TUT206 Oct 04

Recap: bootstrapping

```
sample = np.random.choice(original_data,
size=len(original_data), replace=True)
```

Bootstrapping is a resampling technique used to estimate the sampling distribution of a statistic by taking repeated samples with replacement from the original sample.

Recap: sample mean vs mean

Aspect	Population Mean (Mean)	Sample Mean
Denotation	μ	$ar{x}$
What it Represents	The average of all members of a population	The average of a subset (sample) of the population
Nature	A fixed value	A variable value that depends on the sample chosen
Purpose	Describes the true central value of the population	Estimates the population mean (μ)

Recap: sample mean vs mean

Population Mean	Sample Mean	
$\mu = \frac{\sum_{i=1}^{N} x_i}{N}$	$\overline{X} = \frac{\sum_{i=1}^{n} x_i}{n}$	
N = number of items in the population	n = number of items in the sample	

Recap: variance and standard deviation

Variance and Standard Deviation Formula



	Population	Sample
Variance	$\sigma^2 = \frac{\sum_{i=1}^{N} (x_i - \mu)^2}{N}$	$S^2 = \frac{\sum_{i=1}^{n} (x_i - \overline{x})^2}{n-1}$
Standard Deviation	$\sigma = \sqrt{\frac{\sum_{i=1}^{N} (x_i - \mu)^2}{N}}$	$S = \sqrt{\frac{\sum_{i=1}^{n} (x_i - \overline{x})^2}{n-1}}$

sd = np.std(original_data, ddof=1)

Recap: Standard deviation vs standard error

Aspect	Standard Deviation (SD)	Standard Error (SE)
What it measures	The variability of individual data points in a sample/population	The variability of a sample statistic (e.g., sample mean)
Used for	Describing the spread of a dataset	Describing the accuracy of a sample statistic as an estimate of a population parameter
Formula	Measures the deviation of data points from the mean	Measures the deviation of sample means from the population mean
Effect of sample size	Unaffected by sample size	Decreases as sample size increases

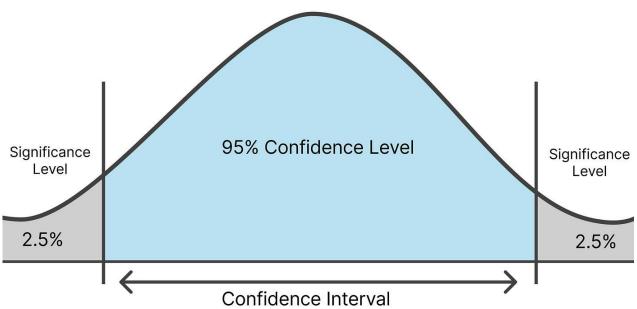
Recap: Standard deviation vs standard error

$$SD = \sqrt{rac{\sum{(x_i - ar{x})^2}}{n-1}}$$

$$SE = \frac{SD}{\sqrt{n}}$$

sd = np.std(original_data, ddof=1)

Recap: confidence interval



A **confidence interval** gives us a range of values within which we are confident the true population parameter lies. For example, a **95% confidence interval** means that we are 95% confident that the interval contains the population mean.

Recap: confidence interval

lower_bound, upper_bound = np.percentile(bootstrapped _means, [2.5, 97.5])

$$CI = \bar{x} \pm z \frac{s}{\sqrt{n}}$$

CI = confidence interval

 \bar{x} = sample mean

z = confidence level value

sample standard deviation

n = sample size

Why is "Single Sample" in Quotes in the TUT Title?

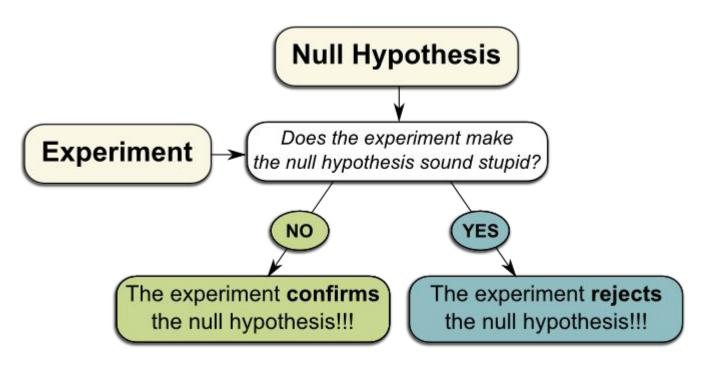
The phrase "single sample" is in quotes because, although we are using only one sample, the idea of generating a sampling distribution (e.g., via bootstrapping) involves simulating many repeated resamples to understand the variability of our sample statistic.

• Null Hypothesis (H_0): Represents the current belief or "status quo". It is what we assume to be true unless there is sufficient evidence to prove otherwise.

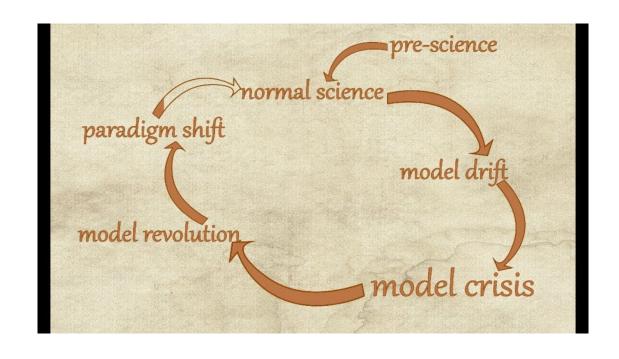
X bar

- ullet Example: $H_0: \mu=\mu_0$, where μ_0 is the hypothesized value of the population mean.
- Alternative Hypothesis (H_1): Represents the new claim or alternative to the null hypothesis.
 - ullet Example: $H_1: \mu
 eq \mu_0$ (Two-tailed test) or $H_1: \mu > \mu_0$ (One-tailed test).

Keep in mind, we can either "reject null hypothesis" or "doesn't reject null hypothesis"



Thomas Kuhn's model of scientific progress, commonly known as the Kuhnian Cycle. This model describes how science evolves over time through different stages



https://colab.research.google.com/drive/1JDlyGaVOKthKzl6Xk7TlpbfDNq70JZp4?usp=sharing

- InitialHealthScore: The health score of the patient before receiving the vaccine or treatment.
- FinalHealthScore: The health score of the patient after receiving the vaccine or treatment.
- HealthScoreChange: Calculated as FinalHealthScore InitialHealthScore, this value indicates whether the patient's health has improved, remained the same, or worsened after the treatment.

The Null Hypothesis [and Alternative Hypothesis]

The null hypothesis usually simply states the "no effect" (on average) assumption

 H_0 : The vaccine has no effect (on average) on patient health $H_1: H_0$ is false

To empasize that "**(on average)**" refers to the pupulation parameter μ (the average effect), it is helpful to more formally (and concisely) express this equivalently as

 $H_0: \mu = 0$ and $H_A: H_0$ is false

Hypothesis Testing

Two-tailed

 H_0 : $\mu = 23$

 H_1 : $\mu \neq 23$



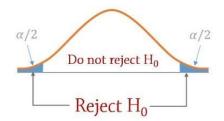
 $H_0: \mu \ge 23$

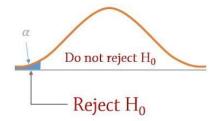
 H_1 : $\mu < 23$

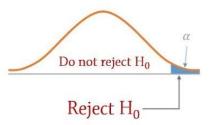
Right-tailed

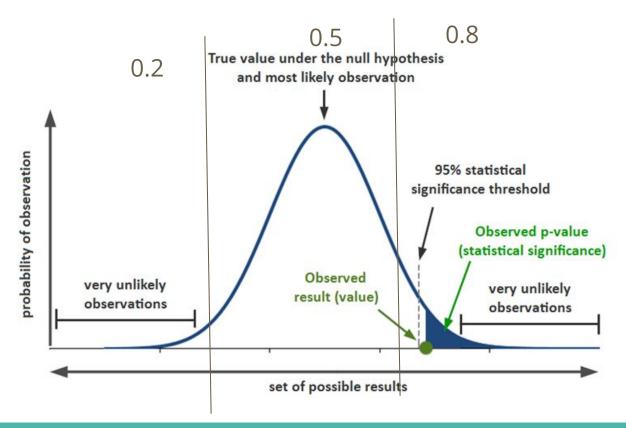
 $H_0: \mu \leq 23$

 H_1 : $\mu > 23$

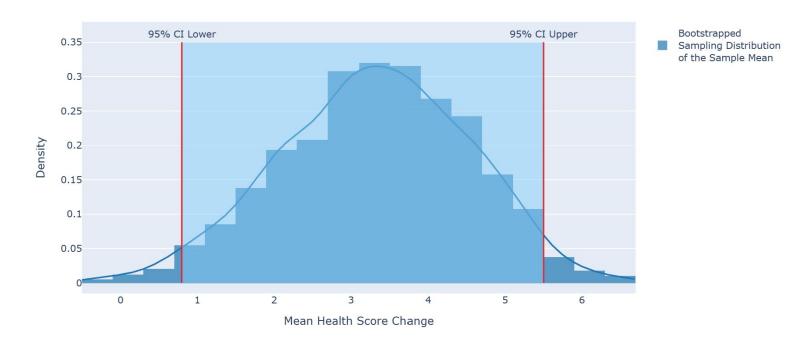








Bootstrapped Sampling Distribution with 95% Confidence Interval



Recap