Package ‘randomizeR’

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Description This tool enables the user to choose a randomization procedure based on sound scientific criteria. It comprises the generation of randomization sequences as well as the assessment of randomization procedures based on carefully selected criteria. Furthermore, ‘randomizeR’ provides a function for the comparison of randomization procedures.

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'survEndp.R' 'getExpectation.R' 'expEndp.R' 'normEndp.R'
'endpoint.R' 'util.R' 'getStat.R' 'power.R' 'imbalance.R'
'corGuess.R' 'logRankDistribution.R' 'doublyF.R' 'testDec.R'
'doublyT.R' 'chronBias.R' 'selBias.R' 'bias.R' 'issue.R'
'assess.R' 'bbcdPar.R' 'bbcdSeq.R' 'ebcPar.R' 'bsdPar.R'
'bsdSeq.R' 'chenPar.R' 'chenSeq.R' 'chronBiasStepT.R'
'combinedBias.R' 'compare.R' 'crPar.R' 'crSeq.R'
'createParam.R' 'derFunc.R' 'desFunc.R' 'getDesFunc.R'
'derringerLs.R' 'derringerRs.R' 'derringerTs.R' 'desScores.R'
'desirability.R' 'ebcSeq.R' 'evaluate.R' 'gbcdPar.R'
'gbcdSeq.R' 'hadaPar.R' 'hadaSeq.R' 'mpPar.R' 'mpSeq.R'
'pbrPar.R' 'pbrSeq.R' 'probUnDes.R' 'tbdSeq.R' 'rpbrSeq.R'
'randomBlockSeq.R' 'randomizeROverview.R' 'randomizeRPackage.R'
'rarPar.R' 'rarSeq.R' 'rpbrPar.R' 'tbdPar.R' 'rtbdPar.R'
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R topics documented:

randomizeR-package .................................................. 3
a ................................................................. 4
abcdPar ............................................................ 5
assess .............................................................. 6
bbcdPar ............................................................ 7
blocks ............................................................... 8
bsdPar ............................................................. 9
chenPar ........................................................... 10
chronBias .......................................................... 11
coin ............................................................... 12
combineBias ....................................................... 13
compare ........................................................... 14
corGuess .......................................................... 15
createParam ...................................................... 16
createSeq ......................................................... 17
crPar ............................................................. 17
derFunc .......................................................... 18
desirability ....................................................... 19
ebcPar ............................................................ 20
evaluate ........................................................... 21
expEndp ........................................................... 23
gbcdPar ............................................................ 24
generateAllSequences ............................................. 25
generateRandomSequences ......................................... 27
getCorGuesses ..................................................... 32
getDesFunc ....................................................... 32
getDesign ........................................................ 33
getDesScores ..................................................... 35
getExpectation ................................................... 36
getProbabilities .................................................. 38
getRandomizationList ............................................ 40
haduPar ........................................................... 40
imbal .............................................................. 41
Description

This tool enables the user to choose a randomization procedure based on sound scientific criteria. It comprises the generation of randomization sequences as well the assessment of randomization procedures based on carefully selected criteria. Furthermore, randomizeR provides a function for the comparison of randomization procedures.
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References

See Also
For functionality for randomization procedures, see randPar and genSeq. For the criteria for the assessment of randomization procedures, see issues. For the assessment and comparison of randomization procedures, see assess and compare.

Function returning the adjusting parameter a slot of an S4 object

Description
Function returning the adjusting parameter a slot of an S4 object

Usage
a(obj)

Arguments
obj object of class randPar
abcdPar

Representing Accelerated Biased Coin Design

Description

Represents the randomization procedure Accelerated Biased Coin Design.

Usage

abcdPar(N, a, groups = LETTERS[1:2])

Arguments

N integer for the total sample size of the trial.

a nonnegative parameter which controls the degree of randomness: For decreasing
a the allocations become deterministic, while for increasing a the randomization
procedure tends to complete randomization.

groups character vector of labels for the different treatments.

Details

This is a class of 'biased coins' where the probability of selecting the under-represented treatment
is dependent from the absolute difference between the two treatment allocations up to the current
step.

Value

S4 object of the class abcdPar.

References

A. B. Antognini and A. Giovagnoli (2004) A new 'biased coin design' for the sequential allocation
651-664

See Also

Other randomization procedures: bbcdPar, bsdPar, chenPar, crPar, createParam(), ebcPar,
gbcdPar, hadaPar, mpPar, pbrPar, rarPar, rpbrPar, rtbdPar, tbdPar, udPar
Assessing randomization sequences

Description
Assesses randomization sequences based on specified issues in clinical trials.

Usage
assess(randSeq, ..., endp)
## S4 method for signature 'randSeq,missing'
assess(randSeq, ..., endp)
## S4 method for signature 'randSeq,endpoint'
assess(randSeq, ..., endp)

Arguments
randSeq object of class randSeq.
... at least one object of class issue or just a list of objects of the class issue.
endp object of class endpoint, or missing.

Details
Randomization sequences behave differently with respect to issues like selection bias, chronological bias, or loss in power estimation. The assess function evaluates the behavior of randomization sequences with respect to these issues. The first argument should be a result of one of the functions genSeq or getAllSeq. The second argument should be any number of issues arising in a clinical trial. The last argument endp may be provided if the assessment should take the distribution of the treatment groups into account, e.g. for power evaluation.

Value
S4 object of class assessment summarizing the assessment of the randomization procedure.

See Also
Representation of randomization procedures: randPar
Generation of randomization sequences: genSeq
issues for the assessment of randomization sequences
Examples

# assess the full set of Random Allocation Rule for N=4 patients
sequences <- getAllSeq(rarPar(4))
issue1 <- corGuess("CS")
issue2 <- corGuess("DS")
issue3 <- imbal("imb")
issue4 <- imbal("maxImb")
assess(sequences, issue1, issue2, issue3, issue4)

# assess one sequence of the Big Stick Design with respect to correct guesses
sequence <- genSeq(bsdPar(10, 2), seed = 1909)
assess(sequence, issue1)

# assess the same sequence with respect to selection bias and power for a normal endpoint
dpn <- normEndp(c(2, 2), c(1, 1))
issue5 <- selBias("CS", 4, "exact")
issue6 <- setPower(2, "exact")
assess(sequence, issue1, issue5, issue6, endp = dpn)

# assess the same sequence with respect to selection bias for an exponential endpoint
dpn <- expEndp(lambda = c(0.5, 0.5), cenRate=0.1, accrualTime=1, cenTime=5)
issue7 <- selBias("CS", 0.1, "exact")
assess(sequence, issue1, issue7, endp = dpn)

# recommended plot for the assessment of rejection probabilities
RP <- getAllSeq(crPar(6))
cB <- chronBias(type = "linT", theta = 1/6, method = "exact")
sB <- selBias(type= "CS", eta = 1/4, method = "exact")
normEndp <- normEndp(c(0, 0), c(1, 1))
A <- assess(RP, cB, sB, endp = normEndp)
D <- A$D
desiredSeq <- round(sum(D[,2][D[,3] <= 0.05 & D[,4] <= 0.05]), digits = 4)
colnames(D) <- c("Seq", "Prob", "SB", "linT")
g <- ggplot(D, aes(x = SB, y = linT))
g <- g + annotate("rect", xmin = 0, xmax = 0.05, ymin = 0, ymax = 0.05, alpha=0.2, fill="green")
g <- g + geom_point(alpha = 1/10, size = 3, col = "orange")
g <- g + geom_vline(xintercept = 0.05, col = "red")
g <- g + geom_hline(yintercept = 0.05, col = "red")
g <- g + geom_text(data = NULL, x = 0, y = 0, label = paste("Proportion:", desiredSeq, hjust=0, vjust=0, size = 7))
g

bbcdPar

Representing Bayesian Biased Coin Design

Description

Represents the randomization procedure Bayesian Biased Coin Design.
Usage

bbcdPar(N, a, groups = LETTERS[1:2])

Arguments

N integer for the total sample size of the trial.

a nonnegative parameter which controls the degree of randomness: For decreasing
a the allocations become deterministic, while for increasing a the randomization
procedure tends to complete randomization.

groups character vector of labels for the different treatments.

details

Extension of Efron’s biased coin design.

Value

S4 object of the class bbcdPar.

References

A. B. Antognini and Maroussa Zagoraiou (2014) Balance and randomness in sequential clinical

See Also

Other randomization procedures: abcPar, bsdPar, chenPar, crPar, createParam(), ebcPar,
gbcdPar, hadaPar, mpPar, pbrPar, rarPar, rpbrPar, rtbdPar, tbdPar, udPar

blocks

Function returning the block slot of an S4 object

Description

Function returning the block slot of an S4 object

Usage

blocks(obj)

Arguments

obj object of class pbrPar
**bsdPar**

*Representing Big Stick Design*

---

**Description**

Represents the randomization procedure Big Stick Design.

**Usage**

```r
bsdPar(N, mti, groups = LETTERS[1:2])
```

**Arguments**

- **N**: integer for the total sample size of the trial.
- **mti**: maximum tolerated imbalance in patient numbers during the trial.
- **groups**: character vector of labels for the different treatments.

**Details**

Tossing a fair coin as long as the difference in group sizes does not exceed the `mti`. If the `mti` is reached a deterministic allocation is done, so that the difference in group sizes is reduced.

**Value**

S4 object of the class `bsdPar`.

**References**


**See Also**

Other randomization procedures: `abcdPar`, `bbcdPar`, `chenPar`, `crPar`, `createParam()`, `ebcPar`, `gbcdPar`, `hadaPar`, `mpPar`, `pbrPar`, `rarPar`, `rpbrPar`, `rtbdPar`, `tbdPar`, `udPar`
chenPar

Representing Chen’s Design

Description

Represents the randomization procedure Chen’s Design.

Usage

chenPar(N, mti = N, p = 0.5, groups = LETTERS[1:2])

Arguments

- **N**: integer for the total sample size of the trial.
- **mti**: maximum tolerated imbalance in patient numbers during the trial.
- **p**: success probability of the biased coin (e.g. in Efron’s Biased Coin Design).
- **groups**: character vector of labels for the different treatments.

Details

Flip a biased coin with probability p in favor of the treatment which is allocated less frequently as long as the difference in group sizes does not exceed the mti. If the mti is reached a deterministic allocation is done, so that the difference in group sizes is reduced. If both treatments have been assigned equally often a fair coin is tossed.

Value

S4 object of the class chenPar.

References


See Also

Other randomization procedures: abcdPar, bbcdPar, bsdPar, crPar, createParam(), ebcPar, gbcdPar, hadaPar, mpPar, pbrPar, rarPar, rpbrPar, rtbdPar, tbdPar, udPar
`chronBias`  

Represents the issue of chronological bias in a clinical trial.

**Usage**

```r
chronBias(type, theta, method, saltus, alpha = 0.05)
```

**Arguments**

- **type** character string, should be one of "linT", "logT", or "stepT", see Details.
- **theta** factor of the time trend for further details see type.
- **method** character string, should be one of "sim" or "exact", see Description.
- **saltus** integer or missing specifying the patient index (i.e. position) of the step in case of step time trend.
- **alpha** significance level

**Details**

Chronological bias can be an issue in the design of a clinical trial. The `chronBias` function is a constructor function for an S4 object of the class `chronBias` representing the issue of chronological bias, s.a. time trends, in a clinical trial. It supports two possible modes, method="sim" and method="exact", and three different types of trend.

If method="sim", the object represents the simulated type-I-error rate given the level alpha, the selection effect eta and the biasing strategy type. When calling assess for a `chronBias` object with method="sim", one test decision is computed for each sequence of randSeq. The type-I-error rate (power) is the proportion of falsely (correctly) rejected null hypotheses.

If method="exact", the object represents the exact type-I-error probability given the level alpha, the selection effect eta and the biasing strategy type. When calling assess for a `chronBias` object with method="exact", the p-value of each randomization sequence is computed. For normal endpoints and two treatment groups these p-values are exact values which can be calculated from the sum of the corresponding quantiles of the doubly noncentral t-distribution. For more than two treatment groups, exact p-values are computed using a doubly noncentral F distribution. For exponential endpoints the p-values are obtained using an approximation formula.

**Types of chronological bias:**

- **type = "linT"** Represents linear time trend. Linear time trend means that the time trend function of the patients, i.e. expected response for normal endpoints, increases evenly by \( \frac{\theta}{N-1} \) with every patient included in the study, until reaching \( \theta \) after \( N \) patients. Linear time trend may occur as a result of gradually relaxing in- or exclusion criteria throughout the trial. It can be represented by the formula:

\[
f(i) = \frac{(i - 1)}{(N - 1)}\theta
\]
type = "logT" Represents logarithmic time trend. Logarithmic time trend means that the time trend function of the patients, i.e. expected response for normal endpoints, increases logarithmically in the patient index by $\theta/\log(N)$ with every patient included in the study, until reaching $\theta$ after $N$ patients. Logarithmic time trend may occur as a result of a learning curve, i.e. in a surgical trial. It can be represented by the formula:

$$\log(i)/\log(N)\theta$$

$\text{type} = "\text{stepT}"$ Represents step trend. Step trend means that the expected response of the patients increases by $\theta$ after a given point ("saltus") in the allocation process. Step trend may occur if a new device is used after the point $c = "\text{saltus}"$, or if the medical personal changes after this point. Step time trend can be represented by the formula:

$$f(i) = 1_{c<i\leq N}\theta$$

Value

S4 object of class chronBias, a formal representation of the issue of chronological bias in a clinical trial.

References


See Also

Other issues: combineBias(), corGuess, imbal, issue, selBias, setPower()

Examples

```r
# create a linear time trend with theta = 0.5 for which the exact rejection probabilities
# are calculated
cbias <- chronBias("linT", 0.5, "exact")

# create a stepwise time trend with theta = 1 after 10 allocations for which the test
# decision is simulated
cbias <- chronBias("stepT", 1, "sim", 10)
```

---

coin

*Function returning the coin slot of an S4 object*

**Description**

Function returning the coin slot of an S4 object
Usage

coin(obj)

Arguments

obj object extending class randPar or randSeq

Description

This class combines a selBias object and a chronBias object to a new object. In the analysis within the new object the two types of bias are treated as additive effect for normal endpoints and as multiplicative effect for exponential endpoints.

Usage

combineBias(selBias, chronBias)

Arguments

selBias object of class selBias
chronBias object of class chronBias

See Also

Other issues: chronBias, corGuess, imbal, issue, selBias, setPower()

Examples

chronBias <- chronBias(type="linT", theta=1, method="sim")
selBias <- selBias(type="CS", eta=1, method="sim")
combineBias(selBias, chronBias)
Compare randomization procedures based on a specified issue in clinical trials.

Usage

```r
compare(issue, ..., endp)
```

## S4 method for signature 'issue,missing'

```r
compare(issue, ..., endp)
```

## S4 method for signature 'issue,endpoint'

```r
compare(issue, ..., endp)
```

Arguments

- `issue`: object of class `issue`.
- `...`: at least one object of class `randSeq` or a list of objects of class `randSeq`.
- `endp`: object of class `endpoint`, or `missing`.

Details

Randomization procedures behave differently with respect to issues like selection bias, chronological bias, or loss in power estimation. The `compare` function evaluates the behavior of randomization procedures with respect to one issue. Its first argument should represent one of the implemented `issues`. The second argument should be any number of objects of the class `randSeq`. These objects represent the randomization procedures for the planned comparison. The last argument `endp` may be provided if the assessment should take the distribution of the treatment groups into account, e.g. for power evaluation.

Value

S4 object of class `comparison` summarizing the comparison of the randomization procedures.

See Also

Representation of randomization procedures: `randPar`

Generation of randomization sequences: `genSeq`

`issues` for the assessment of randomization sequences
Examples

# compare Random Allocation Rule and Big Stick for N = 4 with respect to
correct guesses
RAR <- getAllSeq(rarPar(4))
BSD <- getAllSeq(bsdPar(4, mti = 2))
corGuess <- corGuess("CS")
(comp <- compare(corGuess, RAR, BSD))
plot(comp)

# compare the same procedures with respect to selection bias for a normal endpoint
endp <- normEndp(c(2, 2), c(1, 1))
selBias <- selBias("CS", 4, "exact")
(comp <- compare(selBias, RAR, BSD, endp = endp))
plot(comp)

# compare the same procedures with respect to selection bias for an exponential endpoint
endp <- expEndp(lambda = c(0.5, 0.5), cenRate=0.1, accrualTime=1, cenTime=5)
selBias <- selBias("CS", 0.1, "exact")
(comp <- compare(selBias, RAR, BSD, endp = endp))
plot(comp)

corGuess

Represents the expected number of correct guesses

Description

Represents the expected number of correct guesses of randomization sequences.

Usage

corGuess(type)

Arguments

type character string, should be one of "CS" or "DS", see Details.

Details

Selection bias can be an issue in the design of a clinical trial. The expected number of correct guesses is one measure for selection bias. The corGuess function is a constructor function for an S4 object of the class corGuess representing the issue of correct guesses in a clinical trial. The parameter type takes the following values:

"CS" refers to "convergence strategy", i.e. the investigator predicts the treatment which has hitherto occurred less often.

"DS" refers to "divergence strategy", i.e. the investigator predicts the treatment which has hitherto occurred more often.
createParam

Value

S4 object of class corGuess, a formal representation of the issue of correct guesses in a clinical trial.

References


See Also

Other issues: chronBias, combineBias(), imbal, issue, selBias, setPower()

description

Representing any randomization procedure

Description

Represents any randomization procedure for a two-armed clinical trial.

Usage

createParam(method, N, mti, bc, rb, p, ini, add, filledBlock)

Arguments

method method that is used to generate the (random) allocation sequence. It can take values PBR, RAR, HAD, PWR, EBC, BSD, CR, TBD, UD, and MP.
N integer for the total sample size of the trial.
mti maximum tolerated imbalance in patient numbers during the trial.
bc vector which contains the lengths $k_1, \ldots, k_l$ of each block. This means that the vector bc will have one entry for each block.
rb block lengths of the blocks that can be selected equiprobable at random.
p success probability of the biased coin (e.g. in Efron’s Biased Coin Design).
in integer representing the initial urn composition.
add integer representing the number of balls that are added to the urn in each step.
filledBlock logical whether the last block should be filled or not.

Details

Depending on the input of the user, createParam creates an object representing a randomization procedures for a two-armed clinical trial (see also randPar).

Value

S4 object of the corresponding randomization procedure class.
See Also

Other randomization procedures: abcdPar, bbcdPar, bsdPar, chenPar, crPar, ebcPar, gbdPar, hadaPar, mpPar, pbrPar, rarPar, rpbrPar, rtbdPar, tbdPar, udPar

createSeq

Query to create a randomization sequence of a particular randomization procedure

Description

This function is a query to create an corresponding randomization sequence for a two-armed clinical trial. If file is defined, the generated sequence is automatically saved to the corresponding path.

Usage

createSeq(file)

Arguments

dfile A connection, or a character string naming the file to write to.

Value

an object Param, which is available

crPar

Representing Complete Randomization

Description

Represents the randomization procedure Complete Randomization.

Usage

crPar(N, K = 2, ratio = rep(1, K), groups = LETTERS[1:K])

Arguments

N integer for the total sample size of the trial.
K number of treatment groups (e.g. K=2 if we compare one experimental against one control treatment).

ratio vector of length K. The total sample number N and all used block lengths (bc) have to be divisible by sum(ratio).

groups character vector of labels for the different treatments.
Details
Toss a fair coin \( N \) times in case \( K=2 \) and assign the treatments according to the result of the coin. In case of \( K>2 \), replace the coin by a die with \( K \) sides.

Value
S4 object of the class \texttt{crPar}.

References

See Also
Other randomization procedures: \texttt{abcdPar}, \texttt{bbcdPar}, \texttt{bsdPar}, \texttt{chenPar}, \texttt{createParam()}, \texttt{ebcPar}, \texttt{gbcdPar}, \texttt{hadaPar}, \texttt{mpPar}, \texttt{pbrPar}, \texttt{rarPar}, \texttt{rpbrPar}, \texttt{rtbdPar}, \texttt{tbdPar}, \texttt{udPar}

---

\texttt{derFunc} \hspace{1cm} \textit{Representing Derringer-Suich desirability functions}

Description
Represents the Derringer-Suich desirability approach.

Usage
\texttt{derFunc(TV, SLs, b)}

Arguments
\begin{description}
\item[TV] numeric specifying the optimal desired value called the target value.
\item[SLs] numeric vector of length at most 2 specifying the lower and/or upper specified border.
\item[b] numeric vector of length at most 2 specifying the weight(s) for the punishment of deviations from the target value.
\end{description}

Details
\texttt{derFunc} represents the framework for left, right and two-sided desirability functions introduced by Derringer and Suich (1980). For all three different kinds of desirability functions the parameter \( TV \) must be specified. If the parameter \( SLs \) has length 1, either the left- or right-sided desirability function is created depending from whether the value is smaller (left-sided) or greater (right-sided) than the target value. By specifying \( SLs \) as a vector of length 2 a two-sided desirability function is created where the lower specified border is determined as the smaller value of \( SLs \) and thus the upper specified border is determined as the greater value. If there are no values specified for the weights, then they are automatically set to 1 (linear loss).
**Value**

S4 object of class `derFunc`, a formal representation of desirability functions introduced by Derringer and Suich.

**References**


**See Also**

Other desirability topics: `evaluate()`, `getDesScores()`, `plotDes()`, `plotEv()`, `probUnDes()`

**Examples**

```r
# create an object of a left-sided desirability function
dLeft <- derFunc(0.5, 0.3, 2)

# create an object of a right-sided desirability function
dRight <- derFunc(0.5, 0.8, 1)

# create an object of a two-sided desirability function
dLR <- derFunc(0.5, c(0.3, 0.9), c(3, 1))
```

---

### desirability

**Desirability functions within the scope of clinical trials**

**Description**

Illustrates the interplay between functions related to desirability indices.

**Details**

Currently, randomizr encompasses the class of desirability functions introduced by Derringer and Suich (1980) and corresponding functions to evaluate and compare randomization sequences which have been assessed on the basis of desirability indices of specific issues:

- `derFunc` represents the class of desirability functions according to Derringer-Suich (1980).
- `getDesScores` can be applied to an object of class assessment together with prespecified desirability functions to compare the behavior of randomization sequences (on a common scale [0,1]).
- `plotDes` plots a desScores object on a radar chart.
- `evaluate` performs a comparison of sequences from different randomization sequences on the basis of object of the class `desScores`.
- `plotEv` plots an evaluation object on a radar chart.
- `probUnDes` computes the probability of undesired randomization sequences with respect to certain issues and desirability functions.
Examples

# perform a comparison of randomization sequences from different randomization procedures
# with the help of desirability functions

issue1 <- corGuess("CS")
issue2 <- chronBias(type = "linT", theta = 1/4, method = "exact")
RAR <- getAllSeq(rarPar(4))
BSD <- getAllSeq(bsdPar(4, mti = 2))
A1 <- assess(RAR, issue1, issue2, endp = normEndp(c(0,0), c(1,1)))
A2 <- assess(BSD, issue1, issue2, endp = normEndp(c(0,0), c(1,1)))

d1 <- derFunc(TV = 0.5, 0.75, 2)
d2 <- derFunc(0.05, c(0, 0.1), c(1, 1))

# apply the getDesScores function to the assessment output with the specified desirability
# functions to evaluate the behaviour of randomization sequences on a [0,1] scale

DesScore <- getDesScores(A1, d1, d2, weights = c(5/6, 1/6))
DesScore2 <- getDesScores(A2, d1, d2, weights = c(5/6, 1/6))

# plotting the desScores objects
plotDes(DesScore, quantiles = TRUE)
plotDes(DesScore2, quantiles = TRUE)

# summarize the results of getDesScore with respect to the statistic "mean"
evaluate(DesScore, DesScore2)

# plot the evaluation objects for a visualized comparison
plotEv(evaluate(DesScore, DesScore2))

# display which randomization produces more undesired randomization sequences
# with respect to certain issues and desirability functions
probUnDes(DesScore)
probUnDes(DesScore2)

---

**ebcPar**  
*Representing Efron’s Biased Coin Design*

**Description**

Represents the randomization procedure Efron's Biased Coin Design.

**Usage**

```
ebcPar(N, p, groups = LETTERS[1:2])
```
evaluate

Arguments

- **N** integer for the total sample size of the trial.
- **p** success probability of the biased coin (e.g. in Efron’s Biased Coin Design).
- **groups** character vector of labels for the different treatments.

Details

Flip a biased coin with probability p in favor of the treatment which is allocated less frequently. If both treatments have been assigned equally often a fair coin is tossed.

Value

S4 object of the class ebcPar.

References


See Also

Other randomization procedures: abcdPar, bbcdPar, bsdPar, chenPar, crPar, createParam(), gdbdPar, hadaPar, mpPar, pbrPar, rarPar, rpbrPar, rtbdPar, tbdPar, udPar

Description

Evaluation of several randomization procedures with respect to certain desirability functions applied to specified issues.

Usage

evaluate(..., statistic)

---

## S4 method for signature 'missing'

evaluate(..., statistic)

## S4 method for signature 'character'

evaluate(..., statistic)

Arguments

- **...** at least one object of the class desScores or a list of objects of the class desScores.
- **statistic** character string that specifies on the basis of which statistic the evaluate function should be applied. The statistic can be chosen from "mean", "median", "min" or "max".
Details

The `evaluate` function allows the user to compare and evaluate different randomization procedures. It expects a number of objects that result when applying the `getDesScores` function to an `assess` object and specified desirability functions. The `evaluate` function summarizes the desirability scores of each randomization procedure on the basis of a prespecified statistic and incorporates them into a data frame. If no statistic is specified then it is automatically set to `mean`. If the function is applied to only one object it corresponds simply to `summary(getDesScores(...))`.

Value

S4 object of class `evaluation` Comparison of randomization procedures with respect to desirability functions applied to specified issues, summarized by a prespecified statistic.

References


See Also

Representation of randomization procedures: `randPar`

Generation of randomization sequences: `genSeq`

`issues` for the desirability of randomization sequences

Other desirability topics: `derFunc`, `getDesScores()`, `plotDes()`, `plotEv()`, `probUnDes()`

Examples

```r
corGuess("CS")
corGuess("DS")
getAllSeq(rarPar(4))
getAllSeq(bsdPar(4, mti = 2))
assess(RAR, issue1, issue2)
assess(BSD, issue1, issue2)

tv = 0.1, 0.7, 2
tv = 0.5, c(0.3, 0.8), c(1, 1)
getDesScores(A1, d1, d2, weights = c(5/6, 1/6))
getDesScores(A2, d1, d2, weights = c(5/6, 1/6))

evaluate(DesScore, DesScore2)
evaluate(DesScore, DesScore2, statistic = "max")
```
expEndp

Representation of exponentially distributed endpoints

Description

Represents exponentially distributed endpoints in clinical trials.

Usage

expEndp(lambda, cenRate, accrualTime = 0, cenTime)

Arguments

lambda vector of the exponential rate parameters in each treatment group.
cenRate exponential censoring rate in a survival study.
accrualTime duration of the accrual period in a survival study.
cenTime total duration of a survival study (maximum length of followup).

Details

The expEnd function is a constructor function for an S4 object of the class expEnd representing an exponentially distributed endpoint in a clinical trial. In conjunction with the assess function, exponential endpoints admit the calculation of the 'exact' type-I-error probability and power using an approximation formula.

See Also

Compute exact or simulated type-I-error: assess.
Other endpoint types: normEndp, survEndp

Examples

# set the parameters of two exponentially distributed endpoints
dbp <- expEndp(lambda = c(1, 2), cenTime = 10, cenRate = 0.01)
gbcdPar

Representing Generalized Biased Coin Design

Description

Represents the randomization procedure Generalized Biased Coin Design.

Usage

gbcdPar(N, rho, groups = LETTERS[1:2])

Arguments

N integer for the total sample size of the trial.

rho nonnegative parameter which may be adjusted according to how strongly it is desired to balance the experiment. If \( \rho = 1 \), we have Wei’s urn design with \( \alpha = 0 \). If \( \rho = 0 \), we have complete randomization.

groups character vector of labels for the different treatments.

Details

Generalization of Wei’s urn and Efron’s biased coin design.

Value

S4 object of the class gbcdPar.

References


See Also

Other randomization procedures: abcdPar, bbcdPar, bsdPar, chenPar, crPar, createParam(), ebcPar, hadaPar, mpPar, pbrPar, rarPar, rpbrPar, rtbdPar, tbdPar, udPar
generateAllSequences  Complete set of randomization sequences

Description

Computes all randomization sequences for the given randomization procedure, and stores them in an object along with the parameters belonging to the randomization procedure.

Usage

generateAllSequences(obj)

## S4 method for signature 'abcdPar'
generateAllSequences(obj)

## S4 method for signature 'bbcdPar'
generateAllSequences(obj)

## S4 method for signature 'ebcPar'
generateAllSequences(obj)

## S4 method for signature 'bsdPar'
generateAllSequences(obj)

## S4 method for signature 'chenPar'
generateAllSequences(obj)

## S4 method for signature 'crPar'
generateAllSequences(obj)

## S4 method for signature 'gbcdPar'
generateAllSequences(obj)

## S4 method for signature 'hadaPar'
generateAllSequences(obj)

## S4 method for signature 'mpPar'
generateAllSequences(obj)

## S4 method for signature 'pbrPar'
generateAllSequences(obj)

## S4 method for signature 'rarPar'
generateAllSequences(obj)

## S4 method for signature 'tbdPar'
gen
### S4 method for signature 'udPar'
getAllSeq(obj)

**Arguments**

obj object specifying the randomization procedure, see `randPar` or `createParam`.

**Details**

getAllSeq is a generic function which dispatches different methods depending on the type of input. The set of sequences of a procedure is computed by enumerating all possible sequences and eliminating those that are not possible in the randomization procedure specified by obj. The parameters of the randomization procedure are saved along with the sequences to ensure reproducibility of the results.

**Value**

An object inheriting from `randSeq`, representing the set of randomization sequences for the given parameters. The output consists of the parameters used for the generation of the randomization sequences (see `createParam`) and the matrix `M` that stores the randomization sequences in its rows.

**See Also**

`createParam`

**Examples**

```r
# all randomization sequences of Efron's Biased Coin Design with p = 0.667 for N = 6
myPar <- ebcPar(6, 0.667)
getAllSeq(myPar)

# all randomization sequences of Big Stick Design with mti = 2 for N = 6
myPar <- bsdPar(6, 2)
getAllSeq(myPar)

# all randomization sequences of Permuted Block Randomization with block sizes 4 and 2
myPar <- pbrPar(c(4, 2))
getAllSeq(myPar)
```
generateRandomSequences

Generate random sequences

Description

Generates randomization sequences from a given randomization procedure.

Usage

```r
genSeq(obj, r, seed)
## S4 method for signature 'abcdPar,numeric,numeric'
genSeq(obj, r, seed)

## S4 method for signature 'abcdPar,numeric,missing'
genSeq(obj, r, seed)

## S4 method for signature 'abcdPar,missing,numeric'
genSeq(obj, r, seed)

## S4 method for signature 'abcdPar,missing,missing'
genSeq(obj, r, seed)

## S4 method for signature 'bbcdPar,numeric,numeric'
genSeq(obj, r, seed)

## S4 method for signature 'bbcdPar,numeric,missing'
genSeq(obj, r, seed)

## S4 method for signature 'bbcdPar,missing,numeric'
genSeq(obj, r, seed)

## S4 method for signature 'bbcdPar,missing,missing'
genSeq(obj, r, seed)

## S4 method for signature 'ebcPar,numeric,numeric'
genSeq(obj, r, seed)

## S4 method for signature 'ebcPar,missing,numeric'
genSeq(obj, r, seed)

## S4 method for signature 'ebcPar,numeric,missing'
genSeq(obj, r, seed)

## S4 method for signature 'ebcPar,missing,missing'
genSeq(obj, r, seed)
```
generateRandomSequences

## S4 method for signature 'bsdPar,numeric,numeric'
genSeq(obj, r, seed)

## S4 method for signature 'bsdPar,numeric,missing'
genSeq(obj, r, seed)

## S4 method for signature 'bsdPar,missing,numeric'
genSeq(obj, r, seed)

## S4 method for signature 'bsdPar,missing,missing'
genSeq(obj, r, seed)

## S4 method for signature 'chenPar,numeric,numeric'
genSeq(obj, r, seed)

## S4 method for signature 'chenPar,numeric,missing'
genSeq(obj, r, seed)

## S4 method for signature 'chenPar,missing,numeric'
genSeq(obj, r, seed)

## S4 method for signature 'chenPar,missing,missing'
genSeq(obj, r, seed)

## S4 method for signature 'crPar,numeric,numeric'
genSeq(obj, r, seed)

## S4 method for signature 'crPar,numeric,missing'
genSeq(obj, r, seed)

## S4 method for signature 'crPar,missing,numeric'
genSeq(obj, r, seed)

## S4 method for signature 'crPar,missing,missing'
genSeq(obj, r, seed)

## S4 method for signature 'gbcdPar,numeric,numeric'
genSeq(obj, r, seed)

## S4 method for signature 'gbcdPar,numeric,missing'
genSeq(obj, r, seed)

## S4 method for signature 'gbcdPar,missing,numeric'
genSeq(obj, r, seed)

## S4 method for signature 'gbcdPar,missing,missing'
genSeq(obj, r, seed)
## S4 method for signature 'hadaPar,numeric,numeric'
```
genSeq(obj, r, seed)
```

## S4 method for signature 'hadaPar,missing,numeric'
```
genSeq(obj, r, seed)
```

## S4 method for signature 'hadaPar,numeric,missing'
```
genSeq(obj, r, seed)
```

## S4 method for signature 'hadaPar,missing,missing'
```
genSeq(obj, r, seed)
```

## S4 method for signature 'mpPar,numeric,numeric'
```
genSeq(obj, r, seed)
```

## S4 method for signature 'mpPar,missing,numeric'
```
genSeq(obj, r, seed)
```

## S4 method for signature 'mpPar,numeric,missing'
```
genSeq(obj, r, seed)
```

## S4 method for signature 'mpPar,missing,missing'
```
genSeq(obj, r, seed)
```

## S4 method for signature 'pbrPar,missing,numeric'
```
genSeq(obj, r, seed)
```

## S4 method for signature 'pbrPar,numeric,numeric'
```
genSeq(obj, r, seed)
```

## S4 method for signature 'pbrPar,missing,missing'
```
genSeq(obj, r, seed)
```

## S4 method for signature 'pbrPar,numeric,missing'
```
genSeq(obj, r, seed)
```

## S4 method for signature 'rarPar,numeric,numeric'
```
genSeq(obj, r, seed)
```

## S4 method for signature 'rarPar,missing,numeric'
```
genSeq(obj, r, seed)
```

## S4 method for signature 'rarPar,numeric,missing'
```
genSeq(obj, r, seed)
```

## S4 method for signature 'rarPar,missing,missing'
```
genSeq(obj, r, seed)
```

## S4 method for signature 'rarPar,numeric,missing'
```
genSeq(obj, r, seed)
```

## S4 method for signature 'rarPar,missing,missing'
```
genSeq(obj, r, seed)
```

## S4 method for signature 'rarPar,numeric,missing'
```
genSeq(obj, r, seed)
```

## S4 method for signature 'rarPar,missing,missing'
```
## S4 method for signature 'rpbrPar,missing,numeric'
\texttt{genSeq}(\texttt{obj} \ , \ \texttt{r} \ , \ \texttt{seed})

## S4 method for signature 'rpbrPar,numERIC,numERIC'
\texttt{genSeq}(\texttt{obj} \ , \ \texttt{r} \ , \ \texttt{seed})

## S4 method for signature 'rpbrPar,missing,missing'
\texttt{genSeq}(\texttt{obj} \ , \ \texttt{r} \ , \ \texttt{seed})

## S4 method for signature 'rpbrPar,numERIC,missing'
\texttt{genSeq}(\texttt{obj} \ , \ \texttt{r} \ , \ \texttt{seed})

## S4 method for signature 'tbdPar,numERIC,numERIC'
\texttt{genSeq}(\texttt{obj} \ , \ \texttt{r} \ , \ \texttt{seed})

## S4 method for signature 'tbdPar,missing,numERIC'
\texttt{genSeq}(\texttt{obj} \ , \ \texttt{r} \ , \ \texttt{seed})

## S4 method for signature 'tbdPar,numERIC,missing'
\texttt{genSeq}(\texttt{obj} \ , \ \texttt{r} \ , \ \texttt{seed})

## S4 method for signature 'tbdPar,missing,missing'
\texttt{genSeq}(\texttt{obj} \ , \ \texttt{r} \ , \ \texttt{seed})

## S4 method for signature 'rtbdPar,numERIC,numERIC'
\texttt{genSeq}(\texttt{obj} \ , \ \texttt{r} \ , \ \texttt{seed})

## S4 method for signature 'rtbdPar,missing,numERIC'
\texttt{genSeq}(\texttt{obj} \ , \ \texttt{r} \ , \ \texttt{seed})

## S4 method for signature 'rtbdPar,numERIC,missing'
\texttt{genSeq}(\texttt{obj} \ , \ \texttt{r} \ , \ \texttt{seed})

## S4 method for signature 'rtbdPar,missing,missing'
\texttt{genSeq}(\texttt{obj} \ , \ \texttt{r} \ , \ \texttt{seed})

## S4 method for signature 'udPar,numERIC,numERIC'
\texttt{genSeq}(\texttt{obj} \ , \ \texttt{r} \ , \ \texttt{seed})

## S4 method for signature 'udPar,missing,numERIC'
\texttt{genSeq}(\texttt{obj} \ , \ \texttt{r} \ , \ \texttt{seed})

## S4 method for signature 'udPar,numERIC,missing'
\texttt{genSeq}(\texttt{obj} \ , \ \texttt{r} \ , \ \texttt{seed})

## S4 method for signature 'udPar,missing,missing'
\texttt{genSeq}(\texttt{obj} \ , \ \texttt{r} \ , \ \texttt{seed})
Arguments

<table>
<thead>
<tr>
<th>arg</th>
<th>description</th>
</tr>
</thead>
<tbody>
<tr>
<td>obj</td>
<td>object specifying the randomization procedure, see <code>randPar</code> or <code>createParam</code>.</td>
</tr>
<tr>
<td>r</td>
<td>numeric indicating the number of random sequences to be generated at random, or missing.</td>
</tr>
<tr>
<td>seed</td>
<td>a single value, interpreted as an integer, that specifies the seed for the random number generation.</td>
</tr>
</tbody>
</table>

Details

genSeq generates randomization sequences for a randomization procedure as defined by the input parameters. genSeq has two modes, according to the input.

1. `genSeq(obj,r)`: gives \( r \) random sequences from the design specified by \( obj \), along with the parameters stored in \( obj \).
2. `genSeq(obj)`: gives one random sequences from the design specified by \( obj \), along with the parameters stored in \( obj \).

The sequences are generated by using the Monte-Carlo sampling technique to sample from the true distribution of the sequences according to the randomization procedure specified by \( obj \). The parameters of the randomization procedure are saved along with the sequences to ensure reproducibility of the results.

Value

An object inheriting from `randSeq`, representing the \( r \) randomization sequences generated at random for the specified randomization procedure. The output consists of the parameters used for the generation of the randomization sequences (see `createParam`) and the matrix \( M \) that stores the randomization sequences in its \( r \) rows. If \( r \) is missing, one sequence is generated by default.

Examples

```r
# generate randomization sequences using Complete Randomization for N = 10
myPar <- crPar(10)
genSeq(myPar, 4)
genSeq(myPar)

# generate randomization sequences using the Random Allocation Rule for N = 10
myPar <- rarPar(10)
genSeq(myPar, 4)
genSeq(myPar)

# generate randomization sequences using the Maximal Procedure with mti = 2 and N = 10
myPar <- mpPar(10, 2)
genSeq(myPar, 4)
genSeq(myPar)
```
getCorGuesses | Matrix of the guesses of the investigator

Description

Calculates the guesses of the investigator of a randomization list following the specified guessing strategy.

Usage

gectCorGuesses(randSeq, guessing)

Arguments

randSeq | object of the class randSeq.
guessing | object of the class corGuess.

Value

Matrix of the guesses of the investigator following the specified guessing strategy. No guess is abbreviated with "nG".

Examples

myPar <- bsdPar(10, 2)
M <- genSeq(myPar, 2)
type <- corGuess("CS")
gectCorGuesses(M, type)

getDesFunc | Type of Desirability function

Description

Generates a character vector which specifies the used desirability function and its parameters

Usage

gectDesFunc(obj)

## S4 method for signature 'derringerLs'
gectDesFunc(obj)

## S4 method for signature 'derringerRs'
gectDesFunc(obj)
### S4 method for signature 'derringerTs'
getDesFunc(obj)

### Arguments

- **obj**: object of the class desFunc.

### getDesign

**Design of a randomization procedure**

### Description

Generates a character vector which specifies the used randomization method

### Usage

getDesign(obj)

## S4 method for signature 'abcdPar'
getDesign(obj)

## S4 method for signature 'abcdSeq'
getDesign(obj)

## S4 method for signature 'bbcdPar'
getDesign(obj)

## S4 method for signature 'bbcdSeq'
getDesign(obj)

## S4 method for signature 'ebcPar'
getDesign(obj)

## S4 method for signature 'bsdPar'
getDesign(obj)

## S4 method for signature 'bsdSeq'
getDesign(obj)

## S4 method for signature 'chenPar'
getDesign(obj)

## S4 method for signature 'chenSeq'
getDesign(obj)

## S4 method for signature 'crPar'
getDesign(obj)

## S4 method for signature 'crSeq'
getDesign(obj)

## S4 method for signature 'ebcSeq'
getDesign(obj)

## S4 method for signature 'gbcdPar'
getDesign(obj)

## S4 method for signature 'gbcdSeq'
getDesign(obj)

## S4 method for signature 'hadaPar'
getDesign(obj)

## S4 method for signature 'hadaSeq'
getDesign(obj)

## S4 method for signature 'mpPar'
getDesign(obj)

## S4 method for signature 'mpSeq'
getDesign(obj)

## S4 method for signature 'pbrPar'
getDesign(obj)

## S4 method for signature 'pbrSeq'
getDesign(obj)

## S4 method for signature 'rRtbdSeq'
getDesign(obj)

## S4 method for signature 'rRpbrSeq'
getDesign(obj)

## S4 method for signature 'rarPar'
getDesign(obj)

## S4 method for signature 'rarSeq'
getDesign(obj)

## S4 method for signature 'rpbrPar'
getDesign(obj)

## S4 method for signature 'tbdPar'
getDesign(obj)

## S4 method for signature 'rtbdPar'
getDesign(obj)

## S4 method for signature 'tbdSeq'
getDesign(obj)

## S4 method for signature 'udPar'
getDesign(obj)

## S4 method for signature 'udSeq'
getDesign(obj)

Arguments

**obj**
object of the class randSeq or randPar.

---

getDesScores

*Applying desirability functions on issues of individual randomization sequences*

**Description**

Applying desirability function on issues of individual randomization sequences.

**Usage**

getDesScores(assess, ..., weights)

## S4 method for signature 'assessment,missing'
getDesScores(assess, ..., weights)

## S4 method for signature 'assessment,numeric'
getDesScores(assess, ..., weights)

**Arguments**

**assess**
object of class assessment.

**...**
at least one object of class derFunc or a list of objects of the class derFunc.

**weights**
weights for computing the geometric mean of several desirability scores. If missing, the issues are automatically equally weighted.
Details

Randomization sequences behave differently with respect to issues like selection bias, chronological bias, or loss in power estimation. The `getDesScores` function evaluates the behavior of randomization sequences with respect to these issues. The difference to the `assess` function is that it scales them to [0,1] and makes them easier interpretable. The first argument should be a result of the `assess` function. The second argument should be any number of `derFunc` objects that represent the desirability functions. The last argument `weights` may be provided if the desirability functions should be weighted differently.

Value

S4 object of class `desirability` summarizing the desirability of the randomization procedure.

See Also

Representation of randomization procedures: `randPar`
Generation of randomization sequences: `genSeq`
issues for the desirability of randomization sequences
Other desirability topics: `derFunc`, `evaluate()`, `plotDes()`, `plotEv()`, `probUnDes()`

Examples

```r
# compute the desire-function for the full set of Random Allocation Rule for N = 4
sequences <- getAllSeq(rarPar(4))
issue1 <- corGuess("CS")
issue2 <- chronBias("linT", 0.25, "exact")
endp <- normEndp(mu = c(0,0), sigma = c(1,1))
A <- assess(sequences, issue1, issue2, endp = endp)
d1 <- derFunc(0.5, 0.75, 1)
d2 <- derFunc(0.05, 0.1, 1)
D1 <- getDesScores(A, d1, d2)
summary(D1)

D2 <- getDesScores(A, d1, d2, weights = c(3/4, 1/4))
summary(D2)
```

getExpectation

Get expectations of a randomization list

Description

Generates a matrix of the expectations of the included patients in the clinical trial.
getExpectation

Usage

getExpectation(randSeq, issue, endp)

## S4 method for signature 'randSeq,missing,expEndp'
getExpectation(randSeq, endp)

## S4 method for signature 'randSeq,missing,normEndp'
getExpectation(randSeq, endp)

## S4 method for signature 'randSeq,power,normEndp'
getExpectation(randSeq, issue, endp)

## S4 method for signature 'randSeq,chronBias,normEndp'
getExpectation(randSeq, issue, endp)

## S4 method for signature 'randSeq,chronBias,expEndp'
getExpectation(randSeq, issue, endp)

## S4 method for signature 'randSeq,chronBias,missing'
getExpectation(randSeq, issue)

## S4 method for signature 'randSeq,selBias,normEndp'
getExpectation(randSeq, issue, endp)

## S4 method for signature 'randSeq,selBias,expEndp'
getExpectation(randSeq, issue, endp)

## S4 method for signature 'randSeq,selBias,missing'
getExpectation(randSeq, issue)

## S4 method for signature 'randSeq,combinedBias,normEndp'
getExpectation(randSeq, issue, endp)

## S4 method for signature 'randSeq,combinedBias,expEndp'
getExpectation(randSeq, issue, endp)

## S4 method for signature 'randSeq,combinedBiasStepTrend,normEndp'
getExpectation(randSeq, issue, endp)

## S4 method for signature 'randSeq,combinedBiasStepTrend,expEndp'
getExpectation(randSeq, issue, endp)

Arguments

randSeq object of the class randSeq.
issue object of the class issue (optional).
endp object of the class endpoint (optional).
getProbabilities

Details

It is assumed that the expectations of the included patients in a clinical trial can be influenced in three different ways:

- The strength of selection bias and the guessing strategy of the investigator (see selBias).
- The strength of a linear time trend, which is described by an object of the class chronBias.
- The expectations of the investigated treatment groups can be different (see e.g. normEndp).

Examples

```r
# get Expectation for a normal endpoint
myPar <- bsdPar(10, 2)
M <- genSeq(myPar, 2)
cs <- selBias("CS", 2, "sim")
endp <- normEndp(mu = c(2, 2), sigma = c(1, 1))
getExpectation(M, cs, endp)

# get Expectation for an exponential endpoint
endp <- expEndp(lambda = c(0.5, 1), cenTime = 10, cenRate = 0.01)
getExpectation(M, cs, endp)
```

getProbabilities

Theoretical probability for randomization sequences

Description

Calculate theoretical probability for observed randomization sequences

Usage

```r
getProb(obj)
```

## S4 method for signature 'abcdSeq'
```r
getProb(obj)
```

## S4 method for signature 'bbcdSeq'
```r
getProb(obj)
```

## S4 method for signature 'bsdSeq'
```r
getProb(obj)
```

## S4 method for signature 'chenSeq'
```r
getProb(obj)
```

## S4 method for signature 'crSeq'
```r
getProb(obj)
```
getProbs

getProb(obj)

## S4 method for signature 'ebcSeq'
getProb(obj)

## S4 method for signature 'gbcdSeq'
getProb(obj)

## S4 method for signature 'hadaSeq'
getProb(obj)

## S4 method for signature 'mpSeq'
getProb(obj)

## S4 method for signature 'pbrSeq'
getProb(obj)

## S4 method for signature 'rarSeq'
getProb(obj)

## S4 method for signature 'tbdSeq'
getProb(obj)

## S4 method for signature 'udSeq'
getProb(obj)

Arguments

obj object of a class inheriting from randSeq. Formal representation of a randomization sequences together with the parameters that belong to the procedure that generated the sequences.

Examples

myPar <- bsdPar(10, 2)
M <- genSeq(myPar, 2)
getProb(M)

# all Sequences
par <- pbrPar(bc=c(2,2))
refSet <- getAllSeq(myPar)
probs <- getProb(refSet)

# sequences with probabilities
cbind(probs, refSet$M)
**getRandomizationList**

*Accessor function for the randomization list*

**Description**

Get the randomization list coded in its groups.

**Usage**

```
getRandList(obj)
```

**Arguments**

- `obj` object specifying the randomization procedure, see `randPar` or `createParam`.

**Examples**

```r
myPar <- bsdPar(10, 2)
M <- genSeq(myPar, 2)
getRandList(M)
```

---

**hadaPar**

*Representing Hadamard Randomization*

**Description**

Represents the randomization procedure Hadamard Randomization.

**Usage**

```
hadaPar(N, groups = LETTERS[1:2])
```

**Arguments**

- `N` integer for the total sample size of the trial.
- `groups` character vector of labels for the different treatments.

**Details**

Hadamard randomization has been proposed by R.A. Bailey. The key idea is to use the columns of a special Hadamard Matrix as a randomization scheme. The implemented algorithm uses the Hadamard Matrix with N=12 columns proposed in the paper, see references.

**Value**

S4 object of the class `hadaPar`.
**imbal**

**Note**

getProb and getAllSeq are currently only supported for hadaPar with total sample size N=12.

**References**


**See Also**

Other randomization procedures: abcdPar, bbcdPar, bsdPar, chenPar, crPar, createParam(), ebcPar, gbecPar, mpPar, pbrPar, rarPar, rpbrPar, rtbdPar, tbdPar, udPar

---

**imbal**

*Representing the allocation imbalance*

**Description**

Represents the imbalance of the treatment assignments of patients in a clinical trial.

**Usage**

`imbal(type)`

**Arguments**

- `type` character string, should be one of "imb", "absImb", "loss", or "maxImb", see Details.

**Details**

Balance of the treatment assignment of patients can be an issue in the design of a clinical trial. The `imbal` function is a constructor function for an S4 object of class `imbal` representing the issue of imbalance in a clinical trial. The parameter `type` can take the following values: The type "imb" the final imbalance, i.e. difference in group sizes at the end of a trial "absImb" the absolute value of the final imbalance "loss" the loss in power estimation, i.e. \( \text{imb}^2 / N \) "maxImb" the maximal attained imbalance during the trial

**Value**

S4 object of class `imbal`, a formal representation of the issue of imbalance in a clinical trial.

**References**

### Description

Summarizes the criteria for the assessment of randomization procedures.

### Details

Randomization in clinical trials is supposed to control certain properties in clinical trials. In the randomizeR package, these properties are called issues. It is crucial to decide which of the issues is relevant in the present clinical trial, because a randomization procedure that manages well one issue might behave very badly for another. The issues include

- **Selection bias** can occur if future treatment allocations are predictable due to restricted randomization and unmasking of past treatment assignments. The influence of selection bias on the test decision is represented by the `selBias` class. The measure for the predictability of a randomization procedure is implemented in the `corGuess` class representing the expected number of correct guesses.

- **Chronological bias** can occur if a time trend is present in the data. Time trends occur due to learning curves, relaxed inclusion/exclusion criteria or new co-medication. Chronological bias is represented by the `chronBias` class.

- **Additive combination of chronological and selection bias** may occur if a time trend and selection bias are present in the data. The combined bias is represented by the `combineBias` class.

- **Balance** is important in order to ensure proper power estimation properties of the treatments. However, a high degree of balance favors selection bias. Depending on the clinical context, a randomization procedure should be chosen that admits a suitable imbalance. Imbalance bias is represented by the `imbal` class. The power loss due to imbalance can be assessed directly via the `setPower` class.

### See Also

- Representation of randomization procedures: `randPar`
- Generation of randomization sequences: `genSeq`
- Assessment of randomization sequences: `assess`
- Comparison of randomization sequences: `compare`
- Other issues: `chronBias, combineBias(), corGuess, issue, selBias, setPower()`

---

**issue**

<table>
<thead>
<tr>
<th>Assessment criteria for clinical trials</th>
</tr>
</thead>
</table>

---

**See Also**

- Other issues: `chronBias, combineBias(), corGuess, issue, selBias, setPower()`
Function returning the total sample size slot of an S4 object

**Description**

Function returning the total sample size slot of an S4 object

**Usage**

\[ K(\text{obj}) \]

**Arguments**

- obj: object of class randPar

Method returning the rate parameter of an expEndp S4 object

**Description**

Method returning the rate parameter of an expEndp S4 object

**Usage**

\[ \text{lambda}(\text{obj}) \]

**Arguments**

- obj: object of class expEndp

Function returning the method of an S4 object

**Description**

Function returning the method of an S4 object

**Usage**

\[ \text{method}(\text{obj}) \]

**Arguments**

- obj: object inheriting from randPar
Description

Represents the Maximal Procedure.

Usage

mpPar(N, mti, ratio = c(1, 1), groups = LETTERS[1:2])

Arguments

- **N**: integer for the total sample size of the trial.
- **mti**: maximum tolerated imbalance in patient numbers during the trial.
- **ratio**: vector of length K. The total sample number N and all used block lengths (bc) have to be divisible by sum(ratio).
- **groups**: character vector of labels for the different treatments.

Details

Fix the total sample size N and the mti. Afterwards, the patients are assigned to each treatment arm according to the ratio. All randomization sequences are equiprobable.

Value

S4 object of the class mpPar.

References


See Also

Other randomization procedures: abcdPar, bbcdPar, bsdPar, chenPar, crPar, createParam(), ebcPar, gbcdPar, hadaPar, pbrPar, rarPar, rpbrPar, rtbdPar, tbdPar, udPar
Function returning the MTI slot of an S4 object

Usage

mti(obj)

Arguments

obj object of class bsdPar or mpPar

Access the expectation value slot of a normEndp S4 object

Usage

mu(obj)

Arguments

obj object of class normEndp

Function returning the sample size slot of an S4 object

Usage

N(obj)

Arguments

obj object inheriting from randPar
normEndp  

*Representation of normally distributed endpoints*

### Description

Represents normally distributed endpoints in clinical trials.

### Usage

```r
normEndp(mu, sigma)
```

### Arguments

- **mu**  
  vector of the expected responses of the treatment groups, should have length K (i.e. one entry for each treatment group).

- **sigma**  
  vector of the standard deviations in each treatment group, should have length K (i.e. one entry for each treatment group).

### Details

The `normEndp` function is a constructor function for an S4 object of the class `normEnd` representing a normally distributed endpoint in a clinical trial. In conjunction with the `assess` function, normal endpoints admit the calculation of the exact type-I-error probability and power.

### See Also

- Compute exact or simulated type-I-error: `assess`
- Other endpoint types: `expEndp`, `survEndp`

### Examples

```r
# set the parameters of two normally distributed endpoints
dotp <- normEndp(mu = c(1, 2), sigma = c(1, 1))
```
Arguments

- \(a\) nonnegative parameter which controls the degree of randomness: For decreasing \(a\) the allocations become deterministic, while for increasing \(a\) the randomization procedure tends to complete randomization.
- \(\text{accrualTime}\) duration of the accrual period in a survival study.
- \(\text{add}\) integer representing the number of balls that are added to the urn in each step.
- \(\alpha\) the significance level of the test in each simulation.
- \(b\) vector which contains the lengths \(k_1, \ldots, k_l\) of each block. This means that the vector \(bc\) will have one entry for each block.
- \(\beta\) numeric vector of length at most 2 specifying the weight(s) for the punishment of deviations from the target value.
- \(\text{cenRate}\) exponential censoring rate in a survival study.
- \(\text{cenTime}\) total duration of a survival study (maximum length of followup).
- \(d\) effect size.
- \(\text{df}\) degrees of freedom (i.a. \(N-2\)).
- \(\eta\) numeric specifying the magnitude of selection bias.
- \(\text{file}\) A connection, or a character string naming the file to write to.
- \(\text{filledBlock}\) logical whether the last block should be filled or not.
- \(\text{FTI}\) final tolerated imbalance. This is the difference in number of patients of groups \(A\) and \(B\) that is permitted at the end of a trial. Usually this is set to zero.
- \(\text{groups}\) character vector of labels for the different treatments.
- \(\text{ini}\) integer representing the initial urn composition.
- \(k\) length of the block to be permuted. \(k\) should be divisible by the number of treatment arms.
- \(\text{K}\) number of treatment groups (e.g. \(K=2\) if we compare one experimental against one control treatment).
- \(\text{lb}\) lower bound for the starting value of the poisson distribution.
- \(\lambda\) vector of the expected responses of the treatment groups, should have length \(K\) (i.e. one entry for each treatment group).
- \(N\) integer for the total sample size of the trial.
- \(\text{name}\) name of a variable.
- \(\text{obj}\) object specifying the randomization procedure, see \texttt{randPar} or \texttt{createParam}.
- \(\text{object}\) any R object.
- \(p\) success probability of the biased coin (e.g. in Efron’s Biased Coin Design).
- \(\text{pr}\) vector with patient responses, i.e. each patients resulting value after the treatment.
q
"cut-off" value in \([0.5,1]\). This is the ratio of patients up from which the experimenter imposes selection bias on the data.

r
numeric indicating the number of random sequences to be generated at random, or missing.

ratio
vector of length \(K\). The total sample number \(N\) and all used block lengths (bc) have to be divisible by \(\text{sum(ratio)}\).

rb
block lengths of the blocks that can be selected equiprobable at random.

rho
nonnegative parameter which my be adjusted according to how strongly it is desired to balance the experiment. If \(\rho = 1\), we have Wei's urn design with \(\alpha = 0\). If \(\rho = 0\), we have complete randomization.

rsob
randomization sequence (of one block).

rs
randomization sequence (of all blocks).

S
matrix for the computation of the probabilities in the maximal procedure.

saltus
integer or missing specifying the patient index (i.e. position) of the step in case of step time trend.

seed
a single value, interpreted as an integer, that specifies the seed for the random number generation.

sigma
vector of the standard deviations in each treatment group, should have length \(K\) (i.e. one entry for each treatment group).

SLs
numeric vector of length at most 2 specifying the lower and/or upper specified border.

theta
factor of the time trend for further details see type.

type
character vector indicating which biasing strategy the experimenter is using (selection bias) and which other bias is present in the clinical trial (e.g. time trend). All biases included in the vector are combined (i.e. added up) to form the total bias. Possible values are "none" (if no bias occurs), "CS" (resp. "DS") (if the experimenter uses the convergence (resp. divergence) strategy to invoke selection bias), LinT for linear time trend, LogT for log-linear time trend, StepT for step time trend, SigT for sigmoid time trend, PWR for knowledge of all up to the first observation in each block, MTI the next observation after reaching the maximal tolerated imbalance is reached will be known to the physician.

TV
numeric specifying the optimal desired value called the target value.

ub
upper bound for the last value of the poisson distribution.

varEq
logical parameter for the t.test: Shall the variances be treated as equal (TRUE= t.test) or different (FALSE= Welch.test).

x
a variable \(x\).
**Representing Permuted Block Randomization**

**Description**

Represents the randomization procedure Permuted Block Randomization.

**Usage**

```
pbrPar(bc, K = 2, ratio = rep(1, K), groups = LETTERS[1:K])
```

**Arguments**

- `bc` vector which contains the lengths $k_1, \ldots, k_l$ of each block. This means that the vector `bc` will have one entry for each block.
- `K` number of treatment groups (e.g. $K=2$ if we compare one experimental against one control treatment).
- `ratio` vector of length $K$. The total sample number $N$ and all used block lengths (`bc`) have to be divisible by `sum(ratio)`.
- `groups` character vector of labels for the different treatments.

**Details**

Fix the block constellation `bc`, the number of treatment groups `K`, and the vector of the `ratio`. Afterwards, in each block the patients are assigned according to the ratio to the corresponding treatment groups. All generated randomization sequences are equiprobable.

**Value**

S4 object of the class `pbrPar`.

**References**


**See Also**

Other randomization procedures: `abcdPar`, `bbcdPar`, `bsdPar`, `chenPar`, `crPar`, `createParam()`, `ebcPar`, `gbcdPar`, `hadaPar`, `mpPar`, `rarPar`, `rpbrPar`, `rtbdPar`, `tbdPar`, `udPar`
plot

Generic plotting of comparison objects

Description

Generic plotting of comparison objects

Usage

plot(x, y, ...)

## S4 method for signature 'comparison,character'
plot(x, y)

## S4 method for signature 'comparison,missing'
plot(x, y)

Arguments

x object of class comparison.
y character "boxplot", or "violin", or "missing".
... "missing"

Details

Creates a box- or violinplot of an object x of the class comparison.

Value

A plot created with the additional package ggplot2.

See Also

compare for creating S4 objects of the class comparison

Examples

# compare Random Allocation Rule and Big Stick for N = 4 with respect to
# correct guesses
RAR <- getAllSeq(rarPar(4))
BSD <- getAllSeq(bsdPar(4, mti = 2))
corGuess <- corGuess("CS")
comp <- compare(corGuess, RAR, BSD)
plot(comp)
Description

Plot of an desScore object.

Usage

plotDes(desScore, labels, colAv = "red", quantiles = FALSE)

Arguments

desScore object of type desScore.
labels labels used in the plot. Can be NULL.
colAv color of the line representing the average of the desirability scores in the plot.
quantiles logical whether the quantiles should be depicted in the plot.

See Also

Other desirability topics: derFunc, evaluate(), getDesScores(), plotEv(), probUnDes()

Examples

# compute the desirability scores of the full set of PBR(4)
sequences <- getAllSeq(rarPar(4))
issue1 <- corGuess("CS")
issue2 <- chronBias("linT", 1/4, "exact")
endp <- normEndp(mu = c(0,0), sigma = c(1,1))
A <- assess(sequences, issue1, issue2, endp = endp)
d1 <- derFunc(0.5, 0.75, 1)
d2 <- derFunc(0.05, 0.1, 1)

D <- getDesScores(A, d1, d2)
summary(D)
plotDes(D)
plotDes(D, quantiles = TRUE)
plotEv

Plotting Evaluation

Description

Plot of an evaluation object.

Usage

plotEv(evaluation, labels, cols)

Arguments

evaluation object of type evaluation.

labels labels used in the plot. Can be NULL.

cols colors of the lines representing the desirability scores in the plot. Can be NULL.

See Also

Other desirability topics: derFunc, evaluate(), getDesScores(), plotDes(), probUnDes()

Examples

# compare Random Allocation Rule to Big Stick Design with respect to different issues
# and their corresponding desirability functions
issue1 <- corGuess("CS")
issue2 <- chronBias(type = "linT", theta = 1/4, method = "exact")
RAR <- getAllSeq(rarPar(4))
BSD <- getAllSeq(bsdPar(4, mti = 2))
A1 <- assess(RAR, issue1, issue2, endp = normEndp(c(0,0), c(1,1)))
A2 <- assess(BSD, issue1, issue2, endp = normEndp(c(0,0), c(1,1)))
d1 <- derFunc(TV = 0.5, 0.75, 2)
d2 <- derFunc(0.05, c(0, 0.1), c(1, 1))
DesScore <- getDesScores(A1, d1, d2, weights = c(5/6, 1/6))
DesScore2 <- getDesScores(A2, d1, d2, weights = c(5/6, 1/6))

E <- evaluate(DesScore, DesScore2)
plotEv(E)
plotSeq

Sequence plotting

Description
Plot all randomization sequences of a randSeq object

Usage
plotSeq(sequences, plotAllSeq = FALSE, emph = NA, rs = NA)

Arguments
sequences object of type randSeq
plotAllSeq logical. If plotAllSeq=TRUE, the complete set of randomization sequences will be plotted in light gray.
emph integer indicating which sequence should be highlighted in blue.
rs vector of a randomization sequence that should be highlighted.

probUnDes Computing the probability of having desirability scores of zero

Description
Computing the probability of having desirability scores of zero for each desirability function applied to an issue.

Usage
probUnDes(desScore)

## S4 method for signature 'desScores'
probUnDes(desScore)

Arguments
desScore an object of the class desScores, i.e. an object resulting from applying the function getDesScores

Details
The function probUnDes expects an object that results from the getDesScores function. For each issue it computes the probability that it achieves an undesirable score, i.e. a desirability score of 0. In doing so, it weights the zero desirability scores with the probability that the sequence occurs.
Function returning the block slot of an S4 object

Description

Function returning the block slot of an S4 object

Usage

randBlocks(obj)

Arguments

obj object of class pbrPAr
Description

Randomization procedures in randomizeR are represented by objects that inherit from `randPar`. The representation can then be used in order to generate randomization sequences. In order generate a representation of a randomization procedure, call `createParam` or one of the following functions.

Supported randomization procedures

- Complete Randomization (`crPar`)
- Random Allocation Rule (`rarPar`)
- Permuted Block Randomization (`pbrPar`)
- Permuted Block Randomization with random block length (`rpbrPar`)
- Truncated Binomial Design (`tbdPar`)
- Truncated Binomial Design with random block length (`rtbdPar`)
- Efron’s Biased Coin Design (`ebcPar`)
- Big Stick Design (`bsdPar`)
- Maximal Procedure (`mpPar`)
- Wei’s Urn Design (`udPar`)
- Chen’s Design (`chenPar`)
- Generalized Biased Coin Design (`gbcdPar`)
- Accelerated Biased Coin Design (`abcdPar`)
- Bayesian Biased Coin Design (`bbcdPar`)
- Hadamard Randomization (`hadaPar`)

See Also

Generate randomization sequences `genSeq`. Calculate the the complete set of randomization sequences of a randomization procedure. `getAllSeq`. 
**randSeq-class**  
*An S4 Class for the representation of randomization sequences*

**Description**

This set of classes provides functionality of storing randomization sequences of different randomization procedures along with the parameters representing the design.

**Slots**

- **N** total number of patients included in the trial
- **M** matrix containing randomization sequences of length N in its rows.
- **K** number of treatment groups
- **groups** character string of length K defining the names of the treatment groups

---

**rarPar**  
*Representing Random Allocation Rule*

**Description**

Represents the randomization procedure Random Allocation Rule.

**Usage**

```
rarPar(N, K = 2, ratio = rep(1, K), groups = LETTERS[1:K])
```

**Arguments**

- **N** integer for the total sample size of the trial.
- **K** number of treatment groups (e.g. K=2 if we compare one experimental against one control treatment).
- **ratio** vector of length K. The total sample number N and all used block lengths (bc) have to be divisible by sum(ratio).
- **groups** character vector of labels for the different treatments.

**Details**

Fix a total sample size N the number of treatment groups K, and the vector of the ratio. Afterwards, all patients are assigned according to the ratio to the corresponding treatment groups. All randomization sequences are equiprobable.

**Value**

S4 object of the class.rarPar.
References


See Also

Other randomization procedures: `abcdPar`, `bbcdPar`, `bsdPar`, `chenPar`, `crPar`, `createParam()`, `ebcPar`, `gbcdPar`, `hadaPar`, `mpPar`, `pbrPar`, `rpbrPar`, `rtbdPar`, `tbdPar`, `udPar`

---

`ratio`  
*Function returning the allocation ratio slot of an S4 object*

### Description

Function returning the allocation ratio slot of an S4 object

### Usage

```r
ratio(obj)
```

### Arguments

- `obj`  
  object of class `randPar`

---

`rho`  
*Function returning the adjusting parameter rho slot of an S4 object*

### Description

Function returning the adjusting parameter rho slot of an S4 object

### Usage

```r
rho(obj)
```

### Arguments

- `obj`  
  object of class `randPar`
Representing Randomized Permuted Block Randomization

**Description**

Represents the randomization procedure Randomized Permuted Block Randomization.

**Usage**

```r
rpbrPar(
  N,
  rb,
  K = 2,
  ratio = rep(1, K),
  groups = LETTERS[1:K],
  filledBlock = FALSE
)
```

**Arguments**

- `N` integer for the total sample size of the trial.
- `rb` block lengths of the blocks that can be selected equiprobable at random.
- `K` number of treatment groups (e.g. K=2 if we compare one experimental against one control treatment).
- `ratio` vector of length K. The total sample number N and all used block lengths (bc) have to be divisible by sum(ratio).
- `groups` character vector of labels for the different treatments.
- `filledBlock` logical whether the last block should be filled or not.

**Details**

Fix the possible random block lengths rb, the number of treatment groups K, the sample size N and the vector of the ratio. Afterwards, one block length is randomly selected of the random block lengths. The patients are assigned according to the ratio to the corresponding treatment groups. This procedure is repeated until N patients are assigned. Within each block all possible randomization sequences are equiprobable.

**Value**

S4 object of the class `rpbrPar`.

**References**

## rtbdPar

**Representing Randomized Truncated Binomial Design**

### Description

Represents the randomization procedure Randomized Truncated Binomial Design.

### Usage

```r
rtbdPar(N, rb = N, groups = LETTERS[1:2], filledBlock = FALSE)
```

### Arguments

- `N` integer for the total sample size of the trial.
- `rb` block lengths of the blocks that can be selected equiprobable at random.
- `groups` character vector of labels for the different treatments.
- `filledBlock` logical whether the last block should be filled or not.

### Details

Fix the possible random block lengths `rb` and the sample size of the trial `N`. Afterwards, one block length is randomly selected of the random block lengths. In this block a fair coin is tossed for the patient assignments until half of the patients have been assigned to one of the treatment arms. Afterwards, the block is filled with the other treatment. This procedure is repeated until `N` patients are assigned.

### Value

S4 object of the class `rtbdPar`.

### References


### See Also

Other randomization procedures: `abcdPar`, `bbcdPar`, `bsdPar`, `chenPar`, `crPar`, `createParam()`, `ebcPar`, `gbcdPar`, `hadaPar`, `mpPar`, `pbrPar`, `rarPar`, `rtbdPar`, `tbdPar`, `udPar`
saveAssess  Saving an assess object

Description
Saves the full information of an assess object in a .csv data sheet.

Usage
saveAssess(obj, file = "assessObject.csv")

Arguments
- obj: object of class assessment, e.g. the output of the assess function.
- file: A connection, or a character string naming the file to write to.

Value
Creates a .csv data in the home folder.

See Also
Other saving functions: saveRand()

saveRand  Saving a randomization lists

Description
Saves the parameters of a randSeq object in a .csv data sheet.

Usage
saveRand(obj, file = "randList.csv")

Arguments
- obj: object of class randSeq containing a single randomization sequence.
- file: A connection, or a character string naming the file to write to.

Value
Creates a .csv data in the home folder and saves the randomization list as a column vector.

See Also
Other saving functions: saveAssess()
**seed**

*Function returning the allocation seed slot of an object*

**Description**

Returns the seed that was either generated at random or user specified. The seed can be specified for any random operation e.g. genSeq.

**Usage**

```r
seed(obj)
```

**Arguments**

- **obj** object specifying the randomization procedure, see `randPar` or `createParam`.

**selBias**

*Representing selection bias*

**Description**

Represents the issue of selection bias in a clinical trial.

**Usage**

```r
selBias(type, eta, method, alpha = 0.05)
```

**Arguments**

- **type** character string, should be one of "CS", "CS2" or "DS", see Details.
- **eta** numeric specifying the magnitude of selection bias.
- **method** character string, should be one of "sim" or "exact", see Details.
- **alpha** significance level.

**Details**

Selection bias can be an issue in the design of a clinical trial. The `selBias` function is a constructor function for an S4 object of the class `selBias` representing the issue of third order selection bias in a clinical trial. It supports two possible modes, `method="sim"` and `method="exact"`. This representation is particularly useful in interaction with the `assess` function.

`method="sim"` Represents the simulated type-I-error rate given the level alpha, the selection effect eta and the biasing strategy type. When calling `assess` for a `selBias` object with `method="sim"`, one test decision is computed for each sequence of `randSeq`. The type-I-error rate (power) is the proportion of falsely (correctly) rejected null hypotheses.
method="exact" Represents the exact type-I-error probability given the level alpha, the selection effect eta and the biasing strategy type. When calling assess for a selBias object with method="exact", the p-value of each randomization sequence is computed. For normal endpoints and two treatment groups these p-values are exact values which can be calculated from the sum of the corresponding quantiles of the doubly noncentral t-distribution. For more than two treatment groups, exact p-values are computed using a doubly noncentral F distribution. For exponential endpoints the p-values are obtained using an approximation formula.

It also supports three types of selection bias:

- **type="DS"** Refers to the divergence strategy according to Blackwell and Hodges (1957). Under this guessing strategy, the investigator guesses that the upcoming treatment is the one that has so far been allocated more frequently.

- **type="CS"** Refers to the convergence strategy according to Blackwell and Hodges (1957). Under this guessing strategy, the investigator guesses that the upcoming treatment is the one that has so far been allocated less frequently. In multi-arm trials, type="CS" refers to the first generalization of the convergence strategy according to Uschner et al (2018). The investigator guesses the treatment that had been allocated less frequently whenever all the treatments of the opposite group are larger than the smallest of the present group.

- **type="CS2"** In trials with two treatment arms, type="CS2" is equivalent to type="CS". In multi-arm trials, type="CS2" refers to the second generalization of convergence strategy according to Uschner et al (2018). The investigator guesses the treatment that had been allocated less frequently whenever all the treatments of the opposite group are larger than the smallest of the present group.

**Value**

S4 object of class selBias, a formal representation of the issue of selection bias in a clinical trial.

**References**


**See Also**

Compute exact or simulated rejection probability: `assess`.

Other issues: `chronBias`, `combineBias()`, `corGuess`, `imbal`, `issue`, `setPower()`

**Examples**

```r
# create a selection bias of the convergency strategy type with eta = 0.25 for which # the exact rejection probabilities are calculated
sbias <- selBias("CS", 0.25, "exact")
```
setPower

Representing the power

Description

Represents the expected power of the individual randomization sequences.

Usage

setPower(d, method, alpha = 0.05)

Arguments

d : effect size.
method : character string, should be one of "sim" or "exact", see Description.
alpha : significance level.

Details

The attained power of an individual randomization sequence can be an issue in the design of a clinical trial. The power of a randomization sequence is computed depending on the effect size d and the difference in group sizes.

If method="sim", the object represents the simulated power of an individual randomization sequence. When calling assess for a power object with method="sim", one test decision is computed for each randomization sequence of randSeq. The power is the proportion of falsely (correctly) rejected null hypotheses.

If method="exact", the object represents the exact power of an individual randomization sequence. When calling assess for a power object with method="exact", the exact p-value of each randomization sequence is computed. So far, this is only supported for normal endpoints. Then the power is the sum of the corresponding quantiles of the noncentral t-distribution.

Value

S4 object of class power, a formal representation of the issue of power in a clinical trial.

See Also

Other issues: chronBias, combineBias(), corGuess, imbal, issue, selBias
### sigma

*Function returning the standard deviation slot of a normEndp S4 object*

#### Description

Function returning the standard deviation slot of a normEndp S4 object

#### Usage

```r
sigma(obj)
```

#### Arguments

- `obj` object of class normEndp

### summary

*Summary of assessments of a randomization procedure*

#### Description

Summary of assessments of a randomization procedure

Summary of desirability scores of a randomization procedure

#### Usage

```r
summary(object, ...)
```

```r
## S4 method for signature 'assessment'
summary(object)
```

```r
## S4 method for signature 'desScores'
summary(object)
```

#### Arguments

- `object` assessment object.
- `...` additional arguments affecting the summary that will be produced.
Details

For each issue the assessment of the sequences is summarized to permit a design-based assessment of the randomization procedure. This approach uses the sequence-wise values of the assessment and the probabilities in order to give an overall summary.

For each issue the desirability score of the sequences is summarized to permit a design-based desirability score of the randomization procedure. This approach uses the sequence-wise values of the desirability and the probabilities in order to give an overall summary.

Value

Data frame with a summary of the assessment object.

Data frame with a summary of the desirability scores object.

Examples

```r
# assess the full set of PBR(4)
seq <- getAllSeq(pbrPar(4))
issue <- corGuess("CS")
A <- assess(seq, issue)
summary(A)

# compute the desirability scores of the full set of PBR(4)
seq <- getAllSeq(pbrPar(4))
issue1 <- corGuess("CS")
issue2 <- corGuess("DS")
A <- assess(seq, issue1, issue2)
d1 <- deriv(0.5, x=0.1, y=0.8)
d2 <- deriv(0.1, x=0.7, y=2)
D <- getDesScores(A, d1, d2, weights = c(5/6, 1/6))
summary(D)
```

---

**survEndp**  
*Representation of survival endpoints*

Description

Represents survival endpoints in clinical trials.

Usage

```
survEndp(cenRate, accrualTime, cenTime)
```

Arguments

- `cenRate`: exponential censoring rate in a survival study.
- `accrualTime`: duration of the accrual period in a survival study.
- `cenTime`: total duration of a survival study (maximum length of followup).
Details

The `survEnd` function is a constructor function for an S4 object of the class `survEnd` representing a survival endpoint in a clinical trial.

See Also

Other endpoint types: `expEndp`, `normEndp`

---

tbdPar  

Representing Truncated Binomial Design

Description

Represents the Truncated Binomial Design.

Usage

`tbdPar(bc = N, groups = LETTERS[1:2])`

Arguments

- `bc`  
  vector which contains the lengths $k_1, \ldots, k_l$ of each block. This means that the vector `bc` will have one entry for each block.

- `groups`  
  character vector of labels for the different treatments.

Details

A fair coin is tossed until half of the patients have been assigned to one of the treatment arms. Afterwards, the randomization list is filled with the other treatment.

Value

S4 object of the class `tbdPar`.

References


See Also

Other randomization procedures: `abcdPar`, `bbcdPar`, `bsdPar`, `chenPar`, `crPar`, `createParam()`, `ebcPar`, `gbcdPar`, `hadaPar`, `mpPar`, `pbrPar`, `rarPar`, `rpbrPar`, `rtbdPar`, `udPar`
TV

Function returning the target value slot of an S4 object

Description
Function returning the target value slot of an S4 object

Usage
TV(obj)

Arguments
obj object inheriting from derFunc

type

Get type of an object

Description
Accesses the type slot of an S4 object

Usage
type(obj)

Arguments
obj a bias object (i.e. S4 object inheriting from bias)

Value
Character string specifying the type of bias obj represents, e.g. "linT" in case of chronological bias.
Representing Wei’s Urn Design

Description

Represents Wei’s Urn Design.

Usage

udPar(N, ini, add, groups = LETTERS[1:2])

Arguments

N integer for the total sample size of the trial.
ini integer representing the initial urn composition.
add integer representing the number of balls that are added to the urn in each step.
groups character vector of labels for the different treatments.

Details

An urn is filled with a number of ini balls of both of the treatments. Afterwards, a ball is drawn randomly from the urn. Finally, add balls are added to the urn from the opposite treatment. This procedure is repeated until N patients are assigned.

Value

S4 object of the class udPar.

References


See Also

Other randomization procedures: abcdPar, bbcdPar, bsdPar, chenPar, crPar, createParam(), ebcPar, gbdPar, hadaPar, mpPar, pbrPar, rarPar, rpbrPar, rtbdPar, tbdPar
Index

a, 4
abcdPar, 5, 8–10, 17, 18, 21, 24, 41, 44, 49, 55, 57, 59, 66, 68
assess, 4, 6, 23, 36, 42, 46, 60–62
assess, randSeq, endpoint-method
  (assess), 6
assess, randSeq, missing-method (assess), 6
bbcdPar, 5, 7, 9, 10, 17, 18, 21, 24, 41, 44, 49, 55, 57, 59, 66, 68
blocks, 8
bsdPar, 5, 8, 9, 10, 17, 18, 21, 24, 41, 44, 49, 55, 57, 59, 66, 68
calcProb (getProbabilities), 38
calculateProbabilities
  (getProbabilities), 38
chenPar, 5, 8, 9, 10, 17, 18, 21, 24, 41, 44, 49, 55, 57, 59, 66, 68
chronBias, 11, 13, 16, 38, 42, 62, 63
coin, 12
combineBias, 12, 13, 16, 42, 62, 63
cor, 4, 14, 42, 50
cor, issue, endpoint-method
  (compare), 14
cor, issue, missing-method (compare), 14
corGuess, 12, 13, 15, 42, 62, 63
createParam, 5, 8–10, 16, 18, 21, 24, 26, 31, 40, 41, 44, 47, 49, 55, 57, 59, 61, 66, 68
createSeq, 17
crPar, 5, 8–10, 17, 17, 21, 24, 41, 44, 49, 55, 57, 59, 66, 68
derFunc, 18, 19, 22, 35, 36, 51, 52, 54
desirability, 19
ebcPar, 5, 8–10, 17, 18, 20, 24, 41, 44, 49, 55, 57, 59, 66, 68
evaluate, 19, 21, 36, 51, 52, 54
evaluate, character-method (evaluate), 21
evaluate, missing-method (evaluate), 21
expEndp, 23, 46, 66

gbcdPar, 5, 8–10, 17, 18, 21, 24, 41, 44, 49, 55, 57, 59, 66, 68
generateAllSequences, 25
generateRandomSequences, 27
genSeq, 4, 6, 14, 22, 36, 42, 54, 55
genSeq (generateRandomSequences), 27
genSeq, abcdPar, missing, missing-method
  (generateRandomSequences), 27
genSeq, abcdPar, missing, numeric-method
  (generateRandomSequences), 27
genSeq, abcdPar, numeric, missing-method
  (generateRandomSequences), 27
genSeq, abcdPar, numeric, numeric-method
  (generateRandomSequences), 27
genSeq, bbcdPar, missing, missing-method
  (generateRandomSequences), 27
genSeq, bbcdPar, missing, numeric-method
  (generateRandomSequences), 27
genSeq, bbcdPar, numeric, missing-method
  (generateRandomSequences), 27
genSeq, bbcdPar, numeric, numeric-method
  (generateRandomSequences), 27
genSeq, bsdPar, missing, missing-method
  (generateRandomSequences), 27
genSeq, bsdPar, missing, numeric-method
  (generateRandomSequences), 27
genSeq, bsdPar, numeric, missing-method
  (generateRandomSequences), 27
genSeq, bsdPar, numeric, numeric-method
  (generateRandomSequences), 27
genSeq, chenPar, missing, missing-method
  (generateRandomSequences), 27
genSeq, chenPar, missing, numeric-method
  (generateRandomSequences), 27
genSeq, chenPar, numeric, missing-method
    (generateRandomSequences), 27

genSeq, chenPar, numeric, numeric-method
    (generateRandomSequences), 27

genSeq, crPar, missing, missing-method
    (generateRandomSequences), 27

genSeq, crPar, missing, numeric-method
    (generateRandomSequences), 27

genSeq, crPar, numeric, missing-method
    (generateRandomSequences), 27

genSeq, crPar, numeric, numeric-method
    (generateRandomSequences), 27

genSeq, ebcPar, missing, missing-method
    (generateRandomSequences), 27

genSeq, ebcPar, missing, numeric-method
    (generateRandomSequences), 27

genSeq, ebcPar, numeric, missing-method
    (generateRandomSequences), 27

genSeq, ebcPar, numeric, numeric-method
    (generateRandomSequences), 27

genSeq, gbdPar, missing, missing-method
    (generateRandomSequences), 27

genSeq, gbdPar, missing, numeric-method
    (generateRandomSequences), 27

genSeq, gbdPar, numeric, missing-method
    (generateRandomSequences), 27

genSeq, gbdPar, numeric, numeric-method
    (generateRandomSequences), 27

genSeq, hadaPar, missing, missing-method
    (generateRandomSequences), 27

genSeq, hadaPar, missing, numeric-method
    (generateRandomSequences), 27

genSeq, hadaPar, numeric, missing-method
    (generateRandomSequences), 27

genSeq, hadaPar, numeric, numeric-method
    (generateRandomSequences), 27

genSeq, mpPar, missing, missing-method
    (generateRandomSequences), 27

genSeq, mpPar, missing, numeric-method
    (generateRandomSequences), 27

genSeq, mpPar, numeric, missing-method
    (generateRandomSequences), 27

genSeq, mpPar, numeric, numeric-method
    (generateRandomSequences), 27

genSeq, pbrPar, missing, missing-method
    (generateRandomSequences), 27

genSeq, pbrPar, missing, numeric-method
    (generateRandomSequences), 27

genSeq, pbrPar, numeric, missing-method
    (generateRandomSequences), 27

genSeq, pbrPar, numeric, numeric-method
    (generateRandomSequences), 27

genSeq, rarPar, missing, missing-method
    (generateRandomSequences), 27

genSeq, rarPar, missing, numeric-method
    (generateRandomSequences), 27

genSeq, rarPar, numeric, missing-method
    (generateRandomSequences), 27

genSeq, rarPar, numeric, numeric-method
    (generateRandomSequences), 27

genSeq, rtbdPar, missing, missing-method
    (generateRandomSequences), 27

genSeq, rtbdPar, missing, numeric-method
    (generateRandomSequences), 27

genSeq, rtbdPar, numeric, missing-method
    (generateRandomSequences), 27

genSeq, rtbdPar, numeric, numeric-method
    (generateRandomSequences), 27

genSeq, udPar, missing, missing-method
    (generateRandomSequences), 27

genSeq, udPar, missing, numeric-method
    (generateRandomSequences), 27

genSeq, udPar, numeric, missing-method
    (generateRandomSequences), 27

genSeq, udPar, numeric, numeric-method
    (generateRandomSequences), 27

g getAllSeq, 6, 55
g getAllSeq (generateAllSequences), 25
g getAllSeq (generateAllSequences), 25

g getAllSeq (generateAllSequences), 25

g getAllSeq (generateAllSequences), 25
getAllSeq, bbcdPar-method
   (generateAllSequences), 25
getAllSeq, bsdPar-method
   (generateAllSequences), 25
getAllSeq, chenPar-method
   (generateAllSequences), 25
getAllSeq, crPar-method
   (generateAllSequences), 25
getAllSeq, ebcPar-method
   (generateAllSequences), 25
getAllSeq, gbcdPar-method
   (generateAllSequences), 25
getAllSeq, hadaPar-method
   (generateAllSequences), 25
getAllSeq, mpPar-method
   (generateAllSequences), 25
getAllSeq, pbrPar-method
   (generateAllSequences), 25
getAllSeq, rarPar-method
   (generateAllSequences), 25
generateAllSequences
getDesFunc, derringerLs-method
   (getDesFunc), 32
generateAllSequences
getDesFunc, derringerRs-method
   (getDesFunc), 32
getCorGuesses, 32
generateAllSequences
getDesFunc, derringerTs-method
   (getDesFunc), 32
getDesign, 33
getDesign, abcdPar-method (getDesign), 33
getDesign, abcdSeq-method (getDesign), 33
getDesign, bbcdPar-method (getDesign), 33
getDesign, bbcdSeq-method (getDesign), 33
generateAllSequences
getDesign, bsdPar-method (getDesign), 33
getDesign, bsdSeq-method (getDesign), 33
getDesign, chenPar-method (getDesign), 33
getDesign, chenSeq-method (getDesign), 33
generateAllSequences
getDesign, crPar-method (getDesign), 33
getDesign, crSeq-method (getDesign), 33
generateAllSequences
getDesign, ebcPar-method (getDesign), 33
generateAllSequences
getDesign, ebcSeq-method (getDesign), 33
getDesign, gbcdPar-method (getDesign), 33
getDesign, gbcdSeq-method (getDesign), 33
generateAllSequences
getDesign, hadaPar-method (getDesign), 33
getDesign, mpPar-method (getDesign), 33
getDesign, mpSeq-method (getDesign), 33
getDesign, pbrPar-method (getDesign), 33
generateAllSequences
getDesign, pbrSeq-method (getDesign), 33
getDesign, rarPar-method (getDesign), 33
getDesign, rarSeq-method (getDesign), 33
generateAllSequences
getDesign, rbrPar-method (getDesign), 33
generateAllSequences
getDesign, rRbrPar-method (getDesign), 33
generateAllSequences
getDesign, rRtbdSeq-method (getDesign), 33
getDesign, rtbdPar-method (getDesign), 33
generateAllSequences
getDesign, tbdPar-method (getDesign), 33
getDesign, tbdSeq-method (getDesign), 33
generateAllSequences
getDesign, udPar-method (getDesign), 33
getDesign, udSeq-method (getDesign), 33
generateAllSequences
getDesign, assessment, numeric-method
   (getDesign), 35
getDesign, assessment, numeric-method
   (getDesign), 35
getDesign, assessment, numeric-method
   (getDesign), 35
getDesScores, 33, 35, 51–54
getDesScores, assessment, missing-method
   (getDesScores), 35
getDesScores, assessment, numeric-method
   (getDesScores), 35
getExpectation, 35
getExpectation, randSeq, chronBias, expEndp-method
   (getExpectation), 36
getExpectation, randSeq, chronBias, missing-method
   (getExpectation), 36
getExpectation, randSeq, chronBias, normEndp-method
   (getExpectation), 36
getExpectation, randSeq, combinedBias, expEndp-method
   (getExpectation), 36
getExpectation, randSeq, combinedBias, normEndp-method
   (getExpectation), 36
getExpectation, randSeq, combinedBiasStepTrend, expEndp-method
   (getExpectation), 36
getExpectation, randSeq, combinedBiasStepTrend, normEndp-method
   (getExpectation), 36
getExpectation, randSeq, missing, expEndp-method
   (getExpectation), 36
getExpectation, randSeq, missing, normEndp-method
   (getExpectation), 36
getExpectation, randSeq, power, normEndp-method
   (getExpectation), 36
getExpectation, randSeq, selBias, expEndp-method
   (getExpectation), 36
getExpectation, randSeq, selBias, missing-method
   (getExpectation), 36
getExpectation, randSeq, selBias, normEndp-method
   (getExpectation), 36
(getExpectation), 36
getProb (getProbabilities), 38
getProb,abcdSeq-method
  (getProbabilities), 38
getProb,bbcdSeq-method
  (getProbabilities), 38
getProb,bsdSeq-method
  (getProbabilities), 38
getProb,chenSeq-method
  (getProbabilities), 38
getProb,crSeq-method
  (getProbabilities), 38
getProb,ebcSeq-method
  (getProbabilities), 38
getProb,gbcdSeq-method
  (getProbabilities), 38
getProb,hadaSeq-method
  (getProbabilities), 38
getProb,gbcdSeq-method
  (getProbabilities), 38
getProb,mpSeq-method
  (getProbabilities), 38
getProb,pbrSeq-method
  (getProbabilities), 38
getProb,mpSeq-method
  (getProbabilities), 38
getRandList (getRandomizationList), 40
getRandomizationList, 50
hadapar, 5–38, 17, 18, 21, 26, 24, 41, 44, 49, 55, 56, 59, 66, 68
imbal, 5–38, 12, 13, 16, 41, 42, 62, 63
issue, 5–38, 32, 12, 16, 41, 42, 62, 63
issues, 5–38, 4, 6, 14, 22, 36, 54
issues (issue), 42
K, 5–38, 43
lambda, 5–38, 43
method, 5–38, 43
mpPar, 5–38, 17, 18, 21, 26, 24, 41, 44, 49, 55, 57, 59, 66, 68
mti, 5–38, 45
mu, 5–38, 45

N, 5–38, 45
normEndp, 5–38, 23, 38, 46, 46
overview, 5–38, 46
pbrPar, 5–38, 8–10, 17, 18, 21, 24, 41, 44, 49, 55, 57, 59, 66, 68
plot, 5–38, 50
plot, comparison, character-method
  (plot), 5–38, 50
plot, comparison, missing-method (plot), 5–38, 50
plotDes, 5–38, 19, 22, 36, 51, 52, 54
plotEv, 5–38, 19, 22, 36, 51, 52, 54
plotSeq, 5–38, 53
probUnDes, 5–38, 19, 22, 36, 51, 52, 53
probUnDes, desScores-method (probUnDes), 5–38, 53
ranBlocks, 5–38, 54
randomizeR (randomizeR-package), 3
randomizeR-package, 3
randPar, 5–38, 4, 6, 14, 16, 22, 26, 31, 36, 40, 42, 47, 54, 55, 61
randSeq, 5–38, 26, 31
randSeq-class, 5–38, 56
rarPar, 5–38, 5, 8–10, 17, 18, 21, 24, 41, 44, 49, 55, 56, 59, 66, 68
ratio, 5–38, 57
rho, 5–38, 57
rpbrPar, 5–38, 5, 8–10, 17, 18, 21, 24, 41, 44, 49, 55, 57, 58, 59, 66, 68
rtbdPar, 5–38, 5, 8–10, 17, 18, 21, 24, 41, 44, 49, 55, 57, 59, 59, 66, 68
saveAssess, 5–38, 60, 60
saveRand, 5–38, 60, 60
seed, 5–38, 61
selBias, 5–38, 12, 13, 16, 38, 42, 61, 63
setPower, 5–38, 12, 13, 16, 42, 62, 63
sigma, 5–38, 64
summary, 5–38, 64
summary, assessment-method (summary), 5–38, 64
summary, desScores-method (summary), 5–38, 64
survEndp, 5–38, 23, 46, 65
tbdPar, 5–38, 8–10, 17, 18, 21, 24, 41, 44, 49, 55, 57, 59, 66, 68
TV, 5–38, 67
INDEX

type, 67

udPar, 5, 8–10, 17, 18, 21, 24, 41, 44, 49, 55, 57, 59, 66, 68