Nate Wells

Math 141, 4/15/22

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Outline

In this lecture, we will...

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- Investigate the theoretical distribution for difference in two means.
- Create confidence intervals and perform hypothesis tests using *t* distribution for differences in means.
- Compare inference procedures for two independent samples vs. paired samples

Section 1

t-distribution vs Normal

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- In general, for small sample sizes, neither method should be used if population does not appear Normal. But if it is Normal, theory-based methods will be more accurate.
- For moderate sample sizes with moderate skew, simulation-based methods will be more accurate

t- versus z-procedures

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- To verify, we'll create 1000 95% confidence intervals using (a) the t-distribution and (b) the Normal distribution, and see how many contain the true population mean.
- Suppose we have the following population distribution for measurement errors



mean error is 0, standard deviation of error is 0.01

10000 Samples

The following code collects 10000 samples from the population, each of size 5. It then computes the mean and standard deviation of each sample.

```
set.seed(1023)
samps<-population %>%
 rep sample n(size = 5, reps = 10000) %>%
 group by(replicate) %>%
  summarize(avg = mean(error), st_dev = sd(error))
## # A tibble: 6 x 3
##
    replicate
                          st dev
                     avg
        <int>
                   <dbl>
                          <dbl>
##
             1 -0.00742 0.00554
## 1
## 2
             2 0.00133 0.00885
             3 0.00465 0.00840
## 3
## 4
            4 -0.00598 0.00924
## 5
             5 0.000320 0.00738
## 6
             6 -0.00148
                        0.00855
```

The Confidence Intervals

- The critical value for a 95% confidence interval using...
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• The following code creates confidence intervals for each sample:

```
samps <- samps %>% mutate(
    lower_z = avg - 1.96*st_dev/sqrt(5), upper_z = avg + 1.96*st_dev/sqrt(5),
    lower_t = avg - 2.776*st_dev/sqrt(5), upper_t = avg + 2.776*st_dev/sqrt(5))
```

```
A tibble: 6 x 7
## #
##
    replicate
                        st dev lower z upper z lower t upper t
                    avg
                  <dbl> <dbl>
                                  <dbl>
                                           <db1>
                                                   <dbl>
                                                             <dbl>
##
        <int>
            1 -0.00742 0.00554 -0.0123 -0.00257 -0.0143
                                                         -0.000545
## 1
            2 0.00133 0.00885 -0.00643 0.00908 -0.00966
                                                         0.0123
## 2
## 3
            3 0.00465 0.00840 -0.00272 0.0120 -0.00578 0.0151
## 4
            4 -0.00598 0.00924 -0.0141 0.00212 -0.0174
                                                          0.00549
## 5
            5 0.000320 0.00738 -0.00615 0.00679 -0.00884 0.00949
## 6
            6 -0.00148 0.00855 -0.00897 0.00601 -0.0121
                                                          0.00913
```

Which intervals contain the true mean?

• Since we **know** the population has mean 0, we can determine whether each interval contains the true mean.

```
samps<-samps %>% mutate(
    z_success = ifelse(( lower_z < 0 & upper_z > 0 ) , "yes", "no"),
    t_success = ifelse(( lower_t < 0 & upper_t > 0 ) , "yes", "no"))
```

##	#	A tibble:	6 x 7					
##		replicate	lower_z	upper_z	lower_t	upper_t	z_success	t_success
##		<int></int>	<dbl></dbl>	<dbl></dbl>	<dbl></dbl>	<dbl></dbl>	<chr></chr>	<chr></chr>
##	1	1	-0.0123	-0.00257	-0.0143	-0.000545	no	no
##	2	2	-0.00643	0.00908	-0.00966	0.0123	yes	yes
##	3	3	-0.00272	0.0120	-0.00578	0.0151	yes	yes
##	4	4	-0.0141	0.00212	-0.0174	0.00549	yes	yes
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What proportion of z- and t-intervals contain 0?

```
## # A tibble: 1 x 2
## z_rate t_rate
## <dbl> <dbl>
## 1 0.879 0.949
```

Section 2

Inference for 2 Means

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Differences in Means

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- Groups could be formed from...
 - Two different populations.
 - Two subsets within the same sample distinguished by levels of a categorical variable.
 - Two treatment groups in an experiment.

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Distribution for Difference in Means

• Suppose random samples of size n_1 and n_2 are drawn **independentally** from populations with means μ_1 and μ_2 and standard deviations σ_1 and σ_2 , respectively.

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- The distribution of the difference $\bar{x}_1 \bar{x}_2$ is approximately Normal also



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Practical Considerations

 By the Central Limit Theorem, as both n₁ and n₂ get larger, the distribution of difference in sample means x
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 and standard error $SE = \sqrt{rac{\sigma_1^2}{n_1} + rac{\sigma_2^2}{n_2}}$

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$$t = \frac{(\bar{x}_1 - \bar{x}_2) - (\mu_1 - \mu_2)}{\text{SE}} = \frac{(\bar{x}_1 - \bar{x}_2) - (\mu_1 - \mu_2)}{\sqrt{\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}}}$$

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Theorem

The standardized difference t is approximately t-distributed with degrees of freedom $df = \min\{n_1 - 1, n_2 - 1\}.$

This approximation is appropriate either when both sample sizes are large (i.e. $n_1, n_2 \ge 30$), or when both populations are approximately Normally distributed.

Diamonds are Forever

Question: Do 1.0 carat diamonds command a higher price than .99 carat diamonds, beyond what you would expect due to increase in weight?

• To answer, we collect random samples of 30 1.0 and 23 .99 carat diamonds.
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Normal Conditions

• Our sample sizes are near the minimum conditions to use the Normal approximation. Are ppc Normally distributed for each carat value?





Hypothesis Test

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$$H_0: \mu_1 - \mu_{99} = 0 \qquad H_0: \mu_1 - \mu_{99} > 0$$

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- **8** We compute our test statistic

$$t = \frac{\bar{x}_1 - \bar{x}_{99}}{SE} = \frac{5585 - 4451}{\sqrt{\frac{1614^2}{30} + \frac{1332^2}{23}}} = 2.802$$

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Hypothesis Test II

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p_value<-1 - pt( 2.802, df = 22)
p_value</pre>
```

[1] 0.005194137

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6 Conclude

• At the $\alpha = 0.01$ significance level, we reject the null hypothesis. This sample suggests 1.0 carat diamonds command a higher price than is explained by increase in weight alone.

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```

```
6 Conclude
```

- At the $\alpha = 0.01$ significance level, we reject the null hypothesis. This sample suggests 1.0 carat diamonds command a higher price than is explained by increase in weight alone.
 - However, we cannot be certain the Normal condition is satisfied. The p-value may not be accurate.

Comparison with infer

```
set.seed(101)
diamonds_null <- diamonds %>% specify(ppc ~ carat) %>%
hypothesize(null = "independence") %>%
generate(reps = 5000, type = "permute") %>%
calculate(stat = "diff in means", order = c("1", "0.99"))
diamonds_null %>% visualize()+shade_p_value(obs_stat = 1135, direction = "right")
```



diamonds_null %>% get_p_value(obs_stat = 1135, direction = "right")

```
## # A tibble: 1 x 1
## p_value
## <dbl>
## 1 0.0042
```

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An Equivalent Confidence Interval

Goal: Create a confidence interval that corresponds to **one-sided** $\alpha = 0.01$ significance

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• What is the t* critical value for 98% confidence? t_star<- qt(.99, df = 22) t_star

[1] 2.508325

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An Equivalent Confidence Interval

Goal: Create a confidence interval that corresponds to **one-sided** α = 0.01 significance



• What is the t* critical value for 98% confidence? t_star<- qt(.99, df = 22) t_star

[1] 2.508325

• Note that our observed t statistic was t = 2.802, which was more extreme than the critical value for 98% confidence

Confidence Interval

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which is (118.42, 2149.58).

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- Since this interval **does not** contain 0, we conclude that there IS a price increase for 1.0 carat diamonds.
 - Moreover, this price increase is likely between \$120 and \$2150.

Comparison with infer

```
diamonds_ci <- diamonds_boot %>% get_ci(level = 0.98, type = "percentile")
diamonds_ci
  # A tibble: 1 \times 2
##
##
     lower ci upper ci
##
        <dbl>
                 <dbl>
## 1
         247
                 2113.
diamonds_boot %>%visualize()+ shade_ci(endpoints = diamonds_ci)
```



Simulation–Based Bootstrap Distribution

Section 3

Inference for Paired Samples

Matched Pairs

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 - But if matching is used in sample design, it is **not** appropriate to use the 2 sample procedures. (Why?)
- You can create a new variable recording the **difference** in measurements in each pair of individuals
- This new variable can be used to perform statistical inference using the 1-sample procedures for mean.

- Suppose you intend to design an experiment to determine whether the mean of two populations are equal.
- You could obtain an SRS from each population, compute means for each sample, take the difference, and assess variability based on previous procedures.
 - It *is* possible that any observed effect is not due to the explanatory variable, but to some confounding variable present in one sample but not other.
- To reduce effect of confounding variable, you could match individuals in one sample with similar individuals in the other sample.
 - But if matching is used in sample design, it is **not** appropriate to use the 2 sample procedures. (Why?)
- You can create a new variable recording the **difference** in measurements in each pair of individuals
- This new variable can be used to perform statistical inference using the 1-sample procedures for mean.
 - Rather than looking at the difference in means, we look at the mean of differences!

Inference for Paired Samples

The World's Fastest Swimsuit

In the 2008 Olympics, controversy erupted over whether a new swimsuit design provided an unfair advantage to swimmers. Eventually, the International Swimming Organization banned the new suit. But can a certain suit really make a swimmer faster?


Data

A study analyzed max velocities for 12 pro swimmers with and without the suit:

swimmer	with_suit	without_suit	difference
1	1.57	1.49	0.08
2	1.47	1.37	0.10
3	1.42	1.35	0.07
4	1.35	1.27	0.08
5	1.22	1.12	0.10
6	1.75	1.64	0.11
7	1.64	1.59	0.05
8	1.57	1.52	0.05
9	1.56	1.50	0.06
10	1.53	1.45	0.08
11	1.49	1.44	0.05
12	1.51	1.41	0.10

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• Without performing any statistical inference, what is the likely conclusion to draw from this data?

Inference for Paired Samples

Hypothesis Testing

We want to determine whether the *average* difference in max velocity (with - without) is positive. Let μ be the average difference.

State Hypotheses:

 $H_0: \mu = 0$ $H_a: \mu > 0$

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- 8 Compute relevant statistics

```
## # A tibble: 1 x 3
## x_bar s n
## <dbl> <dbl> <int>
## 1 0.0775 0.0218 12
```

Inference for Paired Samples

Hypothesis Testing, cont'd

8 Compute Test Statistic

$$t = \frac{\bar{x} - \mu_0}{\frac{s}{\sqrt{n}}} = \frac{0.0775}{\frac{0.022}{\sqrt{12}}} = 12.32$$

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④ Obtain p-value: 1-pt(12.32, df = 11)

[1] 4.435835e-08



Conclusion

6 Conclusion?

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 - Were awarded 98% of all medals (including 33 of 36 gold medals).
 - Represented 23 of the total 25 world records broken.