

Statistics 305: Introduction to Biostatistical Methods for Health Sciences

R Demos for Chapters 8-10: Review of Statistical Inference

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Confidence Intervals (Chapter 9)

Example

- ▶ Example from the text, page 223, summarizes data on plasma aluminum levels, in $\mu\text{g}/\text{l}$, for $n = 10$ infants receiving antacids that contain aluminum.
 - ▶ The sample mean of the plasma aluminum levels is $\bar{x} = 37.20\mu\text{g}/\text{l}$, and the sample SD is $s = 7.13$
- ▶ I can't access the data from the text, but I have simulated a data set of $n = 10$ subject with similar properties for this demo.
 - ▶ Read these data into R:

```
uu <- url("http://people.stat.sfu.ca/~jgraham/Teaching/S305_18/Data/pa.csv")
plasmaAlu <- read.csv(uu)
head(plasmaAlu)
```

```
##           alu
## 1 33.20381
## 2 35.55883
## 3 48.31359
## 4 37.70272
## 5 38.12182
## 6 49.42841
```

Simulated Data Summary Statistics

- ▶ Our simulated data are similar to the data from the text, but the sample mean and SD are different:

```
library(dplyr)
summarize(plasmaAlu, mean(alu))
```

```
##    mean(alu)
## 1  37.73208
```

```
summarize(plasmaAlu, sd(alu))
```

```
##    sd(alu)
## 1  6.80048
```

Software Notes

- ▶ Recall from the chapter 2-3 demo that `dplyr` is an add-on package for R that includes useful tools for manipulating datasets in R.
 - ▶ To use `dplyr` functions we must first load the package with `library(dplyr)`.
- ▶ The package consists of 5 main “verbs” for manipulating a dataframe:
 1. `select()`: select columns
 2. `filter()`: filter rows
 3. `arrange()`: re-order or arrange rows
 4. `mutate()`: create new columns
 5. `summarize()`: summarise columns
- ▶ The `summarize()` function takes the dataframe as its first argument, and the summaries to compute as additional arguments.

Do-It-Yourself CIs in R

- ▶ In R, the quantile function `qt()` for the t distribution can be used to find the quantile or critical value (t^*) for the CI when σ is unknown.
 - ▶ When the argument `lower.tail=FALSE`, the first argument, p , is the upper-tail area to the right of the desired quantile, under the t distribution.

```
tstar<-qt(p=(1-0.95)/2,df=9,lower.tail=FALSE)
tstar
```

```
## [1] 2.262157
```

- ▶ Once we have the quantile or critical value, we can calculate the 95% CI.

- ▶ Use assignment operator `<-` to put the critical value into an R object called `tstar`.
- ▶ Then use `summarize()` function in `dplyr` package to get sample mean, sample sd and the number of observations, n . Assign these to an R object `mysummary`.
- ▶ Use the saved objects to calculate lower and upper bounds of CI and put them into the R object `CI`.

```
tstar <- qt(p=(1-0.95)/2,df=9,lower.tail=FALSE)
mysummary <- plasmaAlu %>%
  summarize(xbar=mean(alu),s=sd(alu),n=n()) %>%
  mutate(CI.lower=xbar-tstar*s/sqrt(n),
         CI.upper=xbar+tstar*s/sqrt(n))
mysummary
```

```
##           xbar           s    n CI.lower CI.upper
## 1 37.73208 6.80048 10 32.86731 42.59685
```

Chaining Data Manipulations

- ▶ In the above code chunk we used the “forward pipe”, `%>%` to push the dataset from one data manipulation to another.
- ▶ Push the `plasmaAlu` dataframe through the pipe to use as input to `summarize()`, then take the dataframe output by `summarize` and push it through the pipe to use as input to `mutate()`.
 - ▶ Each data processing step is a verb, and we are to read the result like a sentence: Start with `plasmaAlu`, summarize it (mean, SD and sample size), then mutate it to add the lower and upper CI limits.
 - ▶ Notice that we do not need to explicitly specify the input data to `summarize()` and `mutate()`.

CI's with the `t.test()` Function

- ▶ R's `t.test()` uses data to test hypotheses about a mean, or about differences between two means, but the function also returns summary statistics and a CI.
- ▶ Set the level or coverage probability of the CI with the argument `conf.level` (default $C = 0.95$):

```
with(plasmaAlu,t.test(alu,conf.level=0.95))
```

```
##  
##  One Sample t-test  
##  
## data:  alu  
## t = 17.546, df = 9, p-value = 2.872e-08  
## alternative hypothesis: true mean is not equal to 0  
## 95 percent confidence interval:  
##  32.86731 42.59685  
## sample estimates:  
## mean of x  
##  37.73208
```

Hypothesis Tests (Chapter 10)

Example

- ▶ In the **population** of infants **not taking antacids**, the mean plasma-aluminum levels are known to be $\mu_0 = 4.13 \mu\text{g/l}$.
- ▶ Want to assess whether the mean level μ in infants taking antacids is the same as μ_0 ; i.e. whether

$$H_0 : \mu = 4.13.$$

- ▶ Our alternative hypothesis is $H_a : \mu \neq 4.13$; i.e., the mean plasma-aluminum levels of infants taking antacids is different from infants not taking antacids.

Do-It-Yourself Hypothesis Test

- ▶ The t -statistic is

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

- ▶ We can implement this as follows using the summaries in the object `mysummary` from the CI demo:

```
mysummary
```

```
##           xbar           s    n CI.lower CI.upper
## 1 37.73208 6.80048 10 32.86731 42.59685
```

```
with(mysummary, (xbar - 4.13)/(s/sqrt(n)))
```

```
## [1] 15.62524
```

- ▶ The p -value is $2P(T \geq |15.63|)$ for T with $10 - 1 = 9$ df:

```
2*pt(15.63,df=9,lower.tail=FALSE)
```

```
## [1] 7.887651e-08
```

Using the `t.test()` Function

- ▶ The `t.test()` function will also perform the test.
 - ▶ Specify the null hypothesis $H_0 : \mu = 4.13$ with the `mu` argument.
 - ▶ The function's default is to use the two-sided alternative hypothesis, which in this case is $\mu \neq 4.13$:

```
with(plasmaAlu,t.test(alu,mu=4.13))
```

```
##  
##  One Sample t-test  
##  
## data:  alu  
## t = 15.625, df = 9, p-value = 7.909e-08  
## alternative hypothesis: true mean is not equal to 4.13  
## 95 percent confidence interval:  
##  32.86731 42.59685  
## sample estimates:  
## mean of x  
##  37.73208
```