

Package ‘sensitivymw’

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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.

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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
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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 `tuncatedPbg` 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, γ , 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)

Paul Rosenbaum

Maintainer: Paul R. Rosenbaum <rosenbaum@wharton.upenn.edu>

References

- Huber, P. (1981) *Robust Statistics*. New York: Wiley, 1981.
- Maritz, J. S. (1979) Exact robust confidence intervals for location. *Biometrika* 1979, 66, 163-166.
- Rosenbaum, P. R. (2002) *Observational Studies* (2nd edition). New York: Springer.
- Rosenbaum, P. R. (2007) Sensitivity analysis for m-estimates, tests and confidence intervals in matched observational studies. *Biometrics*, 2007, 63, 456-464.
- Rosenbaum, P. R. (2013) Impact of multiple matched controls on design sensitivity in observational studies. *Biometrics*, 2013, 69, 118-127.
- 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
- Werfel, U., Langen, V., Eickhoff, I. et al. Elevated DNA strand breakage frequencies in lymphocytes of welders exposed to chromium and nickel. *Carcinogenesis*, 1998, 19, 413-418.

erpcp

DNA Damage Among Welders

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 `sensitivymw` 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

Rosenbaum, P. R. Sensitivity analysis for m-estimates, tests and confidence intervals in matched observational studies. *Biometrics*, 2007, 63, 456-464.

Werful, U., Langen, V., Eickhoff, I. et al. Elevated DNA strand breakage frequencies in lymphocytes of welders exposed to chromium and nickel. *Carcinogenesis*, 1998, 19, 413-418.

Examples

```
data(erpccp)
```

```
mercury
```

```
NHANES Mercury/Fish Data
```

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 $\mu\text{-g/dl}$. 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 `senmv` function in the `sensitivitymv` package.

Usage

```
data(mercury)
```

Format

A data frame with 397 observations on the following 3 variables.

Treated Mercury level for treated individual.

Zero Mercury level for a control who ate no fish/shellfish

One Mercury level for a control who ate one serving of fish/shellfish

Source

Data are originally from NHANES 2009-2010.

Data were used as an example in: 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

Examples

```
data(mercury)
```

mscorev	<i>Computes the M-scores used by senmw.</i>
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Description

Of limited interest to most users, `mscorev` computes the M-scores used by `senmw` 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

```
mscorev(yamat, inner = 0, trim = 2.5, qu = 0.5, TonT = FALSE)
```

Arguments

<code>yamat</code>	<code>yamat</code> is a matrix as described in the documentation for <code>senmw</code> or <code>senmv</code> .
<code>inner</code>	<code>inner</code> is the parameter described in the documentation for <code>senmw</code> or <code>senmv</code> .
<code>trim</code>	<code>trim</code> is the parameter described in the documentation for <code>senmw</code> or <code>senmv</code> .
<code>qu</code>	<code>qu</code> is the lambda parameter described in the documentation for <code>senmw</code> or <code>senmv</code> .
<code>TonT</code>	The <code>TonT</code> parameter is not used in the <code>sensitivymw</code> package. It is included so that the same function <code>mscorev</code> works for both the <code>sensitivymw</code> and <code>senstivymv</code> packages. <code>TonT</code> is relevant only when the number of controls varies from one set to another. See the help file for <code>senmv</code> in the <code>sensitivymv</code> package for discussion of the <code>TonT</code> parameter.

Value

Generally, a matrix with the same dimensions as `yamat` 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

Rosenbaum, P. R. (2007) Sensitivity analysis for m-estimates, tests and confidence intervals in matched observational studies. *Biometrics*, 2007, 63, 456-464.

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

Examples

```
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 .
m2	One of three rank score parameters in Rosenbaum (2011, 2014), specifically m_2 .
m	One of three rank score parameters in Rosenbaum (2011, 2014), specifically m .

Value

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

Author(s)

Paul R. Rosenbaum

References

Rosenbaum, P. R. (2011) A new u-statistic with superior design sensitivity in matched observational studies. *Biometrics* 67, 1017-1027.

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

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

<code>smat</code>	A matrix. When called by <code>senmv</code> , <code>smat</code> is a matrix produced by <code>mscorev</code> .
<code>m1</code>	One of three rank score parameters in Rosenbaum (2011, 2014), specifically $m_1 = \underline{m}$.
<code>m2</code>	One of three rank score parameters in Rosenbaum (2011, 2014), specifically $m_2 = \overline{m}$.
<code>m</code>	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

Rosenbaum, P. R. (2011) A new u-statistic with superior design sensitivity in matched observational studies. *Biometrics* 67, 1017-1027.

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

Examples

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

senmw	<i>Sensitivity analysis in observational studies using weighted Huber-Maritz M-statistics.</i>
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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

```
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 $n=\text{length}(y)$ 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,

$\lambda=1/2$, $m_1=m_2=m=1$. The history of the permutational t-test is discussed in the help file for the `senmv` function in the `sensitivymv` 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 $\text{inner} = 1/2$, $\text{trim} = 2$, $\lambda = 1/2$, $m_1=m_2=m=1$. 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.

<code>inner</code>	Inner trimming to increase design sensitivity. See the discussion of λ . Use of $\text{inner}<0$ or $\text{inner}>\text{trim}$ will generate an error. Inner trimming is discussed in Rosenbaum (2013).
<code>trim</code>	Outer trimming for resistance to outliers. Setting $\text{trim} = \text{Inf}$ does no trimming. See the discussion of λ .
<code>lambda</code>	Observations are scaled by the λ 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 λ quantile of the absolute pair differences is 0, then scaling by 0 is impossible and an error may result; the solution is to increase λ . If q_λ is the λ quantile, absolute pair differences smaller than $\text{inner}*q_\lambda$ receive weight 0, absolute pair differences larger than $q_\lambda*\text{trim}$ receive weight 1, and between $\text{inner}*q_\lambda$ and $\text{trim}*q_\lambda$ weights increase linearly from 0 to 1. Use of $\lambda\leq 0$ or $\lambda\geq 1$ will generate an error. If $\text{inner}=0$ and $\text{trim}=\text{Inf}$, then this results in the permutational t-test in which the observations themselves are permuted, and in this case λ is not used. Taking $\lambda = .95$ and $\text{trim} = 1$ is similar to trimming 5 percent of the pair differences.
<code>tau</code>	If $\text{tau}=0$, <code>senmw</code> tests the null hypothesis of no treatment effect. If tau is not 0, <code>senmw</code> tests the null hypothesis that the treatment effect is an additive shift of tau against the alternative that the effect is larger than tau .
<code>m1</code>	One of three parameters that determine the weights. See the discussion of m below.
<code>m2</code>	One of three parameters that determine the weights. See the discussion of m below.
<code>m</code>	One of three parameters that determine the weights. If in doubt about (m_1, m_2, m) , then sensible sturdy choices are <code>method="p"</code> for matched pairs and <code>method="w"</code> for sets with 2 to 4 controls. Properties of different weights (m, m_1, m_2) are discussed in Rosenbaum (2014, sections 4 and 5). Details follow. The triple (m, m_1, m_2) 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 m_1 , and \overline{m} for m_2 . In particular, $(m, m_1, m_2)=(1, 1, 1)$ is unweighted. $(m, m_1, m_2)=(2, 2, 2)$ are (essentially) conventional ranks, as in <code>method="q"</code> . <code>Method="w"</code> has $(m, m_1, m_2)=(20, 12, 20)$ for increasing rank scores that ignore sets with little dispersion. If $m>m_2$, as in $(m, m_1, m_2)=(20, 12, 19)$ for <code>method="l"</code> , the scores are redescending. The function <code>semwCI</code> for confidence intervals and estimates does not permit redescending weights, $m_2<m$.

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; 2014) and Gastwirth, Krieger and Rosenbaum (2000).

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. (2007) Sensitivity analysis for m-estimates, tests and confidence intervals in matched observational studies. *Biometrics*, 2007, 63, 456-464. Discusses the unweighted statistics.

Rosenbaum, P. R. (2013) Impact of multiple matched controls on design sensitivity in observational studies. *Biometrics*, 2013, 69, 118-127. Evaluates the performance of the methods in the 2007 paper above. In particular, this paper compares methods h, p and t.

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:

Huber, P. (1981) *Robust Statistics*. New York: Wiley, 1981. Huber first proposed the use of m-statistics in 1964 in a paper in the *Annals*.

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.

Gastwirth, J. L., Krieger, A. M., and Rosenbaum, P. R. (2000) Asymptotic separability in sensitivity analysis. *Journal of the Royal Statistical Society B* 2000, 62, 545-556. Provides a general large sample approximation when matching with multiple controls, as used in Rosenbaum (2007, Section 4).

Quade, D. (1979) Using weighted rankings in the analysis of complete blocks with additive block effects. *Journal of the American Statistical Association* 1979, 74, 680-683. Weights within block ranks by ranks of within block ranges to increase efficiency in randomized experiments.

Rosenbaum, P. R. (2010) *Design of Observational Studies*. New York: Springer 2010. Section 2.9 contains an elementary textbook discussion of Maritz's permutation distribution for m-statistics.

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.

Tardiff, S. (1987) Efficiency and optimality results for tests based on weighted rankings. *Journal of the American Statistical Association* 1987, 82, 637-644. Extends the study of Quade's (1979) method.

Examples

#Illustrates greater insensitivity reported when weights are use.

```
data(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)
senmw(mercury, gamma=15, m1=14, m2=20, m=20)
senmw(mercury, gamma=15, m1=16, m2=20, m=20)
```

```

senmw(mercury,gamma=15,m1=12,m2=19,m=20)
senmw(mercury,gamma=15,m1=14,m2=19,m=20)
senmw(mercury,gamma=15,m1=16,m2=19,m=20)

#Reproduces part of Table 1 in Rosenbaum (2007). For other parts of this table, see help(senmwCI).
data(erpcp)
senmw(erpcp,gamma=2,trim=1,inner=0,m1=1,m2=1,m=1)
senmw(erpcp,gamma=3,trim=1,inner=0,m1=1,m2=1,m=1)
senmw(erpcp,gamma=4,trim=1,inner=0,m1=1,m2=1,m=1)

```

senmwCI	<i>Point estimate and confidence interval for sensitivity analysis in observational studies using weighted Huber-Maritz M-statistics.</i>
---------	---

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 τ . In a sensitivity analysis with $\gamma > 1$, one obtains an interval of point estimates consistent with a bias of at most γ , and an interval containing all of the confidence intervals that are consistent with a bias of at most γ . 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

<code>y</code>	If <code>y</code> 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 <code>y</code> . If <code>y</code> is a vector, then <code>y</code> is the vector of treated-minus-control pair differences in outcomes in $n=\text{length}(y)$ matched pairs.
<code>gamma</code>	<code>gamma</code> is the sensitivity parameter, <code>gamma=1</code> for a randomization test, <code>gamma>1</code> for sensitivity bounds. Use of <code>gamma<1</code> will generate an error. This parameter <code>gamma</code> is denoted by the upper case Greek letter <code>gamma</code> in the cited literature, for instance Rosenbaum (2007, 2014).
<code>method</code>	The method argument is the same as for the <code>senmw</code> function. See the help file for <code>senmw</code> for more information. <code>Method="l"</code> is not available for confidence intervals.
<code>inner</code>	Inner trimming to increase design sensitivity. See the help file for <code>senmw</code> for more information.
<code>trim</code>	Outer trimming for resistance to outliers. See the help file for <code>senmw</code> for more information.

<code>lambda</code>	Observations are scaled by the lambda quantile of the absolute pair differences. See the help file for <code>senmw</code> for more information.
<code>m1</code>	One of three parameters that determine the weights. See the discussion of <code>m</code> below.
<code>m2</code>	One of three parameters that determine the weights. See the discussion of <code>m</code> below.
<code>m</code>	One of three parameters that determine the weights. See the help file for <code>senmw</code> for more information. <code>m2 < m</code> is not available for confidence intervals.
<code>alpha</code>	<code>1-alpha</code> is the coverage of the confidence interval.
<code>one.sided</code>	If <code>TRUE</code> , the confidence interval is one sided. If <code>FALSE</code> , the confidence interval is two-sided. The default is one-sided.
<code>tol</code>	The <code>senmwCI</code> function calls the R function <code>uniroot</code> , and <code>tol</code> is the <code>tol</code> (or tolerance) parameter in that call. If <code>tol=NULL</code> , <code>senmwCI</code> picks a reasonable tolerance.
<code>interval</code>	The <code>senmwCI</code> function calls the R function <code>uniroot</code> , and <code>interval</code> is the interval parameter in that call. If <code>interval=NULL</code> , <code>senmwCI</code> picks a reasonable interval.
<code>detail</code>	If <code>detail=FALSE</code> , the interval of point estimates and the confidence interval are reported after rounding based on <code>tol</code> . If <code>detail=TRUE</code> , then the results are not rounded, the <code>tol</code> and <code>interval</code> are reported.

Value

<code>PointEstimate</code>	An interval of point estimates allowing for a bias of gamma in treatment assignment. Rounded if <code>detail=FALSE</code> .
<code>CI</code>	An confidence interval allowing for a bias of gamma in treatment assignment. Rounded if <code>detail=FALSE</code> .
<code>search.interval</code>	If <code>detail=TRUE</code> , the interval of parameter values searched to find the estimates and confidence intervals.
<code>tolerance</code>	If <code>detail=TRUE</code> , 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 re-descending rank scores, `m2 < m` or `method="I"`.

Author(s)

Paul R. Rosenbaum

References

Main references:

Rosenbaum, P. R. (2007) Sensitivity analysis for m-estimates, tests and confidence intervals in matched observational studies. *Biometrics*, 2007, 63, 456-464. Discusses the unweighted statistics.

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 sensitivitymw package.

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(erpccp)
senmwCI(erpccp, gamma=2, trim=1, m1=1, m2=1, m=1)
senmw(erpccp, gamma=2, trim=1, m1=1, m2=1, m=1, tau=0.1812)
senmw(erpccp, gamma=2, trim=1, m1=1, m2=1, m=1, tau=0.3403)
senmw(-erpccp, 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

<code>ymat</code>	<code>ymat</code> 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 <code>dim(ymat)[2]-1</code> controls. NAs are not allowed. For variable numbers of controls, see the <code>separable1v</code> function in the <code>sensitivitymv</code> package.
<code>gamma</code>	<code>gamma</code> is the value of the sensitivity parameter; see the documentation for the <code>senmw</code> function in the <code>sensitivitymw</code> package. One should use a value of <code>gamma</code> ≥ 1 .

Value

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

Author(s)

Paul R. Rosenbaum

References

Gastwirth, J. L., Krieger, A. M., and Rosenbaum, P. R. (2000) Asymptotic separability in sensitivity analysis. *Journal of the Royal Statistical Society B* 2000, 62, 545-556.

Rosenbaum, P. R. (2007) Sensitivity analysis for m-estimates, tests and confidence intervals in matched observational studies. *Biometrics*, 2007, 63, 456-464.

Examples

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


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