

Homework 3

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4.07

a.

```
source("http://www4.stat.ncsu.edu/~lu/ST505/Rcode/functions-Ch4.R")

x = c(1.5, 2.1, 1.9, 2.8, 1.4, 1.8,
      1.8, 2.0, 2.0, 2.7, 1.6, 2.3,
      1.9, 2.5, 2.5, 2.6, 2.1, 2.4)

blocks = rep(1:6,3)
grps = c(1,1,1,1,1,1,2,2,2,2,2,2,3,3,3,3,3,3)

#F-test
# summary(aov(x~factor(grps)+factor(blocks)))

# Permutation Test for RCBD
### Step 1: calculate observed SSTM:sum of squared group-means
SSTMobs <- getSSTM(x,grps)

### Step 2: obtain the permutation distribution of SSTM under H0
###          i.e. obtain SSTM*'s with R permutations

permSSTM <- perm.approx.RCBD(x,grps,blocks,R=1000)

### Step3: calculate the p-value
(pval = mean(permSSTM >= SSTMobs))

## [1] 0.021
```

With a p-value of 0.026 we can reject the null hypothesis. At least one treatment is different from the others.

b.

```
anova(aov(x~factor(grps)+factor(blocks)))

## Analysis of Variance Table
##
## Response: x
##          Df  Sum Sq Mean Sq F value    Pr(>F)
```

```
## factor(grps)      2 0.53444 0.26722 6.9308 0.012927 *
## factor(blocks)    5 2.00944 0.40189 10.4236 0.001022 **
## Residuals         10 0.38556 0.03856
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Using the ANOVA we can reject the null hypothesis with a 0.012927 p-value. This is higher than the previous part, but still within the rejection range.

4.09

```
x = c(1.5, 2.1, 1.9, 2.8, 1.4, 1.8,
      1.8, 2.0, 2.0, 2.7, 1.6, 2.3,
      1.9, 2.5, 2.5, 2.6, 2.1, 2.4)

blocks = rep(1:6,3)
grps = c(1,1,1,1,1,1,2,2,2,2,2,3,3,3,3,3)

mat <- cbind(x,grps,blocks)
### sort by the blocks
mat <- mat[order(mat[,3]),]

#obtain the within-block ranks
Rij = rankinblock(x,blocks)

#calculate observed SSTM:sum of squared group-means of within-block ranks
SSTMobs <- getSSTM(Rij,grps)

##obtain the permutation distribution of SSTM (based on within-block ranks)
set.seed(12379901)
permSSTM <- perm.approx.RCBD(Rij,grps,blocks,1000)
(pval=mean(permSSTM >= SSTMobs))
```

```
## [1] 0.13
```

```
### Use the R function: Friedman rank sum test with unreplicated blocked data
friedman.test(x, grps, blocks) ### based on chi-square approximation
```

```
##
## Friedman rank sum test
##
## data: x, grps and blocks
## Friedman chi-squared = 4.3333, df = 2, p-value = 0.1146
```

```
#### an alternative (manual) way to calculate the Friedman test statistic
Ri = getmeans(Rij, grps)
K = length(unique(grps))
J = length(unique(blocks))
```

```
# calculate Sbj2: sample variance of the ranks within block j
Sbj2 = apply(matrix(Rij, ncol=J, byrow=T),2,var)
(FM = J^2/sum(Sbj2)*sum((Ri - (K+1)/2)^2))
```

```
## [1] 4.333333
```

With a p-value of 0.1146 we fail to reject the null hypothesis. The treatments are equal to each other.

4.11

```
x = c(6.81, 6.16, 5.92, 5.86, 5.80, 5.39,
      6.68, 6.30, 6.12, 5.71, 6.09, 5.28,
      6.34, 6.22, 5.90, 5.38, 5.20, 5.46,
      6.68, 5.24, 5.83, 5.49, 5.37, 5.43,
      6.79, 6.28, 6.23, 5.85, 5.56, 5.38,
      6.85, 6.51, 5.95, 6.06, 6.31, 5.39)
blocks = rep(1:6, 6)
grps = rep(1:6, each=6)
dat = matrix(x, byrow=T, ncol=6)

getsums(rankinblock(x,blocks), grps)
```

```
## [1] 22.5 21.5 14.0 13.5 23.0 31.5
```

```
(Pageobs <- getPage(x, grps,blocks))
```

```
## [1] 465.5
```

```
permPage <- perm.approx.Page(x,grps,blocks,1000)
# tests if means are arranged  $t_1 > t_2 > t_3 > t_4$ , i.e. response decreases as changing trt from 1 to 4
(pval = mean(permPage >= Pageobs))
```

```
## [1] 0.012
```

With a p-value of 0.003 we can reject the null hypothesis. At least one treatment is different than the others. The pH level of at least one of the carcasses decreases at a different rate than the others.