Package ‘randomizeBE’
August 19, 2023

Encoding UTF-8
Type Package
Title Create a Random List for Crossover Studies
Version 0.3-6
Date 2023-08-19
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Description Contains a function to randomize subjects, patients in groups of sequences (treatment sequences).
If a blocksize is given, the randomization will be done within blocks.
The randomization may be controlled by a Wald-Wolfowitz runs test.
Functions to obtain the p-value of that test are included.
The package is mainly intended for randomization of bioequivalence studies but may be used also for other clinical crossover studies.
Contains two helper functions sequences() and williams() to get the sequences of commonly used designs in BE studies.

Imports stats
Suggests knitr, rmarkdown
License GPL (>= 2.0)
NeedsCompilation no
Repository CRAN
Date/Publication 2023-08-19 16:10:07 UTC

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Description

Prints the randomization list including a summary if needed.

Usage

## S3 method for class 'rl4'
print(x, sumry=FALSE, ...)

Arguments

x Object of class "rl4".
sumry If set to TRUE a summary of the randomization will be shown. This summary contains the p-value of runs test of randomness if 2 sequences are used.
...
Additional arguments. None used.

Value

Returns invisible x.

Author(s)

D. Labes

See Also

RL4

Examples

# block randomization of 12 subjects for a reference replicate study
# and demonstration of the S3 print method
rl <- RL4(nsubj=12, blocksize=6, seqs=c("TRR","RTR","RRT"), seed=0)
print(rl, sumry=TRUE)
pruns.exact

**Exact cumulative distribution function of runs test**

**Description**
This function calculates the exact cumulative conditional distribution of the Wald-Wolfowitz runs.

**Usage**
```
pruns.exact(r, n1, n2, tail = c("2-sided", "lower", "upper"))
```

**Arguments**
- **r**: Number of runs observed.
- **n1**: Number of +1 items in the sequence.
- **n2**: Number of -1 items in the sequence.
- **tail**: Tail of the cumulative distribution function.
  Default is the 2-tailed value.

**Value**
Numeric value of the cumulative distribution function according to the chosen tail.

**Note**
The 2-sided exact p-value is defined as $P(|R-E(R)|>=|r-E(R)|)$.
The lower (left) tail p-value is defined as $P(R<=r)$.
The upper (right) tail p-value is defined as $P(R>=r)$.
r is the observed value of the random variable R.

**Author(s)**
D. Labes

**Examples**
```
# SPSS "Exact Tests": small sample example, exact p: 0.071
# x <- c(1, 1, 1, 1, 0, 0, 0, 0, 1, 1)
pruns.exact(r=3, n1=4, n2=6)
# 0.07142857
# left tail P(R<=3)=0.04761905
pruns.exact(r=3, n1=4, n2=6, tail="lower")
# right tail P(R>=3)=0.9904762
pruns.exact(r=3, n1=4, n2=6, tail="upper")
# or via runs.pvalue (2-sided)
x <- c(1, 1, 1, 1, 0, 0, 0, 0, 1, 1)
runs.pvalue(x, pmetho="ex")
```
(Block) randomization of subjects, patients into sequence groups

Description

This function creates a randomization list of subjects, patients into sequences of treatments. It is mainly intended for use in crossover studies but may be used also for parallel group designs if for sequences c("T","R") is used.

Usage

RL4(nsubj, seqs = c("TR", "RT"), blocksize, seed=runif(1,max=1E7),
   randctrl=TRUE, pmethod=c("normal", "exact", "cc"), alpha=0.025)

Arguments

nsubj Number of subjects, patients ... to be randomized.
Or a vector of the subject numbers (f.i. 1001:1012)

seqs Character representation of the sequences.
In BE studies for a 2x2 cross-over usually something like c("TR", "RT").
If you prefer the ABC notation write down here f.i. c("AB", "BA").

blocksize Size of the blocks to randomize within.
If blocksize is missing it defaults to 2*number of sequences.
blocksize may be a vector of numbers.
In that case the sizes of the blocks are randomly chosen from that vector.

If blocksize=0 then the randomization takes place in the one block with all subjects.

seed An integer for the initialisation of the random number generator.

randctrl Shall the creation of the randomlist controlled by a runs test of randomness?
Defaults to TRUE.

pmethod A character string describing the method for the p-value calculation of the runs test.
"normal" denotes the normal approximation like the function(s) runs.test() of the packages tseries or lawstat.
"exact" chooses the calculation via exact distribution of the # of runs.
"cc" chooses the continuity correction to the large sample approximation like in the statistical software SPSS.

Default is pmethod="normal".

alpha Critical alpha value for re-creation of the randomlist based on the runs test.
Recommended is alpha=0.025.
Details

As default the randomization is done as block randomization.
If blocksize is given as a vector of numbers the sizes of the blocks are randomly chosen from that vector.
If blocksize=0 then the randomization takes place in the one block with all subjects.

The randomization is in the default settings controlled by a Wald-Wolfowitz runs test of randomness, i.e. if this test shows significant deviation from randomness (p-value<0.025 as default) the randomization list is recreated.
This behavior may be switched off by setting randctrl=FALSE if you don’t see any needfulness for such a control.
The reason for such a control was originally to avoid randomlists with only ’alternating’ sequences f.i. "TR" "RT" "TR" "RT" ...
See http://forum.bebac.at/mix_entry.php?id=8745

In its original form the runs test is only defined for dichotomous outcomes (i.e if 2 sequences are used).
If more than 2 sequences are used the runs test is modified by dichotomizing the sample of sequence numbers into cases < median and > median.
See package lawstat or https://de.wikipedia.org/wiki/Run-Test for this.

Value

Returns a list of class "rl4". This list has the components

- rl: A data.frame with the random list.
- seed: The used seed.
- blocksize: The used blocksize.
- ninseqs: A named vector containing the number of subjects in the sequence groups.
- runs.pvalue: The p-value of a runs test of randomness.
- date: Date and time of creation.

The class rl4 has the S3 method print.rl4.

Note

The blocksize(s) should be a multiple of the used # of sequences. If this is not the case it (they) will be adjusted accordingly.

The number of subjects should be a multiple of the used # of sequences. If this is not the case a warning is thrown that the design is not balanced.

The default for pmethod is the calculation via standard normal approximation. This has shown the ’best’ potential in rejecting the randomness for alternating random lists.
The randomness control does not work properly if more than 2 sequences are used. In that case a test of repeated patterns of sequences in blocks of length=nseq is done additionally to the runs test.
Example (seqno) 1 2 3 1 2 3 ...
The function calculates the 2-sided p-value of the Wald-Wolfowitz runs test after dichotomizing the input vector.

Usage

```r
runs.pvalue(y, pmethod = c("exact", "normal", "cc"))
```
Arguments

- **y**: Numeric vector of data values.
- **pmethod**: A character string describing the method for the p-value calculation of the runs test.
  - "exact" chooses the calculation via exact distribution of the # of runs.
  - "normal" denotes the normal approximation like the function(s) runs.test() of the packages tseries or lawstat.
  - "cc" chooses the continuity correction to the large sample approximation like in the statistical software SPSS.

Details

This function calculates the 2-sided p-value of the runs.test.
The large sample approximations are an adaption from the codes for runs.test() found in the R-packages lawstat and tseries.
The aim of this own was to avoid the heavy footprint of both packages for this small package.

The user can choose the application of a continuity correction to the normal approximation like a SAS implementation http://support.sas.com/kb/33/092.html uses or like SPSS if n<50.

The exact distribution of runs and the p-value based on it are described in the manual of SPSS "Exact tests" to be found f.i. https://www.sussex.ac.uk/its/pdfs/SPSS_Exact_Tests_21.pdf. If pmethod="exact" is chosen and n>30 and n1>12 and n2>12 (see pruns.exact) the continuity corrected version of the normal approximation is used to save time and memory.

Value

Numeric p-value of the 2-sided test.

Author(s)

- D. Labes
- adapted from runs.test() package lawstat
- Authors: Wallace Hui, Yulia R. Gel, Joseph L. Gastwirth, Weiwen Miao
- and from runs.test() package tseries
- Author: A. Trapletti

See Also

pruns.exact

Examples

```r
# alternating sequence 1,2,1,2 ...
# maybe seen as numeric representation of 'TR','RT' ...
# and is used in that way here in this package
x <- rep(c(1, 2), 6)
runs.pvalue(x, pmethod="normal")
```
sequences

# should give 0.002464631
# exact p-value
runs.pvalue(x, pmethod="exact")
# should give 0.004329004
#
# same for 3 numbers (numeric representation of 3 sequences)
x <- rep(c(1, 2, 3),4)
runs.pvalue(x, pmethod="normal")
# should give 0.2502128
# i.e. is seen as compatible with a random sequence!
# exact p-value, default i.e. must not given exolicitely
runs.pvalue(x)
# should give 0.3212121
# i.e. is seen even more as compatible with a random sequence!

sequences   Obtain sequences for BE study designs

Description

The function is intended as helper function to get the sequences for commonly used designs in BE studies.
These sequences may then subsequently used in function RL4().

Usage

sequences(design, tmts = NULL)

Arguments

design       A character value describing the study design. For crossover studies it is "tmts x sequences x periods" without space.
Fi. "2x2x2" is the standard 2-treatments-2-sequence-2-period crossover.
The designs "2x2x2", "3x3x3", "4x4x4" may be abbreviated to "2x2", "3x3", "4x4".
tmts         A character vector with the codes of the treatments.

Details

This function was implemented because I couldn’t remember f.i. all the six sequences of a "3x6x3" design if had to be coded by T1,T2 and R.
The sequences are primarily build within the ABC... notation.
If treatment codes are given the "AB..." in the sequences are replaced by these codes.

The following designs are implemented:
"parallel" = 2-group parallel design
"2x2" = classical 2-treatments-2-sequence-2-period crossover
"3x3" = 3-treatments-3-sequence-3-period crossover (Latin square)
sequences

"3x6x3" = 3-treatments-6-sequence-3-period crossover (Williams design)
"4x4" = 4-treatments-4-sequence-4-period crossover (Latin square)
"2x2x3" = 2-sequence-3-period replicate crossover
"2x2x4" = 2-sequence-4-period full replicate crossover
"2x4x4" = 4-sequence-4-period full replicate crossover
"2x3x3" = 3-sequence-3-period partial (reference) replicate crossover
"2x4x2" = 4-sequence-2-period replicate crossover, Baalams design.

The sequences for the "3x3" and "4x4" designs are randomly derived from the standard Latin squares (in ABC notation)
ABC, BCA, CAB
or in case of the "4x4" design from
ABCD, BDAC, CADB, DCBA.

Value

Returns a character vector with the sequences.

Note

For the higher order designs (designs with more than 2 treatments or replicate crossover designs, respectively) only a selection of possible designs are covered. The design sequences for "4x4" are not guaranteed to be a Williams design. If need a Williams design use function williams() instead.

Author(s)

Detlew Labes

References


See Also

williams, RL4

Examples

# classical 2x2 crossover in TR notation (simple enough to remember sequences("2x2", tmts=c("T","R"))
# 3-treatment-6-sequence-3-period Williams design in ABC notation sequences("3x6x3")
# 3-treatment-3-sequence-3-period design with one Test and two References sequences("3x3", tmts=c("T","R1","R2"))
# 4-treatment-4-period in TxRy notation, two Test and two Reference sequences("4x4", tmts=c("T1","T2","R1","R2"))
**williams**  
*Construct sequences of a Williams design*

**Description**

The function constructs the sequences of a Williams design via the algorithm given by Sheehe and Bross.

**Usage**

```r
williams(ntmt = 4, tmts = NULL)
```

**Arguments**

- `ntmt` Number of treatments. Must be an integer >1.
- `tmts` NULL or a vector of treatment codes.

**Details**

A Williams design is a crossover design in which each subject receives each treatment. The design is balanced over periods. The design has additionally the further feature that every treatment follows every other treatment the same number of times. It is said that these designs are balanced for first order carry over effects.

For an even number of treatments the design is a Latin square. For an odd number the design is a combination of two Latin squares.

Although the balance to first order carry over effects is not absolutely necessary in well planned BE studies with sufficient washout the Williams designs were traditionally used in "3x6x3" "4x4" crossover studies.

The sequences are created originally within the ABC... notation. If `tmts` are given the sequences are returned based on these treatment codes.

**Value**

Returns a character vector of the sequences.

**Note**

If `ntmt>3` the design returned is randomly chosen from the possible designs.

A similar but simpler function was contained in the package `crossdes`. But this package was removed from the CRAN repository.

**Author(s)**

D. Labes
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References


See Also

sequences, RL4

Examples

# Williams design for 4 treatments in ABC... notation
williams()

# The 6 sequences of the Williams design for 3 treatments
# same as sequences(design="3x6x3") except the ordering
williams(ntmt=3)
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