with probability p, and dysfunctional with probability $1 - p$. The engineers on the UW-Madison production line are quite confident that widgets are independent of one another– that is, whether or not one widget is dysfunctional has no bearing on whether or not any other widgets coming off the production line are dysfunctional.

UW ships widgets in batches, and they want to ensure that every batch ships with at least 5 functional widgets in it.

Example: Universal Widgets of Madison II

Thus, we have two related questions to answer:

1. What is a good estimate for p (i.e., a point estimate for p)?
2. How many widgets should be in a batch to ensure that (with high probability) a batch ships with at least 5 functional widgets in it?

We will focus on the first of these two questions, since if we have a good estimate for p, we can get a decent answer to question (2) using Monte Carlo methods.

Step 1: Specify a model I

All of statistics starts with choosing a model for the world, so let's start there.

What would be a good model for this setting?

Since the outcome of interest here is binary (i.e., it is a yes/no or success/failure outcome), it is natural to model whether a widget is functional or dysfunctional as a Bernoulli random variable with success probability p.

That is, we model each widget as being functional with probability p and dysfunctional with probability $1 - p$.

The production engineers are confident that we are safe assuming that widget are **independent**. Of course, in the real world, the independence assumption is probably unrealistic, but we'll let this slide because if we tried to account for dependency we would have a rough time creating a model.

Step 1: Specify a model II

So, we will make the following assumption: *widgets are functional independently with probability p*.

We'll imagine that we take a sample of widgets from the production line at UW-Madison, and use that sample to try and estimate p.

Having chosen a model for our data, the first thing we need to do is implement it in R. For now, we'll make arbitrary choices for the number of widgets `n` and the probability `p` of a widget being functional.

Step 1: Specify a model III

```
n <- 200; # We will examine n=200 widgets
p <- 0.8; # Suppose that 80% of widgets are functional
functional_widgets <- rbinom(1, size=n, p); # Draw one sample of widgets.
functional_widgets; # How many of the n widgets are functional?
## [1] 156
```

Question: why is the binomial distribution the right thing to use, here?

```
# Let's wrap that up in a function for use later.
generate_widgets <- function(n,p) {
  return( rbinom(1, size=n, p) );
}
```

Step 2: Estimating p I

Suppose that we can collect data by observing widgets $1, 2, \ldots, n$.

Let's denote our data by $X_1, X_2, \ldots, X_n$, where $X_i = 1$ if the i-th widget is functional and $X_i = 0$ if it is dysfunctional. That is, recalling our indicator function notation,

$$X_i = 1_{\text{widget } i \text{ is functional}}$$

$1_{\text{condition}} = \begin{cases} 1 & \text{if cond. true} \\ 0 & \text{otherwise} \end{cases}$

If we examine enough widgets, we know that we can estimate p very well using the sample mean

$$\bar{X} = \frac{1}{n}\sum_{i=1}^{n} X_i = \frac{\#\text{ of functional widgets}}{n}.$$

Again, the law of large numbers (which we'll discuss more formally soon), says that once n is big, this estimate will be really close to $\mathbb{E}\bar{X} = p$. More specifically, the more widgets we examine, the more precise our estimate will be (on average).

Step 2: Estimating p II

Unfortunately, widgets aren't free. So, here are two questions:

1. If we are willing to tolerate an error of, say, 2%, how many widgets do we need to examine?
2. Suppose we examine 1000 widgets and observe that 882 of them are functional, so we estimate p to be $882/1000 = 0.882$. How close is this to the true value of p, on average?

Question 1 is a question about *experiment design*. Specifically, it is a question about *sample size*. How many observations (i.e., how much data) do we need to collect in order to get a certain level of estimation precision?

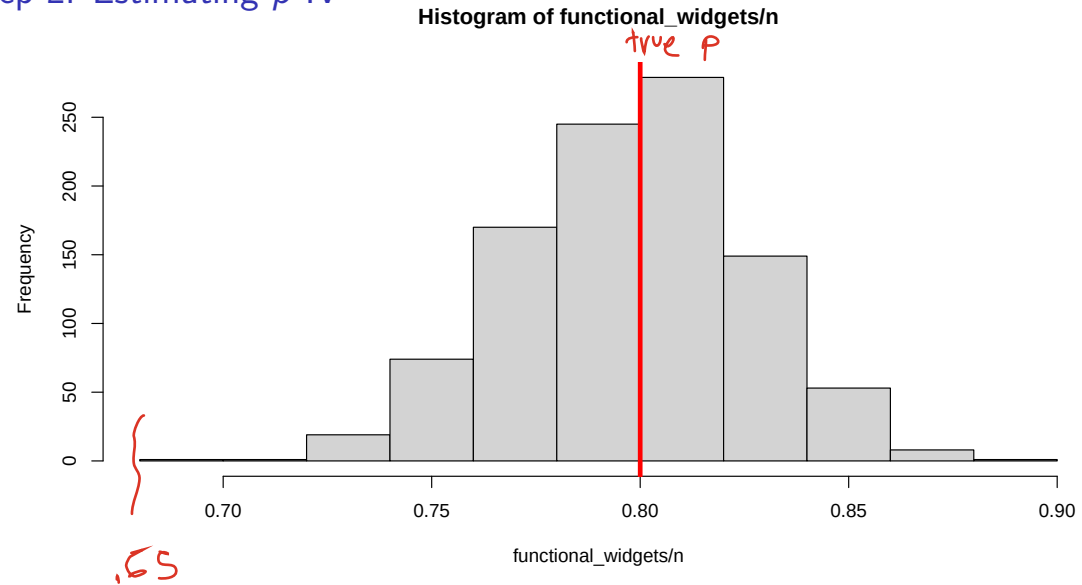
Question 2 is a question about the precision of a specific estimate, namely the sample mean. We will see below that these two questions are, in a certain sense, two sides of the same coin.

So, to start, what do we mean when we say that our estimate will be close to p?

Step 2: Estimating p III

```
# Still n=200 widgets, 80% of which are functional.
n <- 200; p <- 0.8;

# This time, we'll generate lots of iterations of our experiment, and
# we'll make a histogram of our estimates of p.
NMC <- 1000;
functional_widgets <- rep(NA, NMC);
for(i in 1:NMC) {
  functional_widgets[i] <- generate_widgets(n,p)
}

# Plot estimates of p, #functional/#observations
hist( functional_widgets/n );
abline( v=p, col='red', lwd=4 );
```

Step 2: Estimating p IV



Step 2: Estimating p V

Each data point in the above histogram corresponds to a single instance of our experiment, in which we observe $n = 200$ widgets, each of which is functional independently with probability $p = 0.8$ (indicated in red in the plot).

To estimate p, we count up what fraction of the 200 widgets in our sample are functional.

Since the data are random, our estimate of p is also random. The histogram above illustrates that randomness.

Sometimes our estimate is a bit higher than the true value of p, sometimes it is lower. But as we can see, most of the time our estimate is close to p, within about 0.06.

Aside: Estimators, Estimates and Statistics I

Before continuing our investigation of widgets, let's take a moment to discuss things in more generality and establish some vocabulary.

Suppose we have our data $X_1, X_2, \ldots, X_n$. If we performed another experiment, we would presumably see a different set of values for our data. That is reflected in the fact that we model the observations $X_1, X_2, \ldots, X_n$ as being random variables.

So, in our example above, X_i is a Bernoulli random variable representing whether or not widget i is functional.

We might observe that six our of ten widgets are functional, but that could be entirely due to chance– on another day we might observe that seven out of ten are functional, or four out of ten or... etc.

Aside: Estimators, Estimates and Statistics II

We typically summarize our data with a *statistic*, say $S(X_1, X_2, \ldots, X_n)$. This should remind you of our *test statistics* from hypothesis testing. Remember, a *statistic* is just a function of our data– it takes our data as input and spits out a number (or collection of numbers) summarizing our data.

In our example above, we summarized the data with the sample mean $S(X_1, X_2, \ldots, X_n) = n^{-1} \sum_{i=1}^{n} X_i$, but this statistic S can be any function of your data. We usually choose the function S to be so that $S(X_1, X_2, \ldots, X_n)$ will tend to be close to our quantity of interest (e.g., the mean μ in our human heights example, or our probability p in our widgets example).

We call this function S an *estimator* for that quantity of interest.

Aside: Estimators, Estimates and Statistics III

In our widgets example, we are estimating the probability p, and we chose our statistic to be the sample mean of the data (i.e., the fraction of widgets that were functional). That is, we used the sample mean as our estimator for p.

We call a particular value of this estimator (i.e., S applied to a particular choice of data) an *estimate* of our quantity. So, if we observe 162 functional widgets in our sample of $n = 200$ widgets, our estimate of p is $162/200 = 0.81$.

Now, since the data $X_1, X_2, \ldots, X_n$ are random, and $S = S(X_1, X_2, \ldots, X_n)$ is a function of the data, that means that our statistic S is also random. So, in just the same way that X_i has a distribution (e.g., $X_i \sim \text{Bernoulli}(p)$ above), S also has a distribution.

We usually call this distribution the *sampling distribution*, because it describes the behavior of our statistic, which is a function of the sample.

More data, more precision I

So, let's turn back to the first of our two questions: If we are willing to tolerate an error of, say, 2%, how many widgets do we need to examine?

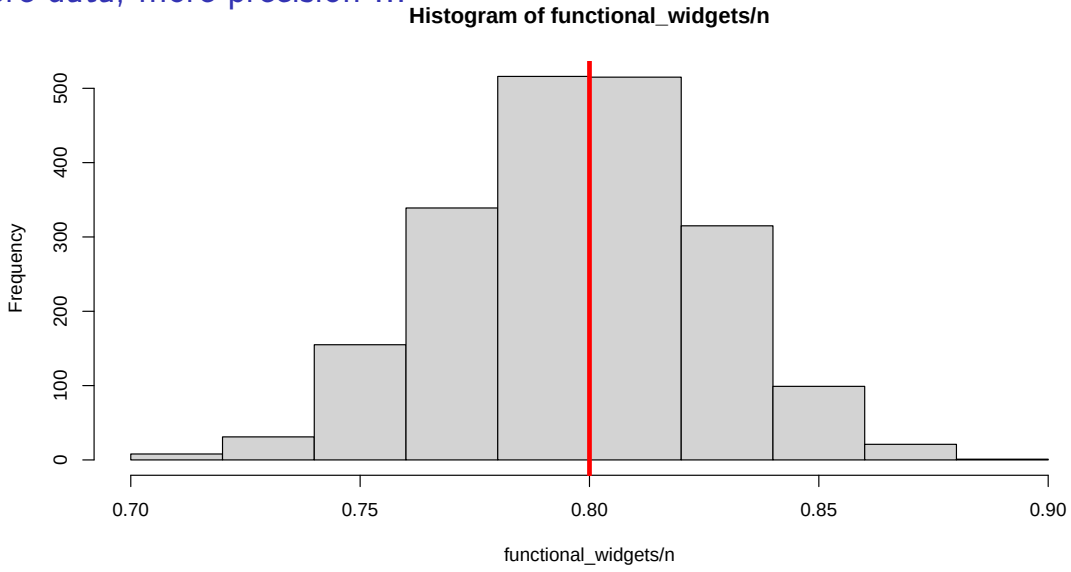
Well, let's start by looking at the histogram of estimates from 2000 different runs with $n = 200$ and $p = 0.8$.

More data, more precision II

sample size

```
n <- 200; p <- 0.8; # Still n=200 widgets, 80% of which are functional.
# We'll generate lots of iterations
NMC <- 2000; # MC replicates
functional_widgets <- rep(NA, NMC);
for(i in 1:NMC) {
  functional_widgets[i] <- generate_widgets(n,p)
}
# Plot estimates of p, #functional/#observations
hist( functional_widgets/n );
# Draw a vertical line at the true value of p
abline( v=p, col='red', lwd=4 );
```

More data, more precision III



More data, more precision IV

```
#This is what proportion of the samples resulted in a an estimate
#within .02 of the true value
mean(abs(functional_widgets/n - p) <= .02)
## [1] 0.5155
```

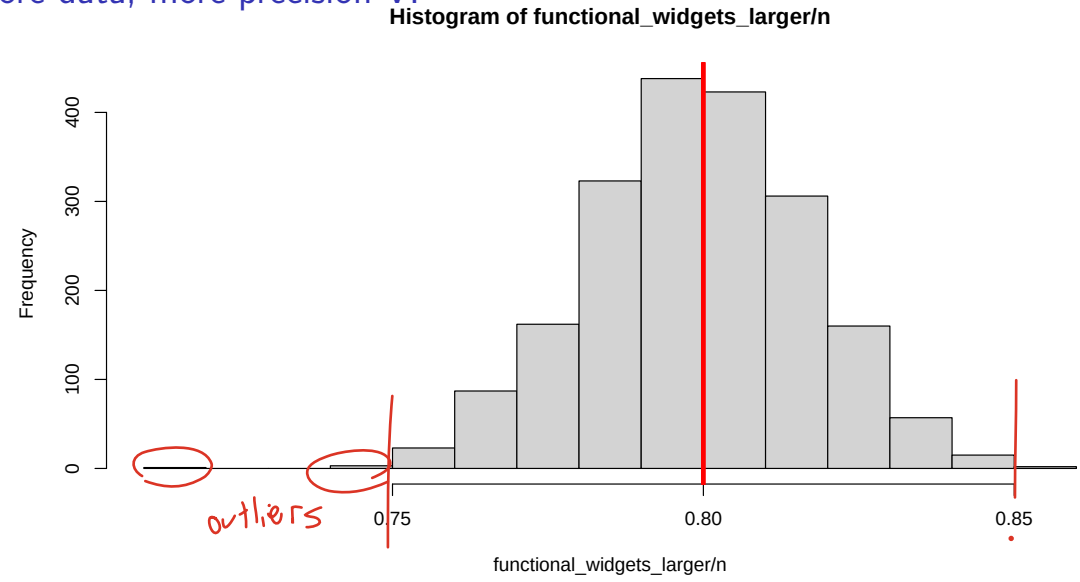
Most of the estimates are between 0.72 and 0.88.

Let's try increasing n from $n = 200$ to $n = 500$. That is, let's try gathering more data, in the form of *more widgets*.

More data, more precision V

```
# n=500 widgets instead of 200, but still 80% are functional.
n <- 500; p <- 0.8;

# We'll generate lots of iterations
NMC <- 2000;
functional_widgets_larger <- rep(NA, NMC);
for(i in 1:NMC) {
  functional_widgets_larger[i] <- generate_widgets(n,p)
}
# Plot estimates of p, #functional/#observations
hist( functional_widgets_larger/n );
# Draw a vertical line at the true value of p
abline( v=p, col='red', lwd=4 );
```

More data, more precision VI

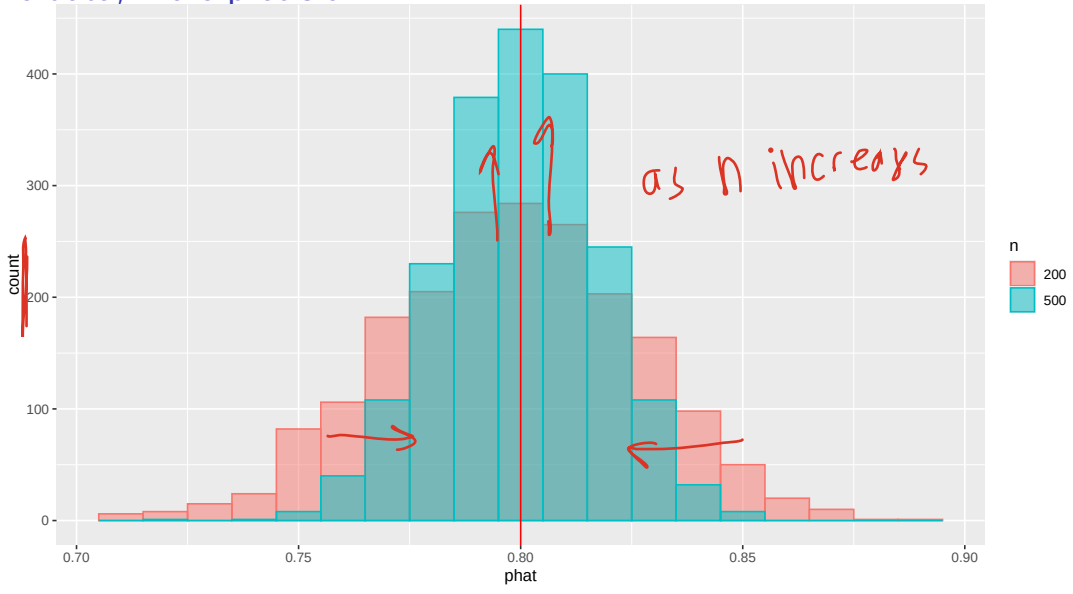


More data, more precision VII

In fact, let's just display them both in one plot.

```
p <- 0.8; # Still n=200 widgets, 80% of which are functional.

# Put the data into a data frame to pass to ggplot2.
phat <- c(functional_widgets/200, functional_widgets_larger/500 );
n <- c( rep(200, 2000), rep(500, 2000) );
df <- data.frame(n=as.factor(n), phat=phat);

library(ggplot2)
pp <- ggplot( df, aes(x=phat, color=n, fill=n));
pp <- pp + geom_histogram( aes(), position='identity', alpha=0.5,
                           binwidth=0.01);
pp <- pp + geom_vline( xintercept=p, color='red');
```

More data, more precision VIII



More data, more precision (cont) I

Looking at the plot, we see that the $n = 500$ estimates (blue) tend to cluster more tightly around the true value of p ($p = 0.8$, indicated by the vertical red line), when compared with the $n = 200$ estimates (orange).

Gathering more data (i.e., observing more widgets) gives us a more precise (on average!) estimate of p.

Just to drive this home, let's increase n even more.

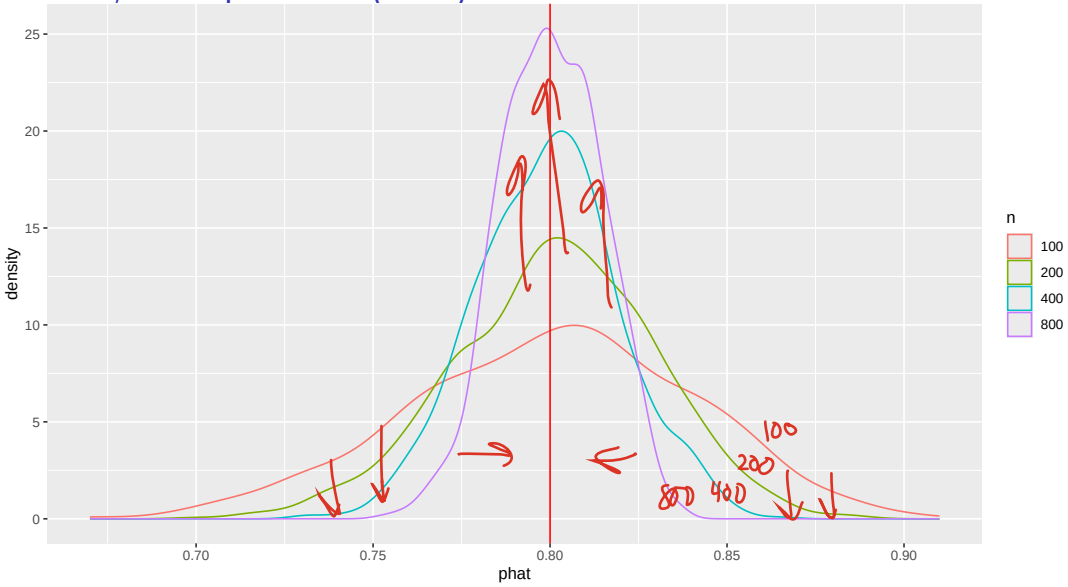
More data, more precision (cont) II

```
p <- 0.8; # Still using 80% functional rate.

# Note: there are "cleaner" ways to build this data frame,
# but those ways are harder to understand on a first glance.
# At this stage of your career, "clumsy but easy to read"
# is better than "short but cryptic"
widgets_100 <- rbinom(1000, size=100, p);
widgets_200 <- rbinom(1000, size=200, p);
widgets_400 <- rbinom(1000, size=400, p);
widgets_800 <- rbinom(1000, size=800, p);

# Compute "p hat", i.e., estimate of p
phat <- c(widgets_100/100, widgets_200/200,
          widgets_400/400, widgets_800/800 );
n <- c( rep(100, 1000), rep(200, 1000), rep(400, 1000), rep(800, 1000) );
```

More data, more precision (cont) III

```
# Put the data into a data frame to pass to ggplot2.
df <- data.frame( 'n'=as.factor(n), 'phat'=phat);
pp <- ggplot( df, aes(x=phat, color=n ));
# Using a smoothed density instead of histogram for easy comparison
pp <- pp + geom_density( lidewidth=4 );
## Warning in geom_density(lidewidth = 4): Ignoring unknown parameters:
## `lidewidth`
pp <- pp + geom_vline( xintercept=p, color='red', lidewidth=3);
## Warning in geom_vline(xintercept = p, color = "red", lidewidth = 3): Ig
## unknown parameters: `lidewidth`
```

More data, more precision (cont) IV



More data, *how much* better precision? I

The plot above certainly seems to indicate that as we increase the number of samples (i.e., the number of widgets n), our estimate becomes more precise, in the sense that it is closer to the true value of p (on average, anyway).

But when we increase our sample from, say $n = 100$ to $n = 800$, like in the experiment above, just how much better does our estimate become?

As a reminder, we are denoting our data by $X_1, X_2, \ldots, X_n$, where $X_i = 1$ if the i-th widget is functional and $X_i = 0$ if it is dysfunctional. That is, recalling our indicator function notation yet again,

$$X_i = 1_{\text{widget } i \text{ is functional}}.$$

$\hat{P}$ r.v.

$\hat{p}$ observed sample proportion.

We are using the sample mean as our estimator,

$$\hat{p} = \hat{p}(X_1, X_2, \ldots, X_n) = \frac{1}{n}\sum_{i=1}^{n} X_i.$$

More data, *how much* better precision? II

Let's consider the variance of this estimator.

Why the variance? Well, remember that for a random variable Z,

$$\operatorname{Var} Z = \mathbb{E}(Z - \mathbb{E}Z)^2.$$

That is, the variance describes how close a variable is *on average* to its expectation.

Now, the expectation of our estimator is

$$\mathbb{E}\hat{p} = \mathbb{E}\frac{1}{n}\sum_{i=1}^{n} X_i = \frac{1}{n}\sum_{i=1}^{n} \mathbb{E}X_i = \frac{1}{n}\sum_{i=1}^{n} p = p,$$

where we used

1. the definition of our estimator $\hat{p}$
2. linearity of expectation: $\mathbb{E}(aX + bY) = a\mathbb{E}X + b\mathbb{E}Y$

More data, *how much* better precision? III

3. the fact that the expectation of an indicator is the probability of the event in the indicator: $\mathbb{E}1_A = \Pr[A]$.
4. basic facts about summation: $\sum_{i=1}^{n} p = np$.

More data, *how much* better precision? IV

So on average, our estimator $\hat{p}$ is equal to the thing we are trying to estimate. That's good! In fact, it's so good that statisticians have a special name for this property: we say that $\hat{p}$ is an *unbiased estimator* of p.

But the fact that our estimator is *on average* equal to p doesn't tell us about how close it is to p. For example, suppose that we have an estimator that is equal to $p + 100$ half the time and $p - 100$ the other half of the time. On average, our estimate is equal to p:

$$\frac{1}{2}(p + 100) + \frac{1}{2}(p - 100) = \frac{p}{2} + 50 + \frac{p}{2} - 50 = p,$$

but our estimate is never *particularly* close to p...

if $E(\hat{\theta}) = \theta$ we say $\hat{\theta}$ is an unbiased estimator of θ.

$\text{Bias}(\hat{\theta}) = E(\hat{\theta}) - \theta$ (bias can be pos, neg or 0)

More data, *how much* better precision? V

So how close is our sample mean

$$\hat{p} = \frac{1}{n} \sum_{i=1}^{n} X_i$$

to p, on average (as measured by the average squared distance)?

Let's try to compute it:

$$\operatorname{Var}(\hat{p}) = \operatorname{Var}\left(\sum_{i=1}^{n} \frac{X_i}{n} \right).$$

Now, our widget indicators $X_1, X_2, \ldots, X_n$ are independent, so we can use the fact that the variance of a sum of independent random variables is just the sum of their variances:

$$\operatorname{Var} \hat{p} = \sum_{i=1}^{n} \operatorname{Var} \frac{X_i}{n}.$$

More data, *how much* better precision? VI

Now, since all of the X_i have the same distribution, we just have to compute

$$\sigma_n^2 = \operatorname{Var} \frac{X_1}{n},$$

and we'll be done, since $\operatorname{Var} \hat{p} = n\sigma_n^2$.

So what is σ_n^2?

$$\operatorname{Var} \frac{X_1}{n} = \mathbb{E}\left(\frac{X_1 - \mathbb{E}X_1}{n}\right)^2 = \mathbb{E}\left(\frac{X_1 - p}{n}\right)^2.$$

or

$$\frac{1}{n^2}\operatorname{Var}(X_1) = \frac{1}{n^2}\left(p(1-p)\right) = \frac{p(1-p)}{n^2}$$

More data, *how much* better precision? VII

Now, X_1 has a discrete distribution: $X_1 = 1$ with probability p and $X_1 = 0$ with probability $1 - p$. So,

$$\begin{aligned}
\operatorname{Var} \frac{X_1}{n} &= \mathbb{E}\left(\frac{X_1 - p}{n}\right)^2 \\
&= \frac{(1-p)^2}{n^2} \Pr[X_1 = 1] + \frac{(-p)^2}{n^2} \Pr[X_1 = 0] \\
&= \frac{(1-p)^2 p + p^2(1-p)}{n} \\
&= \frac{p(1-p)[(1-p) + p]}{n^2} \\
&= \frac{p(1-p)}{n^2}.
\end{aligned}$$

More data, *how much* better precision? VIII

If you've played around with Bernoulli random variables before, that numerator should look familiar– that's the variance of a Bernoulli with success parameter p. The n^2 in the denominator is indicative of a basic fact about variance that you may have seen before, depending on your background: $\operatorname{Var} aX = a^2 \operatorname{Var} X$.

More data, *how much* better precision? IX

Okay, so we have found that

$$\sigma_n^2 = \operatorname{Var} \frac{X_1}{n} = \frac{p(1-p)}{n^2},$$

and we said that $\operatorname{Var} \hat{p} = n\sigma_n^2$, so we have found the variance of our estimator:

$$\operatorname{Var} \hat{p} = n \frac{p(1-p)}{n^2} = \frac{p(1-p)}{n}.$$

$\operatorname{Var}(X_1) = p(1-p) = p(1-p)$

$\operatorname{Var}(\bar{X}) = \frac{p(1-p)}{n}$

Taking stock: more data less variance I

Dang, that was a lot of math. What did we learn as a result of it?

Well, the variance of our estimator $\hat{p}$, based on a sample of size n, is

$$\operatorname{Var} \hat{p} = \frac{p(1-p)}{n}.$$

p doesn't depend on nm so as the sample size n increases, the variance decreases like $1/n$. That is, if we want to decrease the variance of our estimate by $1/2$, we need to double our sample size.

There's one small flaw here. The variance isn't quite the right measure of "how close" our estimate is to our target p. The more appropriate choice is the *standard deviation*.

Taking stock: more data less variance II

In later courses you'll see in detail why this is really the right quantity to care about here, but for now, think of it this way:

Kind of like a physics problem, the "units" of variance is "squared stuff", where "stuff" is the unit that your variable is measured in.

But the "right" way to measure how close we are to something isn't in squared units– that's like an area, not a distance. So we have to take the square root of the variance to get a sensible answer.

So,

$$\operatorname{sd} \hat{p} = \sqrt{\operatorname{Var} \hat{p}} = \frac{\sqrt{p(1-p)}}{\sqrt{n}}.$$

Taking stock: more data less variance III

Now, suppose that we have a sample of size n, and we want to cut "how close our estimate is on average" in half (i.e., decrease the standard deviation by a factor of two).

Multiplying n by 4 decreases $\operatorname{sd} \hat{p}$ by $\sqrt{4} = 2$. So to halve our standard deviation, we have to increase our sample size by 4. To decrease our standard deviation by a factor of ten, we need to increase our sample size by a factor of 100.

That's going to get our of hand quickly, especially if samples are challenging or expensive to get (e.g., subjects in a medical study)...

Aside: probability of "bad" events I

So more data (increasing n) gives us a more precise estimate (i.e., makes our estimate concentrate closer to the true p on average).

But we started our widgets example asking about how to *guarantee* that our estimate is close to the probability p.

There is a problem with this, though. Our data is random, and sometimes we get unlucky. So we can never guarantee that our estimate is close.

Aside: probability of "bad" events II

Let's take a short aside to make this more precise.

We saw in our simulation above that our estimate $\hat{p}$ of p was usually close to p, and making n bigger (i.e., collecting more data) meant that $\hat{p}$ was closer to p, on average.

Can we guarantee that, if n is big enough, then $\hat{p}$ will be arbitrarily close to p?

Unfortunately, the answer is no.

To see what this is the case, let's consider a very specific event: the event that all n of our widgets are functional.

When this happens, our estimate of p is

$$\hat{p} = n^{-1} \sum_{i=1}^{n} X_i = n^{-1} n = 1.$$

Aside: probability of "bad" events III

This event has probability (we're going to use independence of the widgets to write the probability of $X_1 = X_2 = \cdots = X_n = 1$ as a product of probabilities)

$$\Pr[X_1 = 1, X_2 = 1, \ldots, X_n = 1] = \prod_{i=1}^{n} \Pr[X_i = 1] = p^n.$$

Now, unless $p = 0$, this means that the event $X_1 = X_2 = \cdots = X_n = 1$ occurs with *some* positive probability, albeit very small.

That is, no matter how large n is, there is still some small but positive probability that our estimate is simply $\hat{p} = 1$. What that means is that we can never give a 100% guarantee that our estimate is arbitrarily close to the true value of p– there's always a vanishingly small chance that $\hat{p} = 1$.

Aside: probability of "bad" events IV

Now, with that said, notice that as n gets larger, the probability of this bad "all widgets are functional" event gets smaller and smaller. Roughly speaking, this is what we mean when we say that more data gives us a more precise estimate. The probability that our estimate is far from the true value of p gets smaller and smaller as we increase n.

The law of large numbers, which we will (finally) discuss soon, will let us say something both stronger and more precise than this, but the above example is a good illustration of the core idea.

More data, better precision (part II) I

Instead of trying to do more math, let's try and code up an experiment to get a handle on this.

Let's simplify things a bit by writing a function that will generate a random copy of $S(X_1, X_2, \ldots, X_n) = \hat{p}$ given a choice of n and the true value of p.

```
simulate_S <- function( n, p ) {
  functional_widgets <- rbinom(1, size=n, prob=p);
  # Our statistic is the fraction of the n widgets
  # that are functional.
  return(functional_widgets/n);
}

# Simulate n=200 widgets with functional probability p=0.8
simulate_S(200, 0.8)
## [1] 0.84
```

More data, better precision (part II) II

Now, we want to use this function to estimate the probability that our estimate is within 0.02 of p.

That is, we want to estimate

$$\Pr[S \in (p - 0.02, p + 0.02)] = \Pr[|S(X_1, X_2, \ldots, X_n) - p| < 0.02]$$

We *could* explicitly compute this number. After all, we know how to compute the probability distribution of the Bernoulli and/or Binomial distributions.

But instead, let's just use Monte Carlo estimation.

More data, better precision (part II) III

```r
# Here's a function that will take our estimate S (= phat) and check
# if it is within 0.02 of p or not.
check_if_S_is_good <- function( S, p ) {
    return( abs(S-p) < 0.02)
}
# Now, let's simulate a lot of instances of our experiment
# and count up what fraction of the time our estimate is "good"
N_MC <- 2000; # Repeat the experiment 2000 times. N_MC = "number of
              # Monte Carlo (MC) replicates"
n <- 200; p <- 0.8; # Still using n=200, p=0.8

# Create a data frame to store the outcome of our experiment. We are
# initially filling entries with NAs, which we will fill in as we run.
monte_carlo <- data.frame(replicate = 1:N_MC, S = rep(NA, N_MC),
                          S_good = rep(NA, N_MC));
```

More data, better precision (part II) IV

```
# Let's just check what the data frame looks like before we populate it.
head( monte_carlo )
##   replicate  S S_good
## 1         1 NA     NA
## 2         2 NA     NA
## 3         3 NA     NA
## 4         4 NA     NA
## 5         5 NA     NA
## 6         6 NA     NA
```

More data, better precision (part II) V

```
# For each replicate, run the experiment and record results.
# We want to keep track of the value of S and whether or not S was good.
for(i in 1:N_MC){
    monte_carlo$S[i] <- simulate_S( n, p );
    monte_carlo$S_good[i] <- check_if_S_is_good(monte_carlo$S[i], p)
}

sum( monte_carlo$S_good )/N_MC
## [1] 0.5305
```

So about half of our estimates were within 0.02 of p.

Our experiments above suggested that we could improve this by increasing n, so let's try that.

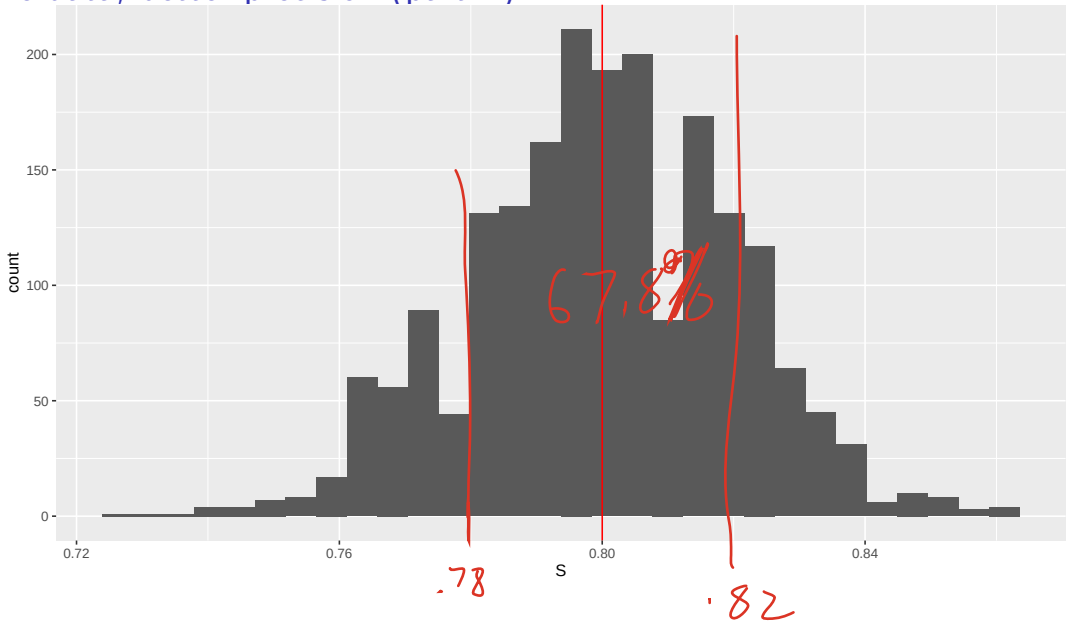
More data, better precision (part II) VI

```
# This is the exact same setup except we're changing n from 200 to 400.
N_MC <- 2000; n <- 400; p <- 0.8;

# Note that we don't really have to create the data frame again. We
# could, if we wanted, just overwrite it, but this is a good habit to
# be in to make sure we don't accidentally "reuse" old data.
monte_carlo <- data.frame( replicate = 1:N_MC, S = rep(NA, N_MC),
                           S_good = rep(NA, N_MC));
for(i in 1:N_MC){
  monte_carlo$S[i] <- simulate_S( n, p );
  monte_carlo$S_good[i] <- check_if_S_is_good(monte_carlo$S[i], p)
}
mean( monte_carlo$S_good )
## [1] 0.678
```

More data, better precision (part II) VII

```
# Just as a check, let's plot a histogram again.
pp <- ggplot(monte_carlo, aes(x = S)) + geom_histogram(bins = 30) +
  geom_vline( xintercept=p, col='red' )
pp
```

More data, better precision (part II) VIII



More data, better precision (part II) IX

Exercise: play around with n in the above code to find how large our sample size has to be so that $\Pr[|S - p| \leq 0.02] \approx 0.95$.

More data, better precision (part II) X

```r
# This is the exact same setup except we're changing n from 200 to 400.
N_MC <- 2000; n <- 1500; p <- 0.8;
# Still using p=0.8 and 2000 Monte Carlo trials.

# Note that we don't really have to create the data frame again. We
# could, if we wanted, just overwrite it, but this is a good habit to
# be in to make sure we don't accidentally "reuse" old data.
monte_carlo <- data.frame( replicate = 1:N_MC,
                           S = rep(NA, N_MC),
                           S_good = rep(NA, N_MC));
for(i in 1:N_MC){
  monte_carlo$S[i] <- simulate_S( n, p );
  monte_carlo$S_good[i] <- check_if_S_is_good(monte_carlo$S[i], p)
}
sum( monte_carlo$S_good )/N_MC
## [1] 0.9435
```

What are we trying to estimate? I

In our discussions above, we are interested in

1. Estimating p and
2. Knowing how good our estimate is (i.e., "how likely is it that we are within 0.02 of the truth?").

Generally, once we compute the statistic S, we could just report it and be done with it. "We estimate p to be 0.785", and leave it at that. That's the problem of *point estimation*. But this leaves open the question of how close our estimate is to the truth.

What are we trying to estimate? II

If we knew p, like in the examples above, we could say how close we are, but we don't know p. So, how can we say how close we are without knowing the true value of the thing we are estimating?

Above, p was defined as a parameter in a model. However, often times, "parameters" can be imagined as something different. Here are two other ways:

- Imagine getting an infinite amount of data. What would be the value of S with an infinite amount of data?
- Imagine repeating the whole experiment lots of different times and on experiment i you created statistic S_i. What is the average of those statistics $S_1, S_2, \ldots$?

What are we trying to estimate? III

For most functions of the data S, these two values are the same thing (though the first one might be a bit easier to think about). However, if they are different (and sometimes they are), it is the second one that we are actually going to use. That second value is in fact the expected value of the statistic, $\mathbb{E}S(X_1, X_2, \ldots, X_n)$, which we will often shorten to just $\mathbb{E}S$, with it being understood that S depends on the data $X_1, X_2, \ldots, X_n$.

What are we trying to estimate? IV

Example: The maximum of the X_i is one statistic for which those two notions are not the same. So is the minimum. Why?

So, to recap, here is the problem:

- S is a random variable.
- We only observe one example of it, but we want to estimate $\mathbb{E}S$.

Point estimation: a good place to begin I

So, we want an estimate of $\mathbb{E}S$. Well, what better estimate than S itself? This isn't an arbitrary decision– there are good mathematical reasons behind this. The simplest of these reasons comes from the definition of the expectation: "on average", $S = \mathbb{E}S$, and S is "usually" close to $\mathbb{E}S$.

We've mentioned the law of large numbers (LLN) a couple of times already this semester. Let's look at it a bit closer.

The *weak law of large numbers* states that if $X_1, X_2, \ldots$ are i.i.d. with mean μ, then for any $\epsilon > 0$,

$$\lim_{n\to\infty} \Pr\left[\left|\frac{1}{n}\sum_{i=1}^{n} X_i - \mu\right| > \epsilon\right] = 0.$$

Restating that in language from calculus class, for every $\epsilon > 0$ and every $\delta > 0$, there

$$\lim_{n\to\infty} \Pr\left[\,|\bar{X} - \mu| > \varepsilon\right] = 0$$

Point estimation: a good place to begin II

exists an n_0 such that if $n \geq n_0$, then

$$\Pr\left[\left|\frac{1}{n}\sum_{i=1}^{n} X_i - \mu\right| > \epsilon\right] \leq \delta.$$

Stated more simply, for any fixed $\epsilon > 0$, we can guarantee that the sample mean $\bar{X}$ is within ϵ of μ with arbitrarily high probability, so long as our sample size n is large enough.

It turns out that this can be extended to include more complicated functions than the sample mean. In fact, so long as S is a "nice" function of the data (and so long as S is constructed in an appropriate way), then S will be close to the parameter that we want to estimate with high probability. That is, for "nice" estimators $S = S(X_1, X_2, \ldots, X_n)$, letting θ denote our parameter of interest,

$$\Pr\left[|S - \theta| > \epsilon\right] \leq \delta.$$

Example: Estimating the rate parameter in the exponential distribution. I

Let's see an example that will also illustrate a useful trick for constructing new estimators.

Suppose that we have data $X_1, X_2, \ldots, X_n$ i.i.d. from an exponential distribution with rate parameter λ. You can look up on Wikipedia that the mean of an exponential with rate λ is $\mathbb{E}X_1 = 1/\lambda$. Suppose that we want to estimate λ. How can we do that?

Well, we know that

$$\mathbb{E}\bar{X} = \frac{1}{n}\sum_{i=1}^{n}\mathbb{E}X_i = \frac{1}{\lambda}.$$

$\bar{X} \approx \frac{1}{\lambda}$

$\Rightarrow \lambda \approx \frac{1}{\bar{X}}$

So the law of large numbers states that for large sample size, the sample mean $\bar{X}$ should be close to $1/\lambda$. But if $\bar{X}$ is close to $1/\lambda$, then $1/\bar{X}$ is close to λ (**exercise:** prove this! Show that if $|\bar{X} - 1/\lambda| \leq \epsilon$ for some small $\epsilon > 0$, then $|1/\bar{X} - \lambda| \leq \epsilon(\lambda + \epsilon)$).

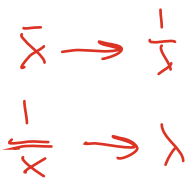
method of moments – base your estimator on $\mathbb{E}X, \mathbb{E}X^2, \mathbb{E}X^3 \ldots$

Example: Estimating the rate parameter in the exponential distribution. II

In this case, then, our estimator is

$$S(X_1, X_2, \ldots, X_n) = \frac{1}{\bar{X}},$$

and for large n, S will be close to λ. That is, as n gets large, $\bar{X}$ is close to $\mathbb{E}\bar{X}$, and therefore $\frac{1}{\bar{X}}$ is close to $1/\mathbb{E}\bar{X}$.

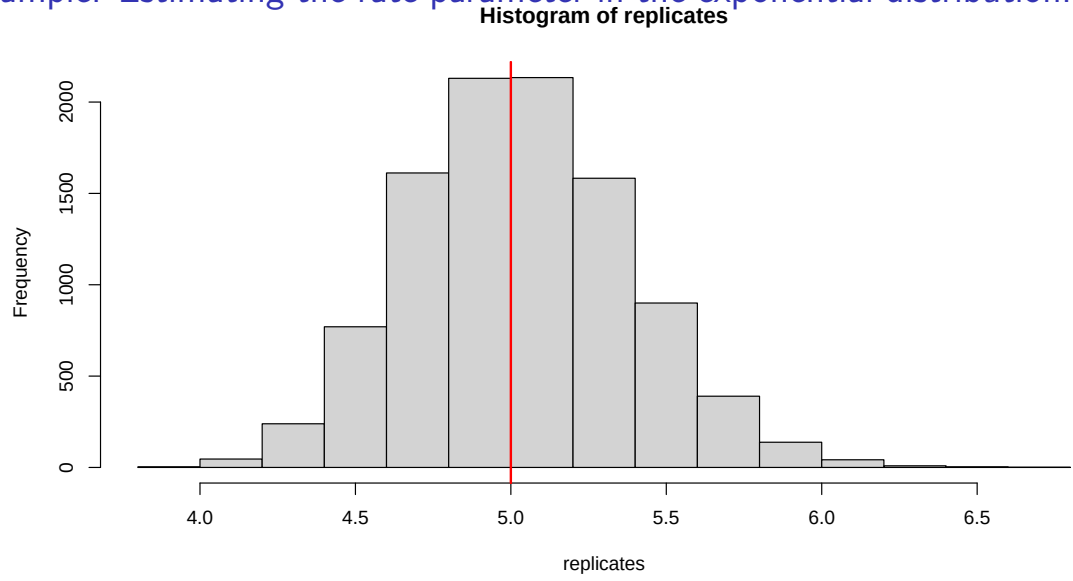


Example: Estimating the rate parameter in the exponential distribution. III

Okay, but this isn't a math class. Let's try simulating and see what happens.

```
run_exprate_expt <- function( n, rate ) {
  data <- rexp(n=n, rate=5);
  Xbar <- mean( data )
  return( 1/Xbar )
}

M <- 1e4;
replicates <- rep(NA, M);
for (i in 1:M ) {
  replicates[i] <- run_exprate_expt(200, rate=5);
}
hist(replicates); abline(v=5, col="red", lwd=2);
```

Example: Estimating the rate parameter in the exponential distribution. IV



Example: Estimating the rate parameter in the exponential distribution. V

This is actually an example of a general technique for doing estimation, called the *method of moments*. We express the parameter we want to estimate (in this case, the rate λ), and we express it in terms of the *moments* of our data, $\mathbb{E}X$, $\mathbb{E}X^2$, $\mathbb{E}X^3$, ...

This is a nice technique, because we know how to estimate moments using the law of large numbers– the sample mean is close to $\mathbb{E}X$, the sample mean of the squares $n^{-1}\sum_i X_i^2$ is close to $\mathbb{E}X^2$, the mean $n^{-1}\sum_i X_i^3$ is close to $\mathbb{E}X^3$, and so on– and we get all of that for free from the law of large numbers.

In the case above, we only needed the first moment. The parameter of interest obeys $\lambda = 1/\mathbb{E}X$.

There are other ways of deriving estimators– most famously maximum likelihood estimation, which we'll talk about a bit later this semester.

For now, the important thing is just that you've seen this and recognize that there are methods out there for *constructing an estimator* once we've written down a model and chosen a parameter of interest in it.

How many samples are enough? I

So we can appeal to the law of large numbers to support our assumption that S is close to $\mathbb{E}S$. But we said above that we also want to communicate how certain we are about this estimate.

There's a problem there– the law of large numbers doesn't tell us anything about how close S is to $\mathbb{E}S$ for finite sample size n. It just says that if n is suitably large, then the probability that S is "far" from $\mathbb{E}S$ is arbitrarily small.

This is the... limitation? of limit results (I'm so sorry).

So, S is close to $\mathbb{E}S$, but we don't know how close.

The best we can do is to create an interval of values that is "usually right", in that it "usually" contains the true value of $\mathbb{E}S$. This is the motivation for *confidence intervals* and *uncertainty quantification*, the subject of next week's lectures.

Review

- Create a parametric model for simulation
- Understand the difference between an estimator, an estimate and a statistic
- Simulate the distribution of an estimator
- See the effect of sample size on the variance of an estimator
- The expected value and variance of $\hat{P}$
- Point estimates for model parameters