Package ‘fugue’

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Type Package
Title Sensitivity Analysis Optimized for Matched Sets of Varied Sizes
Version 0.1.7
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Description As in music, a fugue statistic repeats a theme in small variations. Here, the psi-
function that defines an m-statistic is slightly altered to maintain the same design sensitiv-
ity in matched sets of different sizes. The main functions in the pack-
age are sen() and senCI(). For sensitivity analyses for m-statistics, see Rosenbaum (2007) Bio-
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R topics documented:

  amplify ................................................................. 2
  mscoreInternal ...................................................... 3
  nhland3 ............................................................... 4
  sen ................................................................. 5
  senCI ............................................................... 8
  separable1v ......................................................... 11

Index 13
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 gamma. Each value of gamma amplifies to a curve (lambda, delta) 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 gamma has a two-dimensional interpretation in terms of (lambda, delta).

Usage

amplify(gamma, lambda)

Arguments

gamma  
gamma > 1 is the value of the sensitivity parameter, for instance the parameter in sensmv. length(gamma) > 1 will generate an error.

lambda  
lambda is a vector of values > gamma. An error will result unless lambda[i] > gamma > 1 for every i.

Details

A single value of gamma, say gamma = 2.2 in the example, corresponds to a curve of values of (lambda, delta), 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.

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: gamma corresponds with (lambda, delta) = (gamma, Inf) and (Inf, gamma).

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.
mscoreInternal

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

Author(s)
Paul R. Rosenbaum

References

Examples
attach(nhQandSI
sen(homocysteineLzLmsetLgamma\]QN9I
amplify(QN9Lc(SLSNULTII
detach(nhQandSI

mscoreInternal

Computes M-scores for M-tests and estimates.

Description
Of very limited interest to most users, function mscoreInternal() computes the M-scores used by functions sen().

Usage
mscoreInternal(ymat, inner, trim)

Arguments
ymat
A matrix of outcomes scaled for use in an M-statistic; see the discussion of the parameter lambda in the documentation for the sen function. If the largest matched set has K controls, and there are I matched sets, then ymat is an I x (K+1) matrix. Each row is a matched set. The first column contains the treated individual in the matched set. The remaining columns contain the controls. If a set has fewer than K controls, then its last columns are NAs.

inner
inner is the inner[i] parameter described in the documentation for sen().

trim
trim is the trim[i] parameter described in the documentation for sen().
Value

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

Author(s)

Xinran Li and Paul R. Rosenbaum

References


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nh1and3

*Smoking Matched Sets with 1 or 3 Controls*

Description

Data from NHANES 2005-2006 concerning homocysteine levels in daily smokers ($z=1$) and never smokers ($z=0$), aged 20 and older.

Usage

```r
data("nh1and3")
```

Format

A data frame with 1370 observations consisting of 353 matched pairs and 166 matched sets with 3 controls.

- **SEQN**: NHANES ID number
- **z**: =1 for a daily smoker, =0 for a never smoker
- **mset**: Matched set indicator, for 519 sets, 1, 2, ..., 519
- **homocysteine**: Blood homocysteine level
- **cigsperday30**: Cigarettes smoked per day
- **cotinine**: Cotinine is a biomarker for exposure to nicotine
- **female**: =1 for female, =0 for male
- **age**: Age in years
- **black**: =1 for black, =0 for other
- **education**: NHANES 1-5 score. 3 is a high school degree.
- **povertyr**: Ratio of family income to the poverty level, capped at 5.
Details

Data from NHANES 2005-2006 concerning homocysteine levels in daily smokers (z=1) and never smokers (z=0), aged 20 and older. Daily smokers smoked every day for the last 30 days, smoking an average of at least 10 cigarettes per day. Never smokers smoked fewer than 100 cigarettes in their lives, do not smoke now, and had no tobacco use in the previous 5 days.

Source

NHANES 2005-2006

References


Examples

data(nhland3)
attach(nhland3)
table(table(nhland3$msetII
par(mfrow=c(1,2))
boxplot(homocysteine[1:166]-z[1:166],ylim=c(0,70),main="1-1 match",
 ylab="homocysteine",names=c("Control","Smoker"))
boxplot(homocysteine[167:1370]-z[167:1370],ylim=c(0,70),
 main="1-3 match",ylab="homocysteine",names=c("Control","Smoke"))
detach(nhland3)

Description

Each matched set contains one treated individual and one or more controls. Uses Huber's M-statistic as the basis for the test, for instance, a mean. Matched sets of different sizes use different \( \psi \)-functions, creating what is called a fugue statistic. Performs either a randomization test (Gamma=1) or an analysis of sensitivity to departures from random assignment (Gamma>1). For confidence intervals, use function senCI(). The method is described in Li and Rosenbaum (2019); see also Rosenbaum (2007,2013).

Usage

sen(y, z, mset, gamma = 1, inner = NULL, trim = NULL, lambda = 1/2,
 tau = 0, alternative = "greater")
Arguments

- **y**: A vector of responses with no missing data.
- **z**: Treatment indicator, z=1 for treated, z=0 for control with length(z)==length(y).
- **mset**: Matched set indicator, 1, 2, ..., sum(z) with length(mset)==length(y). Matched set indicators should be either integers or a factor.
- **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. If the largest matched set has k controls, then inner is either a scalar or a vector with k=length(inner). If inner is a scalar, then the same value of inner is used, regardless of the number of controls. Otherwise, inner[1] is used with one control, inner[2] is used with two controls, etc. If inner is NULL, default values of inner=c(.8,.8,.6,.4,0,0,0,...,0) are used.
- **trim**: inner and trim together define the $\psi$-function for the M-statistic. If the largest matched set has k controls, then trim is either a scalar or a vector with k=length(trim). If trim is a scalar, then the same value of trim is used, regardless of the number of controls. Otherwise, trim[1] is used with one control, trim[2] is used with two controls, etc. If trim is NULL, default values of trim=c(3,3,...,3) are used. For each i, 0 <= inner[i] < trim[i] < Inf.
- **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=Inf and inner=0. 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

The novel element in the fugue package is the automatic use of different $\psi$-functions for matched sets of different sizes. These $\psi$-functions have been selected to approximately equate the design sensitivities in sets of unequal sizes when the errors are Normal and the additive effect is half the standard deviation of a matched pair difference; see Li and Rosenbaum (2019). If you disable this automatic feature by manually setting a single value for inner and trim, then the results will agree with senm() in the R package sensitivitymult. For instance, using both sen() in the fugue package and senm() in the sensitivitymult package will yield the same deviate and P-value in: data(nh1and3) attach(nh1and3) sen(homocysteine,z,mset,inner=0,gamma=1.9) senm(homocysteine,z,mset,inner=0,trim=3,gamma=1.9)
Note that the sensitivitymult package is intended to implement methods from Rosenbaum (2016, 2019) that are not implemented in the fugue package.

For the given $\Gamma$, sen() 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, sen() 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, 2018).

**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 sen() 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 a 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.

The examples reproduce some results from Li and Rosenbaum (2019).

**Author(s)**

Xinran Li and Paul R. Rosenbaum.

**References**


### Examples

# Reproduces results from Table 3 of Li and Rosenbaum (2019)
data(nhland3)
attach(nhland3)
sen(homocysteine, z, mset, gamma=1)
sen(homocysteine, z, mset, gamma=1.9)
sen(homocysteine, z, mset, inner=0, gamma=1.9)
amplify(1.9, c(3, 3.5, 4))
detach(nhland3)

---

**senCI**

*Sensitivity Analysis for Point Estimates and Confidence Intervals in an Observational Study.*

### Description

Each matched set contains one treated individual and one or more controls. Uses Huber’s M-statistic as the basis for the test; see Maritz (1979). Matched sets of different sizes use different $\psi$-functions, creating what is called a fugue statistic. Performs either a randomization test ($\Gamma = 1$) or an analysis of sensitivity to departures from random assignment ($\Gamma > 1$). For hypothesis tests, use function `sen()`. The method is described in Li and Rosenbaum (2019); see also Rosenbaum (2007, 2013).

### Usage

```r
senCI(y, z, mset, gamma = 1, inner = NULL, trim = NULL, lambda = 1/2, 
alpha = 0.05, alternative = "greater")
```
Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>y</td>
<td>A vector of responses with no missing data.</td>
</tr>
<tr>
<td>z</td>
<td>Treatment indicator, z=1 for treated, z=0 for control with length(z)==length(y).</td>
</tr>
<tr>
<td>mset</td>
<td>Matched set indicator, 1, 2, ..., sum(z) with length(mset)==length(y). Matched set indicators should be either integers or a factor.</td>
</tr>
<tr>
<td>gamma</td>
<td>Gamma is the sensitivity parameter Γ, where Γ ≥ 1. Setting Γ = 1 is equivalent to assuming ignorable treatment assignment given the matched sets, and it performs a within-set randomization test.</td>
</tr>
<tr>
<td>inner</td>
<td>inner and trim together define the ψ-function for the M-statistic. If the largest matched set has k controls, then inner is either a scalar or a vector with k=length(inner). If inner is a scalar, then the same value of inner is used, regardless of the number of controls. Otherwise, inner[1] is used with one control, inner[2] is used with two controls, etc. If inner is NULL, default values of inner=c(.8,.8,.6,.4,0,0,0,...,0) are used.</td>
</tr>
<tr>
<td>trim</td>
<td>inner and trim together define the ψ-function for the M-statistic. If the largest matched set has k controls, then trim is either a scalar or a vector with k=length(trim). If trim is a scalar, then the same value of trim is used, regardless of the number of controls. Otherwise, trim[1] is used with one control, trim[2] is used with two controls, etc. If trim is NULL, default values of trim=c(3,3,...,3) are used. For each i, 0 &lt;= inner[i] &lt; trim[i] &lt; Inf.</td>
</tr>
<tr>
<td>lambda</td>
<td>Before applying the ψ-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=Inf and inner=0. See Maritz (1979) for the paired case and Rosenbaum (2007) for matched sets. An error will result unless 0 &lt; lambda &lt; 1.</td>
</tr>
<tr>
<td>alpha</td>
<td>The coverage rate of the confidence interval is 1-α. If the bias in treatment assignment is at most Γ, then the confidence interval covers at rate 1-α.</td>
</tr>
<tr>
<td>alternative</td>
<td>If alternative=&quot;greater&quot; or alternative=&quot;less&quot;, the a one-sided confidence interval is returned. If alternative=&quot;twosided&quot;, a somewhat conservative two-sided confidence interval is returned. See the discussion of two-sided tests in the documentation for sen().</td>
</tr>
</tbody>
</table>

Details

The confidence interval inverts the test provided by sen(). See the documentation for sen() for more information.

The upper bound on the P-value is based on the separable approximation described in Gastwirth, Krieger and Rosenbaum (2000); see also Rosenbaum (2007, 2018).

Value

- **point.estimates**
  - For Γ > 1, an interval of point estimates is returned. Γ = 1, the interval is a point.
- **confidence.interval**
  - The confidence interval.
Note

The examples reproduce some results from Li and Rosenbaum (2019).

Author(s)

Xinran Li and Paul R. Rosenbaum.

References

Li, Xinran and Rosenbaum, P. R. (2019) Maintaining high constant design sensitivity in observational studies with matched sets of varying sizes. Manuscript.

Examples

```r
## Not run:
# Reproduces results from Table 3 of Li and Rosenbaum (2019)
data(nhand3)
attach(nhand3)
senCI(homocysteine,z,mset,alternative="twosided")
senCI(homocysteine,z,mset,alternative="less",tau=2.1721733)
senCI(homocysteine,z,mset,alternative="less",gamma=1.75)
# Relationships between confidence intervals and P-value bounds
senCI(homocysteine,z,mset,alternative="twosided",gamma=1.75)
sen(homocysteine,z,mset,alternative="less",tau=2.21721733,gamma=1.75)
sen(homocysteine,z,mset,alternative="less",gamma=1.75)
detach(nhand3)
```

## End(Not run)
separable1v

Asymptotic separable calculations internal to other functions.

Description

Of limited interest to most users, this general purpose function is internal to other functions in the package. It is the same function as in the sensitivitymv package, version 1.3. The function performs the asymptotic separable calculations described in Gastwirth, Krieger and Rosenbaum (2000) and Rosenbaum (2018), as used in section 4 of Rosenbaum (2007). See the sensitivitymv package for an example.

Usage

separable1v(ymat, gamma = 1)

Arguments

ymat is a matrix whose rows are matched sets and whose columns are matched individuals. The first column describes treated individuals. Other columns describe controls. If matched sets contain variable numbers of controls, NAs fill in empty spaces in ymat; see the documentation for senmv. In senmv, the matrix ymat is created by mscorev. Instead, if there were no NAs and ranks within rows were used in ymat, then separable1v would perform a sensitivity analysis for the stratified Wilcoxon two-sample test. Applied directly to data, it performs a sensitivity analysis for the permutational t-test.

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

Value

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

Author(s)

Paul R. Rosenbaum
References


Index

*Topic datasets
   nh1and3, 4

*Topic htest
   sen, 5
   senCI, 8

*Topic robust
   sen, 5
   senCI, 8

amplify, 2

mscoreInternal, 3

nh1and3, 4

sen, 5
senCI, 8
separable1v, 11