

# Package ‘Omixer’

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**Type** Package

**Title** Randomize Samples for -omics Profiling

**Version** 1.2.4

**Description** Omixer - an R package for multivariate and reproducible randomization with lab-friendly sample layouts. Omixer ensures optimal sample distribution across batches with well-documented methods, and can output lab-friendly sample sheets for the wet lab if needed.

**License** MIT + file LICENSE

**Encoding** UTF-8

**LazyData** true

**Imports** dplyr, ggplot2,forcats,tibble,gridExtra,magrittr,readr,tidyselect,grid,stats,stringr,RColorBrewer

**Depends** R (>= 4.0)

**RoxygenNote** 7.1.1

**Suggests** knitr,rmarkdown,BiocStyle,magick,testthat

**VignetteBuilder** knitr

**biocViews** DataRepresentation,ExperimentalDesign,QualityControl,  
Software,Visualization

**BugReports** <l.j.sinke@lumc.nl>

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Omixer Multivariate Randomization

## Description

Omixer provides functions to perform optimal randomization of sample lists prior to omic profiling. This minimizes the correlation between biological factors and technical covariates, whilst ensuring there is insufficient evidence for any of these associations.

## Details

Following this multivariate randomization, Omixer can also be used to smoothly bridge the gap between dry and wet labs, by creating visually intuitive sample sheets.

With clear documentation and the possibility to reproduce any output sample list, Omixer sets the standard for transparency and reproducibility in this often vague methodological step.

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## omixerCorr      *Correlation Tests*

## Description

This function uses appropriate tests of correlation between two variables and stores the estimate and p-value in a list.

## Usage

omixerCorr(x, y)

## Arguments

- x Randomization variable (e.g. age)
  - y Technical covariate (e.g. plate number)

## Details

For two categorical variables, the Cramer's V estimate is stored alongside chi-square p-value. For all other combinations of variables, Pearson's correlation coefficient and p-value are stored.

Please note: variables will be converted to numeric class within this function.

## Value

List of correlation estimate and p-value

## Examples

```
library(tibble)
library(forcats)
library(stringr)

sampleList <- tibble(sampleId=str_pad(1:48, 4, pad="0"),
sex=as_factor(sample(c("m", "f"), 48, replace=TRUE)),
age=round(rnorm(48, mean=30, sd=8), 0),
smoke=as_factor(sample(c("yes", "ex", "never"), 48, replace=TRUE)),
date=sample(seq(as.Date('2008/01/01'), as.Date('2016/01/01'),
by="day"), 48))

omixerCorr(sampleList$age, sampleList$sex)
```

## Description

As the main function of the Omixer package, this function outputs a randomized sample list that minimizes correlations between biological factors and technical covariates.

## Usage

```
omixerRand(
  df,
  sampleId = "sampleId",
  block = "block",
  iterNum = 1000,
  wells,
  div = "none",
  positional = FALSE,
  plateNum = 1,
  layout,
  mask = 0,
  techVars,
  randVars
)
```

## Arguments

|                         |   |
|-------------------------|---|
| <code>df</code>         | Sample list                                   |
| <code>sampleId</code>   | String specifying sample ID variable          |
| <code>block</code>      | Paired sample identifier                      |
| <code>iterNum</code>    | Number of layouts to generate                 |
| <code>wells</code>      | Number of wells on a plate                    |
| <code>div</code>        | Plate subdivisions                            |
| <code>positional</code> | Logical indicator of positional batch effects |
| <code>plateNum</code>   | Number of plates                              |
| <code>layout</code>     | Custom plate layout as data frame             |
| <code>mask</code>       | Wells to be left empty                        |
| <code>techVars</code>   | Technical covariates                          |
| <code>randVars</code>   | Randomization variables                       |

## Value

Selected randomized sample list as a data frame  
 Randomization environment of optimal list generation

## Examples

```
library(tibble)
library(forcats)
library(stringr)

sampleList <- tibble(sampleId=str_pad(1:48, 4, pad="0"),
sex=as_factor(sample(c("m", "f"), 48, replace=TRUE)),
age=round(rnorm(48, mean=30, sd=8), 0),
smoke=as_factor(sample(c("yes", "ex", "never"), 48, replace=TRUE)),
date=sample(seq(as.Date('2008/01/01'), as.Date('2016/01/01'),
by="day"), 48))

randVars <- c("sex", "age", "smoke", "date")

omixerLayout <- omixerRand(sampleList, sampleId="sampleId",
block="block", iterNum=10, wells=48, div="row",
plateNum=1, randVars=randVars)
```

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**omixerSheet**      *Sample Sheet Generation*

---

**Description**

This function will generate visually intuitive plate layouts for the wet lab, with the option to colour code different types of samples (e.g. for studies investigating multiple tissues).

**Usage**

```
omixerSheet(  
  omixerLayout = omixerLayout,  
  group,  
  group.text.size = 3.5,  
  sample.text.size = 4  
)
```

**Arguments**

|                  |  |
|------------------|--|
| omixerLayout     | Randomized sample list                   |
| group            | Colour-coding indicator                  |
| group.text.size  | Change size of group text (default: 3.5) |
| sample.text.size | Change size of sample text (default: 4)  |

**Value**

PDF of sample layout in working directory

**Examples**

```
library(tibble)  
library(forcats)  
library(stringr)  
  
sampleList <- tibble(sampleId=str_pad(1:48, 4, pad="0"),  
  sex=as_factor(sample(c("m", "f"), 48, replace=TRUE)),  
  age=round(rnorm(48, mean=30, sd=8), 0),  
  smoke=as_factor(sample(c("yes", "ex", "never"), 48, replace=TRUE)),  
  date=sample(seq(as.Date('2008/01/01'), as.Date('2016/01/01'),  
    by="day"), 48))  
  
randVars <- c("sex", "age", "smoke", "date")  
  
omixerLayout <- omixerRand(sampleList, sampleId="sampleId",  
  block="block", iterNum=10, wells=48, div="row",  
  plateNum=1, randVars=randVars)
```

```
omixerSheet(omixerLayout)
```

|                       |                                 |
|-----------------------|---------------------------------|
| <i>omixerSpecific</i> | <i>Sample List Regeneration</i> |
|-----------------------|---------------------------------|

## Description

Regenerate an Omixer-produced randomized sample list quickly, after setting up the random environment from *omixerRand*

## Usage

```
omixerSpecific(
  df,
  sampleId = "sampleId",
  block = "block",
  wells,
  div = "none",
  positional = FALSE,
  plateNum = 1,
  layout,
  mask = 0,
  techVars,
  randVars
)
```

## Arguments

|                   |   |
|-------------------|---|
| <i>df</i>         | Sample list                                   |
| <i>sampleId</i>   | String specifying sample ID variable          |
| <i>block</i>      | Paired sample identifier                      |
| <i>wells</i>      | Number of wells on a plate                    |
| <i>div</i>        | Plate subdivisions                            |
| <i>positional</i> | Logical indicator of positional batch effects |
| <i>plateNum</i>   | Number of plates                              |
| <i>layout</i>     | Custom plate layout as data frame             |
| <i>mask</i>       | Wells to be left empty                        |
| <i>techVars</i>   | Technical covariates                          |
| <i>randVars</i>   | Randomization variables                       |

## Value

Chosen layout as a data frame

**Examples**

```
library(tibble)
library(forcats)
library(stringr)

sampleList <- tibble(sampleId=str_pad(1:48, 4, pad="0"),
sex=as_factor(sample(c("m", "f"), 48, replace=TRUE)),
age=round(rnorm(48, mean=30, sd=8), 0),
smoke=as_factor(sample(c("yes", "ex", "never"), 48, replace=TRUE)),
date=sample(seq(as.Date('2008/01/01'), as.Date('2016/01/01'),
by="day"), 48))

randVars <- c("sex", "age", "smoke", "date")

omixerLayout <- omixerSpecific(sampleList, sampleId="sampleId",
block="block", wells=48, div="row",
plateNum=1, randVars=randVars)
```

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