## STAT 477/577 - Technology Guide

Module 2 - Section 6 Matched Pair Designs

Below is an explanation of the R commands and functions needed to calculate McNemar's test for 2 by 2 tables and an extension of McNemar's test to J by J tables.

## • McNemar's Test

The base package in R has a function called mcnemar.test which will calculate the test statistic and p-value for McNemar's test of marginal homogeneity. To obtain the test statistic and p-value from the lecture notes for the equality of the proportion of correct responses from the two histogram questions, we will first read in the data from the file histogramq.csv.

```
hist.data<- read.csv(file.choose(), header = T)
```

Then we will calculate the contingency table for the responses from the two histogram questions.

```
hist.table<- table(hist.data$Question1, hist.data$Question2)
```

Finally, we will use the mcnemar.test function to obtain the test statistic and p-value for the test. Similar to earlier in this module, we will not use the continuity correction to calculate the test statistic.

```
mcnemar.test(hist.table, correct = F)

##

## McNemar's Chi-squared test

##

## data: hist.table

## McNemar's chi-squared = 7.7143, df = 1, p-value = 0.005479
```

If the test determines evidence of a difference between the two marginal probabilities, a confidence interval can be calculated using the function mcnemar.ci. For the histogram example, a 95% confidence interval for the difference in the proportion of correct responses for the two histogram questions is given by:

```
mcnemar.ci(hist.table, conf.level = 0.95)
## Confidence Interval = -0.05198398 -0.009136565
```

## • Extension of McNemar's Test

The base package in R does not include a function for the extension of McNemar's test of marginal homogeneity to J by J tables. A function for calculating the test statistic and p-value called  $\mathtt{stuart.maxwell.mh}$  is included in the R package  $\mathtt{irr}$ . To obtain the test statistic and p-value from the lecture notes for the equality of the distribution of the responses from the two baby questions, we will first read in the data from the file  $\mathtt{babyhat.csv}$ .

```
baby.data<- read.csv(file.choose(), header = T)</pre>
```

Then we will calculate the contingency table for the responses from the two baby questions.

```
baby.table<- table(baby.data$Question1, baby.data$Question2)</pre>
```

Finally, we will use the stuart.maxwell.mh function to obtain the test statistic and p-value for the test.

```
stuart.maxwell.mh(baby.table)

## Stuart-Maxwell marginal homogeneity

##

## Subjects = 195

## Raters = 2

## Chisq = 24.2

##

## Chisq(3) = 24.2

##

## p-value = 2.23e-05
```

The required information for the test from lecture is given in the last two lines of the output. The first line is the test statistic W (with the degrees of freedom) and the second line is the p-value of the test statistic.

Note: this function also works to calculate the test statistic and p-value for McNemar's test.