

# Package ‘SCMA’

October 26, 2017

**Type** Package

**Title** Single-Case Meta-Analysis

**Version** 1.2.1

**Date** 2017-10-25

**Author** Isis Bulte

**Maintainer** Tamal Kumar De <tamalkumar.de@kuleuven.be>

**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).

**License** GPL (>= 2)

**Imports** stats, utils

**NeedsCompilation** no

**Repository** CRAN

**Date/Publication** 2017-10-26 20:32:20 UTC

## R topics documented:

|                        |          |
|------------------------|----------|
| SCMA-package . . . . . | 2        |
| AB . . . . .           | 2        |
| combine . . . . .      | 3        |
| ES . . . . .           | 4        |
| P . . . . .            | 5        |
| <b>Index</b>           | <b>6</b> |

---

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: 1.2.1  
Date: 2017-10-25  
License: GPL version 2 or newer

### Author(s)

Isis Bulte and Patrick Onghena

Maintainer: Tamal Kumar De <tamalkumar.de@kuleuven.be>

---

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

*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/cmcs/SCRT-R.html>

**Examples**

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

---

|    |                               |
|----|-------------------------------|
| ES | <i>measure of effect size</i> |
|----|-------------------------------|

---

**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), "MBD" (multiple-baseline AB design) or "Custom" (user specified design).                                                                                                                                                                                                                                                            |
| ES     | 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), "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.

**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 | <i>P-values</i> |
|---|-----------------|
|---|-----------------|

---

**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)
```

# Index

\*Topic **datasets**

AB, [2](#)

P, [5](#)

\*Topic **meta-analysis**

combine, [3](#)

ES, [4](#)

\*Topic **package**

SCMA-package, [2](#)

\*Topic **single-case designs**

combine, [3](#)

ES, [4](#)

AB, [2](#)

combine, [3](#)

ES, [4](#)

P, [5](#)

SCMA-package, [2](#)