

randomizeR 1.0 Quick Reference Guide

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1 Randomization Procedures (RP)

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| <code>rarPar(N)</code> | Random Allocation rule with N patients |
| <code>crPar(N)</code> | Complete Randomization with N patients |
| <code>rpbrPar(bc)</code> , <code>rpbr(bc)</code> | (randomized) Permuted Block Design |
| <code>ebcPar(N, p)</code> | Efron's Biased Coin Design with N patients and success probability p |
| <code>mpPar(N, mti)</code> | Maximal Procedure with N patients and maximum tolerated imbalance mti |
| <code>bsdPar(N, mti)</code> | Big Stick design with N patients and maximum tolerated imbalance mti |
| <code>udPar(N, ini, add)</code> | Wei's urn design with an initial urn composition of <code>ini</code> balls and in each step <code>add</code> balls are added |
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| <code>createParam(method, N, ...)</code> | Creates object that represents the chosen RP |
| <code>genSeq(obj, r, seed)</code> | Generates random sequences |
| <code>getAllSeq(obj)</code> | Output of all randomization sequences for the given RP |
| <code>getProb(obj)</code> | Calculates theoretical probability for observed randomization sequences |
| <code>getRandList(obj)</code> | Get the randomization list coded in its groups |
| <code>saveRand(obj)</code> | Saves the generated randomization sequence and its input parameters |

2 Assessment of a Randomization Procedure

Assess one randomization procedure according to several specified issues

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| <code>assess(...)</code> | Evaluates the behaviour of randomization sequences with respect to certain issues |
| <code>summary(assess(...))</code> | Summary of assessments (for each issue) of one RP |

3 Issues

Summarizes the criteria for the assessment of randomization

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| <code>selBias(type, eta, method, alpha)</code> | Issue of selection bias in a clinical trial with magnitude of selection bias <code>eta</code> |
| <code>chronBias(type, theta, method, alpha)</code> | Issue of chronological bias in a clinical trial with factor of time trend <code>theta</code> |
| <code>setPower(d, method, alpha)</code> | Expected power of the individual randomization sequences with effect size <code>d</code> |
| <code>normEndp(mu, sigma)</code> | Represents normally distributed endpoints in clinical trials (in conjunction with <code>assess</code> function and issues mentioned above) |

For the parameter `method` there are two possible models supported:

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| <code>method = "sim"</code> | the object represents the simulated type-I-error rate given the significance level <code>alpha</code> |
| <code>method = "exact"</code> | the object represents the exact type-I-error probability given the significance level <code>alpha</code> |
| <code>imbal(type)</code> | Imbalance of the treatment assignments of patients in clinical trial with parameter <code>type</code> that represents the different kinds of imbalance, e.g. final imbalance, maximal attained imbalance |
| <code>corGuess(type)</code> | Expected number of correct guesses of randomization sequences with strategy parameter <code>type</code> , i.e. <code>type = "CS"</code> or <code>type = "DS"</code> |

4 Comparison of Randomization procedures

Compare several randomization procedures according to one issue

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| <code>compare(issue, ...)</code> | Compares randomization procedures based on a specified issue |
| <code>plot(compare(...))</code> | Creates a box- or violinplot of an object of the class <code>comparison</code> |