Package 'multiCA'

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Type Package

Title Multinomial Cochran-Armitage Trend Test

Version 1.2.0

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Depends R(>= 2.10)

Imports bitops, multcomp

Description Implements a generalization of the Cochran-Armitage trend test to multinomial data. In addition to an overall test, multiple testing adjusted p-values for trend in individual outcomes and power calculation is available.

License GPL (>= 2)

Encoding UTF-8

RoxygenNote 7.2.3

Suggests testthat

URL https://github.com/anikoszabo/multiCA

BugReports https://github.com/anikoszabo/multiCA/issues

NeedsCompilation no

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`multiCA-package` *Multinomial Cochran-Armitage Trend Test*

Description

Implements a generalization of the Cochran-Armitage trend test to multinomial data. In addition to an overall test, multiple testing adjusted p-values for trend in individual outcomes and power calculation is available.

Details

The DESCRIPTION file:

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BugReports:	https://github.com/anikoszabo/multiCA/issues
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The main functionality is implemented in the `multiCA.test` function. The `power.multiCA.test` function can be used for power and sample size calculation.

Author(s)

NA

Maintainer: NA

References

Szabo, A. (2018). Test for Trend With a Multinomial Outcome. The American Statistician, 73(4), 313–320.

`cnonct` *Non-centrality parameter for chi-square distribution*

Description

Calculates the non-centrality parameter for a chi-square distribution for a given quantile. This is often needed for sample size calculation for chi-square based tests.

Usage

```
cnonct(x, p, df)
```

Arguments

`x`	a numeric value at which the distribution was evaluated
`p`	a numeric value giving the cumulative probability at `x`
`df`	an integer giving the degrees of freedom of the chi-square variable

Details

The function is modeled after the SAS function CNONCT. If `p` is larger than the cumulative probability of the central chi-square distribution at `x`, then there is no solution and NA is returned.

Examples

```
(ncp <- cnonct(qchisq(0.95, df=10), 0.8, df=10))
## check
pchisq(qchisq(0.95, df=10), df=10, ncp=ncp)  ## 0.8
```

multiCA.test *Multinomial Cochran-Armitage trend test*

Description

The multiCA.test function performs a multinomial generalization of the Cochran-Armitage trend test.

Usage

```
multiCA.test(x, ...)

## Default S3 method:
multiCA.test(
  x,
  scores = 1:ncol(x),
  outcomes = 1:nrow(x),
 p.adjust.method = c("none", "closed.set", "Holm-Shaffer", "single-step", "Westfall"),
  ...
)

## S3 method for class 'formula'
multiCA.test(formula, data, subset, na.action, weights, ...)
```

Arguments

x	a two-dimensional matrix of event counts with the outcomes as rows and ordered groups as columns.
...	other arguments
scores	non-decreasing numeric vector of the same length as the number of ordered groups. Defaults to linearly increasing values
outcomes	integer or character vector defining the set of outcomes (by row index or row name) over which the trend should be tested. Defaults to all outcomes.
p.adjust.method	character string defining the correction method for individual outcome p-values. Defaults to "closed.set" when length(outcomes)<=3, and "Holm-Shaffer" otherwise.
formula	a formula of the form outcome ~ group where outcome is a factor representing the categorical outcome and group is the grouping variable over which the trend is tested.
data	an optional matrix or data frame containing the variables in the formula formula. By default the variables are taken from environment(formula).
subset	an optional vector specifying a subset of observations to be used.
na.action	a function which indicates what should happen when the data contain NAs. Defaults to getOption("na.action").

weights	an integer-valued variable representing the number of times each outcome - group combination was observed.

Value

a list with two components

overall	an object of class "htest" with the results of the overall test
individual	a vector with adjusted p-values for individual outcomes

Author(s)

Aniko Szabo

References

Szabo, A. (2018). Test for Trend With a Multinomial Outcome. The American Statistician, 73(4), 313–320.

Examples

```
data(stroke)
## using formula interface
multiCA.test(Type ~ Year, weights=Freq, data=stroke)

##using Westfall's multiple testing adjustment
multiCA.test(Type ~ Year, weights=Freq, data=stroke, p.adjust.method="Westfall")

## using matrix interface and testing only the first 3 outcomes
strk.mat <- xtabs(Freq ~ Type + Year, data=stroke)
multiCA.test(strk.mat, outcomes=1:3)
```

---

power.CA.test *Power calculations for the Cochran-Armitage trend test*

Description

Power calculations for the Cochran-Armitage trend test

Usage

```
power.CA.test(
  N = NULL,
  power = NULL,
  pvec = NULL,
  scores = seq_along(pvec),
  n.prop = rep(1, length(pvec)),
  sig.level = 0.05,
  alternative = c("two.sided", "less", "greater")
)
```

Arguments

N	integer, the total sample size of the study. If NULL then power needs to be specified.
power	target power. If NULL then N needs to be specified.
pvec	numeric vector of hypothesized outcome probabilities in each group.
scores	non-decreasing numeric vector of the same length as the number of ordered groups giving the trend test scores. Defaults to linearly increasing values.
n.prop	numeric vector describing relative sample sizes of the ordered groups. Will be normalized to sum to 1. Defaults to equal sample sizes.
sig.level	significance level
alternative	character string specifying the alternative hypothesis

Value

object of class "power.htest"

References

Nam, J. (1987). A Simple Approximation for Calculating Sample Sizes for Detecting Linear Trend in Proportions. Biometrics, 43(3), 701-705.

Examples

```
# sample size required to detect with 80% power a decreasing trend over 4 groups
# with 3:2:1:2 sample-size distribution at a 2.5% significance level
power.CA.test(power=0.8, pvec=c(0.4, 0.3, 0.2, 0.1), n.prop=c(3,2,1,2),
              alternative = "less", sig.level=0.025)

# power of a 2-sided test to detect a logistic increase with slope 0.2 over 5 groups
# with groups of size 10 with unequal dose spacing
doses <- c(0,1,2,4,8)
p0 <- 0.05 # event probability at lowest dose
logit.props <- log(p0/(1-p0)) + doses * 0.2
p <- 1 / (1 + exp(-logit.props)) # hypothesized probabilities at each dose
power.CA.test(N = 10 * 5, pvec=p, scores = doses)
```

---

power.multiCA.test *Power calculations for the multinomial Cochran-Armitage trend test*

Description

Given the probabilities of outcomes, compute the power of the overall multinomial Cochran-Armitage trend test or determine the sample size to obtain a target power.

Usage

```
power.multiCA.test(
  N = NULL,
  power = NULL,
  pmatrix = NULL,
  p.ave = NULL,
  p.start = NULL,
  p.end = NULL,
  slopes = NULL,
  scores = 1:G,
  n.prop = rep(1, G),
  G = length(p.ave),
  sig.level = 0.05
)
```

Arguments

N	integer, the total sample size of the study. If NULL then power needs to be specified.
power	target power. If NULL then N needs to be specified.
pmatrix	numeric matrix of hypothesized outcome probabilities in each group, with the outcomes as rows and ordered groups as columns. The columns should add up to 1.
p.ave	numeric vector of average probability of each outcome over the groups weighted by n.prop.
p.start, p.end	numeric vectors of the probability of each outcome for the first / last ordered group
slopes	numeric vector of the hypothesized slope of each outcome when regressed against the column scores with weights n.prop. The values should add up to zero, as the total probability is always 1 and has no trend.
scores	non-decreasing numeric vector of the same length as the number of ordered groups giving the trend test scores. Defaults to linearly increasing values.
n.prop	numeric vector describing relative sample sizes of the ordered groups. Will be normalized to sum to 1. Defaults to equal sample sizes.
G	integer, number of ordered groups
sig.level	significance level

Details

The sample size calculation depends only on p.ave - the weighted average probability of each outcome, and slopes - the weighted regression slope of each outcome.

The values of these two key inputs can be specified in three ways:

1. directly passing p.ave and slopes, or

2. specifying exactly two of the parameters p.ave, slopes, p.start, and p.end. In this case the full matrix of outcome probabilities will be inferred assuming linearity within each outcome.

3. specifying the full matrix of outcome probabilities `pmatrix`.

The calculation is based on approximating the distribution of the test statistic under the alternative with a non-central chi-squared distribution instead of the correct weighted mixture of multiple non-central chi-squares. This results in bias in the power away from 50 underestimated.

Value

object of class "power.htest"

References

Szabo, A. (2018). Test for Trend With a Multinomial Outcome. The American Statistician, 73(4), 313–320.

See Also

`power.CA.test` for simpler (and more precise) power calculation with a binomial outcome

Examples

```
power.multiCA.test(power=0.8, p.start=c(0.1,0.2,0.3,0.4), p.end=c(0.4, 0.3, 0.2, 0.1),
                     G=5, n.prop=c(3,2,1,2,3))

## Power of stroke study with 100 subjects per year and observed trends
data(stroke)
strk.mat <- xtabs(Freq ~ Type + Year, data=stroke)
power.multiCA.test(N=900, pmatrix=prop.table(strk.mat, margin=2))
```

`stroke` *Stroke types over time*

Description

Nakajima et al. (2014) collected information on stroke patients over a 9-year period. For each patient, the type of stroke was classified into one of 5 categories by etiology.

Usage

```
data("stroke")
```

Format

A data frame with 45 observations on the following 3 variables.

`Type` a factor with levels `Small vessel occlusion`, `Large artery atherosclerosis`, `Cardioembolism`, `Other determined aetiology`, and `Undetermined aetiology` giving the etiology of the stroke

`Year` a numeric vector with the year of the observation

`Freq` a numeric vector with the number of patients with a stroke of the given etiology that year

Source

Nakajima, M., Y. Inatomi, T. Yonehara, Y. Hashimoto, T. Hirano, and Y. Ando (2014). Temporal trends in oral intake ability 3 months after acute ischaemic stroke: analysis of a single-centre database from 2003 to 2011. J Rehabil Med 46 (3), 200–205.

Examples

```
data(stroke)
xtabs(Freq ~ Type + Year, data=stroke)

strk.props <- prop.table(xtabs(Freq ~ Year+Type, data=stroke), margin=1)
matplot(strk.props, type="l")
```

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