# Inference and hypothesis testing EDS 222

Tamma Carleton Fall 2023

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- ...the next few weeks. We might need 2.5 weeks for inference + time series. We will focus on going slow enough to fit it all in (we have slack time built in)

Remember week 1? ...why are we we here?

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#### Statistics:

The science of **collecting**, **manipulating**, and **analyzing** empirical data

Statistics enables us to use environmental data to follow the **scientific method** 



#### Thinking about uncertainty

Sampling distributions

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#### Confidence

Confidence intervals

### Thinking about uncertainty

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- We have a *randomly drawn sample* and are trying to learn about the population from our sample
- But our sample statistics would have been different had we randomly drawn a different set of observations!
- This is **natural variability** and it means that all our sample statistics are uncertain estimates of population parameters, even if they are unbiased (e.g., no convenience sampling, no systematic non-response, etc.)

Key question: Is our estimate indicating anything more than sampling variability or "noise"?

• This is the question **statistical inference** and **hypothesis testing** are trying to answer

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- Does this mean there is a gender wage gap, or did we just *happen* to get a few high-earning men and a few low-earning women in this group?
- If we collected another independent sample of 100, would the gap be the same?



Population



Population



**Population relationship** 

 $y_i = 2.53 + 0.57 x_i + u_i$ 

$$y_i=eta_0+eta_1x_i+u_i$$



Sample 1: 30 random individuals



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Population relationship

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Sample relationship

 ${\hat y}_i = 2.36 + 0.61 x_i$ 



Sample 2: 30 random individuals



**Population relationship** 

 $y_i = 2.53 + 0.57 x_i + u_i$ 

Sample relationship

 ${\hat y}_i = 2.79 + 0.56 x_i$ 

#### count: false



Sample 3: 30 random individuals



#### **Population relationship**

 $y_i = 2.53 + 0.57x_i + u_i$ 

#### Sample relationship

 ${\hat y}_i = 3.21 + 0.45 x_i$ 



- On **average**, our regression lines match the population line very nicely.
- However, individual lines

   (samples) can really miss the
   mark.
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Keeping track of uncertainty allows us to test hypotheses about the population using just our sample

# Hypothesis testing: conceptual foundations

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- *H<sub>A</sub>*: **Alternative hypothesis** A hypothesis that the measured quantity is nonzero. In other words: whatever I recovered in my sample is due to true population differences or effects.

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You have a random sample of 100 tagged ducks in Minnesota from 2010 and 2023.

- Mean 2010 latitude: 44.27 degrees N
- Mean 2023 latitude: 46.12 degrees N
- Standard deviation 2023 latitude: 0.92 degrees

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You have a random sample of 100 tagged ducks in Minnesota from 2010 and 2023.

- Mean 2010 latitude: 44.27 degrees N
- Mean 2023 latitude: 46.12 degrees N
- Standard deviation 2023 latitude: 0.92 degrees
- $H_0$ : The average latitude was the same in the two years. That is, $\mu_{2023}-\mu_{2010}=0$
- $H_A$ : The average latitude was not the same in the two years. That is,  $\mu_{2023}-\mu_{2010}
  eq 0$
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Here, the difference in mean latitude between the 2023 sample and the 2010 sample is:

• 46.12 - 44.27 = 1.85

Hypothesis test asks if this point estimate is actually different from zero once we account for sampling variability

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Rejecting the null involves both a **point estimate** and a measure of **uncertainty** or spread in your data

### Hypothesis testing: in practice

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We already know all about these two steps.

- Null and alternative hypotheses will depend entirely on the statistical question of interest.
- Data collection and point estimates (e.g., means, regression parameters, variances, etc.) we have studied at length in this class

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Ack! What is this? Something about how much noise there is in a sample statistic in any given sample...

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Let's turn to some definitions.

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- The sampling distribution describes how sample statistics (e.g., mean, regression parameters) vary from one sample (or study) to the next
- This is *not* the same as the **data distribution**!
  - Distribution of your data = distribution within one sample (e.g., gives you one sample mean)
  - Sampling distribution = distribution across samples (e.g., gives you many sample means)

For example, recall our regression above, where the population model is:

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For example, recall our regression above, where the population model is:

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- A regression using one sample gives us *one* set of coefficients, called the **point estimates**. For example,  $\hat{\beta}_0 = 2.36$  and  $\hat{\beta}_1 = 0.61$
- If we could collect 1000 samples and run that regression 1,000 times, we would recover the **sampling distribution** for each coefficient

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#### But how do we obtain one of these?

You only have one sample of data! Where does the sampling distribution come from?

#### We derive the sampling distribution from applying the Central Limit Theorem

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This is true *even if* the underlying data are not normally distributed!



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#### Question: How big does our sample need to be?

#### Answer: Rule of thumb is $n \geq 30$

But this is not a hard and fast rule! Be cautious about hypothesis testing and inference with small sample sizes.

#### Standard errors

So we know the sample statistic is drawn from a normal distribution...

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#### We need to know the $\mu$ and $\sigma$ of our sampling distribution in order to fully

model the variability of our statistic.



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- $H_0$ : Male and female wages have a mean *difference* of zero.  $\mu_{men}-\mu_{women}=0.$
- $H_0$ : There is *no effect* of neonicotinoid use on colony collapse disorder.  $\beta_1 = 0$ . (Note that linear regression parameters are conditional means -- mean of y conditional on a level of x)

## Standard error of the sample mean

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For example, if we are interested in a sample mean, our friend the **Central Limit Theorem** tells us that:

$$SE=rac{s^2}{\sqrt{n}}$$

where s is the sample standard deviation and n is the sample size.

Q: What happens to the standard error as sample size increases? Why?

## Standard error for regression slope

# The standard deviation of your sampling distribution is called the **standard error**

How you calculate the standard error depends on the research question.

For example, if we are interested in a regression slope, the CLT plus some algebra tell us that:

$$SE = \sqrt{var({\hat eta}_1)} = \sqrt{rac{s^2}{\sum_i (x_i - ar x)^2}}$$

where  $s^2$  is the sample variance of model errors  $\hat{y}_i - y_i$ 

Q: What happens to the standard error as sample size increases? Why?

## SE for comparing two means

# The standard deviation of your sampling distribution is called the **standard error**

How you calculate the standard error depends on the research question.

For example, if we are interested in the *difference* between two means, the CLT plus some algebra tell us that:

$$SE = \sqrt{rac{s_1^2}{n_1} + rac{s_2^2}{n_2}}$$

where  $s_k$  is the sample standard deviation in each of the two samples and  $n_k$  is the sample size in each sample

In all these cases, the SE is the standard deviation of the sampling distribution!

### Summary: Standard errors

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**Standard error** measures how dispersed our sample statistic is around the population parameter of interest (highly dispersed = large SE = a lot of uncertainty about the population parameter from our one sample)

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- I know how that my sample statistic is drawn from a normal distribution with mean  $\mu$  and an estimated standard deviation given by SE.
- This should tell me something about **how unlikely it was** that I happened to draw my point estimate if the null were true, right?
- Yep! But we need a couple more definitions to get all the way there.

#### The 68-95-99.7 rule

#### For a normal distribution:



Probabilities for falling within 1, 2, and 3 standard deviations of the mean in  $$^{36\,/\,57}$$ 

#### Z-score

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Z-score: How many standard deviations is a value from the mean?

$$z=rac{x_i-\mu}{\sigma}$$

where  $\mu$  is the mean and  $\sigma$  is the standard deviation

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*p*-value is the probability of getting a point estimate *at least as extreme* as ours **if the null hypothesis were true.** 

$$p-value=Pr(Z<-|z| ext{ or } Z>|z|)=2*Pr(Z>|z|)$$

where z is the z-score computed using your point estimate.

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$$p-value = Pr(Z < -|z| ext{ or } Z > |z|) = 2*Pr(Z > |z|)$$

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Question: What feature of the normal distribution lets us simplify this to 2 \* Pr(Z > |z|)?

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How do I compute a *p*-value from a test statistic?

- In math: Integrate the sampling distribution's probability density function between  $-\infty$  and -|z|; multiply by 2
- In R: pnorm(), t.test(), summary(lm()),...

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The **Central Limit Theorem** has done a lot of work for us so far. However, it only holds under the following conditions:

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- 2. We have a **large enough sample** (at the very least  $n \geq 30$ )

When n is relatively small, we can still proceed, we just need to use a t-distribution (and T-score -- use pt() in R) instead of a normal distribution (and Z-score)



# Hypothesis testing in five steps

The general framework for implementing a hypothesis test is:

- 1. **Define the null** and alternative hypotheses
- 2. Collect data and compute the **point estimate of the statistic**
- 3. Model the **variability of the statistic**
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- Traditionally, we use a **significance level** of lpha=0.05
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  - $\circ\,$  Reject the null if p < 0.05 and lpha = 0.05
- In general, reject the null if p < lpha.
  - Other common  $\alpha$ s: 0.01, 0.1

## Statistical significance

#### We say a point estimate is "statistically significant" when:

 $p < \alpha$ 

For example:

"[W]e find a **statistically-significant** effect whereby increases in surface UV intensity lowers subsequent COVID-19 growth rates...we estimate that a 1 kJm-2hr-1 increase in local UV reduces local COVID-19 growth rates by .09 (±.04, *p* =.01) percentage points over the ensuing 17 days." --- *Carleton et al., 2021* 

We can **reject the null** hypothesis *or* **fail to reject the null** hypothesis.

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• Failing to reject the null tells us we do not have sufficient evidence to prove there is an effect or a difference

## Constructing confidence intervals

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- Effect sizes are important! We care not just about whether a treatment effects an outcome, but by *how much*

A **confidence interval** is a range of plausible values where we may find the true population value.

• It tells us something about the magnitude of the parameter of interest, as well as our uncertainty around our estimate

When the sampling distribution of a point estimate can be modeled as normal, the point estimate we observe will be within 1.96 standard errors of the true value of interest about 95% of the time (think back to the 68-95-99.7 rule).

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Thus, a 95% confidence interval for such a point estimate can be constructed:

point estimate  $\pm$  1.96 \* SE

We can be 95% confident this interval captures the true value.

Also can see this as: 2\*pnorm(-1.96) = .05

You can build a confidence interval for any level of  $\alpha$ :

```
	ext{point estimate} \pm z_{lpha/2} * SE
```

where  $z_{lpha/2}$  is a "critical value" that varies with significance level lpha.

 $z_{lpha/2}$  is the z-score at which lpha/2 percent of the sampling distribution exceeds that z-score

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Why do the z-scores get larger for higher confidence intervals?

#### A 95% confidence interval visual



## Confidence intervals: Interpretation

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#### Why is this a big deal?

The population parameter *is not random*. So it either **is or is not** inside your CI.

#### Slides created via the R package **xaringan**.

Some slide components were borrowed from Ed Rubin's awesome course materials.