Package 'skrmdb'

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Type Package

Title Package to estimate ED50

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Author David Siev

Maintainer Marie Vendettuoli <marie.c.vendettuoli@aphis.usda.gov>

Description Package to estimate ED50 by the methods of Spearman-Karber,
Reed-Muench, Dragstedt-Behrens. No endorsement, claim, or warranty is
implied for this package. It is made available for investigational or pedagogical use only

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LazyLoad yes

Depends R (>= 3.4.4)

Imports methods, stats

Collate 'class-skrmdb.r' 'skrmdb-package.r' 'aaa.r' 'bbb.r'
'dragbehr.r' 'reedmuench.r' 'skrmdb.R'

RoxygenNote 6.0.1

NeedsCompilation no

R topics documented:

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skrmdb-package   *skrmdb package.*

Description

Includes functions to estimate ED50 by the methods of Spearman-Karber, Reed-Muench, Dragstedt-Behrens.

For internal use only at the USDA Center for Veterinary Biologics

Details

Package:	skrmdb-package
Type:	Package
Version:	4.2.5
Date:	2018-08-03
License:	MIT
LazyLoad:	yes
LazyData:	yes

Resources

- QUICK START: https://github.com/ABS-dev/skrmdb/blob/master/README.md
- PACKAGE VIGNETTE: https://www.aphis.usda.gov/animal_health/vet_biologics/publications/STATWI0001.pdf
- BUG REPORTS: https://github.com/ABS-dev/skrmdb/issues

Author(s)

David Siev <David.Siev@aphis.usda.gov>

DragBehr   *Dragstedt-Behrens estimator*

Description

Gives the Dragstedt-Behrens estimate of median effective dose (ED50)

Usage

```
DragBehr(formula = NULL, data = NULL, y, n, x, warn.me = T, show = F)
```

Arguments

`formula`	a formula of the form `cbind(y,n) ~ x`
`data`	a data frame
`y`	the number responding (response should be monotone increasing)
`n`	the group size
`x`	log dilution or dose
`warn.me`	boolean to give warning message
`show`	boolean to display extended summary

Details

Data input may either be a formula and data frame, or variables may be input directly (see example).

The Dragstedt-Behrens method estimates the median effective dose by interpolating between the two doses that bracket the dose producing median response. It accumulates sums in both directions by assuming that those that responded at a lower dose would respond at a higher dose, and those that did not respond at a higher dose would not respond at a lower dose. The hypothetical fraction that would have responded at a particular dose is estimated from the cumulative sums at that dose. The ED50 is estimated by interpolation on the line that connects the hypothetical fractions of the bracketing doses.

Value

object of SKRMDB class with slots:

`ed`	Estimated median effective dose (ED50)
`eval`	Evaluation method: 'DragBehr'

Note

Many microbiology texts mistakenly present the Dragstedt-Behrens method as the Reed-Muench method.

And yes, it is absurd to have an R function for an archaic method developed to avoid complex calculations.

Input data is expected to be sorted by x (either increasing or decreasing). Use of unsorted data will result in error.

Author(s)

David Siev <David.Siev@aphis.usda.gov>

References

Miller, Rupert G. (1973). Nonparametric estimateors of the mean tolerance in bioassay. *Biometrika.* **60: 535 - 542**.

Behrens, B. (1929) Zur Auswertung der Digitalisblatter im Froschversuch. *Arkiv fur Experimentelle*

Pathologie und Pharmakologie. **140: 237-256**.

Dragstedt, CA., Lang, VF. (1928). Respiratory Stimulants in acute poisoning in rabbits. *J. of Pharmacology* **32: 215–222**.

See Also

The function ReedMuench gives the Reed-Muench estimate of ED50, SKRMDB-class

Examples

```
X <- data.frame(dead=c(0,3,5,8,10,10),total=rep(10,6),dil=1:6)
DragBehr(cbind(dead,total) ~ dil, X)
# or
DragBehr(y=c(0,3,5,8,10,10), n=rep(10,6), x=1:6)

#           db
#      2.906593


## Not run:

## unordered data
X2 <- data.frame(dead = c(10,8,5,3,0), total = rep(10, 5), dil = c(1, 3, 2, 4, 5))
DragBehr(cbind(dead,total) ~ dil, X2)
DragBehr(y = X2$dead, n = X2$total, x = X2$dil)

## monotone decreasing (note that x variable direction is ignored!!)
reverse <- data.frame(dead = c(10, 8, 5, 3, 0), total = rep(10, 5), dil = 5:1)
DragBehr(cbind(dead,total) ~ dil, reverse)
DragBehr(y = reverse$dead, n = reverse$total, x = reverse$dil)

## not monotone
X3 <- data.frame(dead = c(1:3, 5, 4), total = rep(10, 5), dil = 1:5 )
DragBehr(cbind(dead, total) ~ dil, X3)
DragBehr(y = X3$dead, n = X3$total, x = X3$dil)

## End(Not run)
```

---

getED | *Accessor to retrieve the numeric median effective dose from a SKR-MDB or sk object*

Description

This is an accessor function for retrieving the numeric value of effective from a SKRMDB or sk data object object generated by ReedMuench, SpearKarb or DragBehr

Usage

```
getED(x)

## S4 method for signature 'SKRMDB'
getED(object)
```

Arguments

object   class SKRMDB or sk

Author(s)

Marie Vendettuol <marie.c.vendettuoli@aphis.usda.gov>

See Also

[SKRMDB-class](), [sk-class]()

Examples

```
## with an object of class SKRMDB
temp1 <- DragBehr(y=c(0,3,5,8,10,10), n=rep(10,6), x=1:6)
getED(temp1)
##  with an object of class sk
X <- data.frame(dead=c(0,3,5,8,10), total=rep(10,5), dil=1:5)
temp2 <- SpearKarb(cbind(dead,total) ~ dil, X)
getED(temp2)
```

ReedMuench   *Reed-Muench estimator*

Description

Gives the Reed-Muench estimate of median effective dose (ED50)

Usage

```
ReedMuench(formula = NULL, data = NULL, y, n, x, warn.me = T, show = F)
```

Arguments

formula	a formula of the form cbind(y,n) ~ x
data	a data frame
y	the number responding (response should be monotone increasing)
n	the group size
x	log dilution or dose
warn.me	boolean to give warning message
show	boolean to display extended summary

Details

Data input may either be a formula and data frame, or variables may be input directly (see example).

The Reed-Muench method estimates the median effective dose by interpolating between the two doses that bracket the dose producing median response. It accumulates sums in both directions that represent the hypothetical number that would have responded or not at each dose. It does so by assuming that those that responded at a lower dose would respond at a higher dose, and those that did not respond at a higher dose would not respond at a lower dose. The ED50 is the intersection of the lines connecting the two sets of cumulative sums between the bracketing doses.

Value

object of class SKRMDB with slots:

ed	Estimated median effective dose (ED50)
eval	Evaluation method: 'ReedMuench'

Note

Many microbiology texts mistakenly present the Dragstedt-Behrens method as the Reed-Muench method.

And yes, it is absurd to have an R function for an archaic method developed to avoid complex calculations.

Input data is expected to be sorted by X variable (either increasing or decreasing). Use of unsorted X variables will result in error. Y variables are evaluated for monotone, increasing or decreasing; however the estimate will be calculated in the original order regardless.

Author(s)

David Siev <David.Siev@aphis.usda.gov>

References

Miller, Rupert G. (1973). Nonparametric estimateors of the mean tolerance in bioassay. *Biometrika.* **60: 535 − 542**.

Reed LJ, Muench H (1938). A simple method of estimating fifty percent endpoints. *American Journal of Hygiene.* **27:493–497.**

See Also

The function [DragBehr] gives the Dragstedt-Behrens estimate of ED50 [SKRMDB-class]

Examples

```
X <- data.frame(dead=c(0,3,5,8,10,10),total=rep(10,6),dil=1:6)
ReedMuench(cbind(dead,total) ~ dil, X)
# or
ReedMuench(y=c(0,3,5,8,10,10), n=rep(10,6), x=1:6)

#         rm
#   2.916667


## Not run:

## unordered data
X2 <- data.frame(dead = c(10,8,5,3,0), total = rep(10, 5), dil = c(1, 3, 2, 4, 5))
ReedMuench(cbind(dead,total) ~ dil, X2)
ReedMuench(y = X2$dead, n = X2$total, x = X2$dil)
```

```
## monotone decreasing (note that x variable direction is ignored!!)
reverse <- data.frame(dead = c(10, 8, 5, 3, 0), total = rep(10, 5), dil = 5:1)
ReedMuench(cbind(dead,total) ~ dil, reverse)
ReedMuench(y = reverse$dead, n = reverse$total, x = reverse$dil)

## not monotone
X3 <- data.frame(dead = c(1:3, 5, 4), total = rep(10, 5), dil = 1:5 )
ReedMuench(cbind(dead, total) ~ dil, X3)
ReedMuench(y = X3$dead, n = X3$total, x = X3$dil)

## End(Not run)
```

---

sk-class   *Class definition for sk object*

Description

The sk object holds values for the Spear Karb estimator for median estimated dose. It extends the SKRMDB data object with value for variance.

Details

eval Evaluation method. "SpearKarb". Character string.

ed Median effective dose by eval method. Numeric.

sk.var variance. Numeric.

Author(s)

Marie Vendettuoli <marie.c.vendettuoli@aphis.usda.gov>

See Also

SKRMDB-class

Examples

```
new('sk', sk.var = 0.06888889, ed = 2.9, eval = "SpearKarb")
```

SKRMDB-class   *Class definition for SKRMDB object*

Description

The SKRMDB object holds output from functions in the SKRMDB package.

Details

eval Evaluation method. One of 'ReedMeunch', 'SpearKarb', or 'DragBehr'. Character string.

ed Median effective dose by eval method. Numeric.

Author(s)

Marie Vendettuoli <marie.c.vendettuoli@aphis.usda.gov>

See Also

sk-class

Examples

```
new("SKRMDB", ed = 2.906593, eval = "DragBehr")
```

SpearKarb	*Spearman-Karber estimator*

Description

Gives the Spearman-Karber estimate of the mean effective dose

Usage

```
SpearKarb(formula = NULL, data = NULL, y, n, x)
```

Arguments

formula	a formula of the form cbind(y,n) ~ x
data	a data frame
y	the number responding (response should be monotone increasing)
n	the group size
x	log dilution or dose

Details

Data input may either be a formula and data frame, or variables may be input directly (see example).

The Spearman-Karber method gives a non-parametric estimate of the mean of a tolerance distribution from its empirical distribution (EDF). The empirical PMF is derived from the EDF by differencing and the estimator is $\sum x f(x)$. If the EDF does not cover the entire support of x, SpearKarb() extends it by assuming the next lower dilution would produce zero response and the next higher dilution would produce complete response.

Value

object of class sk

ed	estimator of mean response
sk.var	variance
eval	evaluation method: 'SpearKarb'

Note

Input data is expected to be sorted by X variable (either increasing or decreasing). Use of unsorted X variables will result in error. Y variables are evaluated for monotone, increasing or decreasing; however the estimate will be calculated in the original order regardless of direction.

Author(s)

David Siev <David.Siev@aphis.usda.gov>

References

Miller, Rupert G. (1973). Nonparametric estimateors of the mean tolerance in bioassay. *Biometrika.* **60: 535 – 542**.

Karber, G. (1931). Beitrag zur kollektiven Behandlung Parmakogischer Reihenversuche. *Archiv fur Experimentelle Pathologie und Pharmakologie.* **162: 480–487**.

Spearman, C. (1908). The method of "right and wrong cases" ("constant stimuli") without Gauss's formulae. *Brit J. of Psychology.* **2: 227–242.**

Examples

```
X <- data.frame(dead=c(0,3,5,8,10), total=rep(10,5), dil=1:5)
SpearKarb(cbind(dead,total) ~ dil, X)


#        sk      sk.var
#2.90000000 0.06888889


# without zero and complete response
X <- data.frame(dead=c(3,5,8),total=rep(10,3),dil=2:4)
SpearKarb(cbind(dead,total) ~ dil, X)
# or
SpearKarb(y=c(3,5,8), n=rep(10,3), x=2:4)

#         sk      sk.var
#2.90000000 0.06888889


## Not run:
## unordered
X2 <- data.frame(dead = c(10,8,5,3,0), total = rep(10, 5), dil = c(1, 3, 2, 4, 5))
SpearKarb(cbind(dead,total) ~ dil, X2)
SpearKarb(y = X2$dead, n = X2$total, x = X2$dil)

## monotone decreasing (note that x variable direction is ignored!!)
reverse <- data.frame(dead = c(10, 8, 5, 3, 0), total = rep(10, 5), dil = 5:1)
SpearKarb(cbind(dead,total) ~ dil, reverse)
SpearKarb(y = reverse$dead, n = reverse$total, x = reverse$dil)

## not monotone
X3 <- data.frame(dead = c(1:3, 5, 4), total = rep(10, 5), dil = 1:5 )
SpearKarb(cbind(dead, total) ~ dil, X3)
SpearKarb(y = X3$dead, n = X3$total, x = X3$dil)
```

```
## End(Not run)
```

Index