Package ‘sensitivitymw’

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Type Package

Title Sensitivity analysis using weighted M-statistics

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Description Sensitivity analysis analysis in matched observational studies with multiple controls using weighted M-statistics to increase design sensitivity.

License GPL-2

LazyLoad yes

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sensitivitymw-package

Sensitivity analysis for observational studies using weighted M-statistics.

Description

Sensitivity analysis for tests, confidence intervals and estimates in matched observational studies with multiple controls using weighted or unweighted Huber-Maritz M-tests (including the permutational t-test).

Details

Package: sensitivitymw
Type: Package
Version: 1.0
Date: 2013-11-03
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The sensitivitymw package performs sensitivity analyses in matched observational studies with multiple controls using weighted Huber-Maritz M-tests, as proposed in Rosenbaum (2014). Function senmw provides bounds on P-values and function senmwCI provides confidence intervals and point estimates. Package sensitivitymw is a companion to package sensitivitymv, and in particular the functions amplify, truncatedP and truncatedPbg in sensitivitymv are useful when using function senmw in the sensitivitymw package. Package sensitivitymw applies weights to matched sets to increase design sensitivity, whereas sensitivitymv does not use weights. However, package sensitivitymv may be used with variable numbers of controls, whereas sensitivitymw requires a fixed number, say 2 controls for each treated subject.

The sensitivity analysis asks about the magnitude, gamma, of bias in treatment assignment in observational studies that would need to be present to alter the conclusions of a randomization test that assumed matching for observed covariates removes all bias. The method implemented in sensitivitymw is essentially the method described in Rosenbaum (2014); see also Rosenbaum (2007, 2013). For general discussion of sensitivity analyses in observational studies, see Chapter 4 of Rosenbaum (2002).

The main functions in the sensitivitymw package are senmw and senmwCI. Therefore, type help(senmw) and help(senmwCI).

Data set "mercury" is from NHANES and was used as an example in Rosenbaum (2014). Data set "erpcp" is from Werful et al. (1998) and was used as an example in Rosenbaum (2007). See the help files for these data sets for more information. The examples in senmw reproduce some calculations from Table 2 of Rosenbaum (2014), and the examples in senmwCI reproduce some of the calculations in Table 1 of Rosenbaum (2007).

Author(s)

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References


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erpcp

Description

Matched pairs of a welder and a control, matching for age and smoking. The values are DNA elution rates through polycarbonate filters with proteinase K (or erpcp). Data are originally from Werfel et al. (1998) and were used as an example in Rosenbaum (2007). Data are used to illustrate the senmwCI function in the sensitivitymw package.

Usage

data(erpcp)

Format

A data frame with 39 observations on the following 2 variables.

- **welder**: erpcp value for the welder
- **control**: erpcp value for the matched control

Source

Werfel et al. (1998).

References


Examples

data(erpcp)
Description
Data from NHANES. Matrix 397 x 3. n=397 treated people who ate at least 15 servings of fish or shellfish during the previous month are matched to two controls who ate at most one serving of fish or shellfish. The values in mercury record the level of methylmercury in blood in mu-g/dl. Column 1 is treated, columns 2 and 3 are controls. Specifically, column 2 describes an individual who ate no fish or shellfish in the previous month, while column 3 describes an individual who ate exactly one serving of fish or shellfish. Data are used to illustrate the sennmv function in the sensitivitymv package.

Usage
\texttt{data(mercury)}

Format
A data frame with 397 observations on the following 3 variables.
\begin{itemize}
\item \texttt{Treated} Mercury level for treated individual.
\item \texttt{Zero} Mercury level for a control who ate no fish/shellfish
\item \texttt{One} Mercury level for a control who ate one serving of fish/shellfish
\end{itemize}

Source

Examples
\texttt{data(mercury)}

mscorev
\textit{Computes the M-scores used by sennw.}

Description
Of limited interest to most users, mscorev computes the M-scores used by sennw for sensitivity analysis in observational studies using Huber-Maritz M-tests. As discussed in Rosenbaum (2014, section 4.1), the ranges of these M-scores within matched sets are ranked.

Usage
\texttt{mscorev(ymat, inner = 0, trim = 2.5, qu = 0.5, TonT = FALSE)}
multrnks

Arguments

- **ymat**: ymat is a matrix as described in the documentation for senmw or senmv.
- **inner**: inner is the parameter described in the documentation for senmw or senmv.
- **trim**: trim is the parameter described in the documentation for senmw or senmv.
- **qu**: qu is the lambda parameter described in the documentation for senmw or senmv.
- **TonT**: The TonT parameter is not used in the sensitivitymw package. It is included so that the same function mscorev works for both the sensitivitymw and sensitivitymv packages. TonT is relevant only when the number of controls varies from one set to another. See the help file for senmv in the sensitivitymv package for discussion of the TonT parameter.

Value

Generally, a matrix with the same dimensions as ymat containing the M-scores.

Note

The example uses the mercury data set. In particular, the first two rows of the mercury data were discussed in the final paragraph of Rosenbaum (2014, Section 2).

Author(s)

Paul R. Rosenbaum

References


Examples

```r
data(mercury)
mercury[1:2,]
mscorev(mercury,trim=3)[1:2,]
```

multrnks Approximate scores for ranks.

Description

Of limited interest to most users, this function is called by senmw. The function calculates the large sample approximation to a rank score transformation in Lemma 1, expression (9) of Rosenbaum (2011).

For numerical stability in large problems, the approximate rank score transformation in expression (9) of Rosenbaum (2011) is used in place of the exact rank score transformation in expression (8) of Rosenbaum (2011) and expression (5) of Rosenbaum (2014). Exact and approximate rank
scores yield similar bounds on P-values. The exact rank scores involve very large combinatorial coefficients when the same size is very large, whereas the nearly equivalent approximate scores do not.

Usage
multrnks(rk, m1 = 2, m2 = 2, m = 2)

Arguments
rk A vector of ranks that may include average ranks for ties.
m1 One of three rank score parameters in Rosenbaum (2011, 2014), specifically \( m_1 = \underline{m} \).
m2 One of three rank score parameters in Rosenbaum (2011, 2014), specifically \( m_2 = \overline{m} \).
m One of three rank score parameters in Rosenbaum (2011, 2014), specifically \( m = m \).

Value
Vector of length(rk) containing the scores for the ranks in rk.

Author(s)
Paul R. Rosenbaum

References


Examples
multrnks(1:10)
multrnks(1:10,m1=12,m2=20,m=20)

newurks Approximate scores for ranks of row ranges.

Description
Of limited interest to most users, this function is called by senmw. The function calculates the ranges for each row of smat, scores their ranks using the large sample approximation to a rank score transformation in Lemma 1, expression (9) of Rosenbaum (2011), as implemented in the function multrnks, and multiplies the rows by these rank scores. Additional detail is found in the help file for multrnks.
Usage

newurks(smat, m1 = 2, m2 = 2, m = 2)

Arguments

smat
  A matrix. When called by senmv, smat is a matrix produced by mscorev.

m1
  One of three rank score parameters in Rosenbaum (2011, 2014), specifically m1 = underline(m).

m2
  One of three rank score parameters in Rosenbaum (2011, 2014), specifically m2 = overline(m).

m
  One of three rank score parameters in Rosenbaum (2011, 2014), specifically m = m.

Value

The function calculates the ranges for each row of smat, scores the ranks of the ranges using the large sample approximation to a rank score transformation in Lemma 1, expression (9) of Rosenbaum (2011), as implemented in the function multrnks, and multiplies the rows of smat by these rank scores, returning the result.

Author(s)

Paul R. Rosenbaum

References


Examples

data(mercury)
head(newurks(mscorev(mercury)))

senmw

Sensitivity analysis in observational studies using weighted Huber-Maritz M-statistics.

Description

Computes the large sample approximation to the upper bound on the one sided P-value testing the null hypothesis of no treatment effect in a matched observational study with a fixed number of controls matched to each treated subject. Uses an unweighted or a weighted version of Huber-Maritz M-statistics as test statistics, with weights proposed by Rosenbaum (2014). Under many simple models for treatment effects, weighted M-statistics have superior design sensitivity compared to unweighted M-statistics.

For confidence intervals and point estimates, use the senmwCI function rather than senmw.
The `senmw` function requires every treated subject to have the same number of matched controls, e.g., 2 controls matched to each treated subject. If your study has variable numbers of controls matched to treated subjects, consider using `senmv` in the `sensitivitymv` package.

The `senmw` function offers a wide choice of test statistics obtained by varying its arguments. The default is an unweighted M-test using Huber’s psi-function, and it is equivalent to `method = "h"`. The default is safe to use in all contexts, but it is expected to report greater sensitivity to bias than other methods in many contexts: therefore, for matched pairs, `method="p"` is suggested; and for matched sets with 2 to 4 controls per set, `method="w"` is suggested. See below and the references for additional options and discussion.

The one-sided alternative hypothesis is that treatment increases the level of response. See the notes for discussion of other situations.

**Usage**

```r
senmw(y, gamma = 1, method = NULL, inner = 0, trim = 3,
      lambda = 1/2, tau = 0, m1=1, m2=1, m=1)
```

**Arguments**

- **y**
  - If `y` is an n by J matrix, then: (i) the rows are n matched sets, (ii) the first column is the treated response in a set, columns 2 to J contain the responses of controls in the same matched set. Every set must have J-1 controls, and NAs are not allowed in `y`. If `y` is a vector, then `y` is the vector of treated-minus-control pair differences in outcomes in n=length(`y`) matched pairs.

- **gamma**
  - `gamma` is the sensitivity parameter, `gamma=1` for a randomization test, `gamma>1` for sensitivity bounds. Use of `gamma<1` will generate an error. This parameter `gamma` is denoted by the upper case Greek letter `gamma` in the cited literature, for instance Rosenbaum (2007, 2014).

- **method**
  - If `method` is `NULL`, then the method is determined by the parameters, namely `inner`, `trim`, `lambda`, `m1`, `m2`, and `m`. If `method` is not `NULL`, then these parameters are set according to the selected method and stated values of the parameters are ignored. The default values of the parameters are equivalent to `method="h"`. (i) `method = "h"` (Huber, unweighted) is unweighted and sets `inner=0`, `trim=3`, `lambda = 1/2`, `m1=m2=m=1`. Method "h" is equivalent to the default settings. Its psi function levels off at 3 times the median (`lambda = 1/2`) of the absolute pair differences. The unweighted method h is often a good choice in small samples with few pairs or sets (say 20 sets). Unweighted method h is often a reasonable choice when the number of controls in each matched set is 6 or more. (Method "h" is almost the same as the default method for the `senmv` function in the `sensitivitymv` package, except: (a) `senmv` permits variable numbers of controls, (b) `senmv` uses `trim = 2.5`, not `trim = 3`.) (ii) `method = "w"` (weighted). Method "w" sets `inner=0`, `trim=3`, `lambda=1/2`, `m1=12`, `m2=20`, `m=20`. These weights are sturdy, all-purpose weights, often better than `method="h"` with 2-4 controls per matched set. Method="s" will often perform better for short-tailed Normal errors and method="l" will often perform better for long-tailed errors such as the t with 4 degrees of freedom. (iii) `method = "f"` (fixed choice weights). Method "f" sets `inner=0`, `trim=3`, `lambda=1/2`, `m1=14`, `m2=20`, `m=20`. Similar to method="w", method="f" uses all-purpose weights that were suggested, based on various calculations, in section 7.2 of Rosenbaum (2014) as the choice of a person who wants a "fixed choice" of weights.
(iv) method = "s" (weighted for short tails) has weights appropriate for short tailed distributions, such as the Normal distribution. Method "s" sets inner=0, trim=3, lambda=1/2, m1=16, m2=20, m=20.

(v) method = "l" (i.e., lower case letter L, weighted for long tails) has weights appropriate for long tailed distributions, such as the t-distribution with 4 degrees of freedom. It sets inner=0, trim=3, lambda=1/2, m1=12, m2=19, m=20. These weights redescend. The senmwCI function does not permit weights that redescend, and in particular does not permit method = "l".

(vi) method = "q" (Quade) ranks sets using ordinary ranks \((1, 2, ..., n)\) applied to ranges of M-scores within sets, in parallel with Quade (1979) and Tardiff (1987). It sets inner=0, trim=3, lambda=1/2, m1=2, m2=2, m=2.

(vii) method = "t" (permutational t-test) is unweighted and permutes the observations themselves without ranking or scoring. It sets inner=0, trim=Inf, lambda=1/2, m1=m2=m=1. The history of the permutational t-test is discussed in the help file for the senmv function in the sensitivitymv package. Method "t" is the permutation test that uses the treated-minus-control difference in means as a test statistic.

(viii) method = "p" (pairs) is primarily intended for matched pairs, with just one matched control. It is unweighted but uses inner trimming, and it sets inner = 1/2, trim =2, lambda = 1/2, m1=m2=m=1. This method performs well for matched pairs, as seen in the evaluations in Tables 3, 4 and 5 of Rosenbaum (2013) where it is psi_in with \(K=2\) for pairs.

inner

Inner trimming to increase design sensitivity. See the discussion of lambda. Use of inner<0 or inner>trim will generate an error. Inner trimming is discussed in Rosenbaum (2013).

trim

Outer trimming for resistance to outliers. Setting trim = Inf does no trimming. See the discussion of lambda.

lambda

Observations are scaled by the lambda quantile of the absolute pair differences, defaulting to the median of all paired absolute differences; see Rosenbaum (2007, section 4.2) for a precise definition in the case of multiple controls. If the lambda quantile of the absolute pair differences is 0, then scaling by 0 is impossible and an error may result; the solution is to increase lambda. If qu is the lambda quantile, absolute pair differences smaller than inner*qu receive weight 0, absolute pair differences larger than qu*trim receive weight 1, and between inner*qu and trim*qu weights increase linearly from 0 to 1. Use of lambda<=0 or lambda>1 will generate an error. If inner=0 and trim=Inf, then this results in the permutational t-test in which the observations themselves are permuted, and in this case lambda is not used. Taking lambda = .95 and trim = 1 is similar to trimming 5 percent of the pair differences.

tau

If tau=0, sennw tests the null hypothesis of no treatment effect. If tau is not 0, sennw tests the null hypothesis that the treatment effect is an additive shift of tau against the alternative that the effect is larger than tau.

m1

One of three parameters that determine the weights. See the discussion of m below.

m2

One of three parameters that determine the weights. See the discussion of m below.

m

One of three parameters that determine the weights. If in doubt about \((m1,m2,m)\), then sensible sturdy choices are method="p" for matched pairs and method="w" for sets with 2 to 4 controls. Properties of different weights \((m,m1,m2)\) are discussed in Rosenbaum (2014, sections 4 and 5). Details follow. The triple
(m,m1,m2) determines the weights, essentially as in expression (5) in Rosenbaum (2014) or expression (8) in Rosenbaum (2011) where they are called m (for m), underline(m) for m1, and overline(m) for m2. In particular, (m,m1,m2)=(1,1,1) is unweighted. (m,m1,m2)=(2,2,2) are (essentially) conventional ranks, as in method="q". Method="w" has (m,m1,m2)=(20,12,20) for increasing rank scores that ignore sets with little dispersion. If m>m2, as in (m,m1,m2)=(20,12,19) for method="l", the scores are redescending. The function semwCI for confidence intervals and estimates does not permit redescending weights, m2<m.

Value

<table>
<thead>
<tr>
<th>Value</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>pval</td>
<td>Approximate upper bound on the one-sided P-value.</td>
</tr>
<tr>
<td>deviate</td>
<td>Deviate that is compared to the upper tail of the standard Normal distribution to obtain the P-value.</td>
</tr>
<tr>
<td>statistic</td>
<td>Value of the test statistic.</td>
</tr>
<tr>
<td>expectation</td>
<td>Maximum null expectation of the test statistic for the given value of gamma.</td>
</tr>
<tr>
<td>variance</td>
<td>Among null distributions that yield the maximum expectation, variance is the maximum possible variance for the given value of gamma. See Rosenbaum (2007, Section 4; 2014) and Gastwirth, Krieger and Rosenbaum (2000).</td>
</tr>
</tbody>
</table>

Note

The one-sided alternative hypothesis is that treatment increases the level of response. Apply senmw to -y to test against the alternative that the treatment decreases the level of response. One way to perform a two sided test is to perform both tests and double the smaller P-value bound.

When a study has a fixed number of controls, the senmw function may be used in place of the senmv function in the sensitivitymv package, and senmw will be faster (because separable1k in sensitivitymw for fixed controls is faster than separable1v in sensitivitymv for variable controls). The senmw function may be used in conjunction with the following functions from the sensitivitymv package: amplify, truncatedP and truncatedPbg.

The example mercury is from Rosenbaum (2014) and compares the mercury levels in the blood of individuals who ate 15 or more servings of fish or shellfish in the previous month to people who ate at most one serving. Data are from NHANES.

Consistent with theory, in the example, the weighted M-statistics report greater insensitivity to unmeasured biases than do unweighted M-statistics. For example, unweighted method="h" and unweighted m1=1,m2=1,m=1 yield p-values above 0.05 for gamma=15, but weighted method="w" yields a p-value below 0.05 for gamma=19.

Row gamma=15 in Table 2 of Rosenbaum (2014) is reproduced by the example below with various values of m1<=m2<=m.

For numerical stability in large problems, senmw function uses approximate weights (expression (9) in Rosenbaum (2011)) rather than exact weights (expression (8) in Rosenbaum (2011) and expression (5) in Rosenbaum (2014)), so senmw produces ever so slightly different p-value bounds than reported in Table 2 of Rosenbaum (2014). If you are interested in this distinction between approximate and exact rank scores (it isn’t really very interesting), the calculation occurs in the multrnks function, so type help(multrnks).

Author(s)

Paul R. Rosenbaum
References

Main references:
Rosenbaum, P. R. (2014) Weighted M-statistics with superior design sensitivity in matched observational studies with multiple controls. Journal of the American Statistical Association, 2014. DOI: 10.1080/01621459.2013.879261 This paper is the main reference for weighted M-statistics and for the sensitivymw package. It evaluates weights controlled by m1, m2 and m.

Additional references:
Maritz, J. S. (1979) Exact robust confidence intervals for location. Biometrika 1979, 66, 163-166. Proposed exact permutation tests using m-statistics that Maritz inverts to obtain exact confidence limits. The subtle aspect is the scaling which must be invariant to treatment assignment under the null hypothesis, so it differs from the scaling used by Huber.
Rosenbaum, P. R. (2011) A new u-statistic with superior design sensitivity in observational studies. Biometrics 2011, 67, 1017-1021. Introduced the (m,m1,m2) weights in the context of signed rank statistics.

Examples

# Illustrates greater insensitivity reported when weights are use.
data(mercury)
senmw(mercury)
senmw(mercury,gamma=15)
senmw(mercury,method="h", gamma=15)
senmw(mercury,method="w", gamma=15)
senmw(mercury,method="w", gamma=19)
senmw(mercury,method="l", gamma=20)

# Reproduces Table 2, row gamma=15 of Rosenbaum (2014).
senmw(mercury, gamma=15,m1=1,m2=1,m=1)
senmw(mercury, gamma=15,m1=2,m2=2,m=2)
senmw(mercury, gamma=15,m1=12,m2=20,m=20)
senmwCI

Point estimate and confidence interval for sensitivity analysis in observational studies using weighted Huber-Maritz M-statistics.

Description

Obtains point estimates and confidence intervals by inverting the hypothesis test in senmw. For instance, the confidence interval is the set of hypotheses not rejected by the test. Estimates an additive treatment effect tau. In a sensitivity analysis with gamma>1, one obtains an interval of point estimates consistent with a bias of at most gamma, and an interval containing all of the confidence intervals that are consistent with a bias of at most gamma. Because senmwCI calls senmw many times, senmwCI is slower than senmw.

Usage

```
senmwCI(y, gamma = 1, method = NULL, inner = 0, trim = 3,
         lambda = 1/2, m1=1, m2=1, m=1, alpha=0.05,
         one.sided=TRUE, tol=NULL, interval=NULL, detail=FALSE)
```

Arguments

- **y**
  - If y is an n by J matrix, then: (i) the rows are n matched sets, (ii) the first column is the treated response in a set, columns 2 to J contain the responses of controls in the same matched set. Every set must have J-1 controls, and NAs are not allowed in y. If y is a vector, then y is the vector of treated-minus-control pair differences in outcomes in n=length(y) matched pairs.

- **gamma**
  - gamma is the sensitivity parameter, gamma=1 for a randomization test, gamma>1 for sensitivity bounds. Use of gamma<1 will generate an error. This parameter gamma is denoted by the upper case Greek letter gamma in the cited literature, for instance Rosenbaum (2007, 2014).

- **method**
  - The method argument is the same as for the senmw function. See the help file for senmw for more information. Method="l" is not available for confidence intervals.

- **inner**
  - Inner trimming to increase design sensitivity. See the help file for senmw for more information.

- **trim**
  - Outer trimming for resistance to outliers. See the help file for senmw for more information.

- **lambda**
  - Observations are scaled by the lambda quantile of the absolute pair differences. See the help file for senmw for more information.
senmwCI

m1 One of three parameters that determine the weights. See the discussion of m below.
m2 One of three parameters that determine the weights. See the discussion of m below.
m One of three parameters that determine the weights. See the help file for senmw for more information. m2<m is not available for confidence intervals.

alpha 1-alpha is the coverage of the confidence interval.
one.sided If TRUE, the confidence interval is one sided. If FALSE, the confidence interval is two-sided. The default is one-sided.
tol The senmwCI function calls the R function uniroot, and tol is the tol (or tolerance) parameter in that call. If tol=NULL, senmwCI picks a reasonable tolerance.
interval The senmwCI function calls the R function uniroot, and interval is the interval parameter in that call. If interval=NULL, senmwCI picks a reasonable interval.
detail If detail=FALSE, the interval of point estimates and the confidence interval are reported after rounding based on tol. If detail=TRUE, then the results are not rounded, the tol and interval are reported.

Value

PointEstimate An interval of point estimates allowing for a bias of gamma in treatment assignment. Rounded if detail=FALSE.
CI An confidence interval allowing for a bias of gamma in treatment assignment. Rounded if detail=FALSE.
search.interval If detail=TRUE, the interval of parameter values searched to find the estimates and confidence intervals.
tolerance If detail=TRUE, the tolerance used in solving for estimates and confidence intervals.

Note

senmwCI inverts a test to obtain confidence intervals and point estimates; so, it calls senmw many times, solving several equations, and senmwCI is much slower than a single call to senmw. senmwCI finds point estimates and confidence intervals by searching for a value of the parameter tau in "interval" determining the solution tau.hat to an estimating equation with an error of "tol" in solving the equation. If interval=NULL and tol=NULL, senmwCI tries to pick a reasonable finite interval and tol>0. If concerned about these "reasonable values", set detail=TRUE, make the interval longer, the tol smaller, and wait longer for program to run. As illustrated in the examples, if there is reason for concern, the solutions produced by senmwCI can be checked by running senmw with tau set to the endpoints of the various intervals.

Unlike senmw, senmwCI does not permit redescending rank scores, m2<m or method="l".

Author(s)

Paul R. Rosenbaum
References

Main references:


Examples

data(mercury)
senmwCI(mercury,gamma=2,method="w",one.sided=FALSE,detail=TRUE)

#The following example reproduces part of Table 1 in Rosenbaum (2007).
#In particular, the one-sided .95 confidence interval is tau >= 0.1812,
#and the P-value testing tau=0.1812 is 0.05.
#Similarly, the test statistic equals its null expectation at tau=0.3403,
#and when evaluated at -yrpcp the same thing happens at tau=-0.6666.
data(erpcp)
senmw(erpcp,gamma=2,trim=1,m1=1,m2=1,m=1)
senmw(erpcp,gamma=2,trim=1,m1=1,m2=1,m=1,tau=0.1812)
senmw(erpcp,gamma=2,trim=1,m1=1,m2=1,m=1,tau=0.3403)
senmw(-erpcp,gamma=2,trim=1,m1=1,m2=1,m=1,tau=-0.6666)

#This example illustrates the relationship between senmwCI and senmw.
#Note that the endpoints from senmwCI are tested by senmw.
#Also for illustration, the search interval in this case is specified as from 0 to 5.
senmwCI(mercury,gamma=2,method="w",detail=TRUE,interval=c(0,5),one.sided=FALSE)
senmw(mercury,gamma=2,method="w",tau=2.03135)
senmw(-mercury,gamma=2,method="w",tau=-3.166710)
senmw(mercury,gamma=2,method="w",tau=1.775008)
senmw(-mercury,gamma=2,method="w",tau=-3.605779)

separable1k

Asymptotic separable calculations internal to other functions.

Description

This general purpose function is internal to other functions, such as senmw in the sensitivitymw package. The function performs the asymptotic separable calculations described in Gastwirth, Krieger and Rosenbaum (2000), as used in section 4 of Rosenbaum (2007). The example is equivalent to senmw(mercury,gamma=2,method="t"). The function separable1k in the sensitivitymw package and the function separable1v in sensitivitymv package should give the same answer when applied to matched sets with a fixed number of controls; however, separable1k is faster as a consequence of not allowing variable numbers of controls. Speed is important when senmwCI calls senmw repeatedly to obtain a confidence set by inverting a test.

Usage

separable1k(ymat, gamma = 1)
Arguments

ymat  ymat is a matrix whose rows are matched sets and whose columns are matched individuals. The first column describes treated individuals. Other columns describe controls. Every set must have 1 treated subject and \( \text{dim}(ymat)[2]-1 \) controls. NAs are not allowed. For variable numbers of controls, see the separable1v function in the sensitivitymv package.

gamma  gamma is the value of the sensitivity parameter; see the documentation for the senmw function in the sensitivitymv package. One should use a value of gamma >= 1.

Value

pval  Approximate upper bound on the one-sided P-value.

deviate  Deviate that is compared to the upper tail of the standard Normal distribution to obtain the P-value.

statistic  Value of the test statistic.

expectation  Maximum null expectation of the test statistic for the given value of gamma.

variance  Among null distributions that yield the maximum expectation, variance is the maximum possible variance for the given value of gamma. See Rosenbaum (2007, Section 4) and Gastwirth, Krieger and Rosenbaum (2000).

Author(s)

Paul R. Rosenbaum

References


Examples

data(mercury)
separable1k(mercury,gamma=2)
senmw(mercury,method="t",gamma=2)
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