ECON526: Quantitative Economics with Data Science Applications

Uncertainty Quantification in Applied Economics

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Overview

Summary

- Last class, we covered the meaning of causal effects and some of the challenges of estimating them from observational data.
- Today, we will discuss how we measure the uncertainty associated with our estimates of causal effects.
- We will also introduce the bias-variance tradeoff and how it relates to the uncertainty of our estimates.

Bias

Bias

- Remember that the bias of an estimator is the difference between the **expected value of the estimator** and the **true value of the parameter** we are trying to estimate.
- There are a number of types of bias that can arise in our estimators.
- In causal inference, we are often interested in the ATE or ATT.
  - → Much of the discussion of bias in causal inference is focused on the bias of estimators of these quantities.
  - → The estimator we are usually concerned about is the difference in sample means between the treatment and control groups.
  - → This particular bias is given by the formula

$$E[Y \mid T = 1] - E[Y \mid T = 0] = \text{ATT} + E[Y_0 \mid T = 1] - E[Y_0 \mid T = 0]$$

Bias

- Some types of bias are due to the fact that we are using an estimator that is not the best one for the parameter we are trying to estimate.
  - $\longrightarrow$ These types of bias can often be fixed by getting more data, or by tweaking the estimator itself.
  - $\longrightarrow$ For example, while $\hat{\sigma}^2 = \frac{1}{n}\sum_{i=1}^{n}(x - \bar{x})^2$ seems like a natural estimator for the variance of a random variable x, it's expected value is actually $E[\hat{\sigma}^2] = \frac{n-1}{n}\sigma^2 = \sigma^2 - \frac{1}{n}\sigma^2 \leftarrow (\mathbf{bias})$.
  - $\longrightarrow$ We can fix this by using $\frac{1}{n-1}\sum_{i=1}^{n}(x - \bar{x})^2$ instead. (The Bessel correction)
  - $\longrightarrow$ Note that $\lim_{n\to\infty} \frac{1}{n} = 0$, so this bias term vanishes as we get more data. This type of estimator is called **consistent**.

Bias

- Now look back at the formula

$$E[Y \mid T=1] - E[Y \mid T=0] = \text{ATT} + \underbrace{E[Y_0 \mid T=1] - E[Y_0 \mid T=0]}_{\text{bias}}$$

- Notice that there is nothing about this bias term that will force it to go to zero as we get more data.
- These types of bias, like **omitted variable bias**, and **selection bias** are more due to the fact that we are ignoring some important aspect of the data-generating process, therefore they can’t be fixed by simply getting more data.

Standard Errors

Standard Errors

- Usually the estimators we study are based on sample averages of random variables.
  - → If we don't have a lot of data, and the data-generating process has a lot of variation, then our sample average will be very sensitive to the particular sample we draw.
  - → As we get more data, the sample average will be closer to the true mean and less sensitive to the particular sample we draw.
- The equation for the standard error of a sample average is: $\mathbf{SE} = \frac{\sigma}{\sqrt{n}}$
  - → Where σ is the standard deviation of the random variable and n is our sample size.
  - → This is called Moivre's equation

Example: School Size and Academic Performance in Brazil

Standard Errors

- The standard error of a sample average is a measure of the uncertainty of our estimate of the true mean.
- To see why this might be important, let's look at an example.
- For this, we will use a dataset that contains ENEM scores for students in Brazil, from different schools, over a three year time period.

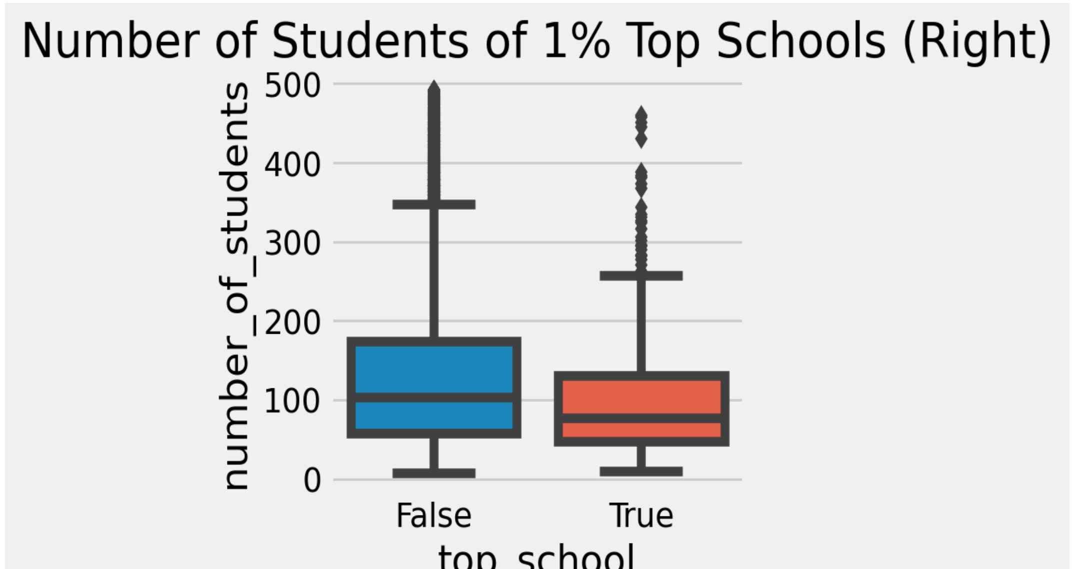
```python
df = pd.read_csv("./data/enem_scores.csv")
df.sort_values(by="avg_score", ascending=False).head(5)
```

	year	school_id	number_of_students	avg_score
16670	2007	33062633	68	82.97
16796	2007	33065403	172	82.04
16668	2005	33062633	59	81.89
16794	2005	33065403	177	81.66

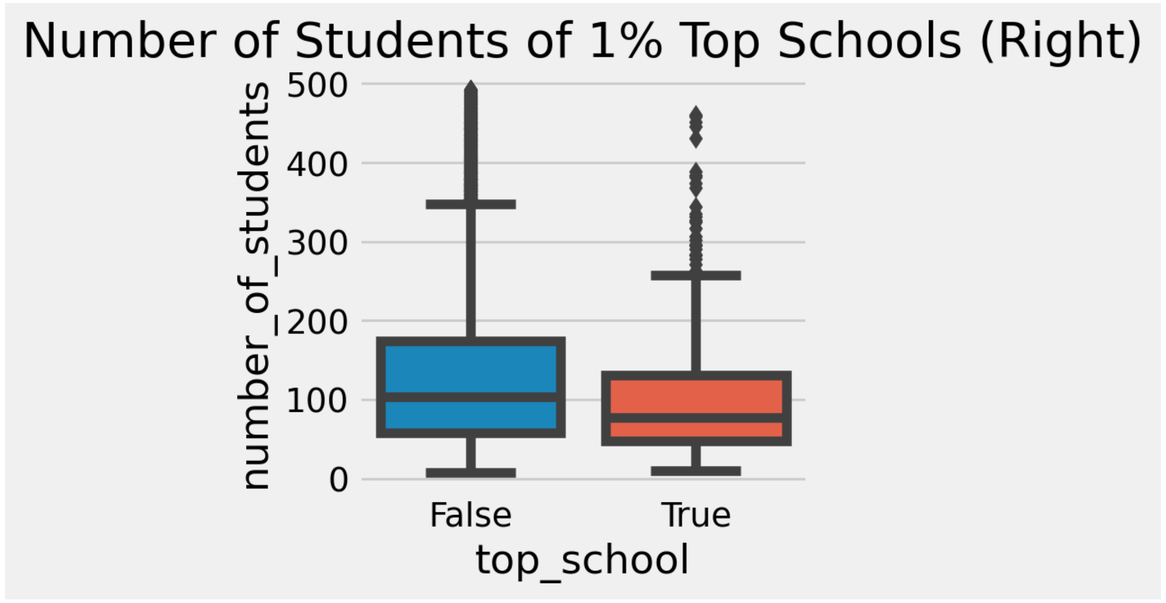
Standard Errors - Example

- We want to discover if there is a relationship between school quality and student performance.
- As a first step, let’s split out the top 1% of schools by average score, and compare the number of students in those schools to the number of students in the rest of the schools.

```
plot_data = (df
  .assign(top_school = df["avg_score"] >= np.quantil
  [["top_school", "number_of_students"]]
  .query(f"number_of_students<{np.quantile(df['numbe

plt.figure(figsize=(3,3))
sns.boxplot(x="top_school", y="number_of_students",
plt.title("Number of Students of 1% Top Schools (Rig
```



Standard Errors - Example

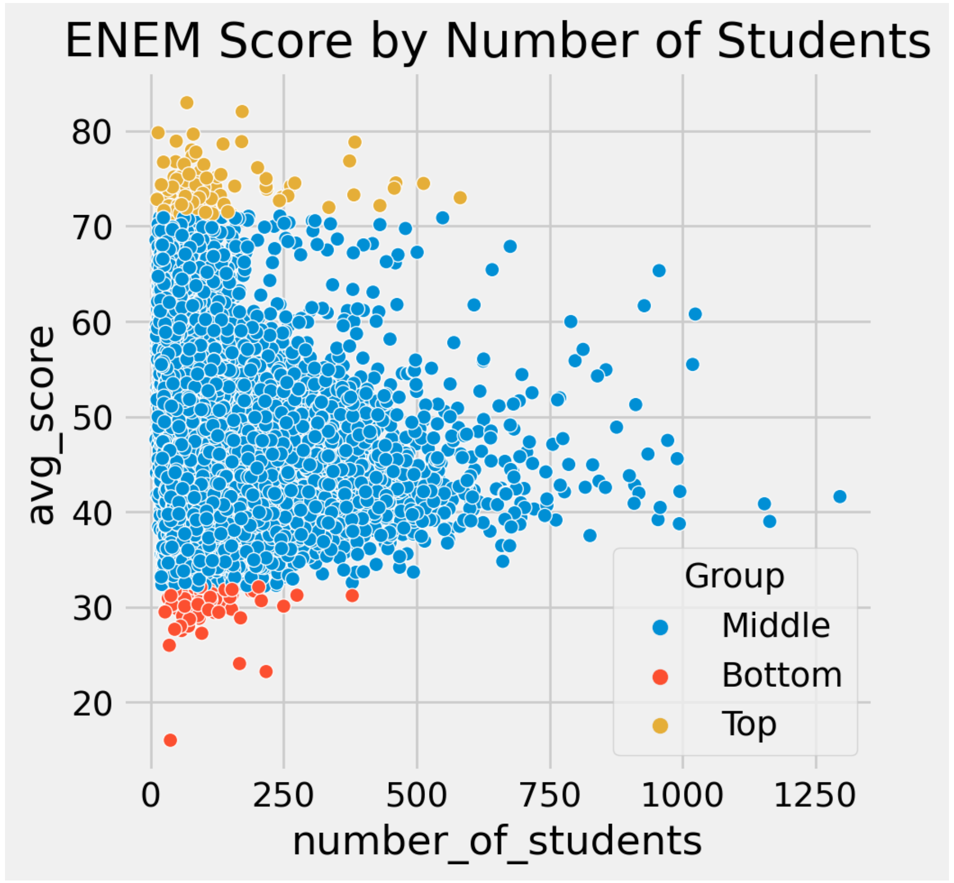


- We can see that the top 1% of schools have a lot fewer students than the rest of the schools.
- This might lead us to draw some conclusions, like “smaller schools are better”.

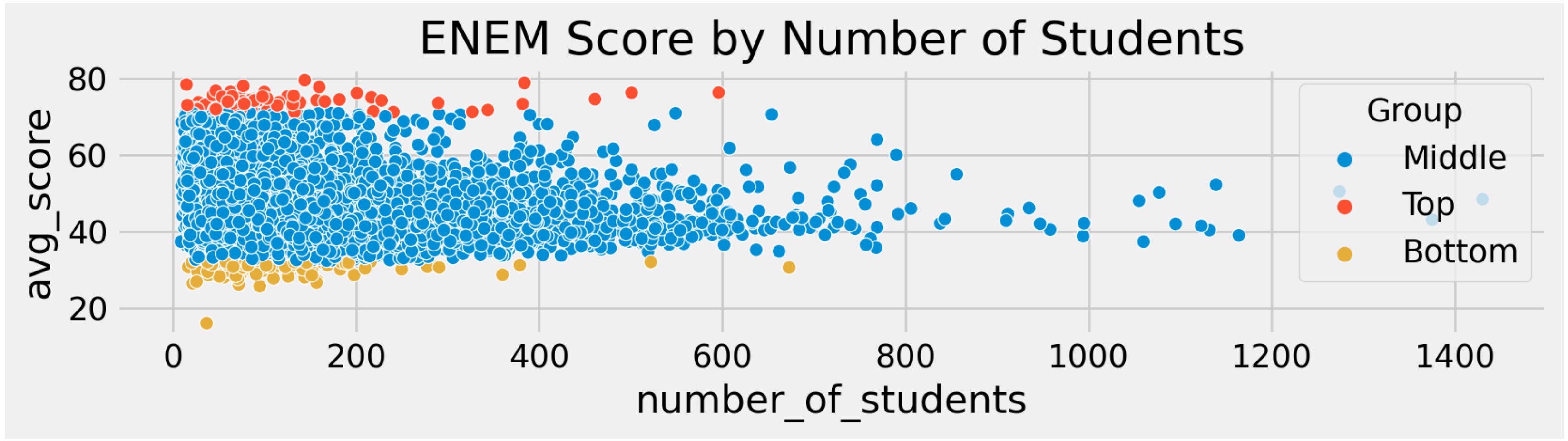
Standard Errors - Example

- Now let's take a look at the full distribution of scores by school size.

```python
q_99 = np.quantile(df["avg_score"], .99)
q_01 = np.quantile(df["avg_score"], .01)

plot_data = (df
  .sample(10000)
  .assign(Group = lambda d: np.select([d["avg_score"]
    ["Top", "Bottom"], "Middle")))
plt.figure(figsize=(5,5))
sns.scatterplot(y="avg_score", x="number_of_students
plt.title("ENEM Score by Number of Students");
```



Standard Errors - Example



- This captures exactly what we would expect if there was no relationship between school size and student performance.
- Our false conclusion is a direct result of the formula $\mathbf{SE} = \frac{\sigma}{\sqrt{n}}$.
- Since each observation in our dataset is a *sample average*, the schools with a lot of students give very precise estimates of the true mean, while the schools with fewer students give noisier estimates.

Example: An Evaluation of Online Learning

Standard Errors in a Causal Context

- Let's return to causal inference.
- We will explore the following data, which contain the results of an RCT that randomized students into online and face-to-face sections of a course.
- This dataset contains observations of 323 students who were randomized into three different class formats. It comes from:
  - → Alpert et al. 2016 *AER*. A Randomized Assessment of Online Learning.

	gender	asian	black	hawaiian	hispanic	unknown	white	format_ol
0	0	0.0	0.0	0.0	0.0	0.0	1.0	0
1	1	0.0	0.0	0.0	0.0	0.0	1.0	0
2	1	0.0	0.0	0.0	0.0	0.0	1.0	0

Standard Errors in a Causal Context

- Since these data come from an RCT, we can estimate the ATE by simply comparing the average scores of the different treatment groups.

```python
(data
 .assign(class_format = np.select(
  [data["format_ol"].astype(bool), data["format_blended"].astype(bool)],
    ["online", "blended"],
    default="face_to_face"
 ))
 .groupby(["class_format"])
 .mean())
```

	gender	asian	black	hawaiian	hispanic	unkn
class_format						
blended	0.550459	0.217949	0.102564	0.025641	0.012821	0.012
face_to_face	0.633333	0.202020	0.070707	0.000000	0.010101	0.000
online	0.542553	0.228571	0.028571	0.014286	0.028571	0.000

Standard Errors in a Causal Context

	gender	asian	black	hawaiian	hispanic	unkn
class_format						
blended	0.550459	0.217949	0.102564	0.025641	0.012821	0.012
face_to_face	0.633333	0.202020	0.070707	0.000000	0.010101	0.000
online	0.542553	0.228571	0.028571	0.014286	0.028571	0.000

- For reference, the averages of these variables are:

	gender	asian	black	hawaiian	hispanic	unknown	w
0	0.578947	0.214575	0.068826	0.012146	0.016194	0.004049	0.684

Standard Errors in a Causal Context

- Now let’s take a closer look at the average scores by treatment group.

```python
exam_scores = (data
 .assign(class_format = np.select(
  [data["format_ol"].astype(bool), data["format_blen
    ["online", "blended"],
    default="face_to_face"
 ))
 .groupby(["class_format"])
 .mean())["falsexam"]
exam_scores
```

```
class_format
blended         77.093731
face_to_face    78.547485
online          73.635263
Name: falsexam, dtype: float64
```

- Since these data come from an RCT, we can estimate the ATE by simply comparing the average scores of the different treatment groups, relative to the control group (face-to-face).

```python
print(f"Online format changed test scores by {(exam_
print(f"Blended format changed test scores by {(exam
```

```
Online format changed test scores by -4.912 points.
Blended format changed test scores by -1.454 points.
```

Standard Errors in a Causal Context

- Online format decreased test scores by almost 5 points, while the blended format decreased test scores by almost 2 points.
  - → *Relative* to the face-to-face format.
- But because of the relatively small sample, there's a chance that our estimates are wrong.
  - → We can use the standard error of the sample average to quantify the uncertainty of our estimates.
  - → Having a low standard error (relative to the size of the effect) gives us more *confidence* that the estimate is correct.

```python
online = data.query("format_ol==1")["falsexam"]
face_to_face = data.query("format_ol==0 & format_ble
def se(y: pd.Series):
    return y.std() / np.sqrt(len(y))
```

```
SE for Online: 1.54 points
SE for Face to Face: 0.872 points
```

Confidence Intervals

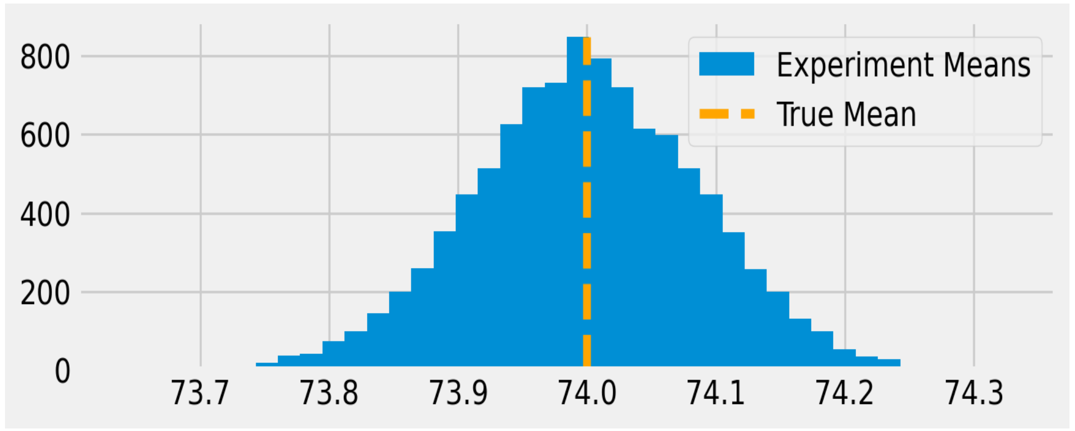
Confidence Intervals

- We can use the standard error of the sample average to construct a **confidence interval** around our estimate.
- A confidence interval is a range of values that we are confident contains the true value of the parameter we are trying to estimate.
- The confidence interval is constructed by taking the sample average and adding and subtracting a multiple of the standard error.
  - $\rightarrow$ The multiple we use is determined by *how* confident we want to be that the true value is in the interval.
  - $\rightarrow$ If the estimator takes a normal distribution, then we can use the quantiles of the normal distribution to determine the multiple.

Confidence Intervals

- Let's suppose we have a true abstract distribution of students' test scores to better grasp this.
- Imagine it is a normal distribution with a true mean of 74 and a true standard deviation of 2.
- We can simulate a sample of 500 students from this distribution and calculate the sample average.

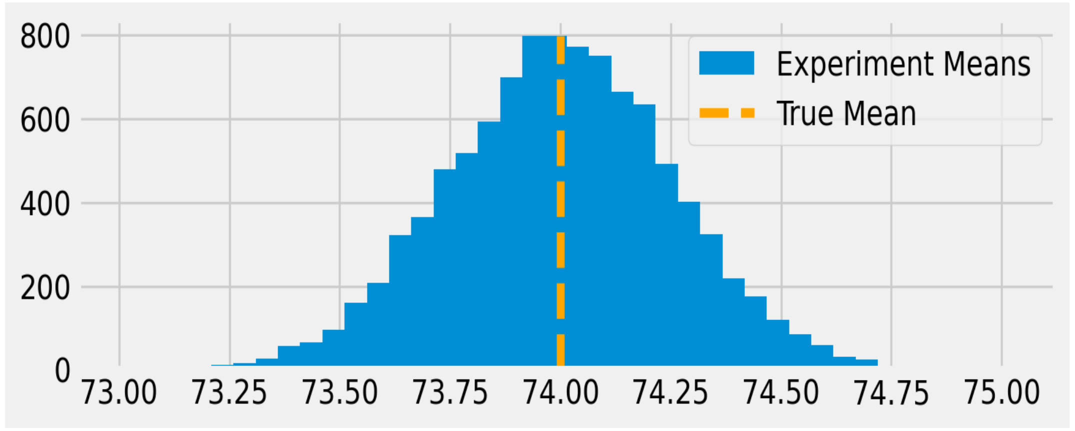
```
def run_experiment():
    return np.random.normal(74, 2, 500)

np.random.seed(42)

plt.figure(figsize=(8,2.5))
freq, bins, img = plt.hist([run_experiment().mean()
plt.vlines(74, ymin=0, ymax=freq.max(), linestyles="
plt.legend();
```



Aside: Central Limit Theorem

- Let's try the same thing, but with the data coming from a uniform distribution.

```python
# these numbers are not realistic, but they have ave
def run_experiment_unif():
    return np.random.uniform(64, 84, 500)

np.random.seed(42)

plt.figure(figsize=(8,2.5))
freq, bins, img = plt.hist([run_experiment_unif().me
plt.vlines(74, ymin=0, ymax=freq.max(), linestyles="
plt.legend();
```



- In fact, the **central limit theorem** tells us that the sample average of *any* * distribution will be normally distributed as the sample size gets large.
  - → *As long as the mean and variance of the distribution are finite.

Confidence Intervals

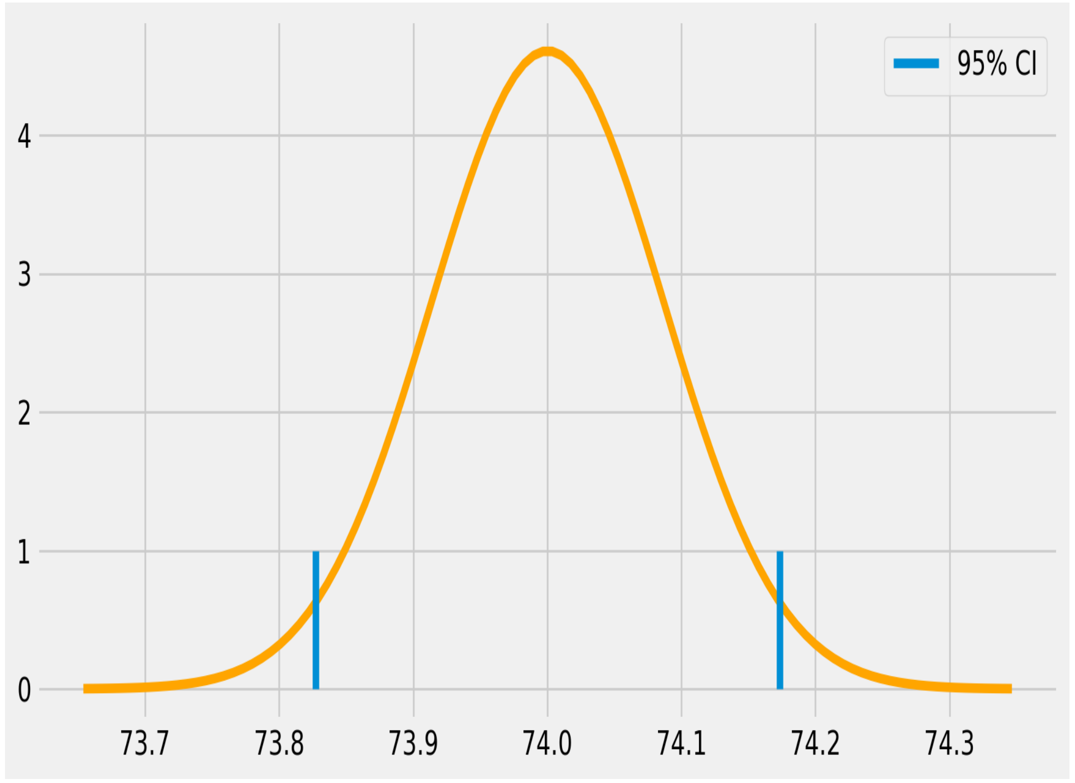
- Of course, usually we won't have the luxury of simulating our experiment thousands of times to get a sense of the distribution of our estimator.
- But we can use the CLT, and the approximate normality of the sample mean, to construct a confidence interval around our estimate.
- Confidence intervals are coupled with a probability (usually 90%, 95%, or 99%).
  - $\longrightarrow$ This probability tells us the percentage of times that we would expect an experiment to produce an estimate within the interval.

Confidence Intervals

- These confidence intervals would look something like this:

```python
np.random.seed(321)
exp_data = run_experiment()
exp_se = exp_data.std() / np.sqrt(len(exp_data))
exp_mu = exp_data.mean()
ci = (exp_mu - 2 * exp_se, exp_mu + 2 * exp_se)
print(ci)
x = np.linspace(exp_mu - 4*exp_se, exp_mu + 4*exp_se
y = stats.norm.pdf(x, exp_mu, exp_se)
plt.plot(x, y, color="orange")
plt.vlines(ci[1], ymin=0, ymax=1)
plt.vlines(ci[0], ymin=0, ymax=1, label="95% CI")
plt.legend()
plt.show()
```

```
(73.82718114045632, 74.17341543460314)
```



Confidence Intervals

- Back to our classroom experiment, we can construct the confidence interval for the mean exam score in both online and face-to-face formats.

```python
def ci(y: pd.Series):
    return (y.mean() - 2 * se(y), y.mean() + 2 * se(

print("95% CI for Online:", ci(online))
print("95% for Face to Face:", ci(face_to_face))
```

```
95% CI for Online: (70.56094429049804, 76.7095818797147)
95% for Face to Face: (76.80278229206951,
80.29218687459715)
```

- Not only are the means different, but the confidence intervals also do not overlap.
  - → This gives us a good amount of certainty that online format actually does decrease test scores.

Confidence Intervals

- Without confidence intervals, point estimates are not very useful.
  - → We can’t tell if the difference between the means is due to chance or not.
  - → We can’t tell if the difference is large or small.
  - → Therefore some measure of uncertainty should *always* be reported along with the point estimate.
- A common mistake is to interpret the confidence interval as the probability that the true value is in the interval.
  - → This is not technically correct.
  - → The true value is either in the interval or it is not.
  - → Really, the confidence interval should be interpreted as the frequency with which the interval would contain the true value, if the experiment were repeated many times.

Hypothesis Testing

Hypothesis Testing

- Another way to quantify the uncertainty of our estimates is to use **hypothesis testing**.
  - → Is the difference in means statistically different from zero (or some other value)?
- Recall that the sum or difference of two independent normal random variables is also normally distributed.
  - → Therefore, we can use the CLT to construct a test statistic that is normally distributed.
- The resulting mean will be the sum or difference between the two distributions, while the variance will always be the sum of their variances:
  - → $N(\mu_1, \sigma_1^2) - N(\mu_2, \sigma_2^2) = N(\mu_1 - \mu_2, \sigma_1^2 + \sigma_2^2)$
  - → $N(\mu_1, \sigma_1^2) + N(\mu_2, \sigma_2^2) = N(\mu_1 + \mu_2, \sigma_1^2 + \sigma_2^2)$

Hypothesis Testing

- Hypothesis testing is another way to quantify the uncertainty of our estimates.
  - $\rightarrow$ It is very closely related to confidence intervals.
- If we have two normal distributions, and want to test if the difference between the means is zero, we can construct a test statistic that is normally distributed.
  - $\rightarrow$ $\mu_{diff} = \mu_1 - \mu_2$
  - $\rightarrow$ $SE_{diff} = \sqrt{\sigma_1^2/n_1 + \sigma_2^2/n_2}$

Hypothesis Testing

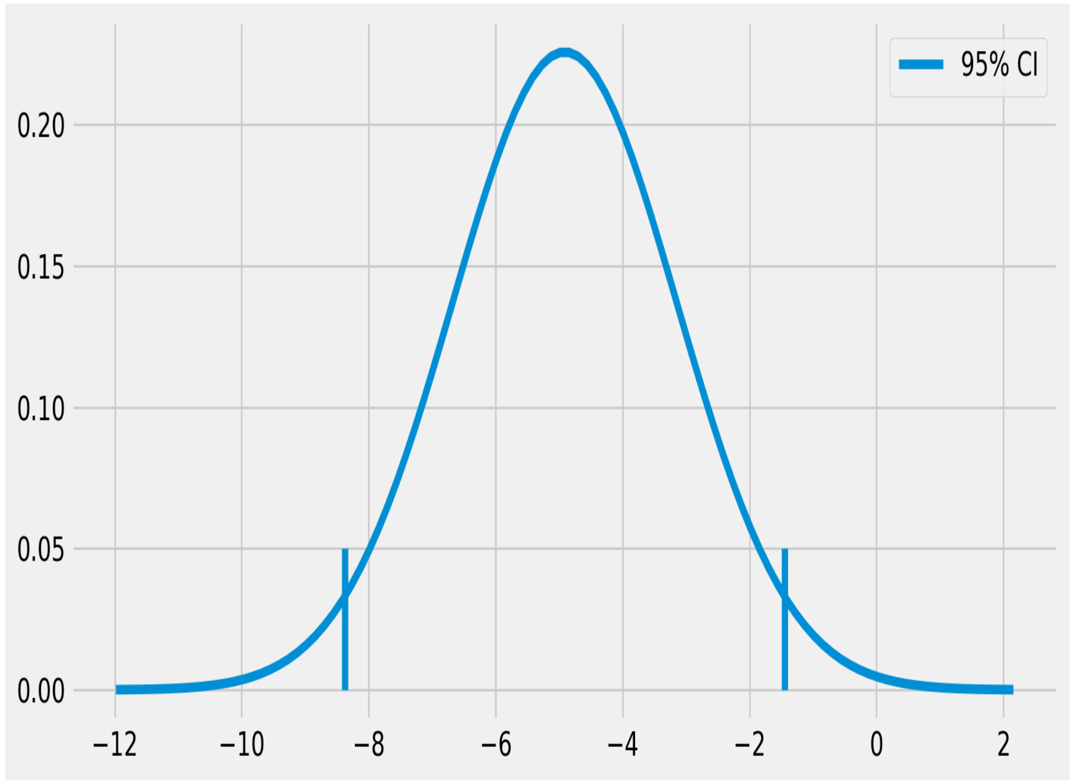
- Returning to our classroom experiment, we can construct a hypothesis test to determine if the difference in means is different from zero.
- The null hypothesis is that the difference in means is zero.
  → $H_0 : \mu_{online} - \mu_{face-to-face} = 0$
- The alternative hypothesis is that the difference in means is *not* zero.
  → $H_1 : \mu_{online} - \mu_{face-to-face} \neq 0$
- Notice that the alternative hypothesis is not that the difference is *positive* or *negative*.
  → This is because we are using a two-sided test.
  → We are testing if the difference is *different* from zero, not if it is *greater* or *less* than zero.
  → The hypotheses are mutually exclusive and collectively exhaustive.

Hypothesis Testing

```python
diff_mu = online.mean() - face_to_face.mean()
diff_se = np.sqrt(face_to_face.var()/len(face_to_face) + online.var()/len(online))
ci = (diff_mu - 1.96*diff_se, diff_mu + 1.96*diff_se)
print(ci)
```

```
(-8.376410208363385, -1.4480327880905248)
```

```python
x = np.linspace(diff_mu - 4*diff_se, diff_mu + 4*dif
y = stats.norm.pdf(x, diff_mu, diff_se)
plt.plot(x, y)
plt.vlines(ci[1], ymin=0, ymax=.05)
plt.vlines(ci[0], ymin=0, ymax=.05, label="95% CI")
plt.legend()
plt.show()
```



Hypothesis Testing

- Based on the results, we can see that based on our original standard errors, we are 95% confident that the true difference in means is between -8.37 and -1.63.
- Therefore, we can reject the null hypothesis that the difference in means is zero, at the 5% level.
- Alternatively, we can say that the difference in means is *statistically significant at the 5% level*.

Hypothesis Testing

- We can also construct a z-statistic to test the null hypothesis.

  $\rightarrow z = \frac{\mu_{diff} - H_0}{SE_{diff}} = \frac{\mu_1 - \mu_2 - 0}{\sqrt{\sigma_1^2/n_1 + \sigma_2^2/n_2}}$
- The z-statistic is the number of standard errors that the difference in means is from the null hypothesis.
- Under the null hypothesis, the z-statistic is normally distributed with mean zero and variance one.

  $\rightarrow z \sim N(0, 1)$
- Therefore, we can simply calculate the z-statistic and compare it to the quantiles of the normal distribution to determine if the difference in means is statistically significant.

P-Values

P-Values

- With all of the previous methods, we have been able to answer yes-or-no questions about our estimates.
  - → Is the difference in means statistically different from zero at the 95% level?
  - → Is the difference in means statistically significant at the 5% level?
- However, a more useful question might be *how* different are the means?
  - → Is the difference in means large or small?
  - → Is the difference in means practically significant?
- To answer these questions, we can use **p-values**.

P-Values

- The p-value is the probability of observing a test (z) statistic at least as extreme as the one we calculate, *if the null hypothesis is true*.
- P-values allow us to quantify uncertainty without needing to specify a confidence level.
  - $\rightarrow$ We can simply report the p-value and let the reader decide what level of uncertainty they are comfortable with.
- The p-value is calculated by taking the area under the normal distribution curve that is more extreme than the test statistic.
  - $\rightarrow$ The p-values is *not* the probability that the null hypothesis is true $P(H_0 \mid data)$.
  - $\rightarrow$ Instead it is the probability of observing the data, under the null $P(data \mid H_0)$.

P-Values

- Let's calculate the p-value for our classroom experiment.

```python
z = diff_mu / diff_se
p_value = 2 * (1 - stats.norm.cdf(z))
print(f"z-statistic: {z:.3}")
print(f"p-value: {p_value:.3}")
```

```
z-statistic: -2.78
p-value: 1.99
```

- The p-value of 0.0027 tells us that we can reject the null hypothesis at the 5% level.
  - → The difference in means is statistically significant at the 5% level. (The 95% confidence interval does not contain zero.)
  - → In fact, we could reject the null hypothesis at the 1% level as well. (The 99% confidence interval does not contain zero.)
  - → However, we could not reject the null hypothesis at the 0.1% (or 0.2%) level. (The 99.9% confidence interval does contain zero.)

Monte-Carlo Methods and Bootstrapping

Monte-Carlo Methods

- We can use Monte-Carlo simulation to simulate the distribution of an estimator, and get some idea of how it will perform.
  - $\longrightarrow$ This is especially useful for estimators that are not asymptotically normal.
  - $\longrightarrow$ For example the minimum or maximum of a uniform distribution is not asymptotically normal.
- Monte-Carlo simulations involve simulating the experiment many times, and calculating the estimator each time, similar to what we did with the `run_experiment` function before.
  - $\longrightarrow$ This knowledge can also be used to construct confidence intervals.

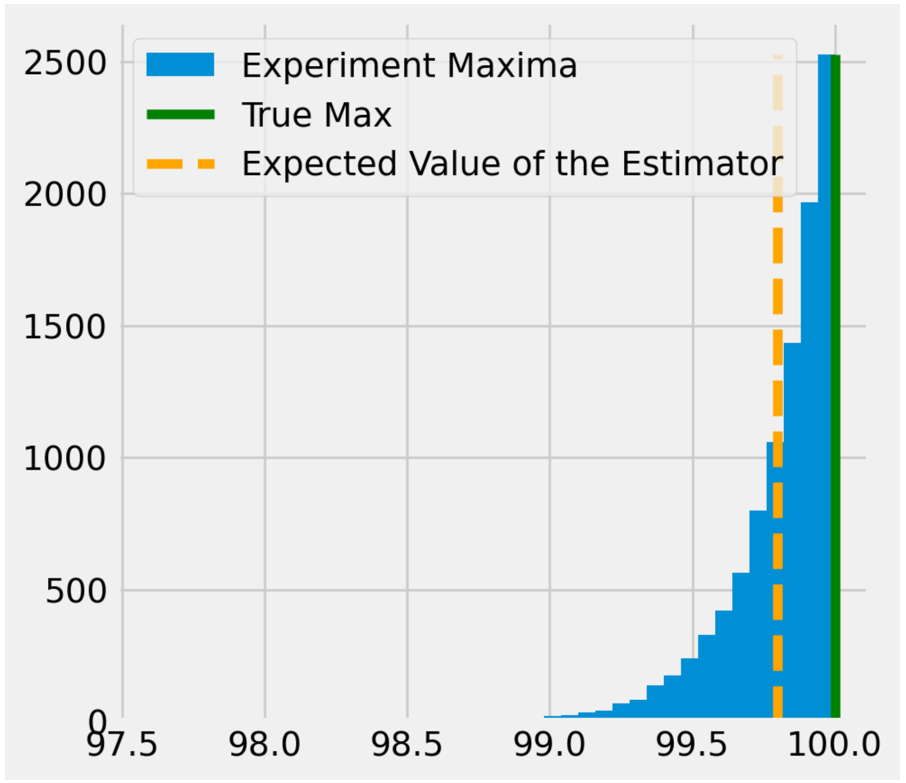
Monte-Carlo Methods

- Let's say that instead of the mean, we want to estimate the `maximum` parameter of a uniform distribution.
  - $\rightarrow$ $X \sim U(0, \alpha)$
  - $\rightarrow$ $\hat{\alpha} = \max_i(X_i)$ (?)
- Note that this is an example of an estimator that is not based on a sample average.
  - $\rightarrow$ Therefore, the CLT does not apply, and the estimator is *not* asymptotically normal.
- We can use the same type of simulations as before to get an idea of how this intuitive estimator is distributed.

Monte-Carlo Methods

```python
def run_experiment_unif(lb = 0, ub = 100):
    return np.random.uniform(lb, ub, 500)

np.random.seed(421)
plt.figure(figsize=(5,5))
max_estimates = np.array([run_experiment_unif().max(
freq, bins, img = plt.hist(max_estimates, bins=40, l
plt.vlines(100, ymin=0, ymax=freq.max(), label="True
plt.vlines(np.mean(max_estimates), ymin=0, ymax=freq
plt.legend();
print("The standard error of our estimator is approx
```

```
The standard error of our estimator is approximately
0.20073906450653084
```



Monte-Carlo Methods

- While the distribution of the estimator is not normal, we can still construct an empirical confidence interval by taking the quantiles of the distribution of the estimator.

  $\longrightarrow$ This gives us some kind of measure of how uncertain we are about the true value of the parameter, given our estimate and the data we have.

- By looking at the graph, we can tell that this estimator is actually biased! Even though it is an intuitive (and consistent estimator), because we have a finite sample, the maximum of the sample is always going to be less than the true maximum.

  $\longrightarrow$ What is the expected value of $\max_i(X_i)$? (*it's not α!*)

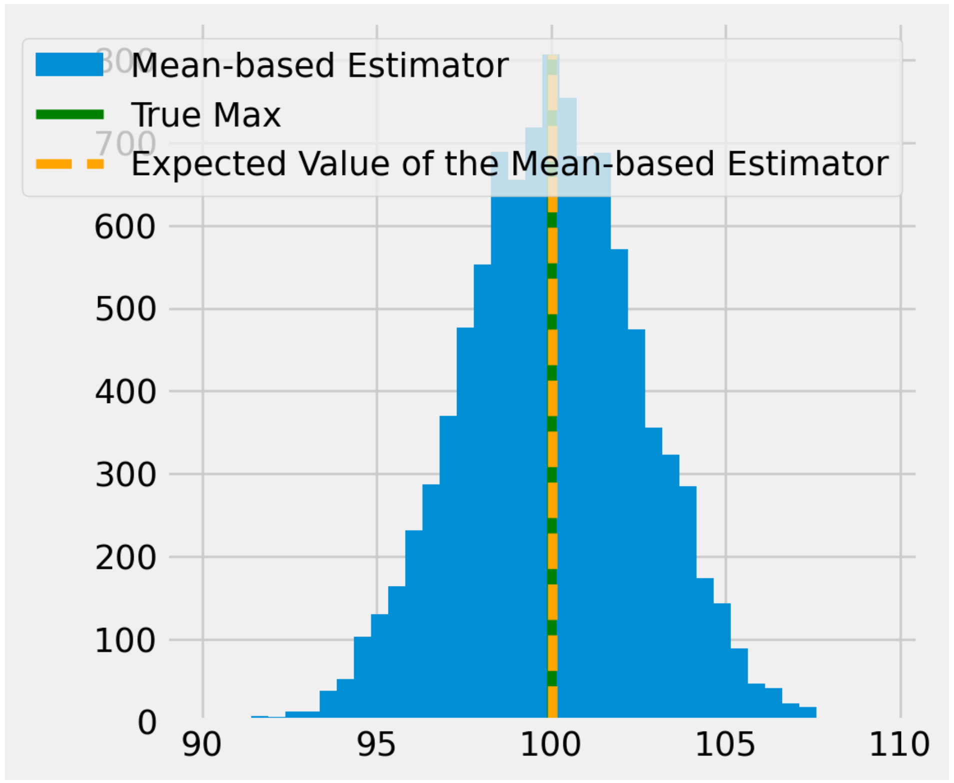
Monte-Carlo Methods

- Another estimator that we could try is using $\hat{\alpha}_2 = 2\bar{X}$
  - $\rightarrow$ Since the lower bound is 0, the mean of the uniform distribution is $\frac{\alpha}{2}$.
  - $\rightarrow$ The expected value $E[\bar{X}] = \frac{\alpha}{2}$, so $E[2\bar{X}] = \alpha$, and this estimator is actually unbiased.
- We can uses Monte-Carlo simulation to get an idea of how this estimator is distributed.

Monte-Carlo Methods

```
plt.figure(figsize=(5,5))
np.random.seed(421)
mean_estimates = np.array([2*run_experiment_unif().m
freq, bins, img = plt.hist(mean_estimates, bins=40,
plt.vlines(100, ymin=0, ymax=freq.max(), label="True
plt.vlines(np.mean(mean_estimates), ymin=0, ymax=fre
plt.legend();
print("The standard error of our mean-based estimato
```

```
The standard error of our mean-based estimator is
approximately 2.580268375420416
```



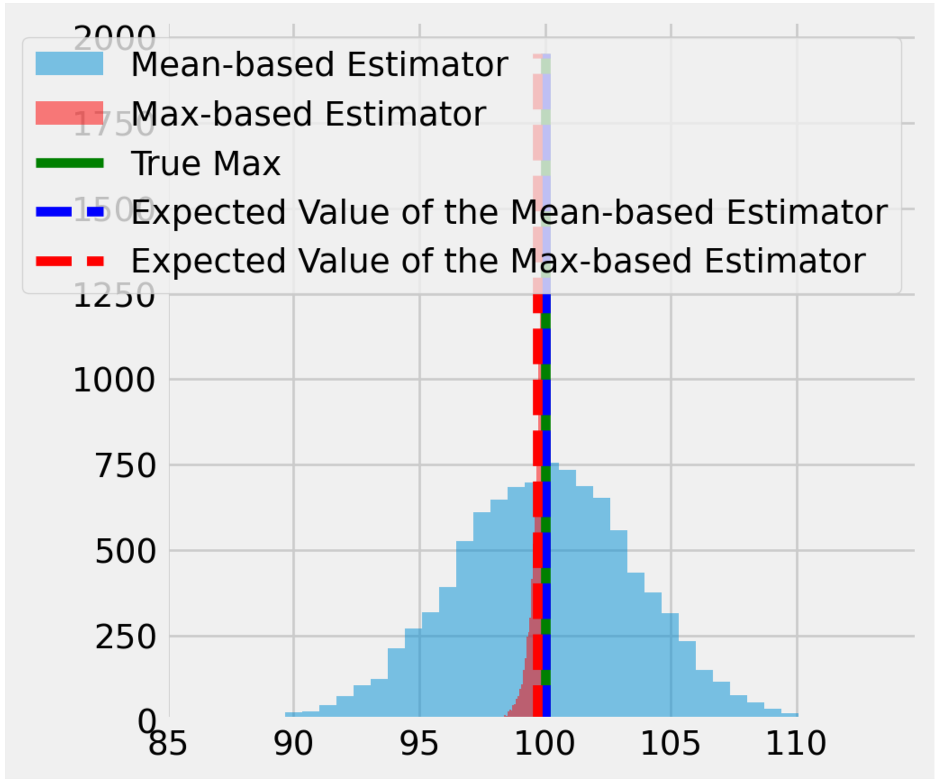
Bootstrapping

- Monte-carlo is a good option when we know the distribution of the estimator, but what if we don't?
- In this case, we can use **bootstrapping** to construct confidence intervals.
  - $\longrightarrow$ Bootstrapping is a non-parametric method for estimating the distribution of an estimator.
  - $\longrightarrow$ It is based on the idea of **resampling** the data.
- Resampling is to create a new sample by drawing observations from the original sample *with replacement*.
  - $\longrightarrow$ This means that some observations will be sampled more than once, and some will not be sampled at all.
  - $\longrightarrow$ The new sample will be the same size as the original sample.
- Let's see what this would look like in our uniform distribution example

Bootstrapping

```
plt.figure(figsize=(5,5))
experiment = run_experiment_unif(ub=100)
resample = lambda sample_size: np.random.choice(run_
mean_estimates = np.array([2*resample(500).mean() fo
max_estimates = np.array([resample(500).max() for _
freq, bins, img = plt.hist(mean_estimates, bins=40,
freq2,bins2,img2 = plt.hist(max_estimates, bins=40,
plt.vlines(100, ymin=0, ymax=freq2.max(), label="Tru
plt.vlines(np.mean(mean_estimates), ymin=0, ymax=fre
plt.vlines(np.mean(max_estimates), ymin=0, ymax=freq
plt.legend();
print("The bootstrap standard error of our mean-base
print("The bootstrap standard error of our max-based
```

```
The bootstrap standard error of our mean-based estimator
is approximately 3.622011142890086
The bootstrap standard error of our max-based estimator
is approximately 0.31176197251081217
```



Bootstrapping

- Bootstrapping can be a good way to approximate the distribution of an estimator when we don't have an analytical solution.
  - → However, it can be computationally expensive, since we need to run the estimation many times.
- Generally, we can think of bootstrap errors as being a "coarse" approximation to the true standard errors. That is, they are likely to be different than the asymptotic standard errors.
  - → They may be either larger or smaller than the asymptotic standard errors.
  - → They are likely to be larger when the sample size is small, and smaller when the sample size is large.
  - → This is not a hard-and-fast rule, and it depends on the estimator.
  - → Even though we don't have to make any assumptions about the distribution of the estimator, we still do have to make an assumption about

The Bias-Variance Tradeoff

The Bias-Variance Tradeoff

- The bias-variance tradeoff is a fundamental concept in statistics and machine learning.
- There is a often a tradeoff between the bias and variance of an estimator.
  - $\longrightarrow$ An estimator with low bias will have high variance.
  - $\longrightarrow$ An estimator with low variance will have high bias.
- While we generally want to minimize both bias and variance, it can often be the case that introducing a little bias will reduce the variance of the estimator by a large amount.
- If you are choosing between estimators that are consistent, then it might be ok to introduce a little bias if it buys you a lot of reduction in the variance.

The Bias-Variance Tradeoff

- Let's look at another example.
- Rembember our first example of a biased estimator, the sample variance.
- The simple sample variance (without the Bessel correction) is biased because $E[\frac{1}{n}\sum_{i=1}^{n}(x_i - \bar{x})^2] = \frac{n-1}{n}\sigma^2$.
  - $\longrightarrow$ The bias term is $\frac{1}{n}\sigma^2$.
- For an unbiased estimator, we simply need to replace $\frac{1}{n}$ with $\frac{1}{n-1}$.
  - $\longrightarrow$ This gets rid of the bias term, and it is still consistent (since the difference between $\frac{1}{n}$ and $\frac{1}{n-1}$ goes to zero as n gets large).

The Bias-Variance Tradeoff

- Let's consider instead the whole class of estimators of the form $\hat{\sigma}^2_c = c\sum_{i=1}^{n}(x_i - \bar{x})^2$.
  - $\rightarrow$ The simple sample variance is the special case where $c = \frac{1}{n}$.
  - $\rightarrow$ The unbiased sample variance is the special case where $c = \frac{1}{n-1}$.
- Remember that $E[\hat{\sigma}^2_{\frac{1}{n}}] = \frac{n-1}{n}\sigma^2$.
  - $\rightarrow$ The bias term is $\frac{1}{n}\sigma^2$.
  - $\rightarrow$ We can use the linearity of expectation to calculate the bias of any estimator of this form.
  - $\rightarrow$ $E[\hat{\sigma}^2_c] = c(n-1)\sigma^2$.
- Therefore, in order to minimize the bias, we need to choose $c = \frac{1}{n-1}$.

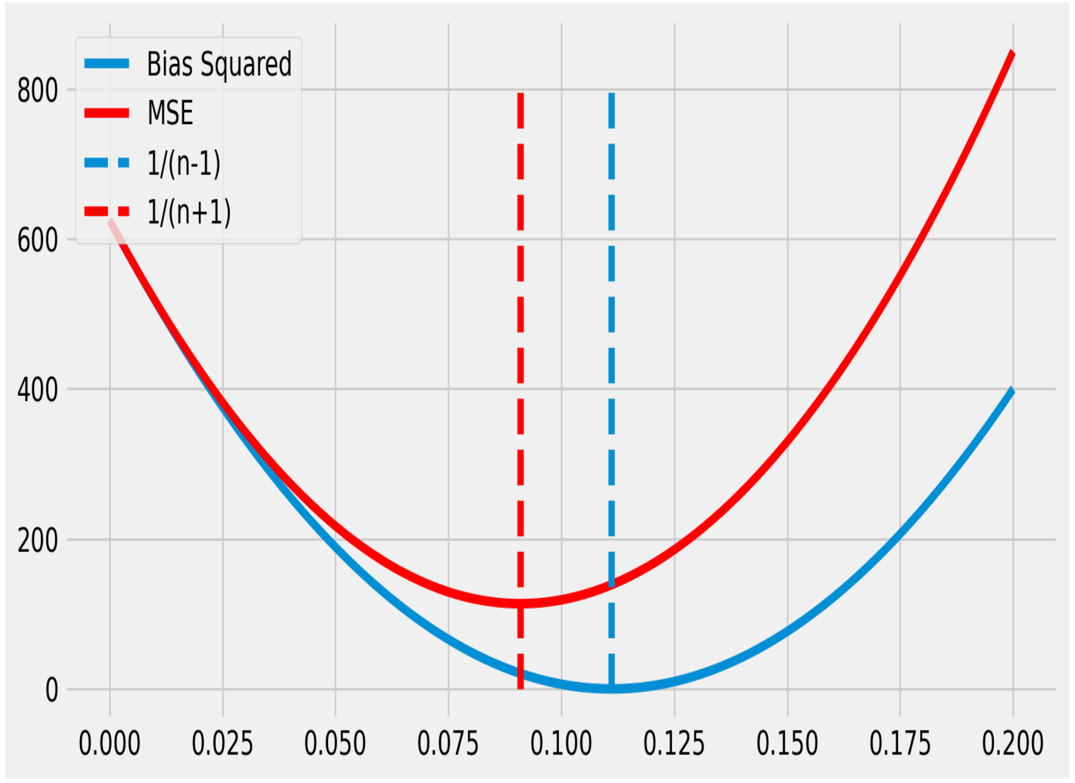
The Bias-Variance Tradeoff

- However, we can also calculate the variance of this estimator.
  - $\rightarrow$ $Var(\hat{\sigma}_c^2) = 2c^2\sigma^4(n-1)$
- Instead of finding the value of c that minimizes the bias, we can find the value of c that minimizes the variance (MSE) of the estimator.
  - $\rightarrow$ $MSE(\hat{\sigma}_c^2) = E[(\hat{\sigma}_c^2 - \sigma^2)^2] = E[\hat{\sigma}_c^2 - \sigma^2]^2 + Var(\hat{\sigma}_c^2)$
  - $\rightarrow$ ($Var(\hat{\sigma}_c^2)$ is the variance of the estimator, or the square of its standard error.)
  - $\rightarrow$ Plugging in our formula for the variance, $MSE(\hat{\sigma}_c^2) = (c(n-1)-1)^2\sigma^4 + 2c^2\sigma^4(n-1)$.
- If we wanted to minimize the standard error of the estimate, instead of the bias, minimizing this MSE would actually lead us to choose $c = \frac{1}{n+1}$.

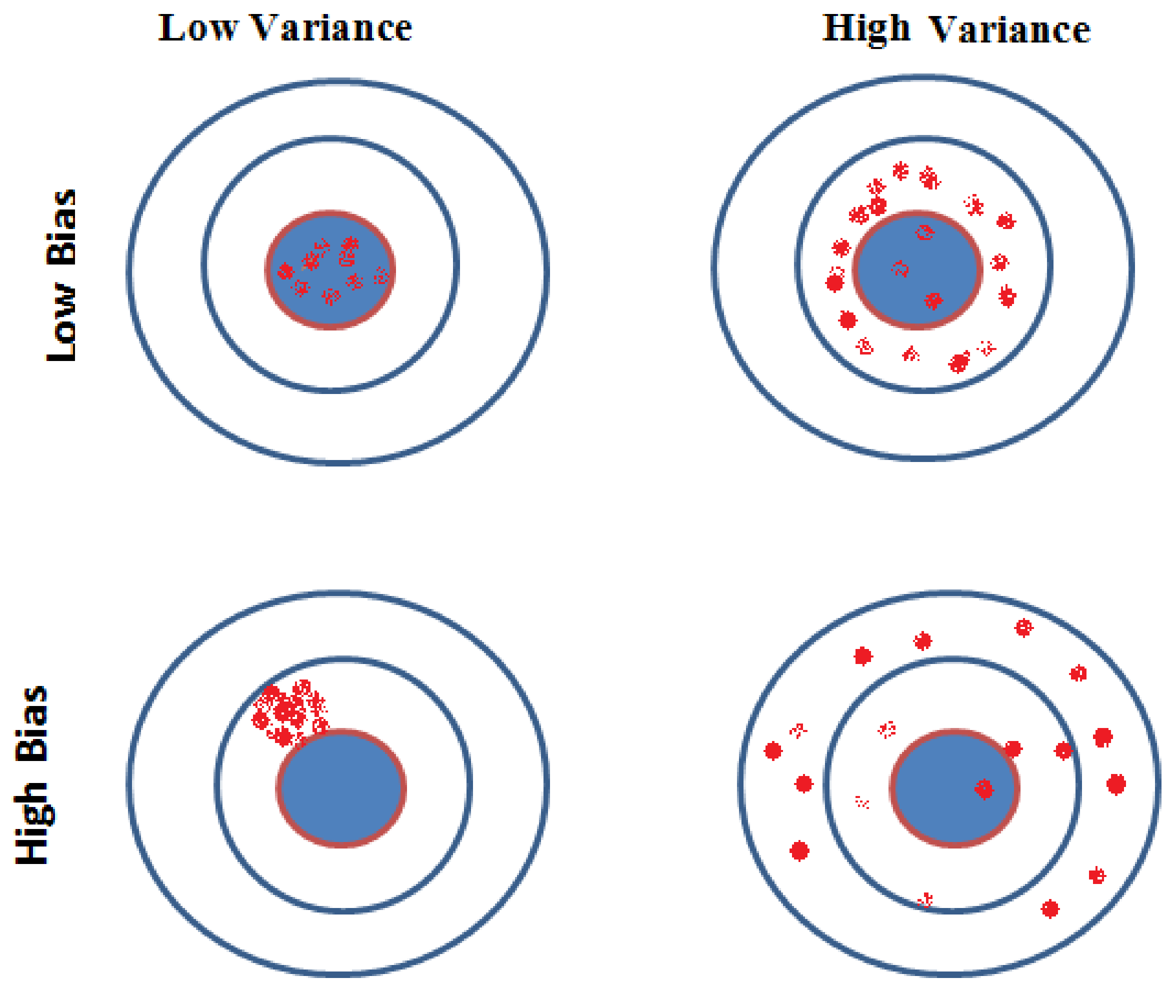
The Bias-Variance Tradeoff

- Let's plot the bias and variance of the estimator for different values of c.

```python
def bias_sq(c,sigma=5,n=10):
    return (c * (n-1)-1)**2 * sigma**4

def mse(c,sigma=5,n=10):
    return (c*(n-1)-1)**2 * sigma**4 + 2 * c**2 * si

n = 10
sigma = 5
c = np.linspace(0, 0.2, 100)
plt.plot(c, bias_sq(c), label="Bias Squared")
plt.plot(c, mse(c), label="MSE", color = "red")
plt.vlines(1/(n-1), ymin=0, ymax=800, linestyles="da
plt.vlines(1/(n+1), ymin=0, ymax=800, linestyles="da

plt.legend(loc="upper left")
plt.show()
```

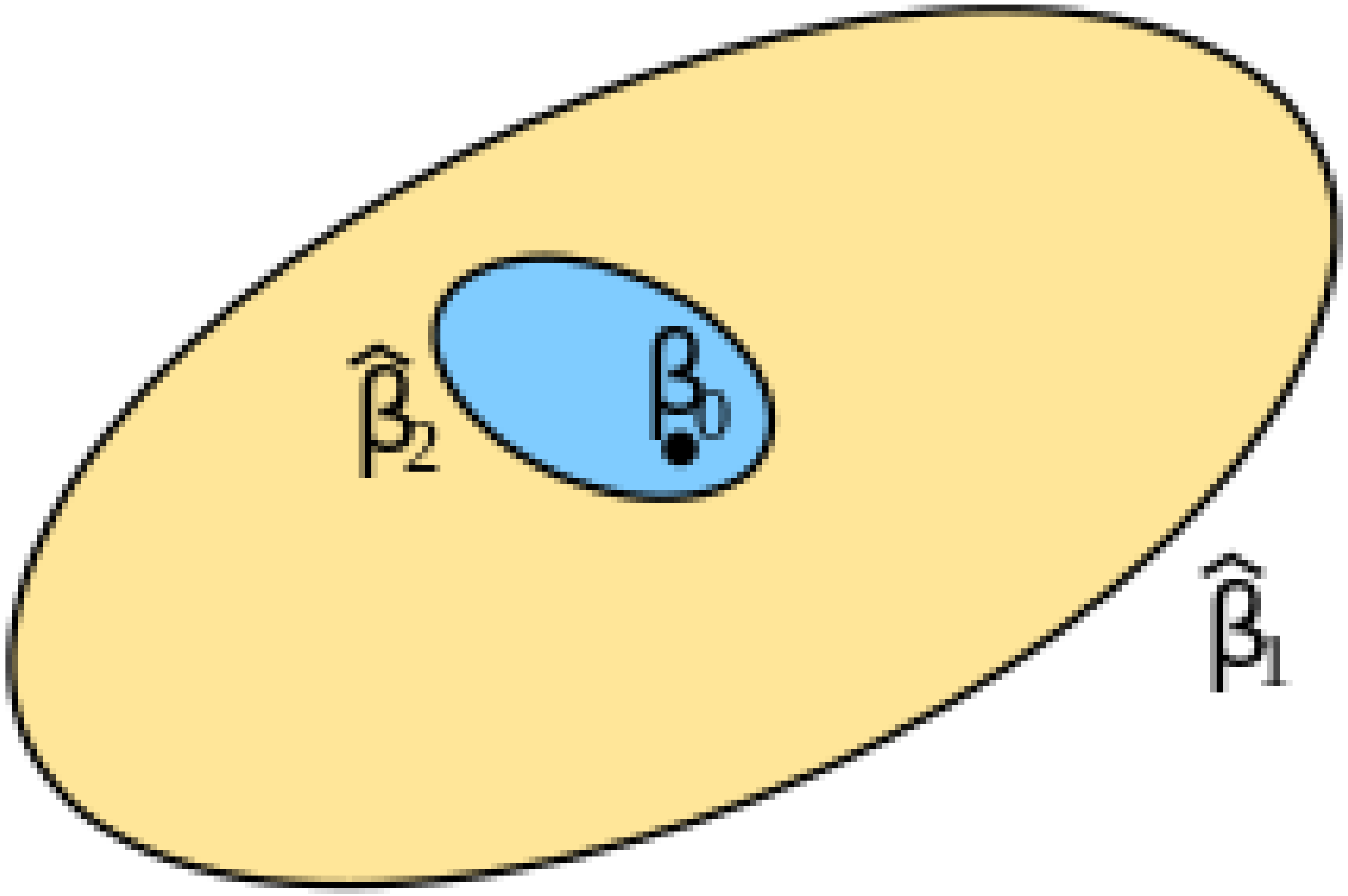


The Bias-Variance Tradeoff



Source: https://en.wikipedia.org/wiki/Bias_of_an_estimator

The Bias-Variance Tradeoff



Source: https://www.shiksha.com/online-courses/articles/bias-and-variance/

Credits

This lecture draws heavily from Causal Inference for the Brave and True: Stats Review - The Most Dangerous Equation by Matheus Facure.