## Discussion 10: 2 Sample T tests and Bootstrap T

1. Consider an experiment where medical researchers wish to test the efficacy of a new antibiotic, labeled A. They will compare it to the old gold-standard antibiotic labeled B – for which there is not yet any known resistance. To conduct the test, the researchers will prepare 20 agar plates. As the antibiotics themselves are produced by modified bacteria, the plates will be steralized and seeded with e-Coli-half of the agar plates will be seeded with either the bacteria producing antibiotic A or antibiotic B. After two weeks, the proportion of e-Coli is measured on each plate:

```
A: 0.10, 0.12, 0.08, 0.14, 0.08, 0.11, 0.13, 0.09, 0.12, 0.15
```

B: 0.14, 0.13, 0.10, 0.19, 0.01, 0.28, 0.46, 0.24, 0.07, 0.10

- (a) What problems might exist in analyzing this particular experiment?
- (b) If we ignore these problems, what is the appropriate set of hypotheses if we wish to determine whether the mean proportion of e-Coli present is the same with the two antibiotics?
- (c) What kind of tests could we perform and why? (Hint: think about the assumptions of each test.)
- (d) Conduct the test(s) by hand at the 5% after computing the summary statistics (as applicable). Confirm your findings with R What are the p-values for those tests you identified in a? How do the conclusions of the tests compare?
- (e) Suppose during the researcher's literature review, they saw that other studies have proposed that antibiotic B has a proportion of 15% e-Coli after two weeks in agar plates prepared as they had. If instead of preparing agar plates with antibiotic B and collecting sample data, they used .15 as a true proportion of e-Coli with antibiotic B, how would their process change? Which experiment and analysis (original scenerio vs that proposed in this part) would be the most informative?
- 2. Consider the original two sample experiment as above, but suppose this was the sample data observed:

```
A: 5.42, 3.54, 2.14, 9.56, 17.16, 1.98, 1.30, 2.01, 2.23, 2.04, 2.10, 2.12, 2.09, 2.07
```

B: 0.31, 0.27, 0.93, 0.92, 0.18, 0.90, 0.64, 2.42, 2.87, 2.15, 2.53, 2.75, 2.34, 2.38

Repeat c) and d) from above.

3. Consider the same experiment as above, but with this new data set:

A: 2.61, 2.07, 2.28, 2.08, 2.12, 1.69, 1.85

B: 1.61, 1.90, 1.74, 1.83, 1.87, 1.79, 1.94, 1.68

Repeat c) and d) from above.

```
AA<-c(0.10, 0.12, 0.08, 0.14, 0.08, 0.11, 0.13, 0.09, 0.12, 0.15)
BB < -c(0.14, 0.13, 0.10, 0.19, 0.01, 0.28, 0.46, 0.24, 0.07, 0.10)
(xbar.AA<-mean(AA)); (s.AA<-sd(AA))</pre>
(xbar.BB<-mean(BB)); (s.BB<-sd(BB))</pre>
Ex1.combo<-c(AA, BB)
Ex1.labels<-c(rep("AA", length(AA)),rep("BB", length(BB)))</pre>
Ex1.df<-data.frame(Ex1.combo, Ex1.labels)</pre>
stripchart(Ex1.combo~Ex1.labels, method="stack")
qqnorm(AA)
qqnorm(BB)
na=length(AA)
nb=length(BB)
df < (var(AA)/na+var(BB)/nb)^2/((var(AA)/na)^2/(na-1)+(var(BB)/nb)^2/(nb-1))
t.test(AA, BB, var.equal = FALSE, alternative = "two.sided")
#By Hand in R
(Ex1.tobs < -(xbar.AA-xbar.BB-0)/sqrt(s.AA^2/10+s.BB^2/10))
p.val<-2*pt(Ex1.tobs, df)</pre>
p.val
#Bootstrap for Two Sample Test
boottwo <- function(dat1, dat2, nboot) {</pre>
  bootstat <- numeric(nboot)</pre>
  truediff <- mean(dat1) - mean(dat2)</pre>
 n1 <- length(dat1)</pre>
  n2 <- length(dat2)
  for (i in 1:nboot) {
    samp1 <- sample(dat1, size = n1, replace = T)</pre>
    samp2 <- sample(dat2, size = n2, replace = T)</pre>
    bootmean1 <- mean(samp1)</pre>
    bootmean2 <- mean(samp2)</pre>
    bootvar1 <- var(samp1)</pre>
    bootvar2 <- var(samp2)</pre>
    bootstat[i] <- (bootmean1 - bootmean2 - truediff)/sqrt((bootvar1/n1) + (bootvar2/n2))</pre>
return(bootstat)
n.boot<-10000
set.seed(1)
Ex1.boot<-boottwo(AA, BB, n.boot)</pre>
(m.low<-sum(Ex1.boot<= Ex1.tobs)) #521
(m.up < -sum(Ex1.boot >= Ex1.tobs)) #9479
(pval < -2*min(m.low, m.up)/n.boot) #0.1042
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#Question 2
AA.2<-c(5.42, 3.54, 2.14, 9.56, 17.16, 1.98, 1.30, 2.01, 2.23, 2.04, 2.10, 2.12, 2.09, 2.07)
BB.2<-c(0.31, 0.27, 0.93, 0.92, 0.18, 0.90, 0.64, 2.42, 2.87, 2.15, 2.53, 2.75, 2.34, 2.38)
(xbar.AA2 < -mean(AA.2)); (s.AA2 < -sd(AA.2))
(xbar.BB2<-mean(BB.2)); (s.BB2<-sd(BB.2))
Ex2.combo<-c(AA.2, BB.2)
Ex2.labels<-c(rep("AA2", length(AA.2)),rep("BB2", length(BB.2)))</pre>
Ex2.df<-data.frame(Ex2.combo, Ex2.labels)</pre>
stripchart(Ex2.combo~Ex2.labels, method="stack")
boxplot(Ex2.combo~Ex2.labels)
qqnorm(AA.2)
qqnorm(BB.2)
(Ex2.t < -(xbar.AA2-xbar.BB2-0)/sqrt(s.AA2^2/10+s.BB2^2/10))
Ex2.boot<-boottwo(AA.2, BB.2, n.boot)</pre>
hist(Ex2.boot)
(m.low2 < -sum(Ex2.boot <= Ex2.t)) #9883
(m.up2 < -sum(Ex2.boot >= Ex2.t)) #117
(pval2 < -2*min(m.low2, m.up2)/n.boot)
#Exercise 3
AA.3<-c(2.19, 2.07, 2.28, 2.08, 2.12, 1.88, 1.99)
BB.3<-c(1.99, 1.90, 1.74, 1.83, 1.87, 1.79, 1.94, 1.71)
(xbar.AA3<-mean(AA.3)); (s.AA3<-sd(AA.3))
(xbar.BB3<-mean(BB.3)); (s.BB3<-sd(BB.3))
Ex3.combo<-c(AA.3, BB.3)
Ex3.labels<-c(rep("AA3", length(AA.3)),rep("BB3", length(BB.3)))</pre>
Ex3.df<-data.frame(Ex3.combo, Ex3.labels)</pre>
stripchart(Ex3.combo~Ex3.labels, method="stack")
boxplot(Ex3.combo~Ex3.labels)
qqnorm(AA.3)
qqnorm(BB.3)
#T.test Equal Variance
t.test(AA.3, BB.3, var.equal=TRUE, alternative="two.sided")
#T.test Non Equal Variance
t.test(AA.3, BB.3, var.equal=FALSE, alternative="two.sided")
#Bootstrap
(Ex3.tobs<-(xbar.AA3-xbar.BB3-0)/sqrt(s.AA3^2/7+s.BB3^2/8))
Ex3.boot<-boottwo(AA.3, BB.3, n.boot)
(m.low3<-sum(Ex3.boot<=Ex3.tobs))</pre>
(m.up3 < -sum(Ex3.boot > = Ex3.tobs))
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pval3<-min(m.low3,m.up3)/n.boot
pval3</pre>