

Package ‘SCMA’

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SCMA-package

Single-Case Meta-Analysis

Description

A package for probability combining (additive and multiplicative method) and for calculating some effect size measures on single-case data (SMD, PND and PEM).

Details

Package: SCMA
Type: Package
Version: 1.1
Date: 2014-01-13
License: GPL version 2 or newer

Author(s)

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AB

Hypothetical AB data

Description

Hypothetical data collected in an AB phase design with 27 measurement times.

Usage

```
data(AB)
```

Format

A data frame with 27 observations.

- The first column contains the condition/phase labels ("A" and "B").
- The second column contains the obtained scores.
- The rows and columns are not labeled.

References

Bulte, I., & Onghena, P. (2012). When the truth hits you between the eyes: A software tool for the visual analysis of single-case experimental data. *Methodology*, 8, 104-114.

Examples

```
data(AB)
```

combine	<i>Statistical combination of p-values</i>
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Description

Calculates a general p-value by statistically combining the p-values of a number of independent studies, to determine whether a general significant result is obtained.

Usage

```
combine(method, pvalues = read.table(file.choose(new = FALSE)))
```

Arguments

method	Indicates which combining function should be used: "x" (multiplicative) or "+" (additive)
pvalues	File in which the p-values can be found. Default: a window pops up in which the appropriate file can be selected.

Details

When using the default 'pvalues' argument, a window will pop up to ask in what file the pvalues can be found. This text file containing the pvalues should consist of 1 column with all the obtained pvalues.

Author(s)

Isis Bulte

References

Bulte, I., & Onghena, P. (2008). An R package for single-case randomization tests. *Behavior Research Methods*, 40, 467-478.

Bulte, I., & Onghena, P. (2009). Randomization tests for multiple baseline designs: An extension of the SCRT-R package. *Behavior Research Methods*, 41, 477-485.

<http://ppw.kuleuven.be/cmcs/SCRT-R.html>

Examples

```
data(P)
combine(method="+", pvalues=P)
```

ES *measure of effect size*

Description

Calculates the specified effect size measure.

Usage

```
ES(design, ES, data = read.table(file.choose(new = FALSE)))
```

Arguments

design	Type of single-case design: "AB", "ABA", "ABAB", "CRD"(completely randomized design), "RBD" (randomized block design), "ATD" (alternating treatments design), or "MBD" (multiple-baseline AB design).
ES	the type of effect size that has to be calculated: "SMD" (standardized mean difference), "SMDpool" (pooled standardized mean difference), "PND+" / "PND-" (percentage of nonoverlapping data, depending on the expected direction of the treatment effect), or "PEM+" / "PEM-" (percentage of data points exceeding the median, depending on the expected direction of the treatment effect)
data	File in which the data can be found. Default: a window pops up in which the appropriate file can be selected.

Details

When using the default 'data' argument, a window will pop up to ask in what file the data can be found. This text file containing the data should consist of two columns for single-case phase and alternation designs: the first with the condition labels and the second with the obtained scores. For multiple-baseline designs it should consist of these two columns for EACH unit. This way, each row represents one measurement occasion. It is important not to label the rows or columns.

Author(s)

Isis Bulte

References

Bulte, I., & Onghena, P. (2008). An R package for single-case randomization tests. *Behavior Research Methods*, 40, 467-478.

Bulte, I., & Onghena, P. (2009). Randomization tests for multiple baseline designs: An extension of the SCRT-R package. *Behavior Research Methods*, 41, 477-485.

<http://ppw.kuleuven.be/cmcs/SCRT-R.html>

Examples

```
data(AB)
ES(design = "AB", ES = "SMD", data = AB)
```

P

P-values

Description

Each p-value (i.e., each row) corresponds to one participant in the study.

Usage

```
data(P)
```

Format

A data frame with 7 observations on the following variable.

V1 P-value

Examples

```
data(P)
```

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