Package: SCRT (via r-universe)

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Type Package

Title Single-Case Randomization Tests

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Imports graphics, utils

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Description Design single-case phase, alternation and
multiple-baseline experiments, and conduct randomization tests
on data gathered by means of such designs, as discussed in
Bulte and Onghena (2013) <doi:10.22237/jmasm/1383280020>.

License GPL (>= 2)

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Contents

SCRT-package   *Single-Case Randomization Tests*

Description

Design single-case phase, alternation and multiple-baseline experiments, and conduct randomization-tion tests on data gathered by means of such designs.

Details

Package:	SCRT
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

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

ABAB   *Hypothetical ABAB data*

Description

Hypothetical data from Onghena (1992), collected in an ABAB design with 24 measurement times.

Usage

```
data(ABAB)
```

Format

A data frame with 24 observations.

- The first column contains the condition/phase labels ("A1", "B1", "A2", "B2").
- The second column contains the obtained scores.
- The rows and columns are not labeled.

Source

Onghena, P. (1992). Randomization tests for extensions and variations of AB single-case experimental designs: A rejoinder. Behavioral Assessment, 14, 153-171.

References

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

Examples

```
data(ABAB)
```

---

assignments   *All assignments possibilities*

Description

All assignment possibilities for the specified design are enumerated.

Usage

```
assignments(design, save = "no", MT, limit,
starts = file.choose(new = FALSE), assignments = 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).
save	Save the possible assignments to a file (save="yes") or just see them as output in the R console (default: save="no").
MT	Measurement times: number of observations.
limit	For phase designs: minimum number of observations per phase. For alternating treatments designs: maximum number of consecutive administrations of the same condition.
starts	Only for multiple baseline designs: location of the file where the possible start points can be found. Default: a window pops up in which the file can be selected.
assignments	Only for user specified designs: location of the file where all the possible assignments can be found. Default: a window pops up in which the file can be selected.

Details

When choosing to save the possible assignments to a file, a window will pop up (for multiple baseline designs or user specified designs this is the second pop-up window!!!) to ask where to save them. This location can be an existing file, as well as a new file that can be created by giving a file name and the extension .txt. In this latter case a confirmation is required ("The file does not exist yet. Create the file?").

For multiple baseline designs, when using the default `starts` argument, first a window pops up in which is asked in what file the possible start points can be found. In this startpoint file, each row should contain all possibilities for one unit, separated by a tab. The rows and columns should not be labeled.

For user specified designs, when using the default `assignments` argument, first a window pops up in which is asked in what file all the possible assignments can be found. In this file, each row should contain the sequence of conditions in one possible assignment, separated by a tab. There should be one row for every possible assignment. The rows and columns should not be labeled.

For multiple baseline designs, the possible combinations of start points for each unit are returned. There may be duplicates among these assignments if there are overlaps between the start points for different subjects, this is a result of the subjects also being randomized to the set of start points.

For all other designs, the possible sequences of conditions are returned (e.g., "A" "A" "A" "A" "B" "B" "B").

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.

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See Also

quantity to calculate the number of assignment possibilities.

selectdesign to randomly select one of the assignment possibilities.

Examples

```
assignments(design = "ABAB", save = "no", MT = 24, limit = 4)
```

---

distribution.random   *Nonexhaustive randomization distribution*

Description

The nonexhaustive randomization distribution is generated by a random sample of all assignment possibilities.

Usage

```
distribution.random(design, statistic, save = "no",
number, limit, data = read.table(file.choose(new = FALSE)),
starts = file.choose(new = FALSE), assignments = 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).

statistic
: Test statistic. For alternation designs, multiple-baseline designs and AB phase designs, there are 3 built-in possibilities: "A-B", "B-A", and "|A-B|", which stand for the (absolute value of the) difference between condition means. For phase designs with more than 2 phases, 3 more built-in options are available: "PA-PB", "PB-PA", and "|PA-PB|" refer to the (absolute value of the) difference between the means of phase means. Additionally, it is possible to specify a custom test statistic using the variable identifiers "A" and "B" (or in the case of phase deisgns with more than 2 phases, "A1", "B1", "A2", "B2", "A" and "B") and any of the basic R functions. For example, "abs(mean(A) - mean(B))" can be used as a test statistic and it will be the same as using "|A-B|".

save
: Save the randomization distribution to a file (save="yes") or just see it as output in the R console (default: save="no").

number
: Number of randomizations required. Please note that the observed test statistic is always included in the randomization distribution.

limit
: For phase designs: minimum number of observations per phase. For alternating treatments designs: maximum number of consecutive administrations of the same condition.

data
: File in which the data can be found. Default: a window pops up in which the file can be selected.

starts
: Only for multiple baseline designs: location of the file where the possible start points can be found. Default: a window pops up in which the file can be selected.

assignments
: Only for user specified designs: location of the file where all the possible assignments can be found. Default: a window pops up in which the 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.

For multiple baseline designs, when using the default starts argument, second a window pops up in which is asked in what file the possible start points can be found. In this startpoint file, each row

should contain all possibilities for one unit, separated by a tab. The rows and columns should not be labeled.

For user specified designs, when using the default `assignments` argument, second a window pops up in which is asked in what file all the possible assignments can be found. In this file, each row should contain the sequence of conditions in one possible assignment, separated by a tab. There should be one row for every possible assignment. The rows and columns should not be labeled.

Missing data should be indicated as `NA`. When there is missing data, randomization distribution is generated as usual, but instead of randomly reshuffling numerical scores only, the missing data markers (`NA`) are also included in the reshuffling. For test statistic calculations, missing data are omitted.

When choosing to save the randomization distribution to a file, next a window will pop up (for multiple baseline designs or user specified designs this is the third pop-up window, for all other designs it is the second window) to ask where to save it. This location can be an existing file, as well as a new file that can be created by giving a file name and the extension .txt. In this latter case a confirmation is required ("The file does not exist yet. Create the file?").

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.

Edgington, E.S., & Onghena, P. (2007). Randomization Tests (4th ed.). Boca Raton, FL: Chapman & Hall/CRC.

Hope, A.C.A. (1968). A simplified Monte Carlo significance test procedure. Journal of the Royal Statistical Society, Series B 30, 582-598.

Onghena, P. & May, R.B. (1995). Pitfalls in computing and interpreting randomization test p values: A commentary on Chen and Dunlap. Behavior Research Methods, Instruments, & Computers, 27, 408-411.

http://ppw.kuleuven.be/home/english/research/mesrg

See Also

`pvalue.random` to obtain the corresponding p-value for the nonexhaustive randomization distribution.

`observed` to calculate the observed test statistic.

`distribution.systematic` to generate the exhaustive randomization distribution and `pvalue.systematic` to obtain the corresponding p-value.

Examples

```
data(ABAB)
distribution.random(design = "ABAB", statistic = "PA-PB", save = "no",
number = 100, limit = 4, data = ABAB)
```

---

distribution.systematic

Exhaustive randomization distribution

Description

The exhaustive randomization distribution is generated by a complete enumeration of all assignment possibilities.

Usage

```
distribution.systematic(design, statistic, save = "no",
limit, data = read.table(file.choose(new = FALSE)),
starts = file.choose(new = FALSE), assignments = 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).
statistic	Test statistic. For alternation designs, multiple-baseline designs and AB phase designs, there are 3 built-in possibilities: "A-B", "B-A", and "|A-B|", which stand for the (absolute value of the) difference between condition means. For phase designs with more than 2 phases, 3 more built-in options are available: "PA-PB", "PB-PA", and "|PA-PB|" refer to the (absolute value of the) difference between the means of phase means. Additionally, it is possible to specify a custom test statistic using the variable identifiers "A" and "B" (or in the case of phase deisgns with more than 2 phases, "A1", "B1", "A2", "B2", "A" and "B") and any of the basic R functions. For example, "abs(mean(A) - mean(B))" can be used as a test statistic and it will be the same as using "|A-B|".
save	Save the randomization distribution to a file (save="yes") or just see it as output in the R console (default: save="no").
limit	For phase designs: minimum number of observations per phase. For alternating treatments designs: maximum number of consecutive administrations of the same condition.
data	File in which the data can be found. Default: a window pops up in which the file can be selected.
starts	Only for multiple baseline designs: location of the file where the possible start points can be found. Default: a window pops up in which the file can be selected.
assignments	Only for user specified designs: location of the file where all the possible assignments can be found. Default: a window pops up in which the 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.

For multiple baseline designs, when using the default `starts` argument, second a window pops up in which is asked in what file the possible start points can be found. In this startpoint file, each row should contain all possibilities for one unit, separated by a tab. The rows and columns should not be labeled.

For user specified designs, when using the default `assignments` argument, second a window pops up in which is asked in what file all the possible assignments can be found. In this file, each row should contain the sequence of conditions in one possible assignment, separated by a tab. There should be one row for every possible assignment. The rows and columns should not be labeled.

Missing data should be indicated as `NA`. When there is missing data, randomization distribution is generated as usual, but instead of randomly reshuffling numerical scores only, the missing data markers (`NA`) are also included in the reshuffling. For test statistic calculations, missing data are omitted.

When choosing to save the randomization distribution to a file, next a window will pop up (for multiple baseline designs this is the third pop-up window, for all other designs it is the second window) to ask where to save it. This location can be an existing file, as well as a new file that can be created by giving a file name and the extension .txt. In this latter case a confirmation is required ("The file does not exist yet. Create the file?").

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.

Edgington, E.S., & Onghena, P. (2007). Randomization Tests (4th ed.). Boca Raton, FL: Chapman & Hall/CRC.

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See Also

`pvalue.systematic` to obtain the corresponding p-value for the exhaustive randomization distribution.

`observed` to calculate the observed test statistic.

`distribution.random` to generate the nonexhaustive randomization distribution and `pvalue.random` to obtain the corresponding p-value.

Examples

```
data(ABAB)
distribution.systematic(design = "ABAB", statistic = "PA-PB",
```

graph1 9

```
save = "no", limit = 4, data = ABAB)
```

---

graph1   *Graphical representation of single-case data*

Description

The observed single-case data are plotted.

Usage

```
graph1(design,data=read.table(file.choose(new=FALSE)),
xlab="Measurement Times",ylab="Scores")
```

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).
data	File in which the data can be found. Default: a window pops up in which the file can be selected.
xlab	Label x axis
ylab	Label y axis

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.

For alternation designs, after the plot is drawn, the location of the legend should be indicated by a left mouse click.

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

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.

Bulte, I., & Onghena, P. (in press). When the Truth Hits You Between the Eyes: A Software Tool for the Visual Analysis of Single-Case Experimental Data. Manuscript accepted for publication in Methodology.

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Examples

```
data(ABAB)
graph1(design = "ABAB", data = ABAB)
```

---

observed   *Observed test statistic*

Description

The observed test statistic is calculated from the obtained raw data.

Usage

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

Arguments

design   Type of single-case design: "AB", "ABA", "ABAB", "CRD" (completely random-
              ized design), "RBD" (randomized block design), "ATD" (alternating treatments
              design), "MBD" (multiple-baseline AB design) or "Custom" (user specified de-
              sign).

statistic   Test statistic. For alternation designs, multiple-baseline designs and AB phase
              designs, there are 3 built-in possibilities: "A-B", "B-A", and "|A-B|", which
              stand for the (absolute value of the) difference between condition means. For
              phase designs with more than 2 phases, 3 more built-in options are available:
              "PA-PB", "PB-PA", and "|PA-PB|" refer to the (absolute value of the) difference
              between the means of phase means. Additionally, it is possible to specify a
              custom test statistic using the variable identifiers "A" and "B" (or in the case of
              phase deisgns with more than 2 phases, "A1", "B1", "A2", "B2", "A" and "B")
              and any of the basic R functions. For example, "abs(mean(A) - mean(B))" can
              be used as a test statistic and it will be the same as using "|A-B|".

data   File in which the data can be found. Default: a window pops up in which the
              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.

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.

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See Also

distribution.systematic to generate the exhaustive randomization distribtion and pvalue.systematic to obtain the corresponding p-value.

distribution.random to generate the nonexhaustive randomization distribution and pvalue.random to obtain the corresponding p-value.

Examples

```
data(ABAB)
observed(design = "ABAB", statistic = "PA-PB", data = ABAB)
```

---

pvalue.random   *P-value using the Monte Carlo procedure*

Description

The P-value corresponding to the observed value of the test statistic is obtained by locating this value in the randomization distribution generated by a random sample of all assignment possibilities (the nonexhaustive randomization distribution).

Usage

```
pvalue.random(design, statistic, save = "no",
number, limit, data = read.table(file.choose(new = FALSE)),
starts = file.choose(new = FALSE), assignments = file.choose(new = FALSE))
```

Arguments

design   Type of single-case design: "AB", "ABA", "ABAB", "CRD" (completely random-
               ized design), "RBD" (randomized block design), "ATD" (alternating treatments
               design), "MBD" (multiple-baseline AB design) or "Custom" (user specified de-
               sign).

statistic   Test statistic. For alternation designs, multiple-baseline designs and AB phase
               designs, there are 3 built-in possibilities: "A-B", "B-A", and "|A-B|", which
               stand for the (absolute value of the) difference between condition means. For
               phase designs with more than 2 phases, 3 more built-in options are available:
               "PA-PB", "PB-PA", and "|PA-PB|" refer to the (absolute value of the) difference
               between the means of phase means. Additionally, it is possible to specify a

custom test statistic using the variable identifiers "A" and "B" (or in the case of phase deisgns with more than 2 phases, "A1", "B1", "A2", "B2", "A" and "B") and any of the basic R functions. For example, "abs(mean(A) - mean(B))" can be used as a test statistic and it will be the same as using "|A-B|".

save   Save the randomization distribution to a file (save="yes") or just see it as output in the R console (default: save="no").

number   Number of randomizations required. Please note that the observed test statistic is always included in the randomization distribution.

limit   For phase designs: minimum number of observations per phase. For alternating treatments designs: maximum number of consecutive administrations of the same condition.

data   File in which the data can be found. Default: a window pops up in which the file can be selected.

starts   Only for multiple baseline designs: location of the file where the possible start points can be found. Default: a window pops up in which the file can be selected.

assignments   Only for user specified designs: location of the file where all the possible assignments can be found. Default: a window pops up in which the 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.

For multiple baseline designs, when using the default starts argument, second a window pops up in which is asked in what file the possible start points can be found. In this startpoint file, each row should contain all possibilities for one unit, separated by a tab. The rows and columns should not be labeled.

For user specified designs, when using the default assignments argument, second a window pops up in which is asked in what file all the possible assignments can be found. In this file, each row should contain the sequence of conditions in one possible assignment, separated by a tab. There should be one row for every possible assignment. The rows and columns should not be labeled.

Missing data should be indicated as NA. When there is missing data, randomization distribution is generated as usual, but instead of randomly reshuffling numerical scores only, the missing data markers (NA) are also included in the reshuffling. For test statistic calculations, missing data are omitted. If test statistic cannot be calculated for a particular randomization due to insufficient data for a treatment condition, the test statistic from this randomization is conservatively considered more extreme than the observed test statistic.

When choosing to save the randomization distribution to a file, next a window will pop up (for multiple baseline designs or user specified designs this is the third pop-up window, for all other designs it is the second window) to ask where to save it. This location can be an existing file, as well as a new file that can be created by giving a file name and the extension .txt. In this latter case a confirmation is required ("The file does not exist yet. Create the file?").

References

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

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Hope, A.C.A. (1968). A simplified Monte Carlo significance test procedure. Journal of the Royal Statistical Society, Series B 30, 582-598.

Onghena, P. & May, R.B. (1995). Pitfalls in computing and interpreting randomization test p values: A commentary on Chen and Dunlap. Behavior Research Methods, Instruments, & Computers, 27, 408-411.

http://ppw.kuleuven.be/home/english/research/mesrg

See Also

distribution.random to generate the corresponding nonexhaustive randomization distribution.

observed to calculate the observed test statistic.

distribution.systematic to generate the exhaustive randomization distribution and pvalue.systematic to obtain the corresponding p-value.

Examples

```
data(ABAB)
pvalue.random(design = "ABAB", statistic = "PA-PB", save = "no",
number = 100, limit = 4, data = ABAB)
```

---

pvalue.systematic   *P-value using the systematic procedure*

Description

The P-value corresponding to the observed value of the test statistic is obtained by locating this value in the randomization distribution generated by complete enumeration of all assignment possibilities (the exhaustive randomization distribution).

Usage

```
pvalue.systematic(design, statistic, save = "no",
limit, data = read.table(file.choose(new = FALSE)),
starts = file.choose(new = FALSE), assignments = 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).

statistic
: Test statistic. For alternation designs, multiple-baseline designs and AB phase designs, there are 3 built-in possibilities: "A-B", "B-A", and "|A-B|", which stand for the (absolute value of the) difference between condition means. For phase designs with more than 2 phases, 3 more built-in options are available: "PA-PB", "PB-PA", and "|PA-PB|" refer to the (absolute value of the) difference between the means of phase means. Additionally, it is possible to specify a custom test statistic using the variable identifiers "A" and "B" (or in the case of phase deisgns with more than 2 phases, "A1", "B1", "A2", "B2", "A" and "B") and any of the basic R functions. For example, "abs(mean(A) - mean(B))" can be used as a test statistic and it will be the same as using "|A-B|".

save
: Save the randomization distribution to a file (save="yes") or just see it as output in the R console (default: save="no").

limit
: For phase designs: minimum number of observations per phase. For alternating treatments designs: maximum number of consecutive administrations of the same condition.

data
: File in which the data can be found. Default: a window pops up in which the file can be selected.

starts
: Only for multiple baseline designs: location of the file where the possible start points can be found. Default: a window pops up in which the file can be selected.

assignments
: Only for user specified designs: location of the file where all the possible assignments can be found. Default: a window pops up in which the 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.

For multiple baseline designs, when using the default `starts` argument, second a window pops up in which is asked in what file the possible start points can be found. In this startpoint file, each row should contain all possibilities for one unit, separated by a tab. The rows and columns should not be labeled.

For user specified designs, when using the default `assignments` argument, second a window pops up in which is asked in what file all the possible assignments can be found. In this file, each row should contain the sequence of conditions in one possible assignment, separated by a tab. There should be one row for every possible assignment. The rows and columns should not be labeled.

Missing data should be indicated as `NA`. When there is missing data, randomization distribution is generated as usual, but instead of randomly reshuffling numerical scores only, the missing data

markers (NA) are also included in the reshuffling. For test statistic calculations, missing data are omitted. If test statistic cannot be calculated for a particular randomization due to insufficient data for a treatment condition, the test statistic from this randomization is conservatively considered more extreme than the observed test statistic.

When choosing to save the randomization distribution to a file, next a window will pop up (for multiple baseline designs or user specified designs this is the third pop-up window, for all other designs it is the second window) to ask where to save it. This location can be an existing file, as well as a new file that can be created by giving a file name and the extension .txt. In this latter case a confirmation is required ("The file does not exist yet. Create the file?").

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.

Edgington, E.S., & Onghena, P. (2007). Randomization Tests (4th ed.). Boca Raton, FL: Chapman & Hall/CRC.

http://ppw.kuleuven.be/home/english/research/mesrg

See Also

distribution.systematic to generate the corresponding exhaustive randomization distribution.

observed to calculate the observed test statistic.

distribution.random to generate the nonexhaustive randomization distribution and pvalue.random to obtain the corresponding p-value.

Examples

```
data(ABAB)
pvalue.systematic(design = "ABAB", statistic = "PA-PB", save = "no",
limit = 4, data = ABAB)
```

---

quantity   *Number of assignment possibilities*

Description

The number of assignment possibilities for the specified design is calculated.

Usage

```
quantity(design, MT, limit, starts = file.choose(new = FALSE),
assignments = 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).
MT	Measurement times: number of observations.
limit	For phase designs: minimum number of observations per phase. For alternating treatments designs: maximum number of consecutive administrations of the same condition.
starts	Only for multiple baseline designs: location of the file where the possible start points can be found. Default: a window pops up in which the file can be selected.
assignments	Only for user specified designs: location of the file where all the possible assignments can be found. Default: a window pops up in which the file can be selected.

Details

For multiple baseline designs, when using the default starts argument, only the design argument is required. In this default version a window pops up in which is asked in what file the possible start points can be found. In this startpoint file, each row should contain all possibilities for one unit, separated by a tab. The rows and columns should not be labeled.

The number of possible assignments for a multiple baseline design is calculated assuming NO overlap between the possible start points of the different units (staggered administration).

For user specified designs, when using the default assignments argument, a window pops up in which is asked in what file all the possible assignments can be found. In this file, each row should contain the sequence of conditions in one possible assignment, separated by a tab. There should be one row for every possible assignment. The rows and columns should not be labeled.

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/home/english/research/mesrg

See Also

assignments to enumerate all assignment possibilities.

selectdesign to randomly select one of the assignment possibilities.

Examples

```
quantity(design = "ABAB", MT = 24, limit = 4)
```

---

selectdesign	*Selection on one assignment possibility*

Description

One assignment possibility is randomly selected from all theoretical possibilities.

Usage

```
selectdesign(design, MT, limit, starts = file.choose(new=FALSE),
assignments = 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).
MT	Measurement times: number of observations.
limit	For phase designs: minimum number of observations per phase. For alternating treatments designs: maximum number of consecutive administrations of the same condition.
starts	Only for multiple baseline designs: location of the file where the possible start points can be found. Default: a window pops up in which the file can be selected.
assignments	Only for user specified designs: location of the file where all the possible assignments can be found. Default: a window pops up in which the file can be selected.

Details

For multiple baseline designs, when using the default starts argument, only the design argument is required. In this default version a window pops up in which is asked in what file the possible start points can be found. In this startpoint file, each row should contain all possibilities for one unit, separated by a tab. The rows and columns should not be labeled.

For user specified designs, when using the default assignments argument, first a window pops up in which is asked in what file all the possible assignments can be found. In this file, each row should contain the sequence of conditions in one possible assignment, separated by a tab. There should be one row for every possible assignment. The rows and columns should not be labeled.

For multiple baseline designs, a possible combination of start points for each unit is returned. For all other designs, a possible sequence of conditions is returned (e.g., "A" "A" "A" "A" "B" "B" "B").

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/home/english/research/mesrg

See Also

quantity to calculate the number of assignment possibilities.

assignments to enumerate all assignment possibilities.

Examples

```
selectdesign(design = "ABAB", MT = 24, limit = 4)
```

Index