Lab02 - t tests and confidence intervals for ANOVA

Your Name Here

Goals

The goal in this lab is to get some practice working with t-based inference for ANOVA models in R.

Loading packages

Here are some packages with functionality you may need for this lab. Run this code chunk now.

```
library(readr)
library(dplyr)
```

```
## Warning: package 'dplyr' was built under R version 3.5.2
```

```
##
## Attaching package: 'dplyr'
```

```
## The following objects are masked from 'package:stats':
##
##     filter, lag
```

```
## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```
library(ggplot2)
```

```
## Warning: package 'ggplot2' was built under R version 3.5.2
```

```
library(gridExtra)
```

```
##
## Attaching package: 'gridExtra'
```

```
## The following object is masked from 'package:dplyr':
##
##     combine
```

```
library(mosaic)
```

```
## Warning: package 'mosaic' was built under R version 3.5.2
```

```
## Loading required package: lattice
```

```
## Loading required package: ggformula
```

```
## Warning: package 'ggformula' was built under R version 3.5.2
```

```
## Loading required package: ggstance
```

```
##
## Attaching package: 'ggstance'
```

```
## The following objects are masked from 'package:ggplot2':
##
##     geom_errorbarh, GeomErrorbarh
```

```
##
## New to ggformula?  Try the tutorials:
##  learnr::run_tutorial("introduction", package = "ggformula")
##  learnr::run_tutorial("refining", package = "ggformula")

## Loading required package: mosaicData

## Loading required package: Matrix

##
## The 'mosaic' package masks several functions from core packages in order to add
## additional features.  The original behavior of these functions should not be affected by this.
##
## Note: If you use the Matrix package, be sure to load it BEFORE loading mosaic.

##
## Attaching package: 'mosaic'

## The following object is masked from 'package:Matrix':
##
##     mean

## The following object is masked from 'package:ggplot2':
##
##     stat

## The following objects are masked from 'package:dplyr':
##
##     count, do, tally

## The following objects are masked from 'package:stats':
##
##     binom.test, cor, cor.test, cov, fivenum, IQR, median,
##     prop.test, quantile, sd, t.test, var

## The following objects are masked from 'package:base':
##
##     max, mean, min, prod, range, sample, sum
```

```r
library(gmodels)

options("pillar.sigfig" = 10) # print 10 significant digits in summarize output
```

Reading in the Spock data

The following R code reads in the data set for the Spock Trial and takes a first look at the data. Run this code now; no need to modify it.

```r
juries <- read_csv("http://www.evanlray.com/data/sleuth3/ex0502_women_jurors.csv")
```

```
## Parsed with column specification:
## cols(
##   Percent = col_double(),
##   Judge = col_character()
## )
```

```r
dim(juries)
```

```
## [1] 46  2
```

```
head(juries)
```

```
## # A tibble: 6 x 2
##       Percent Judge
##         <dbl> <chr>
## 1  6.4        Spock's
## 2  8.700000000 Spock's
## 3 13.3        Spock's
## 4 13.6        Spock's
## 5 15          Spock's
## 6 15.2        Spock's
```

```
juries %>% count(Judge)
```

```
## # A tibble: 7 x 2
##   Judge       n
##   <chr>   <int>
## 1 A           5
## 2 B           6
## 3 C           9
## 4 D           2
## 5 E           6
## 6 F           9
## 7 Spock's     9
```

Make some plots

Use this space to make some plots of the Spock trial data.

t tests and confidence intervals

Use this space to conduct hypothesis tests and find confidence intervals.

Example 2 (a) from page 9 of http://www.evanlray.com/stat242_f2019/materials/20190913_ anova/anova_pairwise.pdf

Conduct a hypothesis test of the claim that the mean percent of potential jurors who are women in venires assembled by Spock's judge is the same as the mean percent of potential jurors who are women in venires assembled by judge A. Also find and report a 95% confidence interval for the difference inmeans for those two judges. State your null and alternative hypotheses in terms of equations and written sentences. What are the constants $C_1, \ldots, C_I$ to use for this procedure?

μ_1 = "population" mean percent of women in jury pools for Judge A μ_2 = "population" mean percent of women in jury pools for Judge B μ_3 = "population" mean percent of women in jury pools for Judge C μ_4 = "population" mean percent of women in jury pools for Judge D μ_5 = "population" mean percent of women in jury pools for Judge E μ_6 = "population" mean percent of women in jury pools for Judge F μ_7 = "population" mean percent of women in jury pools for Spock's Judge

Null Hypothesis: $\mu_1 - \mu_7 = 0$ (population means for Judge A and Spock's judge are the same)

Alternative Hypothesis: $\mu_1 - \mu_7 \neq 0$ (population means for Judge A and Spock's judge are different)

In terms of all 7 means, the null hypothesis says

$(1)\mu_1 + 0 * \mu_2 + 0 * \mu_3 + 0 * \mu_4 + 0 * \mu_5 + 0 * \mu_6 + (-1)\mu_7 = 0$

```
model_fit <- lm(Percent ~ Judge, data = juries)
fit.contrast(model_fit, "Judge", c(1, 0, 0, 0, 0, 0, -1), conf = 0.95)
```

```
##                                Estimate Std. Error  t value     Pr(>|t|)
## Judge c=( 1 0 0 0 0 0 -1 ) 19.49778   3.856562 5.055741 1.050245e-05
##                                lower CI upper CI
## Judge c=( 1 0 0 0 0 0 -1 ) 11.69715 27.29841
## attr(,"class")
## [1] "fit_contrast"
```

The p-value for the test is $1.05 * 10^{-5}$ providing strong evidence againt the null hypothesis that the population mean percent of women in jury pools is the same for Judge A and Spock's judge.

We are 95% confident that the difference in population mean percent women between Judge A and Spock's judge is between 11.7 and 27.3.

Example 2 (b) from page 9 of http://www.evanlray.com/stat242_f2019/materials/20190913_anova/anova_pairwise.pdf

Conduct a hypothesis test of the claim that the mean percent of potential jurors who are women in venires assembled by Spock's judge is the same as the mean percent of potential jurors who are women across all 6 other judges. Also find and report a 95% confidence interval for the difference in means between Spock's judge and the average across all 6 other judges. State your null and alternative hypotheses interms of equations and written sentences. What are the constants $C_1, \ldots, C_I$ to use for this procedure?

Null hypothesis: $\mu_7 = (1/6)\mu_1 + (1/6)\mu_2 + \cdots + (1/6)\mu_6$

OR

Null hypothesis: $(1/6)\mu_1 + (1/6)\mu_2 + \cdots + (1/6)\mu_6 - \mu_7 = 0$

```
fit.contrast(model_fit, "Judge", c(1/6, 1/6, 1/6, 1/6, 1/6, 1/6, -1), conf = 0.95)
```

```
##
## Judge c=( 0.166666666666667 0.166666666666667 0.166666666666667 0.166666666666667 0.166666666666667 (
##
## Judge c=( 0.166666666666667 0.166666666666667 0.166666666666667 0.166666666666667 0.166666666666667 (
##
## Judge c=( 0.166666666666667 0.166666666666667 0.166666666666667 0.166666666666667 0.166666666666667 (
##
## Judge c=( 0.166666666666667 0.166666666666667 0.166666666666667 0.166666666666667 0.166666666666667 (
##
## Judge c=( 0.166666666666667 0.166666666666667 0.166666666666667 0.166666666666667 0.166666666666667 (
##
## Judge c=( 0.166666666666667 0.166666666666667 0.166666666666667 0.166666666666667 0.166666666666667 (
## attr(,"class")
## [1] "fit_contrast"
```

The p-value for this test is $1.5 * 10^{-6}$.

We are 95 percent confident that the difference in population means between Spock's judge and the average across all 6 other judges is between 9.63 and 20.32.

For 95% of all samples, an interval calculated using this procedure would contain the difference in population means between Spock's judge and the average across all 6 other judges.

Questions from page 5 of http://www.evanlray.com/stat242_f2019/materials/20190916_lm_summary/lm_summary.pdf

Look at the output from calling `summary` on your linear model fit object

```
summary(model_fit)
```

```
##
## Call:
## lm(formula = Percent ~ Judge, data = juries)
##
## Residuals:
##     Min     1Q  Median     3Q     Max
## -17.320  -4.367  -0.250   3.319  14.780
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   34.1200     3.0921  11.034 1.47e-13 ***
## JudgeB        -0.5033     4.1868  -0.120   0.9049
## JudgeC        -5.0200     3.8566  -1.302   0.2007
## JudgeD        -7.1200     5.7848  -1.231   0.2258
## JudgeE        -7.1533     4.1868  -1.709   0.0955 .
## JudgeF        -7.3200     3.8566  -1.898   0.0651 .
## JudgeSpock's -19.4978     3.8566  -5.056 1.05e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 6.914 on 39 degrees of freedom
## Multiple R-squared:  0.5083, Adjusted R-squared:  0.4326
## F-statistic: 6.718 on 6 and 39 DF,  p-value: 6.096e-05
```

Estimated mean = 34.12 - 0.5 (JudgeB) - 5 JudgeC - 7 JudgeD - 7 JudgeE - 7 JudgeF - 19 JudgeSpock's

What is the baseline category for the explanatory variable in this model?

Judge A.

- A comes first alphabetically, so it's our default reference category.
- Nothing about JudgeA in the summary output.

What are the possible values of the `JudgeSpock's` variable, and in what circumstances does the variable equal each of those values?

1 if we're talking about Spock's judge and 0 if not

What is the `Estimate` labelled `(Intercept)` an estimate of? Be as precise as possible.

It is an estimate of the population mean for Judge A (the reference category).

What is the `Estimate` labelled `JudgeSpock's` an estimate of? Be as precise as possible.

It is an estimate of the difference in population means for Spock's judge and Judge A.

Use the output from `summary` to conduct a test of the null hypothesis that $\mu_A = \mu_{Spock's}$.

This will be based on the p-value in the row of the output table labelled JudgeSpock's.

The p-value is 1.05e-05, providing very strong evidence against the claim the the population means are the same for Judge A and Spock's judge.

Could you use the output from `summary` to conduct a test of the null hypothesis that $\mu_B = \mu_{Spock's}$? (The answer is no – why not?)

With this output, we can only look at differences between a given judge and the reference judge, Judge A.

```
model.matrix(model_fit)
```

```
##    (Intercept) JudgeB JudgeC JudgeD JudgeE JudgeF JudgeSpock's
## 1            1      0      0      0      0      0            1
## 2            1      0      0      0      0      0            1
## 3            1      0      0      0      0      0            1
## 4            1      0      0      0      0      0            1
## 5            1      0      0      0      0      0            1
## 6            1      0      0      0      0      0            1
## 7            1      0      0      0      0      0            1
## 8            1      0      0      0      0      0            1
## 9            1      0      0      0      0      0            1
## 10           1      0      0      0      0      0            0
## 11           1      0      0      0      0      0            0
## 12           1      0      0      0      0      0            0
## 13           1      0      0      0      0      0            0
## 14           1      0      0      0      0      0            0
## 15           1      1      0      0      0      0            0
## 16           1      1      0      0      0      0            0
## 17           1      1      0      0      0      0            0
## 18           1      1      0      0      0      0            0
## 19           1      1      0      0      0      0            0
## 20           1      1      0      0      0      0            0
## 21           1      0      1      0      0      0            0
## 22           1      0      1      0      0      0            0
## 23           1      0      1      0      0      0            0
## 24           1      0      1      0      0      0            0
## 25           1      0      1      0      0      0            0
## 26           1      0      1      0      0      0            0
## 27           1      0      1      0      0      0            0
## 28           1      0      1      0      0      0            0
## 29           1      0      1      0      0      0            0
## 30           1      0      0      1      0      0            0
## 31           1      0      0      1      0      0            0
## 32           1      0      0      0      1      0            0
## 33           1      0      0      0      1      0            0
## 34           1      0      0      0      1      0            0
## 35           1      0      0      0      1      0            0
## 36           1      0      0      0      1      0            0
## 37           1      0      0      0      1      0            0
## 38           1      0      0      0      0      1            0
## 39           1      0      0      0      0      1            0
## 40           1      0      0      0      0      1            0
## 41           1      0      0      0      0      1            0
```

```
## 42                1       0       0       0       0       1               0
## 43                1       0       0       0       0       1               0
## 44                1       0       0       0       0       1               0
## 45                1       0       0       0       0       1               0
## 46                1       0       0       0       0       1               0
## attr(,"assign")
## [1] 0 1 1 1 1 1 1
## attr(,"contrasts")
## attr(,"contrasts")$Judge
## [1] "contr.treatment"
```