

# Non-parametric Statistics: Notes 2

## Two-sample methods

Gregory Matthews <sup>1</sup>

<sup>1</sup>Department of Mathematics and Statistics  
Loyola University Chicago

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# Outline

Permutation Tests

Wicoxon Rank Sum and Mann-Whitney U Test

Tests for equality of scale parameters

# Permutation test

- ▶ Let's say we want to test formally if there is a difference between two groups.
- ▶ For instance, we could compare a new procedure to an old procedure.

# Two sample tests

- ▶ How would you do this parametrically?
- ▶ We use a t-test with the assumption of normality
- ▶ Or you can use asymptotic theory and the Central Limit Theorem (CLT)

# Permutation test

```
dat<-data.frame(score=c(37,49,55,57,23,31,46),method=c(rep("N",4),rep("O",3)))
dat
```

```
##   score method
## 1    37      N
## 2    49      N
## 3    55      N
## 4    57      N
## 5    23      O
## 6    31      O
## 7    46      O
```

```
#Compute the observed means
```

```
scoreMeans<-tapply(dat$score,dat$method,mean)
scoreMeans
```

```
##           N           O
## 49.50000 33.33333
```

```
obsDiffMeans<-diff(scoreMeans)
```

```
#Compute the observed medians
```

```
scoreMedians<-tapply(dat$score,dat$method,median)
scoreMedians
```

```
##   N   O
## 52 31
```

```
obsDiffMedians<-diff(scoreMedians)
```

# Permutation test

```
library(gtools)
perms<-combinations(7,4)
dim(perms)

## [1] 35 4

permDiffs<-rep(NA,dim(perms)[1])
for (i in 1:dim(perms)[1]){
  scoresTemp<-c(dat$score[perms[i,]],dat$score[setdiff(c(1:7),perms[i,])])
  datPermuted<-data.frame(score=scoresTemp,method=dat$method)
  permDiffs[i]<-diff(tapply(datPermuted$score,datPermuted$method,mean))
}
```

# Permutation test

```
#all differences of all permutations.
sort(permDiffs)

## [1] -21.4166667 -16.1666667 -14.4166667 -12.6666667 -10.9166667
## [6] -10.9166667 -9.7500000 -8.0000000 -7.4166667 -6.2500000
## [11] -6.2500000 -5.6666667 -2.7500000 -2.1666667 -1.5833333
## [16] -1.0000000 -1.0000000 -0.4166667 0.7500000 2.5000000
## [21] 2.5000000 3.6666667 4.2500000 4.2500000 5.4166667
## [26] 6.0000000 7.1666667 7.7500000 8.9166667 8.9166667
## [31] 12.4166667 13.0000000 14.1666667 17.6666667 19.4166667

#observed difference of means
obsDiffMeans

## 0
## -16.16667
```

# Permutation test

- ▶ How can we use these simulated values to construct a p-value?
- ▶ Well, what is a p-value?
- ▶ It's the probability of observing something as or more extreme than what was actually observed.
- ▶ How many of the observations were AS or MORE extreme than what we actually observed?



# Permutation test

```
#One-Sided p-value
```

```
sum(permDiffs<=obsDiffMeans)/length(permDiffs)
```

```
## [1] 0.05714286
```

```
#Two-Sided p-value
```

```
(sum(permDiffs<=obsDiffMeans)+sum(permDiffs>=abs(obsDiffMea
```

```
## [1] 0.1142857
```

```
#http://spark.rstudio.com/ahmed/permutation/
```

# Permutation test

- ▶ The test we just did was exact in the sense that we looked at all possible permutations.
- ▶ However, sometimes the number of permutations is very large and so we simply take a sample of all possibilities.
- ▶ Let's look at that.

# Permutation test

```
dat<-data.frame(score=c(37,49,55,57,23,31,46),
                 method=c(rep("N",4),rep("O",3)))
dat

##   score method
## 1    37      N
## 2    49      N
## 3    55      N
## 4    57      N
## 5    23      O
## 6    31      O
## 7    46      O

scoreMeans<-tapply(dat$score,dat$method,mean)
scoreMeans

##           N           O
## 49.50000 33.33333

diff(scoreMeans)

##           O
## -16.16667

scoreMedians<-tapply(dat$score,dat$method,median)
```

# Permutation test

```
set.seed(1234)
```

```
nsim<-1000
permDiffs<-rep(NA,nsim)
for (i in 1:nsim){print(i)
  datPermuted<-data.frame(score=
    sample(dat$score,replace=FALSE),method=dat$method)
  permDiffs[i]<-diff(tapply(datPermuted$score,
    datPermuted$method,mean))
}
```

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

```
## [1] 2
```

```
## [1] 3
```

```
## [1] 4
```

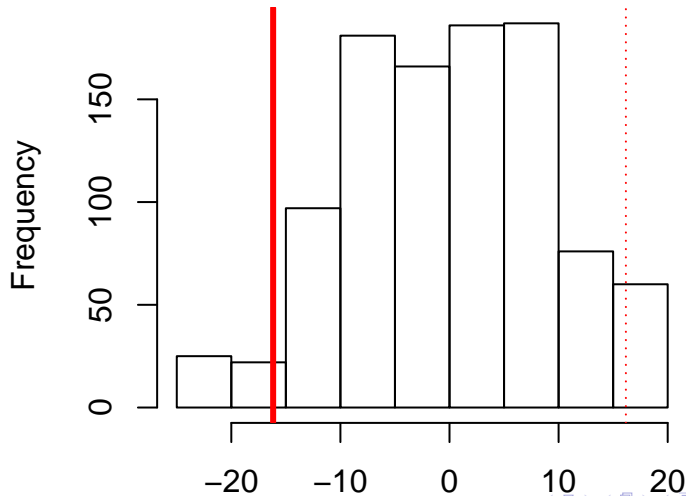
```
## [1] 5
```

```
## [1] 6
```

```
## [1] 7
```

## Permutation test

### Histogram of permDiffs



# Permutation test

```
lower<-sum(permDiffs<=diff(scoreMeans))
higher<-sum(permDiffs>=abs(diff(scoreMeans)))
#How do we constuct a p-value now?
#Two sided p-value
(lower+higher)/nsim

## [1] 0.107

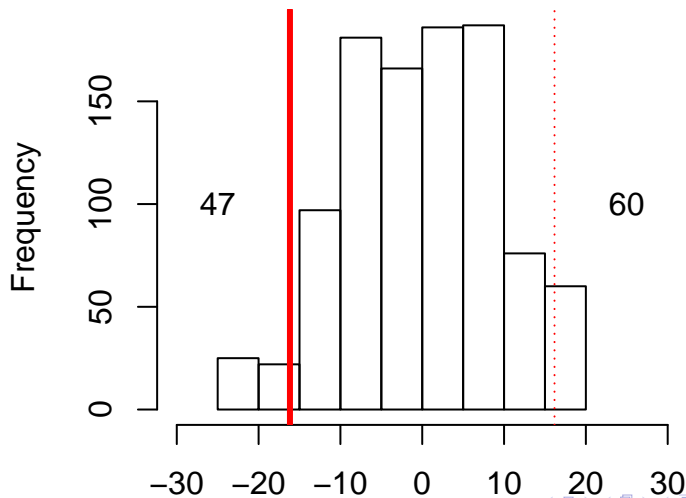
#One sided lower p-value
lower/nsim

## [1] 0.047

#Note: the two-sided p-value is not the
#one-sided p-value times 2 here.
#Why not?
```

## Permutation test

### Histogram of permDiffs



```
#R package for these permutation tests
library(perm)
permTS(dat$score~dat$method,alternative="two.sided",exact=TRUE)

##
## Exact Permutation Test (network algorithm)
##
## data: dat$score by dat$method
## p-value = 0.1143
## alternative hypothesis: true mean dat$method=N - mean dat$method=0 is not equal to 0
## sample estimates:
## mean dat$method=N - mean dat$method=0
##                                16.16667
```



- ▶ SAS procedure is “npar1way”.

# Wilcoxon Rank Sum and Mann-Whitney U Test

## Wilcoxon Rank Sum

- ▶ Let's say we have two groups as before.
- ▶ Take all of the data in both groups, combine them, and then rank them.
- ▶ Add up the ranks from group 1 (or group 2, either will work).
- ▶ Call this sum  $W_1$ .
- ▶ Do a permutation test based on the ranks to find a p-value.

# Wilcoxon Rank Sum and Mann-Whitney U Test

## Mann-Whitney U Test

Value	Brand	Rank
3.6	Brand 1	1
3.8	Brand 2	2
3.9	Brand 1	3
4.0	Brand 1	4
4.1	Brand 2	5
4.3	Brand 1	6
4.5	Brand 2	7
4.8	Brand 2	8
		$W_2 = 22$

# Wilcoxon Rank Sum and Mann-Whitney U Test

## Mann-Whitney U Test

	Brand 1	Brand 2	
0	3.6	3.8	1
1	3.9	4.1	3
1	4.0	4.5	4
2	4.3	4.8	4
Sum=4			Sum=12

$$U = \max(4, 12) = 12$$

# Wilcoxon Rank Sum and Mann-Whitney U Test

Linearly related tests

$$W_2 = \frac{1}{2}n(n+1) + U$$

Check it:

$$22 = \frac{1}{2}4(5) + 12$$

```
dat<-data.frame(scores=c(3.6,3.9,4.0,4.3,3.8,4.1,4.5,4.8),  
                  brand=c(1,1,1,1,2,2,2,2))  
dat$rank<-rank(dat$scores)  
W2<-sum(dat$rank[dat$brand==2])  
W2  
  
## [1] 22
```

```
set.seed(1234)
```

```
nsims<-10000  
rankSumPerms<-rep(NA,nsims)  
for (i in 1:nsims){  
  rankSumPerms[i]<- sum(sample(1:8,4,replace=FALSE))  
}  
#pvalue  
sum(rankSumPerms>=W2)/nsims  
  
## [1] 0.1739
```

## Tests for equality of scale parameters

- ▶ Siegel-Tukey
- ▶ Ansari-Bradley



# Siegel-Tukey

- ▶ Arrange observations from smallest to largest.
- ▶ Assign 1 to the smallest observation, 2 to the **largest** observation, 3 to the next largest, 4 to the next smallest observation, etc.
- ▶ Perform the Wilcoxon rank-sum test. Smaller ranks are associated with the group with larger variability.
- ▶ Problem is why start the ranking with the smallest? Could just as easily start with the largest. (Ansari-Bradley!)

- ▶ Arrange observations from smallest to largest.
- ▶ Assign 1 to the smallest and largest observations, 2 to the next smallest and next largest, etc.
- ▶ Compute the Wilcoxon rank-sum and compute a p-value.  
(Can't use a traditional Wilcoxon rank-sum table. But we shouldn't be using tables anyway! It's 2016!)

```
dat[c(1,2,6,7),]
```

```
##      scores trt
## 1  6.378803   1
## 2 10.832288   1
## 6 12.530279   2
## 7  7.126300   2
```

*#Some code for Ansari Bradley*

```
dat<-dat[order(dat$scores),]
dat$rank<-c(1:(dim(dat)[1]/2),(dim(dat)[1]/2):1)
abs(diff(tapply(dat$rank,dat$trt,mean)))
```

```
##      2
## 1.2
```

```
#Now simulate a null distribution.  
#Some code for Ansari Bradley  
nsim<-1000  
ok<-rep(NA,nsim)  
for (i in 1:nsim){print(i)  
dat<-dat[sample(1:10,10,replace=FALSE),]  
dat$rank<-c(1:(dim(dat)[1]/2),(dim(dat)[1]/2):1)  
ok[i]<-abs(diff((tapply(dat$rank,dat$trt,mean))))  
}
```

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

```
## [1] 2
```

```
## [1] 3
```

```
## [1] 4
```

```
## [1] 5
```

```
## [1] 6
```

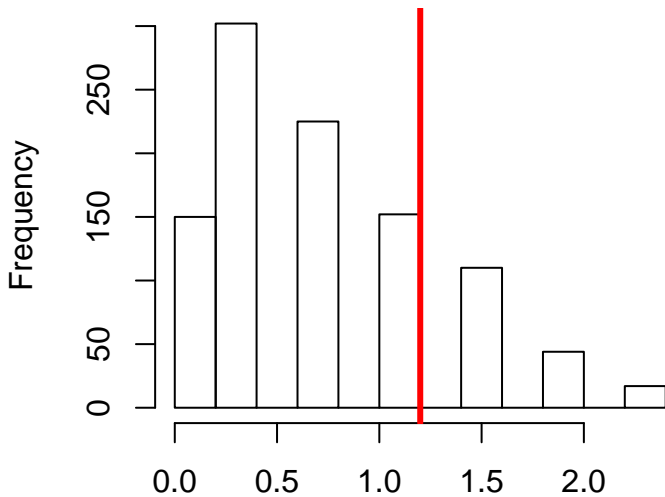
```
## [1] 7
```

```
## [1] 8
```

```
## [1] 9
```

```
## [1] 10
```

# Histogram of ok



*#P-value for this test:*

```
sum(ok>=1.2)/nsim
```

```
## [1] 0.323
```

```
#let's try it again, but with a small change  
#Some code for Ansari Bradley  
dat<-dat[order(dat$scores),]  
dat$rank<-c(1:(dim(dat)[1]/2),(dim(dat)[1]/2):1)  
min(tapply(dat$rank,dat$trt,mean))  
  
## [1] 2.4
```

```
#Now simulate a null distribution.  
#Some code for Ansari Bradley  
nsim<-1000  
ok<-rep(NA,nsim)  
for (i in 1:nsim){print(i)  
dat<-dat[sample(1:10,10,replace=FALSE),]  
dat$rank<-c(1:(dim(dat)[1]/2),(dim(dat)[1]/2):1)  
ok[i]<-min((tapply(dat$rank,dat$trt,mean)))  
}
```

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

```
## [1] 2
```

```
## [1] 3
```

```
## [1] 4
```

```
## [1] 5
```

```
## [1] 6
```

```
## [1] 7
```

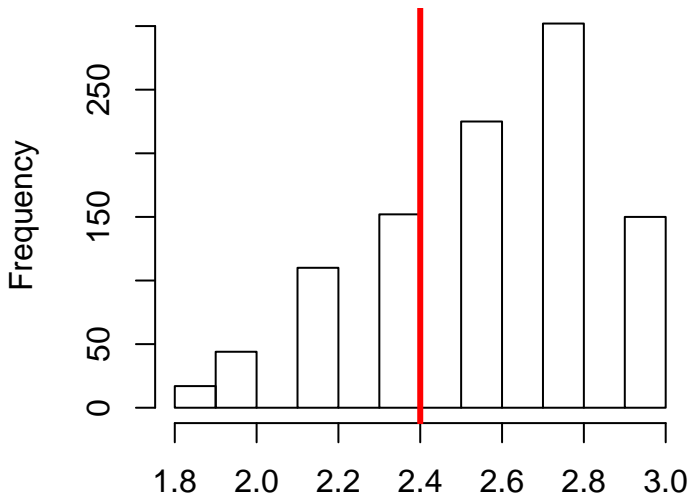
```
## [1] 8
```

```
## [1] 9
```

```
## [1] 10
```



## Histogram of ok



*#P-value for this test:*

```
sum(ok<=2.4)/nsim
```

```
## [1] 0.323
```