Package 'SCMA'

Type Package

Title Single-Case Meta-Analysis

Version 1.3.1

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Depends R (>= 2.11.1)

Description
Perform meta-analysis of single-case experiments, including calculating various effect size measures (SMD, PND, PEM and NAP) and probability combining (additive and multiplicative method), as discussed in Bulte and Onghena (2013) <doi:10.22237/jmasm/1383280020>.

License GPL (>= 2)

Imports stats, utils

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NeedsCompilation no

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R topics documented:

SCMA-package   *Single-Case Meta-Analysis*

Description

Perform meta-analysis of single-case experiments, including calculating various effect size measures (SMD, PND, PEM and NAP) and probability combining (additive and multiplicative method).

Details

Package:	SCMA
Type:	Package
Version:	1.3.1
Date:	2019-12-20
License:	GPL version 2 or newer

Author(s)

Isis Bulte, Tamal Kumar De, Patrick Onghena

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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)
```

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combine   *Statistical combination of p-values*

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/cmes/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 ran-
                domized design), "RBD" (randomized block design), "ATD" (alternating treat-
                ments design), "MBD" (multiple-baseline AB design) or "Custom" (user speci-
                fied design).

ES   Type of effect size that has to be calculated: "SMD" (standardized mean dif-
                ference), "SMDpool" (pooled standardized mean difference), "PND+" / "PND-
                " (percentage of nonoverlapping data, depending on the expected direction of
                the treatment effect), "PEM+" / "PEM-" (percentage of data points exceeding
                the median, depending on the expected direction of the treatment effect), or
                "NAP+" / "NAP-" (nonoverlap of all pairs, 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.

Missing data should be indicated as NA. For calculations, missing data are omitted.

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/cmes/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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