Package ‘ed50’

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Type Package
Title Estimate ED50 and Its Confidence Interval
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Description Functions of five estimation method for ED50 (50 percent effective dose) are provided, and they are respectively Dixon-Mood method (1948) <doi:10.2307/2280071>, Choi's original turning point method (1990) <doi:10.2307/2531453> and it's modified version given by us, as well as logistic regression and isotonic regression. Besides, the package also supports comparison between two estimation results.
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bootBC.ci  
Estimate Confidence Interval of ED50 Using Isotonic Regression

Description
Estimate confidence interval of ED50 using isotonic regression based on bootstrap method.

Usage
bootBC.ci(tObserved, tBoot, conf = 0.95)

Arguments
- tObserved: the vector of observed statistics.
- tBoot: The matrix with R rows each of which is a bootstrap replicate of the statistics.
- conf: Confidence level.

Examples
library(ed50)
library(boot)
pavaData <- preparePava(groupS)
bootResult <- boot(data = groupS,
  statistic = bootIsotonicRegression,
  R = 10,
  sim = 'parametric',
  ran.gen = bootIsotonicResample,
  mle = list(baselinePava = pavaData,
    firstDose = 2.5,
    PROBABILITY.GAMMA = 0.5),
  baselinePava = pavaData,
  PROBABILITY.GAMMA = 0.5)
bootBC.ci(tObserved = bootResult$@3,
  tBoot = bootResult$[3],
  conf = 0.95)

bootIsotonicRegression
Isotonic Regression Function

Description
Function of isotonic regression.
**Usage**

```r
go.bootIsotonicResample(data, PROBABILITY.GAMMA = 0.5, baselinePava)
```

**Arguments**

- **data**: the same dataframe called by the boot function.
- **PROBABILITY.GAMMA**: the target effect probability in the BCD experiment; default = 0.5 and need not be specified.
- **baselinePava**: the dataframe prepared by the function `preparePava`.

**Examples**

```r
library(ed50)
pavaData <- preparePava(groupS)
bootIsotonicRegression(data = groupS, PROBABILITY.GAMMA = 0.5, baselinePava = pavaData)
```

---

**bootIsotonicResample** *The resample function of isotonic regression*

**Description**

The function is designed as an argument for the boot function of the Canty Bootstrap package.

**Usage**

```r
bootIsotonicResample(data, mle)
```

**Arguments**

- **data**: Original experiment data.
- **mle**: A list of additional arguments to be used by `bootIsotonicResample`.

**Examples**

```r
library(ed50)
pavaData <- preparePava(groupS)
bootIsotonicResample(data = groupS, mle = list(baselinePava = pavaData, firstDose = 2.5, PROBABILITY.GAMMA = 0.5))
```
compare  

Compare ED50 Estimation of Independent Two-sample Case

Description

Test the statistical difference of two independent estimation results of ED50.

Usage

```r
compare(group1, group2, alpha = 0.05)
```

Arguments

- `group1`: A list object of ED50 estimation.
- `group2`: Another list object of ED50 estimation to be compared with.
- `alpha`: The significant level of test. 0.05 is the default value.

Value

The difference between two groups of ED50 estimation in terms of statistical significance.

References


Examples

```r
library(ed50)
ans1 <- estimate(groupS$doseSequence, groupS$responseSequence, method = 'ModTurPoint')
ans2 <- estimate(groupSN$doseSequence, groupSN$responseSequence, method = 'Dixon-Mood')
compare(ans1, ans2)
```

estimate  

Estimate ED50

Description

Estimate 50 percent effective dose using different methods.

Usage

```r
estimate(doseSequence, doseResponse, confidence = 0.95,
method = c("Dixon-Mood", "Choi", "ModTurPoint", "Logistic",
"Isotonic"), tpCiScale = 2.4/qnorm(0.975), boot.n = 10000)
```
Arguments

doseSequence  A sequence of doses given in order
doseResponse  A sequence of response results shown in order
certainty    The confidence level of interval estimate
method        The method used to estimate ED50, there are five methods here, respectively Dixon-Mood, Choi (Choi’s Original Turning Point), ModTurPoint (Modified Turning Point), Logistic (Logistic Regression) and Isotonic (Isotonic Regression). The default is Dixon-Mood.
tpCiScale     The scale level to enlarge the confidence interval estimated by Modified Turning Point Method. The default value is \(2.4/\text{qnorm}(0.975)\).
boot.n        The number of boot process if Logistic method is chosen to estimate ED50.

Value

A list of estimation result consisting of method of estimation, ED50 estimate, standard error of ED50 estimate, confidence level and estimate of confidence interval.

References


Examples

```r
library(ed50)
estimate(groups\$doseSequence, groups\$responseSequence, method = 'Dixon-Mood')
estimate(groups\$doseSequence, groups\$responseSequence, method = 'Logistic', boot.n = 1000)
```

Description

The function is used to generate simulation data of up-and-down experiment, and provide three cases that tolerance distribution obeys normal, triangle or chi-square distribution.

Usage

generateData(number, useTurPoint = FALSE, start, doseStep = 1,
distribution = c("Normal", "Triangle", "Chi-square"), normalMean = 0,
normalStd = 1, triMean = 0, triWidth = 2, chiDegree = 1)
Arguments

- **number**: The number of experiments in a trial.
- **useTurPoint**: A logical value indicating whether the parameter **number** refers to the amount of turning points. The default value is `FALSE`.
- **start**: The first dose level given in this trail.
- **doseStep**: A fix value that represents the difference between two adjacent dose levels.
- **distribution**: The tolerance distribution, including normal, triangle and chi-square distribution, and the default distribution is N(0, 1).
- **normalMean**: Parameter mean of normal distribution, the default value is 0.
- **normalStd**: Parameter std of normal distribution, the default value is 1.
- **triMean**: Parameter mean of triangle distribution, the default value is 0.
- **triWidth**: Parameter width of triangle distribution, the default value is 2.
- **chiDegree**: Parameter degree of freedom of chi-square distribution, the default value is 1.

Value

A data frame.

Examples

```r
library(ed5P)
generateData(number = 20, start = 2, doseStep = 0.2, distribution = 'Normal')
generateData(number = 40, start = 2, doseStep = 0.2, distribution = 'Chi-square')
```

---

**groupS**

*A Real Experiment Dose Data*

Description

A group of real experiment data based on up-and-down method.

Usage

`groupS`

Format

A data of 36 samples and 2 variables:

- **responseSequence**: A value of 0 or 1 indicating the experiment outcome. 0 refers to a failure outcome while 1 refers to a success.
- **doseSequence**: The dose given in each experiment.
Source

The data is from the article in the references below.

References


<table>
<thead>
<tr>
<th>groupSN</th>
<th>A Real Experiment Dose Data</th>
</tr>
</thead>
</table>

Description

A group of real experiment data based on up-and-down method.

Usage

groupSN

Format

A data of 38 samples and 2 variables:

- responseSequence A value of 0 or 1 indicating the experiment outcome. 0 refers to a failure outcome while 1 refers to a success.
- doseSequence The dose given in each experiment.

Source

The data is from the article in the references below.

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preparePava

### gTableOrigin

**G Table**

<table>
<thead>
<tr>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>A table containing parameter G used in Dixon-Mood method.</td>
</tr>
</tbody>
</table>

<table>
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<tr>
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<tbody>
<tr>
<td>gTableOrigin</td>
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</tbody>
</table>

<table>
<thead>
<tr>
<th>Format</th>
</tr>
</thead>
<tbody>
<tr>
<td>A data table containing 3 columns:</td>
</tr>
<tr>
<td><strong>Ratio</strong> The ratio of dose step and estimate standard error</td>
</tr>
<tr>
<td><strong>G1</strong> The value of parameter G when the estimate of ED50 falls on a dose level</td>
</tr>
<tr>
<td><strong>G2</strong> The value of parameter G when the estimate of ED50 falls between two dose levels</td>
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</table>

<table>
<thead>
<tr>
<th>Source</th>
</tr>
</thead>
<tbody>
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<td>The table is obtained from Figure 2 in the reference below</td>
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</tbody>
</table>

<table>
<thead>
<tr>
<th>References</th>
</tr>
</thead>
</table>

preparePava

**Covert Data Using PAVA Algorithm**

<table>
<thead>
<tr>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Covert data using PAVA algorithm, the result is used for isotonic regression estimation.</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Usage</th>
</tr>
</thead>
<tbody>
<tr>
<td>preparePava(data)</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Arguments</th>
</tr>
</thead>
<tbody>
<tr>
<td>data A data frame of dose experiments.</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Examples</th>
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<tbody>
<tr>
<td>library(ed50)</td>
</tr>
<tr>
<td>preparePava(groupS)</td>
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<tr>
<td>preparePava(groupSN)</td>
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