fisher_mcnemar

```r
library(tidyverse)
```

Fisher's Exact Test

Example 1

Tea-time experiment.

```r
# define data
tea_exp = matrix(c(3,1,1,3),nrow=2)

# one-tailed test
fisher.test(tea_exp, alternative = "greater")
```

```
    Fisher's Exact Test for Count Data

data:  tea_exp
p-value = 0.2429
alternative hypothesis: true odds ratio is greater than 1
95 percent confidence interval:
 0.3135693       Inf
sample estimates:
odds ratio
  6.408309
```

```r
# two-sided test
fisher.test(tea_exp)
```

```
    Fisher's Exact Test for Count Data

data:  tea_exp
p-value = 0.4857
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
   0.2117329 621.9337505
sample estimates:
odds ratio
  6.408309
```

```r
# use chi-squared test
chisq.test(tea_exp)
```

```
Warning in chisq.test(tea_exp): Chi-squared approximation may be incorrect
```

```
    Pearson's Chi-squared test with Yates' continuity correction

data:  tea_exp
X-squared = 0.5, df = 1, p-value = 0.4795
```

Notice that the two-sided p-value from Fisher is greater than the one generated by chi-square.
This supports the conclusion that Fisher Exat Test is more conservative (harder to reject)

Example 2

```r
# define data
practice_data = matrix(c(1,8,9,3), nrow=2,
                      dimnames=list(c("diet","non-diet"), c("men","women")))

# perform chi-squared
chisq.test(practice_data)
```

```
Warning in chisq.test(practice_data): Chi-squared approximation may be incorrect
```

```
    Pearson's Chi-squared test with Yates' continuity correction

data:  practice_data
X-squared = 6.0494, df = 1, p-value = 0.01391
```

```r
  # fishers test
  fisher.test(practice_data)
```

```
    Fisher's Exact Test for Count Data

data:  practice_data
p-value = 0.007519
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
 0.0008560335 0.6145334348
sample estimates:
odds ratio
0.05080595
```

Mcnemar Test for Binomial Matched-Pair Data

Two procedures are tested on the same 75 subjects in order to identify the absence/presence of the disease.

```r
  # define data
  procedure_data = matrix(c(41,8,14,12), nrow=2, byrow=T,
                          dimnames=list(c("positive","negative"),c("positive","negative")))

  # perform test
  mcnemar.test(procedure_data)
```

```
    McNemar's Chi-squared test with continuity correction

data:  procedure_data
McNemar's chi-squared = 1.1364, df = 1, p-value = 0.2864
```

```
# What if you performed a chi-squared test instead?
chisq.test(procedure_data)
```

    Pearson's Chi-squared test with Yates' continuity correction

data: procedure_data
X-squared = 6.278, df = 1, p-value = 0.01222