

# Package ‘sensitivityfull’

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**Type** Package

**Title** Sensitivity Analysis for Full Matching in Observational Studies

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**Description** Sensitivity to unmeasured biases in an observational study that is a full match. Function `senfm()` performs tests and function `senfmCI()` creates confidence intervals. The method uses Huber's M-statistics, including least squares, and is described in Rosenbaum (2007, Biometrics) <DOI:10.1111/j.1541-0420.2006.00717.x>.

**Imports** stats

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mscoref *Computes M-scores for a Full Match*

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### Description

Of limited interest to most users, mscoref() computes the scores that form the basis for the hypothesis test performed by senfm.

### Usage

```
mscoref(ymat, treated1, inner = 0, trim = 3, qu = 0.5)
```

### Arguments

ymat	If there are I matched sets and the largest matched set contains J individuals, then y is an I by J matrix with one row for each matched set. If matched set i contains one treated individual and k controls, where k is at least 1 and at most J-1, then y[i,1] is the treated individual's response, y[i,2],...,y[i,k+1] are the responses of the k controls, and y[i,k+2],...,y[i,J] are equal to NA. If matched set i contains one control and k>1 treated individuals, then y[i,1] is the control's response, y[i,2],...,y[i,k+1] are the responses of the k treated individuals, and y[i,k+2],...,y[i,J] are equal to NA.
treated1	The vector treated1 is a logical vector of length I, where treated1[i]=TRUE if there is one treated subject in matched set i and treated1[i]=FALSE if there is more than one treated subject in matched set i.
inner	inner and trim together define the $\psi$ -function for the M-statistic. The default values yield a version of Huber's $\psi$ -function, while setting inner = 0 and trim = Inf uses the mean within each matched set. The $\psi$ -function is an odd function, so $\psi(w) = -\psi(-w)$ . For $w \geq 0$ , the $\psi$ -function is $\psi(w) = 0$ for $0 \leq w \leq \text{inner}$ , is $\psi(w) = \text{trim}$ for $w \geq \text{trim}$ , and rises linearly from 0 to trim for $\text{inner} < w < \text{trim}$ .
trim	inner and trim together define the $\psi$ -function for the M-statistic. See inner.
qu	Before applying the $\psi$ -function to treated-minus-control differences, the differences are scaled by dividing by the qu quantile of all within set absolute differences. Typically, qu = 1/2 for the median. The value of qu has no effect if trim=0 and inner=Inf. See Maritz (1979) for the paired case and Rosenbaum (2007) for matched sets.

### Value

Returns a matrix with the same dimensions as ymat and the same pattern of NAs. The returned value in position [i,j] compares ymat[i,j] to the other observations in row i of ymat, scoring the differences using  $\psi$ -function, totalling them, and applying a weight. Matched sets of unequal size are weighted using weights that would be efficient in a randomization test under a simple model with additive set and treatment effects and errors with constant variance. See Rosenbaum (2007, section 4.2).

When a matched set contains one control and several treated subjects, this is reflected in the returned scores by a sign reversal.

### Author(s)

Paul R. Rosenbaum

### References

- Huber, P. (1981) *Robust Statistics*. New York: John Wiley.
- Maritz, J. S. (1979). A note on exact robust confidence intervals for location. *Biometrika* 66 163–166.
- Rosenbaum, P. R. (2007). Sensitivity analysis for m-estimates, tests and confidence intervals in matched observational studies. *Biometrics* 63 456–64. (R package *sensitivitymv*)
- Rosenbaum, P. R. (2010). *Design of Observational Studies*. New York: Springer. Table 2.12, page 60, illustrates the calculations for the simple case of matched pairs.
- Rosenbaum, P. R. (2013). Impact of multiple matched controls on design sensitivity in observational studies. *Biometrics* 69 118–127. (Introduces inner trimming to increase design sensitivity.)

### Examples

```
# The artificial example that follows has I=9
# matched sets. The first 3 sets have one treated
# individual and two controls with treated subjects
# in column 1. The next 3 sets are
# matched pairs, with treated subjects in column 1.
# The next 3 sets have one control and two treated
# subjects, with the control in column 1. Simulated
# from a Normal distribution with an additive effect
# of tau=1.

y<-c(2.2, 1.4, 1.6, 2.4, 0.7, 1.3, 1.2, 0.6, 0.3,
0.5, -0.1, -1.3, -0.3, 0.1, 0.4, 3.0, 1.1, 1.4, -0.8,
0.1, 0.8, NA, NA, NA, 1.1, 0.5, 1.8)
y<-matrix(y,9,3)
treated1<-c(rep(TRUE,6),rep(FALSE,3))

mscoref(y,treated1) # Huber scores
mscoref(y,treated1,inner=0.5,trim=3) #inner trimmed scores
mscoref(y,treated1,qu=.9,trim=1) #trimming the outer 10 percent

# For an additional example, install and load package sensitivitymv
# The following example is a match with variable controls.
# Both mscorev() (in sensitivitymv) and mscoref() (in sensitivityfull)
# reproduce the example in Rosenbaum (2007, Table 3).
# data(tbmetaphase)
# mscorev(tbmetaphase,trim=1)
# mscoref(tbmetaphase,rep(TRUE,15),trim=1)
```

senfm

*Sensitivity Analysis for a Full Match in an Observational Study.***Description**

In a full match, each matched set contains either one treated individual and one or more controls or one control and one or more treated individuals. Uses Huber's M-statistic as the basis for the test, for instance, a mean. Performs either a randomization test or an analysis of sensitivity to departures from random assignment. For confidence intervals, use function `senfmCI()`.

**Usage**

```
senfm(y, treated1, gamma = 1, inner = 0, trim = 3, lambda = 1/2,
      tau = 0, alternative="greater")
```

**Arguments**

- y** If there are  $I$  matched sets and the largest matched set contains  $J$  individuals, then  $y$  is an  $I$  by  $J$  matrix with one row for each matched set. If matched set  $i$  contains one treated individual and  $k$  controls, where  $k$  is at least 1 and at most  $J-1$ , then  $y[i,1]$  is the treated individual's response,  $y[i,2], \dots, y[i,k+1]$  are the responses of the  $k$  controls, and  $y[i,k+2], \dots, y[i,J]$  are equal to NA. If matched set  $i$  contains one control and  $k > 1$  treated individuals, then  $y[i,1]$  is the control's response,  $y[i,2], \dots, y[i,k+1]$  are the responses of the  $k$  treated individuals, and  $y[i,k+2], \dots, y[i,J]$  are equal to NA. Although  $y$  can contain NA's,  $y[i,1]$  and  $y[i,2]$  must not be NA for every  $i$ .
- treated1** The vector `treated1` is a logical vector of length  $I$ , where `treated1[i]=TRUE` if there is one treated subject in matched set  $i$  and `treated1[i]=FALSE` if there is more than one treated subject in matched set  $i$ .
- gamma**  $\gamma$  is the sensitivity parameter  $\Gamma$ , where  $\Gamma \geq 1$ . Setting  $\Gamma = 1$  is equivalent to assuming ignorable treatment assignment given the matched sets, and it performs a within-set randomization test.
- inner** `inner` and `trim` together define the  $\psi$ -function for the M-statistic. The default values yield a version of Huber's  $\psi$ -function, while setting `inner = 0` and `trim = Inf` uses the mean within each matched set. The  $\psi$ -function is an odd function, so  $\psi(w) = -\psi(-w)$ . For  $w \geq 0$ , the  $\psi$ -function is  $\psi(w) = 0$  for  $0 \leq w \leq \text{inner}$ , is  $\psi(w) = \text{trim}$  for  $w \geq \text{trim}$ , and rises linearly from 0 to `trim` for  $\text{inner} < w < \text{trim}$ . An error will result unless  $0 \leq \text{inner} \leq \text{trim}$ . Taking `trim < Inf` limits the influence of outliers; see Huber (1981). Taking `inner > 0` often increases design sensitivity; see Rosenbaum (2013).
- trim** `inner` and `trim` together define the  $\psi$ -function for the M-statistic. See `inner`.
- lambda** Before applying the  $\psi$ -function to treated-minus-control differences, the differences are scaled by dividing by the `lambda` quantile of all within set absolute differences. Typically, `lambda = 1/2` for the median. The value of `lambda` has

	no effect if trim=0 and inner=Inf. See Maritz (1979) for the paired case and Rosenbaum (2007) for matched sets. An error will result unless $0 < \lambda < 1$ .
tau	The null hypothesis asserts that the treatment has an additive effect, tau. By default, tau=0, so by default the null hypothesis is Fisher's sharp null hypothesis of no treatment effect.
alternative	If alternative="greater", the null hypothesis of a treatment effect of tau is tested against the alternative of a treatment effect larger than tau. If alternative="less", the null hypothesis of a treatment effect of tau is tested against the alternative of a treatment effect smaller than tau. In particular, alternative="less" is equivalent to: (i) alternative="greater", (ii) y replaced by -y, and (iii) tau replaced by -tau. See the note for discussion of two-sided sensitivity analyses.

### Details

For the given  $\Gamma$ , senfm() computes the upper bound on the 1-sided P-value testing the null hypothesis of an additive treatment effect tau against the alternative hypothesis of a treatment effect larger than tau. By default, senfm() tests the null hypothesis of no treatment effect against the alternative of a positive treatment effect. The P-value is an approximate P-value based on a Normal approximation to the null distribution; see Rosenbaum (2007).

Matched sets of unequal size are weighted using weights that would be efficient in a randomization test under a simple model with additive set and treatment effects and errors with constant variance; see Rosenbaum (2007).

The upper bound on the P-value is based on the separable approximation described in Gastwirth, Krieger and Rosenbaum (2000); see also Rosenbaum (2007).

### Value

pval	The upper bound on the 1-sided P-value.
deviate	The deviate that was compared to the Normal distribution to produce pval.
statistic	The value of the M-statistic.
expectation	The maximum expectation of the M-statistic for the given $\Gamma$ .
variance	The maximum variance of the M-statistic among treatment assignments that achieve the maximum expectation. Part of the separable approximation.

### Note

The function senfm() performs 1-sided tests. One approach to a 2-sided,  $\alpha$ -level test does both 1-sided tests at level  $\alpha/2$ , and rejects the null hypothesis if either 1-sided test rejects. Equivalently, a bound on the two sided P-value is the smaller of 1 and twice the smaller of the two 1-sided P-values. This approach views a 2-sided test as two 1-sided tests with a Bonferroni correction; see Cox (1977, Section 4.2). In all cases, this approach is valid large sample test: a true null hypothesis is falsely rejected with probability at most  $\alpha$  if the bias in treatment assignment is at most  $\Gamma$ ; so, this procedure is entirely safe to use. For a randomization test,  $\Gamma = 1$ , this Bonferroni procedure is not typically conservative. For large  $\Gamma$ , this Bonferroni procedure tends to be somewhat conservative.

Related packages are sensitivitymv, sensitivitymw and sensitivity2x2k. sensitivitymv is for matched sets with one treated subject and a variable number of controls. sensitivitymw is for matched sets

with one treated subject and a fixed number of controls, including matched pairs. For their special cases, `sensitivitymv` and `sensitivitymw` contain additional features not available in `sensitivityfull`. `sensitivitymw` is faster and computes confidence intervals and point estimates. `sensitivitymv` also implements methods from Rosenbaum (2014). `sensitivity2x2xk` is for 2x2xk contingency tables, treatment x outcome x covariates; see Rosenbaum and Small (2016).

Rosenbaum (2007) describes the method for matching with variable numbers of controls, but only very minor adjustments are required for full matching, and `senfm()` implements these adjustments.

### Author(s)

Paul R. Rosenbaum.

### References

- Cox, D. R. (1977). The role of significance tests (with Discussion). *Scand. J. Statist.* 4, 49-70.
- Hansen, B. B. (2007). `Optmatch`. *R News* 7 18-24. (R package `optmatch`) (`Optmatch` can create an optimal full match.)
- Hansen, B. B. and Klopfer, S. O. (2006). Optimal full matching and related designs via network flows. *J. Comput. Graph. Statist.* 15 609-627. (R package `optmatch`)
- Huber, P. (1981) *Robust Statistics*. New York: John Wiley. (M-estimates based on M-statistics.)
- Maritz, J. S. (1979). A note on exact robust confidence intervals for location. *Biometrika* 66 163–166. (Introduces exact permutation tests based on M-statistics by redefining the scaling parameter.)
- Rosenbaum, P. R. (1991). A characterization of optimal designs for observational studies. *J. Roy. Statist. Soc. B* 53 597-610. (Introduces full matching.)
- Rosenbaum, P. R. (2007). Sensitivity analysis for m-estimates, tests and confidence intervals in matched observational studies. *Biometrics* 63 456-64. (R package `sensitivitymv`)
- Rosenbaum, P. R. (2013). Impact of multiple matched controls on design sensitivity in observational studies. *Biometrics* 69 118-127. (Introduces inner trimming.)
- Rosenbaum, P. R. (2014). Weighted M-statistics with superior design sensitivity in matched observational studies with multiple controls. *J. Am. Statist. Assoc.* 109 1145-1158. (R package `sensitivitymw`)
- Rosenbaum, P. R. and Small, D. S. (2016). An adaptive Mantel-Haenszel test for sensitivity analysis in observational studies. *Biometrics*, to appear.

### Examples

```
# The artificial example that follows has I=9
# matched sets. The first 3 sets have one treated
# individual and two controls with treated subjects
# in column 1. The next 3 sets are
# matched pairs, with treated subjects in column 1.
# The next 3 sets have one control and two treated
# subjects, with the control in column 1. Simulated
# from a Normal distribution with an additive effect
# of tau=1.

y<-c(2.2, 1.4, 1.6, 2.4, 0.7, 1.3, 1.2, 0.6, 0.3,
```

```

0.5, -0.1, -1.3, -0.3, 0.1, 0.4, 3.0, 1.1, 1.4, -0.8,
0.1, 0.8, NA, NA, NA, 1.1, 0.5, 1.8)
y<-matrix(y,9,3)
treated1<-c(rep(TRUE,6),rep(FALSE,3))

#Randomization test of no effect, Huber scores:
senfm(y,treated1)

#Sensitivity analysis, Huber scores:
senfm(y,treated1,gamma=2)

#Randomization test of tau=1 vs tau>1
senfm(y,treated1,tau=1)

#Randomization test of tau=1 vs tau<1
senfm(y,treated1,tau=1,alternative="less")

#Same randomization test of tau=1 vs tau<1
senfm(-y,treated1,tau=-1)

#Sensitivity analysis testing tau=1 at gamma=2
senfm(y,treated1,tau=1,gamma=2,alternative="greater")
senfm(y,treated1,tau=1,gamma=2,alternative="less")

# For an additional example, install and load package sensitivitymv
# The following example is a match with variable controls.
# So this example has one treated subject per matched set.
# Both mscorev (in sensitivitymv) and mscoref (in sensitivityfull)
# reproduce parts of the example in Rosenbaum (2007, Section 4).
# data(tbmetaphase)
# senmv(tbmetaphase,gamma=2,trim=1)
# senfm(tbmetaphase,rep(TRUE,15),gamma=2,trim=1)
# senmv(tbmetaphase,gamma=2,trim=1,tau=0.94)
# senfm(tbmetaphase,rep(TRUE,15),gamma=2,trim=1,tau=.94)
# senmv(tbmetaphase,gamma=2,trim=1,tau=0.945)
# senfm(tbmetaphase,rep(TRUE,15),gamma=2,trim=1,tau=.945)
# mscoref(tbmetaphase,rep(TRUE,15),trim=1)

```

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senfmCI

*Sensitivity Analysis for a Confidence Interval in a Full Match.*


---

## Description

In a full match, each matched set contains either one treated individual and one or more controls or one control and one or more treated individuals. Uses Huber's M-statistic as the basis for a confidence interval for an additive constant treatment effect,  $\tau$ . Performs either a randomization inference or an analysis of sensitivity to departures from random assignment. The confidence interval inverts the test in the function `senfm()` in the `sensitivityfull` package.

**Usage**

```
senfmCI(y, treated1, gamma=1, inner=0, trim=3, lambda=1/2,
        alpha=0.05, twosided=TRUE, upper=TRUE)
```

**Arguments**

- y** If there are  $I$  matched sets and the largest matched set contains  $J$  individuals, then  $y$  is an  $I$  by  $J$  matrix with one row for each matched set. If matched set  $i$  contains one treated individual and  $k$  controls, where  $k$  is at least 1 and at most  $J-1$ , then  $y[i,1]$  is the treated individual's response,  $y[i,2], \dots, y[i,k+1]$  are the responses of the  $k$  controls, and  $y[i,k+2], \dots, y[i,J]$  are equal to NA. If matched set  $i$  contains one control and  $k > 1$  treated individuals, then  $y[i,1]$  is the control's response,  $y[i,2], \dots, y[i,k+1]$  are the responses of the  $k$  treated individuals, and  $y[i,k+2], \dots, y[i,J]$  are equal to NA. Although  $y$  may, and typically does, contain NA's,  $y[i,1]$  and  $y[i,2]$  must not be NA for all  $i$ .
- If you have matched pairs, not matched sets, use the `senmwCI` function in the `sensitivymw` package.
- treated1** The vector `treated1` is a logical vector of length  $I$ , where `treated1[i]=TRUE` if there is one treated subject in matched set  $i$  and `treated1[i]=FALSE` if there is more than one treated subject in matched set  $i$ .
- gamma** `gamma` is the sensitivity parameter  $\Gamma$ , where  $\Gamma \geq 1$ . Setting  $\Gamma = 1$  is equivalent to assuming ignorable treatment assignment given the matched sets, and it returns a randomization-based confidence interval.
- inner** `inner` and `trim` together define the  $\psi$ -function for the  $M$ -statistic. The default values yield a version of Huber's  $\psi$ -function, while setting `inner = 0` and `trim = Inf` uses the mean within each matched set. The  $\psi$ -function is an odd function, so  $\psi(w) = -\psi(-w)$ . For  $w \geq 0$ , the  $\psi$ -function is  $\psi(w) = 0$  for  $0 \leq w \leq \text{inner}$ , is  $\psi(w) = \text{trim}$  for  $w \geq \text{trim}$ , and rises linearly from 0 to `trim` for `inner < w < trim`.
- An error will result unless  $0 \leq \text{inner} \leq \text{trim}$ .
- Taking `trim < Inf` limits the influence of outliers; see Huber (1981). Taking `inner > 0` often increases design sensitivity; see Rosenbaum (2013).
- trim** `inner` and `trim` together define the  $\psi$ -function for the  $M$ -statistic. See `inner`.
- lambda** Before applying the  $\psi$ -function to treated-minus-control differences, the differences are scaled by dividing by the `lambda` quantile of all within set absolute differences. Typically, `lambda = 1/2` for the median. The value of `lambda` has no effect if `trim=0` and `inner=Inf`. See Maritz (1979) for the paired case and Rosenbaum (2007) for matched sets.
- An error will result unless  $0 < \text{lambda} < 1$ .
- alpha** The coverage rate of the confidence interval is  $1-\text{alpha}$ . If the bias in treatment assignment is at most  $\Gamma$ , then the confidence interval will cover the true  $\tau$  with probability at least  $1 - \alpha$ .
- twosided** If `twosided==TRUE`, then a two-sided  $1 - \alpha$  confidence interval is constructed. If `twosided==FALSE`, then a one-sided  $1 - \alpha$  confidence interval is constructed. The two sided interval is the intersection of two one-sided  $1 - \alpha/2$  intervals.

upper            If `twosided==TRUE`, then upper is ignored. If `twosided==FALSE` and `upper=TRUE`, then an upper  $1 - \alpha$  confidence interval is constructed. If `twosided==FALSE` and `upper=FALSE`, then a lower  $1 - \alpha$  confidence interval is constructed.

### Details

For the given  $\Gamma$ , `senfmCI()` inverts the test in the function `senfm()` to produce the confidence interval. That is, it tests every  $\tau$  and retains the values not rejected at level  $\alpha$ .

The test is a large sample approximation based on a Normal approximation to the null distribution; see Rosenbaum (2007).

Matched sets of unequal size are weighted using weights that would be efficient in a randomization test under a simple model with additive set and treatment effects and errors with constant variance; see Rosenbaum (2007).

The upper bound on the P-value is based on the separable approximation described in Gastwirth, Krieger and Rosenbaum (2000); see also Rosenbaum (2007).

### Value

PointEstimates

The interval of point estimates of  $\tau$ . If `gamma=1`, then the interval is a single point estimate.

ConfidenceInterval

The confidence interval for  $\tau$ .

description

Reminder of the coverage rate, `gamma`, and type of interval.

### Note

In a sensitivity analysis, a one-sided confidence interval is not conservative; however, two-sided intervals formed as the intersection of two one-sided  $1 - \alpha/2$  intervals are somewhat conservative. See the discussion of two-sided tests in the documentation for `senfm()`.

### Author(s)

Paul R. Rosenbaum.

### References

Hansen, B. B. (2007). *Optmatch*. R News 7 18-24. (R package `optmatch`) (*Optmatch* can create an optimal full match.)

Hansen, B. B. and Klopfer, S. O. (2006). Optimal full matching and related designs via network flows. *J. Comput. Graph. Statist.* 15 609-627. (R package `optmatch`)

Huber, P. (1981) *Robust Statistics*. New York: John Wiley. (M-estimates based on M-statistics.)

Maritz, J. S. (1979). A note on exact robust confidence intervals for location. *Biometrika* 66 163–166. (Introduces exact permutation tests based on M-statistics by redefining the scaling parameter.)

Rosenbaum, P. R. (1991). A characterization of optimal designs for observational studies. *J. Roy. Statist. Soc. B* 53 597-610. (Introduces full matching.)

Rosenbaum, P. R. (2007). Sensitivity analysis for m-estimates, tests and confidence intervals in matched observational studies. *Biometrics* 63 456-64. (R package sensitivitymv)

Rosenbaum, P. R. (2013). Impact of multiple matched controls on design sensitivity in observational studies. *Biometrics* 69 118-127. (Introduces inner trimming.)

Rosenbaum, P. R. (2014). Weighted M-statistics with superior design sensitivity in matched observational studies with multiple controls. *J. Am. Statist. Assoc.* 109 1145-1158. (R package sensitivitymw)

## Examples

```
# The artificial example that follows has I=9
# matched sets. The first 3 sets have one treated
# individual and two controls with treated subjects
# in column 1. The next 3 sets are
# matched pairs, with treated subjects in column 1.
# The next 3 sets have one control and two treated
# subjects, with the control in column 1. Simulated
# from a Normal distribution with an additive effect
# of tau=1.

y<-c(2.2, 1.4, 1.6, 2.4, 0.7, 1.3, 1.2, 0.6, 0.3,
0.5, -0.1, -1.3, -0.3, 0.1, 0.4, 3.0, 1.1, 1.4, -0.8,
0.1, 0.8, NA, NA, NA, 1.1, 0.5, 1.8)
y<-matrix(y,9,3)
treated1<-c(rep(TRUE,6),rep(FALSE,3))

# Randomization interval and point estimate, Huber scores:
senfmCI(y,treated1)

# Uses senfm() to show how senfmCI() inverts the test.
senfm(y,treated1,tau=0.6172307) #P-value is 0.025
senfm(y,treated1,tau=2.0612746,alternative = "less") #P-value is 0.025
senfm(y,treated1,tau=1.345436) #Statistic is 0

senfmCI(y,treated1,gamma=1.5) #Sensitivity of two-sided CI
# The next two calculations relate one and two-sided intervals
senfmCI(y,treated1,gamma=1.5,twosided=FALSE,upper=TRUE,alpha=0.025)
senfmCI(y,treated1,gamma=1.5,twosided=FALSE,upper=FALSE,alpha=0.025)

# If an estimator is approximately Normal, then +/- a standard
# error is approximately a 2/3 confidence interval. Going the
# other way, people sometimes suggest looking at a 2/3
# confidence interval as analogous to +/- a standard error.
senfmCI(y,treated1,gamma=1.5,alpha=1/3)

# For an additional example, install and load package sensitivitymw
# library(sensitivitymw)
# The mercury data is 397 triples, 1 treated, 2 controls.
# It is the example in Rosenbaum (2014).
# data(mercury)
# help(mercury)
# In this balanced design, senmwCI() and senfmCI() give the same CI.
```

```
# senmCI(mercury, gamma=3)
# senfmCI(mercury, rep(TRUE, 397), gamma=3, twosided=FALSE)
```

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separable1f	<i>Computes the Separable Approximation.</i>
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### Description

Of limited interest to most users, `separable1f()` is called by the main function, `senfm()`, in computing the sensitivity analysis. `separable1f()` is given scores produced by `mscoref()` and computes the separable approximation to the upper bound on the P-value.

### Usage

```
separable1f(yamat, gamma = 1)
```

### Arguments

<code>yamat</code>	A matrix of scores produced by <code>mscoref</code> .
<code>gamma</code>	The sensitivity parameter $\Gamma \geq 1$ .

### Details

See Gastwirth, Krieger and Rosenbaum (2000) and Rosenbaum (2007, section 4) for discussion of the separable approximation.

### Value

<code>pval</code>	The upper bound on the 1-sided P-value.
<code>deviate</code>	The deviate that was compared to the Normal distribution to produce <code>pval</code> .
<code>statistic</code>	The value of the score-statistic.
<code>expectation</code>	The maximum expectation of the score-statistic for the given $\Gamma$ .
<code>variance</code>	The maximum variance of the score-statistic among treatment assignments that achieve the maximum expectation. Part of the separable approximation.

### Author(s)

Paul R. Rosenbaum

### References

Gastwirth, J. L., Krieger, A. M. and Rosenbaum, P. R. (2000). Asymptotic separability in sensitivity analysis. *J. Roy. Statist. Soc. B.* 62 545-555.

Rosenbaum, P. R. (2007). Sensitivity analysis for m-estimates, tests and confidence intervals in matched observational studies. *Biometrics* 63 456-64. (See section 4.) (R package `sensitivitymv`)

**Examples**

```
# The artificial example that follows has I=9
# matched sets. The first 3 sets have one treated
# individual and two controls with treated subjects
# in column 1. The next 3 sets are
# matched pairs, with treated subjects in column 1.
# The next 3 sets have one control and two treated
# subjects, with the control in column 1. Simulated
# from a Normal distribution with an additive effect
# of tau=1.

y<-c(2.2, 1.4, 1.6, 2.4, 0.7, 1.3, 1.2, 0.6, 0.3,
0.5, -0.1, -1.3, -0.3, 0.1, 0.4, 3.0, 1.1, 1.4, -0.8,
0.1, 0.8, NA, NA, NA, 1.1, 0.5, 1.8)
y<-matrix(y,9,3)
treated1<-c(rep(TRUE,6),rep(FALSE,3))

# The same calculation done in two equivalent ways.
separable1f(mscoref(y,treated1),gamma=2)
senfm(y,treated1,gamma=2)
```

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