Conducting and Interpreting t-Tests

One-sample t-test

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Import the data

```
# import nhanes 2015-2016
nhanes.2016 <- read.csv("/Users/harrisj/Box/teaching/Teaching/Fall2020/d

# check the data
summary(object = nhanes.2016)
```

```
##       SEQN           cycle                SDDSRVYR     RIDSTATR     RIAGENDR
##  Min.   :83732   Length:9544        Min.   :9   Min.   :2   Min.   :1.00
##  1st Qu.:86222   Class :character   1st Qu.:9   1st Qu.:2   1st Qu.:1.00
##  Median :88726   Mode  :character   Median :9   Median :2   Median :2.00
##  Mean   :88720                      Mean   :9   Mean   :2   Mean   :1.51
##  3rd Qu.:91210                      3rd Qu.:9   3rd Qu.:2   3rd Qu.:2.00
##  Max.   :93702                      Max.   :9   Max.   :2   Max.   :2.00
##
##     RIDAGEYR        RIDAGEMN        RIDRETH1        RIDRETH3        RIDEXMON
##  Min.   : 0.00   Min.   : 0.00   Min.   :1.00   Min.   :1.000   Min.   :1.00
##  1st Qu.: 9.00   1st Qu.: 5.00   1st Qu.:2.00   1st Qu.:2.000   1st Qu.:1.00
##  Median :27.00   Median :10.00   Median :3.00   Median :3.000   Median :2.00
##  Mean   :31.87   Mean   :10.76   Mean   :3.01   Mean   :3.216   Mean   :1.51
##  3rd Qu.:53.00   3rd Qu.:17.00   3rd Qu.:4.00   3rd Qu.:4.000   3rd Qu.:2.00
##  Max.   :80.00   Max.   :24.00   Max.   :5.00   Max.   :7.000   Max.   :2.00
##                  NA's   :8882
##     RIDEXAGM        DMQMILIZ        DMQADFC         DMDBORN4
##  Min.   :  0.0   Min.   :1.000   Min.   :1.000   Min.   : 1.000
##  1st Qu.: 41.0   1st Qu.:2.000   1st Qu.:1.000   1st Qu.: 1.000
##  Median :100.0   Median :2.000   Median :2.000   Median : 1.000
##  Mean   :104.5   Mean   :1.914   Mean   :1.531   Mean   : 1.244
```

Comparing a sample mean to a population mean with a one sample t-test

- Comparing the mean sbp in the NHANES data to a hypothesized value like 120 can be done with a **one sample t-test**.

- The *one sample t-test* compares *a sample mean* to *a hypothesized or population mean*. It is one of three types of t-tests:

  - **one-sample t-test**: compares a mean to a population or hypothesized value
  - **independent samples t-test**: compares the means of two unrelated groups
  - **paired samples t-test**: compares the means of two related groups

NHST for one sample t-test

The NHST process:

- Write the null and alternate hypotheses.
- Compute the test statistic.
- Calculate the probability that your test statistic is at least as big as it is if there is no relationship (i.e., the null is true).
- If the probability that the null is true is very small, usually less than 5%, reject the null hypothesis.
- If the probability that the null is true is not small, usually 5% or greater, retain the null hypothesis.

NHST Step 1: Write the null and alternate hypothesis

- The first step is to write the null hypothesis for statistical testing.
- The null hypothesis is a statement that claims there is **no difference** or **no relationship** between things.
- In this case, the null hypothesis could state that the mean systolic blood pressure of adults in the US is no different from the hypothesized value of 120.
    - H0: There is no difference between mean systolic blood pressure in the US and the cutoff for normal blood pressure, 120 mmHG.
    - HA: There is a difference between mean systolic blood pressure in the US and the cutoff for normal blood pressure, 120 mmHG.

NHST Step 2: Compute the test statistic

- The one-sample t-test uses the t-statistic (sort of like a z-statistic) as the test statistic, but with the standard error as the denominator rather than the standard deviation.
    - The standard error approximates the standard deviation in the population.

$$t = \frac{m_x - \mu_x}{\frac{s_x}{\sqrt{n_x}}}$$

- The m_x represents the mean of of the variable x, the variable to be tested
- μ_x is the population mean or hypothesized value of the variable
- s_x is the sample standard deviation of x
- and n is the sample size

Getting relevant descriptive statistics

```
# mean and sd of systolic blood pressure
nhanes.2016 %>%
  drop_na(BPXSY1) %>%
  summarize(m.sbp = mean(BPXSY1),
            sd.sbp = sd(BPXSY1),
            n.spb = n())
```

```
##      m.sbp   sd.sbp n.spb
## 1 120.5394 18.61692  7145
```

Computing the t-statistic manually

$$t = \frac{120.5394 - 120}{\frac{18.61692}{\sqrt{7145}}} = 2.45$$

- With a t of 2.45, the sample mean of 120.5394 was 2.45 standard errors above the hypothesized value of 120.

Computing the t-statistic with R

```r
# comparing mean of BPXSY1 to 120
t.test(x = nhanes.2016$BPXSY1, mu = 120)
```

```
##
##  One Sample t-test
##
## data:  nhanes.2016$BPXSY1
## t = 2.4491, df = 7144, p-value = 0.01435
## alternative hypothesis: true mean is not equal to 120
## 95 percent confidence interval:
##  120.1077 120.9711
## sample estimates:
## mean of x
##  120.5394
```

- Note: The df value for the one-sample t-test is computed by subtracting 1 from the sample size.

NHST Step 3: Compute the probability for the test statistic (p-value)

- The t-statistic was 2.4491.
- Like the chi-squared statistic, the t-statistic has a distribution made up of all the possible values of t and how probable each value is to occur.
- In the case of t, the distribution looks similar to a normal distribution.

The t-distribution

- Shading under the curve for the t-statistic value of 2.4491 and higher might be useful to understand the probability.

- The shading represents the probability of getting a t-statistic that is 2.4491 or greater **if the null hypothesis were true**:

Interpreting the area under the curve

- The shaded section was very small, indicating that a t-statistic of 2.4491 or greater has a low probability **when the null hypothesis is true**.
- The output from the t-test showed this probability was 0.014, the p-value.
- The interpretation of this value was that there is a 1.4% probability that a t-statistic would be 2.4491 or greater **if the null hypothesis were true**.
- That is, there is a 1.4% probability of getting a t-statistic of 2.4491 or greater for a mean of 120.54 in this sample if it came from a population with a mean systolic blood pressure of 120.
- Usually a t-statistic, or any test statistic, with a probability of occurring of less than 5% of the time is considered to be **statistically significant**.

t-distributions and rejection regions

- For a t-distribution with 7,144 degrees of freedom, the cutoff for values of the t-statistic that would be occur less than 5% of the time are shown by the shaded areas, which make up the **critical region** or **rejection region** for the null hypothesis since the values of t in these shaded areas happen so infrequently when the null hypothesis is true that it should be rejected.

- The t-statistics falling into this critical region therefore suggest a **statistically significant** result (Figure \@ref(fig:tdf7144c)).

- Any value of the t-statistic that is in the shaded tales of the distribution happens with a probability of less than 5% **when the null hypothesis is true**.

NHST Steps 4 & 5: Interpret the probability and write a conclusion

- In this case, the t-statistic is in the shaded region which is the rejection region.
- This is sufficient evidence to reject the null hypothesis in favor of the alternate hypothesis.
- Even though the difference between the mean systolic blood pressure of 120.54 and the hypothesized value of 120 is small, it is statistically significant.
- The probability of this sample coming from a population where the mean systolic blood pressure is actually 120 is just 1.4%.
- This sample is likely to be from a population with a higher mean blood pressure.
- In summary:
    - The mean systolic blood pressure in a sample of 7,145 people was 120.54 (sd = 18.62). A one-sample t-test found this mean to be statistically significantly different from the hypothesized mean of 120 [$t(7144) = 2.449$; $p = 0.014$]. The sample likely came from a population with a mean systolic blood pressure not equal to 120.