

# Package ‘permute’

September 26, 2024

**Title** Run Permutation Tests and Construct Associated Confidence Intervals

**Version** 1.0.0

**Description** Implements permutation tests for any test statistic and randomization scheme and constructs associated confidence intervals as described in Glazer and Stark (2024) <[doi:10.48550/arXiv.2405.05238](https://doi.org/10.48550/arXiv.2405.05238)>.

**License** GPL (>= 3)

**Encoding** UTF-8

**RoxygenNote** 7.3.2

**Suggests** testthat (>= 3.0.0)

**Config/testthat.edition** 3

**NeedsCompilation** no

**Author** Amanda Glazer [aut, cre] (<<https://orcid.org/0000-0002-3229-7924>>)

**Maintainer** Amanda Glazer <amanda.glazer@austin.utexas.edu>

**Repository** CRAN

**Date/Publication** 2024-09-26 11:20:02 UTC

## Contents

|                               |    |
|-------------------------------|----|
| adjust_p_value . . . . .      | 2  |
| diff_in_means . . . . .       | 2  |
| diff_inmedians . . . . .      | 3  |
| fisher . . . . .              | 4  |
| liptak . . . . .              | 4  |
| npc . . . . .                 | 5  |
| one_sample . . . . .          | 6  |
| one_sample_mean . . . . .     | 7  |
| one_way_anova_stat . . . . .  | 8  |
| permutation_test . . . . .    | 8  |
| permutation_test_ci . . . . . | 10 |
| permute_group . . . . .       | 11 |
| permute_sign . . . . .        | 12 |

|                               |    |
|-------------------------------|----|
| strat_permute_group . . . . . | 12 |
| tippett . . . . .             | 13 |
| ttest_stat . . . . .          | 14 |
| two_sample . . . . .          | 14 |

|              |           |
|--------------|-----------|
| <b>Index</b> | <b>16</b> |
|--------------|-----------|

---

|                       |   |
|-----------------------|---|
| <b>adjust_p_value</b> | <i>Adjust p-values for multiple testing</i> |
|-----------------------|---|

---

## Description

This function takes an array of p-values and returns adjusted p-values using user-inputted FWER or FDR correction method

## Usage

```
adjust_p_value(pvalues, method = "holm-bonferroni")
```

## Arguments

|         |  |
|---------|--|
| pvalues | Array of p-values  |
| method  | The FWER or FDR correction to use, either 'holm-bonferroni', 'bonferroni', or 'benjamini-hochberg' |

## Value

Adjusted p-values

## Examples

```
adjust_p_value(pvalues = c(.05, .1, .5), method='holm-bonferroni')
```

---

|                      |                                      |
|----------------------|--------------------------------------|
| <b>diff_in_means</b> | <i>Calculate difference in means</i> |
|----------------------|--------------------------------------|

---

## Description

This function takes a data frame, and group and outcome column names as input and returns the difference in mean outcome between the two groups

## Usage

```
diff_in_means(df, group_col, outcome_col, treatment_value = NULL)
```

**Arguments**

|                 |   |
|-----------------|---|
| df              | A data frame  |
| group_col       | The name of the column in df that corresponds to the group label      |
| outcome_col     | The name of the column in df that corresponds to the outcome variable |
| treatment_value | The value of group_col to be considered 'treatment'                   |

**Value**

The difference in mean outcome between the two groups

**Examples**

```
data <- data.frame(group = c(rep(1, 4), rep(2, 4)),
                     outcome = c(rep(3, 4), rep(5, 4)))

diff_in_means(df = data,
               group_col = "group",
               outcome_col = "outcome",
               treatment_value = 1)
```

|                 |  |
|-----------------|--|
| diff_in_medians | <i>Calculate difference in medians</i> |
|-----------------|--|

**Description**

This function takes a data frame, and group and outcome column names as input and returns the difference in median outcome between the two groups

**Usage**

```
diff_in_medians(df, group_col, outcome_col, treatment_value = NULL)
```

**Arguments**

|                 |   |
|-----------------|---|
| df              | A data frame  |
| group_col       | The name of the column in df that corresponds to the group label      |
| outcome_col     | The name of the column in df that corresponds to the outcome variable |
| treatment_value | The value of group_col to be considered 'treatment'                   |

**Value**

The difference in median outcome between the two groups

## Examples

```
data <- data.frame(group = c(rep(1, 4), rep(2, 4)),
                    outcome = c(rep(3, 4), rep(5, 4)))

diff_in_medians(df = data,
                 group_col = "group",
                 outcome_col = "outcome",
                 treatment_value = 1)
```

**fisher**

*Fisher combining function*

## Description

This function takes an array of p-values and returns a combined p-value using fisher's combining function:  $-2 \sum_i \log(p_i)$

## Usage

```
fisher(pvalues)
```

## Arguments

|         |                   |
|---------|-------------------|
| pvalues | Array of p-values |
|---------|-------------------|

## Value

Combined p-value using fisher's method

## Examples

```
fisher(pvalues = c(.05, .1, .5))
```

**liptak**

*Liptak combining function*

## Description

This function takes an array of p-values and returns a combined p-value using Liptak's combining function:  $\sum_i \Phi^{-1}(1 - p_i)$  where  $\Phi$  is the CDF of the Normal distribution

## Usage

```
liptak(pvalues)
```

**Arguments**

|         |                   |
|---------|-------------------|
| pvalues | Array of p-values |
|---------|-------------------|

**Value**

Combined p-value using Liptak's method

**Examples**

```
liptak(pvalues = c(.05, .1, .5))
```

|     |                |
|-----|----------------|
| npc | <i>Run NPC</i> |
|-----|----------------|

**Description**

This function takes a data frame and group and outcome column names as input and returns the nonparametric combination of tests (NPC) omnibus p-value

**Usage**

```
npc(
  df,
  group_col,
  outcome_cols,
  strata_col = NULL,
  test_stat = "diff_in_means",
  perm_func = permute_group,
  combn = "fisher",
  shift = 0,
  reps = 10000,
  perm_set = NULL,
  complete_enum = FALSE,
  seed = NULL
)
```

**Arguments**

|              |  |
|--------------|--|
| df           | A data frame   |
| group_col    | The name of the column in df that corresponds to the group label                             |
| outcome_cols | The names of the columns in df that corresponds to the outcome variable                      |
| strata_col   | The name of the column in df that corresponds to the strata                                  |
| test_stat    | Test statistic function  |
| perm_func    | Function to permute group, default is permute_group which randomly permutes group assignment |

|                            |   |
|----------------------------|---|
| <code>combn</code>         | Combining function method to use, takes values 'fisher', 'tippett', or 'liptak', or a user defined function |
| <code>shift</code>         | Value of shift to apply in one- or two-sample problem   |
| <code>reps</code>          | Number of iterations to use when calculating permutation p-value  |
| <code>perm_set</code>      | Matrix of permutations to use instead of reps iterations of perm_func                                       |
| <code>complete_enum</code> | Boolean, whether to calculate P-value under complete enumeration of permutations                            |
| <code>seed</code>          | An integer seed value   |

**Value**

The omnibus p-value

**Examples**

```
data <- data.frame(group = c(rep(1, 4), rep(2, 4)),
out1 = c(0, 1, 0, 0, 1, 1, 1, 0),
out2 = rep(1, 8))
output <- npc(df = data, group_col = "group",
              outcome_cols = c("out1", "out2"), perm_func = permute_group,
              combn = "fisher", reps = 10^4, seed=42)
```

---

`one_sample`

*One-sample permutation test*

---

**Description**

This function runs a permutation test for the one-sample problem by calling the `permutation_test` function using the one-sample mean test statistic.

**Usage**

```
one_sample(x, shift = 0, alternative = "greater", reps = 10^4, seed = NULL)
```

**Arguments**

|                          |  |
|--------------------------|--|
| <code>x</code>           | array of data  |
| <code>shift</code>       | Value of shift to apply in one-sample problem                    |
| <code>alternative</code> | String, two-sided or one-sided (greater or less) p-value         |
| <code>reps</code>        | Number of iterations to use when calculating permutation p-value |
| <code>seed</code>        | An integer seed value  |

**Value**

The permutation test p-value

## Examples

```
one_sample(x = c(-1, 1, 2), seed = 42)
```

---

one\_sample\_mean

*Calculate the one-sample problem test statistic*

---

## Description

This function takes a data frame, and group and outcome column names as input and returns the mean of the product of the outcome and group. This test statistic is used for the one-sample problem.

## Usage

```
one_sample_mean(df, group_col, outcome_col)
```

## Arguments

|             |   |
|-------------|---|
| df          | A data frame  |
| group_col   | The name of the column in df that corresponds to the group label      |
| outcome_col | The name of the column in df that corresponds to the outcome variable |

## Value

The one-sample problem test statistic: the mean of the product of the outcome and group

## Examples

```
data <- data.frame(group = c(rep(1, 4), rep(2, 4)),
                     outcome = c(rep(3, 4), rep(5, 4)))

one_sample_mean(df = data,
                 group_col = "group",
                 outcome_col = "outcome")
```

`one_way_anova_stat`      *Calculate one-way anova test statistic*

### Description

This function takes a data frame, and group and outcome column names as input and returns the one-way anova test statistic

### Usage

```
one_way_anova_stat(df, group_col, outcome_col)
```

### Arguments

|                          |   |
|--------------------------|---|
| <code>df</code>          | A data frame  |
| <code>group_col</code>   | The name of the column in df that corresponds to the group label      |
| <code>outcome_col</code> | The name of the column in df that corresponds to the outcome variable |

### Value

The one-way anova test statistic:  $\sum_{g=1}^G n_g(\bar{X}_g - \bar{X})^2$  where  $g$  indexes the groups

`permutation_test`      *Run permutation test*

### Description

Run permutation test with user inputted data, test statistic, and permutation function

### Usage

```
permutation_test(
  df,
  group_col,
  outcome_col,
  strata_col = NULL,
  test_stat = "diff_in_means",
  perm_func = permute_group,
  alternative = "two-sided",
  shift = 0,
  reps = 10000,
  perm_set = NULL,
  complete_enum = FALSE,
  return_test_dist = FALSE,
  return_perm_dist = FALSE,
  seed = NULL
)
```

## Arguments

|                  |   |
|------------------|---|
| df               | A data frame  |
| group_col        | The name of the column in df that corresponds to the group label  |
| outcome_col      | The name of the column in df that corresponds to the outcome variable                                   |
| strata_col       | The name of the column in df that corresponds to the strata   |
| test_stat        | Test statistic function   |
| perm_func        | Function to permute group   |
| alternative      | String, two-sided or one-sided (greater or less) p-value; options are 'greater', 'less', or 'two-sided' |
| shift            | Value of shift to apply in one- or two-sample problem   |
| reps             | Number of iterations to use when calculating permutation p-value  |
| perm_set         | Matrix of group assignments to use instead of reps iterations of perm_func                              |
| complete_enum    | Boolean, whether to calculate P-value under complete enumeration of permutations                        |
| return_test_dist | Boolean, whether to return test statistic distribution under permutations                               |
| return_perm_dist | Boolean, whether to return a matrix where each row is the group assignment under that permutation       |
| seed             | An integer seed value   |

## Value

p\_value: the permutation test p-value

test\_stat\_dist: array, the distribution of the test statistic under the set of permutations, if return\_test\_dist is set to TRUE

perm\_indices\_mat: matrix, each row corresponds to a permutation used in the permutation test calculation

## Examples

```
data <- data.frame(group = c(rep(1, 10), rep(2, 10)), outcome = c(rep(1, 10), rep(1, 10)))

permutation_test(df = data, group_col = "group", outcome_col = "outcome",
test_stat = "diff_in_means", perm_func = permute_group, alternative = "greater",
shift = 0, reps = 10, return_perm_dist = TRUE, return_test_dist = TRUE, seed = 42)
```

---

`permutation_test_ci`     *Construct confidence interval by inverting permutation tests*

---

## Description

This function constructs a confidence interval by inverting permutation tests and applying the method in Glazer and Stark, 2024.

## Usage

```
permutation_test_ci(
  df,
  group_col,
  outcome_col,
  strata_col = NULL,
  test_stat = "diff_in_means",
  perm_func = permute_group,
  upper_bracket = NULL,
  lower_bracket = NULL,
  cl = 0.95,
  e = 0.1,
  reps = 10000,
  perm_set = NULL,
  seed = 42
)
```

## Arguments

|                            |  |
|----------------------------|--|
| <code>df</code>            | A data frame   |
| <code>group_col</code>     | The name of the column in <code>df</code> that corresponds to the group label                        |
| <code>outcome_col</code>   | The name of the column in <code>df</code> that corresponds to the outcome variable                   |
| <code>strata_col</code>    | The name of the column in <code>df</code> that corresponds to the strata                             |
| <code>test_stat</code>     | Test statistic function  |
| <code>perm_func</code>     | Function to permute group  |
| <code>upper_bracket</code> | Array with 2 values that bracket upper confidence bound  |
| <code>lower_bracket</code> | Array with 2 values that bracket lower confidence bound  |
| <code>cl</code>            | Confidence level, default 0.95   |
| <code>e</code>             | Maximum distance from true confidence bound value  |
| <code>reps</code>          | Number of iterations to use when calculating permutation p-value                                     |
| <code>perm_set</code>      | Matrix of group assignments to use instead of <code>reps</code> iterations of <code>perm_func</code> |
| <code>seed</code>          | An integer seed value  |

**Value**

A list containing the permutation test p-value, and the test statistic distribution if applicable

**Examples**

```
x <- c(35.3, 35.9, 37.2, 33.0, 31.9, 33.7, 36.0, 35.0, 33.3, 33.6, 37.9, 35.6, 29.0, 33.7, 35.7)
y <- c(32.5, 34.0, 34.4, 31.8, 35.0, 34.6, 33.5, 33.6, 31.5, 33.8, 34.6)
df <- data.frame(outcome = c(x, y), group = c(rep(1, length(x)), rep(0, length(y))))
permutation_test_ci(df = df, group_col = "group", outcome_col = "outcome", strata_col = NULL,
                     test_stat = "diff_in_means", perm_func = permute_group,
                     upper_bracket = NULL, lower_bracket = NULL,
                     cl = 0.95, e = 0.01, reps = 10^3, seed = 42)
```

permute\_group

*Unstratified group permutation***Description**

This function takes a data frame and group column name as input and returns the dataframe with the group column randomly permuted

**Usage**

```
permute_group(df, group_col, strata_col = NULL, seed = NULL)
```

**Arguments**

|            |  |
|------------|--|
| df         | A data frame   |
| group_col  | String, the name of the column in df that corresponds to the group label                                 |
| strata_col | The name of the column in df that corresponds to the strata, should be NULL for unstratified permutation |
| seed       | An integer seed value  |

**Value**

The inputted data frame with the group column randomly shuffled

**Examples**

```
data <- data.frame(group_label = c(1, 2, 2, 1, 2, 1), outcome = 1:6)
permute_group(df = data, group_col = "group_label", strata_col = NULL, seed = 42)
```

|              |                         |
|--------------|-------------------------|
| permute_sign | <i>Sign permutation</i> |
|--------------|-------------------------|

## Description

This function takes a data frame and group and outcome column name as input and returns the dataframe with the group column replaced with randomly assigned signs

## Usage

```
permute_sign(df, group_col, strata_col = NULL, seed = NULL)
```

## Arguments

|            |   |
|------------|---|
| df         | A data frame  |
| group_col  | The name of the column in df that corresponds to the group label                              |
| strata_col | The name of the column in df that corresponds to the strata, should be NULL for this function |
| seed       | An integer seed value   |

## Value

The inputted data frame with the group column replaced with randomly assigned signs

## Examples

```
data <- data.frame(group_label = rep(1, 6), outcome = 1:6)
permute_group(df = data, group_col = "group_label", strata_col = NULL, seed = 42)
```

|                     |                                     |
|---------------------|-------------------------------------|
| strat_permute_group | <i>Stratified group permutation</i> |
|---------------------|-------------------------------------|

## Description

This function takes a data frame and group and strata column name as input and returns the dataframe with the group column randomly permuted by strata

## Usage

```
strat_permute_group(df, group_col, strata_col, seed = NULL)
```

**Arguments**

|            |  |
|------------|--|
| df         | A data frame   |
| group_col  | The name of the column in df that corresponds to the group label |
| strata_col | The name of the column in df that corresponds to the strata      |
| seed       | An integer seed value  |

**Value**

The inputted data frame with the group column randomly shuffled by strata

**Examples**

```
data <- data.frame(group_label = c(1, 2, 2, 1, 2, 1), stratum = c(1, 1, 1, 2, 2, 2), outcome = 1:6)
permute_group(df = data, group_col = "group_label", strata_col = "stratum", seed = 42)
```

tippett

*Tippett combining function***Description**

This function takes an array of p-values and returns a combined p-value using Tippett's combining function:  $\max_i \{1 - p_i\}$

**Usage**

```
tippett(pvalues)
```

**Arguments**

|         |                   |
|---------|-------------------|
| pvalues | Array of p-values |
|---------|-------------------|

**Value**

Combined p-value using Tippett's method

**Examples**

```
tippett(pvalues = c(.05, .1, .5))
```

|                   |                                   |
|-------------------|-----------------------------------|
| <b>ttest_stat</b> | <i>Calculate t-test statistic</i> |
|-------------------|-----------------------------------|

### Description

This function takes a data frame, and group and outcome column names as input and returns the t test statistic

### Usage

```
ttest_stat(df, group_col, outcome_col)
```

### Arguments

|                          |   |
|--------------------------|---|
| <code>df</code>          | A data frame  |
| <code>group_col</code>   | The name of the column in df that corresponds to the group label      |
| <code>outcome_col</code> | The name of the column in df that corresponds to the outcome variable |

### Value

The t test statistic

|                   |                                    |
|-------------------|------------------------------------|
| <b>two_sample</b> | <i>Two-sample permutation test</i> |
|-------------------|------------------------------------|

### Description

This function runs a permutation test with difference in means test statistic for the two-sample problem by calling the `permutation_test` function.

### Usage

```
two_sample(x, y, shift = 0, alternative = "greater", reps = 10^4, seed = NULL)
```

### Arguments

|                          |   |
|--------------------------|---|
| <code>x</code>           | array of data for treatment group   |
| <code>y</code>           | array of data for control group   |
| <code>shift</code>       | Value of shift to apply in two-sample problem   |
| <code>alternative</code> | String, two-sided or one-sided (greater or less) p-value; options are 'greater', 'less', or 'two-sided' |
| <code>reps</code>        | Number of iterations to use when calculating permutation p-value  |
| <code>seed</code>        | An integer seed value   |

**Value**

The permutation test p-value

**Examples**

```
two_sample(x = c(10, 9, 11), y = c(12, 11, 13), alternative = "less", seed = 42)
```

# Index

adjust\_p\_value, 2  
diff\_in\_means, 2  
diff\_inmedians, 3  
fisher, 4  
liptak, 4  
npc, 5  
one\_sample, 6  
one\_sample\_mean, 7  
one\_way\_anova\_stat, 8  
permutation\_test, 8  
permutation\_test\_ci, 10  
permute\_group, 11  
permute\_sign, 12  
strat\_permute\_group, 12  
tippett, 13  
ttest\_stat, 14  
two\_sample, 14