Package ‘clust.bin.pair’

February 15, 2018

Title  Statistical Methods for Analyzing Clustered Matched Pair Data
Version 0.1.2

Depends R (>= 3.2.4)
License MIT + file LICENSE
Encoding UTF-8
LazyData true
URL https://github.com/dgopstein/clust.bin.pair

BugReports https://github.com/dgopstein/clust.bin.pair/issues

Imports
Suggests testthat
RoxygenNote 5.0.1
NeedsCompilation no
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Repository CRAN
Date/Publication 2018-02-15 17:44:57 UTC
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clust.bin.pair Statistical test for clustered binary matched pair data

Description

A single interface for several adjustments to the McNemar test for marginal homogeneity that correct for clustered data.

Usage

clust.bin.pair(ak, bk, ck, dk, method = "yang")

Arguments

ak
bk
ck
dk
method

type containing counts per group of Success/Success results.
type containing counts per group of Success/Failure results.
type containing counts per group of Failure/Success results.
type containing counts per group of Failure/Failure results.
a character string specifying the method to calculate the statistic. Must be one of "yang" (default), "durkalski", "obuchowski", "eliasziw". A value of "mcnemar" can also be supplied for comparison.

Value

A list with class "htest" containing the following components:

statistic
p.value
method
data.name

type of the test statistic.
type of the test applied.
a character string giving the names of the data.
References


Examples

```r
with(psychiatry, clust.bin.pair(ah, bh, ch, dh, method="eliasziw"))

tc <- nested.to.contingency(thyroids$x.pet, thyroids$x.spect)
clust.bin.pair(tc$ak, tc$bk, tc$ck, tc$dk, method="obuchowski")

oc <- with(obfuscation, paired.to.contingency(group = list(subject, atom),
       t1 = control, t2 = treatment))
clust.bin.pair(oc$ak, oc$bk, oc$ck, oc$dk, method="durkalski")
```

### nested.to.contingency

Convert between nested results and the canonical contingency tables

**Description**

Sum all concordant and discordant pairs from each nested group into a contingency table.

**Usage**

```r
nested.to.contingency(t1, t2)
```

**Arguments**

- `t1` lists of pre-treatment measures
- `t2` lists of post-treatment measures

**Value**

Contingency tables represented in the rows of a matrix
Examples

```r
nested.to.contingency(thyroids$x.pet, thyroids$x.spec)
```

---

<table>
<thead>
<tr>
<th>obfuscation</th>
<th>Obfuscated C code misinterpretation data</th>
</tr>
</thead>
</table>

Description

Data from Gopstein et. al.'s experiment on the misinterpretation of C code. Subjects were asked to hand evaluate pairs of functionally equivalent code. Half of the questions were intentionally obfuscated to elicit confusion.

Usage

```r
data(obfuscation)
```

Format

A data frame with 57 rows and 4 variables:

- **subject**: the ID of the study participant
- **atom**: the type of obfuscation being evaluated
- **control**: whether the subject answered the un-obfuscated question correctly
- **treatment**: whether the subject answered the obfuscated question correctly

Source

Atoms of Confusion

Examples

```r
data(obfuscation)

oc <- paired.to.contingency(group = obfuscation[,c("subject", "atom")],
                           t1 = obfuscation$control,
                           t2 = obfuscation$treatment)

clust.bin.pair(oc$k, oc$bk, oc$ck, oc$dk, method="durkalski")
```
paired.to.contingency  
*Convert between paired results and the canonical contingency tables*

**Description**

Group results by common clustering then tally the concordant and discordant pairs.

**Usage**

`paired.to.contingency(group, t1, t2)`

**Arguments**

- `group` List of grouping values
- `t1` pre-treatment measures
- `t2` post-treatment measures

**Value**

Contingency tables represented in the rows of a matrix

**Examples**

```r
paired.to.contingency(list(obfuscation$subject, obfuscation$atom),
                      obfuscation$control, obfuscation$treatment)
```

---

**psychiatry**  
*Psychiatrist and patient disagreement data*

**Description**

Psychiatrists and their patients were surveyed in pairs regarding patient concerns and treatment. Each psychiatrist was asked whether each question item was relevant to their patient and each of their patients were asked the same. The data can be evaluated to answer the question of whether there was patient/doctor agreement in each item. The sample was 29 psychiatrists, each with 1-8 patients, for a total of N = 135 matched pairs.

**Usage**

`data(psychiatry)`
Format

A data frame with 29 rows and 7 variables:

- psychiatrist: the ID of the psychiatrist
- Nh: the number of the psychiatrist’s patients participating in the experiment
- ah: both participants answered 1
- bh: patient answered 1, psychiatrist answered 0
- ch: patient answered 0, psychiatrist answered 1
- dh: both participants answered 0
- Wh: Normalized difference: (bh - ch) / Nh

Source


References


Examples

data(psychiatry)

psychiatry$Wh = round((psychiatry$bh - psychiatry$ch) / psychiatry$Nh, 2)

clust.bin.pair(psychiatry$ah, psychiatry$bh, psychiatry$ch, psychiatry$dh, method="eliasziw")

---

thyroids

*PET and SPECT data for diagnosing hyperparathyroidism*

Description

Following surgery which confirmed the absence of hyperparathyroidism two diagnostic tests, PET and SPECT, were performed. Their measures of true negatives and false positives are reported. Data reported in Obuchowki 1998.

Usage

data(thyroids)
Format

A data frame with 21 rows and 6 variables:

- **patient**: ID of the patient
- **n.glands**: number of glands tested from the patient
- **n.pet**: number of true negatives from the PET test
- **x.pet**: individual results per gland from the PET test
- **n.spect**: number of true negatives from the SPECT test
- **x.spect**: individual results per gland from the SPECT test

Source


Examples

data(thyroids)

```r
thyroids$n.glands <- sapply(thyroids$x.pet, length)
thyroids$n.glands <- sapply(thyroids$x.spect, length)

thyroids$n.pet <- sapply(thyroids$x.pet, function(x) length(which(x == 1)))
thyroids$n.spect <- sapply(thyroids$x.spect, function(x) length(which(x == 1)))

tc <- nestedNtoNcontingency(thyroids$x.pet, thyroids$x.spect)
clust.bin.pair(tc[, 'ak'], tc[, 'bk'], tc[, 'ck'], tc[, 'dk'], method="obuchowski")
do.call(clust.bin.pair, data.frame(tc))
```
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