Lesson 08: Statistical Inference, Estimation for Single Populations

References

- Black, Chapter 8 Statistical Inference: Estimation for Single Populations (pp. 260-294)
- Davies, Chapter 17 Sampling Distribution and Confidence (pp. 378-384)
- Stowell, Chapter 5 Summary Statistics for Continuous Variables (pp. 70-71), Chapter 6 Tabular Data (pp.84-86)

Exercises:

1) Assume a random sample of size 100 is drawn from a normal distribution with variance 1. The average value of the sample is 50. Find a 95% confidence interval for the mean.

```
n <- 100         # sample size
mean <- 50       # mean of sample
sd <- sqrt(1)    # standard deviation of population

margin.of.error <- qnorm(1-(0.05/2)) * sd/sqrt(n)

conf.int <- c(mean - margin.of.error, mean + margin.of.error)
conf.int
```

```
## [1] 49.804 50.196
```

2) Assume the standard deviation for a normal distribution is equal to 100 units. Also assume we want to estimate the unknown mean with a 95% confidence interval of total width 8 units. Calculate the sample size required.

```
z_score <- qnorm(0.025, mean = 0, sd = 1, lower.tail = FALSE)
sample_size <- (z_score*100.0/4.0)**2
round(sample_size)
```

```
## [1] 2401
```

3) A random sample of 1600 registered voters are contacted and asked a variety of questions. For one question, 60% of the voters expressed approval and 40% disapproval. Calculate a 95% confidence interval for the proportion expressing approval.

```
# Here we will use a built-in R function for testing a proportion.
# prop.test(x, n, p = NULL,
#    alternative = c("two.sided", "less", "greater"),
#    conf.level = 0.95, correct = TRUE
# x a vector of counts of successes, a one-dimensional table with two entries,
#   or a two-dimensional table (or matrix) with 2 columns, giving the counts of
#   successes and failures, respectively.
# n a vector of counts of trials; ignored if x is a matrix or a table.
```

```r
# p a vector of probabilities of success. The length of p must be the same
#   as the number of groups specified by x, and its elements must be greater
#   than 0 and less than 1.
# alternative: a character string specifying the alternative hypothesis,
#   must be one of "two.sided" (default), "greater" or "less". You can specify
#   just the initial letter. Only used for testing the null that a single proportion
# equals a given value, or that two proportions are equal; ignored otherwise.
# conf.level: confidence level of the returned confidence interval.
#   Must be a single number between 0 and 1. Only used when testing the
#   null that a single proportion equals a given value, or that two proportions
#   are equal; ignored otherwise.
# correct: a logical indicating whether Yates' continuity correction should be
#   applied where possible.
prop.test(x = 1600 * 0.6, n = 1600,
    alternative = "two.sided", conf.level = 0.95)
```

```
##
##  1-sample proportions test with continuity correction
##
## data:  1600 * 0.6 out of 1600, null probability 0.5
## X-squared = 63.601, df = 1, p-value = 1.524e-15
## alternative hypothesis: true p is not equal to 0.5
## 95 percent confidence interval:
##  0.5754686 0.6240461
## sample estimates:
##   p
## 0.6
```

```r
# If we were to store prop.test in an R object, we could examine its structure.
prop_test_object <- prop.test(x = 1600 * 0.6, n = 1600,
    alternative = "two.sided", conf.level = 0.95)
print(str(prop_test_object))
```

```
## List of 9
##  $ statistic  : Named num 63.6
##   ..- attr(*, "names")= chr "X-squared"
##  $ parameter  : Named int 1
##   ..- attr(*, "names")= chr "df"
##  $ p.value    : num 1.52e-15
##  $ estimate   : Named num 0.6
##   ..- attr(*, "names")= chr "p"
##  $ null.value : Named num 0.5
##   ..- attr(*, "names")= chr "p"
##  $ conf.int   : atomic [1:2] 0.575 0.624
##   ..- attr(*, "conf.level")= num 0.95
##  $ alternative: chr "two.sided"
##  $ method     : chr "1-sample proportions test with continuity correction"
##  $ data.name  : chr "1600 * 0.6 out of 1600, null probability 0.5"
##  - attr(*, "class")= chr "htest"
## NULL
```

```r
# Notice that this object is a list and the confidence interval lower
# and uppler limits themselves can be extracted from the object as
as.numeric(prop_test_object$conf.int)
```

```
## [1] 0.5754686 0.6240461
```

5) A random sample of consumers are presented with two beverages in random order and asked which they prefer most. All the consumers expressed a preference. One beverage was preferred 85% of the time. Use this number to determine how large a sample of consumers would be needed to generate a 95% confidence interval with an overall width just less than 2% (i.e. from 84% to 86%)?

```r
p <- 0.85
z_score <-  qnorm(0.025, mean = 0, sd = 1, lower.tail = FALSE)
sample_size <- (z_score**2)*p*(1-p)/(0.01)**2
round(sample_size)
```

```
## [1] 4898
```

```r
sample_size <- (z_score**2)*(0.25)/(0.01)**2
round(sample_size)
```

```
## [1] 9604
```

Data Set: hot_dogs.csv (Original source: Consumer Reports, June 1986, pp. 366-367)

Description: Results of a laboratory analysis of calories and sodium content of major hot dog brands. Researchers for Consumer Reports analyzed three types of hot dog: beef, poultry, and meat (mostly pork and beef, but up to 15% poultry meat). Fifty four observations are reported.

Variable Names:

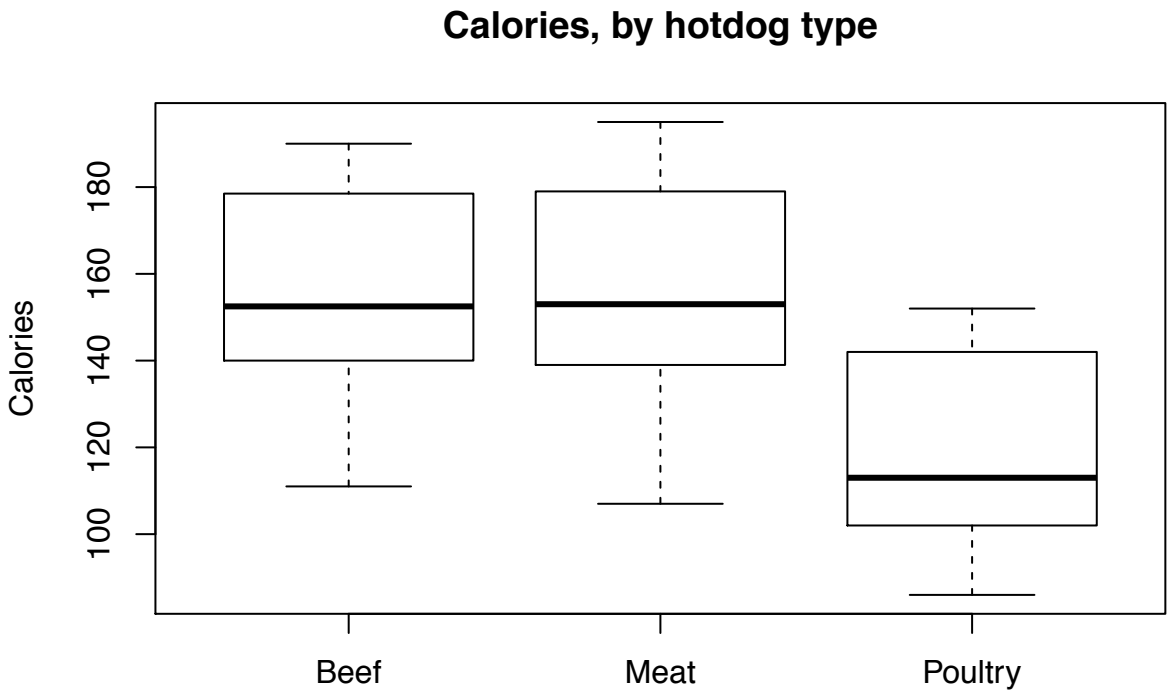
1. Type = Type of hotdog (beef, meat, or poultry)
2. Calories = Calories per hot dog
3. Sodium = Milligrams of sodium per hot dog

1) Create boxplots and find 95% confidence intervals for the mean amount of calories in each Type of hot dog: beef, meat and poultry. Construct 99% one-sided lower confidence intervals for the mean amount of calories in each Type of hot dog: beef, meat and poultry.

```r
# Read the comma-delimited text file creating a data frame object in R,
# then examine its structure:
hotdogs <- read.csv("hot_dogs.csv")
str(hotdogs)
```

```
## 'data.frame':    54 obs. of  3 variables:
##  $ Type    : Factor w/ 3 levels "Beef","Meat",..: 1 1 1 1 1 1 1 1 1 1 ...
##  $ Calories: int  186 181 176 149 184 190 158 139 175 148 ...
##  $ Sodium  : int  495 477 425 322 482 587 370 322 479 375 ...
```

```r
with(hotdogs, boxplot(Calories ~ Type, main = "Calories, by hotdog type",
  ylab = "Calories"))
```




```r
# Reading ahead in this lesson, we see that most of the questions
# concern subsets of the data by hotdog type. To respond to the
# questions, we will create three subset data frames.
beef <- subset(hotdogs, subset = (Type == "Beef"))
meat <- subset(hotdogs, subset = (Type == "Meat"))
poultry <- subset(hotdogs, subset = (Type == "Poultry"))

# Here we know of an R function to compute the confidence interval.
with(beef, t.test(Calories)$conf.int)
```

```
## [1] 146.2532 167.4468
## attr(,"conf.level")
## [1] 0.95
```

```r
with(meat, t.test(Calories)$conf.int)
```

```
## [1] 145.7308 171.6809
## attr(,"conf.level")
## [1] 0.95
```

```r
with(poultry, t.test(Calories)$conf.int)
```

```
## [1] 107.1698 130.3596
## attr(,"conf.level")
## [1] 0.95
```

```r
# Construct 99% one-sided lower confidence intervals for the mean amount of
# calories in each Type of hot dog:  beef, meat and poultry.

# One-sided confidence intervals can also be created.
t.test(beef$Calories, alternative = "less", conf.level = 0.99)
```

```
##
##  One Sample t-test
##
## data:  beef$Calories
## t = 30.98, df = 19, p-value = 1
## alternative hypothesis: true mean is less than 0
## 99 percent confidence interval:
##      -Inf 169.7072
## sample estimates:
## mean of x
##    156.85
```

```r
t.test(meat$Calories, alternative = "less", conf.level = 0.99)
```

```
##
##  One Sample t-test
##
## data:  meat$Calories
## t = 25.93, df = 16, p-value = 1
## alternative hypothesis: true mean is less than 0
## 99 percent confidence interval:
##      -Inf 174.5183
## sample estimates:
## mean of x
##  158.7059
```

```r
t.test(poultry$Calories, alternative = "less", conf.level = 0.99)
```

```
##
##  One Sample t-test
##
## data:  poultry$Calories
## t = 21.714, df = 16, p-value = 1
## alternative hypothesis: true mean is less than 0
## 99 percent confidence interval:
##      -Inf 132.8951
## sample estimates:
## mean of x
##  118.7647
```

2) Find a 95% confidence interval for the variance in the amount of calories found for each type of hotdog: beef, meat and poultry.

```
# Here, we set up a user-defined function.
# Note that this is a chi-square test... so we use qchisq() function
# qchisq(p, df, ncp = 0, lower.tail = TRUE, log.p = FALSE)  # quantiles
var.conf.int = function(x, conf.level = 0.95) {
  df <- length(x) - 1
  chilower <- qchisq((1 - conf.level)/2, df, lower.tail = TRUE)
  chiupper <- qchisq((1 - conf.level)/2, df, lower.tail = FALSE)
  v <- var(x)
  c(df * v/chiupper, df * v/chilower)
}
with(beef, var.conf.int(Calories))
```

```
## [1]  296.495 1093.643
```

```
with(meat, var.conf.int(Calories))
```

```
## [1]  353.2469 1475.1049
```

```
with(poultry, var.conf.int(Calories))
```

```
## [1]  282.0926 1177.9754
```