

# randomizeR 1.0 Quick Reference Guide

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## 1 Randomization Procedures (RP)

<code>rarPar(N)</code>	Random Allocation rule with N patients
<code>crPar(N)</code>	Complete Randomization with N patients
<code>rpbrPar(bc), rpbr(bc)</code>	(randomized) Permuted Block Design
<code>ebcPar(N, p)</code>	Efron's Biased Coin Design with N patients and success probability <code>p</code>
<code>mpPar(N, mti)</code>	Maximal Procedure with N patients and maximum tolerated imbalance <code>mti</code>
<code>bsdPar(N, mti)</code>	Big Stick design with N patients and maximum tolerated imbalance <code>mti</code>
<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
<code>:</code>	
<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

<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

<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:

<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

<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>