Notes and Exercises Chapter 20 – Inference for Quantitative Variables

Name _____

Math 217 **Date** _____

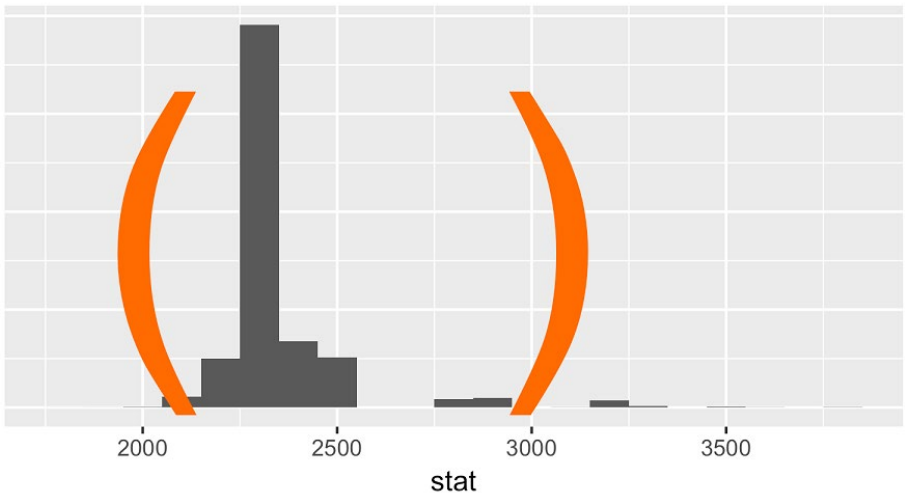
Saidi

19.1 Bootstrap confidence interval for a mean

The inferential analysis methods in this chapter are grounded in quantifying how one dataset differs from another when they are both taken from the same population, but we aren't ever going to take more than one sample of observations. It does not make sense to take repeated samples from the same population because if you have the ability to take more samples, a larger sample size will benefit you more than taking two samples from the population.

Instead, of taking repeated samples from the actual population, we use bootstrapping to measure how the samples behave under an estimate of the population.

Start with a single sample and look at the distribution from a histogram.



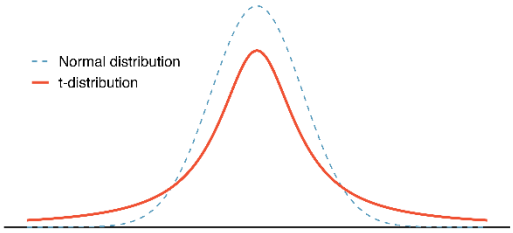
SE for confidence interval for *t*-distribution

The amount of discrepancy between $\bar{y}$ and μ is described using probability terms with the SAMPLING distribution of $\bar{Y}$, and the standard deviation of $\bar{Y}$ is given as the **standard error of the mean**, which is $SE_{\bar{x}} = \frac{\sigma}{\sqrt{n}} \approx \frac{s}{\sqrt{n}}$ (this is sometimes called the ***estimated standard error***, since *s* is already an estimate of σ.

As with the sample proportion, the variability of the sample mean is well described by the mathematical theory given by the Central Limit Theorem. However, because of missing information about the inherent variability in the population (σ), **a t-distribution is used** in place of the standard normal when performing hypothesis test or confidence interval analyses.

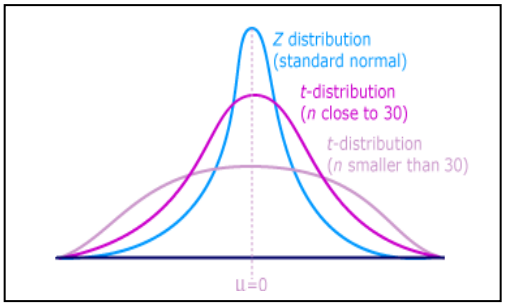
The *t*-distribution is symmetric and bell curved, but has bigger tails than the normal curve, because of the larger standard deviation. It is dependent on the sample size, because the distribution requires the ***degrees of freedom (df)***, which is n-1.

The extra thick tails of the t-distribution are exactly the correction needed to resolve the problem (due to extra variability of the T score) of using s in place of σ in the SE calculation.



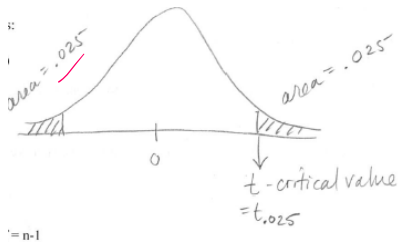
Comparison of a t-distribution and a normal distribution

Notation



$t_{0.025}$ - two-tailed 5% critical value means:

(use the upper tail area of 2.5% probability with df = n-1)



Confidence Interval for μ

$$\bar{x} \pm t^*_{0.025} SE_{\bar{x}} = \bar{x} \pm t^*_{0.025} \left(\frac{s}{\sqrt{n}}\right)$$

** $df = n - 1$

** $t^*_{0.025}$ comes from `qt(.975, df = degrees of freedom)`

$$\left(\bar{x} - t_{n-1,\alpha/2} \cdot \frac{s}{\sqrt{n}}, \bar{x} + t_{n-1,\alpha/2} \cdot \frac{s}{\sqrt{n}}\right)$$

19.2.2 Evaluating the two conditions required for modeling $\bar{x}$

Two conditions are required to apply the Central Limit Theorem for a sample mean $\bar{x}$:

- **Independence.** The sample observations must be independent. The most common way to satisfy this condition is when the sample is a simple random sample from the population.
- **Normality.** When a sample is small, we also require that the sample observations come from a normally distributed population. We can relax this condition more and more for larger and larger sample sizes. This condition is obviously vague, making it difficult to evaluate, so next we introduce a couple rules of thumb to make checking this condition easier.

General rule for performing the normality check.

$$\bar{x} \sim N\left(mean = \mu, SE = \frac{\sigma}{\sqrt{n}}\right)$$

There is no perfect way to check the normality condition, so instead we use two general rules based on the number and magnitude of extreme observations. Note, it often takes practice to get a sense for whether a normal approximation is appropriate.

- **Small n:** If the sample size n is small and there are **no clear outliers** in the data, then we typically assume the data come from a nearly normal distribution to satisfy the condition.
- **Large n:** If the sample size n is large and there are no **particularly extreme** outliers, then we typically assume the sampling distribution of $\bar{x}$ is nearly normal, even if the underlying distribution of individual observations is not.

If n is small ($n < 15$), the population must be basically normally distributed

If $15 < n < 30$, the population distribution should not have any strong skewing or outliers

If n is large ($n \geq 30$), the population may have some skewing or outliers (This is basically the CLT).

When n is 30 or more, you could use normal distribution calculations rather than t-distribution calculations BUT for our class, from now on, we will use t-distributions for quantitative variables.

Every data analysis should begin with an inspection of the graph of the data to see the shape of the distribution.

To be **more accurate:** 1. Widen the interval by

- Increasing the confidence level
- Decreasing the sample size

To be **more precise:** 2. Narrow the interval by

- Decreasing the confidence level
- Increasing the sample size

19.2.5 One sample t-tests

The test statistic for assessing a single mean is a T.

The t test statistic is a ratio of how the sample mean differs from the hypothesized mean as compared to how the observations vary.

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

When the null hypothesis is true and the conditions are met, it has a t-distribution with df=n−1.

Conditions:

- Independent observations.
- Large samples and no extreme outliers.

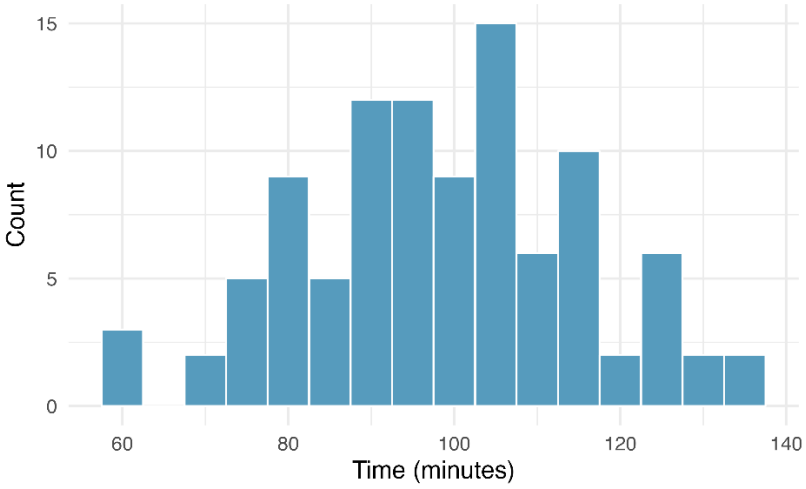
Example:
Is the typical US runner getting faster or slower over time? We consider this question in the context of the Cherry Blossom Race, which is a 10-mile race in Washington, DC each spring. **The average time for all runners who finished the Cherry Blossom Race in 2006 was 93.29 minutes**. We want to determine using data from 100 participants in the 2017 Cherry Blossom Race whether runners in this race are getting faster or slower, versus the other possibility that there has been no change.

The `run17` data can be found in the **cherryblossom** R package.

1. What are appropriate hypotheses for this context?

2. Check conditions for normality:
   a. Independent observations?

   b. Check shape of distribution (histogram below) and sample size



If conditions are met, perform the computations for a t test comparing the null (from 2006) of a mean of 93.29 minutes to the 2017 mean.

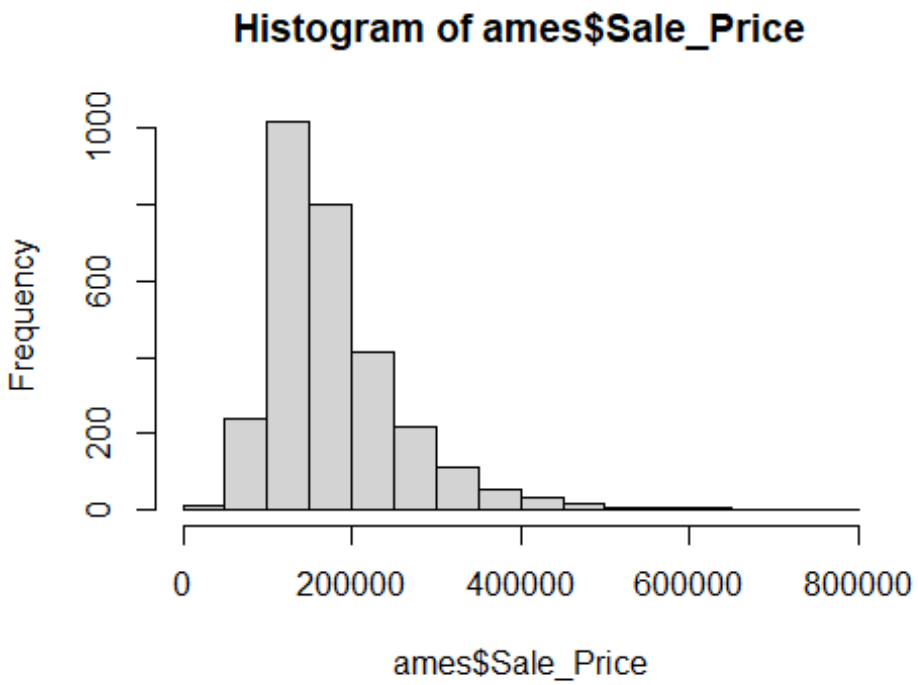
Chapter 19 notes - single mean

R Saidi

Load the libraries and dataset

```
library(tidyverse)
library(openintro)
library(tidymodels)
data("ames")
head(ames)
```

```
# A tibble: 6 × 74
  MS_SubClass              MS_Zoning Lot_Frontage Lot_Area Street Alley Lot_Shape
  <fct>                    <fct>            <dbl>    <int> <fct>  <fct> <fct>
1 One_Story_1946_and_New… Resident…           141    31770 Pave   No_A… Slightly…
2 One_Story_1946_and_New… Resident…            80    11622 Pave   No_A… Regular
3 One_Story_1946_and_New… Resident…            81    14267 Pave   No_A… Slightly…
4 One_Story_1946_and_New… Resident…            93    11160 Pave   No_A… Regular
5 Two_Story_1946_and_New… Resident…            74    13830 Pave   No_A… Slightly…
6 Two_Story_1946_and_New… Resident…            78     9978 Pave   No_A… Slightly…
#
```



The simple code to create a 95% CI for single mean

Use t.test(). You must indicate the variable of interest

```
t.test(ames$Sale_Price, conf.level = .95)


    One Sample t-test

data:  ames$Sale_Price
t = 122.5, df = 2929, p-value < 0.00000000000000022
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 177902.3 183689.9
sample estimates:
mean of x
 180796.1
```

We are 95% confident that the mean sale price for homes in Ames is between $177,902.30 and $183,689.90.

##Answer the question:

Test to determine if the mean home sale price in Ames was different from the national average at that time from 2006-2010.

The average home price in the US in 2010 was $222,900.

```
t.test(ames$Sale_Price, mu=222900)


    One Sample t-test
```

```
data:  ames$Sale_Price
t = -28.529, df = 2929, p-value < 0.00000000000000022
alternative hypothesis: true mean is not equal to 222900
95 percent confidence interval:
 177902.3 183689.9
sample estimates:
mean of x
 180796.1
```

T test

Use the Cherry Blossom dataset from 2017

```
data("run17")
```

Mutate the variable net_sec to convert to minutes

```
run17_1 <- run17 |>
  mutate(minutes = net_sec/60)
head(run17_1)
```

```
# A tibble: 6 × 10
    bib name         sex     age city   net_sec clock_sec pace_sec event minutes
  <int> <chr>        <chr> <int> <chr>    <dbl>     <dbl>    <dbl> <chr>   <dbl>
1     6 Hiwot G.     F        21 Ethio…    3217      3217      321 10 M…    53.6
2    22 Buze D.      F        22 Ethio…    3232      3232      323 10 M…    53.9
3    16 Gladys K.    F        31 Kenya     3276      3276      327 10 M…    54.6
4     4 Mamitu D.    F        33 Ethio…    3285      3285      328 10 M…    54.8
5    20 Karolina N.  F        35 Poland    3288      3288      328 10 M…    54.8
6     8 Firehiwot D. F        33 Ethio…    3316      3316      331 10 M…    55.3
```

Generate a sample of size 100 from the population

```
# create a vector of size 100 for minutes from 2017
run17_samp <- sample(run17_1$minutes, size = 100, replace = FALSE)
summary(run17_samp)
```

```
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  30.52   82.02   95.97   91.88  106.43  130.28
```

Perform the t test comparing the mean for 2017 to the mean from 2006

The mean from 2006 was 93.29 minutes

Here is the format for the single mean t test

t.test(x, mu = 0, alternative = “two.sided”) t.test(x, mu = 0, alternative = “less”) t.test(x, mu = 0, alternative = “greater”)

```
# compare the mean from the samples from 2017 to the mean in 2006
t.test(run17_samp, mu = 93.29, alternative = "two.sided")
```

```
    One Sample t-test

data:  run17_samp
```

```
t = -0.61627, df = 99, p-value = 0.5391
alternative hypothesis: true mean is not equal to 93.29
95 percent confidence interval:
 87.36061 96.40906
sample estimates:
mean of x
 91.88483
```

t = -0.66655, df = 99, p-value = 0.5066

Fail to reject the null. There is no compelling evidence that the mean in 2017 is different from the mean in 2006.

Now using tidymodels code for a 95% CI for the ames house prices.

This is a two-part exercise: First, generate 15000 bootstrap distributions of sale_price in the ames data frame and record the median of each bootstrap distribution.

• Specify that sale_price is the response variable. • Generate 15000 bootstrap replicates. • Calculate the median of each distribution.

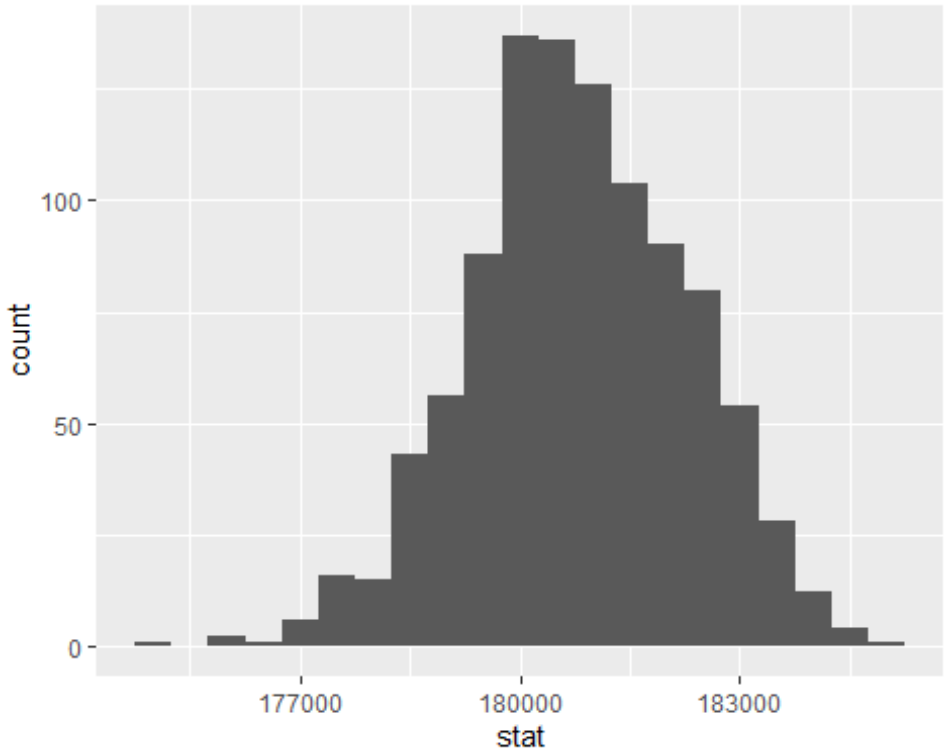
```
# Generate bootstrap distribution of means
sale_mean_ci <- ames |>
  # Specify the variable of interest
  specify(response = Sale_Price) |>
  # Generate 10000 bootstrap samples
  generate(reps = 1000, type = "bootstrap") |>
  # Calculate the mean of each bootstrap sample
  calculate(stat = "mean")   # change this to "median" to see how this changes

# Take a peek
head(sale_mean_ci)
```

```
Response: Sale_Price (numeric)
# A tibble: 6 × 2
  replicate    stat
      <int>   <dbl>
1         1 182180.
2         2 181786.
3         3 179963.
4         4 180308.
5         5 179413.
6         6 180631.
```

Plot a histogram of the boostrap replications

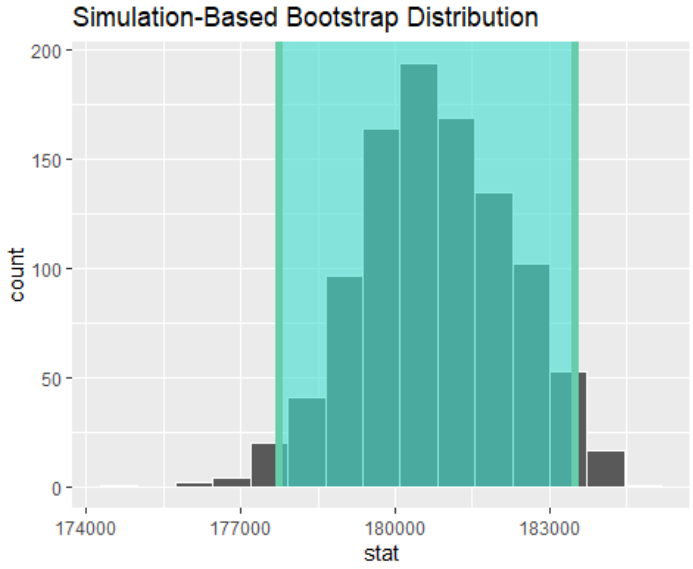
Look at the shape of the distribution

```
# Plot the sale_mean_ci statistic
ggplot(sale_mean_ci, aes(x = stat)) +
  # Make it a histogram with a binwidth of 500
  geom_histogram(binwidth = 500)
```



Calculate the 95% CI using the percentile method

```
# Calculate the 95% CI via percentile method
sale_mean_ci |>
  summarize(
    l = quantile(stat, 0.025),
    u = quantile(stat, 0.975)
  )

# A tibble: 1 × 2
        l       u
    <dbl>   <dbl>
1 177741. 183509.

sale_ci <- sale_mean_ci |>
  get_confidence_interval(level =.95)
sale_ci

# A tibble: 1 × 2
  lower_ci upper_ci
     <dbl>    <dbl>
1  177741.  183509.

sale_mean_ci %>%
  visualize() +
  shade_confidence_interval(endpoints = sale_ci, level=.95)
```



We are 95% confident that the true median home sale price in Ames is between $177,925.10 and $183,698.20.

Perform the hypothesis test using tidymodels

Answer the question: Test to determine if the mean home sale price in Ames was different from the national average at that time from 2006-2010.

The average home price in the US in 2010 was $222,900.

Calculate the observed mean

```
# Calculate observed mean
price_mean_obs <- ames |>
  # Summarize to calculate the mean observed sale price
  summarize(mean_price = mean(Sale_Price))
price_mean_obs
```

```
# A tibble: 1 × 1
  mean_price
       <dbl>
1    180796.
```

Use “specify”, “hypothesize”, “generate” and “calculate”

```
sale_mean_ht <- ames |>
  # Specify sale_price as the response
  specify(response = Sale_Price) |>
  # Set the hypothesis that national home price is 222900
  hypothesize(null = "point", mu = 222900) |>
  # Generate 10000 bootstrap replicates
  generate(reps = 1000, type = "bootstrap") |>
  # Calculate the mean
  calculate(stat = "mean")
head(sale_mean_ht)
```

```
Response: Sale_Price (numeric)
Null Hypothesis: point
# A tibble: 6 × 2
```

```
  replicate    stat
      <int>   <dbl>
1         1 224440.
2         2 222402.
3         3 221122.
4         4 223405.
5         5 221828.
6         6 224044.
```

Calculate the p-value

The p-value is 0. Reject the null. The mean sale price of homes in Ames is different (and much less than) the national home price in 2010.

```
pvalue <- get_p_value(sale_mean_ht, price_mean_obs, "two-sided")
```

```
Warning: Please be cautious in reporting a p-value of 0. This result is an approximation
based on the number of `reps` chosen in the `generate()` step.
```

```
# A tibble: 1 × 7
  statistic  t_df p_value alternative estimate lower_ci upper_ci
      <dbl> <dbl>   <dbl> <chr>          <dbl>    <dbl>    <dbl>
1      123.  2929       0 two.sided    180796.  177902.  183690.
```

We can see that the 95% CI is (177902, 183690).

Homework Chapter 19

1. Review section 19.3 (the chapter review)
2. Suggested problems from textbook section 19.4 exercises: 3, 5, 6, 12, 15, 17, 22
3. Suggested tutorials:

    5 – Bootstrapping to estimate single means parameter

    6 – Introducing the t-distribution