Package: matchedcc (via r-universe)

February 20, 2025

Type Package

Title 'Stata'-Like Matched Case-Control Analysis

Version 0.1.1.9000

Date 2024-11-19

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Description Calculate multiple statistics with confidence intervals for matched case-control data including risk difference, risk ratio, relative difference, and the odds ratio. Results are equivalent to those from 'Stata', and you can choose how to format your input data. Methods used are those described on page 56 of the 'Stata' documentation for ``Epitab - Tables for Epidemologists'' <`https://www.stata.com/manuals/repitab.pdf`>.

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Encoding UTF-8

RoxygenNote 7.3.2

Roxygen list(markdown = TRUE)

URL `https://github.com/simpar1471/matchedcc/`, `https://simpar1471.github.io/matchedcc/`

BugReports `https://github.com/simpar1471/matchedcc/issues`

Depends R (>= 4.1.0)

Imports checkmate, stats, cli, binom

Suggests testthat (>= 3.0.0), readr, vctrs, stringr, purrr, knitr, rmarkdown, RStata

LazyData true

Config/Needs/website rmarkdown

Repository https://simpar1471.r-universe.dev

RemoteUrl https://github.com/simpar1471/matchedcc

RemoteRef HEAD

RemoteSha 278932d54dd50e05be4c569f6d90eed4ce99a05f

Contents

`mcc` *Stata-like analysis of unstratified matched-case control data*

Description

Using data from vectors, data from a 2x2 contingency table, or individual cell counts, `mcc()` and `mcci()` will calculate McNemar's χ^2; point estimates and confidence intervals for the difference, ratio, and relative difference of proportion of pairs with the exposure; and the odds ratio with a confidence interval.

Usage

```
mcc(cases = NULL, controls = NULL, table = NULL, conf_level = 0.95)

mcci(a, b, c, d, conf_level = 0.95)
```

Arguments

`cases, controls` Numeric vectors of the same length, with values of `0` (unexposed) and `1` (exposed). The default for these variables is `NULL`, and an error will be thrown if you attempt to provide these parameters as well as `table`. If provided, these variables are used to construct a 2x2 matrix in the same format as `table`.

`table` A 2x2 integerish (see `checkmate::check_integerish()`) matrix with matched case-control data. The default value of `table` is `NULL`, and an error will be thrown if you provide `table` as well as `cases` and `controls`.

The table should have the following format, where each cell represents a pair of a matched case and control:

Cases	**Controls**	
	Exposed	Unexposed
Exposed	a	b
Unexposed	c	d

`conf_level` Numeric scalar from `0.1` to `0.9999`. Controls level at which to calculate confidence intervals. Default = `0.95` (95% confidence intervals).

`a, b, c, d` Single integerish values with cell counts that correspond to a 2x2 table of matched case control data.

Value

A named list with 5 elements:

`data` A 3x3 matrix generated using the data provided, formatted for matched case-control analysis and with row/column totals.

`mcnemar_chi2` Results from analysing the matched case-control data with `mcnemar.test()`, *without* Yates' continuity correction.

`mcnemar_exact_p` Result of an exact test of H_0: $OR = 1$, calculated using the binomial distribution.

`proportions` A two-element numeric vector with the proportion of of cases and controls with the exposure.

`statistics` A 4 row, 3 column numeric matrix with point estimates and confidence intervals for the ratio, difference, and relative difference in the proportion of cases/controls with the exposure, and the odds ratio.

References

Exact Chi-squared statistic: McNemar, Q. (1947) *Note on the sampling error of the difference between correlated proportions or percentages* **Psychometrika** 12(2): 153–157. doi:10.1007/bf02295996

Other steps: Agresti, A. (2013) *Categorical Data Analysis* 3rd ed. Hoboken, NJ: Wiley. pp. 414-417.

Examples

```
data <- matchedcc::mccxmpl
mcc(cases = data$case, controls = data$control)

# Convert data into 2x2 table
data$case_fctr <- factor(data$case, levels = c(1, 0),
                         labels = c("6+ cups", "0 cups"))
data$control_fctr <- factor(data$control, levels = c(1, 0),
                            labels = c("6+ cups", "0 cups"))
mcc(table = table(data$control_fctr, data$case_fctr))

# Alternatively, provide cell counts to `mcci()`
table <- table(data$control_fctr, data$case_fctr)
mcci(a = table[1,1],
     b = table[1,2],
     c = table[2,1],
     d = table[2,2])
```

`mccxmpl` *Example data for matched case-control analysis*

Description

A subset of data from Jick *et al.* (1973) with data on a matched case-control study on myocardial infarction and drinking 6+ cups of coffee per day. Cases and controls were matched after excluding people who drank 1 to 5 cups of coffee per day.

Usage

```
mccxmpl
```

Format

`mccxmpl`**:**

A data frame with 27 rows and 2 columns:

`case` Integer variable of either `1` (exposed) or `0` (not exposed)

`control` Integer variable of either `1` (exposed) or `0` (not exposed)

Source

In Stata 18 - run the commands:

```
webuse mccxmpl, clear
expand pop
keep case control
```

References

Jick, H. *et al.* (1973). Coffee and myocardial infarction. **New England Journal of Medicine** 289: 63–67. doi:10.1056/NEJM197307122890203.

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