

Package ‘PairedRand’

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Title Paired Randomization Functions

Version 0.1.0

Description

Provides tools for generating simulated study data, creating matched participant pairs using optimal nonbipartite matching, randomizing participants within pairs into study groups, and assessing post-randomization balance using descriptive summary statistics and standardized mean differences. The matching methodology is based on Lu et al. (2011) <[doi:10.1198/tast.2011.08294](https://doi.org/10.1198/tast.2011.08294)>.

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Encoding UTF-8

Imports dplyr, gtsummary, magrittr, nbpMatching, tidyr, tidyselect

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```
create_matched_randomization
```

Create Matched Randomization

Description

The following function creates matched pair. With the matched pair, randomization is performed. SMD helps assess balance, but caution is required when interpreting results in small samples

Usage

```
create_matched_randomization(
  dat_in,
  group_label = c("SelfHelp", "Group"),
  seed = 177
)
```

Arguments

<code>dat_in</code>	Input dataset
<code>group_label</code>	The label for the two randomization group
<code>seed</code>	Seed for reproducibility

Value

A list containing:

dat_in_matched A data frame containing participants organized into matched pairs based on similarity across baseline variables. The variable `Pair` identifies each matched pair.

dat_in_matched_rand A data frame containing matched participants and their randomized study group assignments. This dataset is used for study implementation and assessment of balance between study groups.

dist_matrix An object of class `distancematrix` from the `nbpMatching` package. The distance matrix quantifies similarity between participants and is used by the optimal nonbipartite matching algorithm to identify matched pairs. Smaller distances indicate greater similarity between participants.

Examples

```
dat_in <- data.frame(
  id = 1:4,
  age = c(25, 30, 35, 40),
  trait = c("A", "B", "A", "B")
)

results <- create_matched_randomization(dat_in, group_label = c("Treated", "Control"))
print(results$dat_in_matched_rand)
```

dat_sim	<i>Data Simulation</i>
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Description

The following code generates a simulated dataset that will be used in running functions in the package

Usage

```
dat_sim(n_rows = 100, num_vars = 5, cat_vars = 3, cat_lev = 3, seed = 100)
```

Arguments

n_rows	Number of rows in the simulated dataset
num_vars	Number of numeric variables
cat_vars	Number of categorical variables
cat_lev	Number of levels for each categorical variable
seed	Seed for reproducibility

Value

A data frame containing simulated study data. The first column is a unique participant identifier (ID), followed by numeric variables (N_1, N_2, ...) and categorical variables (C_1, C_2, ...).

Examples

```
n_rows <- 100
num_vars <- 5
cat_vars <- 3
cat_lev <- 3
seed <- 100
dat_out <- dat_sim(n_rows, num_vars, cat_vars, cat_lev, seed)
```

summ_stats	<i>Summary Statistics</i>
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Description

The following code generates summary statistics to describe balance across two arms Note: To save the output from summ_stats as an Excel file, refer to the as_hux_xlsx() function from the gtsummary package

Usage

```
summ_stats(dat_in, lab_list, arm = "randomization_group")
```

Arguments

<code>dat_in</code>	Dataset generated after randomization within pairs
<code>lab_list</code>	Variable labels for the dataset (can be set to NULL if not needed)
<code>arm</code>	Variable indicating the randomization group

Value

A gtsummary object of class `tbl_strata` containing descriptive statistics by study group, overall summary statistics, standardized mean differences (SMDs), and confidence intervals for assessing balance between randomized groups.

Examples

```
dat_in <- data.frame(
  id = 1:4,
  age = c(25, 30, 35, 40),
  trait = c("A", "B", "A", "B")
)

results <- create_matched_randomization(dat_in, group_label = c("Treated", "Control"))
results_matched_rand <- results$dat_in_matched_rand
dat_in <- results_matched_rand %>% dplyr::select(-c(Pair,ID))
results_matched_summary <- summ_stats(dat_in, lab_list = NULL, arm = "Group")
```

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