

Package ‘ExpDesignR’

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Type Package

Title Experimental Design and Randomization Methods for Biomedical and Veterinary Research

Version 0.1.0

Description Generates randomized experimental designs for biomedical, veterinary, agricultural, and clinical research, including simple, block, stratified, and cluster randomization, Latin square and crossover designs, allocation summaries, schedule export, and visualization of treatment allocations. The methods are based on established principles of randomization and experimental design; see Rosenberger and Lachin (2015, ISBN:9781118742242) and Jones and Kenward (2014, ISBN:9781439861424).

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Depends R (>= 4.2.0)

Imports stats, utils, tibble, dplyr, ggplot2, rlang

Suggests testthat (>= 3.0.0), covr, spelling, knitr, rmarkdown

URL <https://github.com/vinodhpm/ExpDesignR>

BugReports <https://github.com/vinodhpm/ExpDesignR/issues>

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Author Vinodhkumar Obli Rajendran [aut, cre],
Keerthi Aaradhana [aut]

Maintainer Vinodhkumar Obli Rajendran <vinodhkumar.rajendran@gmail.com>

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allocation_summary	<i>Allocation Summary</i>
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Description

Summarizes treatment allocations from a randomization schedule.

Usage

```
allocation_summary(schedule, group_col = "Group")
```

Arguments

- schedule A data frame or tibble produced by an ExpDesignR randomization function.
- group_col Name of the treatment group column.

Value

A tibble summarizing the number and percentage of subjects in each treatment group.

Examples

```
sch <- simple_randomization(  
  n = 20,  
  groups = c("Control", "Treatment"),  
  seed = 123  
)  
  
allocation_summary(sch)
```

block_randomization	<i>Block Randomization</i>
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Description

Generates a randomized allocation schedule using fixed block randomization.

Usage

```
block_randomization(n, groups, block_size = 4, seed = NULL)
```

Arguments

n	Total number of subjects.
groups	Character vector of treatment groups.
block_size	Size of each block. Must be a multiple of the number of treatment groups.
seed	Optional random seed.

Value

A tibble with subject allocation.

Examples

```
block_randomization(  
  n = 24,  
  groups = c("Control", "Treatment"),  
  block_size = 4,  
  seed = 123  
)
```

cluster_randomization	<i>Cluster Randomization</i>
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Description

Randomly assigns clusters (e.g., villages, farms, schools, hospitals) to treatment groups.

Usage

```
cluster_randomization(clusters, groups, seed = NULL)
```

Arguments

clusters	Character or numeric vector of cluster IDs.
groups	Character vector of treatment groups.
seed	Optional random seed.

Value

A tibble containing cluster assignments.

Examples

```
cluster_randomization(
  clusters = paste0("Farm_", 1:20),
  groups = c("Control", "Treatment"),
  seed = 123
)
```

crossover_design

Crossover Design

Description

Generates a crossover design for clinical, veterinary, pharmaceutical and agricultural experiments.

Usage

```
crossover_design(
  treatments,
  subjects,
  periods = length(treatments),
  seed = NULL
)
```

Arguments

treatments	Character vector of treatment labels.
subjects	Number of subjects.
periods	Number of study periods.
seed	Optional random seed.

Value

A tibble containing the crossover schedule.

Examples

```
crossover_design(  
  treatments = c("A", "B"),  
  subjects = 8,  
  periods = 2,  
  seed = 123  
)
```

export_schedule	<i>Export Randomization Schedule</i>
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Description

Export a randomization schedule to a CSV file.

Usage

```
export_schedule(schedule, file, row.names = FALSE)
```

Arguments

schedule	A data frame or tibble generated by ExpDesignR.
file	Character. Output CSV filename or path. This argument must be supplied explicitly.
row.names	Logical. Should row names be written?

Value

Invisibly returns the input schedule unchanged. The function writes the schedule to the CSV file specified by file.

Examples

```
sch <- simple_randomization(  
  n = 20,  
  groups = c("Control", "Treatment"),  
  seed = 123  
)  
  
tf <- tempfile(fileext = ".csv")  
  
export_schedule(  
  sch,  
  file = tf  
)  
  
unlink(tf)
```

latin_square	<i>Latin Square Design</i>
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Description

Generates a Latin Square design for experimental studies.

Usage

```
latin_square(treatments, randomize = TRUE, seed = NULL)
```

Arguments

treatments	Character vector of treatment labels.
randomize	Logical. Should rows, columns and treatments be randomized? Default is TRUE.
seed	Optional random seed.

Value

A matrix representing a Latin square.

Examples

```
latin_square(  
  treatments = LETTERS[1:4],  
  seed = 123  
)
```

plot_randomization	<i>Plot Randomization Schedule</i>
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Description

Creates a bar chart showing the number of subjects allocated to each treatment group.

Usage

```
plot_randomization(  
  schedule,  
  group_col = "Group",  
  fill = "#2C7FB8",  
  title = "Treatment Allocation"  
)
```

Arguments

schedule	A data frame produced by ExpDesignR.
group_col	Character. Name of the treatment column.
fill	Character. Fill colour.
title	Character. Plot title.

Value

A ggplot object.

Examples

```
sch <- simple_randomization(  
  n = 40,  
  groups = c("Control", "Treatment"),  
  seed = 123  
)  
  
plot_randomization(sch)
```

simple_randomization *Simple Randomization*

Description

Generate a simple random allocation schedule.

Usage

```
simple_randomization(n, groups, seed = NULL)
```

Arguments

n	Number of subjects.
groups	Character vector of treatment groups.
seed	Optional random seed.

Value

A tibble containing subject IDs and assigned groups.

Examples

```
simple_randomization(  
  n = 20,  
  groups = c("Control", "Treatment"),  
  seed = 123  
)
```

`stratified_randomization`*Stratified Randomization*

Description

Generates a randomized allocation schedule within each stratum.

Usage

```
stratified_randomization(data, strata, groups, seed = NULL)
```

Arguments

<code>data</code>	A data frame containing the study subjects.
<code>strata</code>	Character vector specifying one or more stratification variables.
<code>groups</code>	Character vector of treatment groups.
<code>seed</code>	Optional random seed.

Value

A tibble containing the original data with an additional treatment allocation column.

Examples

```
df <- data.frame(  
  ID = 1:20,  
  Sex = rep(c("Male", "Female"), each = 10),  
  Age = rep(c("Young", "Adult"), times = 10)  
)  
  
stratified_randomization(  
  data = df,  
  strata = c("Sex"),  
  groups = c("Control", "Treatment"),  
  seed = 123  
)
```


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