Inference for Means

Nate Wells

Math 141, 4/13/22

Outline

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- Investigate the *t* distribution.
- Create confidence intervals and perform hypothesis tests using *t* distribution for sample means.

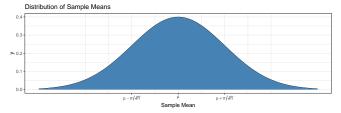
Section 1

The *t*-distribution

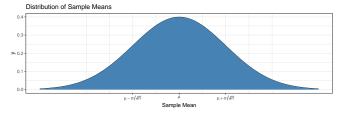
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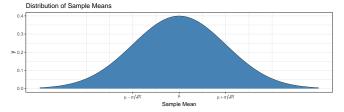


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- Note that smaller σ and larger *n* both correspond to smaller standard error.
- As *n* increases, Normal approximation becomes more accurate, even if population is skewed.

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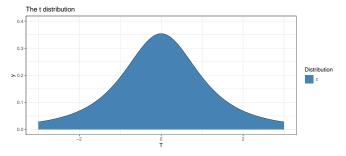
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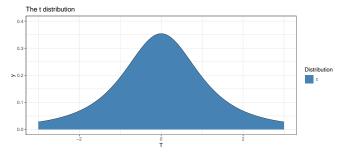
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- Instead, the standardized statistic z follows a t-distribution
 - The *t*-distribution was first studied in 1908 by William Gosset, who published under the pseudonym *Student*.

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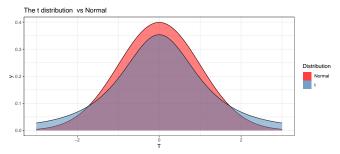


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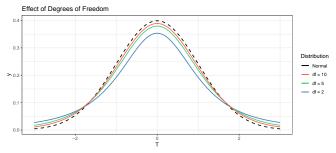


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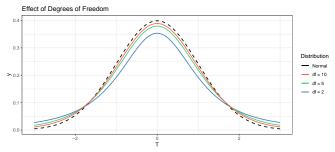
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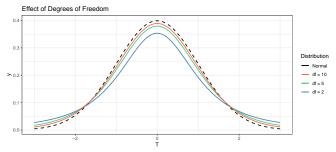


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- As degrees of freedom increases, the *t* distribution gets closer to the Normal distribution.
 - For $df \ge 30$, the t distribution is nearly indistinguishable from the Normal

Distribution of Sample Means using t-distribution

Theorem

Suppose a sample of size n is collected from a population with mean μ . The distribution of the sample mean \bar{x} has the following characteristics:

- **Center**: The mean is equal to μ
- **Spread**: The standard error is equal to $\frac{s}{\sqrt{n}}$ (where s is the sample st. dev.)
- Shape: The standardized statistic follows approximately a t-distribution with n − 1 degrees of freedom.

For small sample sizes ($n \le 30$), the t-distribution is only a good approximation if the population distribution is approximately Normal.

Section 2

Statistical Inference

The Origin Story

A batch of stout beer is best when it has an *original gravity* (OG) close to 1.071. The particular OG of a batch depends on a number factors (like temperature, rest time, recipe, etc.).



If we can only obtain a small number of measurements from the batch, how can we quantify whether the deviations we observe are due to random sampling, and not an actual deviation in OG?

Confidence Intervals

The t-procedures for Confidence Intervals

A C% confidence interval for a population mean μ using a sample of size *n* is

$$\bar{\mathbf{x}} \pm t^* \frac{s}{\sqrt{n}}$$

where \bar{x} and s are the mean and standard deviation of the sample, and where t^* is the critical value for C% confidence in the *t*-distribution with n-1 degrees of freedom.

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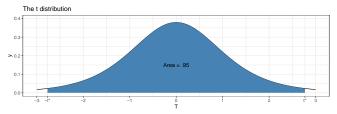
- Since our sample size is small $(n \le 30)$, we need to make sure our population is approximately Normal.
 - Fortunately, the only variability here is due to measurement errors, which are known to be approximately Normally distributed.
- Our sample mean and standard deviation are

xbar s ## 1 1.069 0.006348

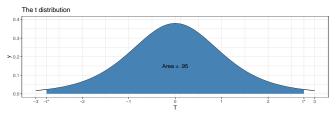
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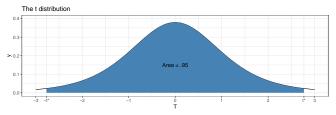


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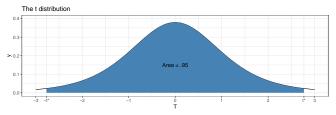
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- Use the function qt to get quantiles for a t-distribution (just like qnorm for Normal) qt(p = 0.975, df = 4)
- ## [1] 2.776
- Note that the t* critical value of 95% confidence is larger than the z* critical value qnorm(p = 0.975)
- ## [1] 1.96

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- Thus, the range of plausible values for the OG of the beer is (1.061, 1.076) at 95% confidence.
- As $\mu = 1.071$ is within this interval, it is plausible that the batch has the desired OG.

Comparison using infer

```
If we instead use infer...
```

```
set.seed(1908)
beer %>%
  specify(response = OG) %>%
  generate(reps = 5000, type = "bootstrap" ) %>%
  calculate(stat = "mean") %>%
  get_ci(level = .95, type = "percentile")
## # A tibble: 1 x 2
## lower_ci upper_ci
```

```
## <dbl> <dbl> ## 1 1.06 1.07
```

• The bootstrap interval is a bit narrower than the theory-based interval:

[1] 1.061 1.076

Hypothesis Tests

The *t*-test for Single Mean

To test $H_0: \mu = \mu_0$ against $H_a: \mu \neq \mu_0$ (or 1-sided alternatives), use the *t*-statistic

$$t = \frac{\bar{x} - \mu_0}{\frac{s}{\sqrt{n}}}$$

where \bar{x} and s are the mean and standard deviation of the sample with size n. The distribution of t is approximated by the t-distribution with n - 1 degrees of freedom.

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• Therefore, our *t*-statistic is

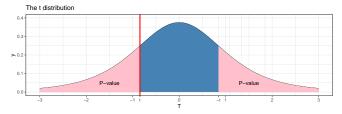
$$t = \frac{\bar{x} - \mu_0}{\frac{s}{\sqrt{n}}} = \frac{1.0686 - 1.071}{\frac{0.0063}{\sqrt{5}}} = -0.845$$

The P-Value

• Plotting our *t*-statistic against the theoretical *t*-distribution with df = 4

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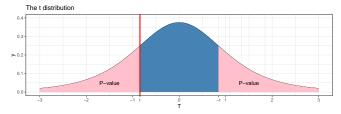
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- The exact P-value is twice the area left of *t*:
- ## [1] 0.4457
 - At significance $\alpha = 0.05$, we do not have enough evidence to reject the null hypothesis.

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- The exact P-value is twice the area left of *t*:
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 - At significance $\alpha = 0.05$, we do not have enough evidence to reject the null hypothesis.
 - Our sample is consistent with a true mean OG of $\mu = 1.071$.

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set.seed(1908)
beer %>%
  specify(response = 0G) %>%
  hypothesize(null = "point", mu = 1.071) %>%
  generate(reps = 5000, type = "bootstrap" ) %>%
  calculate(stat = "mean") %>%
  get_p_value(obs_stat = 1.069, direction = "both")
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• The bootstrap p-value is a bit larger than the theory-based p-value:

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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

It is important to use the t-distribution (rather than the Normal distribution) for confidence intervals and hypothesis tests when the sample size is small.

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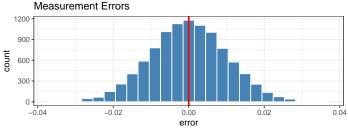
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• To verify, we'll create 1000 95% confidence intervals using (a) the t-distribution and (b) the Normal distribution, and see how many contain the true population mean.

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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 critical value for a 95% confidence interval using...
 - the standard Normal distribution is $z^* = 1.96$.
 - the *t* distribution with 4 df is $t^* = 2.776$.

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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
                   avg st dev lower z upper z lower t upper t
                 <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
##	5	5	-0.00615	0.00679	-0.00884	0.00949	yes	yes
##	6	6	-0.00897	0.00601	-0.0121	0.00913	yes	yes

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
##	5	5	-0.00615	0.00679	-0.00884	0.00949	yes	yes
##	6	6	-0.00897	0.00601	-0.0121	0.00913	yes	yes

• 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
```