Discussion 9 Soln

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 sterilized 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?

      Answer: Were the agar plates seeded with the exact same number of the relevant bacteria?, Do the bacteria producing antibiotics A and B reproduce at the same rate? (maybe one grows very quickly but other grows for a longer time?) Could there be other interactions besides the presence of the antibiotic between the two bacteria in each plate which might effect the outcome?

   (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? *Answer:* $H_o : \mu_a - \mu_b = 0$ *vs* $H_A : \mu_a - \mu_b \neq 0$

   (c) What kind of tests could we perform and why? (Hint: think about the assumptions of each test.) *Answer: Summary Statistics:* $\bar{x}_{aa} = 0.112; s_{aa} = 0.0244$ *and* $\bar{x}_{bb} = 0.172; s_{bb} = 0.129$ *, Based on the stripchart and the sample sd,* $s_{aa}/s_{bb} = 0.0244/0.129 = 0.19$ *we see that the variances between the two groups is very dissimilar, so we should not use the equal variance assumption. The qqnorm plots looks pretty linear, so we could do the (1) welch's 2 sample t test. We can also do a bootstrap (though this technique seems less necessary)*

   (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 c? How do the conclusions of the tests compare?

      Answer: For Welch's t test, we can do much of it by hand: $t_{obs} = \frac{\bar{X}_a - \bar{X}_b - 0}{\sqrt{s_a^2/n_a + s_b^2/n_b}} = \frac{0.112 - 0.172}{\sqrt{0.0244^2/10 + 0.1288^2/10}} = \frac{-0.06}{0.04146} = -1.447$ *we also need df which is* $v = df = \frac{[0.0244^2/10 + 0.129^2/10]^2}{\frac{(0.0244^2/10)^2}{9} + \frac{(0.129^2/10)^2}{9}} = 9.5855 \approx 9$ *and pvalue=*$2 * P(T_9) < -1.447$ *so* $0.10 < pvalue < 0.20$ *from the t table. We get an exact p value of 0.1796 and a very close df. We need to use the computer for the bootstrap (where code is given below). From a bootstrap with set.seed(1), I got a 2 sided p value of 0.1042.*

   (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?

Answer: They could have just done a 1 sample t test with A being the sample and comparing the mean of sample A to .15. I think the two sample is probably more reliable, because then the data is being generated by the same researchers. In some ways that is "controlling for" the practicioner (ie, they or the environment is affecting both sets of agar plates and therefore both antibiotic growth rates similarly -maybe they have really clean plates which inhibit (or support) E.coli growth for both?)

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.

   Answer: The qqplots and boxplots show strong evidence of a non normal population, thus bootstrap would be best. Computations shown below. From bootstrap I got tobs=1.724978, p=0.0234

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

   A : 2.19, 2.07, 2.28, 2.08, 2.12, 1.88, 1.99

   B : 1.99, 1.90, 1.74, 1.83, 1.87, 1.79, 1.94, 1.71

   Repeat c) and d) from above.

   Answer: The qqplots and boxplots show no evidence of a non normal population, thus I can perform a t test. (bootstrap or wilcoxon can also be done, but less necessary All computations shown below. Since the sample SD are approximately equal, we could do a equal variance t test (though may not want to make this assumption with such a small sample). With equal variance assumption, I first calculate the pooled variance: $s_p = \sqrt{\frac{6*0.130^2+7*0.097^2}{7+8-2}} = 0.11343$. Then I got: $t_{obs} = \frac{2.087-1.846-0}{0.11343*\sqrt{1/7+1/8}} = 4.10$, df = 7+8-2=13, from table: $0.001 < p-value < .002$ from R: p-value = 0.001259, and with non equal variance (in R) I got tobs = 4.0151, df = 11.039, p-value = 0.002019: From bootstrap (with seed 1) I got tobs=4.0151, p=0.0012. All methods gave me strong evidence against null which looks appropriate based on graph.

```
#Ex 1:
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))
```
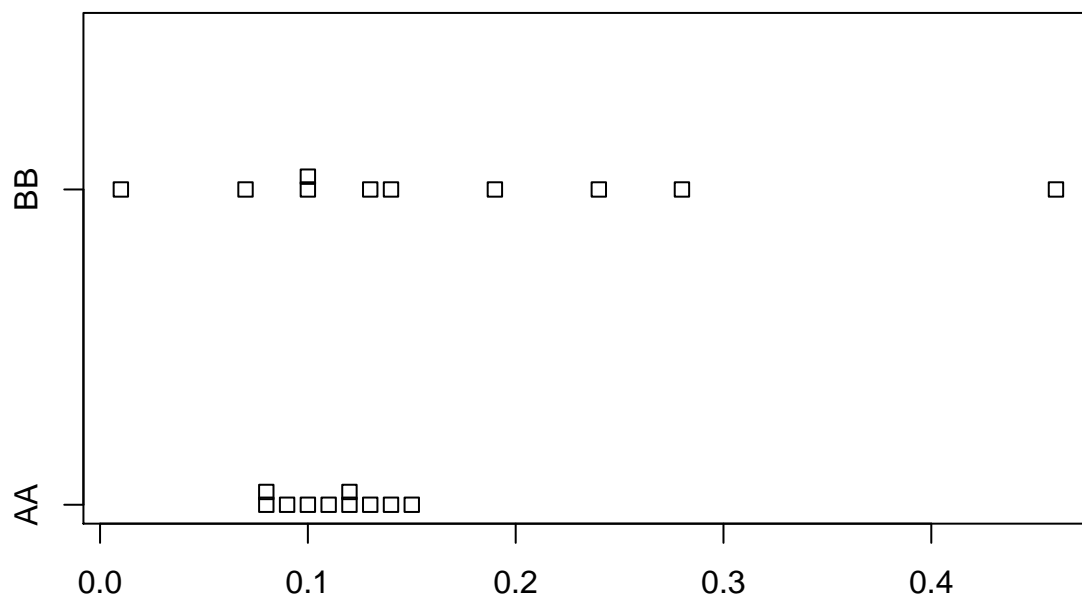
```
## [1] 0.112
```

```
## [1] 0.02440401
```

```
(xbar.BB<-mean(BB)); (s.BB<-sd(BB))
```

```
## [1] 0.172
```

```
## [1] 0.1288237
```

```
Ex1.combo<-c(AA, BB)
Ex1.labels<-c(rep("AA", length(AA)),rep("BB", length(BB)))
Ex1.df<-data.frame(Ex1.combo, Ex1.labels)

stripchart(Ex1.combo~Ex1.labels, method="stack")
```
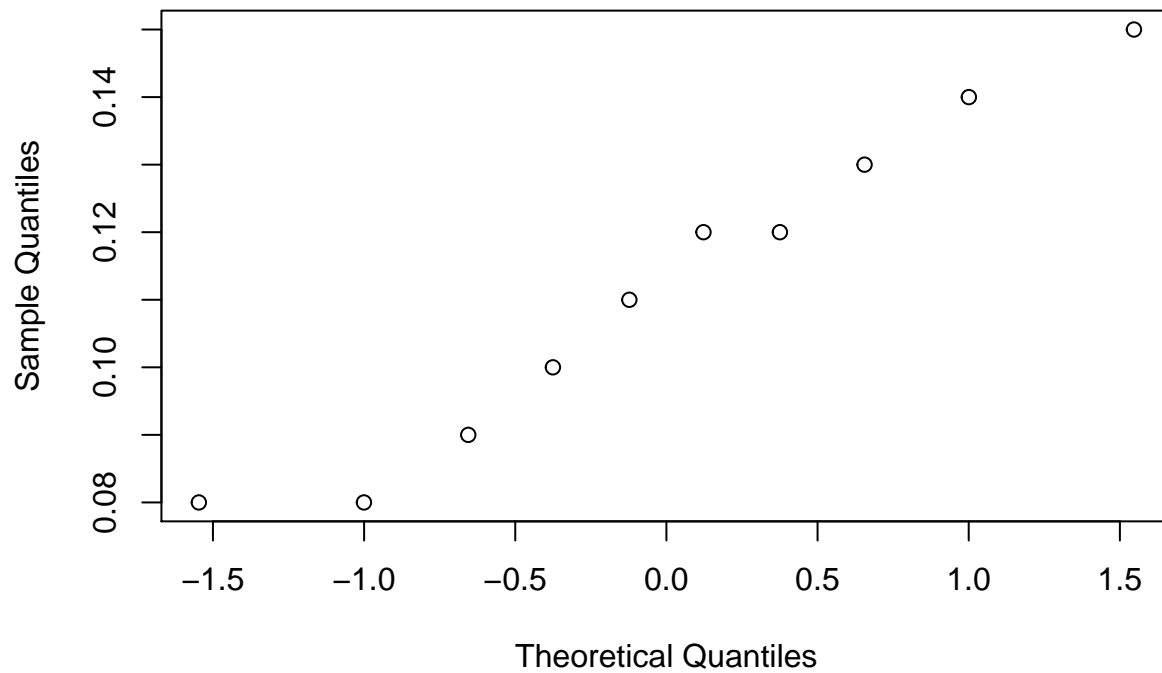
Ex1.combo

Normal Q–Q Plot

Normal Q–Q Plot
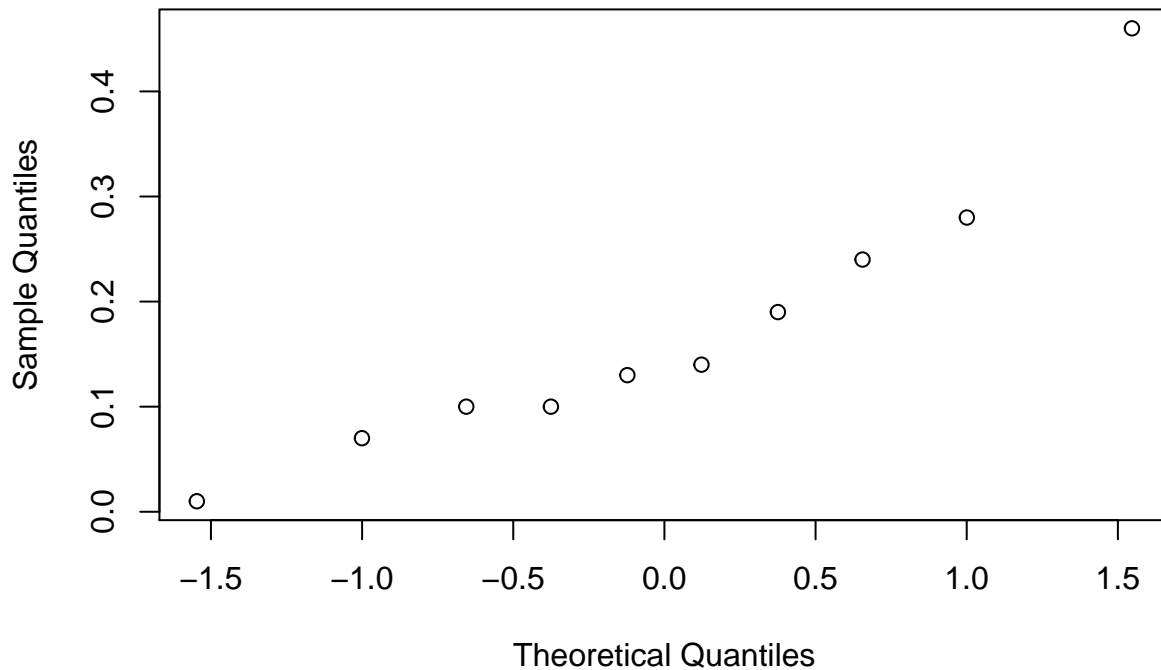

```
na=length(AA)
nb=length(BB)
df<-(var(AA)/na+var(BB)/nb)^2/((var(AA)/na)^2/(na-1)+(var(BB)/nb)^2/(nb-1))
df
```

```
## [1] 9.645125
```

```
t.test(AA, BB, var.equal = FALSE, alternative = "two.sided")
```

```
##
##  Welch Two Sample t-test
##
## data:  AA and BB
## t = -1.4471, df = 9.6451, p-value = 0.1796
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.15284628  0.03284628
## sample estimates:
## mean of x mean of y
##     0.112     0.172
```

```
#By Hand in R
(Ex1.tobs<-(xbar.AA-xbar.BB-0)/sqrt(s.AA^2/10+s.BB^2/10))
```

```
## [1] -1.447102
```

```
p.val<-2*pt(Ex1.tobs, df)
p.val
```

```
## [1] 0.1795755
```

```
#Bootstrap for Two Sample Test
boottwo <- function(dat1, dat2, nboot) {
```

```r
  bootstat <- numeric(nboot)
  truediff <- mean(dat1) - mean(dat2)
  n1 <- length(dat1)
  n2 <- length(dat2)
  for (i in 1:nboot) {
    samp1 <- sample(dat1, size = n1, replace = T)
    samp2 <- sample(dat2, size = n2, replace = T)
    bootmean1 <- mean(samp1)
    bootmean2 <- mean(samp2)
    bootvar1 <- var(samp1)
    bootvar2 <- var(samp2)
    bootstat[i] <- (bootmean1 - bootmean2 - truediff)/sqrt((bootvar1/n1) + (bootvar2/n2))
  }
return(bootstat)
}

n.boot<-10000

set.seed(1)
Ex1.boot<-boottwo(AA, BB, n.boot)
(m.low<-sum(Ex1.boot<= Ex1.tobs))   #521
```

```
## [1] 521
```

```r
(m.up<-sum(Ex1.boot >= Ex1.tobs))    #9479
```

```
## [1] 9479
```

```r
(pval<-2*min(m.low, m.up)/n.boot)   #0.1042
```

```
## [1] 0.1042
```

```r
#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))
```

```
## [1] 3.982857
```

```
## [1] 4.355413
```

```r
(xbar.BB2<-mean(BB.2)); (s.BB2<-sd(BB.2))
```
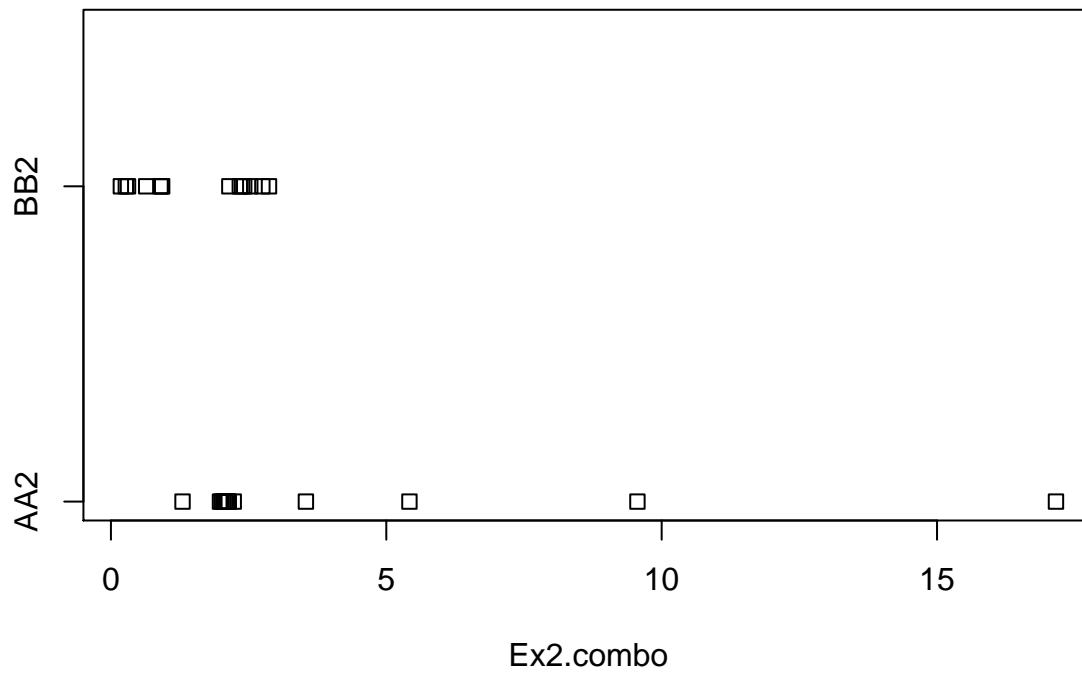
```
## [1] 1.542143
```
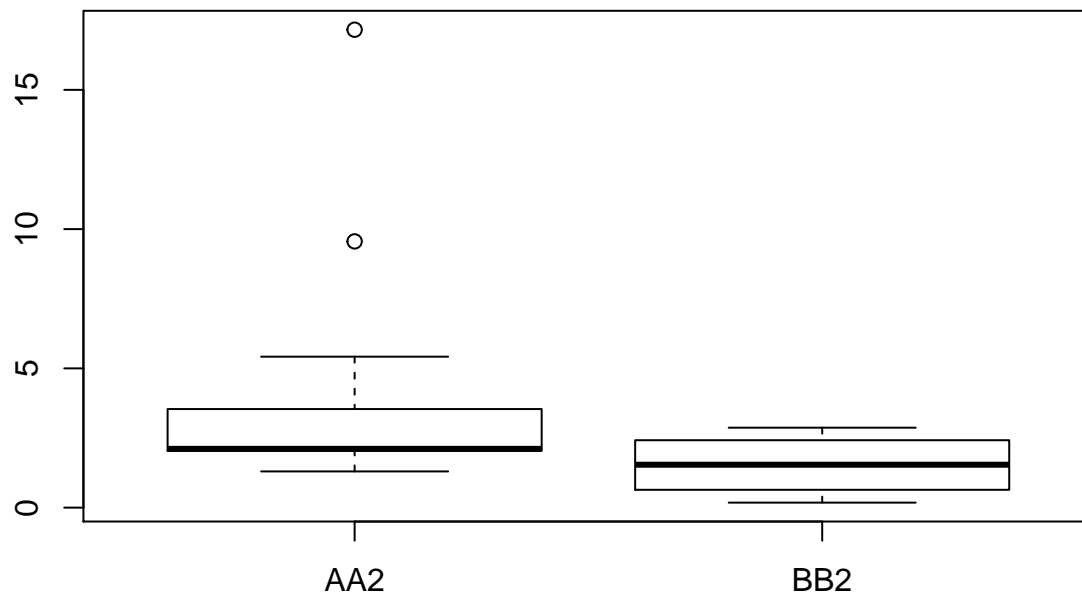
```
## [1] 1.024944
```

```r
Ex2.combo<-c(AA.2, BB.2)
Ex2.labels<-c(rep("AA2", length(AA.2)),rep("BB2", length(BB.2)))
Ex2.df<-data.frame(Ex2.combo, Ex2.labels)

stripchart(Ex2.combo~Ex2.labels, method="stack")
```
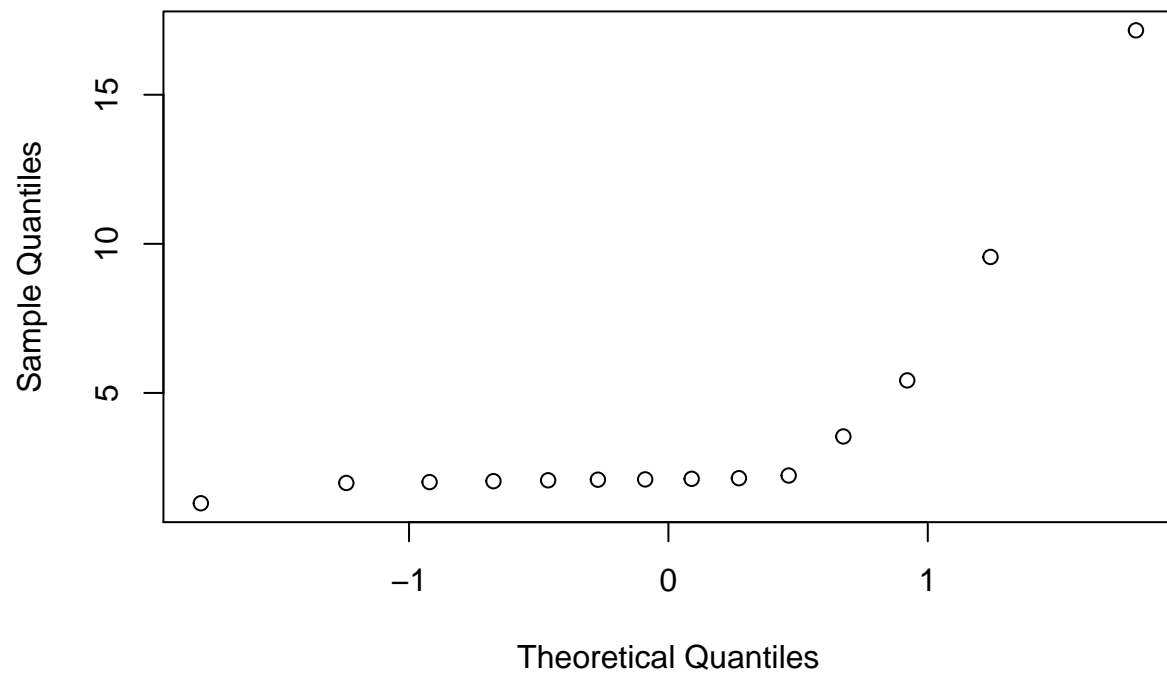
```
boxplot(Ex2.combo~Ex2.labels)
```
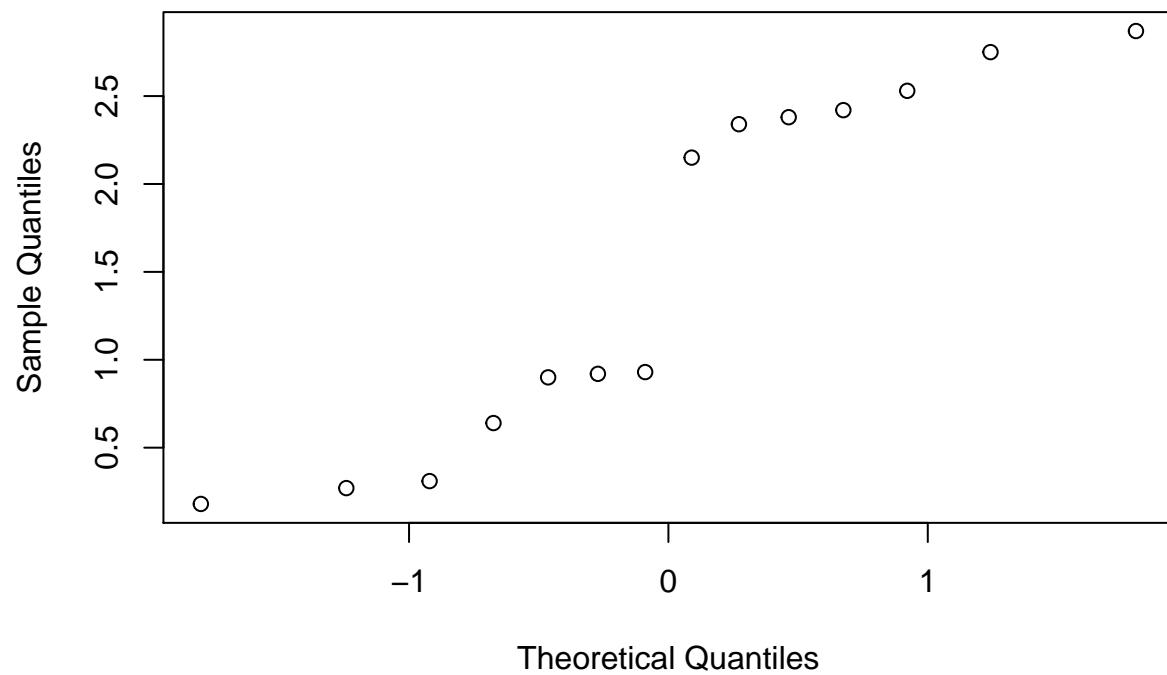


```
qqnorm(AA.2)
```

Normal Q–Q Plot


```r
qqnorm(BB.2)
```
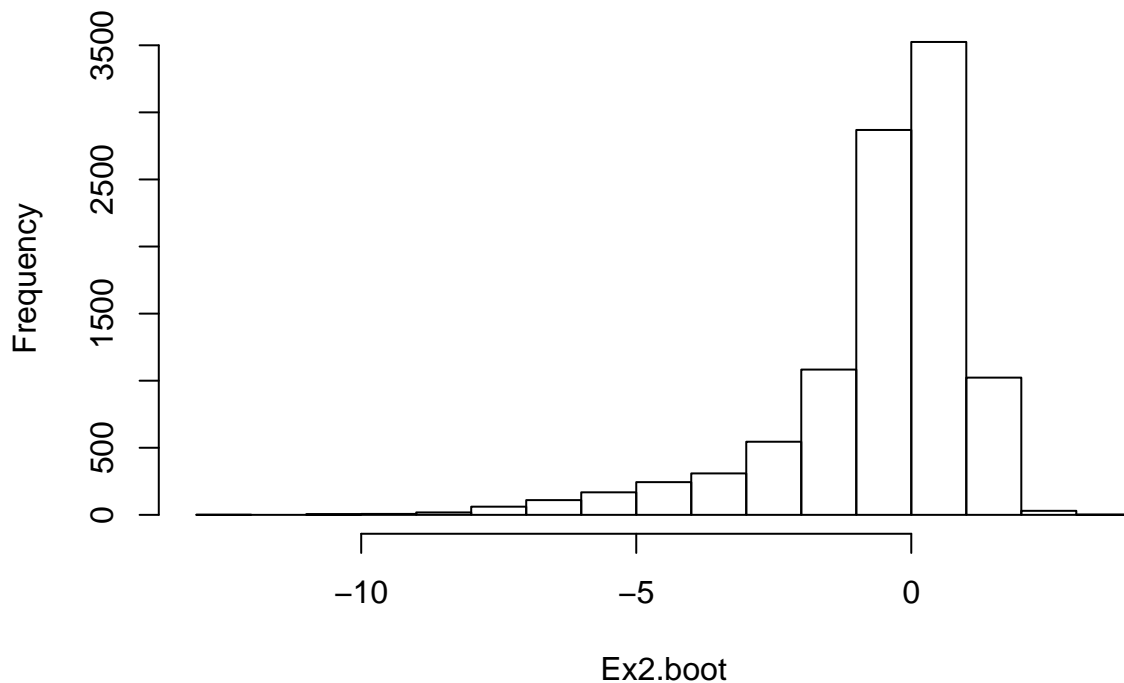
Normal Q–Q Plot


```r
(Ex2.t<-(xbar.AA2-xbar.BB2-0)/sqrt(s.AA2^2/10+s.BB2^2/10))
```

```
## [1] 1.724978
```

```
set.seed(1)
Ex2.boot<-boottwo(AA.2, BB.2, n.boot)
hist(Ex2.boot)
```

Histogram of Ex2.boot

Ex2.boot

```
(m.low2<-sum(Ex2.boot<= Ex2.t))   #9883
```

[1] 9883

```
(m.up2<-sum(Ex2.boot >= Ex2.t))   #117
```

[1] 117

```
(pval2<-2*min(m.low2, m.up2)/n.boot)
```

[1] 0.0234

```
#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))
```

[1] 2.087143
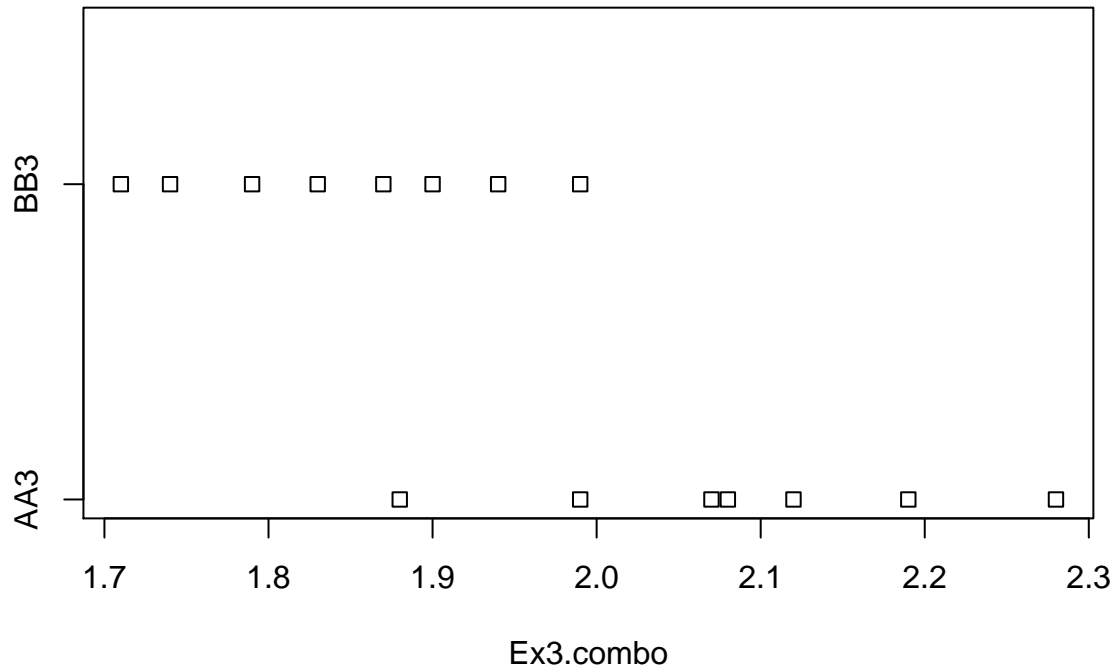
[1] 0.1300915

```
(xbar.BB3<-mean(BB.3)); (s.BB3<-sd(BB.3))
```
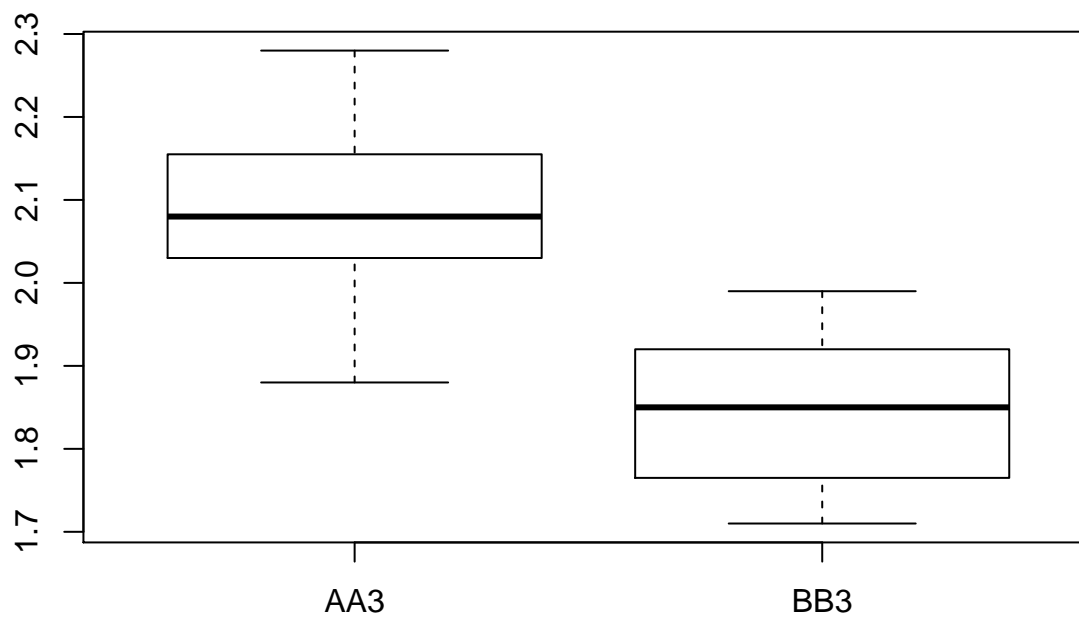
[1] 1.84625

[1] 0.09723866

```
Ex3.combo<-c(AA.3, BB.3)
Ex3.labels<-c(rep("AA3", length(AA.3)),rep("BB3", length(BB.3)))
Ex3.df<-data.frame(Ex3.combo, Ex3.labels)

stripchart(Ex3.combo~Ex3.labels, method="stack")
```
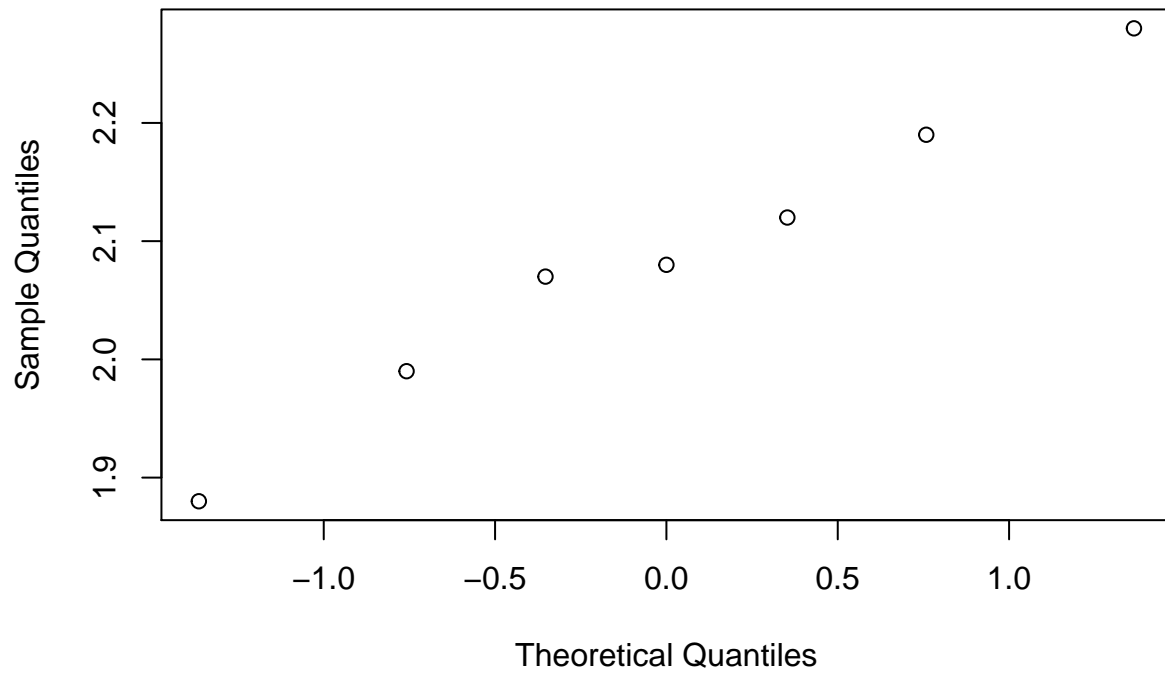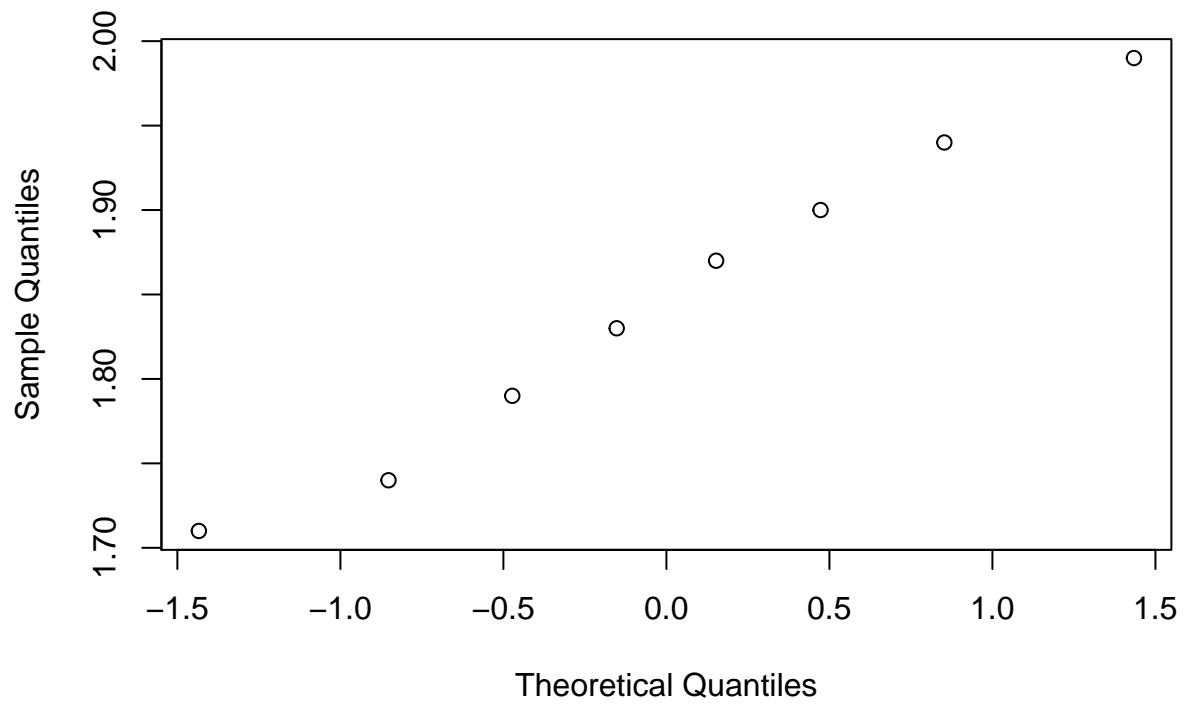


```
boxplot(Ex3.combo~Ex3.labels)
```



```
qqnorm(AA.3)
```

Normal Q–Q Plot


```r
qqnorm(BB.3)
```

Normal Q–Q Plot


```r
#T.test Equal Variance
t.test(AA.3, BB.3, var.equal=TRUE, alternative="two.sided")
```

```
##
##  Two Sample t-test
##
## data:  AA.3 and BB.3
## t = 4.0977, df = 13, p-value = 0.001259
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  0.1138900 0.3678958
## sample estimates:
## mean of x mean of y
##  2.087143  1.846250
```

```r
#T.test Non Equal Variance
t.test(AA.3, BB.3, var.equal=FALSE, alternative="two.sided")
```

```
##
##  Welch Two Sample t-test
##
## data:  AA.3 and BB.3
## t = 4.0151, df = 11.039, p-value = 0.002019
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  0.1088978 0.3728879
## sample estimates:
## mean of x mean of y
##  2.087143  1.846250
```

```r
#Bootstrap
(Ex3.tobs<-(xbar.AA3-xbar.BB3-0)/sqrt(s.AA3^2/7+s.BB3^2/8))
```

```
## [1] 4.0151
```

```r
set.seed(1)
Ex3.boot<-boottwo(AA.3, BB.3, n.boot)
(m.low3<-sum(Ex3.boot<=Ex3.tobs))
```

```
## [1] 9988
```

```r
(m.up3<-sum(Ex3.boot>=Ex3.tobs))
```

```
## [1] 12
```

```r
pval3<-min(m.low3,m.up3)/n.boot
pval3
```

```
## [1] 0.0012
```