

Package ‘TestingSimilarity’

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Type Package

Title Bootstrap Test for Similarity of Dose Response Curves Concerning the Maximum Absolute Deviation

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Description Provides a bootstrap test which decides whether two dose response curves can be assumed as equal concerning their maximum absolute deviation. A plenty of choices for the model types are available, which can be found in the 'DoseFinding' package, which is used for the fitting of the models.

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Imports lattice, DoseFinding, alabama

LazyData TRUE

NeedsCompilation no

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betaMod	<i>Implementation of Beta models</i>
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Description

Beta model:

$$m(d, \theta) = E_0 + E_{max} B(\delta_1, \delta_2) (d/scal)^{\delta_1} (1 - d/scal)^{\delta_2}$$

with

$$B(\delta_1, \delta_2) = (\delta_1 + \delta_2)^{\delta_1 + \delta_2} / (\delta_1^{\delta_1} \delta_2^{\delta_2})$$

and *scal* is a fixed dose scaling parameter.

Usage

betaMod(d, e, scal)

Arguments

d	real-valued argument to the function (dose variable)
e	model parameter
scal	fixed dose scaling parameter

Value

Response value.

bootstrap_test	<i>Bootstrap test for testing dose response curves for similarity concerning the maximum absolute deviation</i>
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Description

Function for testing whether two dose response curves can be assumed as equal concerning the hypotheses

$$H_0 : \max_{x \in \mathcal{X}} |m_1(d, \theta_1) - m_2(d, \theta_2)| \geq \epsilon \text{ vs. } H_1 : \max_{x \in \mathcal{X}} |m_1(d, \theta_1) - m_2(d, \theta_2)| < \epsilon.$$

See <http://arxiv.org/pdf/1505.05266.pdf> for details.

Arguments

data1, data2	data frame for each of the two groups containing the variables referenced in dose and resp
m1, m2	model types. Built-in models are "linlog", "linear", "quadratic", "emax", "exponential", "sigEmax", "betaMod" and "logistic"
epsilon	positive argument specifying the hypotheses of the test
B	number of bootstrap replications. If missing, default value of B is 5000
bnds1, bnds2	bounds for the non-linear model parameters. If not specified, they will be generated automatically
plot	if TRUE, a plot of the absolute difference curve of the two estimated models will be given
scal, off	fixed dose scaling/offset parameter for the Beta/ Linear in log model. If not specified, they are 1.2*max(dose) and 1 respectively

Value

A list containing the p.value, the maximum absolute difference of the models, the estimated model parameters and the number of bootstrap replications. Furthermore plots of the two models are given.

References

<http://arxiv.org/pdf/1505.05266.pdf>

Examples

```
library("DoseFinding")
library("alabama")
data(IBScovars)
male<-IBScovars[1:118,]
female<-IBScovars[119:369,]
bootstrap_test(male, female, "linear", "emax", epsilon=0.35, B=300)
```

 dff

Implementation of absolute difference function

Description

Function calculating the absolute difference of two dose response models:

$$dff(d, \theta_1, \theta_2) = |m_1(d, \theta_1) - m_2(d, \theta_2)|$$

Usage

```
dff(d, alpha, beta, m1, m2)
```

Arguments

d	real-valued argument to the function (dose variable)
alpha,beta	model parameters (real vectors)
m1,m2	model types. Built-in models are "linlog", "linear", "quadratic", "emax", "exponential", "sigEmax", "betaMod" and "logistic"

Value

Response value for the absolute difference of two models.

emax *Implementation of EMAX models*

Description

Emax model:

$$m(d, \theta) = E_0 + E_{max} \frac{d}{ED_{50} + d}$$

Usage

emax(d, e)

Arguments

d	real-valued argument to the function (dose variable)
e	model parameter

Value

Response value.

exponential *Implementation of exponential models*

Description

Exponential model:

$$m(d, \theta) = E_0 + E_1(\exp(d/\delta) - 1)$$

Usage

exponential(d, e)

Arguments

d real-valued argument to the function (dose variable)
e model parameter

Value

Response value.

linear

Implementation of linear models

Description

Linear model:

$$m(d, \theta) = E_0 + \delta d$$

Usage

linear(d, e)

Arguments

d real-valued argument to the function (dose variable)
e model parameter

Value

Response value.

linlog

Implementation of linear in log models

Description

Linear in log Model model:

$$m(d, \theta) = E_0 + \delta \log(d + off)$$

and *off* is a fixed offset parameter.

Usage

linlog(d, e, off)

Arguments

d	real-valued argument to the function (dose variable)
e	model parameter
off	fixed offset parameter

Value

Response value.

logistic	<i>Implementation of logistic models</i>
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Description

Logistic model:

$$m(d, \theta) = E_0 + \frac{E_{max}}{1 + \exp[(ED_{50} - d)/\delta]}$$

Usage

logistic(d, e)

Arguments

d	real-valued argument to the function (dose variable)
e	model parameter

Value

Response value.

quadratic	<i>Implementation of quadratic models</i>
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Description

Quadratic model:

$$m(d, \theta) = E_0 + \beta_1 d + \beta_2 d^2$$

Usage

quadratic(d, e)

Arguments

d	real-valued argument to the function (dose variable)
e	model parameter

Value

Response value.

sigEmax

Implementation of Sigmoid Emax models

Description

Sigmoid Emax Model model:

$$m(d, \theta) = E_0 + E_{max} \frac{d^h}{ED_{50}^h + d^h}$$

Usage

sigEmax(d, e)

Arguments

d	real-valued argument to the function (dose variable)
e	model parameter

Value

Response value

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