Hi.

Hi everybody.

Students Hi.

It’s my pleasure today to introduce Professor Rebecca Andridge.

Professor Andridge has a Bachelors’ in Economics in Stanford and her Master’s and PhD in Biostatistics from the University of Michigan.

She an expert in group randomized trials and methods of missing data especially for that ever so tricky case that is not,

or so where data is missing not at random.

She’s been faculty in Biostatistics in Ohio State University since 2009.

She’s an award-winning educator and a 2020 Fellow of the Americans Associates, and we’re very honored to have a huge day.

Let’s welcome professor Andridge.

Thank you for the very generous introduction.

I have to tell you, it’s so exciting to see a room full of students.

I am currently teaching online class and the students don’t all congregate in a room.

So it’s like been years since I’ve seen this.

So I’m of course gonna share my slides.

I want to warn everybody that I am working from home today.
And while we will not be interrupted by my children, we might be interrupted or I might be interrupted by the construction going on in my house, my cats or my fellow work at home husband. So I’m gonna try to keep the distractions to a minimum but that is the way of the world in 2020, in the pandemic life. So today I’m gonna be talking about some work I’ve done with some colleagues actually at the University of Michigan. Talking about selection bias in proportions estimated from non-probability samples. So I’m gonna start with some background and definitions and we’ll start with kind of overview of what’s the problem we’re trying to address. So big data are everywhere, right? We all have heard that phrase being bandied about, big data. They’re everywhere and they’re cheap. You got Twitter data, internet search data, online surveys, things like predicting the flu using Instagram, right? All these massive sources of data. And these data often, I would say pretty much all the ways arise from what are called non-probability samples.
So when we have a non-probability sample we can’t use what are called design based methods for inference, you actually have to use model based approaches. So I’m not gonna assume that everybody knows all these words that I’ve found out here, so I’m gonna go into some definitions. Our goal is to develop an index of selection bias that lets us get at how bad the problem might be, how much bias might we have due to non-random selection into our sample? A probability sample is a situation where you’re collecting data where each unit in the population has a known positive probability of selection. And randomness is involved in the selection of which units come into the sample, right? So this is your stereotypical complex survey design or your sample survey. Large government sponsored surveys like the National Health and Nutrition Examination Survey, NHANES or NHIS or any number of large surveys that you’ve probably come across, you know, in application and your biostatistics courses.
So for these large surveys we do what’s called design-based inference. That’s where we rely on the design of the data collection mechanism in order for us to get unbiased estimates of population quantities, and we can do this without making any model assumptions.

So we don’t have to assume that let’s say body mass index has a normal distribution. We literally don’t have to specify distribution at all.

It’s all about the random selection into the sample that lets us get our estimates and be assured that we have unbiased estimates.

So here’s an example in case there are folks out in the audience who don’t have experience with the sort of complex survey design or design features.

This is a really silly little example of a stratified sample.

So here I have a population of two different types of animals.

I have cats and I have dogs. And in this population I happen to have 12 cats and 8 dogs.

Stratified sample where I took two cats and two dogs.
are known for all of the units, right?

Because I know that there's a two out of eight chance

I pick a dog and a two out of 12 chance

So the probability a cat is selected is 1/6

then the probability of dog is selected is 1/4.

Now, how do I estimate a proportion of interest?

Let's say it's the proportion of orange animals in the population.

Like here in my sample,

I have one of four orange animals,

but if I chose that as my estimator

I'd be ignoring the fact that I know how I selected

these animals into my sample.

So what we do is we wait the sample units to produce design unbiased estimates, right?

Because this one dog kinda counts differently than one cat, right?

Because there were only eight dogs

to begin with but there were 12 cats.

So if I want to estimate the proportion of orange animals

I would say this cat is a weight is six

because there's two of them and 12 total.

So 12 divided by two is six.

So there's six in the numerator.

And then the denominator is the sum of the weights

of all the selected units,
the cats are each six and the dogs are each four.
So I actually get my estimate a proportion of
30%.
So instead of 25%.
So that kind of weighted estimator is what we do in probability sampling.
And we don’t have to say what the distribution of dogs or cats is in the sample
we entirely rely on the selection mechanism.
What ended up happening in the real world a lot of the time is we don’t actually get to use
those kinds of complex designs.
And instead we collect data through what’s called a non-probability sample.
So in a non-probability sample, it’s pretty easy to define.
You cannot calculate the probability of selection into the sample, right?
So we simply don’t know what the mechanism was that made at unit enter our sample.
I know there’s the biostatistics students in the audience,
you’ve all probably done a lot of data analysis.
And I would venture a guess that a lot of the times
are non-probability samples, right?
A lot of the times there are convenience samples.

I work a lot with biomedical researchers studying cancer patients. Well guess what, it’s almost always a convenient sample of cancer patients, right?

Who will agree to be in the study? Who can I find to be in my study? Other types of non-probability samples include things like voluntary or self-selection sampling, quota sampling, that’s a really old, old school method from polling back many years ago. Judgment sampling or snowball sampling.

So there’s a lot of different ways you can get non-probability samples. So if we go back to the dog and cat example, if I didn’t know anything about how these animals got into my sample and I just saw the four of them, and one of them was orange, I guess, I’m gonna guess 25% of my population is orange. Right?

I don’t have any other information I can’t recreate the population like I could with the weighting. Where I knew how many cats in the population did each of my sampled cats represent and similarly for the dogs.
So of course our best guess looking at these data would just be 25%, right? One out of the four animals is orange. So when you think about a non-probability sample, how much faith do you put in that estimate, that proportion? Hard to say, right? It depends on what you believe about the population and how you selected this non-probability sample but you do not have the safety net of the probability sample that guaranteed you’re gonna get an unbiased estimate of repeated applications of the sampling. So I’ve already used the word selection bias a lot and sort of being assuming that, you know what I mean. So now I’m gonna come back to it and define it. So selection bias is bias arising when part of the target population is not in the sample population, right? So when there’s a mismatch between who got into your sample and who was supposed to get into your sample, right? Who’s the population? Or in a more general statistical kind of way, when some population units are sampled at a different rate.
than you meant. It’s lik you meant for there to be a certain selection probability for orange animals or for dogs but it didn’t actually end up that way. This will end up down the path of selection bias. And I will note that again, as you are biostats students you’ve probably had some epidemiology. And epidemiologists talk about selection bias as well. It’s the same concept, right? That concept of who is ending up in your sample. And is there some sort of a bias in the mechanism? So selection bias is in fact the predominant concern with non-probability samples. In these non-probability samples, the units in the sample might be really different from the units not in the sample, but we can’t tell how different they are. Whether we’re talking about people, dogs, cats, hospitals, whatever we’re talking about. However, these units got into my sample, I don’t know. So I don’t know if the people in my sample look like my population or not. And an important key thing to know is that probability samples when we have a low response rates, right?
So when there are a lot of people not responding, you’re basically ending up back at a non-probability sample, right? Where we have this beautiful design, we know everybody’s sampling weight, we draw a sample, oops, ut then only 30% of people respond to my sample. You’re basically injecting that bias back in again. Sort of undoing the beauty of the probability sample.

So when we think about a selection bias and selection into a sample, we can categorize them in two ways. And Dr. McDougal, actually, when he was giving you my brief little bio used the words that I’m sure you’ve used in your classes before like ignorable and non-ignorable. These are usually are more commonly applied to missingness, right? So ignorable missingness mechanisms and non-ignorable missingness mechanisms. Missing at random, missing completely at random or missing not at random, right? Same exact framework here. But instead of talking about missingness we’re talking about selection into the sample. So when we have an ignorable selection mechanism,
that means the probability of selection depends on things I observed. Right, it depends on the observed characteristics. When I have a non-negotiable selection mechanism now that probability of selection depends on observed characteristics. Again, this is not really a new concept if you understood about missing data, just apply to selection into the sample. So in a probability sample we might have different probabilities of selection for different types of units like for cats versus for dogs. But we know exactly how they differ, right? It’s because I designed my survey based on his characteristic of dog versus cat and I know exactly the status of dog versus cat for my entire population in order to do that selection. So I absolutely can estimate the proportion of orange, animals unbiasedly in the sense of taking repeated stratified samples and estimating that proportion. I hadn’t guaranteed that I’m gonna get an unbiased estimate, right? So this selection mechanism is definitely not non-ignorable, right?
This is definitely an ignorable selection mechanism in the sense that it only depends on observed characteristics. But if my four animals had just come from, I don’t know where? Convenience. Well now why did they end up in my sample? It could depend on something that we didn’t observe.

What breed of dog it was? The age of the dog, the color of the dog. It could have been pretty much anything, right? That’s the problem with the convenient sample.

You don’t know why those units often self-selected to be into your sample. So now I’m gonna head into the kind of ugly statistical notation portion of this stock. So we’ll start with estimated proportions. So we’ll use Y as our binary indicator for the outcome, okay? But here I’m gonna talk about Y more generally as all the survey data. So we’ll start with Y as all the survey data, then we’re gonna narrow it down to Y as the binary indicator? So we can partition our survey data into the data for the units we got in the sample.
and the data for units that are not in the sample. I so selected into the sample versus not selected into the sample. But for everybody I have Z, I have some fully observed what are often called design variables. So this is where we are using information that we know about an entire population to select our sample in the world of probability sampling. And then S is the selection indicator. So these three variables have a joint distribution. And most of the time, what we care about is Y given Z. Right, we’re interested in estimating some outcome characteristic conditional on some other characteristic, right? Average weight for dogs, average weight for cats, right? Y given Z. But Y given Z is only part of the issue, there’s also a selection mechanism, right? So there’s also this function of how do you predict selection S with Y and Z. And I’m using this additional Greek letter psi here to denote additional variables that might be involved, right?
'Cause selection could depend on more than just Y and Z.
It could depend on something outside of that set of variables.
So when we have probability sampling, we have what’s called an extremely ignorable selection mechanism, which means selection can depend on Z, like when we stratified on animal type but it cannot depend on Y. Either the selected units Y or the excluded units Y doesn’t depend on either. Kind of vaguely like the MCAR of selection mechanisms.
It doesn’t depend on Y at all. Observed or unobserved. But it can depend on Z. So that makes it different than MCAR. Including a unit into the sample is independent of those survey outcomes Y and also any unobserved variables, right? That phi here, that phi goes away. So selection only depends on Z. So if I’m interested in this inference target I can ignore the selection mechanism. So this is kind of parallels that idea in the missingness, in the missing data literature, right? If I have an ignorable missingness mechanism I can ignore that part of it. I don’t have to worry about modeling
the probability that a unit is selected.

But the bad news in our non-probability sampling,

very, very arguably true

that you could have non ignorable selection, right?

It’s easy to make an argument for why the people

who ended up into your sample, your convenient sample are different than the people

who don’t enter your sample.

Both of these big data examples.

Think about Twitter data.

Well, I mean, you know,

the people who use Twitter are different

than the people who don’t use Twitter, right?

In lots of different ways.

So if you’re going to think about drawing

some kind of inference about the population,

you can’t just ignore that selection mechanism.

You need to think about how do they enter

into your Twitter sample

and how might they be different than the people

who did not enter into your Twitter sample.

So when we’re thinking about the selection mechanism

basically nothing goes away, right?

We can’t ignore this selection mechanism.

But we have to think

about it when we want to make inference,
even when our inference is about Y given Z, right?

Even when we don’t actually care about the selection mechanism.

So the problem with probability samples is that it’s often very, very hard to model S or we don’t really have a good set of data with which to model the probability someone ended up in your sample.

And that’s basically what you have to do to generalize to the population, right?

There’s methods that exist for non-probability samples require you to do something along the lines of finding another dataset that has similar characteristics and model the probability of being in the probability sample, right?

So that’s doable in many situations but what we’re looking for is a method that doesn’t require you to do that but instead says, let’s do a sensitivity analysis. Let’s say, how big of a problem might selection bias be if we ignored the selection mechanism, right?

If we just sort of took our sample on faith as if it were an SRS from the population. How wrong would we be depending on how bad our selection bias problem is?
So there has been previous work done in this area, in surveys often. Try to think about how confident are we that we can generalize to the population even when we’re doing a probability sample. So there’s work on thinking about the representativeness of a sample. So that’s again, the generalizability to the population. So there’s something called an R-indicator, which is a function of response probabilities or propensities, but it doesn’t involve the survey variables. So it’s literally comparing the probability of response to a survey for different demographic, across different demographic characteristics, for example. Right. And seeing who is more likely to respond then who else? And if there are those differences then adjustments need to be made. There’s also something called the H1 indicator, which does bring Y into the equation but it assumes ignorable selection. So it’s going to assume that the Y excluded gets dropped out. The selection mechanism is only depends on things that you observe, so you can ignore it, right? So it’s ignorable.
So that’s not what we’re interested in. Cause we’re really worried in the non probability space that we can’t ignore the selection mechanism. And there isn’t relatively new indicator called that they called the SMUB, S-M-U-B. That is an index that actually extends this idea of selection bias to allow for non ignorable selection. So it lets you say, well, what would my point estimate be for a mean if selection were in fact ignorable,

and now let’s go to the other extreme, suppose selection only depends on Y. And I’m trying to estimate average weight and whether or not you entered my sample is entirely dependent on your weight. That’s really not ignorable. And then it kinda bounds the potential magnitude for the problem. So that SMUB, this estimator is really close to what we want but we want it for proportions.

especially because in survey work and in large datasets, we very often have categorical data or very, very often binary data. If you think about if you’ve ever participated in an online survey or filled out those kinds of things very often, right, You’re checking a box.
It’s multiple choice, select all that apply.

It’s lots and lots of binary data floating around out there.

And I’ll show you a couple of examples.

So that was a lot of kind of me talking at you about the framework.

Now, let me bring this down to a solid example application.

So I’m going to use the national survey of family growth as a fake population.

So I want you to pretend that I have a population of about 20,000 people.

In this particular case, in this fake population, it’s a very high selection fraction.

That in and of itself is very unusual, right?
A non-probability sample is usually very, very small compared to the full population, let’s say of the United States if that’s who we’re trying to generalize to. But for the purposes of illustration it helps to have a pretty high selection fraction. And we’ll assume that the outcome we’re interested in is whether or not the individual has ever been married. So this is person level data, right? Ever been married. And it is...

we wanna estimate it by gender, and I will note that the NSFG only calculate or only captures gender as a binary variable. This is a very long standing survey, been going on since the seventies. We know our understanding of gender as a construct has grown a lot since the seventies but this survey, and in fact many governmental surveys still treat gender as a binary variable. So that’s our limitation here but I just want to acknowledge that. So in this particular case, we know the true selection bias, right? Because I actually have all roughly 20,000 people so that therefore I can calculate what’s the truth,
and then I can use my smartphone sample and say, "Well, how much bias is there?"
So it turns out that in the full sample 46.8% of the females have never been married. And 56.6% of the males had never been married.
But if I use my selected sample of smartphone users I'm getting a, well, very close, but slightly smaller estimate for females. 46.6% never married. And for males it's like about a percentage point lower than the truth, 55.5%.
So not a huge amount of bias here. My smartphone users are not all that non-representative with respect to the entire sample, at least with respect to whether or not they've ever been married.
So when we have binary data, an important point of reference is what happens if we assume everybody not in my sample is a one, right? What if everybody not in my sample was never married
or everyone not in my sample is a no to never married, right? So like has, has ever been married?
And these are what's called the Manski bounds. When you fill in all zeros or fill in old bonds for the missing values or the values
for those non-selected folks.

So we can bound the bias.

So the bias of this estimate of 46.6 or 46.6%

has to be by definition

between negative 0.098 and positive 0.085.

Because those are the two ends of putting all zeros

or all ones for the people who are not in my sample.

So this is unlike a continuous variable, right?

Where we can’t actually put a finite bound on the bias.

We can with a proportion, right?

So this is why, for example,

if any of you ever work on smoking cessation studies

often they do sensitivity analysis.

People who drop out assume they’re all smoking, right?

Or assume they’re all not smoking.

They’re not calling it that

but they’re getting the Manski bounds.

Okay.

So the question is, can we do better than the Manski bounds?

Because these are actually pretty wide bounds,

relative to the size of the true bias,

and these are very wide.

And imagine a survey where we didn’t have 80% selected.

What if we had 10% selected?

Well, then the Manski bounds are gonna be useless, right?
plug in, all zeros plug in all ones, you’re gonna get these insane estimates that are nowhere close to what you observed.

So going back to the statistical notation, this is where I said we’re going to use $Y$ in a slightly different way.

Now, $Y$, and now forward is the binary variable of interest.

In this case, in this NSFG example it was never married.

We have a bunch of auxiliary variables that we observed for everybody in the selected sample; age, race, education, et cetera, and I’m gonna call those $Z$.

Assume also that we have summary statistics on $Z$ for the selected cases.

So I don’t observe $Z$ for everybody, right? All my non-smartphone users, I don’t know for each one of them, what is their gender?

What is their age? What is their race?

But I don’t actually observe that.

But I observed some kinda summary statistic.

But a mean vector and a covariance matrix of $Z$.

So I have some source of what does my population look like at an aggregate level?

And in practice, this would come from something like census data or in a very large probability sample,
something where we would be pretty confident
This is reflective of the population.
Will note that if we have data for the population
and not the non-selected,
then we can kinda do subtraction, right?
We can take the data for the population
and aggregate and go backwards
to figure out what it would be for the non-selected
by effectively backing out the selected cases.
And similarly another problem
is that we don’t have the variance.
We could just assume it’s what we observe
in the selected cases.
So how are we gonna use this in order
to estimate of selection bias,
what we’re gonna come up
with this measure of unadjusted bias for proportions
called the MUBP.
So the MUBP is an extension of the SMUB
that was for means, for continuous variables
to binary outcomes, right?
To proportions.
High-level, it’s based on pattern-mixture models.
It requires you to make explicit assumptions
about the distribution of the selection mechanism,
and it provides you a sensitivity analysis,
basically make different assumptions on S,
I don’t know what that distribution is, and you’re gonna get a range of bias. So that’s that idea of how wrong might we be? So we’re trying to just tighten those bounds compared to the Manski bounce. Where we don’t wanna have to rely on plug in all zeros, plug in all ones, we wanna shrink that interval to give us something a little bit more meaningful. So the basic idea behind how this works before I show you the formulas is we can measure the degree of selection bias in $Z$, right? Because we observed $Z$ for our selected sample, and we observed at an aggregate for the population. So I can see, for example, that if in my selected sample, I have 55% females but in the population it’s 50% females. Well, I can see that bias. Right, I can do that comparison. So absolutely I can tell you how much selection bias there is for all of my auxiliary variables. So if my outcome $Y$ is related to my $Z$s then knowing something about the selection bias in $Z$ tells me something about the selection bias in $Y$. 
It doesn’t tell me exactly the selection bias in Y but it gives me some information in the selection bias in Y.

So in the extreme imagine if your Zs in your selected sample in aggregate looked exactly like the population.

Well, then you’d be pretty confident, right? That there’s not an enormous amount of selection bias in Y assuming that Y was related to the Z.

So we’re gonna use pattern-mixture models to explicitly model that distribution of S, right?

And we’re especially gonna focus on the case when selection depends on Y.

It depends on our binary outcome of interest. So again, Y is that binary variable interest, we only have it for the selected sample.

In the NSFG example it’s whether the woman or man has ever been married.

We have Z variables available for the selected cases in micro data and an aggregate for the non-selected sample.

a demographic characteristics like age, education, marital status, et cetera. And the way that we’re gonna go about doing this is we’re gonna try to get back to the idea of normality, because then as you all know, when everything’s normal
it’s great, right?

It’s easy to work with the normal distribution. So the way we can do that with a binary variable is we can think about latent variables.

So we’re going to think about a latent variable called $U$. That is an underlying, unobserved latent variables. So unobserved for everybody, including our selected sample. And it’s basically thresholded.

And when $U$ crosses zero, well, then $Y$ goes from zero to one.

So I’m sure many, all of you have seen probit regression, and this is how probit regression is justified, via latent variables.

So we’re going to take our $Z$s that we have for the selected cases, and essentially reduce the dimensionality.

We’re gonna take the $Z$s, run a probate regression of $Y$ on $Z$ in the selected cases, pull out the linear predictor and pull out the linear predictor from the regression, right?

The $X$ beta, right?

Sorry, $Z$ beta. And I’m gonna call that $X$.

That is my proxy for $Y$ or my $Y$ hat, right?

It’s just the predicted value from the regression.
And I can get that for every single observation in my selected sample, of course, right? Just plug in each individual's Z values and get out their Y hat. That's my proxy value. And it's called the proxy because it's the prediction, right? It's our sort of best guess at Y based on this model. So I can get it for every observation in my selected sample, but very importantly I can also get it on average for the non-selective sample. So I have all my beta hats for my probit regression, and I'm gonna plug in Z-bar. And I'm going to plug in the average value of my Zs. And that's going to give me the average value of X for the non-selected cases. I don't have an actual observed value for all those non-selective cases but I have the average, right? So I could think about comparing the average Z value in the aggregate, in the non-selected cases to that average Z among my selected cases. And that is of course exactly where we're gonna get those index from. So I have my selection indicator S, so in the smartphone example,
that’s S equals one for the smartphone users
and S equals zero for the non-smartphone users
who weren’t in my sample.

And importantly, I’m going to allow there to be some other covariates V floating around in here that are independent of Y and X
but could be related to selection.

So it could be related to how you got into my sample but importantly, not related to the outcome.

Notice that all my mus, all my sigmas, my rho, they’ve all got a superscript of j, right?

So that’s whether your S equals zero or S equals one.

So two totally different bi-variate normal distributions depending on if you’re selected or non-selected.

And then we have a marginal distribution
just Bernoulli, for the selection indicator. However, I’m sure you all immediately are thinking, “Well, that’s great, but I don’t have any information to estimate some of these parameters for the non-selected cases.” Clearly, for the selected cases, right? S equals one. I can estimate all of these things. But I can’t estimate them for the non-selected sample because I might observe X-bar. I don’t observe anything having to do with you. ’Cause I have no Y information. So in order to identify this model and be able to come up with estimates for all of these parameters, we have to make an assumption about the selection mechanism. So we assume that the probability of selection into my sample is a function of U. So we’re allowing it to be not ignorable. Remember that’s underlying Y and X, that proxy which is a function of Z. So that’s observed and V, those other variables. And in particular, we’re assuming that it’s this funny looking form of combination of X and U.
That depends on this sensitivity parameter phi. 
So phi it’s one minus phi times X and phi times U. 
So that’s essentially weighting the contributions of those two pieces. 
How much of selection is dependent on the thing that I observe or the proxy builds off the auxiliary variables and how much of it is depending on the underlying latent U related to Y, that’s definitely not observed for the non-selected. Okay. And there’s a little X star here, that’s sort of a technical detail. We’re rescaling the proxy. So it has the same variance as U, very unimportant mathematical detail. So we have this joint distribution that is conditional on selection status. And in addition to, we need that one assumption to identify things. We also have the latent variable problem. So latent variables do not have separately identifiable mean and variance, right? So that’s just... Outside of the scope of this talk that’s just a fact, right?
So without loss of generality we're gonna set the variance of the latent variable for the select a sample equal to one. So it's just the scale of the latent variable. So what we actually care about is a function of you, right?

It's the probability Y equals one marginally in my entire population. And so the probability Y equals one is a probability U is greater than zero. That's that relationship. And so it's a weighted average of the proportion in the selected sample and the proportion in the non-selected sample, right? These are just...

If U has this normal distribution this is how we get down to the probability U equals zero. Like those are those two pieces. So the key parameter that governs how this MUBP works is a correlation, right?

It's the strength of the relationship between Y and your covariates. How good of a model do you have for Y, right? So remember we think back to that example of what if I had no biases Z. Or if Y wasn’t related to Z, well, then who cares that there is no bias in Z.
But we want there to be a strong relationship between Z and Y so that we can kind of infer from Z to Y.

So that correlation in this latent variable framework is called the biserial correlation of the binary X and the continuous.

I mean, sorry, the binary Y and the continuous X, right?

There’s lots of different flavors of correlation, biserial is the name for this one that’s a binary Y and a continuous X when we’re thinking about the latent variable framework.

Importantly, you can estimate this in the selected sample, right?

So I can estimate the correlation between you and X among the selected sample.

I can’t for the non-selected sample, of course, but I can for the selected sample. So the non-identifiable parameters of that pattern-mixture model, here they are.

Like the mean for the latent variable, the variance for the latent variable and that correlation for the non-selected sample are in fact identified when we make this assumption on the selection mechanism.

So let’s think about some concrete scenarios.

What if phi was zero?
If $\phi$ is zero,
we look up here at this part of the formula,
well, then $\phi$ drops out it.
So therefore selection only depends on $X$
and those extra variables $V$ that don’t really matter
because $V$ isn’t related to $X$ or $Y$.
This is an ignorable selection mechanism, okay.
If on the other hand $\phi$ is one,
well, then it entirely depends on $U$.
$X$ doesn’t matter at all.
This is your worst, worst, worst case scenario, right?
Where whether or not you’re in my sample only depends
on $U$ and therefore only depends on the value of $Y$.
And so this is extremely not ignorable selection.
And of course the truth is likely to lie somewhere in between, right?
Some sort of non-ignorable mechanism,
a $\phi$ between zero and one, so that $U$ matters
but it’s not the only thing that matters.
Right, that $X$ matters as well.
Okay.
So this is a kind of moderate,
non-ignorable selection.
That’s most likely the closest to reality
with these non-probability samples.
So for a specified value of $\phi$. 
So we pick a value for our sensitivity parameter. There's no information in the data about it. We just pick it and we can actually estimate the mean of Y and compare that to the selected sample proportion. So we take this select a sample proportion, subtract what we get as the truth for that particular value of phi, and that's our measure of bias, right? So this second piece that's being subtracted here depends on phi. Right, it depends on what your value of your selected parameter is, or selection for your sensitivity parameter is. So in a nutshell, pick a selection mechanism by specifying specifying phi, estimate the overall proportion, and then subtract to get your measure of bias. And again, we don’t know whether we’re getting the right answer because it’s depending on the sensitivity parameter but it’s at least going to allow us to bound the problem. So the formula is quite messy, but it gives some insight into how this index works. This measure of bias is the selected sample mean minus that estimator, right? This is the overall mean of Y based on those latent variables.
And what gets plugged in here importantly for the mean and the variance for the non-selected cases depends on a component that I’ve got colored blue here, and a component that I’ve got color red. So if we look at the red piece this is the comparison of the proxy mean for the unselected and the selected cases. This is that bias in Z, the selection bias in Z, and it’s just been standardized by its estimated variance, right? So that’s how much selection bias was present in Z via X, right. Via using it to predict in the appropriate regression. Similarly, down here, how different is the variance of the selected and unselected cases for X. How much bias, selection bias is there in estimating the variance? So we’re going to use that difference and scale the observed mean, right? There’s that observed the estimated mean of U in the selected sample and how much it’s gonna shift by is it depends on the selection, the sensitivity parameter phi, and also that by serial correlation.
So this is why the by serial correlation is so important. It is gonna dominate how much of the bias in X we're going to transfer over into Y. So if phi were zero, so if we wanna assume that it is an ignorable selection mechanism, then this thing in blue here, think about plugging zero here, zero here, zero everywhere, is just gonna reduce down to that correlation. So we're gonna shift the mean of U for the non-selective cases based on the correlation times that difference in X. Whereas if we have phi equals one, this thing in blue turns into one over the correlation. So here is where thinking about the magnitude of the correlation helps. If the correlation is really big, right? If the correlation is 0.8, 0.9, something really large than phi and... I mean, sorry, then rho and one over rho are very close, right? 0.8 and 1/0.8 are pretty close. So if we're thinking about bounding this between phi equals zero and equals one, our interval is gonna be relatively small. But if the correlation is small, the correlation were 0.2, oh, oh, right?
We’re gonna get a really big interval because that correlation, we’re gonna shift with the factor of multiplied by 0.2 but then one over 0.2. That’s gonna be a really big shift in that mean of the latent variable U and therefore the mean of Y.

So how do we get these estimates? We have two possibilities. We can use what we call modified maximum likelihood estimation. It’s not true. Maximum likelihood because we estimate the biserial correlation with something called a two step method, right? So instead of doing a full, maximum likelihood, we kind of take this cheat in which we set that mean of X for the selected cases equal to what we observe, and then conditional not to estimate the by serial correlation. Alternatively, and we feel is a much more attractive approach is to be Bayesian about this. And as a sensitivity analysis we would plug in zero one and maybe 0.5 in the middle as the values sensitivity parameter. Alternatively, and we feel is a much more attractive approach is to be Bayesian about this. So in this MML estimation, we are implicitly assuming that we know the betas.
from that probate regression.

That we’re essentially treating X like we know it.

But we don’t know X, right?

That probate regression, those parameters have error associated with them.

Right?

And you can imagine that the bigger your selected sample,

the more precisely estimating those betas,

that’s not being reflected at all in the modified maximum likelihood.

So instead we can be Bayesian.

Put non-informative priors on all the identified parameters.

That’s gonna let those, the error in those betas be propagated.

And so we’ll incorporate that uncertainty.

And we can actually, additionally put a prior on phi, right?

So we could just say let’s have it be uniform across zero one.

And we can see what does it look like if we in totality,

if we assume that phi is somewhere evenly distributed

across that interval.

We’ve done other things as well.

We’ve taken like discreet priors.

Oh, let’s put a point mass on 0.5 and one

or other different, right?
You can do whatever you want for that prior.
So let’s go back to the example
see what it looks like.
If we have the proportion ever married for females
on the left and males on the right,
the true bias is the black dot.
And so the black is the true bias.
The little tiny diamond is the MUBP for 0.5.
An so that’s plugging in that average value.
Some selection mechanism that depends on why some,
somewhere in the middle.
So we’re actually coming pretty close.
That happens to be, that’s pretty close.
And the intervals in green
are the modified maximum likelihood intervals
from phi equals zero to phi equals one,
and the Bayesian intervals are longer, right?
Naturally.
We’re incorporating the uncertainty.
Essentially these MUBP,
modified maximum likely intervals are too short.
And we admit that these are too short.
If we plug in all zeros and all ones
for that small proportion of my NSFG population
that we aren’t selected into the sample,
we get huge bounds relative to our indicator.
Right?
So remember when I showed you that slide, that bounded, we know the bias has to be between these two values. That’s what’s going on here. That’s what these two values are. But using the information in Z we’re able to much, much narrow or make an estimate on where our selection bias is.

So we got much tighter bounds. An important fact here is that we have pretty good predictors. Our correlation, the biserial correlation is about 0.7 or 0.8. So these things are pretty correlated with whether you’ve been married, age, education, right?

Well, as it turns out those variables we have on everybody; age, education, gender, those things are not actually that good of predictors, of low income, very low correlation. So our index reflects that. Or you get much, Y, your intervals. Sort of closer to the Manski bounds. And in fact, it’s exactly returning one of those bounds.
The filling in all zeros bound is returned by this index.
So that’s actually an attractive feature.
Right?
We’re sort of bounded at the worst possible case.
on one end of the bias
but we are still capturing the truth.
The Manski bounds are basically useless,
right in this particular case.
So that’s a toy example.
Just gonna quickly show you a real example,
and I’m actually gonna to skip
over the incentive experiment,
which well, very, very interesting
is there’s a lot to talk about,
and I’d rather jump straight to the presidential polls.
So there’s very much in the news now,
and over the past several years,
this idea of failure of political polling
and this recent high profile failure
of pre-election polls in the US.
So polls are probability samples
but they have very, very, very low response rates.
I don’t know how much you know about how they’re done,
but they’re very, very low response rate.
But think about what we’re getting at in a poll,
a binary variable, are you going to vote for Donald Trump?
Yes or no?

Are you gonna vote for Joe Biden?

These binary variables.

We want to estimate proportions.

That’s what political polls aimed to do.

Pre-election polls.

So we have these political polls with these failures.

So we’re thinking, maybe it’s a selection bias problem.

And that there is some of this people

are entering into this poll differentially,

depending on who they’re going to vote for.

So think of it this way,

and I’m gonna use Trump as the example

’cause we’re going to estimate,

I’m gonna try to estimate

the proportion of people who will vote

for Former President Trump in the 2020 election.

So, might Trump supporters

just inherently be less likely to answer the call, right?

To answer that poll or to refuse to answer the question

even conditional demographic characteristics, right?

So two people who otherwise look the same

with respect to those Z variables, age, race, education,

the one who’s the Trump supporter, someone might argue,
you might be more suspicious of the government and the polls, and not want to answer and not come into this poll, not be selected. As it would be depending on why. So the MUBP could be used to try to adjust poll estimates. Say, well, there’s your estimate from the poll but what if selection were not ignorable? How different would our estimate of the proportion voting for Trump? So in this example, our proportion of interest is the percent of people who are gonna vote for Trump. The sample that we used are publicly available data from seven different pre-election polls conducted in seven different states by ABC in 2020. And the way these polls work is it’s a random digit dialing survey. So that’s literally randomly dialing phone numbers. Many of whom get throughout ’cause their business, et cetera, very, very low response rates, 10% or lower. Very, very low response rates to these kinds of polls. They do, however, try to do some weighting. So it’s not as if they just take that sample and say, there we go let’s estimate the proportion for Trump.
We do waiting adjustments and they use what’s called inter proportional fitting or raking to get the distribution of key variables in the sample to look like the population. So they use census margins for, again, it’s gender as binary, unfortunately, age, education, race, ethnicity, and party identification. So, because we’re doing this after the election we know the truth. We have access to the true official election outcomes in each state. So I know the actual proportion of why. And my population is likely voters, because that’s who we’re trying to target with these pre-election polls. You wanna know what’s the estimated proportion would vote for Trump among the likely voters. So the tricky thing is that population is hard to come by summary statistics. Likely voters, right? It’s easy to get summary statistics from all people in the US or all people of voting age in the US but not likely voters. So here Y is an indicator for voting for Trump. Z is auxiliary variable in the ABC poll.
So all those variables I mentioned before gender age, etcetera. We actually have very strong predictors of why basically because of these political ideation, not surprisingly the people who identify as Democrats, very unlikely to be voting for Trump. The data set that we found that can give us population level estimates of the mean of Z for the non-selected sample is a dataset from AP/NORC. It’s called their VoteCast Data. And they conduct these large surveys and provide an indicator of likely voter. So we can basically use this dataset to describe the demographic characteristics of likely voters, instead of just all people who are 18 and older in the US. The subtle issue is of course, these AP VoteCast data are not without error, but we’re going to pretend that they are without error. And that’s like a whole other papers. How do we handle the fact that my population data have error? So we’re gonna use the unweighted ABC poll data as the selected sample and estimate the MUBP.
1183 00:46:25.530 --> 00:46:27.270 with the Bayesian approach with phi
1184 00:46:27.270 --> 00:46:29.270 from the uniform distribution.
1185 00:46:29.270 --> 00:46:32.280 The poll selection fraction is very, very, very
1186 00:46:32.280 --> 00:46:34.030 Right, these polls in each state
1187 00:46:34.030 --> 00:46:36.050 have about a thousand people in them
1188 00:46:36.050 --> 00:46:38.060 but we’ve got millions of voters in each state.
1189 00:46:38.060 --> 00:46:40.040 So the selection fraction is very, very, very
1190 00:46:40.040 --> 00:46:42.090 total opposite of the smartphone example.
1191 00:46:42.980 --> 00:46:45.760 So we’ll just jump straight into the answer,
1192 00:46:45.760 --> 00:46:46.593 did it work?
1193 00:46:46.593 --> 00:46:48.090 Right, this is really exciting.
1194 00:46:48.090 --> 00:46:51.820 So the red circle is the true proportion,
1195 00:46:51.820 --> 00:46:53.410 oh, sorry, the true bias,
1196 00:46:53.410 --> 00:46:54.720 this should say bias down here.
1197 00:46:54.720 --> 00:46:55.600 In each of the states.
1198 00:46:55.600 --> 00:46:56.540 So these are the seven states
1199 00:46:56.540 --> 00:46:59.270 we looked at Arizona, Florida, Michigan, Minnesota,
1200 00:46:59.270 --> 00:47:01.550 North Carolina, Pennsylvania, and Wisconsin.
1201 00:47:01.550 --> 00:47:05.960 So this horizontal line here at zero that’s no
1202 00:47:05.960 --> 00:47:08.140 bias, right?
1203 00:47:08.140 --> 00:47:09.490 would have no bias.
1204 00:47:09.490 --> 00:47:12.920 And we can see then in Arizona where sort
1205 00:47:12.920 --> 00:47:14.060 of overestimated
1206 00:47:14.060 --> 00:47:16.277 we’ve got underestimated the support for
1207 00:47:16.277 --> 00:47:19.140 And so that was really the failure was the
underestimation
of the support for Trump.

Notice that our Bayesian bounds cover the true bias everywhere except in Pennsylvania and Wisconsin.

And so Wisconsin had an enormous bias, or they way under called the support for Trump in Wisconsin by 10 percentage points. Huge problem.

So our bounds are suggesting that there was a negative bias from the poll. So even though we didn’t capture the truth, we’ve at least crossed the threshold saying very likely that you are under calling the support for Trump.

So how do estimates using the MUBP compared to the ABC poll?

Well, we can use the MUBP bounds to basically shift the ABC poll estimates.

So we’re calling those MUBP adjusted, right? So we’ve got the truth is...

The true proportion who voted for Trump are now these red triangles and then the black circles are the point estimates.

from three different methods of estimation, obtaining an estimate.

Unweighted from the poll weighted estimate from the poll.
and the adjusted by our measure of selection bias,
the non-ignorable selection bias is the last one.
Is MUBP adjusted.
So we can see that in some cases
our adjustment and the polls are pretty similar, right?
But look at, for example, Wisconsin,
all the way over here on the right.
So again, remember I said, we didn’t cover the truth
our indicator is the only one, right?
That’s got that much higher shift up towards Trump.
So this is us saying, well,
if there were an underlying selection mechanism
saying that Trump supporters
were inherently less likely to enter this poll,
this is what would happen.
Or this is what your estimated support for Trump would be.
It’s shifted up.
We’ve got a similar sort of success story
I’ll say in Minnesota,
we’re both of the ABC estimators did not cover the truth
in these pre-election polls but ours did, right.
We were able to sort of shift up and say,
look, if there were selection bias
that depended on whether or not you supported Trump
we would captured that.

So the important idea here is, you know,

before the election, we wouldn’t have these red triangles.

But it’s important to be able to see

that this is saying you’re under calling

the support for Trump

if there were a non-negligible selection, right?

So it’s that idea of a sensitivity analysis?

How bad would we be doing?

And what we would say is in Minnesota and Wisconsin

we’d be very worried

about under calling the support for Trump.

So what have I just shown you?

I’ll summarize.

The MUBP is a sensitivity analysis tool

to assess the potential for non-ignorable selection bias.

If we have a phi equals zero, an ignorable selection,

we can adjust that away via weighting

or some other method, right?

So if it’s not ignorable, I mean, if it is ignorable

we can ignore the selection mechanism.

On the other extreme if phi is one,

totally not ignorable,

selection is only depending on that outcome

we’re trying to measure.

Somewhere in between we’ve got the 0.5.

That if you really needed a point estimate
1287 00:50:31.970 --> 00:50:33.610 of the bias, that would be 0.5.
1288 00:50:33.610 --> 00:50:36.630 And in fact, that’s what this black dot is.
1289 00:50:36.630 --> 00:50:40.003 That’s the adjustment at 0.5 for our adjusted estimator.
1290 00:50:41.420 --> 00:50:45.210 This MUBP is tailored to binary outcomes,
1291 00:50:45.210 --> 00:50:47.923 and it is an improvement over the normal base SMUB.
1292 00:50:47.923 --> 00:50:48.980 I didn’t show you the,
1293 00:50:48.980 --> 00:50:51.930 so the results from simulations that basically show
1294 00:50:51.930 --> 00:50:54.550 if you use the normal method on a binary outcome
1295 00:50:54.550 --> 00:50:56.020 you get these huge bounds.
1296 00:50:56.020 --> 00:50:58.180 You go outside of the Manski bounds, right?
1297 00:50:58.180 --> 00:51:01.010 'Cause it’s not properly bounded between zero and one,
1298 00:51:01.010 --> 00:51:03.300 or your proportion isn’t properly bounded.
1299 00:51:03.300 --> 00:51:05.910 And importantly, our measure only requires
1300 00:51:05.910 --> 00:51:08.140 summary statistics for Z,
1301 00:51:08.140 --> 00:51:11.160 for the population or for the non-selected sample.
1302 00:51:11.160 --> 00:51:13.750 So I don’t have to have a whole separate data set
1303 00:51:13.750 --> 00:51:15.660 where I have everybody who didn’t get selected
1304 00:51:15.660 --> 00:51:16.493 into my sample,
1305 00:51:16.493 --> 00:51:19.703 I just need to know the average of these co-variants, right.
1306 00:51:19.703 --> 00:51:23.380 I just needs to know Z-bar in order to get my average
1307 00:51:23.380 --> 00:51:25.580 proxy for the non-selected.
1308 00:51:25.580 --> 00:51:27.100 With weak information,
1309 00:51:27.100 --> 00:51:30.410 so if my model is poor then my Manski bounds
1310 00:51:30.410 --> 00:51:31.560 are gonna be what’s returned.
1311 00:51:31.560 --> 00:51:34.200 So that’s a good feature of this index.
1312 00:51:34.200 --> 00:51:35.670 Is that it is naturally bound
1313 00:51:35.670 --> 00:51:38.000 unlike the normal model version.
1314 00:51:38.000 --> 00:51:41.020 And we have done additional work to move
1315 00:51:41.020 --> 00:51:43.140 beyond just estimating means and proportions
1316 00:51:43.140 --> 00:51:45.950 into linear regression and probate progression.
1317 00:51:45.950 --> 00:51:48.360 So we’ve have indices of selection bias
1318 00:51:48.360 --> 00:51:49.630 for regression coefficients.
1319 00:51:49.630 --> 00:51:52.780 So instead of wanting to know the mean of
1320 00:51:52.780 --> 00:51:54.900 or the proportion with Y equals one,
1321 00:51:54.900 --> 00:51:57.210 what if you wanted to do a regression of Y
1322 00:51:57.210 --> 00:51:58.700 on some covariates?
1323 00:51:58.700 --> 00:52:01.590 So we have a paper out in the animals of
1324 00:52:01.590 --> 00:52:04.750 that extends those two regression coefficients.
1325 00:52:04.750 --> 00:52:06.740 So I believe I’m pretty much right on the
time
1326 00:52:06.740 --> 00:52:09.240 I was supposed to end, so I’ll say Thank you
everyone.
1327 00:52:09.240 --> 00:52:11.170 And I’m happy to take questions.
1328 00:52:11.170 --> 00:52:12.250 I’ll put on my references
1329 00:52:12.250 --> 00:52:15.423 of my meeny, miny fonts, yes.
1330 00:52:15.810 --> 00:52:21.960 Robert Does anybody have any questions?
1331 00:52:21.960 --> 00:52:26.443 From the room?
1332 00:52:26.443 --> 00:52:34.331 So.
1333 00:52:34.331 --> 00:52:37.820 Dr. Rebecca Let me stop my share.
1334 00:52:37.820 --> 00:52:38.653 Student Hey.
1335 00:52:38.653 --> 00:52:41.360 I have a very basic one,
1336 00:52:41.360 --> 00:52:43.740 mostly more of curiosity (indistinct)
Sure, sure.

What is it that caused the...

We know after the fact that in your example that there was the direction of the bias, but why is it that it only shifted in the Trump direction?

Why?

You don’t know in advance if something is more likely

You don’t know in advance if something is more likely or less likely?

Okay.

So excellent question.

So that is effectively, the direction of the shift is going to match...

The direction of the shift in the mean of Y, when the proportion is going to match the shift in X, right?

So if what you get as your mean for your proxy, for the non-selected sample is bigger than for your selected sample then your proportion is gonna get shifted in that direction?

It’s only ever going to shift it to match the bias in X.

And so then, which way that shifts Y depends on what the relationship is between the covariates Z and X in the probate regression. But it will always shift it in a particular direction.
I will notice that I fully admit, our index actually shifted the wrong direction in one particular case. Right?

So actually in Florida, we actually shifted down when we shouldn’t. Right.

So here’s the way to estimate and we’re shifting down, but actually the truth is higher.

So we’re not always getting it right when that X is shifting in the correct direction. Right?

So it isn’t true that we always... It’s true that it always shifts the direction of X, but it’s not a hundred percent true that X always shifts in the exact same way as Y. Just most of the time.

There was evidence of underestimating the Trump support, and that was in fact reflected in that probate regression, right in that relationship.

The people who replied to the poll were older, they were higher educated, right? And so those older, higher educated people in aggregate were less likely to vote for Trump.

So that’s why we ended up under calling the support...
for Trump when we don’t account for that potential non-ignorable selection bias.

Good question though.

Robert Go it, Thank you.

Any other questions (indistinct)

Anybody?

I know I talk fast and that was a lot of stuff so you know, like get it.

Alright.

Well, Andridge, Thank you again.

And.

(students clapping)

Thank you.

Thank you for having me.

Robert Yeah.