Analysis of Two and Three Categorical Variables

Riley Smith

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Contents

Setting Things Up in `R`

```
source("SETUP.R")
options(width = 70)
knitr::opts_chunk$set(tidy = FALSE, echo = TRUE,
    cache = FALSE, fig.keep = "high", fig.show = "asis",
    results = "asis", autodep = T, Rplot = TRUE,
    dev = "pdf", fig.path = "graphics/reuters/rplot_",
    fig.width = 7, fig.asp = 1, out.width = "\\linewidth")
library(foreign)  ## read.spss() ##
library(car)  ## recode() ##
dat <- read.spss("data/reuters.sav", to.data.frame = TRUE)
dat <- within(dat, {
    recode(response, c("1=0", "2=1", "3=2"))
})
```

Notes on the `R`-code above: `SETUP.R` is the default `R`-script I source in the `"setup"` `code-chunk`[1] at the beginning of all `R markdown` documents. It contains global arguments for loading commonly used

[1] see `help(package = knitr)`

packages, setting options, and defining various R-object utilities and functions. I also use this script as a record of functions I create while working in `R`. The script is heavily commented throughout for explanatory purposes, as well as for giving credit where it is due (I've tried to keep up with all of the `R-code`, `LaTex`, and `R markdown` sources, but may have missed some along the way).

AFTER SOURCING `SETUP.R` and setting a few output options (`options()` & `opts_chunk$set()`), I load the `{foreign}` and `{car}` packages for the `read.spss()` and `recode()` functions, respectively. Then I read in (`read.spss()`) the Reuters polling dataset, "`reuters.sav`" and store it in `R` as a `dataframe` named "`dat`". Finally, I re-code the values for the "`dat$response`" variable, using the `{car}` package's `recode()` function to undo default numeric values 1,2,3 and label values.

Note: *This last recoding step seems unneccessary to me. I included it here based on Jason Newsom's code and in-class explanation, but when I run the rest of the analysis below without recoding, the results are the same. Is there a specific situation in which setting a discrete variable's values to '`0, 1, 2, ...`', versus '`1, 2, 3, ...`' is consequential to the analysis? Or is this a matter of personal preference for coding discrete variables? I think it would make more logical sense to me if, in this case, '`0`' strictly reflected '`No Response`', but that is not the case here, as '`0`' reflects both '`Other`' and '`No Response`'. Further, should '`Other`' responses not be coded as separate from '`No Response`', given that an '`Other`' response is absolutely qualitatively distinct from '`No Response`'?*

Reuters 2016 Polling Data Analysis

See Newsom 2016-CDA Handout-4

Data-Cleaning & Preparation

A few things need to happen to help optimize the information we put into and get out of the binomial hypothesis testing for the polling data. Specifically, I want set all values of "`other`" to "`NA`" in `dat$response`, then drop all "`NA`" values since the analysis is only interested in responses for the two major candidates (i.e., *Clinton and Trump*).

Note that the common method for binomial tests in `R` is to use `exact.test = TRUE`, which is actually the most conservative approach and also no ideal for binomial tests. Use `prop.test()` for *approximate* tests. *(source: Jason Newsom)*

However, there are also some existing "`NAs`" in "`dat$party`", which need to be re-coded as well to avoid excluding rows with acceptable data values in `dat$response`.

`sapply()`, `apply()`, and `vapply()` are great function to get to know if you find yourself doing a ton of data cleaning/mining.

```
Risna <- function(x) sum(is.na(x))
#   ## Getting a count of NA values in the original dataframe ##
sapply(dat, Risna)

>>
>> ---------------------------------------
>> id   response   party   partmiss   ind
>> ---- ---------- ------- ---------- -----
>> 0    0          377     0          0
>> ---------------------------------------

R.na <- function(x, v = 0){
    ## x = object to be manipulated,
    ## v = value to assign to NAs ##
    x <- ifelse(is.na(x), v, x)
    return(x)
    }
```

`R.na()`: *"If x = NA (`is.na()`), replace x with v, otherwise leave x alone."*

Table 1: Summary information for '**party**' data column *before* recoding `NAs`

M	0.42
SD	0.49
Min	0.00
Max	1.00
NAs	377.00

```
unique(dat$party)
```

0, 1 and *NA*

```
dat$party <- sapply(dat$party, R.na, v = 99)
```

Table 2: Summary information for '**party**' data column *after* recoding `NAs`

M	24.59
SD	42.42
Min	0.00
Max	99.00
NAs	0.00

0, 1 and *99*

```
dat$response <- recode_factor(dat$response,
                              "other/no opinion" = NA_character_)
## see "recode_factor()" in the {dplyr} package ##
dat <- na.omit(dat)
sapply(dat, R.isna) ## bye-bye NAs! ... again ##
```

id	response	party	partmiss	ind
0	0	0	0	0

```
## but this time we only lost data for rows with NA
## in dat$response (but we did lose ALL of the data
## for those rows, as these were removed from the
## dataframe entirely, though the original datafile remains untouched).
```

Now the data are, in my opinion, ready for analysis.

Analysis: Differences in Proportions of (non-"other") Polling Responses

```
levels(dat$response)
```

Trump and *Clinton*

```
poll.t <- table(dat$response)
## Why not make a table of the poll response counts for each candidate? ... ##
```

Table 4: Frequency Table of Polling Data

Response	Frequency
Trump	554
Clinton	677

DEFINITION OF A CONVENIENCE FUNCTION FOR THE BINOMIAL TEST. I'm combining the `prop.test()` & `binom.test()` functions (`{pkg:stats}`) because I think it's kind of ridiculous that there is not already a combined function for these. I also don't particularly enjoy the default output format for either of these functions, so I'm breaking the function writing rule of simplicity (AKA: *"Curly's Law"*) and implementing some formatting tasks within the function as well.

Arguments (`R.binom_test()`):

`p`. The target proportion to be tested against the null hypothesis (H_0; π_0; see `pi0` below). *Synonymous Arguments:* `x` in `prop.test()` & `binom.test()`.

`N`. The size of the sample from which 'p' is taken. *Synonymous Arguments:* `n` in `prop.test()` & `binom.test()`. *Synonymous Arguments:* `n` in `prop.test()` & `binom.test()`.

`pi0`. [Default = `0.5`]. A vector of probabilities of success corresponding to the value(s) in `p`. These probabilities represent the null hypothesis value (H_0; π_0) against which `p` is to be tested. *Synonymous Arguments:* `p` & `conf.level` (inverse) in `prop.test()` & `binom.test()`.

`exact`. Logical [Default = `FALSE`]. Should the the hypothesis be tested using an exact binomial test (i.e., `binom.test()`). If `FALSE` (the default), a test of equal or given proportions, depending on the lengths of `p` and `pi0` is conducted using `prop.test()`

`correct`. Logical Default = `FALSE`]. Synonymous with the `correct` argument in `prop.test()`.

`digits`. [Default = `2`]. Number of digits to use when rounding (`round()`) the final output values (does not influence the test calcu-

lation).

`...`. Additional arguments to be passed to either `prop.test()` or `binom.test()`, depending on the value set for `exact` (e.g., `alternative`).

Value (`R.binomTest()`): Returns a `data.frame` object containing the values returned by either `prop.test()` or `binom.test()`, depending on the value set for `exact`.

```
R.binom_test <- function(p, N, pi0 = 0.5, exact = FALSE, correct = FALSE,
                        digits = 2, ...){
    if (exact) { ## Hypothesis Testing
        BT <- stats::binom.test(x = p, n = N, p = pi0, ...)
        }
        else {
            BT <- stats::prop.test(x = p, n = N, p = pi0,
                                  correct = correct, ...)
        }
    ## The rest deals with formatting the output ##
        BT$data.name <- paste0(p, " out of ", N, " null probability ",
                               BT$null.value)
        ## Above, I modified the default output value for *.test$data.name
            ## to print the actual data values, rather than the object
            ## names the values are stored under (see output below) ##
        BTCI <- paste0(round(BT$conf.int[[1]], digits = digits), ", ",
                       round(BT$conf.int[[2]], digits = digits))
        BT$p.value <- round(BT$p.value, digits = 7)
        BT.df <- data.frame(c(BT[c("alternative",
                                  "null.value",
                                  "parameter",
                                  "estimate",
                                  "statistic",
                                  "p.value")],
                              BTCI))
        row.names(BT.df) <- NULL
        return(BT.df)
}
```

Approximate Test (`prop.test()`)

```
pt <- R.binom_test(p = poll.t["Clinton"], N = nrow(dat), pi0 = 0.5)
    ## ... Now we know where values for prop.test() came from :) ##
        ## There's more than one way to do that, by the way, but
        ## creating the table will come in handy later on too. ##
```

Table 5: 1-sample proportions test without continuity correction: *677 out of 1231*

H_1	π_0	df	p	χ_2	*p-value*	CI
two.sided	0.5	1	0.55	12	0.00046	0.52, 0.58

Exact Test (`binom.test()`)

```
et <- R.binom_test(p = poll.t["Clinton"],
                   N = nrow(dat), pi0 = 0.5,
                   exact = TRUE)
```

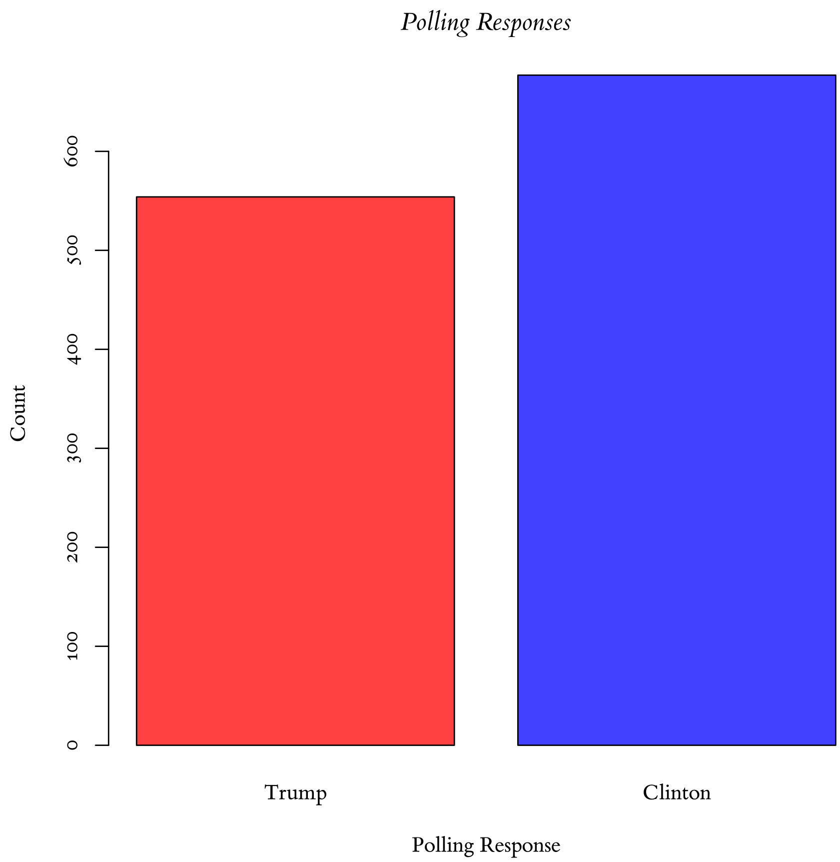
Table 6: 1-sample *exact* binomial test with continuity correction: *677 out of 1231*

H_1	π_0	n_{trials}	p	$n_{successes}$	*p-value*	CI
two.sided	0.5	1231	0.55	677	5e-04	0.52, 0.58

Plotting!

Bar Plot of Polling Data (using R's Base Graphics)

```
electpal <- c("red", "blue")
electpal <- sapply(electpal, adjustcolor, alpha = 0.75, USE.NAMES = FALSE)

palette(electpal)
barplot(poll.t, ylab = "Count",
        xlab = "Polling Response",
        family = "ETBembo",
        col = electpal, main = "Polling Responses")
```

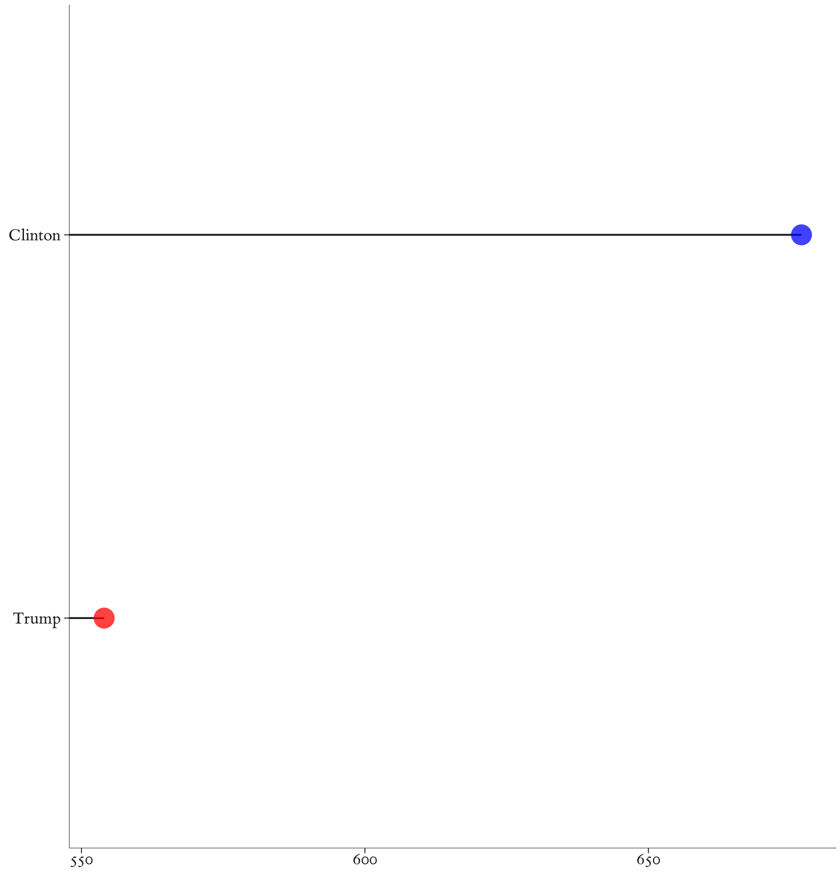


Dot-Plot of Polling Data using the `ggplot2` package.

This would actually be interesting to do with repeated-measures data with the candidates on the `Y-axis` and time (in months/weeks) on the `X-axis`.

```
poll.df <- as.data.frame(poll.t)
names( poll.df) <- c("Response", "Frequency")
 poll.df$N <- rep(x = nrow(dat), times = nrow( poll.df))
n <-  poll.df[, 2]
bpoll <- ggplot( poll.df, aes(x = Frequency, y = Response)) +
    geom_segment(aes(yend = Response), xend = 0, colour = mypal[20]) +
```

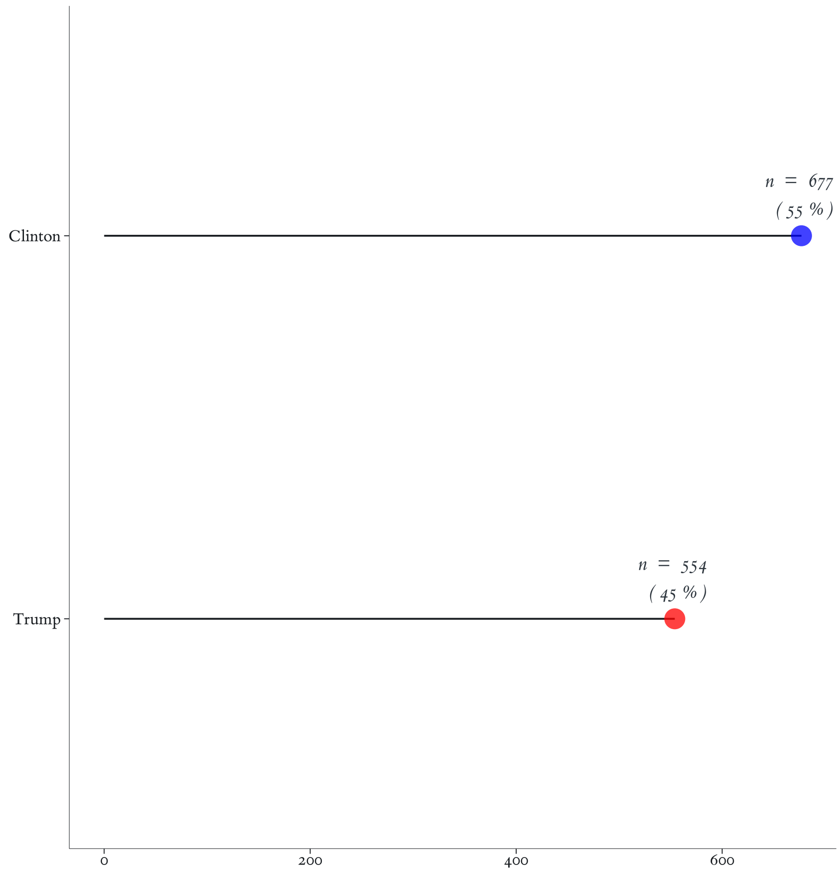
```
    geom_point(size = 5, aes(colour = Response)) +
    scale_colour_manual(values = electpal, guide = FALSE) +
    labs(y = "", x = "") + thm_tft(xline = TRUE, yline = TRUE)
bpoll
```



Don't forget to set the x-and-y-limits! Otherwise, you could be presenting a potentially misleading visualization of the data. Since these are polling data, there is a true "zero" such that `0` would reflect `0` votes for a given candidate in a given poll.[2] The data should thus be represented according to its appropriate scale limits.

[2] \textit{This has happened for one of the two current major party presidential candidates in the very recent past - I will not say who.}

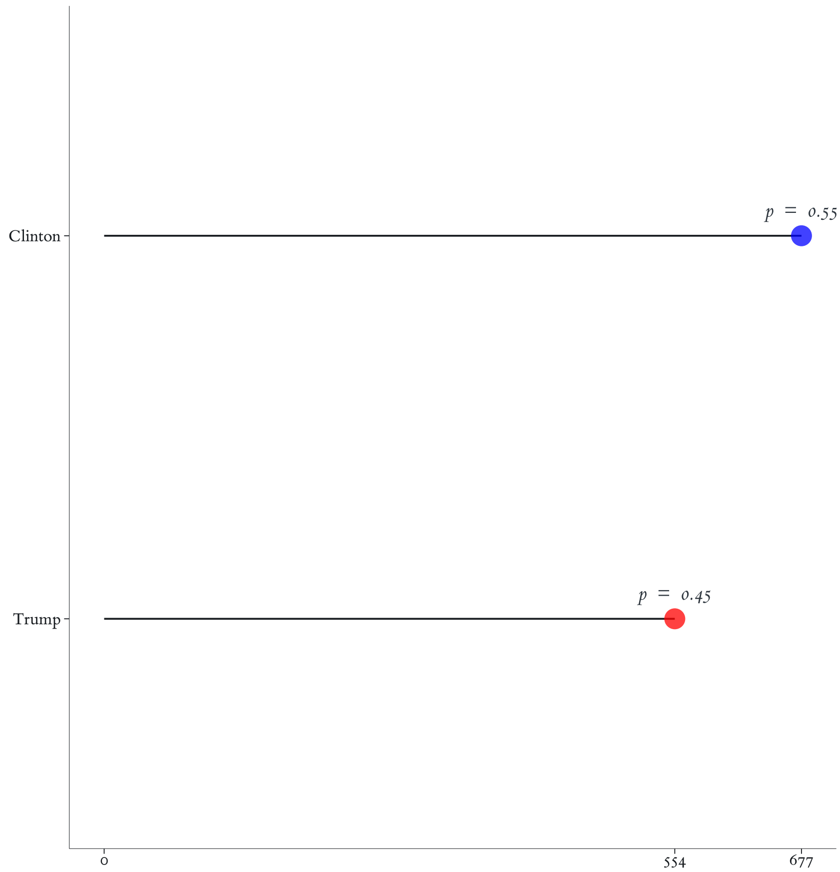
```
bpoll + xlim(0, max( poll.df$Frequency)) +
    geom_text(vjust = -0.5, hjust = 0.5, stat = 'identity',
              position = 'identity', colour = mypal[19],
              size = rel(4), aes(family = "ETBembo", fontface = "italic",
                                 label = paste("n  = ", n,
                                               "\n", "(",
                                               round(n/ poll.df$N*100),
                                               "%",")")))
```



Further, in plots like these, where discrete data with a relatively small number of categories[3] are juxtaposed with a continuous scale, setting the continuous axis' limits (in this case the `x-axis`) can help to further disambiguate the information.

[3] My persona rule of thumb for what constitutes a "relatively small category" is $N_{categories} \leq 5$

```
bpoll2 <- bpoll + scale_x_continuous(breaks = c(0, n),
                                     limits = c(0, max(n)))

bpoll2 + geom_text(vjust = -1.5, hjust = 0.5, stat = 'identity',
                   position = 'identity', colour = mypal[19],
                   size = rel(4), aes(family = "ETBembo",
                                     fontface = "italic",
                                     label = paste("p  = ",
                                                   round(n/ poll.df$N,
                                                         digits = 2))))
```



*Categorical Data Visualization - **Mosaic Plots***

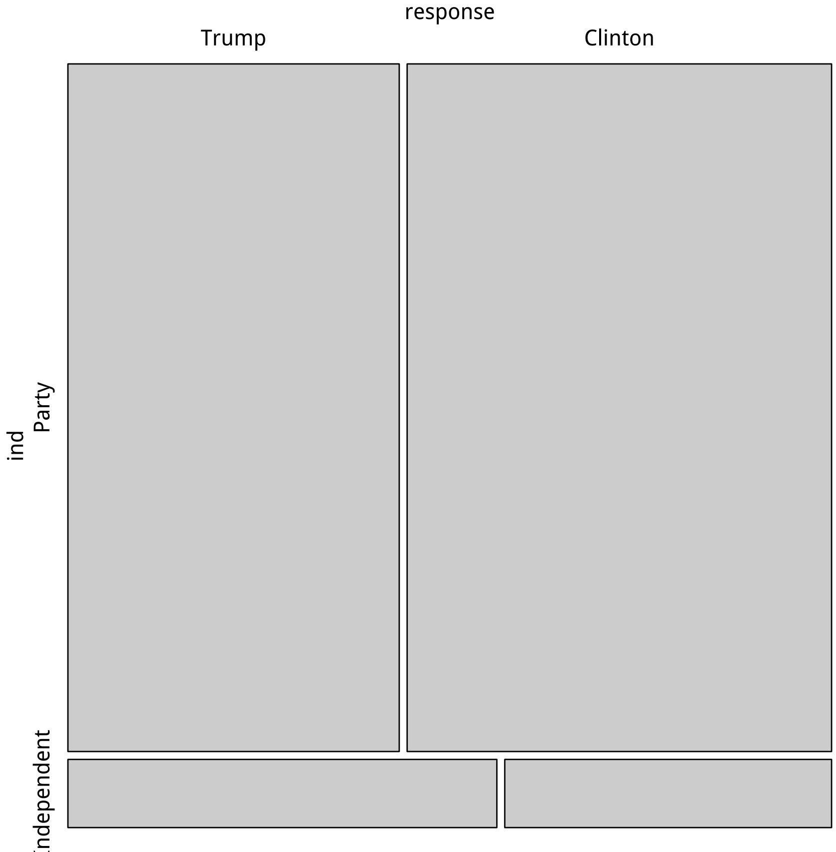
The below R-Code is copied directly from [Dr. Jason Newsom's *"Mosaic Plots"* handout]

```
dat <- within(dat, {
    resp.F <- factor(response)
    ind.F <- factor(ind)
})

tbl <- table(dat$ind.F, dat$resp.F)
tbl
```

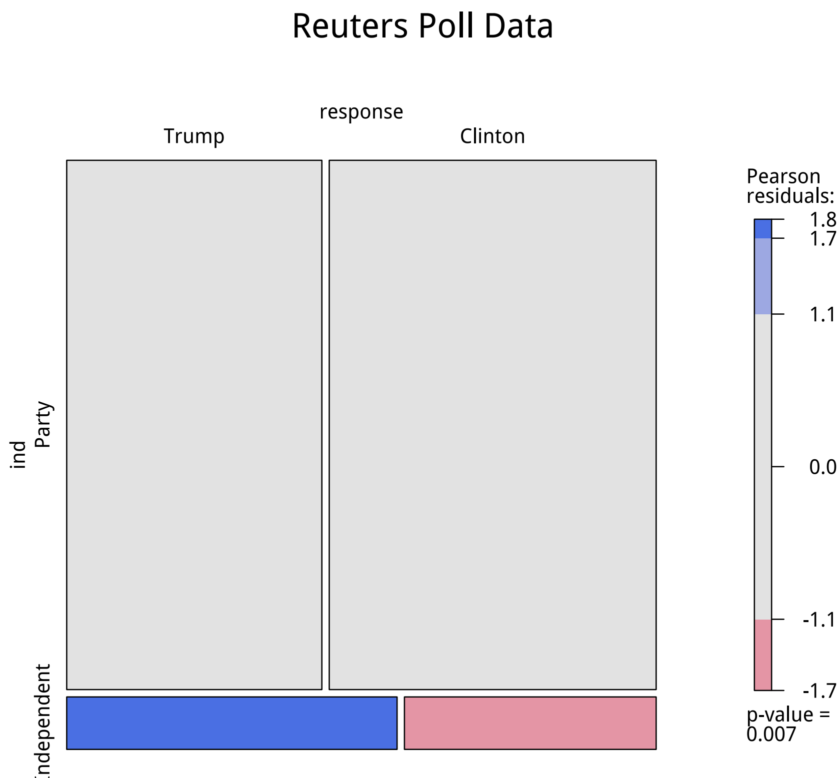
	Trump	Clinton
0	491	629
1	63	48

```
library(vcd)

dimnames(tbl) <- list(ind = c("Party", "Independent"),
                      response = c("Trump","Clinton"))
```

```
mosaic(tbl)
```




```
mosaic(tbl,main = "Reuters Poll Data", gp = shading_max)
```


Reuters Poll Data
response
Trump
Clinton
Party
ind
Independent
Pearson
residuals:
1.8
1.7
1.1
0.0
-1.1
-1.7
p-value =
0.007

Three-Way Contingency Table Analysis

```
cnt <- array( ## What we want to generate directly from the data ##
    c(100, 139, 106, 128, 157, 140, 89, 77),
    dim = c(2, 2, 2),
    dimnames = list(
    sex = c("Male", "Female"),
    ind = c("Affiliate", "Independent"),
    response = c("Clinton", "Trump")
))
library(DescTools)
## what the results of the BD & MH tests should be: ##
BreslowDayTest(cnt, correct = FALSE)
```

Table 8: Breslow-Day test on Homogeneity of Odds Ratios: `cnt`

Test statistic	df	P value
0.1691	1	0.6809

```
mantelhaen.test(cnt, correct = TRUE) ## For comparison only, since JTN's handout
```

Table 9: Mantel-Haenszel chi-squared test with continuity correction: `cnt`

Test statistic	df	P value	Alternative hypothesis
0.346	1	0.5564	two.sided

```
                                    ## uses the default MH test method, which
                                    ## includes Yate's correction ##
mantelhaen.test(cnt, correct = FALSE)
```

Table 10: Mantel-Haenszel chi-squared test without continuity correction: `cnt`

Test statistic	df	P value	Alternative hypothesis
0.4293	1	0.5123	two.sided

```
dat <- R.rspss("data/cnnpoll.sav", vlabs = T)
ft <- with(dat, {
```

```
    ftable(dat, row.vars = 1:2, col.vars = 3)
})
ft
```

		"ind"	"party affiliate"	"independent"
"response"	"sex"			
"CLINTON"	"MALE"		100	106
	"FEMALE"		157	89
"TRUMP"	"MALE"		139	128
	"FEMALE"		140	77

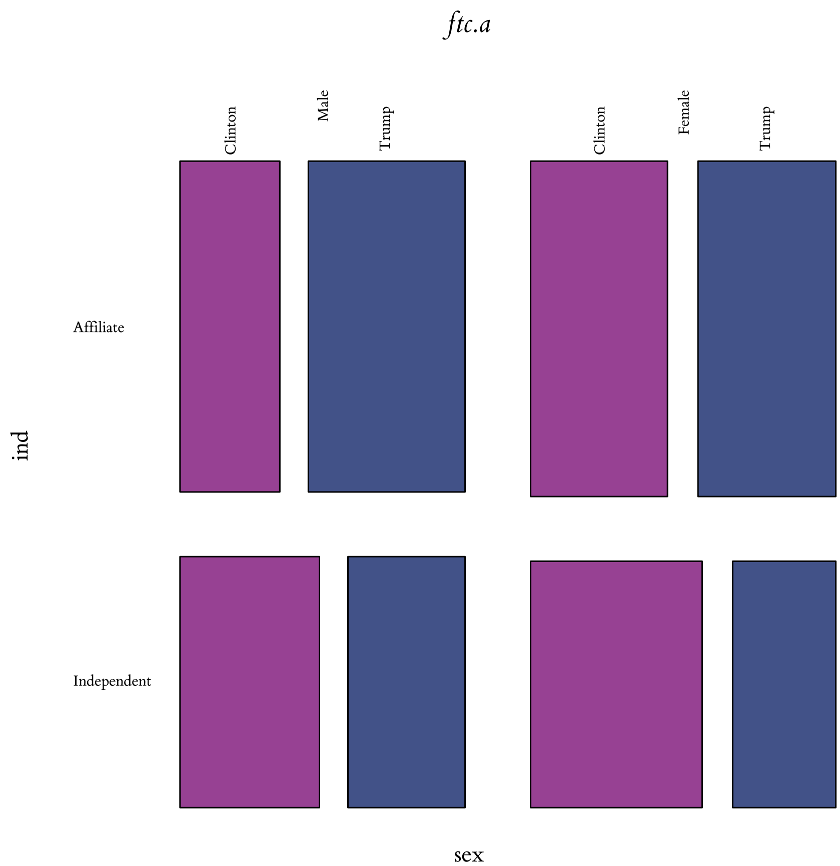
```
ftc <- matrix(ft, nrow = 4, byrow = T)
ftc
```

100	157
139	140
106	89
128	77

```
ftc.a <- array(ftc, dim = c(2, 2, 2), dimnames = list(
    sex = c("Male", "Female"),
    ind = c("Affiliate", "Independent"),
    response = c("Clinton", "Trump")))
ftc.a
```

100, 139, 106, 128, 157, 140, 89 and *77*

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




```
library(DescTools)
BreslowDayTest(ftc.a, correct = FALSE)
```

Table 13: Breslow-Day test on Homogeneity of Odds Ratios: `ftc.a`

Test statistic	df	P value
0.1691	1	0.6809

```
mantelhaen.test(ftc.a, correct = TRUE) ## For comparison only, since JTN's handout
```

Table 14: Mantel-Haenszel chi-squared test with continuity correction: `ftc.a`

Test statistic	df	P value	Alternative hypothesis
0.346	1	0.5564	two.sided

```
                                    ## uses the default MH test method, which
                                    ## includes Yate's correction ##
mantelhaen.test(ftc.a, correct = FALSE)
```

Table 15: Mantel-Haenszel chi-squared test without continuity correction: `ftc.a`

Test statistic	df	P value	Alternative hypothesis
0.4293	1	0.5123	two.sided

Matched Pairs

```
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 17: 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
```

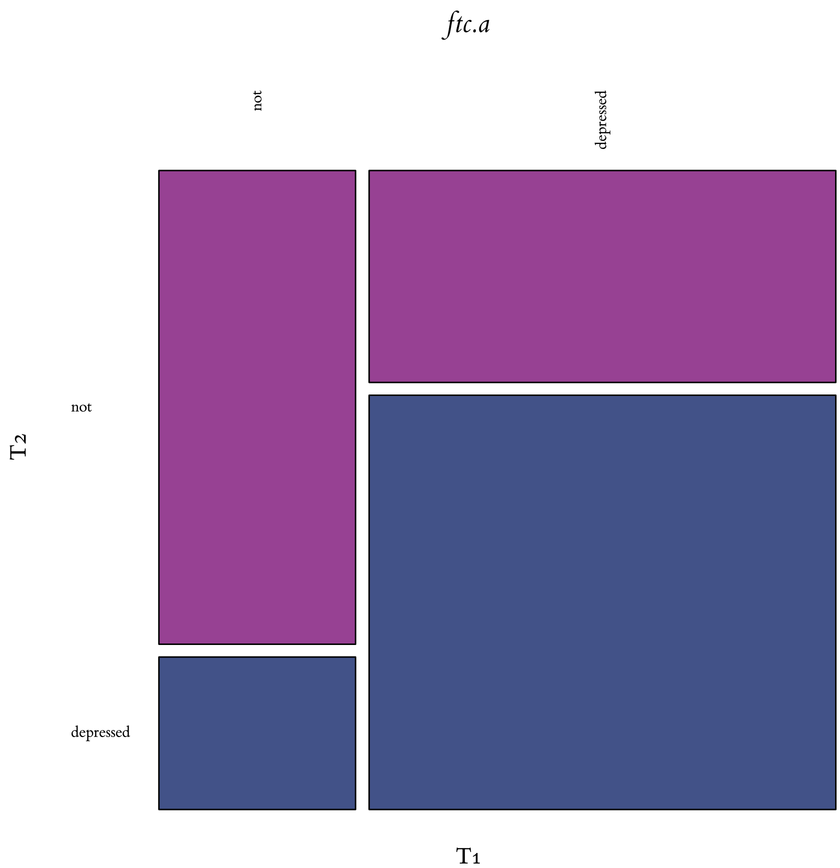
	not	depressed
not	146	47
depressed	155	303

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

Table 22: 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)])
```


ftc.a
not
depressed
T2
not
depressed
T1

Loglinear Model Analysis

```
dat <- R.rspss("data/reuters.sav", vlabs = F)
R.msmm(dat)
```

	M	SD	Min	Max	NAs
id	769.5	444.1	1	1538	0
response	0.84	0.73	0	2	0
party	0.42	0.49	0	1	377
partmiss	0.25	0.43	0	1	0
ind	0.14	0.35	0	1	0

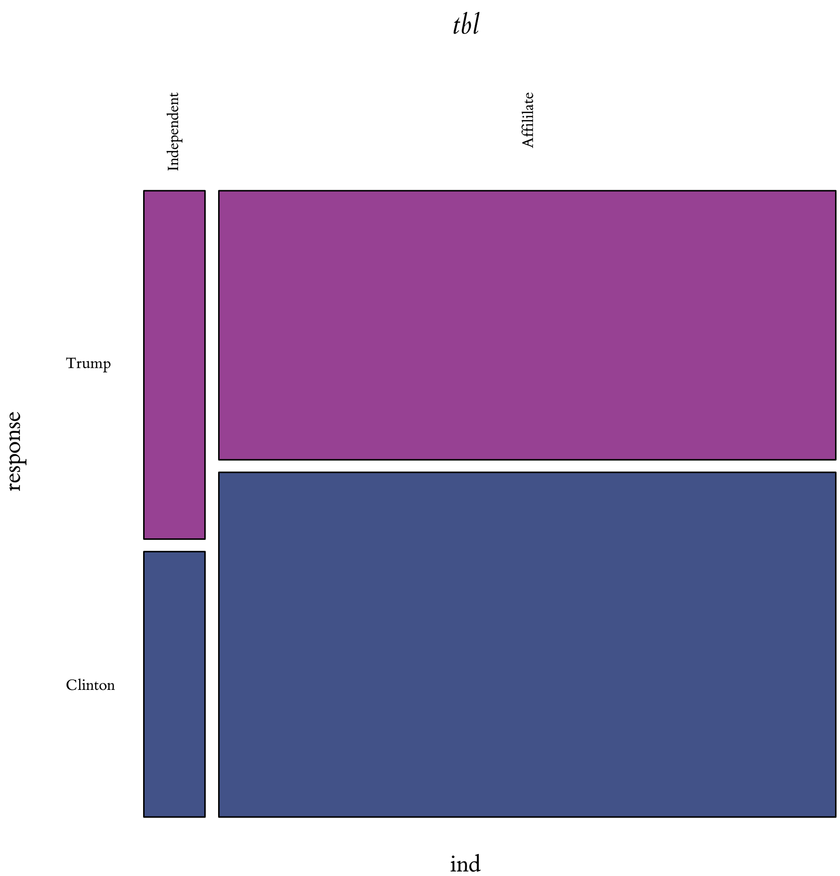
```
dat <- dat[, -3]
dat <- subset(dat, response < 2)
dat <- within(dat, {
    ind.f <- factor(ind,
                    levels = unique(ind),
                    labels = c("Independent",
                               "Affililate"))
    response.f <- factor(response,
                         levels = c(0, 1),
                         labels = c("Trump",
                                    "Clinton"))
})
summary(dat)
```

Table 24: Table continues below

id	response	partmiss	ind	response.f
Min. : 1.0	Min. :0.00	Min. :0.00000	Min. :0.00000	Trump :554
1st Qu.: 308.5	1st Qu.:0.00	1st Qu.:0.00000	1st Qu.:0.00000	Clinton:677
Median : 616.0	Median :1.00	Median :0.00000	Median :0.00000	
Mean : 616.0	Mean :0.55	Mean :0.05686	Mean :0.09017	
3rd Qu.: 923.5	3rd Qu.:1.00	3rd Qu.:0.00000	3rd Qu.:0.00000	
Max. :1231.0	Max. :1.00	Max. :1.00000	Max. :1.00000	

ind.f
Independent:
111
Affililate :1120

```
tbl <- table(dat$ind.f, dat$response.f)
dimnames(tbl) <- list(ind = levels(dat$ind.f), response = levels(dat$response.f))
mosaicplot(tbl, type = "deviance", las = 2, color = mypal.a75[c(5, 16)])
```




```
library(MASS)
logmodel <- loglm( ~ ind + response, digits = 4, data = tbl)
```

[ToDo]

- [ ] *Find method for entering expected values into binomial test function(s) (e.g., when you want to compare Oregon's polling estimates to those of the general US population).*

References[4]

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[4] **Note:** This document was created using ***R***-*v3.3.2* R Core Team, *R*, and the following ***R***-*packages*: *base-v3.3.* R Core Team, *R*, *bibtex-v0.4.* Francois, *Bibtex*, *car-v2.1.* Fox and Weisberg, *An R Companion to Applied Regression*, *dplyr-v0.5.* Wickham and Francois, *Dplyr*, *DT-v0.2.* Xie, *DT*, *extrafont-v0.17.* Chang, *Extrafont*, *ggplot2-v2.1.* Wickham, *Ggplot2*, *knitcitations-v1.0.* Boettiger, *knitcitations*, *knitr-v1.14.* Xie, *Dynamic Documents with R and Knitr*, *pander-v0.6.* Daroczi and Tsegelskyi, *Pander*, *papaja-v0.1.* Aust and Barth, *Papaja*, *plyr-v1.8.* Wickham, "The Split-Apply-Combine Strategy for Data Analysis.", *rmarkdown-v1.1.* Allaire et al., *rmarkdown*, *scales-v0.4.* Wickham, *Scales*, *tidyr-v0.6.* Wickham, *Tidyr*, *ggthemes-v3.2.* Arnold, *Ggthemes*, *gtable-v0.2.* Wickham, *Gtable*, *kableExtra-v0.0.* Zhu, *KableExtra*, *tufte-v0.2.* Xie and Allaire, *Tufte*, *MASS-v7.3.* Venables and Ripley, *Modern Applied Statistics with S*, *vcd-v1.4.* Meyer, Zeileis, and Hornik, "Residual-Based Shadings for Visualizing (Conditional) Independence".", *devtools-v1.12.* Wickham and Chang, *Devtools*, *highlight-v0.4.* Francois, *Highlight*, *sysfonts-v0.5.* Qiu and others, *Sysfonts*, and *showtext-v0.4.* Qiu, *Showtext*

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