Package ‘meta.shrinkage’

January 3, 2022

Type Package
Title Meta-Analyses for Simultaneously Estimating Individual Means
Version 0.1.2
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Description Implement meta-analyses for simultaneously estimating individual means with shrinkage, isotonic regression and pretests. Include our original implementation of the isotonic regression via the pool-adjacent-violators algorithm (PAVA) algorithm.
This methodology is published in Taketomi et al.(2021) <doi:10.3390/axioms10040267>.
License GPL-2
Encoding UTF-8
NeedsCompilation no
Repository CRAN
Date/Publication 2022-01-03 16:50:05 UTC

R topics documented:

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gpt 

The General Pretest(GPT) Estimator for Sparse Means

Description

This function is used to calculate the general pretest(GPT) estimator for individual means under sparse means. The methodology is described in detail in Section 3.3 of Taketomi et al. (2021). An example shows the application of this method to the gastric cancer data of GASTRIC group (2013).
Usage

gpt(y,s,alpha1=0.05,alpha2=0.10,q=0.5)

Arguments

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<td>y</td>
<td>a vector for estimates</td>
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<tr>
<td>s</td>
<td>a vector for standard errors of y</td>
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<tr>
<td>alpha1</td>
<td>significance level for testing (0&lt;alpha1&lt;1)</td>
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Value

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Author(s)

Nanami Taketomi, Takeshi Emura

References


Examples

#Estimates from the gastric cancer studies(Taketomi et al.(2021); GASTRIC group (2013))
y<-c(-0.18312,-0.72266,-0.48507,-0.23961,-0.13226,-0.27228,-0.5867,-0.13969,
     -0.1004,-0.31143,-0.04949,-0.11685,-0.13044,0.04391)

#Standard errors(Taketomi et al. (2021))
s<-c(0.15372,0.28686,0.33192,0.21558,0.14691,0.14416,0.24885,
    0.14542,0.16404,0.17038,0.19818,0.16476,0.19268,0.17632)

#Pretest(PT) estimator and general pretest(GPT) estimator

gpt(y,s)
James-Stein (JS) Estimator and Positive-Part JS Estimator for Means

Description
This function computes the James-Stein (JS) shrinkage estimators for means. The detail of this estimation is described in Section 3.1 of Taketomi et al. (2021). An example shows the application of this method to the gastric cancer data of GASTRIC group (2013).

Usage
js(y, s)

Arguments
y  a vector for estimates
s  a vector for standard errors of y

Value
JS  James-Stein (JS) estimator for y
JS_plus  positive-part JS estimator for y

Author(s)
Nanami Taketomi, Takeshi Emura

References


Examples
# Estimates from the gastric cancer studies (Taketomi et al. (2021); GASTRIC group (2013))
y<-c(-0.18312,-0.72266,-0.48507,-0.23961,-0.13226,-0.27228,-0.5867,-0.13969,
    -0.1004,-0.31143,-0.04949,-0.11685,-0.13044,0.04391)

# Standard errors (Taketomi et al. (2021))
s<-c(0.15372,0.28686,0.33192,0.21558,0.14691,0.14416,0.24885,
    0.14542,0.16404,0.17038,0.19818,0.14676,0.19268,0.17632)

# JS estimator and JS-plus estimator
js(y, s)
rjs

Restricted James-Stein (JS) Estimator Under Ordered Means

Description
This function is used to calculate the James-Stein (JS) shrinkage estimator under ordered means. The calculation of this estimator includes pooled-adjacent-violators algorithm (PAVA). Technical details are described in Taketomi et al. (2021). An example shows the application to the COVID-19 data from Pranata et al. (2020). This application is also described in Section 5.2 of Taketomi et al. (2021).

Usage
rjs(y, s, x=1:length(y), id=1:length(y), decreasing=FALSE)

Arguments
- **y**: a vector for estimates
- **s**: a vector for standard errors of y
- **x**: a numeric vector for covariates to define the order of studies. Default implies the serial number assigned to the dataset.
- **id**: a vector for the names of studies. The elements of this vector are numeric or character.
- **decreasing**: logical scalar - Whether to sort the dataset in decreasing order by x or not.

Value
- **id**: the names of studies
- **x**: a numeric vector for a covariate that is used to sort the dataset.
- **RJS**: Restricted JS estimator
- **RJS_plus**: positive-part restricted JS estimator

Author(s)
Nanami Taketomi, Takeshi Emura

References
# Examples

Examples from the COVID-19 data (Taketomi et al. (2021); Pranata et al. (2020))

```r
y <- c(0.6881, 0.5933, 1.1756, 0.5365, 0.5878, 0.4637, 0.5247, 1.2326, 2.8904, 1.1378)
```

standard errors of estimates

```r
s <- c(0.6732, 0.2754, 0.2821, 0.2493, 0.1713, 0.3302, 0.0956, 0.3272, 0.1489, 1.4263, 0.2097)
```

The proportions of males of each study

```r
x <- c(56.4, 63.0, 52.0, 49.0, 62.1, 49.5, 82.0, 58.0, 47.9, 45.0, 62.0)
```

Note that in rjs function, y is sorted by x before calculating RML estimator.

The names of studies

```r
```

rjs(y, s, x, id, decreasing = TRUE)

---

rml  

The Ordered Restricted Maximum Likelihood Estimator under Ordered Means

## Description

This function provides the restricted maximum likelihood (RML) estimator under ordered means using Pooled-Adjacent-Violators Algorithm (PAVA). The technical details and examples for this estimator are described in Section 3.2 of Taketomi et al. (2021). An example shows the application to the COVID-19 data from Pranata et al. (2020). This application is also described in Section 5.2 of Taketomi et al. (2021).

## Usage

```r
rml(y, x=1:length(y), id=1:length(y), decreasing=FALSE, test=FALSE)
```

## Arguments

- `y`: a vector of estimates
- `x`: a numeric vector for a covariate that is interested in the relationship between ordered means. Default implies the serial number assigned to the dataset.
- `id`: a vector for the names of studies. The elements of this vector are numeric or character.
- `decreasing`: logical scalar - Whether to sort the dataset in decreasing order by x or not. If decreasing=TRUE, RML in the output is estimators under the assumption that the y is monotonically decreasing with respect to x.
test

logical scalar - Whether to test for correlation between x and y, and to fit the lowess. If test=TRUE, the scatter plot of x and y and the curve fitting of lowess are described in the output.

Value

id

the names of studies

x

a numeric vector for a covariate that is used to sort the dataset.

RML

the ordered restricted estimator for y using PAVA

Author(s)

Nanami Taketomi, Takeshi Emura

References


Examples

#Estimates from the COVID-19 data (Taketomi et al.(2021); Pranata et al.(2020))
y<-c(0.6881,0.5933,1.1756,0.5365,0.678,0.5878,0.4637,0.5247,1.2326,2.8904,1.1378)

#Proportions of males of each study
x<-c(56.4,63.0,52.0,49.0,62.1,49.5,82.0,58.0,47.9,45.0,62.0)

#Under the assumption that y is monotonically decreasing with respect to x,
#input decreasing=TRUE(the dataset is sorted by in decreasing order by x).
rml(y,x,decreasing=TRUE)

#If test=TRUE, we can confirm Kendall's tau and lowess plot for x and y.
rml(y,x,decreasing=TRUE,test=TRUE)

#If x and decreasing are default, the dataset is sorted by
#in the serial numbers of studies
#and RML in the output is under the assumption
#that y is monotonically increasing with respect to serial numbers.
rml(y)

#If x is default and decreasing=TRUE, the dataset is sorted by
#in decreasing the serial numbers of studies
#and RML in the output is under the assumption
that y is monotonically decreasing with respect to serial numbers.
```
rml(y, decreasing=TRUE)
```
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