

# LDI Seminar Series in Biostatistics: Lecture 2

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September 25, 2017

- Slides, tutorial, video will be available eventually through LDI
- For now I will upload slides (before the lecture) to my personal Github page:
- <http://github.com/kevinmcgregor/LDI-Biostatistics-Seminar>
- Tutorials and instructions posted there as well.
- Email: [kevin.mcgregor@mail.mcgill.ca](mailto:kevin.mcgregor@mail.mcgill.ca)

# Last time

- Outlined difference between population parameters and statistics.
- Defined some simple descriptive statistics.
- Showed some simple types of plots.

- We've seen some tools for doing an initial data exploration.
- We know how to calculate estimates of several population parameters.
- We don't yet know how to determine if our results are “significant”.
- Can do this through *hypothesis testing*.

# Research question

- Before performing a statistical test, we need to define what parameter we're investigating, and in what way it's being tested
- Consider two hypotheses corresponding to two possible states of the world: the null hypothesis ( $H_0$ ) and the alternate hypothesis ( $H_1$  or  $H_a$ ). Usually boils down to:

$H_0$  : Nothing interesting to see

$H_1$  : Hey, there could be something here!

# Hypothesis testing examples

- A sample of grad students at McGill is taken and an IQ test is administered... do McGill grad students have a different IQ on average than the general population ( $=100$ )?

$H_0$  : Average IQ in McGill grad students equal to 100

$H_1$  : Average IQ in McGill grad students not equal to 100

- Mean survival time in patients taking drug  $A$  vs.  $B$ :

$H_0$  : Mean survival time is the same between groups

$H_1$  : Mean survival time differs between groups

# Hypothesis testing

- Always define the hypotheses with respect to parameters... never with respect to statistics!
- In the IQ example, if  $\bar{x}$  is the mean IQ in the sample, and  $\mu$  is the mean IQ among McGill grad students:

$$H_0 : \mu = 100$$

$$H_1 : \mu \neq 100$$

- Never this!

$$H_0 : \bar{x} = 100$$

$$H_1 : \bar{x} \neq 100$$

# Types of errors

		Reality	
		$H_0$ False	$H_0$ True
Test	Reject $H_0$	Correct rejection $H_0$ ✓ = Power = $1 - \beta$	✗ Type I error = $\alpha$
	Accept $H_0$	✗ Type II error	✓ Correct acceptance of $H_0$

[https://commons.wikimedia.org/wiki/File:Inferential\\_Statistics\\_Decision\\_Making\\_Table.png](https://commons.wikimedia.org/wiki/File:Inferential_Statistics_Decision_Making_Table.png)

The types of errors that could be made in a hypothesis test.

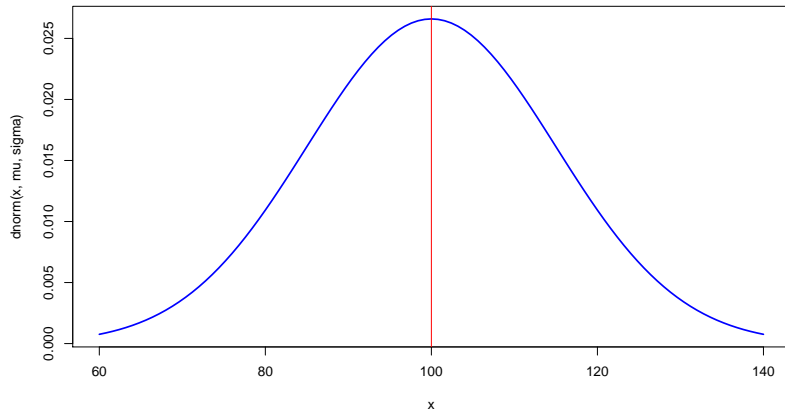


# Deciding on the hypothesis

- Start by assuming null hypothesis
- Collect data and calculate “test statistic”
- If there's enough evidence based on the test statistic, reject the null hypothesis. Otherwise, do not reject the null hypothesis.
- *Never* accept either hypothesis.

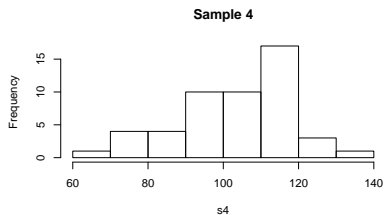
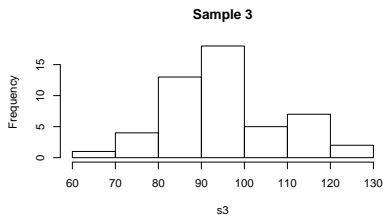
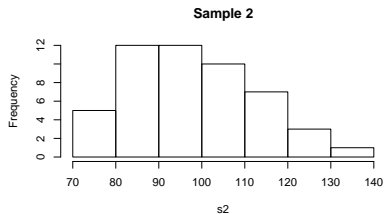
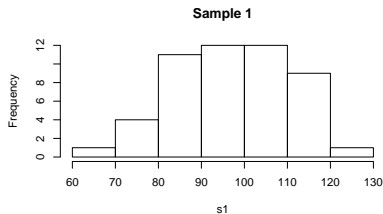
- A *test statistic* usually involves three main components:
  - Estimate of the parameter of interest
  - Measure of variation of estimate (how reliable is the estimate?)
  - Sample size
- The measure of variation is the tricky part. Let's illustrate using the sample mean.

# Population normal distribution



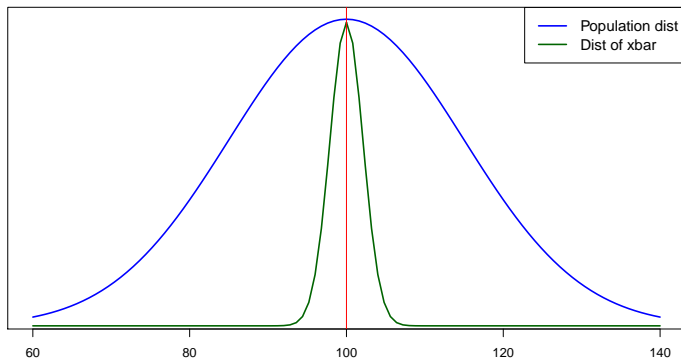
Population normal distribution:  $\mu = 100$ ,  $\sigma = 15$

# Possible samples



Four samples of size 50: Sample means are: 97.34, 98.10, 95.41, 102.91

# Normal distribution and $\bar{x}$ distribution



All possible values of  $\bar{x}$  from sample size  $n = 50$  form a normal distribution too!

# Standard error of the mean

- If we could take repeated samples from a normally distributed population, the sample means would also form a normal distribution.
- A large amount of variation in this distribution means we're less confident about the estimated value of  $\bar{x}$ .
- If the population distribution has standard deviation  $\sigma$ , and we take samples of size  $n$ , then the standard deviation of all possible sample means is:

$$sd(\bar{x}) = \frac{\sigma}{\sqrt{n}}$$

- Known as the *standard error of the mean*.

# Estimated standard error of the mean

- Usually, we don't know the true population standard deviation  $\sigma$
- So instead, we use the sample standard deviation  $s$  to get an estimate:

$$s = \sqrt{\frac{(x_1 - \bar{x})^2 + \cdots + (x_n - \bar{x})^2}{n - 1}}$$

- Then the estimate for the standard error of the mean is:

$$\hat{sd}(\bar{x}) = \frac{s}{\sqrt{n}}$$

- The estimated value for the standard error of the mean is also known as the *standard error of the mean* (yeah, seriously)

## One-sample $t$ -test



# Simple statistical test

- One of the simplest statistical tests we can perform is testing whether the population mean is equal to some fixed quantity  $c$  (assuming normal distribution).
- Hypotheses:

$$H_0 : \mu = c$$

$$H_1 : \mu \neq c$$

- If we don't know the true population standard deviation  $\sigma$ , this test is called the *one-sample t-test*.

# Assumptions of the one-sample $t$ -test

- Assume that the underlying observations  $x_1, \dots, x_n$  come from a normal distribution.
  - For a large sample size  $n$ , don't necessarily need this assumption!
- Data observations must be independent.
- No significant outliers.

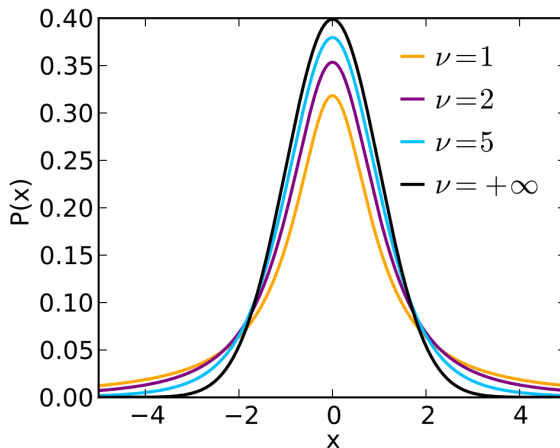
# One-sample $t$ -test

- Test statistic for the one-sample  $t$ -test:

$$t = \frac{\bar{x} - c}{s/\sqrt{n}}$$

- Reject null hypothesis if this is large in absolute value
  - Means sample mean  $\bar{x}$  is far away from null hypothesis value  $c$  relative to overall amount of variation.
- Need to define threshold to make decision on whether to reject or not reject null hypothesis.

# Student's $t$ -distribution

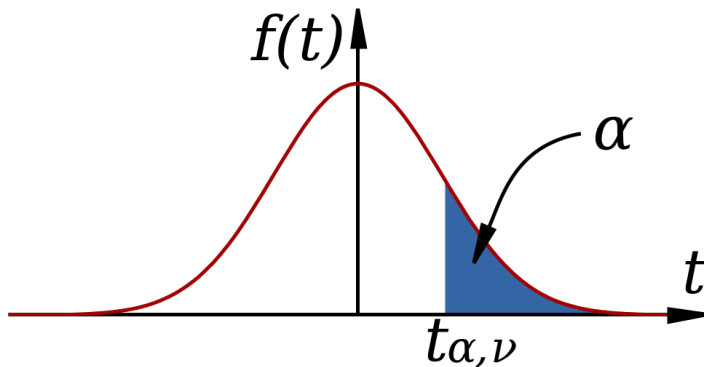


Under  $H_0$ :  $t$  statistic follows a  $t$ -distribution with  $n - 1$  degrees of freedom.

# Extreme values in $t$ -distribution

- We reject the null hypothesis if there were a small probability (say,  $< \alpha$ ) of getting the observed value or a more extreme value, of  $t$ .
  - $\alpha$  is called the significance level of the test. Smaller  $\alpha$  means a more strict threshold.
  - By convention we often choose  $\alpha = 0.05$ . However **this is completely arbitrary**. There's nothing special about this value.
- We're interested in extreme values in both tails of the distribution. But the  $t$ -distribution is symmetric, so we can just consider the absolute value of the  $t$  statistic and compare to the upper tail.

# Tail of $t$ -distribution



$t_{\alpha, \nu}$  is the  $t$ -value corresponding to a tail probability of  $\alpha$  in a distribution with  $\nu$  ( $= n - 1$ ) degrees of freedom. Found in a table or using software.

# Performing the one-sample $t$ -test

- Start by calculating the sample mean  $\bar{x}$  and sample standard deviation  $s$ .
- Then calculate the test statistic:

$$t = \frac{\bar{x} - c}{s/\sqrt{n}}$$

- Choose significance level  $0 < \alpha < 1$ .
- Compare  $|t|$  to the critical value  $t_{\alpha, n-1}$ 
  - If  $|t| > t_{\alpha, n-1}$ , then reject the null hypothesis.
  - Otherwise, do not reject the null hypothesis.

## $t$ -test example

Systolic blood pressure calculated for a sample of 50 medical residents at the JGH. Sample average turns out to be  $\bar{x} = 128$  and standard deviation  $s = 9$ . Assume that the average SBP for medical residents across Canada is 120. Is the average SBP in this group significantly different from the population mean?

- $H_0 : \mu = 120, H_1 : \mu \neq 120$
- Test at level  $\alpha = 0.05$
- Calculate  $t$ -statistic:  $\frac{\bar{x}-120}{s/\sqrt{n}} = \frac{128-120}{9/\sqrt{50}} = 6.29$
- Calculate critical value:  $t_{\alpha,n-1} = t_{0.05,49} = 1.68$
- Our  $t$ -statistic is greater than the critical value ( $6.29 > 1.68$ ), so we reject  $H_0$ .



- The alternate way of determining significance is through the infamous  $p$ -value.
- The  $p$ -value can be used to determine significance in pretty much every statistical test, which is part of the reason why it's so popular.
- Have to be very careful with  $p$ -values!

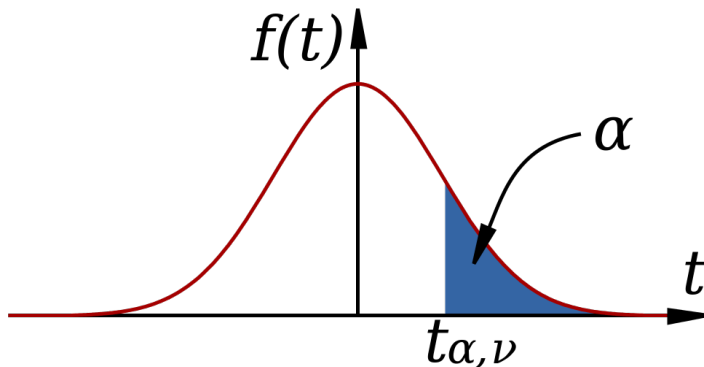
# Coin flip example



- Want to test whether a coin is “fair” (i.e. has equal chance of coming up heads vs. tails)
- Can do an experiment to test this hypothesis. Say we flip the coin 100 times and we get 55 heads.
- If the coin were fair, then the probability of getting 55 or more heads is about 13%.
- If we had observed 65 heads, the same probability would be about 0.08%.

# Definition of $p$ -value

- The calculated probability is a  $p$ -value.
- A  $p$ -value is defined as the probability, **under the null hypothesis**, that we would obtain the result we got or a more extreme result.
- If that probability is small, then we have evidence against the null hypothesis.
- Can compare the  $p$ -value against some significance level  $\alpha$ .



In a one-sample  $t$ -test, we just calculate  $t$  as before, and calculate the tail probability. If it's less than  $\alpha$ , we reject the null hypothesis.

# Systolic blood pressure example

- In our blood pressure example from before, we calculated  $t = 6.29$ .
- The tail probability to the right of 6.29 in a  $t$ -distribution with 49 degrees of freedom is  $p = 8.34 \times 10^{-8}$
- Significant at  $\alpha = 0.05$ , since  $8.34 \times 10^{-8} < 0.05$
- This procedure is exactly equivalent to testing against the critical value as we did before.

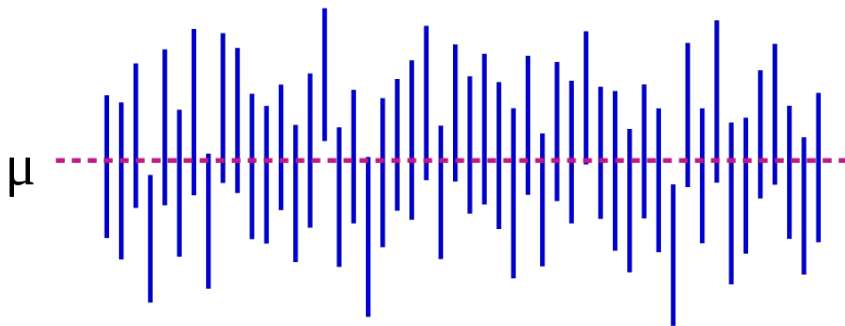
# What $p$ -values are **not**

- The  $p$ -value is *not* the probability that the null hypothesis is true.
- The  $p$ -value does *not* tell us whether either hypothesis is true.
- The  $p$ -value does *not* tell us anything about effect size. An extremely small  $p$ -value does not mean that something is important. It only tells us how strong the evidence is against the null hypothesis.
- $p < 0.05$  does *not* mean anything special. The choice of the significance threshold is arbitrary.

# Confidence intervals

- Another important measure in hypothesis testing is the *confidence interval*.
- Gives an interval of the form (lower value, upper value) which we're "confident" contains the true population parameter.
- Our confidence is expressed through a percentage. E.g. a 95% confidence interval would contain the true parameter approximately 95% of the time if samples from the population had been taken repeatedly.

# Confidence intervals



Taking repeated samples would result in the confidence interval containing the true parameter most of the time.

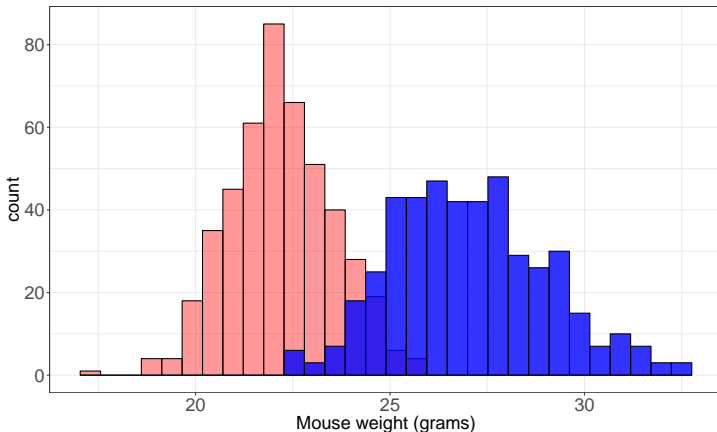


# Confidence interval for systolic blood pressure example

- In the  $t$ -test, the  $100 \times (1 - \alpha)\%$  confidence interval is
$$\bar{x} \pm t_{\alpha/2, n-1} \cdot \frac{s}{\sqrt{n}}$$
- In the blood pressure example we can calculate a 95% confidence interval as (125.44, 130.56).
- Can compare the confidence interval to the value 120 to determine significance. Since our  $100 \times (1 - \alpha)\% = 95\%$  confidence interval does not overlap with the value 120, then the result is significant at level  $\alpha = 0.05$ .
- Another equivalent method of testing significance.

## Independent-samples $t$ -test

# Mouse weight



Remember the mouse weight histogram? Have male/female mice. How to test whether the mean weight differs between male/female mice?

# Independent-samples $t$ -test

- We can test the difference between the means of two groups through the independent-samples  $t$ -test.
- Assume the true mean for groups 1 and 2 are  $\mu_1$  and  $\mu_2$ , respectively. Then our hypotheses are:

$$H_0 : \mu_1 = \mu_2$$

$$H_1 : \mu_1 \neq \mu_2$$

- Equivalently,

$$H_0 : \mu_1 - \mu_2 = 0$$

$$H_1 : \mu_1 - \mu_2 \neq 0$$

# Assumptions of the independent-samples $t$ -test

- Assume that the underlying observations in each group come from a normal distribution.
- The variance should be equal in each of the two groups.
- Data observations must be independent within groups and across groups.
- No significant outliers.

# Formula for the independent-samples $t$ -test

Sample size in each group is  $n_1$  and  $n_2$ , the sample means in each group are  $\bar{x}_1$  and  $\bar{x}_2$ , and the sample variances in each group are  $s_1^2$  and  $s_2^2$ . Then the test statistic is:

$$t = \frac{\bar{x}_1 - \bar{x}_2}{s_p \cdot \sqrt{\frac{1}{n_1} + \frac{1}{n_2}}}$$

where

$$s_p = \sqrt{\frac{(n_1 - 1)s_1^2 + (n_2 - 1)s_2^2}{n_1 + n_2 - 2}}$$

# Mouse weight data example

- 467 female mice, 454 male mice. Mean in each group is: males 27.04g, females 22.22g. Difference = 4.81
- Resulting  $p$ -value is less than  $1 \times 10^{-16}$ . Implies significance difference in means at level  $\alpha = 0.05$ .
- 95% confidence interval is (4.59, 5.03). When comparing means we look to see whether the interval covers the value 0.

# Take-home message

- Always need to be clear about what parameter you're testing and how you're testing it.
- Determining significance involves looking at both the parameter estimate, and an estimation of the theoretical variance of that estimate if we could take repeated samples.
- Don't worry too much about the calculations... more important to know how to properly interpret  $p$ -values and confidence intervals.



Thank you! - Merci!

Questions?