

Package ‘weightedRank’

May 8, 2023

Type Package

Title Sensitivity Analysis Using Weighted Rank Statistics

Version 0.2.5

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()` and `ef2C()`.

License GPL-2

Encoding UTF-8

LazyData true

Imports stats, graphics, mvtnorm, sensitivitymv

Suggests sensitivitymw, sensitivitymult, DOS2

Depends R (>= 3.5.0)

NeedsCompilation no

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Repository CRAN

Date/Publication 2023-05-08 15:50:02 UTC

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 weightedRank-package *Sensitivity Analysis Using Weighted Rank Statistics*

Description

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Details

The DESCRIPTION file:

```
Package:      weightedRank
Type:        Package
Title:       Sensitivity Analysis Using Weighted Rank Statistics
Version:     0.2.5
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() and ef2C().
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Depends:     R (>= 3.5.0)
Author:      Paul Rosenbaum [aut, cre]
Maintainer:  Paul Rosenbaum <rosenbaum@wharton.upenn.edu>
```

Index of help topics:

aBP	Binge Drinking and Blood Pressure
aHDL	Alcohol and HDL Cholesterol
amplify	Amplification of sensitivity analysis in observational studies.
dwgtRank	Weighted Rank Statistics for Evidence Factors with Two Control Groups
ef2C	Evidence Factors For Matched Triples With Two Control Groups
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. The function `ef2C()` is used to extract two evidence factors when a treated group is compared to two different control groups.

Author(s)

NA

Maintainer: NA

References

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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. (2021) <[doi:10.1201/9781003039648](https://doi.org/10.1201/9781003039648)> Replication and Evidence Factors in Observational Studies. Chapman and Hall/CRC.

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)
```

aBP

Binge Drinking and Blood Pressure

Description

A matched observational study from NHANES with two control groups, examining the possible effects of on blood pressure of frequent binge drinking of alcohol.

Usage

```
data("aBP")
```

Format

A data frame with 621 observations on the following 13 variables.

SEQN NHANES identification number

age Age in years

female 1=female, 0=male

education Education, with levels: "<9th" = less than 9th grade, "9-11" = grades 9 to 11, "HS" = high school, "SomeCol" = Some College, ">=BA" = BA degree or more

bmi BMI or body-mass index

waisthip Waist-to-hip ratio

vigorR Engages in vigorous recreational exercise, 1=yes, 0=no

smokenow Do you smoke now? Answers: Everyday, Some days, No

bpRX Reports currently taking medication for high blood pressure

bpSystolic Systolic blood pressure, mm Hg. Average of up to three readings.

bpDiastolic Diastolic blood pressure, mm Hg. Average of up to three readings.

group Drinking group, B=currently engages in frequent binge drinking, N=never binged regularly, and drank at most one drink per week in the last year, P=binged on most days for some period in the past but stopped, nevery binged in the last year, and drank at most one drink per week in the last year. See Details.

mset Matched set indicator, 1, 2, ..., 207. There are 207 blocks of size 3, each containing one B, one N and one P.

Details

The data are from data from the 2017-2020 National Health and Nutrition Examination Survey (which was interrupted by COVID-19, so it is not a survey). There were 5624 people who were at least 20 years of age, with an alcohol use survey, blood pressure measurements and covariates used here. Blood pressure measurements are the average of up to three measurements. One question asked about binge drinking in the past, defined as 4 drinks for women or 5 drinks for men. Question ALQ151 asks (essentially): "Was there ever a time or times in your life when you drank 4/5 or more drinks of any kind of alcoholic beverage almost every day?" Another question ALQ142 asked about binge drinking last year: "During the past 12 months, about how often did you have 4/5 or more drinks of any alcoholic beverage?" Question ALQ121 about the overall frequency of alcohol consumption in the past 12 months. Proper use of ALQ121 and ALQ142 accounts for certain screening questions. By definition, group "binge" responded by saying that they engaged in binge drinking on 3 or more days each week in the past 12 months. By definition, group "never" responded to ALQ142 saying they never binged in the past 12 months, responded to ALQ151 saying they had no past time when they binged almost every day, and drank any alcohol on at most one day a week in the past 12 months. By definition, group "past" said yes to question ALQ151, so there was a period in their life of binge drinking almost every day, but they never binged in the past 12 months, and drank alcohol on at most one day a week in the past 12 months. There were 9232 people aged

20 or more. Of these, 9187 had covariate information, aside from BMI and waist/hip ratio. Of these, 7876 had an alcohol survey. Of these, 7281 had at least one measurement of diastolic and systolic blood pressure. Of these, 7076 had body measurements, namely BMI and waist/hip ratio. The three treatment groups — binge, never and past — are mutually exclusive but not exhaustive, and 5624 people fell in one of the groups. All 207 members of the binge group were matched to one control from each control group. Before matching, the never group had 3995 people and the past group had 505 people. The never group was large enough to closely match two or three controls to each member of the binge group, but that was not done in this illustrative example. Up to 3 repeated measures of blood pressure were often present, and the analysis uses their average.

Note

The data are used as an example in Rosenbaum (2023).

Source

US National Health and Nutrition Examination Survey (<https://www.cdc.gov/nchs/nhanes/index.htm>)

References

Roerecke, M., Kaczorowski, J., Tobe, S. W., Gmel, G., Hasan, O. S. and Rehm, J. (2017). <doi:10.1016/S2468-2667(17)30003-8> The effect of a reduction in alcohol consumption on blood pressure: a systematic review and meta-analysis. *Lancet Public Health*, 2, e108-e120.

Rosenbaum, P. R. (2023) A second evidence factor associated with a second control group. Manuscript.

Examples

```
# The following code creates Figure 2 in Rosenbaum (2023)

data(aBP)
attach(aBP)

yD<-t(matrix(bpDiastolic,3,207))
yS<-t(matrix(bpSystolic,3,207))
vS<-c(yS[,1]-yS[,2],yS[,1]-yS[,3],yS[,2]-yS[,3])
vD<-c(yD[,1]-yD[,2],yD[,1]-yD[,3],yD[,2]-yD[,3])
y<-(yD/median(abs(vD)))+(yS/median(abs(vS)))

par(mfrow=c(1,3))
graphics::boxplot(yD[,1]-yD[,2],yD[,1]-yD[,3],yD[,2]-yD[,3],las=1,
  main="",ylab="Difference mm Hg",
  names=c("B-N","B-P","N-P"),cex.main=.9,
  cex.axis=.8,cex.lab=.9,xlab="Diastolic Difference")
graphics::abline(h=0)
wx<-round(stats::wilcox.test(yD[,1]-yD[,2],conf.int=TRUE)$conf.int,1)
graphics::segments(1,wx[1],1,wx[2],col="black",lwd=2)
wx<-round(stats::wilcox.test(yD[,1]-yD[,3],conf.int=TRUE)$conf.int,1)
graphics::segments(2,wx[1],2,wx[2],col="black",lwd=2)
wx<-round(stats::wilcox.test(yD[,2]-yD[,3],conf.int=TRUE)$conf.int,1)
```

```

graphics::segments(3,wx[1],3,wx[2],col="black",lwd=2)

graphics::boxplot(yS[,1]-yS[,2],yS[,1]-yS[,3],yS[,2]-yS[,3],las=1,
  main="",ylab="Difference mm Hg",
  names=c("B-N","B-P","N-P"),cex.main=.9,
  cex.axis=.8,cex.lab=.9,xlab="Systolic Difference")
graphics::abline(h=0)
wx<-round(stats::wilcox.test(yS[,1]-yS[,2],conf.int=TRUE)$conf.int,1)
graphics::segments(1,wx[1],1,wx[2],col="black",lwd=2)
wx<-round(stats::wilcox.test(yS[,1]-yS[,3],conf.int=TRUE)$conf.int,1)
graphics::segments(2,wx[1],2,wx[2],col="black",lwd=2)
wx<-round(stats::wilcox.test(yS[,2]-yS[,3],conf.int=TRUE)$conf.int,1)
graphics::segments(3,wx[1],3,wx[2],col="black",lwd=2)

graphics::boxplot(y[,1]-y[,2],y[,1]-y[,3],y[,2]-y[,3],las=1,
  main="",ylab="(Diastolic/10.7)+(Systolic/14.7)",
  names=c("B-N","B-P","N-P"),cex.main=.9,
  cex.axis=.8,cex.lab=.9,xlab="Combined Difference")
graphics::abline(h=0)
wx<-round(stats::wilcox.test(y[,1]-y[,2],conf.int=TRUE)$conf.int,1)
graphics::segments(1,wx[1],1,wx[2],col="black",lwd=2)
wx<-round(stats::wilcox.test(y[,1]-y[,3],conf.int=TRUE)$conf.int,1)
graphics::segments(2,wx[1],2,wx[2],col="black",lwd=2)
wx<-round(stats::wilcox.test(y[,2]-y[,3],conf.int=TRUE)$conf.int,1)
graphics::segments(3,wx[1],3,wx[2],col="black",lwd=2)
graphics::abline(h=0)
par(mfrow=c(1,1))
detach(aBP)

```

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
```

amplify

Amplification of sensitivity analysis in observational studies.

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 <code>i</code> .

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 $\gamma = (\lambda \cdot \delta + 1) / (\lambda + \delta)$. 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

- Gastwirth, J. L., Krieger, A. M., Rosenbaum, P. R. (1998) <doi:10.1093/biomet/85.4.907> Dual and simultaneous sensitivity analysis for matched pairs. *Biometrika*, 85, 907-920.
- Rosenbaum, P. R. and Silber, J. H. (2009) <doi:10.1198/jasa.2009.tm08470> Amplification of sensitivity analysis in observational studies. *Journal of the American Statistical Association*, 104, 1398-1405.
- Rosenbaum, P. R. (2017) <doi:10.4159/9780674982697> *Observation and Experiment: An Introduction to Causal Inference*. Cambridge, MA: Harvard University Press. Table 9.1.
- Rosenbaum, P. R. (2020) <doi:10.1007/978-3-030-46405-9> *Design of Observational Studies* (2nd ed.) NY: Springer. Section 3.6.
- Wolfe, D. A. (1974) <doi:10.2307/2286025> A characterization of population weighted symmetry and related results. *Journal of the American Statistical Association*, 69, 819-822.

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)
```

dwgtRank

Weighted Rank Statistics for Evidence Factors with Two Control Groups

Description

In an observational complete block design, dwgtRank computes a sensitivity analysis for a weighted rank statistic designed to perform well when the comparison of a treated group and two control groups is conducted as two nearly independent evidence factors; see Rosenbaum (2023b). For this task, a suggested setting of m , m_1 , m_2 , scores and range is given in a note in the documentation below. A simpler way to use the suggested settings is to use the function `ef2C` instead.

Usage

```
dwgtRank(y, gamma = 1, m = 2, m1 = 2, m2 = 2, phifunc = NULL,
         alternative = "greater", scores = NULL, range = TRUE)
```

Arguments

y	With I blocks and J individuals in each block, y is an I x J matrix or dataframe containing the outcomes. The first column of y is compared to columns 2, ..., J. J must be at least 2.
gamma	A real number ≥ 1 giving the value of the sensitivity parameter. $\text{gamma}=1$ yields a randomization test.
m	One of three parameters that define the weights that attach to blocks. The three parameters are integers with $1 \leq m1 \leq m2 \leq m$. See Details.
m1	See m.
m2	See m.
phifunc	An optional function that can be used to substitute your own weights for the weights defined by (m, m1, m2). The function must map [0,1] into [0,1]. If phifunc is NULL, then the weight function is defined by (m, m1, m2). If phifunc is not NULL, then it defines the weights and (m, m1, m2) are ignored.
alternative	For an upper-tailed test, use the default, <code>alternative="greater"</code> . For a lower-tailed test, use <code>alternative="less"</code> . An error will result if <code>alternative</code> is something besides "greater" or "less". In this context, a two-sided test is best viewed as two one-sided tests with a Bonferroni correction, e.g., testing in both tails at level 0.025 to ensure overall level of 0.05; see Cox (1977). For more information, see the notes.
scores	If <code>scores</code> is NULL, the scores are 1, 2, ..., J. Otherwise, <code>scores</code> should specify the J scores for the J within-block ranks. If <code>scores</code> are specified, there must be J scores, but the J scores need not be distinct.
range	If <code>range=TRUE</code> , then the within-block ranges are calculated, ranked from 1 to I, and scored (m, m1, m2) or <code>phifunc</code> . If <code>range=FALSE</code> , then the within-block gap between the largest response and the average of the remaining J-1 responses is used instead.

Details

The method uses a weighted rank statistic to compare the first column of y to the rest; see Rosenbaum (2023a,b). Weighted rank statistics generalize the methods of Quade (1979) and Tardif (1987). Quade (1979) applied unscored ranks to the I within block ranges, and used unscored ranks within-blocks. In contrast, here, the scores of ranks of ranges or gaps are based on expression (9) in Rosenbaum (2011a); see also Rosenbaum (2014) where weighted M-statistics are used instead of weighted rank statistics. If $J=2$, the method agrees exactly with the method for pairs in Rosenbaum (2011a).

Using $m=1, m1=1, m2=1$, is the same as the stratified Wilcoxon rank sum with I strata, ignoring the ranges or gaps; see Lehmann 1975, Chapter 3). Using $m=2, m1=2, m2=2$ applies unscored ranks to the I ranges or gaps. Using $m=5, m1=5, m2=5$ is the suggestion of Conover and Salsburg (1988), and $m=8, m1=8, m2=8$ is a more extreme version of the same theme. In pairs, $J=2, m=8, m1=7,$

$m_2=8$ performs well in Rosenbaum (2011a), as does $m=8$, $m_1=6$, $m_2=8$. Detailed evaluations in terms of design sensitivity and Bahadur efficiency are in Rosenbaum (2023a,b).

Value

pval	Upper bound on the one-sided P-value.
detail	A vector with the standardized deviate, the statistic, its null expectation and variance and the value of gamma.

Note

SUGGESTED SETTINGS FOR m , m_1 , m_2 , range AND scores WHEN USED WITH TWO CONTROL GROUPS. These suggested settings are more conveniently implemented in the function ef2C. Rosenbaum (2023b) considered a matched block design with I blocks of size 3, containing one treated individual and one control from each of two control groups. The two evidence factors are: (1) compare treated to the first control group, and (2) compare the second control group to the pooled group that does not distinguish the treated individual and the control from the first control group. For the matched pair comparison (1) with one control group, the suggested settings are ($m=8$, $m_1=7$, $m_2=8$), together with the defaults of range=TRUE and scores=NULL; see Rosenbaum (2011a). For comparison (2), Rosenbaum (2023b) evaluated 40 statistics, judging best the statistic with ($m=8$, $m_1=8$, $m_2=8$), range=FALSE, scores=c(1,2,5), as illustrated below. This statistic had good Bahadur efficiency of a sensitivity analysis against several simple alternative hypotheses involving a treatment effect and no unmeasured bias.

If we expect the treated group to have higher responses than controls, then comparison (1) sets alternative to greater and comparison (2) sets alternative to less. If we expect the treated group to have lower responses than controls, then comparison (1) sets alternative to less and comparison (2) sets alternative to greater. See also the note about alternatives.

Suppose that the data are initially in an $I \times 3$ matrix with outcomes for treated in the first column, control group 1 in the second column, and control group 2 in the third column. The dwgtRank function always compares the first column to the remaining columns. So, the first factor applies the function to $y[,1:2]$ and the second factor applies the function to $y[,3:1]$. Note carefully here that $y[,3:1]$ has reversed the order of the columns, so column 3 is compared with the other two columns. If the treatment is expected to cause an increase in the response, then comparison (1) applies the function to $y[,1:2]$ with alternative = greater, and comparison (2) applies the function to $y[,3:1]$ with alternative = less. This is illustrated in the example below which reproduces analyses from Rosenbaum (2023b). If the treatment is expected to cause a decrease in the response, then repeat these steps with y replaced by $-y$, so the treatment is expected to increase $-y$.

Note

ALTERNATIVE. Setting alternative to less is the same as changing the sign of the within-block scored rank, that is, changing $\phi(a_{ij})$ to $-\phi(a_{ij})$ in Rosenbaum (2023b); see especially equation (1) in the on-line supplement to that paper. Note carefully that setting alternative to less does not change the between block ranks, even when range=FALSE. In general, in dwgtRank, changing the alternative will give a different answer from changing y to $-y$ if range=FALSE because, unlike the range, the gap is not invariant to the sign change. I suggest using function ef2C – the recommended analysis – before trying out variations on that analysis using dwgtRank.

The dwgtRank function was designed for the evidence factor analysis with two different control groups in blocks of size 3, and this is reflected in the way alternative is defined when range=FALSE. For a simple analysis in the suggested form, use ef2C instead of dwgtRank; it calls dwgtRank with appropriate settings. If you wish to explore alternative settings for this problem, use dwgtRank. For several controls from a single control group, use wgtRank instead of dwgtRank.

Note

TIES WITHIN BLOCKS. If there are ties within blocks, then these are resolved as follows. If scores are not specified, so the within block ranks are intended to be 1, 2, ..., J, then average ranks are used for ties. If scores are specified, then ties are resolved by the ties.method="min" in the rank function in base R. This means that tied observations are all given the same rank, hence the same score, and that score corresponds with the smallest rank to which a tied group is entitled. Suppose the scores are scores=c(1,2,5) for J=3. If all three observations are different, then the smallest observation gets score 1, the middle gets 2, and the largest gets 5. If the three values are, say, 16, 14, 14 in a block, they get ranks 3, 1, 1, with scores 5, 1, 1. If the three values are 16, 16, 14 in a block, they get ranks 2, 2, 1, with scores 2, 2, 1. This is in keeping with the idea that we want to emphasize those blocks in which one observation stands well above the rest. In the example, there are no within-block ties, so the issue does not arise.

TIES BETWEEN BLOCKS. If there are ties among the I blocks in the within-block ranges or gaps, then average ranks are used for ties.

Note

This function compares the first column of y to the other columns. To implement the second evidence factor analysis in Rosenbaum (2023b), the second control group must be placed in the first column. See the examples, where y is y[,1:2] for the first evidence factor, but y becomes y[,3:1] for the second evidence factor. All of this is automated in the function ef2C.

Author(s)

Paul R. Rosenbaum

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Examples

The calculation below reproduce analyses from Rosenbaum (2023b).

```
data(aBP)
attach(aBP)

yD<-t(matrix(bpDiastolic,3,207))
yS<-t(matrix(bpSystolic,3,207))
vS<-c(yS[,1]-yS[,2],yS[,1]-yS[,3],yS[,2]-yS[,3])
vD<-c(yD[,1]-yD[,2],yD[,1]-yD[,3],yD[,2]-yD[,3])
y<-(yD/median(abs(vD)))+(yS/median(abs(vS)))
```

```

# The following analysis contrasts the second P control
# with the pooled group consisting of the treated B
# binge drinker and the N control. That contrast creates
# a second evidence factor, not redundant with the comparison
# of B and N, yet avoids dilution of the effect by using
# a statistic like that of Conover and Salsburg (1988)
# that allows for nonresponders.

# SECOND EVIDENCE FACTOR: CONTROL2 VS TREATED+CONTROL1
dwgtRank(y[,3:1],gamma=1.45,alternative="less",
         scores=c(1,2,5),range=FALSE,m=8,m1=8,m2=8)

amplify(1.45, 2.5)

# This is a much less sensitive result than is obtained
# from the stratified Wilcoxon rank sum statistic wiht
# I strata,

dwgtRank(y[,3:1],gamma=1.45,alternative="less",
         scores=c(1,2,3),m=1,m1=1,m2=1)

# and theory leads us to expect this difference
# in performance of the two statistics; see Rosenbaum (2023b)

# EVIDENCE FACTOR ANALYSIS, COMBINING TWO FACTORS
# The evidence factor analysis compares treated to the first control group,
# then compares the second control group to the pooled group consisting of
# treated and first control, then combines the two analyses using meta-analysis.
# Treated/first-control matched pairs are compared using the method in
# Rosenbaum (2011).

p1<-dwgtRank(y[,1:2],gamma=2.3,alternative="greater",
             m=8,m1=7,m2=8)$pval
p2<-dwgtRank(y[,3:1],gamma=1.45,alternative="less",
             scores=c(1,2,5),range=FALSE,m=8,m1=8,m2=8)$pval
c(p1,p2)
sensitivitymv::truncatedP(c(p1,p2))
amplify(2.3,4)
amplify(1.45,2.5)

# THE COMBINED ANALYSIS IS INSENSITIVE TO LARGER BIASES
# The combined analysis is insensitive to larger biases
# than are its components
p1<-dwgtRank(y[,1:2],gamma=2.6,alternative="greater",
             m=8,m1=7,m2=8)$pval
p2<-dwgtRank(y[,3:1],gamma=1.7,alternative="less",
             scores=c(1,2,5),range=FALSE,m=8,m1=8,m2=8)$pval
c(p1,p2)
sensitivitymv::truncatedP(c(p1,p2))

amplify(2.6,5)
amplify(1.7,3)

```

```

# CONNECTION WITH OTHER PACKAGES
# Although dwgtRank() computes the matched pair P-value bound,
dwgtRank(y[,1:2],gamma=2.3,alternative="greater",
         m=8,m1=7,m2=8)$pval
# a simpler way to do it uses senU() in the DOS2 package
DOS2::senU(y[,1]-y[,2],m=8,m1=7,m2=8,gamma=2.3)
# where senU also provides bounds on point estimates and confidence
# intervals for each gamma
DOS2::senU(y[,1]-y[,2],m=8,m1=7,m2=8,gamma=1.5,conf.int=TRUE)

detach(aBP)
rm(p1,p2)
rm(y)

# USING SIMULATION TO GET THE GENERAL IDEAS OF DESIGN SENSITIVITY
# AND THE BAHADUR EFFICIENCY OF A SENSITIVITY ANALYSIS

# IN THIS LARGE SAMPLE SIZE, THE DESIGN SENSITIVITY PREDICTS
# U888 WILL HAVE MORE POWER THAN U555, AND IT DOES.
# SEE TABLE 2 OF ROSENBAUM (2023b), NORMAL tau=1/2
# FOR U888/125/GAP AND U555/125/GAP
set.seed(1)
ss<-10000
ysim<-matrix(rnorm(3*ss),ss,3)
ysim[,1]<-ysim[,1]+sqrt(2)/2 # This is tau=1/2 for Normal errors
# Compare U888/125/gap and U555/125/gap
dwgtRank(ysim[,3:1],gamma=3,alternative="less",scores=c(1,2,5),
         range=FALSE,m=8,m1=8,m2=8)$pval
dwgtRank(ysim[,3:1],gamma=3,alternative="less",scores=c(1,2,5),
         range=FALSE,m=5,m1=5,m2=5)$pval
# IF YOU INCREASED ss FROM 10000, AS ABOVE, TO INFINITY, THE
# POWER FUNCTION WOULD TEND TO A STEP FUNCTION WITH A SINGLE
# STEP DOWN FROM POWER 1 TO POWER 0 AT THE DESIGN SENSITIVITY.

# IN THIS SMALLER SAMPLE SIZE, THE BAHADUR EFFICIENCY PREDICTS
# U555 WILL HAVE MORE POWER THAN U888, AND IT DOES.
# SEE TABLE 3 OF ROSENBAUM (2023b), NORMAL tau=1/2
# FOR U888/125/GAP AND U555/125/GAP AT UPSILON = 1.5
set.seed(1)
ss<-100
ysim<-matrix(rnorm(3*ss),ss,3)
ysim[,1]<-ysim[,1]+sqrt(2)/2 # This is tau=1/2 for Normal errors
# Compare U888/125/gap and U555/125/gap
dwgtRank(ysim[,3:1],gamma=1.5,alternative="less",scores=c(1,2,5),
         range=FALSE,m=8,m1=8,m2=8)$pval
dwgtRank(ysim[,3:1],gamma=1.5,alternative="less",scores=c(1,2,5),
         range=FALSE,m=5,m1=5,m2=5)$pval

```


Description

In an observational complete block design, with blocks of size three, each containing a treated individual and one control from each of two control groups, ef2C performs the evidence factor analysis suggested in Rosenbaum (2023). One factor compares the treated group to the first control group in a matched pairs analysis. The other factor pools the treated group and the first control group and compares it to the second control group.

Usage

```
ef2C(y, gamma = 1, upsilon = 1, alternative = "greater",
     trunc = 0.2)
```

Arguments

y	With I blocks and 3 individuals in each block, y is an I x 3 matrix or dataframe containing the outcomes. The first column is the response of the treated individual. The second response is the response of the control from the first control group. The third response is the response of the control from the second control group.
gamma	A real number ≥ 1 giving the value of the sensitivity parameter for the comparison of the treated group and the first control group. gamma=1 yields a randomization test.
upsilon	A real number ≥ 1 giving the value of the sensitivity parameter for the comparison of the second control group and the combination of the treated group plus the first control group. upsilon=1 yields a randomization test.
alternative	Use alternative="greater" if the treatment is expected to cause an increase in the response in y. Use alternative="less" if the treatment is expected to cause a decrease in the response in y. In this context, a two-sided test is best viewed as two one-sided tests with a Bonferroni correction, e.g., testing in both tails at level 0.025 to ensure overall level of 0.05; see Cox (1977). For more information, see the notes.
trunc	The two P-values from the two factors are combined using the truncated product of P-values due to Zaykin et al. (2002): it is the P-value derived from the product of those P-values that are less than trunc. For more information, see the notes.

Details

This is the recommended analysis in Rosenbaum (2023). The example below reproduces some results from the example in that paper. That paper considered 40 test statistics in terms of the Bahadur efficiency of a sensitivity – all of these analyses can be reproduced by the more flexible but more complicated dwgtRank function.

The comparison of the treated group and the first control group is equivalent to `dwgtRank(y[,1:2], gamma=gamma, m=8, m1=7)` and these settings are motivated by results in Rosenbaum (2011, 2015). Notice that `y[,1:2]` uses the first two columns of y.

The comparison of the second control group and the merger of the treated group with the first control group is equivalent to `dwgtRank(y[,3:1], gamma=upsilon, m=8, m1=8, m2=8, range=FALSE, alter-`

native="less", scores=c(1,2,5)), and these settings are motivated by results in Rosenbaum (2023). Notice that `y[,3:1]` compares the third column to the pooled group consisting of columns 1 and 2.

Value

<code>pvals</code>	Upper bounds on the one-sided P-values for the two factors and their combination.
<code>detail</code>	A matrix with some details of the computations that produced the P-values.

Note

The two P-values from the two factors are combined using the truncated product of P-values due to Zaykin et al. (2002): it is the P-value derived from the product of those P-values that are less than `trunc`. Taking `trunc=1` yields Fisher's method for combining independent P-values. Fisher's method is not ideal when combining P-value bounds produced by sensitivity analyses; see Hsu et al. (2013). Reasonable values are `trunc=.1`, `trunc=.15` and `trunc=.2`. As illustrated in the example below, lower truncation values produce smaller combined P-values when the P-values are below the truncation point, but a P-value that barely exceeds the truncation point is effectively discarded. Hsu et al. (2013) compare truncation values when used in a sensitivity analysis. For discussion of combining sensitivity analyses as independent, see the required conditions in Rosenbaum (2011b, 2021). These conditions hold for the comparison performed by `ef2C`.

Note

The setting `alternative = "less"` simply replaces `y` by `-y` before testing in the upper tail.

Note

For a deeper understanding, see the documentation of `dwgtRank`. That function is more general, but it requires more attention to detail by the user. The documentation for `dwgtRank` also produces additional analyses from Rosenbaum (2023).

Author(s)

Paul R. Rosenbaum

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Examples

```
# The calculation below reproduce analyses from Rosenbaum (2023).

data(aBP)
attach(aBP)

yD<-t(matrix(bpDiastolic,3,207))
yS<-t(matrix(bpSystolic,3,207))
vS<-c(yS[,1]-yS[,2],yS[,1]-yS[,3],yS[,2]-yS[,3])
vD<-c(yD[,1]-yD[,2],yD[,1]-yD[,3],yD[,2]-yD[,3])
y<-(yD/median(abs(vD)))+(yS/median(abs(vS)))

# EVIDENCE FACTOR ANALYSIS, COMBINING TWO FACTORS
# The evidence factor analysis compares treated to the first control group,
# then compares the second control group to the pooled group consisting of
# treated and first control, then combines the two analyses using meta-analysis.
# Treated/first-control matched pairs are compared using the method in
# Rosenbaum (2011).

ef2C(y,gamma=2.3,upsilon=1.45)
amplify(2.3,4)
amplify(1.45,2.5)

# THE COMBINED ANALYSIS IS INSENSITIVE TO LARGER BIASES
# The combined analysis is insensitive to larger biases
# than are its components
ef2C(y,gamma=2.6,upsilon=1.7)
amplify(2.6, 5)
amplify(1.7,c(2.7,3))

# The calculations above are also produced in the
# example for dwgtRank, where alternative
# analyses from Rosenbaum (2023) are compared.

#####
```

```
# Comparing truncation points to understand trunc:
ef2C(y,gamma=2.6,upsilon=1.7,trunc=.2) # Default
ef2C(y,gamma=2.6,upsilon=1.7,trunc=1) # Fisher's method
ef2C(y,gamma=2.6,upsilon=1.7,trunc=.1)
ef2C(y,gamma=2.5,upsilon=1.6,trunc=.2)
ef2C(y,gamma=2.5,upsilon=1.6,trunc=.1)
# See Hsu et al. (2013) for discussion of the
# truncation point for a sensitivity analysis.
```

wgtRank

Sensitivity Analysis for Weighted Rank Statistics in Block Designs

Description

Uses a weighted rank statistic to perform a sensitivity analysis for an $I \times J$ 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 ϕ 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. γ is the sensitivity parameter. Two individuals with the same observed covariates may differ in their odds of treatment by at most a factor of γ ; 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

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Rosenbaum, P. R. (2018). <doi:10.1214/18-AOAS1153> Sensitivity analysis for stratified comparisons in an observational study of the effect of smoking on homocysteine levels. *The Annals of Applied Statistics*, 12(4), 2312-2334.

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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$hdl,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. An 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 ranks. 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 gamma.
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 wgtRank() 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)

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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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