Package ‘QCAfalsePositive’

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Title  Tests for Type I Error in Qualitative Comparative Analysis (QCA)
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Description  Implements tests for Type I error in Qualitative Comparative Analysis (QCA) that take into account the multiple hypothesis tests inherent in the procedure. Tests can be carried out on three variants of QCA: crisp-set QCA (csQCA), multi-value QCA (mvQCA) and fuzzy-set QCA (fsQCA). For fsQCA, the fsQCApermTest() command implements a permutation test that provides 95% confidence intervals for the number of counterexamples and degree of consistency, respectively. The distributions of permuted values can be plotted against the observed values. For csQCA and mvQCA, simple binomial tests are implemented in csQCAbinTest() and mvQCAbinTest(), respectively.

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Determinants of the Arab Spring uprising

Description
A dataset containing fuzzy-set membership scores for ten sets of state characteristics (per-capita GDP, economic inequality, etc.) across 20 states in northern Africa and the Arab Peninsula at the time of the Arab Spring uprisings of 2010-12.

Usage

Arab.Spring

Format
A data frame with 20 rows and 10 variables, measured as fuzzy set membership scores.

- Gdppc: per-capita GDP
- Gini: economic inequality
- Unemp: unemployment
- Urban: degree of urbanization
- Youth: size of youth bulge
- Mobile: mobile phone usage
- Internet: internet penetration
- Fuel: fuel-dependence of economy
- Pol: regime fragility
- Success: social movement success

Source
csQCAbinTest

A Simple Binomial Test for Type I Error in csQCA

Description

A Binomial test for crisp-set qualitative comparative analysis (csQCA), designed to calculate the probability of a false positive given the number of hypotheses implicitly tested and the number of confirming cases.

Usage

```r
csqCABinTest(freq.y, configs, total.configs, adj.method = "holm")
```

Arguments

- `freq.y`: The frequency with which the dependent variable occurs in the sample (the number of 1s divided by the total number of cases).
- `configs`: A list of configurations and the number of cases in which each configuration occurs.
- `total.configs`: The total number of configurations used in the original csQCA analysis. This will generally equal the number of lines in the truth table used for Boolean minimization.
- `adj.method`: The method used to calculate adjusted p-values (see `p.adjust` for details).

Value

An object containing the results of the Binomial test.

Examples

```r
test <- csqCABinTest(freq.y=0.7, configs=list(ab=5, bCD=3, Ce=2),
                    total.configs=20)
summary(test)
```

fsQCApermTest

A Simple Permutation Test for Type I Error in fsQCA

Description

A permutation test for fuzzy-set qualitative comparative analysis (fsQCA), designed to calculate the probability of a false positive given the number of hypotheses implicitly tested and the distribution of the data.
Usage

fsQCApermTest(y, configs, total.configs, num.iter = 10000, my.seed = 123,
adj.method = "holm")

Arguments

y The outcome variable of interest.
configs A list of configurations to be tested against y.
total.configs The total number of configurations used in the original fsQCA analysis. This will generally equal the number of lines in the truth table used for Boolean minimization.
num.iter The number of iterations to use for the permutation test. Larger numbers of iterations result in more precise p-values.
my.seed The seed used to generate random numbers.
adj.method The method used to calculate adjusted p-values (see p.adjust for details).

Value

An object containing the aggregate results of the permutation test as well as the individual permutations.

Examples

data(social.revolutions)
attach(social.revolutions)

intersect <- pmin(breakdown, pop.ins)
intersect2 <- pmin(breakdown, (1-pop.ins))
intersect3 <- pmin((1-breakdown), pop.ins)
intersect4 <- pmin((1-breakdown), (1-pop.ins))

test <- fsQCApermTest(y=soc.rev, configs=list(BI=intersect, Bi=intersect2,
bi=intersect3, bi=intersect4), total.configs=4)
summary(test)
plot(test)

mvQCAbinTest A Simple Binomial Test for Type I Error in mvQCA

Description

A Binomial test for multi-value qualitative comparative analysis (mvQCA), designed to calculate the probability of a false positive given the number of hypotheses implicitly tested and the number of confirming cases.
p.threshold.adjust

Usage

mvQCAbinTest(freq.y, configs, total.configs, adj.method = "holm")

Arguments

freq.y The frequency with which the dependent variable occurs in the sample (the number of 1s divided by the total number of cases).
configs A list of configurations and the number of cases in which each configuration occurs.
total.configs The total number of configurations used in the original mvQCA analysis. This will generally equal the number of lines in the truth table used for Boolean minimization.
adj.method The method used to calculate adjusted p-values (see p.adjust for details).

Value

An object containing the results of the Binomial test.

Examples

test <- mvQCAbinTest(freq.y=0.7, configs=list(aB=5, bCD=S, Ce=RI), total.configs=20)
summary(test)

p.threshold.adjust Calculate Vector of p-value Thresholds for Multiple Inference

Description

Internal function. Calculates the adjusted thresholds for multiple significance tests, assuming that the original threshold for a single test is p<0.05. Used by fsQCApermTest to calculate confidence intervals.

Usage

p.threshold.adjust(total.configs, my.method)

Arguments

total.configs The total number of hypotheses tested, or the number of configurations utilized by the Quine-McCluskey algorithm in fsQCA (including logical remainders, if they are used in the analysis).
my.method The adjustment method used to calculate p-values (see p.adjust for details).

Value

Numeric vector giving adjusted p-value thresholds, from smallest to largest.
Examples

p.threshold.adjust(10, "holm")

plot.fsQCApt

Plot Results of fsQCA Permutation Test

Description

Plots distributions of consistencies and counterexamples from permutation tests of fsQCA data, including confidence intervals adjusted to account for multiple inference. Also prints observed consistency values and number of counterexamples as black dots along the x-axis, for comparison.

Usage

```r
## S3 method for class 'fsQCApt'
plot(x, y = x$config.names, statistic = "both", ...)
```

Arguments

- `x`: Object returned by `fsQCApermTest`.
- `y`: A vector of configurations to examine. Default behavior is to examine all configurations.
- `statistic`: The statistic to examine (consistency, counterexamples, or both).
- `...`: Additional parameters to pass on.

Value

Plots of distributions of consistencies, counterexamples, or both.

Examples

```r
data(social.revolutions)
attach(social.revolutions)

intersect <- pmin(breakdown, pop.ins)
intersect2 <- pmin(breakdown, (1-pop.ins))
intersect3 <- pmin((1-breakdown), pop.ins)
intersect4 <- pmin((1-breakdown), (1-pop.ins))

test <- fsQCApermTest(y=soc.rev, configs=list(BI=intersect, Bi=intersect2, bi=intersect3, bi=intersect4), total.configs=4)
plot(test)
plot(test, "bi", statistic="consistency")
plot(test, c("BI", "Bi"), statistic="both")
plot(test, statistic="consistency")
plot(test, "BI")
```
social.revolutions

Determinants of social revolutions.

Description
A data frame containing hypothetical fuzzy-set membership scores for three sets of state characteristics (social revolution, state breakdown, and popular insurrection) across twenty cases.

Usage
social.revolutions

Format
A data frame with 20 rows and 3 variables, measured as degree of fuzzy-set membership.

- soc.rev: presence of social revolution
- breakdown: degree of state breakdown
- pop.ins: presence of popular insurrection ...

Source

summary.csQCAbt
Summarize Binomial Tests for csQCA Data

Description
Displays number of confirming cases and raw and adjusted p-scores following Binomial test of csQCA data.

Usage
## S3 method for class 'csQCAbt'
summary(object, ...)

Arguments
object Object returned by csQCAbinTest.
...
Additional parameters to pass on.

Value
Matrix of values for counterexamples and consistency.
Examples

test <- csQCAbinTest(freq.y=0.7, configs=list(aB=5, bCD=3, Ce=2),
                   total.configs=20)
summary(test)

summary.fsQCApt

Summarize Permutation Tests for fsQCA Data

Description

Displays observed values, confidence intervals, and raw and adjusted p-scores for both consistency
and counterexamples following permutation test of fsQCA data.

Usage

## S3 method for class 'fsQCApt'
summary(object, ...)

Arguments

object Object returned by fsQCApermTest.
...
Additional parameters to pass on.

Value

Two matrices of values for counterexamples and consistency.

Examples

data(social.revolutions)
attach(social.revolutions)

intersect <- pmin(breakdown, pop.ins)
intersect2 <- pmin(breakdown, (1-pop.ins))
intersect3 <- pmin((1-breakdown), pop.ins)
intersect4 <- pmin((1-breakdown), (1-pop.ins))

test <- fsQCApermTest(y=soc.rev, configs=list(BI=intersect, Bi=intersect2,
                       bi=intersect3, bi=intersect4), total.configs=4)
summary(test)
**summary.mvQCAbt**

*Summarize Binomial Tests for mvQCA Data*

**Description**

Displays number of confirming cases and raw and adjusted p-scores following Binomial test of mvQCA data.

**Usage**

```r
## S3 method for class 'mvQCAbt'
summary(object, ...)  
```

**Arguments**

- `object` Object returned by `mvQCAbinTest`.
- `...` Additional parameters to pass on.

**Value**

Matrix of values for counterexamples and consistency.

**Examples**

```r
test <- mvQCAbinTest(freq.y=0.7, configs=list(aB=5, bCD=3, Ce=2),  
total.configs=20)
summary(test)
```
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