

# Package ‘TestingSimilarity’

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**Type** Package

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

**Version** 1.1

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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](https://doi.org/10.1080/01621459.2017.1281813)> for details.

**License** GPL-3

**Depends** lattice, DoseFinding, alabama

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betaMod	<i>Implementation of Beta models</i>
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**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.

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bootstrap_test	<i>Bootstrap test for the equivalence of dose response curves via 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

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

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)
```

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 dff

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*Implementation of absolute difference function*


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**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.

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emax	<i>Implementation of EMAX models</i>
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**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.

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exponential	<i>Implementation of exponential models</i>
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**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.

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linear                    *Implementation of linear models*

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**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.

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linlog                    *Implementation of linear in log models*

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**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.

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logistic	<i>Implementation of logistic models</i>
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**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.

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quadratic	<i>Implementation of quadratic models</i>
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**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.

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sigEmax

*Implementation of Sigmoid Emax models*

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**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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