

Package ‘simdistr’

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Type Package

Title Assessment of Data Trial Distributions According to the Carlisle-Stouffer Method

Version 1.0.1

Author Bernardo Sousa-Pinto [aut, cre],
Joao Julio Cerqueira [ctb],
Cristina Costa-Santos [ctb],
John B Carlisle [ctb],
John A Loadsman [ctb],
Armando Teixeira-Pinto [aut],
Hernani Goncalves [aut]

Maintainer Bernardo Sousa-Pinto <bernardo@med.up.pt>

Description Assessment of the distributions of baseline continuous and categorical variables in randomised trials. This method is based on the Carlisle-Stouffer method with Monte Carlo simulations. It calculates p-values for each trial baseline variable, as well as combined p-values for each trial - these p-values measure how compatible are distributions of trials baseline variables with random sampling. This package also allows for graphically plotting the cumulative frequencies of computed p-values.

Please note that code was partly adapted from Carlisle JB, Loadsman JA. (2017) <doi:10.1111/anae.13650>.

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License GPL-2

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LazyData true

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example_trials	<i>Data of baseline variables of seven randomised trials.</i>
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Description

A dataset containing baseline variables' data from seven randomised trials authored by Yuhji Saitoh and tested by Carlisle JB and Loadsman JA (Anaesthesia 2017; Appendix S2 references number 1, 2, 4, 5, 7, 9 and 14). Results obtained with this example can be compared with results in the Table 1 of Carlisle JB and Loadsman JA. Small differences are to be expected, as p-values are obtained by means of simulations. For the sake of a faster testing, the example sets the number of simulations at 100. However, we recommend at least 5000 simulations to be performed in order to obtain more accurate results.

Usage

```
data(example_trials)
```

Format

A data frame with 93 rows and 9 variables:

1. trial - trial identification number;
2. variable - variable identification number;
3. group - group of participants identification number;
4. participants - number of participants;
5. mean - reported mean or proportion;
6. sd - reported standard-deviation (for continuous variables only);
7. decimals - number of decimal places to which the corresponding mean or proportion was reported;
8. type - type of variable. 1 indicates a continuous variable; 2 indicates a categorical variable;
9. name - name of the randomised trial (first author name and publication year) to which data concern.

Source

Data was retrieved from the following trials authored by Yuhji Saitoh:

1. Saitoh Y, Toyooka H, Amaha K. Recoveries of post-tetanic twitch and train-of-four responses after administration of vecuronium with different inhalation anaesthetics and neuroleptanaesthesia. *British Journal of Anaesthesia* 1993; 70: 402-4.
2. Saitoh Y, Toyooka H, Amaha K. Post-tetanic burst: a new monitoring method for intense neuromuscular block. *British Journal of Anaesthesia* 1995; 74: 293-5.
3. Saitoh Y, Fujii Y, Toyooka H, Amaha K. Post-tetanic burst count: a stimulating pattern for profound neuromuscular blockade. *Canadian Journal of Anesthesia* 1995; 42: 1096-1100.
4. Saitoh Y, Tanaka H, Toyooka H, Amaha K. Recovery of post-tetanic and train-of-four responses at the first dorsal interosseous and adductor pollicis muscles in patients receiving vecuronium. *Canadian Journal of Anesthesia* 1996; 43: 362-7.
5. Saitoh Y, Nakazawa K, Makita K, Tanaka H, Toyooka H. Evaluation of residual neuromuscular blockade using modified double burst stimulation. *Acta Anaesthesiologica Scandinavica* 1997; 41: 741-5.
6. Saitoh Y, Nakazawa K, Makita K, Tanaka H, Toyooka H. Visual evaluation of train-of-four and double burst stimulation, fade at various currents, using a rubber band. *European Journal of Anaesthesiology* 1997; 14: 327-32.
7. Saitoh Y, Narumi Y, Fujii Y, Ueki M, Makita K. Electromyographic assessment of neuromuscular block at the gastrocnemius muscle. *British Journal of Anaesthesia* 1999; 82: 329-32. Retraction in: *British Journal of Anaesthesia* 2013; 110: 669.

Examples

```
sim_distr(100,example_trials,TRUE)
```

sim_distr	<i>Assessment of Data Trial Distributions According to the Carlisle-Stouffer Method</i>
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Description

Assessment of the distributions of baseline continuous and categorical variables in randomised trials, assuming normal distributions for the former and binomial distributions for the latter. The method used is based on the Carlisle-Stouffer method with Monte Carlo simulations. It calculates p-values for each trial baseline variable, as well as combined p-values for each trial - these p-values measure how compatible are distributions of trials baseline variables with random sampling. This package also allows for graphically plotting the cumulative frequencies of obtained p-values.

Usage

```
sim_distr(m, dataframe, plot_flag)
```

Arguments

m	An integer specifying the number of Monte Carlo simulations to be run.
dataframe	A dataframe with 9 columns with order and content as specified in the "Details" section.
plot_flag	A logical indicating whether cumulative frequencies of p-values are to be plotted in a graph; if TRUE a plot is provided.

Value

1. A dataframe with p-values for each variable in each assessed trial - each trial is displayed in a different row. For each trial, each variable ("V") is displayed in a different column; variables are listed in the same order they are presented in the original dataframe.
2. A dataframe with combined (overall) p-values for each assessed trial - each trial is displayed in a different row.
3. A graph plotting the cumulative frequency of obtained variable p-values (optional).

Details

The dataframe must necessarily have 9 columns with the following order and content:

1. Trial number: An integer that sequentially identifies the randomised trial from which data concern. Therefore, all rows with data from the first randomised trial should be identified with the number 1 in this first column, data from the second trial should be identified with number 2, etc.
2. Variable number for each trial: An integer that sequentially identifies the different variables assessed within each trial. Therefore, for each trial, all rows with data from the first reported variable should be identified with the number 1, data from the second variable should be identified with number 2, etc.
3. Group: An integer that sequentially identifies the different groups of participants for which each variable was assessed.
4. Number of participants: An integer corresponding to the number of assessed individuals in each group.
5. Reported mean value (continuous variables) or proportion (categorical variables): A number with the reported result (mean or proportion) obtained for the corresponding variable in each group. Proportions must NOT be presented as percentages.
6. Reported standard-deviation: A number with the reported standard-deviation obtained for the corresponding variable in each group. This column only concerns continuous variables, and should be left blank for categorical variables.
7. Number of decimal places: An integer that indicates the number of decimal places to which the corresponding mean or proportion was reported (e.g., 1 for "2.5").
8. Variable type: 1 for continuous variables; 2 for categorical variables.
9. Name: A character sequence (e.g., with author name and publication year) that names the randomised trial from which data concern.

The example dataframe - `example_trials` - provides a model regarding the required organisation and content of the dataframe. For the sake of a faster testing, the example sets the number of simulations at 100. However, we recommend at least 5000 simulations to be performed in order to obtain more accurate results.

Source

The code for computing p-values for continuous variables is an adaptation of the code provided in AppendixS1 of Carlisle JB and Loadsman JA, 2017, *Anaesthesia*.

References

1. Carlisle JB, Loadsman JA. Evidence for non-random sampling in randomised, controlled trials by Yuhji Saitoh. *Anaesthesia* 2017;72:17-27
2. Carlisle JB, Dexter F, Pandit JJ, Shafer SL, Yentis SM. Calculating the probability of random sampling for continuous variables in submitted or published randomised controlled trials. *Anaesthesia* 2015;70:848-858

Examples

```
sim_distr(100,example_trials, TRUE)
```

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