

Package ‘weightedRank’

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Type Package

Title Sensitivity Analysis Using Weighted Rank Statistics

Version 0.1.6

Description Performs a sensitivity analysis using weighted rank tests in observational studies with I blocks of size J; see Rosenbaum (2018) <[doi:10.1214/18-AOAS1153](https://doi.org/10.1214/18-AOAS1153)>. The package can perform adaptive inference in block designs; see Rosenbaum (2012) <[doi:10.1093/biomet/ass032](https://doi.org/10.1093/biomet/ass032)>. The main functions are `wgtRank()` and `wgtRanktt()`.

License GPL-2

Encoding UTF-8

LazyData true

Imports stats, graphics, mvtnorm

Suggests sensitivitymw, sensitivitymult

Depends R (>= 3.5.0)

NeedsCompilation no

Author Paul Rosenbaum [aut, cre]

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

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 weightedRank-package *Sensitivity Analysis Using Weighted Rank Statistics*

Description

Performs a sensitivity analysis using weighted rank tests in observational studies with I blocks of size J; see Rosenbaum (2018) <doi:10.1214/18-AOAS1153>. The package can perform adaptive inference in block designs; see Rosenbaum (2012) <doi:10.1093/biomet/ass032>. The main functions are wgtRank() and wgtRanktt().

Details

The DESCRIPTION file:

```
Package:      weightedRank
Type:        Package
Title:       Sensitivity Analysis Using Weighted Rank Statistics
Version:     0.1.6
Authors@R:   person("Paul", "Rosenbaum", email = "rosenbaum@wharton.upenn.edu", role = c("aut", "cre"))
Description: Performs a sensitivity analysis using weighted rank tests in observational studies with I blocks of size J; see Rosenbaum (2018) <doi:10.1214/18-AOAS1153>. The package can perform adaptive inference in block designs; see Rosenbaum (2012) <doi:10.1093/biomet/ass032>. The main functions are wgtRank() and wgtRanktt().
License:     GPL-2
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Imports:     stats, graphics, mvtnorm
Suggests:   sensitivitymw, sensitivitymult
Depends:    R (>= 3.5.0)
Author:     Paul Rosenbaum [aut, cre]
Maintainer: Paul Rosenbaum <rosenbaum@wharton.upenn.edu>
```

Index of help topics:

aHDL	Alcohol and HDL Cholesterol
amplify	Amplification of sensitivity analysis in observational studies.
weightedRank-package	Sensitivity Analysis Using Weighted Rank Statistics
wgtRank	Sensitivity Analysis for Weighted Rank Statistics in Block Designs
wgtRanktt	Adaptive Inference Using Two Test Statistics in a Block Design

The package conducts either fixed or adaptive sensitivity analyses for observational studies with I blocks and J individuals in each block, one treated and J-1 controls. The two main functions are wgtRank() for a fixed test statistic, and wgtRanktt() for an adaptive choice of one of two test statistics.

Author(s)

NA

Maintainer: NA

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Rosenbaum, P. R. (2011) <[doi:10.1111/j.1541-0420.2010.01535.x](https://doi.org/10.1111/j.1541-0420.2010.01535.x)> A new U-Statistic with superior design sensitivity in matched observational studies. *Biometrics*, 67(3), 1017-1027.

Rosenbaum, P. R. (2012) <[doi:10.1093/biomet/ass032](https://doi.org/10.1093/biomet/ass032)> Testing one hypothesis twice in observational studies. *Biometrika*, 99(4), 763-774.

Rosenbaum, P. R. (2022) Bahadur efficiency of observational block designs. Manuscript.

Tardif, S. (1987) <[doi:10.2307/2289476](https://doi.org/10.2307/2289476)> Efficiency and optimality results for tests based on weighted rankings. *Journal of the American Statistical Association*, 82(398), 637-644.

Examples

```
data(aHDL)
y<-t(matrix(aHDL$hdl,4,406))
wgtRank(y,phi="u878",gamma=6) # New U-statistic weights (8,7,8)
wgtRanktt(y,phi1="u868",phi2="u878",gamma=5.9)
```

aHDL

Alcohol and HDL Cholesterol

Description

A small observational study of light daily alcohol consumption and HDL cholesterol – so-called good cholesterol – derived from NHANES 2013-2014 and 2015-2016. There are 406 matched sets of four individuals, making 1624 individuals in total. Sets were matched for age, female and education in five ordered categories.

Usage

```
data("aHDL")
```

Format

A data frame with 1624 observations on the following 11 variables.

nh NHANES 2013-2014 is 1314, and NHANES 2015-2016 is 1516

SEQN NHANES ID number

age Age in years

female 1=female, 0=male

education 1 is <9th grade, 3 is high school, 5 is a BA degree

z 1=light almost daily alcohol, 0=little or no alcohol last year.

grp Treated group and control groups. Daily=light almost daily alcohol, Never=fewer than 12 drinks during entire life, Rarely=more than 12 drinks in life, but fewer than 12 in the past year, and never had a period of daily binge drinking, PastBinge = a past history of binge drinking on most days, but currently drinks once a week or less. For details, see Rosenbaum (2022a, Appendix).

grpL Short labels for plotting formed as the first letters of grp. D < N < R < B

hdl HDL cholesterol level mg/dL

mmercury Methylmercury level ug/L

mset Matched set indicator, 1, 2, ..., 406. The 1624 observations are in 406 matched sets, each of size 4.

Details

There is a debate about whether light daily alcohol consumption – a single glass of red wine – shortens or lengthens life. LoConte et al. (2018) emphasize that alcohol is a carcinogen. Suh et al. (1992) claim reduced cardiovascular mortality brought about by an increase in high density lipoprotein (HDL) cholesterol, the so-called good cholesterol. There is on-going debate about whether there are cardiovascular benefits, and if they exist, whether they are large enough to offset an increased risk of cancer. This example looks at a small corner of the larger debate, namely the effect on HDL cholesterol.

The example contains several attempts to detect unmeasured confounding bias, if present. There is a secondary outcome thought to be unaffected by alcohol consumption, namely methylmercury levels in the blood, likely an indicator of the consumption of fish, not of alcohol; see Pedersen et al. (1994) and WHO (2021). There are also three control groups, all with little present alcohol consumption, but with different uses of alcohol in the past; see the definition of variable grp above.

The appendix to Rosenbaum (2022a) describes the data and matching in detail. It is used as an example in Rosenbaum (2022b).

The help file for `boxplotTT()` applies the tail transformation to this example, reproducing a plot from Rosenbaum (2022b).

This data set is also included in the `tailTransform` package. See also the `informedSen` package which contains a part of this data set.

Source

US National Health and Nutrition Examination Survey (NHANES), 2013-2014 and 2015-2016.

References

LoConte, N. K., Brewster, A. M., Kaur, J. S., Merrill, J. K., and Alberg, A. J. (2018). Alcohol and cancer: a statement of the American Society of Clinical Oncology. *Journal of Clinical Oncology* 36, 83-93. <doi:10.1200/JCO.2017.76.1155>

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Examples

```
data(aHDL)
table(aHDL$grp, aHDL$grpL) # Short labels for plotting
boxplot(aHDL$age~aHDL$grp, xlab="Group", ylab="Age")
boxplot(aHDL$education~aHDL$grp, xlab="Group", ylab="Education")
table(aHDL$female, aHDL$grpL)
table(aHDL$z, aHDL$grpL)

# The sets were also matched for is.na(aHDL$mmercury), for use
# in Rosenbaum (2022a). About half of the matched sets
# have values for mmercury.
table(is.na(aHDL$mmercury), aHDL$grp)

# See also the informedSen package for additional analysis
```

Description

Uses the method in Rosenbaum and Silber (2009) to interpret a value of the sensitivity parameter γ . Each value of γ amplifies to a curve (λ, δ) in a two-dimensional sensitivity analysis, the inference being the same for all points on the curve. That is, a one-dimensional sensitivity analysis in terms of γ has a two-dimensional interpretation in terms of (λ, δ) .

Usage

```
amplify(gamma, lambda)
```

Arguments

gamma	gamma > 1 is the value of the sensitivity parameter, for instance the parameter in <code>senmv</code> . <code>length(gamma)>1</code> will generate an error.
lambda	lambda is a vector of values > gamma. An error will result unless <code>lambda[i] > gamma > 1</code> for every i.

Details

A single value of gamma, say $\gamma = 2.2$ in the example, corresponds to a curve of values of (λ, δ) , including (3, 7), (4, 4.33), (5, 3.57), and (7, 3) in the example. An unobserved covariate that is associated with a $\lambda = 3$ fold increase in the odds of treatment and a $\delta = 7$ fold increase in the odds of a positive pair difference is equivalent to $\gamma = 2.2$.

The curve is $\gamma = (\lambda * \delta + 1) / (\lambda + \delta)$. Amplify is given one gamma and a vector of lambdas and solves for the vector of deltas. The calculation is elementary.

This interpretation of gamma is developed in detail in Rosenbaum and Silber (2009), and it makes use of Wolfe's (1974) family of semiparametric deformations of an arbitrary symmetric distribution. See also Rosenbaum (2020, Section 3.6). For an elementary discussion, see Rosenbaum (2017, Table 9.1).

Strictly speaking, the amplification describes matched pairs, not matched sets. The `senm` function views a k-to-1 matched set with k controls matched to one treated individual as a collection of k correlated treated-minus-control matched pair differences; see Rosenbaum (2007). For matched sets, it is natural to think of the amplification as describing any one of the k matched pair differences in a k-to-1 matched set.

The curve has asymptotes that the function `amplify` does not compute: γ corresponds with $(\lambda, \delta) = (\gamma, \infty)$ and (∞, γ) .

A related though distinct idea is developed in Gastwirth et al (1998). The two approaches agree when the outcome is binary, that is, for McNemar's test.

Value

Returns a vector of values of delta of `length(lambda)` with names lambda.

Note

The `amplify` function is also in the `sensitivitymv` package where a different example is used.

Author(s)

Paul R. Rosenbaum

References

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Examples

```
# Consider a treated-control match pair as the unit of measure,
# analogous to one meter or one foot. The calculation
# amplify(4,7) says that, in a matched pair, gamma=4
# is the same a bias that increases the odds of treatment
# 7-fold and increases the odds of positive matched-pair
# difference in outcomes 9-fold.
amplify(4,7)
# It is also true that, in a matched pair, gamma=4
# is the same a bias that increases the odds of treatment
# 9-fold and increases the odds of positive matched-pair
# difference in outcomes 7-fold.
amplify(4,9)
# It is also true that, in a matched pair, gamma=4
# is the same a bias that increases the odds of treatment
# 5-fold and increases the odds of positive matched-pair
# difference in outcomes 19-fold.
amplify(4,5)
# The amplify function can produce the entire curve at once:
amplify(4,5:19)
```

wgtRank

Sensitivity Analysis for Weighted Rank Statistics in Block Designs

Description

Uses a weighted rank statistic to perform a sensitivity analysis for an I x J observational block design in which each of I blocks contains one treated individual and J-1 controls.

Usage

```
wgtRank(y, phi = "u868", phifunc = NULL, gamma = 1)
```

Arguments

y	A matrix or data frame with I rows and J columns. Column 1 contains the response of the treated individuals and columns 2 through J contain the responses of controls in the same block. An error will result if y contains NAs.
phi	The weight function to be applied to the ranks of the within block ranges. The options are: (i) "wilc" for the stratified Wilcoxon test, which gives every block the same weight, (ii) "quade" which ranks the within block ranges from 1 to I, and is closely related to Quade's (1979) statistic; see also Tardif (1987), (iii) "u868" based on Rosenbaum (2011), (iv) u878 based on Rosenbaum (2011). Note that phi is ignored if phifunc is not NULL.
phifunc	If not NULL, a user specified weight function for the ranks of the within block rates. The function should map [0,1] into [0,1]. The function is applied to the ranks divided by the sample size. See the example.
gamma	A single number greater than or equal to 1. gamma is the sensitivity parameter. Two individuals with the same observed covariates may differ in their odds of treatment by at most a factor of gamma; see Rosenbaum (1987; 2017, Chapter 9).

Details

This method is developed and evaluated in Rosenbaum (2022).

To test in the lower tail – to test against the alternative that treated responses are lower than control responses, apply the function to -y. For a two-sided test, do both one-sided tests and apply the Bonferroni inequality, doubling the smaller of the two one-sided P-value bounds; see Cox (1977, Section 4.2).

Value

pval	Upper bound on the one-sided P-value when testing the null hypothesis of no treatment effect against the alternative hypothesis that treated responses are higher than control responses.
detail	Details of the computation of pval: the standardized deviate, the test statistic, its null expectation, its null variance and the value of gamma.

Note

The computations use the separable approximation discussed in Gastwirth et al. (2000) and Rosenbaum (2018). Compare with the method in Rosenbaum (2014) and the R package sensitivitymw.

Author(s)

Paul R. Rosenbaum

References

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- Tardif, S. (1987). <doi:10.2307/2289476> Efficiency and optimality results for tests based on weighted rankings. *Journal of the American Statistical Association*, 82(398), 637-644.

See Also

An alternative approach avoids rank tests and uses weighted M-statistics instead, as in the `sensitivitymw` package and Rosenbaum (2014). However, Bahadur efficiency calculations are available for weighted rank statistics; see Rosenbaum (2022).

Examples

```
data(aHDL)
y<-t(matrix(aHDL$hd1,4,406))
wgtRank(y,phi="wilc",gamma=3.5) # Stratified Wilcoxon rank sum test
wgtRank(y,phi="quade",gamma=3.5) # Quade's test
wgtRank(y,phi="quade",gamma=4.5) # Quade's test, larger gamma
wgtRank(y,phi="quade",gamma=4.6) # Quade's test, larger gamma
wgtRank(y,phi="u868",gamma=5.4) # New U-statistic weights (8,6,8)
wgtRank(y,phi="u878",gamma=6) # New U-statistic weights (8,7,8)
```

```
# As an aid to interpreting gamma, see the amplify function.
amplify(3.5,8)
amplify(4.6,8)
amplify(5.4,8)
amplify(6,8)

# A user defined weight function, brown, analogous to Brown (1981).
brown<-function(v){((v>=.333)+(v>=.667))/2}
wgtRank(y,phifunc=brown,gamma=4.7)
```

wgtRanktt

Adaptive Inference Using Two Test Statistics in a Block Design

Description

Tests twice, using the better of two test statistics; see Rosenbaum (2012, 2022).

Usage

```
wgtRanktt(y, phi1 = "u868", phi2 = "u878", phifunc1 = NULL, phifunc2 = NULL, gamma = 1)
```

Arguments

y	A matrix or data frame with I rows and J columns. Column 1 contains the response of the treated individuals and columns 2 through J contain the responses of controls in the same block. A error will result if y contains NAs.
phi1	The weight function to be applied to the ranks of the within block ranges. The options are: (i) "wilc" for the stratified Wilcoxon test, which gives every block the same weight, (ii) "quade" which ranks the within block ranges from 1 to I, and is closely related to Quade's (1979) statistic; see also Tardif (1987), (iii) "u868" based on Rosenbaum (2011), (iv) u878 based on Rosenbaum (2011). Note that phi is ignored if phifunc is not NULL.
phi2	See phi1.
phifunc1	If not NULL, a user specified weight function for the ranks of the within block rates. The function should map [0,1] into [0,1]. The function is applied to the ranks divided by the sample size. See the example.
phifunc2	See phifunc1.
gamma	A single number greater than or equal to 1. gamma is the sensitivity parameter. Two individuals with the same observed covariates may differ in their odds of treatment by at most a factor of gamma; see Rosenbaum (1987; 2017, Chapter 9).

Value

jointP	Upper bound on the one-sided joint P-value obtained from two test statistics in the presence of a bias of at most γ .
cor12	Correlation of the two test statistics at the treatment assignment distribution that provides the joint upper bound. Often, this correlation is high, so the joint distribution that is used here is much less conservative than use of the Bonferroni inequality when testing twice.
detail	Details about the two statistics separately. Equivalent to the result from <code>wgRank()</code> run twice with different test statistics.

Note

For discussion of testing twice in matched pairs, see Rosenbaum (2012).

Testing twice is also possible in block designs using weighted rank statistics because the same value of the unobserved covariate provides the upper bound for both statistics when using the separable approximation in Gastwirth et al. (2000) and Rosenbaum (2018, Remarks 4 and 5). See also Rosenbaum (2022) where the Bahadur efficiency of such tests is computed.

Other packages that use testing twice in a different way are "sensitivity2x2xk" and "testtwice". The "testtwice" package is restricted to matched pairs, and "sensitivity2x2xk" is for binary outcomes. With some attention to detail (e.g., the handling of zero pair differences), in the case of matched pairs, the "testtwice" package and the `wgtRanktt()` function will yield identical results. In that sense, `wgtRanktt()` extends the method to blocks designs.

Testing twice achieves the larger Bahadur efficiency of the two component statistics; see Berk and Jones (1978).

Author(s)

Paul R. Rosenbaum

References

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- Quade, D. (1979) <[doi:10.2307/2286991](https://doi.org/10.2307/2286991)> Using weighted rankings in the analysis of complete blocks with additive block effects. *Journal of the American Statistical Association*, 74, 680-683.
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- Rosenbaum, P. R. (2012) <doi:10.1093/biomet/ass032> Testing one hypothesis twice in observational studies. *Biometrika*, 99(4), 763-774.
- Rosenbaum, P. R. (2014) <doi:10.1080/01621459.2013.879261> Weighted M-statistics with superior design sensitivity in matched observational studies with multiple controls. *Journal of the American Statistical Association*, 109(507), 1145-1158.
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- Tardif, S. (1987) <doi:10.2307/2289476> Efficiency and optimality results for tests based on weighted rankings. *Journal of the American Statistical Association*, 82(398), 637-644.

Examples

```
data(aHDL)
y<-t(matrix(aHDL$hdl,4,406))

# This is the simplest example of a general property. The
# example simply illustrates, but does not fully exploit
# the property. In this case, use of the stratified
# Wilcoxon statistic is a mistake, because Quade's
# statistic correctly reports insensitivity to a bias
# of gamma=4.5, but the stratified Wilcoxon statistic
# is sensitive at gamma=3.5. The adaptive procedure
# that does both tests and corrects for multiple testing
# is insensitive to gamma=4.4; so, it is almost as good
# as knowing what you cannot know, namely that Quade's
# statistic is the better choice in this one example.
# The price paid for testing twice is very small;
# see Berk and Jones (1978) and Rosenbaum (2012, 2022).
wgtRank(y,phi="wilc",gamma=3.5)
wgtRank(y,phi="quade",gamma=3.5)
wgtRank(y,phi="wilc",gamma=4.5)
wgtRank(y,phi="quade",gamma=4.5)
wgtRanktt(y,phi1="wilc",phi2="quade",gamma=4.4)

# Sensitivity to gamma=3.5 is very different from
# sensitivity to gamma=4.4; see documentation for amplify.
amplify(3.5,8)
amplify(4.4,8)
```

```
# In this example, u878 exhibits greater insensitivity to bias
# than u868. However, adaptive inference using both is almost
# as good as the better statistic, yet it strongly controls the
# family-wise error rate despite testing twice;
# see Rosenbaum (2012,2022).
wgtRank(y,phi="u868",gamma=6) # New U-statistic weights (8,6,8)
wgtRank(y,phi="u878",gamma=6) # New U-statistic weights (8,7,8)
wgtRanktt(y,phi1="u868",phi2="u878",gamma=5.9)

# A user defined weight function, brown, analogous to Brown (1981).
brown<-function(v){((v>=.333)+(v>=.667))/2}
# In this example, the joint test rejects based on u878
wgtRanktt(y,phi1="u878",phifunc2=brown,gamma=5.8)
```

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