Package ‘TestingSimilarity’

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Type Package

Title Bootstrap Test for the 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. See <doi:10.1080/01621459.2017.1281813> for details.

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Contents

`betaMod` *Implementation of Beta models*

Description

Beta model:

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

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` *Bootstrap test for the equivalence of dose response curves via the maximum absolute deviation*

Description

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

$$H_0 : \max_{d\in\mathcal{D}} |m_1(d, \beta_1) - m_2(d, \beta_2)| \geq \epsilon\ vs.\ H_1 : \max_{d\in\mathcal{D}} |m_1(d, \beta_1) - m_2(d, \beta_2)| < \epsilon,$$

where

$$\mathcal{D}$$

denotes the dose range. See https://doi.org/10.1080/01621459.2017.1281813 for details.

Usage

```
bootstrap_test(data1, data2, m1, m2, epsilon, B = 2000, bnds1 = NULL,
  bnds2 = NULL, plot = FALSE, scal = NULL, off = NULL)
```

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

https://doi.org/10.1080/01621459.2017.1281813

Examples

```
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:

$$dff(d, \beta_1, \beta_2) = |m_1(d, \beta_1) - m_2(d, \beta_2)|$$

Usage

```
dff(d, beta1, beta2, m1, m2)
```

Arguments

`d`	real-valued argument to the function (dose variable)
`beta1, beta2`	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:

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

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:

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

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:

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

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:

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

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` *Implementation of logistic models*

Description

Logistic model:

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

Usage

```
logistic(d, e)
```

Arguments

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

Value

Response value.

`quadratic` *Implementation of quadratic models*

Description

Quadratic model:

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

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:

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

Usage

```
sigEmax(d, e)
```

Arguments

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

Value

Response value

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