

Chapter 11

11.1

For the data in 11.2, perform the paired T test for means using the weights for the east and south sides of the trees.

```
data <- data.table::fread(paste0(data.dir,"corkall_dat.txt"))
t.test(data$E - data$S)
```

One Sample t-test

```
data: data$E - data$S
t = -1.7514, df = 27, p-value = 0.09122
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 -7.6002671  0.6002671
sample estimates:
mean of x
 -3.5
```

11.2

Repeat the previous except using 20% trimmed means. Verify the p-value is 0.0049.

```
trimci(data$E - data$S)

[1] "The p-value returned by this function is based on the"
[1] "null value specified by the argument null.value, which defaults to 0"
[1] "To get a measure of effect size using a Winsorized measure of scale, use trimciv2"

$ci
[1] -7.30965260 -0.02368073

$estimate
[1] -3.666667

$test.stat
[1] -2.12353

$se
[1] 1.726685

$p.value
[1] 0.04868652
```

```
$n  
[1] 28
```

11.3

Compare the marginal 20% trimmed means with `yuend` and verify that the p-value is now 0.121.

```
yuend(data$E, data$S, tr=.2)
```

```
$ci  
[1] -8.657220  1.101665
```

```
$p.value  
[1] 0.1207526
```

```
$est1  
[1] 43.61111
```

```
$est2  
[1] 47.38889
```

```
$dif  
[1] -3.777778
```

```
$se  
[1] 2.312734
```

```
$teststat  
[1] -1.633468
```

```
$n  
[1] 28
```

```
$df  
[1] 17
```

11.4

Generally, why is it possible to get a different p-value comparing the marginal trimmed means rather than testing the hypothesis that trimmed mean of the difference scores is zero?

The sample trimmed mean of the difference scores is not necessarily equal to the difference between the trimmed marginals.

11.5

Is it possible that the marginal trimmed means are equal but the trimmed mean based on the difference scores is not equal?

Yes, the population trimmed mean of the difference scores is not necessarily equal to the difference between the population trimmed means.

11.6

Repeat E1 using a bootstrap-t method to compare the means.

```
with(data, trimcibt(N - S, tr=0))
```

```
$estimate
```

```
[1] 0.8571429
```

```
$ci
```

```
[1] -1.949428 3.663714
```

```
$test.stat
```

```
[1] 0.5690203
```

```
$p.value
```

```
[1] 0.5292154
```

```
$n
```

```
[1] 28
```

11.7

Repeat the previous using a 20% trimmed mean.

```
with(data, trimcibt(N - S, tr=.2))
```

```
$estimate
```

```
[1] 0.9444444
```

```
$ci
```

```
[1] -2.972017 4.860906
```

```
$test.stat
```

```
[1] 0.4530047
```

```
$p.value
```

```
[1] 0.5993322
```

```
$n  
[1] 28
```

11.8

Consider the following data for two dependent groups:

G1: 10, 14, 15, 18, 20, 29, 30, 40

G2: 40, 8, 15, 20, 10, 8, 2, 3

Compare the groups with a sign test and the Wilcoxon signed rank test ($\alpha = 0.05$)

```
x <- c(10, 14, 15, 18, 20, 29, 30, 40)  
y <- c(40, 8, 15, 20, 10, 8, 2, 3)
```

```
signt(x,y)
```

```
$Prob_x_less_than_y  
[1] 0.2857143
```

```
$ci  
lower upper  
0.053 0.659
```

```
$n  
[1] 8
```

```
$N  
[1] 7
```

```
$p.value  
NULL
```

```
wilcox.test(x, y)
```

```
Warning in wilcox.test.default(x, y): cannot compute exact p-value with ties
```

```
Wilcoxon rank sum test with continuity correction
```

```
data: x and y  
W = 49, p-value = 0.08199  
alternative hypothesis: true location shift is not equal to 0
```

11.9

For the dependent groups:

G1: 86, 71, 77, 68, 91, 72, 77, 91, 70, 71, 88, 87

G2: 88, 77, 76, 64, 96, 72, 65, 90, 65, 80, 81, 72

Apply the Wilcoxon signed rank test with $\alpha = 0.05$. Verify that $W = 0.7565$.

```
x <- c(86, 71, 77, 68, 91, 72, 77, 91, 70, 71, 88, 87)
y <- c(88, 77, 76, 64, 96, 72, 65, 90, 65, 80, 81, 72)
```

```
wilcox.test(x,y,paired=TRUE)
```

```
Warning in wilcox.test.default(x, y, paired = TRUE): cannot compute exact p-
value with ties
```

```
Warning in wilcox.test.default(x, y, paired = TRUE): cannot compute exact p-
value with zeroes
```

Wilcoxon signed rank test with continuity correction

data: x and y

V = 41.5, p-value = 0.4765

alternative hypothesis: true location shift is not equal to 0

11.10

Using the Indometh data, compare times 2 and 3 using means based on difference scores and verify that the p-value is 0.014.

```
g1 <- which(Indometh[,2]==0.5)
g2 <- which(Indometh[,2]==0.75)
trimci(Indometh[g1,3]-Indometh[g2,3],tr=0)
```

```
[1] "The p-value returned by this function is based on the"
[1] "null value specified by the argument null.value, which defaults to 0"
[1] "To get a measure of effect size using a Winsorized measure of scale, use trimciv2"
```

\$ci

```
[1] 0.1206732 0.6859935
```

\$estimate

```
[1] 0.4033333
```

\$test.stat

```
[1] 3.668014
```

```
$se  
[1] 0.1099596
```

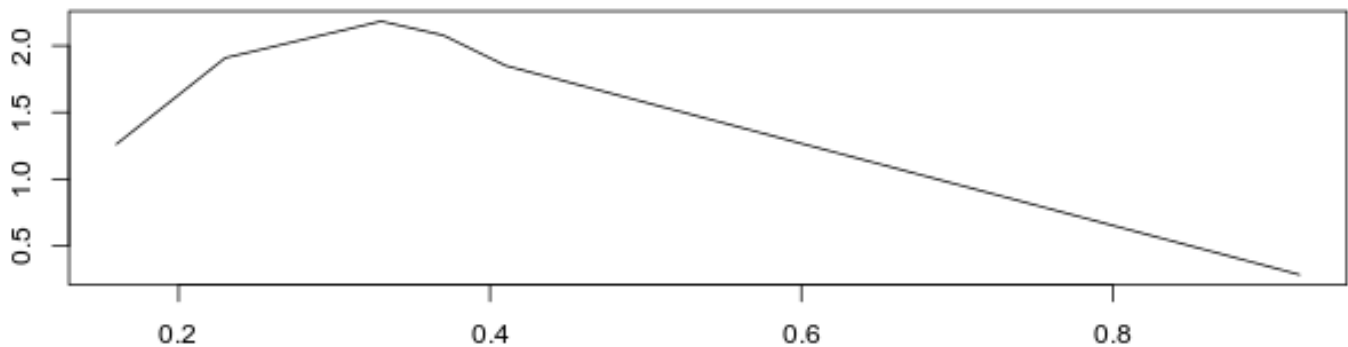
```
$p.value  
[1] 0.01447331
```

```
$n  
[1] 6
```

11.11

Continuing with the previous, plot the differences.

```
akerd(Indometh[g1,3]-Indometh[g2,3])
```



```
[1] "Done"
```

11.12

Use R to test the hypothesis that the differences scores have a mean, 20% trimmed mean and median of zero.

```
data.before <- data.table::fread(paste0(data.dir, "CESD_before_dat.txt"))
```

```
Warning in data.table::fread(paste0(data.dir, "CESD_before_dat.txt")): Discarded  
single-line footer: <<18 6 10>>
```

```
data.after <- data.table::fread(paste0(data.dir, "CESD_after_dat.txt"))
```

```
Warning in data.table::fread(paste0(data.dir, "CESD_after_dat.txt")): Discarded
```

single-line footer: <<11 13 0>>

```
trimci(data.before - data.after, tr = 0)
```

```
[1] "The p-value returned by this function is based on the"
[1] "null value specified by the argument null.value, which defaults to 0"
[1] "To get a measure of effect size using a Winsorized measure of scale, use trimciv2"

$ci
[1] 0.370193 2.346251

$estimate
[1] 1.358222

$test.stat
[1] 2.704745

$se
[1] 0.5021628

$p.value
[1] 0.007208604

$n
[1] 315
```

11.13

For the data in the previous exercise, test the hypothesis that the marginal 20% trimmed means are equal.

```
sintv2(data.before - data.after)
```

```
$median
[1] 1

$n
[1] 315

$ci.low
[1] 0

$ci.up
[1] 1.353732

$p.value
[1] 0.92
```

11.15

For the data using in Ex 12, use `comdvar` to compare the marginal variances.

```
yuend(data.before, data.after)
```

```
$ci  
[1] -0.7549867  8.1908841
```

```
$p.value  
[1] 0.1006342
```

```
$est1  
[1] 14.02564
```

```
$est2  
[1] 10.30769
```

```
$dif  
[1] 3.717949
```

```
$se  
[1] 2.209518
```

```
$teststat  
[1] 1.682697
```

```
$n  
[1] 63
```

```
$df  
[1] 38
```

11.16

Test the hypothesis that the means of these three measures are equal (CESD1, CESD2, CESD3).

```
data <- data.table::fread(paste0(data.dir, "CESDMF123_dat.txt"))
```

```
rmanova(data[, 2:4], tr = 0)
```

```
[1] "The number of groups to be compared is"  
[1] 3
```

```
$test  
[1] 1.24193
```



```
$df
[1] 1.889864 134.180342

$p.value
[1] 0.2908471

$tmeans
[1] 13.59722 12.05778 12.44444

$ehat
[1] 0.9215089

$etil
[1] 0.944932
```

11.17

For the data in the previous exercise, test the hypothesis of identical distributions using the two rank based methods.

```
bprnm(data[, 2:4])
```

```
$test.stat
[1] 1.444947

$nu1
[1] 1.852673

$p.value
[1] 0.2363027
```

```
friedman.test(as.matrix(data[, 2:4]))
```

Friedman rank sum test

```
data: as.matrix(data[, 2:4])
Friedman chi-squared = 0.98519, df = 2, p-value = 0.611
```

11.18

Perform a 2-by-3 between-by-within ANOVA based on 10% trimmed means.

```
M <- bw2list(data, 5, c(2:4))
```

```
[1] "Levels for between factor:"
```

```
[1] 2 1
```

```
bwtrim(2, 3, M, tr=0.1)
```

```
$Qa
```

```
[1] 2.292791
```

```
$Qa.p.value
```

```
      [,1]
```

```
[1,] 0.1435347
```

```
$Qb
```

```
[1] 1.123135
```

```
$Qb.p.value
```

```
      [,1]
```

```
[1,] 0.3443356
```

```
$Qab
```

```
[1] 2.435661
```

```
$Qab.p.value
```

```
      [,1]
```

```
[1,] 0.1122762
```