

Matched Pairs Analysis

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09 November 2016

Contents

References **R** 4

Data: *data/dep.sav*

$$McNemar's \chi^2 = \frac{(n_{21} - n_{12})^2}{n_{21} + n_{12}}$$

```
cnt <- array( ## What we want to generate directly from the data ##
  c(146, 155, 47, 303),
  dim = c(2, 2),
  dimnames = list(w1dep = c("not", "depressed"),
    w2dep = c("not", "depressed"))
  )
cnt
```

	not	depressed
not	146	47
depressed	155	303

```
## What the results of the McNemar's Test should be: ##
mcnemar.test(cnt, correct = FALSE)
```

Table 2: McNemar's Chi-squared test: cnt

Test statistic	df	P value
57.74	1	2.988e-14 * *

```
dat <- read.spss("data/dep.sav", to.data.frame = T)
sapply(dat, R.isna) ## THANK YOU!!!! (no NAs to deal with) ##
```

w1dep	w2dep	w3dep
0	0	0

```
# ## ... except the factor labels are kind of obnoxious for output... ##
```

```

dat <- within(dat, {
  levels(w1dep) <- c("not", "depressed")
  levels(w2dep) <- c("not", "depressed")
})
names(dat) <- c("T1", "T2", "T3")

ft <- with(dat, {
  ftable(dat, row.vars = 1, col.vars = 2)
})
ft

```

	"T2"	"not"	"depressed"
"T1"			
"not"		146	155
"depressed"		47	303

```

ftc <- matrix(ft, nrow = 2, byrow = T)
ftc

```

146	47
155	303

```

ftc.a <- array(ftc, dim = c(2, 2), dimnames = list(
  T1 = c("not", "depressed"),
  T2 = c("not", "depressed")))
ftc.a

```

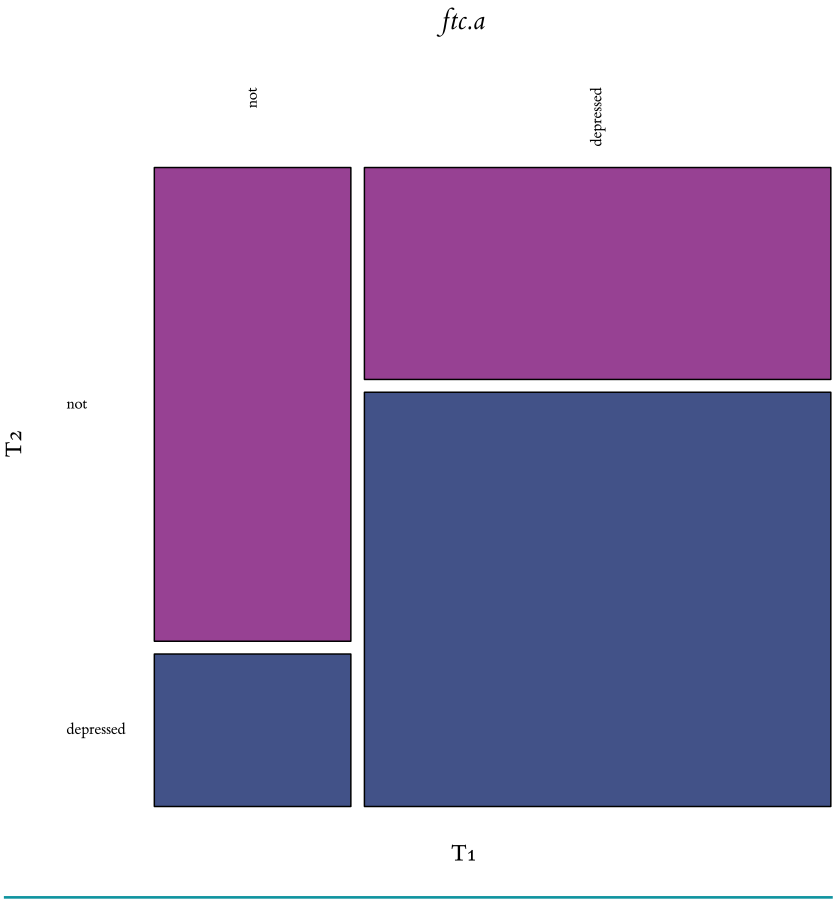
	not	depressed
not	146	47
depressed	155	303

```
mcnemar.test(ftc.a, correct = FALSE)
```

Table 7: McNemar's Chi-squared test: ftc.a

Test statistic	df	P value
57.74	1	2.988e-14 * *

```
mosaicplot(ftc.a, type = "deviance", las = 2, color = mypal.a75[c(5, 16)])
```



References^{R1}

R Core Team. *R: A Language and Environment for Statistical Computing*. Vienna, Austria: R Foundation for Statistical Computing, 2016. <https://www.R-project.org/>.

¹ V 3.3.2, R Core Team, *R*.