Package ‘npboottpmr’

February 23, 2024

Title  Nonparametric Bootstrap Test with Pooled Resampling

Version 0.2.1

Description  Addressing crucial research questions often necessitates a small sample size due to factors such as distinctive target populations, rarity of the event under study, time and cost constraints, ethical concerns, or group-level unit of analysis. Many readily available analytic methods, however, do not accommodate small sample sizes, and the choice of the best method can be unclear. The ‘npboottpmr’ package enables the execution of nonparametric bootstrap tests with pooled resampling to help fill this gap. Grounded in the statistical methods for small sample size studies detailed in Dwivedi, Mallawaarachchi, and Alvarado (2017) <doi:10.1002/sim.7263>, the package facilitates a range of statistical tests, encompassing independent t-tests, paired t-tests, and one-way Analysis of Variance (ANOVA) F-tests. The nonparboot() function undertakes essential computations, yielding detailed outputs which include test statistics, effect sizes, confidence intervals, and bootstrap distributions. Further, ‘npboottpmr’ incorporates an interactive ‘shiny’ web application, nonparboot_app(), offering intuitive, user-friendly data exploration.

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Encoding UTF-8

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URL https://github.com/mightymetrika/npboottpmr

BugReports https://github.com/mightymetrika/npboottpmr/issues

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Simulated Data for F-test

Description

A simulated data set to experiment with nonparboot() with test = "F"

Usage

data_f

Format

data_f:
A data frame with 15 rows and 2 columns:
x  A numeric variable
grp  A factor variable with group labels
**data_f_md**

Source

Simulated data

---

**data_f_id**  
*Simulated Data for F-test Using Identically Distributed Data*

Description

A simulated data set to experiment with `nonparboot()` with `test = "F"` when all groups are drawn from identical distributions

Usage

data_f_id

Format

data_f_id:
A data frame with 15 rows and 2 columns:

- **x** A numeric variable
- **grp** A factor variable with group labels

Source

Simulated data

---

**data_f_mi**  
*Simulated Data for F-test with Missing Outcomes*

Description

A simulated data set to experiment with `nonparboot()` with `test = "F"` and missing outcomes

Usage

data_f_mi

Format

data_f_mi:
A data frame with 15 rows and 2 columns:

- **x** A numeric variable
- **grp** A factor variable with group labels

Source

Simulated data
**data_pt**

*Simulated Data for Paired T-test*

**Description**

A simulated data set to experiment with nonparboot() with test = "pt"

**Usage**

```r
data_pt
```

**Format**

- `data_pt`:
  - A data frame with 10 rows and 2 columns:
  - `x` A numeric variable
  - `y` A numeric variable

**Source**

Simulated data

---

**data_pt_id**

*Simulated Data for Paired T-test Using Identically Distributed Data*

**Description**

A simulated data set to experiment with nonparboot() with test = "pt" when both variables are drawn from identical distributions

**Usage**

```r
data_pt_id
```

**Format**

- `data_pt_id`:
  - A data frame with 10 rows and 2 columns:
  - `x` A numeric variable
  - `y` A numeric variable

**Source**

Simulated data
**data_pt_mi**  
*Simulated Data for Paired T-test with Missing Data*

**Description**  
A simulated data set to experiment with nonparboot() with test = "pt" and missing values

**Usage**  
`data_pt_mi`

**Format**  
`data_pt_mi`:  
A data frame with 10 rows and 2 columns:  
- `x` A numeric variable  
- `y` A numeric variable

**Source**  
Simulated data

---

**data_t**  
*Simulated Data for Independent T-test*

**Description**  
A simulated data set to experiment with nonparboot() with test = "t"

**Usage**  
`data_t`

**Format**  
`data_t`:  
A data frame with 10 rows and 2 columns:  
- `x` A numeric variable  
- `grp` A factor variable with group labels

**Source**  
Simulated data
data_t_mi

Simulated Data for Independent T-test with Missing Outcomes

Description

A simulated data set to experiment with nonparboot() with test = "t" and missing outcome values

Usage

data_t_mi

Format

data_t_mi:
A data frame with 10 rows and 2 columns:
- x  A numeric variable
- grp  A factor variable with group labels

Source

Simulated data

nonparboot

Nonparametric Bootstrap Test with Pooled Resampling for Small Sample Sizes

Description

This function performs a nonparametric bootstrap test with pooled resampling for small sample sizes, as described in Dwivedi et al. (2017). It supports t-tests (independent and paired) and F-tests (one-way ANOVA), with a user-specified number of bootstrap resamples.

Usage

nonparboot(
  data,
  x,
  y = NULL,
  grp = NULL,
  nboot,
  test = c("t", "pt", "F"),
  conf.level = 0.95,
  seed = NULL,
  na_rm = FALSE
)
Arguments

data A data frame containing the variables to be analyzed.
x A character string specifying the column in `data` to be used as the primary variable.
y An optional character string specifying the column in `data` to be used as the second variable for paired t-tests. Default is NULL.
grp An optional character string specifying the column in `data` to be used as the grouping variable for independent t-tests and F-tests. Default is NULL.
nboot An integer specifying the number of bootstrap resamples to perform.
test A character string specifying the type of test to perform. Must be one of "t", "pt", or "F" for independent t-test, paired t-test, or F-test, respectively. Default is "t".
conf.level A numeric value between 0 and 1 specifying the confidence level for confidence intervals. Default is 0.95.
seed An optional value interpreted as an integer to set the seed for the random number generator, for reproducibility. Default is NULL (no seed).
na_rm Remove observations with missing values. Default is FALSE.

Value
A list with the following components:

• p.value: The p-value of the test.
• orig.stat: The test statistic calculated from the original data.
• ci.stat: The confidence interval for the test statistic from the bootstrap distribution.
• bootstrap.stat.dist: The distribution of the test statistic values from the bootstrap resamples.
• effect.size: The effect size (mean difference or eta-squared) calculated from the original data.
• ci.effect.size: The confidence interval for the effect size from the bootstrap distribution.
• bootstrap.effect.dist: The distribution of effect size values from the bootstrap resamples.

References

Examples

# Example usage of nonparboot
np_res <- nonparboot(iris, x = "Sepal.Length", grp = "Species", nboot = 1000, test = "F")
print(np_res$p.value)
**nonparboot_app**  
*Shiny App for Nonparametric Bootstrap Tests with Pooled Resampling*

**Description**

This function creates a Shiny app for performing nonparametric bootstrap tests with pooled resampling. The app allows you to conduct an independent t-test, a paired t-test, or a one-way ANOVA, depending on your input.

**Usage**

`nonparboot_app()`

**Value**

An interactive Shiny app.

**References**


**Examples**

```r
if(interactive()){
    nonparboot_app()
}
```

---

**replext**  
*Replext Simulation Shiny App*

**Description**

This application attempts to replicate and extend the simulation results from the paper by Dwivedi et al. (2017). The application includes a user interface for selecting simulation parameters and a server logic to process the simulation and handle user interactions.

**Usage**

`replext()`
Details

The app’s user interface consists of:

- A numeric input for setting an optional random number seed.
- A dropdown menu to select a cell block for the simulation, which is populated using the `getCellBlocks` function.
- Dynamic UI elements for inputting simulation parameters, generated based on the selected cell block.
- A button to run the simulation.
- A download button to export the simulation results.

The server logic of the app handles:

- Rendering the dynamic UI elements for simulation parameters.
- Observing the simulation run event and processing the simulation using the `runSimulation` function.
- Rendering a table to display the simulation results.
- Handling the data download request and exporting the results as a CSV file.

References


Examples

```r
if(interactive()){
  replext()
}
```

---

**replext_t2_c1.1**  
*Replicate and Extend Simulation Results from Table 2 Cell 1.1*

**Description**

This function attempts to replicate and extend the simulation results from Table 2 cell block 1.1 of the paper by Dwivedi et al. (2017). The default parameter values aim to replicate the results from the paper, while modifying the parameter values allows for an extension of the results.
Usage

replext_t2_c1.1(
  M1 = 5,
  S1 = 1,
  M2 = 5,
  S2 = 1,
  Sk1 = NULL,
  Sk2 = NULL,
  n1 = c(3, 4, 5, 6, 7, 8, 9, 10, 15),
  n2 = c(3, 4, 5, 6, 7, 8, 9, 10, 15),
  n_simulations = 10000,
  nboot = 1000,
  conf.level = 0.95
)

Arguments

M1  Mean for the first group, default is 5.
S1  Standard deviation for the first group, default is 1.
M2  Mean for the second group, default is 5.
S2  Standard deviation for the second group, default is 1.
Sk1 Skewness parameter for the first group, default is NULL (normal distribution).
Sk2 Skewness parameter for the second group, default is NULL (normal distribution).
n1  Vector of sample sizes for the first group.
n2  Vector of sample sizes for the second group, must be the same length as n1.
n_simulations  Number of simulations to run, default is 10,000.
nboot  Number of bootstrap samples, default is 1000.
conf.level  Confidence level for calculating p-value thresholds, default is 0.95.

Value

A data frame with columns for each sample size pair (n1, n2) and the proportions of significant p-values for each test (ST, WT, NPBTT, WRST, PTT).

References


Examples

replext_t2_c1.1(n1 = c(4), n2 = c(4), n_simulations = 1)
Replicate and Extend Simulation Results from Table 2 Cell 1.2

Description

This function is a wrapper around replext_t2_c1.1 and is specifically used for replicating and extending the simulation results from Table 2 cell block 1.2 of the paper by Dwivedi et al. (2017). It sets the standard deviation of the second group ($S_2$) to 3 by default.

Usage

```r
replext_t2_c1.2(
  M1 = 5,
  S1 = 1,
  M2 = 5,
  S2 = 3,
  Sk1 = NULL,
  Sk2 = NULL,
  n1 = c(3, 4, 5, 6, 7, 8, 9, 10, 15),
  n2 = c(3, 4, 5, 6, 7, 8, 9, 10, 15),
  n_simulations = 10000,
  nboot = 1000,
  conf.level = 0.95
)
```

Arguments

- **M1**: Mean for the first group, default is 5.
- **S1**: Standard deviation for the first group, default is 1.
- **M2**: Mean for the second group, default is 5.
- **S2**: Standard deviation for the second group, default is 3.
- **Sk1**: Skewness parameter for the first group, default is NULL (normal distribution).
- **Sk2**: Skewness parameter for the second group, default is NULL (normal distribution).
- **n1**: Vector of sample sizes for the first group.
- **n2**: Vector of sample sizes for the second group, must be the same length as n1.
- **n_simulations**: Number of simulations to run, default is 10,000.
- **nboot**: Number of bootstrap samples, default is 1000.
- **conf.level**: Confidence level for calculating p-value thresholds, default is 0.95.

Value

A data frame with columns for each sample size pair ($n_1, n_2$) and the proportions of significant p-values for each test (ST, WT, NPBTT, WRST, PTT).
References


See Also

replext_t2_c1.1

Examples

replext_t2_c1.2(n1 = c(4), n2 = c(4), n_simulations = 1)

replext_t2_c2.1 Replicate and Extend Simulation Results from Table 2 Cell 2.1

Description

This function is intended to replicate and extend the simulation results from Table 2 cell block 2.1 in the paper by Dwivedi et al. (2017). It is designed for scenarios with the same skewed distribution and equal variance in both groups. The function acts as a wrapper around replext_t2_c1.1, applying specific skewness parameters as required for the cell.

Usage

replext_t2_c2.1(
  M1 = 5,
  S1 = 1,
  M2 = 5,
  S2 = 1,
  Sk1 = 0.8,
  Sk2 = 0.8,
  n1 = c(3, 4, 5, 6, 7, 8, 9, 10, 15),
  n2 = c(3, 4, 5, 6, 7, 8, 9, 10, 15),
  n_simulations = 10000,
  nboot = 1000,
  conf.level = 0.95
)

Arguments

M1 Mean for the first group, default is 5.
S1 Standard deviation for the first group, default is 1.
M2 Mean for the second group, default is 5.
S2 Standard deviation for the second group, default is 1.
repext_t2_c2.2

Sk1  Skewness parameter for the first group, default is 0.8.
Sk2  Skewness parameter for the second group, default is 0.8.
n1   Vector of sample sizes for the first group.
n2   Vector of sample sizes for the second group, must be the same length as n1.
n_simulations Number of simulations to run, default is 10,000.
nboot Number of bootstrap samples, default is 1000.
conf.level Confidence level for calculating p-value thresholds, default is 0.95.

Value

A data frame with columns for each sample size pair (n1, n2) and the proportions of significant p-values for each test (ST, WT, NPBTT, WRST, PTT).

References


See Also

repext_t2_c1.1

Examples

repext_t2_c2.1(n1 = c(4), n2 = c(4), n_simulations = 1)

repext_t2_c2.2

Replicate and Extend Simulation Results from Table 2 Cell 2.2

Description

This function is designed to replicate and extend the simulation results from Table 2 cell block 2.2 of the paper by Dwivedi et al. (2017). It handles scenarios with same skewed distribution but with different variances in the two groups. The function is a wrapper around repext_t2_c1.1, setting specific skewness and variance parameters as per the cell’s requirements.

Usage

repext_t2_c2.2(
  M1 = 5,
  S1 = 1,
  M2 = 5,
  S2 = 3,
  Sk1 = 0.8,
)
Sk2 = 0.8,
n1 = c(3, 4, 5, 6, 7, 8, 9, 10, 15),
n2 = c(3, 4, 5, 6, 7, 8, 9, 10, 15),
n_simulations = 10000,
nboot = 1000,
conf.level = 0.95
)

Arguments

M1 Mean for the first group, default is 5.
S1 Standard deviation for the first group, default is 1.
M2 Mean for the second group, default is 5.
S2 Standard deviation for the second group, default is 3.
Sk1 Skewness parameter for the first group, default is 0.8.
Sk2 Skewness parameter for the second group, default is 0.8.
n1 Vector of sample sizes for the first group.
n2 Vector of sample sizes for the second group, must be the same length as n1.
n_simulations Number of simulations to run, default is 10,000.
nboot Number of bootstrap samples, default is 1000.
conf.level Confidence level for calculating p-value thresholds, default is 0.95.

Value

A data frame with columns for each sample size pair (n1, n2) and the proportions of significant p-values for each test (ST, WT, NPBTT, WRST, PTT).

References


See Also

replext_t2_c1.1

Examples

replext_t2_c2.2(n1 = c(4), n2 = c(4), n_simulations = 1)
Description

This function is designed to replicate and extend the simulation results from Table 2 cell block 3.1 of the paper by Dwivedi et al. (2017). It handles scenarios with different skewed distributions but equal variance in the two groups. The function is a wrapper around `replext_t2_c3.1`, setting specific skewness parameters as per the cell’s requirements.

Usage

```r
replext_t2_c3.1(
  M1 = 5,
  S1 = 1,
  M2 = 5,
  S2 = 1,
  Sk1 = 0.8,
  Sk2 = 1,
  n1 = c(3, 4, 5, 6, 7, 8, 9, 10, 15),
  n2 = c(3, 4, 5, 6, 7, 8, 9, 10, 15),
  n_simulations = 10000,
  nboot = 1000,
  conf.level = 0.95
)
```

Arguments

- `M1`: Mean for the first group, default is 5.
- `S1`: Standard deviation for the first group, default is 1.
- `M2`: Mean for the second group, default is 5.
- `S2`: Standard deviation for the second group, default is 1.
- `Sk1`: Skewness parameter for the first group, default is 0.8.
- `Sk2`: Skewness parameter for the second group, default is 1.0.
- `n1`: Vector of sample sizes for the first group.
- `n2`: Vector of sample sizes for the second group, must be the same length as `n1`.
- `n_simulations`: Number of simulations to run, default is 10,000.
- `nboot`: Number of bootstrap samples, default is 1000.
- `conf.level`: Confidence level for calculating p-value thresholds, default is 0.95.

Value

A data frame with columns for each sample size pair (n1, n2) and the proportions of significant p-values for each test (ST, WT, NPBTT, WRST, PTT).
**References**


**See Also**

replext_t2_c1.1

**Examples**

replext_t2_c3.1(n1 = c(4), n2 = c(4), n_simulations = 1)

---

**Description**

This function aims to replicate and extend the simulation results from Table 2 cell block 3.2 in the paper by Dwivedi et al. (2017). It is tailored for scenarios with different skewed distributions and unequal variance between the two groups. The function serves as a wrapper around replext_t2_c1.1, utilizing specific skewness parameters and variances as described in the cell.

**Usage**

replext_t2_c3.2(
  M1 = 5,
  S1 = 1,
  M2 = 5,
  S2 = 3,
  Sk1 = 0.8,
  Sk2 = 1,
  n1 = c(3, 4, 5, 6, 7, 8, 9, 10, 15),
  n2 = c(3, 4, 5, 6, 7, 8, 9, 10, 15),
  n_simulations = 10000,
  nboot = 1000,
  conf.level = 0.95
)

**Arguments**

- **M1**: Mean for the first group, default is 5.
- **S1**: Standard deviation for the first group, default is 1.
- **M2**: Mean for the second group, default is 5.
- **S2**: Standard deviation for the second group, default is 3.
Sk1  Skewness parameter for the first group, default is 0.8.
Sk2  Skewness parameter for the second group, default is 1.0.
n1   Vector of sample sizes for the first group.
n2   Vector of sample sizes for the second group, must be the same length as n1.
n_simulations  Number of simulations to run, default is 10,000.
nboot  Number of bootstrap samples, default is 1000.
conf.level   Confidence level for calculating p-value thresholds, default is 0.95.

Value

A data frame with columns for each sample size pair (n1, n2) and the proportions of significant p-values for each test (ST, WT, NPBTT, WRST, PTT).

References


See Also

replext_t2_c1.1

Examples

replext_t2_c3.2(n1 = c(4), n2 = c(4), n_simulations = 1)
Usage

replext_t2_c4.1(
  M1 = 5,
  S1 = 1,
  M2 = 5,
  S2 = 1,
  Sk1 = 0.8,
  Sk2 = 0.8,
  n1 = c(4, 3, 5, 4, 6, 4, 3, 4, 5, 6),
  n2 = c(2, 4, 3, 5, 6, 7, 11, 10, 9),
  n_simulations = 10000,
  nboot = 1000,
  conf.level = 0.95
)

Arguments

M1          Mean for the first group, default is 5.
S1          Standard deviation for the first group, default is 1.
M2          Mean for the second group, default is 5.
S2          Standard deviation for the second group, default is 1.
Sk1         Skewness parameter for the first group, default is 0.8.
Sk2         Skewness parameter for the second group, default is 0.8.
n1          Vector of sample sizes for the first group.
n2          Vector of sample sizes for the second group, designed for unequal sample sizes.
n_simulations Number of simulations to run, default is 10,000.
nboot       Number of bootstrap samples, default is 1000.
conf.level  Confidence level for calculating p-value thresholds, default is 0.95.

Value

A data frame with columns for each sample size pair (n1, n2) and the proportions of significant
p-values for each test (ST, WT, NPBTT, WRST, PTT).

References

Dwivedi AK, Mallawaarachchi I, Alvarado LA. Analysis of small sample size studies using non-
parametric bootstrap test with pooled resampling method. Stat Med. 2017 Jun 30;36(14):2187-

See Also

replext_t2_c1.1
Examples

replext_t2_c4.1(n1 = c(4), n2 = c(2), n_simulations = 1)

---

replext_t2_c4.2  Replicate and Extend Simulation Results from Table 2 Cell 4.2

Description

This function is designed to replicate and extend the simulation results from Table 2 cell block 4.2 in the paper by Dwivedi et al. (2017). It is tailored for scenarios with unequal sample sizes, same skewed distribution, but different variances between the two groups. The function acts as a wrapper around replext_t2_c1.1, setting specific skewness parameters, variances, and sample sizes as described in the cell.

Usage

replext_t2_c4.2(
  M1 = 5,
  S1 = 1,
  M2 = 5,
  S2 = 3,
  Sk1 = 0.8,
  Sk2 = 0.8,
  n1 = c(4, 3, 5, 4, 6, 4, 3, 4, 5, 6),
  n2 = c(2, 4, 3, 5, 3, 6, 7, 11, 10, 9),
  n_simulations = 10000,
  nboot = 1000,
  conf.level = 0.95
)

Arguments

- **M1**: Mean for the first group, default is 5.
- **S1**: Standard deviation for the first group, default is 1.
- **M2**: Mean for the second group, default is 5.
- **S2**: Standard deviation for the second group, default is 3.
- **Sk1**: Skewness parameter for the first group, default is 0.8.
- **Sk2**: Skewness parameter for the second group, default is 0.8.
- **n1**: Vector of sample sizes for the first group.
- **n2**: Vector of sample sizes for the second group, designed for unequal sample sizes.
- **n_simulations**: Number of simulations to run, default is 10,000.
- **nboot**: Number of bootstrap samples, default is 1000.
- **conf.level**: Confidence level for calculating p-value thresholds, default is 0.95.
Value

A data frame with columns for each sample size pair (n1, n2) and the proportions of significant p-values for each test (ST, WT, NPBTT, WRST, PTT).

References


See Also

replext_t2_c1.1

Examples

replext_t2_c4.2(n1 = c(4), n2 = c(2), n_simulations = 1)

---

replext_t3_c1.1

Replicate and Extend Simulation Results for Statistical Power from Table 3 Cell 1.1

Description

This function is tailored to replicate and extend the simulation results for assessing statistical power from Table 3 cell block 1.1 in the paper by Dwivedi et al. (2017). It compares two groups with different means but equal variance and optional skewness. The function is a wrapper around replext_t2_c1.1, adapted for statistical power analysis.

Usage

replext_t3_c1.1(
    M1 = 5,
    S1 = 1,
    M2 = 7,
    S2 = 1,
    Sk1 = NULL,
    Sk2 = NULL,
    n1 = c(3, 4, 5, 6, 7, 8, 9, 10, 15, 25, 50, 100),
    n2 = c(3, 4, 5, 6, 7, 8, 9, 10, 15, 25, 50, 100),
    n_simulations = 10000,
    nboot = 1000,
    conf.level = 0.95
)
Arguments

- **M1**: Mean for the first group, default is 5.
- **S1**: Standard deviation for the first group, default is 1.
- **M2**: Mean for the second group, default is 7.
- **S2**: Standard deviation for the second group, default is 1.
- **Sk1**: Skewness parameter for the first group, default is NULL (normal distribution).
- **Sk2**: Skewness parameter for the second group, default is NULL (normal distribution).
- **n1**: Vector of sample sizes for the first group.
- **n2**: Vector of sample sizes for the second group, must be the same length as n1.
- **n_simulations**: Number of simulations to run, default is 10,000.
- **nboot**: Number of bootstrap samples, default is 1000.
- **conf.level**: Confidence level for calculating p-value thresholds, default is 0.95.

Value

A data frame with columns for each sample size pair (n1, n2) and the proportions of significant p-values for each test (ST, WT, NPBTT, WRST, PTT), representing statistical power.

References


See Also

replext_t2_c1.1

Examples

replext_t3_c1.1(n1 = c(10), n2 = c(10), n_simulations = 1)

Description

This function is designed to replicate and extend the statistical power analysis from Table 3 cell block 1.2 in the paper by Dwivedi et al. It focuses on scenarios with normal distribution having different means and unequal variances across two groups. It utilizes replext_t2_c1.1 for its calculations by setting specific means and standard deviations.
Usage

replext_t3_c1.2(
  M1 = 5,
  S1 = 1,
  M2 = 7,
  S2 = 3,
  Sk1 = NULL,
  Sk2 = NULL,
  n1 = c(3, 4, 5, 6, 7, 8, 9, 10, 15, 25, 50, 100),
  n2 = c(3, 4, 5, 6, 7, 8, 9, 10, 15, 25, 50, 100),
  n_simulations = 10000,
  nboot = 1000,
  conf.level = 0.95
)

Arguments

M1 Mean for the first group, default is 5.
S1 Standard deviation for the first group, default is 1.
M2 Mean for the second group, default is 7.
S2 Standard deviation for the second group, default is 3.
Sk1 Skewness parameter for the first group, default is NULL (normal distribution).
Sk2 Skewness parameter for the second group, default is NULL (normal distribution).
n1 Vector of sample sizes for the first group.
n2 Vector of sample sizes for the second group, must be the same length as n1.
n_simulations Number of simulations to run, default is 10,000.
nboot Number of bootstrap samples, default is 1000.
conf.level Confidence level for calculating p-value thresholds, default is 0.95.

Value

A data frame with columns for each sample size pair (n1, n2) and the proportions of significant p-values for each test (ST, WT, NPBTT, WRST, PTT), representing the power analysis.

References


See Also

replext_t2_c1.1
Replext_t3_c2.1

Description

This function is geared towards replicating and extending the statistical power analysis from Table 3 cell block 2.1 of the paper by Dwivedi et al. (2017). It deals with scenarios involving skewed distributions with equal variance and different means in the two groups. It acts as a wrapper around replext_t2_c1.1, with specific adjustments for skewness parameters and means.

Usage

replext_t3_c2.1(
  M1 = 5,
  S1 = 1,
  M2 = 7,
  S2 = 1,
  Sk1 = 0.8,
  Sk2 = 0.8,
  n1 = c(3, 4, 5, 6, 7, 8, 9, 10, 15, 25, 50, 100),
  n2 = c(3, 4, 5, 6, 7, 8, 9, 10, 15, 25, 50, 100),
  n_simulations = 10000,
  nboot = 1000,
  conf.level = 0.95
)

Arguments

M1 Mean for the first group, default is 5.
S1 Standard deviation for the first group, default is 1.
M2 Mean for the second group, default is 7.
S2 Standard deviation for the second group, default is 1.
Sk1 Skewness parameter for the first group, default is 0.8.
Sk2 Skewness parameter for the second group, default is 0.8.
n1 Vector of sample sizes for the first group.
n2 Vector of sample sizes for the second group, must be the same length as n1.
n_simulations Number of simulations to run, default is 10,000.
nboot Number of bootstrap samples, default is 1000.
conf.level Confidence level for calculating p-value thresholds, default is 0.95.
**Value**

A data frame with columns for each sample size pair \((n_1, n_2)\) and the proportions of significant p-values for each test (ST, WT, NPBTT, WRST, PTT), reflecting the power analysis.

**References**


**See Also**

replext_t2_c1.1

**Examples**

```r
replext_t3_c2.1(n1 = c(10), n2 = c(10), n_simulations = 1)
```

---

**Description**

This function aims to replicate and extend the statistical power analysis from Table 3 cell block 2.2 in the paper by Dwivedi et al. (2017). It deals with scenarios involving skewed distributions with different variances and means in the two groups. It is a wrapper around replext_t2_c1.1, with adjusted means, variances, and skewness parameters.

**Usage**

```r
replext_t3_c2.2(
  M1 = 5,
  S1 = 1,
  M2 = 7,
  S2 = 3,
  Sk1 = 0.8,
  Sk2 = 0.8,
  n1 = c(3, 4, 5, 6, 7, 8, 9, 10, 15, 25, 50, 100),
  n2 = c(3, 4, 5, 6, 7, 8, 9, 10, 15, 25, 50, 100),
  n_simulations = 10000,
  nboot = 1000,
  conf.level = 0.95
)
```
Arguments

- **M1**: Mean for the first group, default is 5.
- **S1**: Standard deviation for the first group, default is 1.
- **M2**: Mean for the second group, default is 7.
- **S2**: Standard deviation for the second group, default is 3.
- **Sk1**: Skewness parameter for the first group, default is 0.8.
- **Sk2**: Skewness parameter for the second group, default is 0.8.
- **n1**: Vector of sample sizes for the first group.
- **n2**: Vector of sample sizes for the second group, must be the same length as n1.
- **n_simulations**: Number of simulations to run, default is 10,000.
- **nboot**: Number of bootstrap samples, default is 1000.
- **conf.level**: Confidence level for calculating p-value thresholds, default is 0.95.

Value

A data frame with columns for each sample size pair (n1, n2) and the proportions of significant p-values for each test (ST, WT, NPBTT, WRST, PTT), representing the power analysis.

References


See Also

- replicate_t2_c1.1

Examples

```r
replext_t3_c2.2(n1 = c(10), n2 = c(10), n_simulations = 1)
```

Description

This function is aimed at replicating and extending the statistical power analysis from Table 3 cell block 3.1 in the paper by Dwivedi et al. (2017). It addresses scenarios with different skewed distributions but equal variance and different means in the two groups. It utilizes replext_t2_c1.1 for calculations by setting specific skewness parameters.
Usage

replext_t3_c3.1(
  M1 = 5,
  S1 = 1,
  M2 = 7,
  S2 = 1,
  Sk1 = 0.8,
  Sk2 = 1,
  n1 = c(3, 4, 5, 6, 7, 8, 9, 10, 15, 25, 50, 100),
  n2 = c(3, 4, 5, 6, 7, 8, 9, 10, 15, 25, 50, 100),
  n_simulations = 10000,
  nboot = 1000,
  conf.level = 0.95
)

Arguments

M1  Mean for the first group, default is 5.
S1  Standard deviation for the first group, default is 1.
M2  Mean for the second group, default is 7.
S2  Standard deviation for the second group, default is 1.
Sk1 Skewness parameter for the first group, default is 0.8.
Sk2 Skewness parameter for the second group, default is 1.0.
n1  Vector of sample sizes for the first group.
n2  Vector of sample sizes for the second group, must be the same length as n1.
n_simulations  Number of simulations to run, default is 10,000.
nboot  Number of bootstrap samples, default is 1000.
conf.level  Confidence level for calculating p-value thresholds, default is 0.95.

Value

A data frame with columns for each sample size pair (n1, n2) and the proportions of significant p-values for each test (ST, WT, NPBTT, WRST, PTT), indicating the power analysis.

References


See Also

replext_t2_c1.1
Examples

replext_t3_c3.1(n1 = c(10), n2 = c(10), n_simulations = 1)

---

replext_t3_c3.2  Replicate and Extend Statistical Power Analysis from Table 3 Cell 3.2

Description

This function aims to replicate and extend the statistical power analysis from Table 3 cell block 3.2 in the paper by Dwivedi et al. (2017). It is designed for scenarios involving different skewed distributions with different variances and different means in the two groups. The function is a wrapper around replext_t2_c1.1, applying specific skewness parameters, means, and variances.

Usage

replext_t3_c3.2(
  M1 = 5,
  S1 = 1,
  M2 = 7,
  S2 = 3,
  Sk1 = 0.8,
  Sk2 = 1,
  n1 = c(3, 4, 5, 6, 7, 8, 9, 10, 15, 25, 50, 100),
  n2 = c(3, 4, 5, 6, 7, 8, 9, 10, 15, 25, 50, 100),
  n_simulations = 10000,
  nboot = 1000,
  conf.level = 0.95
)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>M1</td>
<td>Mean for the first group, default is 5.</td>
</tr>
<tr>
<td>S1</td>
<td>Standard deviation for the first group, default is 1.</td>
</tr>
<tr>
<td>M2</td>
<td>Mean for the second group, default is 7.</td>
</tr>
<tr>
<td>S2</td>
<td>Standard deviation for the second group, default is 3.</td>
</tr>
<tr>
<td>Sk1</td>
<td>Skewness parameter for the first group, default is 0.8.</td>
</tr>
<tr>
<td>Sk2</td>
<td>Skewness parameter for the second group, default is 1.0.</td>
</tr>
<tr>
<td>n1</td>
<td>Vector of sample sizes for the first group.</td>
</tr>
<tr>
<td>n2</td>
<td>Vector of sample sizes for the second group, must be the same length as n1.</td>
</tr>
<tr>
<td>n_simulations</td>
<td>Number of simulations to run, default is 10,000.</td>
</tr>
<tr>
<td>nboot</td>
<td>Number of bootstrap samples, default is 1000.</td>
</tr>
<tr>
<td>conf.level</td>
<td>Confidence level for calculating p-value thresholds, default is 0.95.</td>
</tr>
</tbody>
</table>
Value

A data frame with columns for each sample size pair (n1, n2) and the proportions of significant p-values for each test (ST, WT, NPBTT, WRST, PTT), indicating the power analysis.

References


See Also

replext_t2_c1.1

Examples

replext_t3_c3.2(n1 = c(10), n2 = c(10), n_simulations = 1)
Arguments

- **M1**: Mean for the first group, default is 5.
- **S1**: Standard deviation for the first group, default is 1.
- **M2**: Mean for the second group, default is 7.
- **S2**: Standard deviation for the second group, default is 1.
- **Sk1**: Skewness parameter for the first group, default is 0.8.
- **Sk2**: Skewness parameter for the second group, default is 0.8.
- **n1**: Vector of sample sizes for the first group, specific to unequal sample size scenarios.
- **n2**: Vector of sample sizes for the second group, corresponding to n1.
- **n_simulations**: Number of simulations to run, default is 10,000.
- **nboot**: Number of bootstrap samples, default is 1000.
- **conf.level**: Confidence level for calculating p-value thresholds, default is 0.95.

Value

A data frame with columns for each sample size pair (n1, n2) and the proportions of significant p-values for each test (ST, WT, NPBTT, WRST, PTT), reflecting the power analysis.

References


See Also

- `replext_t2_c1.1`

Examples

```r
replext_t3_c4.1(n1 = c(4), n2 = c(3), n_simulations = 1)
```

Description

This function is designed to replicate and extend the statistical power analysis from Table 3 cell block 4.2 in the paper by Dwivedi et al. (2017). It addresses scenarios with unequal sample sizes, the same skewed distribution, but different variances between the two groups. The function acts as a wrapper around `replext_t2_c1.1`, applying specific skewness parameters, variances, and unequal sample sizes.
Usage

replext_t3_c4.2(
    M1 = 5,
    S1 = 1,
    M2 = 7,
    S2 = 3,
    Sk1 = 0.8,
    Sk2 = 0.8,
    n1 = c(4, 3, 5, 4, 6, 4),
    n2 = c(2, 4, 3, 5, 3, 6),
    n_simulations = 10000,
    nboot = 1000,
    conf.level = 0.95
)

Arguments

M1  Mean for the first group, default is 5.
S1  Standard deviation for the first group, default is 1.
M2  Mean for the second group, default is 7.
S2  Standard deviation for the second group, default is 3.
Sk1 Skewness parameter for the first group, default is 0.8.
Sk2 Skewness parameter for the second group, default is 0.8.
n1  Vector of sample sizes for the first group.
n2  Vector of sample sizes for the second group, designed for unequal sample sizes.
n_simulations Number of simulations to run, default is 10,000.
nboot Number of bootstrap samples, default is 1000.
conf.level Confidence level for calculating p-value thresholds, default is 0.95.

Value

A data frame with columns for each sample size pair (n1, n2) and the proportions of significant p-values for each test (ST, WT, NPBTT, WRST, PTT), representing the power analysis.

References


See Also

replext_t2_c1.1
Examples

replext_t3_c4.2(n1 = c(6), n2 = c(3), n_simulations = 1)

Description

This function is designed to replicate and extend the statistical power analysis from Table 3 cell block 5.1 in the paper by Dwivedi et al. (2017). It focuses on scenarios with normal distribution and unequal sample sizes, using the same means and variances for both groups. It acts as a wrapper around replext_t2_c1.1, with modifications in means and sample sizes.

Usage

replext_t3_c5.1(
  M1 = 5,
  S1 = 1,
  M2 = 7,
  S2 = 1,
  Sk1 = NULL,
  Sk2 = NULL,
  n1 = c(3, 4, 5, 6),
  n2 = c(7, 11, 10, 9),
  n_simulations = 10000,
  nboot = 1000,
  conf.level = 0.95
)

Arguments

M1 Mean for the first group, default is 5.
S1 Standard deviation for the first group, default is 1.
M2 Mean for the second group, default is 7.
S2 Standard deviation for the second group, default is 1.
Sk1 Skewness parameter for the first group, default is NULL (normal distribution).
Sk2 Skewness parameter for the second group, default is NULL (normal distribution).
n1 Vector of sample sizes for the first group.
n2 Vector of unequal sample sizes for the second group.
n_simulations Number of simulations to run, default is 10,000.
nboot Number of bootstrap samples, default is 1000.
conf.level Confidence level for calculating p-value thresholds, default is 0.95.
Replicate and Extend Statistical Power Analysis from Table 3 Cell 5.2

Description

This function is tailored to replicate and extend the statistical power analysis from Table 3 cell block 5.2 in the paper by Dwivedi et al. (2017). It covers scenarios with normal distribution, unequal sample sizes, and different variances in the two groups. The function uses `replext_t2_c1.1` for its calculations, with adjusted means, variances, and sample sizes.

Usage

```r
replext_t3_c5.2(
  M1 = 5,
  S1 = 1,
  M2 = 7,
  S2 = 3,
  Sk1 = NULL,
  Sk2 = NULL,
  n1 = c(3, 4, 5, 6),
  n2 = c(7, 11, 10, 9),
  n_simulations = 10000,
  nboot = 1000,
  conf.level = 0.95
)
```

Value

A data frame with columns for each sample size pair (n1, n2) and the proportions of significant p-values for each test (ST, WT, NPBTT, WRST, PTT), representing the power analysis.

References


See Also

`replext_t2_c1.1`

Examples

```r
replext_t3_c5.1(n1 = c(4), n2 = c(11), n_simulations = 1)
```
Arguments

- **M1**: Mean for the first group, default is 5.
- **S1**: Standard deviation for the first group, default is 1.
- **M2**: Mean for the second group, default is 7.
- **S2**: Standard deviation for the second group, default is 3.
- **Sk1**: Skewness parameter for the first group, default is NULL (normal distribution).
- **Sk2**: Skewness parameter for the second group, default is NULL (normal distribution).
- **n1**: Vector of sample sizes for the first group.
- **n2**: Vector of unequal sample sizes for the second group.
- **n_simulations**: Number of simulations to run, default is 10,000.
- **nboot**: Number of bootstrap samples, default is 1000.
- **conf.level**: Confidence level for calculating p-value thresholds, default is 0.95.

Value

A data frame with columns for each sample size pair (n1, n2) and the proportions of significant p-values for each test (ST, WT, NPBTT, WRST, PTT), indicating the power analysis.

References


See Also

replext_t2_c1.1

Examples

replext_t3_c5.2(n1 = c(4), n2 = c(11), n_simulations = 1)

Description

This function aims to replicate and extend the simulation results from Table 4 cell 1.1 of the paper by Dwivedi et al. (2017). The default parameters are set to replicate the results for the lognormal distribution scenarios as presented in the paper, while modifying the parameter values allows for an extension of these results.
Usage

replext_t4_c1.1(
  rdist = "rlnorm",
  par1_1 = 1,
  par2_1 = 0.6,
  par1_2 = 2,
  par2_2 = 1,
  n1 = c(5, 5, 10),
  n2 = c(5, 10, 10),
  n_simulations = 10000,
  nboot = 1000,
  conf.level = 0.95
)

Arguments

rdist Distribution type, default is 'rlnorm' (lognormal). Other options are 'rpois' (Poisson), 'rchisq' (Chi-squared), and 'rcauchy' (Cauchy).
par1_1 First parameter for the first group’s distribution, default is 1.
par2_1 Second parameter for the first group’s distribution, default is 0.6.
par1_2 First parameter for the second group’s distribution, default is 2.
par2_2 Second parameter for the second group’s distribution, default is 1.
n1 Vector of sample sizes for the first group.
n2 Vector of sample sizes for the second group, must be the same length as n1.
n_simulations Number of simulations to run, default is 10,000.
nboot Number of bootstrap samples, default is 1000.
conf.level Confidence level for calculating p-value thresholds, default is 0.95.

Value

A data frame with columns for each sample size pair (n1, n2) and the proportions of significant p-values for each test (ST, WT, NPBTT, WRST, PTTa, PTTe).

Note

When using rlnorm (lognormal distribution), 'par1' represents 'meanlog' (the mean of the logarithms) and 'par2' represents 'sdlog' (the standard deviation of the logarithms). For rpois (Poisson distribution), 'par1' is 'lambda' (the rate parameter). In the case of rchisq (Chi-squared distribution), 'par1' is 'df' (degrees of freedom) and 'par2' is 'ncp' (non-centrality parameter). Lastly, for rcauchy (Cauchy distribution), 'par1' is the 'location' parameter and 'par2' is the 'scale' parameter.

References

Replext_t4_c2.1

Examples

replext_t4_c1.1(n1 = c(10), n2 = c(10), n_simulations = 1)

---

Replext_t4_c2.1 Replicate and Extend Simulation Results from Table 4 Cell 2.1

Description

This function is a specialized wrapper around ‘replext_t4_c1.1’ designed to replicate and extend the simulation results from Table 4 cell 2.1 of the paper by Dwivedi et al. (2017). The default parameters are modified to align with the Poisson distribution scenarios as described in the paper. Adjusting the parameters enables the extension of these results.

Usage

replext_t4_c2.1(
  rdist = "rpois",
  par1_1 = 5,
  par2_1 = NULL,
  par1_2 = 10,
  par2_2 = NULL,
  n1 = c(5, 5, 10),
  n2 = c(5, 10, 10),
  n_simulations = 10000,
  nboot = 1000,
  conf.level = 0.95
)

Arguments

- **rdist**: Distribution type, with the default set to ‘rpois’ (Poisson). Other options include ‘rlnorm’ (lognormal), ‘rchisq’ (Chi-squared), and ‘rcauchy’ (Cauchy).
- **par1_1**: First parameter for the first group’s distribution, default is 5 for Poisson’s lambda.
- **par2_1**: Second parameter for the first group’s distribution, typically NULL for Poisson.
- **par1_2**: First parameter for the second group’s distribution, default is 10 for Poisson’s lambda.
- **par2_2**: Second parameter for the second group’s distribution, typically NULL for Poisson.
- **n1**: Vector of sample sizes for the first group.
- **n2**: Vector of sample sizes for the second group, must be the same length as n1.
- **n_simulations**: Number of simulations to run, default is 10,000.
- **nboot**: Number of bootstrap samples, default is 1000.
- **conf.level**: Confidence level for calculating p-value thresholds, default is 0.95.
Value

A data frame with columns for each sample size pair (n1, n2) and the proportions of significant p-values for each test (ST, WT, NPBTT, WRST, PTTa, PTTe).

Note

When using rlnorm (lognormal distribution), 'par1' represents 'meanlog' (the mean of the logarithms) and 'par2' represents 'sdlog' (the standard deviation of the logarithms). For rpois (Poisson distribution), 'par1' is 'lambda' (the rate parameter). In the case of rchisq (Chi-squared distribution), 'par1' is 'df' (degrees of freedom) and 'par2' is 'ncp' (non-centrality parameter). Lastly, for rcauchy (Cauchy distribution), 'par1' is the 'location' parameter and 'par2' is the 'scale' parameter.

References


Examples

replext_t4_c2.1(n1 = c(10), n2 = c(10),n_simulations = 1)

Replext_t4_c3.1 Replicate and Extend Simulation Results from Table 4 Cell 3.1

Description

This function is a specialized wrapper around 'replext_t4_c1.1' intended to replicate and extend the simulation results from Table 4 cell 3.1 of the paper by Dwivedi et al. (2017). The default parameters are configured to match the Chi-squared distribution scenarios as detailed in the paper. Adjusting these parameters allows users to extend these results further.

Usage

replext_t4_c3.1(
  rdist = "rchisq",
  par1_1 = 3,
  par2_1 = 0,
  par1_2 = 6,
  par2_2 = 0,
  n1 = c(5, 5, 10),
  n2 = c(5, 10, 10),
  n_simulations = 10000,
  nboot = 1000,
  conf.level = 0.95
)
Arguments

- **rdist**: Distribution type, with the default set to 'rchisq' (Chi-squared). Other options include 'rlnorm' (lognormal), 'rpois' (Poisson), and 'rcauchy' (Cauchy).
- **par1_1**: First parameter for the first group’s distribution, default is 3 for Chi-squared’s degrees of freedom (df).
- **par2_1**: Second parameter for the first group’s distribution, typically 0 for Chi-squared.
- **par1_2**: First parameter for the second group’s distribution, default is 6 for Chi-squared’s degrees of freedom (df).
- **par2_2**: Second parameter for the second group’s distribution, typically 0 for Chi-squared.
- **n1**: Vector of sample sizes for the first group.
- **n2**: Vector of sample sizes for the second group, must be the same length as n1.
- **n_simulations**: Number of simulations to run, default is 10,000.
- **nboot**: Number of bootstrap samples, default is 1000.
- **conf.level**: Confidence level for calculating p-value thresholds, default is 0.95.

Value

A data frame with columns for each sample size pair (n1, n2) and the proportions of significant p-values for each test (ST, WT, NPBTT, WRST, PTTa, PTTe).

Note

When using rlnorm (lognormal distribution), 'par1' represents 'meanlog' (the mean of the logarithms) and 'par2' represents 'sdlog' (the standard deviation of the logarithms). For rpois (Poisson distribution), 'par1' is 'lambda' (the rate parameter). In the case of rchisq (Chi-squared distribution), 'par1' is 'df' (degrees of freedom) and 'par2' is 'ncp' (non-centrality parameter). Lastly, for rcauchy (Cauchy distribution), 'par1' is the 'location' parameter and 'par2' is the 'scale' parameter.

References


Examples

replext_t4_c3.1(n1 = c(10), n2 = c(10), n_simulations = 1)
Replicate and Extend Simulation Results from Table 4 Cell 4.1

Description

This function is a specialized wrapper around 'replext_t4_c1.1', tailored to replicate and extend the simulation results from Table 4 cell 4.1 of the paper by Dwivedi et al. (2017). It sets the default parameters to correspond with the lognormal distribution scenarios for this specific cell, allowing for both replication and extension of the results.

Usage

replext_t4_c4.1(  
  rdist = "rlnorm",  
  par1_1 = 1,  
  par2_1 = 0.6,  
  par1_2 = 3,  
  par2_2 = 4,  
  n1 = c(5, 5, 10),  
  n2 = c(5, 10, 10),  
  n_simulations = 10000,  
  nboot = 1000,  
  conf.level = 0.95  
)

Arguments

rdist Distribution type, with the default set to 'rlnorm' (lognormal). Other options include 'rpois' (Poisson), 'rchisq' (Chi-squared), and 'rcauchy' (Cauchy).
par1_1 First parameter (meanlog) for the first group’s distribution, default is 1.
par2_1 Second parameter (sdlog) for the first group’s distribution, default is 0.6.
par1_2 First parameter (meanlog) for the second group’s distribution, default is 3.
par2_2 Second parameter (sdlog) for the second group’s distribution, default is 4.
n1 Vector of sample sizes for the first group.
n2 Vector of sample sizes for the second group, must be the same length as n1.
n_simulations Number of simulations to run, default is 10,000.
nboot Number of bootstrap samples, default is 1000.
conf.level Confidence level for calculating p-value thresholds, default is 0.95.

Value

A data frame with columns for each sample size pair (n1, n2) and the proportions of significant p-values for each test (ST, WT, NPBTT, WRST, PTTa, PTTe).
Note

When using rlnorm (lognormal distribution), 'par1' represents 'meanlog' (the mean of the logarithms) and 'par2' represents 'sdlog' (the standard deviation of the logarithms). For rpois (Poisson distribution), 'par1' is 'lambda' (the rate parameter). In the case of rchisq (Chi-squared distribution), 'par1' is 'df' (degrees of freedom) and 'par2' is 'ncp' (non-centrality parameter). Lastly, for rcauchy (Cauchy distribution), 'par1' is the 'location' parameter and 'par2' is the 'scale' parameter.

References


Examples

replext_t4_c4.1(n1 = c(10), n2 = c(10), n_simulations = 1)

---

replext_t4_c5.1  Replicate and Extend Simulation Results from Table 4 Cell 5.1

Description

This function is a specialized version of 'replext_t4_c4.1', designed to replicate and extend the simulation results from Table 4 cell 5.1 of the paper by Dwivedi et al. (2017). It adjusts the default parameters to match the Cauchy distribution scenarios as described in this particular cell, facilitating both replication and extension of these results.

Usage

replext_t4_c5.1(
  rdist = "rcauchy",
  par1_1 = 5,
  par2_1 = 2,
  par1_2 = 10,
  par2_2 = 4,
  n1 = c(5, 5, 10),
  n2 = c(5, 10, 10),
  n_simulations = 10000,
  nboot = 1000,
  conf.level = 0.95
)
Arguments

- **rdist**: Distribution type, with the default set to ‘rcauchy’ (Cauchy). Other options include ‘rlnorm’ (lognormal), ‘rpois’ (Poisson), and ‘rchisq’ (Chi-squared).
- **par1_1**: First parameter (location) for the first group’s distribution, default is 5.
- **par2_1**: Second parameter (scale) for the first group’s distribution, default is 2.
- **par1_2**: First parameter (location) for the second group’s distribution, default is 10.
- **par2_2**: Second parameter (scale) for the second group’s distribution, default is 4.
- **n1**: Vector of sample sizes for the first group.
- **n2**: Vector of sample sizes for the second group, must be the same length as n1.
- **n_simulations**: Number of simulations to run, default is 10,000.
- **nboot**: Number of bootstrap samples, default is 1000.
- **conf.level**: Confidence level for calculating p-value thresholds, default is 0.95.

Value

A data frame with columns for each sample size pair (n1, n2) and the proportions of significant p-values for each test (ST, WT, NPBTT, WRST, PTTa, PTTe).

Note

When using rlnorm (lognormal distribution), ‘par1’ represents ‘meanlog’ (the mean of the logarithms) and ‘par2’ represents ‘sdlog’ (the standard deviation of the logarithms). For rpois (Poisson distribution), ‘par1’ is ‘lambda’ (the rate parameter). In the case of rchisq (Chi-squared distribution), ‘par1’ is ‘df’ (degrees of freedom) and ‘par2’ ‘ncp’ (non-centrality parameter). Lastly, for rcauchy (Cauchy distribution), ‘par1’ is the ’location’ parameter and ‘par2’ is the ’scale’ parameter.

References


Examples

replext_t4_c5.1(n1 = c(10), n2 = c(10), n_simulations = 1)
Description

This function, a specialized variant of `replext_t4_c1.1`, is designed to replicate and extend the simulation results from Table 4 cell 6.1 of the paper by Dwivedi et al. (2017). It employs different distributions for the two groups, using Chi-squared and Poisson distributions respectively, in line with the specific cell conditions.

Usage

```r
replext_t4_c6.1(
  rdist = c("rchisq", "rpois"),
  par1_1 = 6,
  par2_1 = 0,
  par1_2 = 10,
  par2_2 = NULL,
  n1 = c(5, 5, 10),
  n2 = c(5, 10, 10),
  n_simulations = 10000,
  nboot = 1000,
  conf.level = 0.95
)
```

Arguments

- `rdist`: Vector of distribution types, with the defaults set to 'rchisq' (Chi-squared) for the first group and 'rpois' (Poisson) for the second group. Other options include 'rlnorm' (lognormal) and 'rcauchy' (Cauchy).
- `par1_1`: First parameter for the first group’s distribution, default is 6 for Chi-squared’s degrees of freedom.
- `par2_1`: Second parameter for the first group’s distribution, typically 0 for Chi-squared.
- `par1_2`: First parameter for the second group’s distribution, default is 10 for Poisson’s lambda.
- `par2_2`: Second parameter for the second group’s distribution, typically NULL for Poisson.
- `n1`: Vector of sample sizes for the first group.
- `n2`: Vector of sample sizes for the second group, must be the same length as n1.
- `n_simulations`: Number of simulations to run, default is 10,000.
- `nboot`: Number of bootstrap samples, default is 1000.
- `conf.level`: Confidence level for calculating p-value thresholds, default is 0.95.
A data frame with columns for each sample size pair (n1, n2) and the proportions of significant p-values for each test (ST, WT, NPBTT, WRST, PTTa, PTTe).

Note

When using rlnorm (lognormal distribution), 'par1' represents 'meanlog' (the mean of the logarithms) and 'par2' represents 'sdlog' (the standard deviation of the logarithms). For rpois (Poisson distribution), 'par1' is 'lambda' (the rate parameter). In the case of rchisq (Chi-squared distribution), 'par1' is 'df' (degrees of freedom) and 'par2' is typically 0 as 'ncp' (non-centrality parameter) is not often used. Lastly, for rcauchy (Cauchy distribution), 'par1' is the 'location' parameter and 'par2' is the 'scale' parameter.

References


Examples

```r
replext_t4_c6.1(n1 = c(10), n2 = c(10), n_simulations = 1)
```

---

**replext_t4_c7.1  Replicate and Extend Simulation Results from Table 4 Cell 7.1**

**Description**

This function is a customized version of 'replext_t4_c1.1', created to replicate and extend the simulation results from Table 4 cell 7.1 of the paper by Dwivedi et al. (2017). It is configured to use different distributions for each group, specifically a lognormal distribution for the first group and a Chi-squared distribution for the second group, aligning with the specific cell conditions.

**Usage**

```r
replext_t4_c7.1(
  rdist = c("rlnorm", "rchisq"),
  par1_1 = 1,
  par2_1 = 0.6,
  par1_2 = 6,
  par2_2 = 0,
  n1 = c(5, 5, 10),
  n2 = c(5, 10, 10),
  n_simulations = 10000,
  nboot = 1000,
  conf.level = 0.95
)
```
Arguments

rdist 
Vector of distribution types, with the defaults set to 'rlnorm' (lognormal) for the first group and 'rchisq' (Chi-squared) for the second group. Other options include 'rpois' (Poisson) and 'rcauchy' (Cauchy).

par1_1 
First parameter (meanlog) for the first group’s lognormal distribution, default is 1.

par2_1 
Second parameter (sdlog) for the first group’s lognormal distribution, default is 0.6.

par1_2 
First parameter (df) for the second group’s Chi-squared distribution, default is 6.

par2_2 
Second parameter for the second group’s Chi-squared distribution, typically 0.

n1 
Vector of sample sizes for the first group.

n2 
Vector of sample sizes for the second group, must be the same length as n1.

n_simulations 
Number of simulations to run, default is 10,000.

nboot 
Number of bootstrap samples, default is 1000.

conf.level 
Confidence level for calculating p-value thresholds, default is 0.95.

Value

A data frame with columns for each sample size pair (n1, n2) and the proportions of significant p-values for each test (ST, WT, NPBTT, WRST, PTTa, PTTe).

Note

When using rlnorm (lognormal distribution), 'par1' represents 'meanlog' (the mean of the logarithms) and 'par2' represents 'sdlog' (the standard deviation of the logarithms). For rpois (Poisson distribution), 'par1' is 'lambda' (the rate parameter). In the case of rchisq (Chi-squared distribution), 'par1' is 'df' (degrees of freedom) and 'par2' is typically 0 as 'ncp' (non-centrality parameter) is not often used. Lastly, for rcauchy (Cauchy distribution), 'par1' is the 'location' parameter and 'par2' is the 'scale' parameter.

References


Examples

replext_t4_c7.1(n1 = c(10), n2 = c(10), n_simulations = 1)
Description

This function aims to replicate and extend the simulation results from Table 5 cell 1.1 of the paper by Dwivedi et al. (2017) for paired distributions with the option to use either normal or skew normal distributions. It allows specifying means, standard deviations, skewness, and correlation for two paired distributions.

Usage

```r
replext_t5_c1.1(
  M1 = 5,
  S1 = 1,
  M2 = 5,
  S2 = 1,
  Sk1 = 0,
  Sk2 = 0,
  correl = 0.8,
  n = c(3, 4, 5, 6, 7, 8, 9, 10, 15, 25),
  n_simulations = 10000,
  nboot = 1000,
  conf.level = 0.95
)
```

Arguments

- **M1**: Mean for the first group, default is 5.
- **S1**: Standard deviation for the first group, default is 1.
- **M2**: Mean for the second group, default is 5.
- **S2**: Standard deviation for the second group, default is 1.
- **Sk1**: Skewness parameter for the first group, default is 0 (normal distribution).
- **Sk2**: Skewness parameter for the second group, default is 0 (normal distribution).
- **correl**: Correlation between the two groups, default is 0.8.
- **n**: Vector of sample sizes for the paired groups.
- **n_simulations**: Number of simulations to run, default is 10,000.
- **nboot**: Number of bootstrap samples, default is 1000.
- **conf.level**: Confidence level for calculating p-value thresholds, default is 0.95.

Value

A data frame with columns for each sample size and the proportions of significant p-values for each test (PT, NPBTT, WRST, PTT).
References


Examples

```r
replext_t5_c1.1(n = c(10), n_simulations = 1)
```

```
replext_t5_c1.2
Replicate and Extend Simulation Results for Paired Distributions with Different Variances
```

Description

This function is a wrapper around `replext_t5_c1.1` and is specifically aimed at replicating and extending simulation results from Table 5 cell 1.2 of the paper by Dwivedi et al. (2017). It is tailored for paired distributions with the option to use either normal or skew normal distributions, differing in standard deviations between the two groups.

Usage

```r
replext_t5_c1.2(  
  M1 = 5,  
  S1 = 1,  
  M2 = 5,  
  S2 = 3,  
  Sk1 = 0,  
  Sk2 = 0,  
  correl = 0.8,  
  n = c(3, 4, 5, 6, 7, 8, 9, 10, 15, 25),  
  n_simulations = 10000,  
  nboot = 1000,  
  conf.level = 0.95  
)
```

Arguments

- `M1`: Mean for the first group, default is 5.
- `S1`: Standard deviation for the first group, default is 1.
- `M2`: Mean for the second group, default is 5.
- `S2`: Standard deviation for the second group, default is 3.
- `Sk1`: Skewness parameter for the first group, default is 0 (normal distribution).
- `Sk2`: Skewness parameter for the second group, default is 0 (normal distribution).
correl  Correlation between the two groups, default is 0.8.

n  Vector of sample sizes for the paired groups.
n_simulations  Number of simulations to run, default is 10,000.
nboot  Number of bootstrap samples, default is 1000.
conf.level  Confidence level for calculating p-value thresholds, default is 0.95.

Value

A data frame with columns for each sample size and the proportions of significant p-values for each test (PT, NPBTT, WRST, PTT), similar to 'replext_t5_c1.1' but with differing standard deviations for the groups.

References


Examples

```r
replext_t5_c1.2(n = c(10), n_simulations = 1)
```

```
replext_t5_c1.3
Repackage and Extend Simulation Results for Paired Distributions with Skewness

Description

This function, serving as a wrapper around 'replext_t5_c1.1', is designed to replicate and extend the simulation results from Table 5 cell 1.3 of the paper by Dwivedi et al. (2017). It focuses on paired distributions featuring both normal and skew normal distributions, with specified skewness parameters for each group.

Usage

```r
replext_t5_c1.3(
  M1 = 5,
  S1 = 1,
  M2 = 5,
  S2 = 1,
  Sk1 = 0.5,
  Sk2 = 0.5,
  correl = 0.8,
  n = c(3, 4, 5, 6, 7, 8, 9, 10, 15, 25),
  n_simulations = 10000,
  nboot = 1000,
  conf.level = 0.95
)
```
Arguments

- **M1**: Mean for the first group, default is 5.
- **S1**: Standard deviation for the first group, default is 1.
- **M2**: Mean for the second group, default is 5.
- **S2**: Standard deviation for the second group, default is 1.
- **Sk1**: Skewness parameter for the first group, default is 0.5.
- **Sk2**: Skewness parameter for the second group, default is 0.5.
- **correl**: Correlation between the two groups, default is 0.8.
- **n**: Vector of sample sizes for the paired groups.
- **n_simulations**: Number of simulations to run, default is 10,000.
- **nboot**: Number of bootstrap samples, default is 1000.
- **conf.level**: Confidence level for calculating p-value thresholds, default is 0.95.

Value

A data frame with columns for each sample size and the proportions of significant p-values for each test (PT, NPBTT, WRST, PTT), similar to 'replext_t5_c1.1' but with skewness parameters for the groups.

References


Examples

replext_t5_c1.3(n = c(10), n_simulations = 1)
Usage

replext_t5_c2.1(
  M1 = 5,
  S1 = 1,
  M2 = 5,
  S2 = 3,
  Sk1 = 0.5,
  Sk2 = 0.5,
  correl = 0.8,
  n = c(3, 4, 5, 6, 7, 8, 9, 10, 15, 25),
  n_simulations = 10000,
  nboot = 1000,
  conf.level = 0.95
)

Arguments

M1  Mean for the first group, default is 5.
S1  Standard deviation for the first group, default is 1.
M2  Mean for the second group, default is 5.
S2  Standard deviation for the second group, default is 3.
Sk1 Skewness parameter for the first group, default is 0.5 (indicating skew normal distribution).
Sk2 Skewness parameter for the second group, default is 0.5 (indicating skew normal distribution).
correl Correlation between the two groups, default is 0.8.
n  Vector of sample sizes for the paired groups.
n_simulations Number of simulations to run, default is 10,000.
nboot Number of bootstrap samples, default is 1000.
conf.level Confidence level for calculating p-value thresholds, default is 0.95.

Value

A data frame with columns for each sample size and the proportions of significant p-values for each test (PT, NPBTT, WRST, PTT), similar to ‘replext_t5_c1.1’ but with variations in standard deviations and skewness.

References


Examples

replext_t5_c2.1(n = c(10), n_simulations = 1)
Replicate and Extend Simulation Results for Paired Distributions with Different Skewness Levels

Description

This function is a specialized version of `replext_t5_c1.1`, tailored to replicate and extend the simulation results from Table 5 cell 2.2 of the paper by Dwivedi et al. (2017). It is designed for paired distributions that exhibit both normal and skew normal characteristics, with different skewness parameters for each group while maintaining the same means and standard deviations.

Usage

```r
replext_t5_c2.2(
  M1 = 5,
  S1 = 1,
  M2 = 5,
  S2 = 1,
  Sk1 = 0.2,
  Sk2 = 0.8,
  correl = 0.8,
  n = c(3, 4, 5, 6, 7, 8, 9, 10, 15, 25),
  n_simulations = 10000,
  nboot = 1000,
  conf.level = 0.95
)
```

Arguments

- **M1**: Mean for the first group, default is 5.
- **S1**: Standard deviation for the first group, default is 1.
- **M2**: Mean for the second group, default is 5.
- **S2**: Standard deviation for the second group, default is 1.
- **Sk1**: Skewness parameter for the first group, default is 0.2.
- **Sk2**: Skewness parameter for the second group, default is 0.8.
- **correl**: Correlation between the two groups, default is 0.8.
- **n**: Vector of sample sizes for the paired groups.
- **n_simulations**: Number of simulations to run, default is 10,000.
- **nboot**: Number of bootstrap samples, default is 1000.
- **conf.level**: Confidence level for calculating p-value thresholds, default is 0.95.

Value

A data frame with columns for each sample size and the proportions of significant p-values for each test (PT, NPBTT, WRST, PTT), with a focus on differing skewness levels between the two groups.
**References**

**Examples**
replext_t5_c2.2(n = c(10), n_simulations = 1)

---

**replext_t5_c2.3** Replicate and Extend Simulation Results for Paired Distributions with Varied Skewness and Standard Deviations

**Description**
replext_t5_c2.3 is a wrapper function around replext_t5_c1.1, specifically designed to replicate and extend the simulation results from Table 5 cell 2.3 of the paper by Dwivedi et al. (2017). It focuses on paired distributions that exhibit skew normal characteristics with differing skewness parameters and standard deviations for each group.

**Usage**
```r
replext_t5_c2.3(
  M1 = 5,
  S1 = 1,
  M2 = 5,
  S2 = 3,
  Sk1 = 0.2,
  Sk2 = 0.8,
  correl = 0.8,
  n = c(3, 4, 5, 6, 7, 8, 9, 10, 15, 25),
  n_simulations = 10000,
  nboot = 1000,
  conf.level = 0.95
)
```

**Arguments**
- **M1**: Mean for the first group, default is 5.
- **S1**: Standard deviation for the first group, default is 1.
- **M2**: Mean for the second group, default is 5.
- **S2**: Standard deviation for the second group, default is 3.
- **Sk1**: Skewness parameter for the first group, default is 0.2.
- **Sk2**: Skewness parameter for the second group, default is 0.8.
correl  Correlation between the two groups, default is 0.8.
n  Vector of sample sizes for the paired groups.
n_simulations  Number of simulations to run, default is 10,000.
nboot  Number of bootstrap samples, default is 1000.
conf.level  Confidence level for calculating p-value thresholds, default is 0.95.

Value

A data frame with columns for each sample size and the proportions of significant p-values for each test (PT, NPBTT, WRST, PTT), focusing on variations in skewness and standard deviations between the groups.

References


Examples

replext_t5_c2.3(n = c(10), n_simulations = 1)
Arguments

- **M1**: Mean for the first group, default is 5.
- **S1**: Standard deviation for the first group, default is 1.
- **M2**: Mean for the second group, default is 7.
- **S2**: Standard deviation for the second group, default is 1.
- **Sk1**: Skewness parameter for the first group, default is 0 (normal distribution).
- **Sk2**: Skewness parameter for the second group, default is 0 (normal distribution).
- **correl**: Correlation between the two groups, default is 0.8.
- **n**: Vector of sample sizes for the paired groups.
- **n_simulations**: Number of simulations to run, default is 10,000.
- **nboot**: Number of bootstrap samples, default is 1000.
- **conf.level**: Confidence level for calculating p-value thresholds, default is 0.95.

Value

A data frame with columns for each sample size and the proportions of significant p-values for each test (PT, NPBTT, WRST, PTT), similar to ’replext_t5_c1.1’ but with differing standard deviations for the groups.

References


Examples

```r
replext_t6_c1.1(n = c(10), n_simulations = 1)
```

---

**replext_t6_c1.2**  
Replicate and Extend Statistical Power Simulation Results for Paired Distributions with Different Variances

Description

This function is a wrapper around ’replext_t5_c1.1’ and is specifically aimed at replicating and extending statistical power simulation results from Table 6 cell 1.2 of the paper by Dwivedi et al. (2017).
Usage

replext_t6_c1.2(
  M1 = 5,
  S1 = 1,
  M2 = 7,
  S2 = 3,
  Sk1 = 0,
  Sk2 = 0,
  correl = 0.8,
  n = c(3, 4, 5, 6, 7, 8, 9, 10, 15, 25, 50, 100),
  n_simulations = 10000,
  nboot = 1000,
  conf_level = 0.95
)

Arguments

M1          Mean for the first group, default is 5.
S1          Standard deviation for the first group, default is 1.
M2          Mean for the second group, default is 7.
S2          Standard deviation for the second group, default is 3.
Sk1         Skewness parameter for the first group, default is 0 (normal distribution).
Sk2         Skewness parameter for the second group, default is 0 (normal distribution).
correl      Correlation between the two groups, default is 0.8.
n           Vector of sample sizes for the paired groups.
n_simulations Number of simulations to run, default is 10,000.
nboot       Number of bootstrap samples, default is 1000.
conf_level  Confidence level for calculating p-value thresholds, default is 0.95.

Value

A data frame with columns for each sample size and the proportions of significant p-values for each test (PT, NPBTT, WRST, PTT), similar to `replext_t5_c1.1` but with differing standard deviations for the groups.

References


Examples

replext_t6_c1.2(n = c(10), n_simulations = 1)
Description

This function, serving as a wrapper around 'replext_t5_c1.1', is designed to replicate and extend the statistical power simulation results from Table 6 cell 1.3 of the paper by Dwivedi et al. (2017).

Usage

```r
replext_t6_c1.3(  
  M1 = 5,  
  S1 = 1,  
  M2 = 7,  
  S2 = 1,  
  Sk1 = 0.5,  
  Sk2 = 0.5,  
  correl = 0.8,  
  n = c(3, 4, 5, 6, 7, 8, 9, 10, 15, 25, 50, 100),  
  n_simulations = 10000,  
  nboot = 1000,  
  conf.level = 0.95  
)
```

Arguments

- `M1`: Mean for the first group, default is 5.
- `S1`: Standard deviation for the first group, default is 1.
- `M2`: Mean for the second group, default is 7.
- `S2`: Standard deviation for the second group, default is 1.
- `Sk1`: Skewness parameter for the first group, default is 0.5.
- `Sk2`: Skewness parameter for the second group, default is 0.5.
- `correl`: Correlation between the two groups, default is 0.8.
- `n`: Vector of sample sizes for the paired groups.
- `n_simulations`: Number of simulations to run, default is 10,000.
- `nboot`: Number of bootstrap samples, default is 1000.
- `conf.level`: Confidence level for calculating p-value thresholds, default is 0.95.

Value

A data frame with columns for each sample size and the proportions of significant p-values for each test (PT, NPBTT, WRST, PTT), similar to 'replext_t5_c1.1' but with skewness parameters for the groups.
References


Examples

replext_t6_c1.3(n = c(10), n_simulations = 1)

---

replext_t6_c2.1

Replicate and Extend Statistical Power Simulation Results for Paired Distributions with Skewness and Different Variances

Description

This function is a wrapper around ‘replext_t5_c1.1’, targeting the replication and extension of statistical power simulation results from Table 6 cell 2.1 of the paper by Dwivedi et al. (2017).

Usage

replext_t6_c2.1(
  M1 = 5,
  S1 = 1,
  M2 = 7,
  S2 = 3,
  Sk1 = 0.5,
  Sk2 = 0.5,
  correl = 0.8,
  n = c(3, 4, 5, 6, 7, 8, 9, 10, 15, 25, 50, 100),
  n_simulations = 10000,
  nboot = 1000,
  conf.level = 0.95
)

Arguments

  M1           Mean for the first group, default is 5.
  S1           Standard deviation for the first group, default is 1.
  M2           Mean for the second group, default is 7.
  S2           Standard deviation for the second group, default is 3.
  Sk1          Skewness parameter for the first group, default is 0.5 (indicating skew normal distribution).
  Sk2          Skewness parameter for the second group, default is 0.5 (indicating skew normal distribution).
Description

This function is a specialized version of `replext_t5_c1.1`, tailored to replicate and extend the statistical power simulation results from Table 6 cell 2.2 of the paper by Dwivedi et al. (2017).

Usage

```r
replext_t6_c2.2(
  M1 = 5,
  S1 = 1,
  M2 = 7,
  S2 = 1,
  Sk1 = 0.2,
  Sk2 = 0.8,
  correl = 0.8,
  n = c(3, 4, 5, 6, 7, 8, 9, 10, 15, 25, 50, 100),
  n_simulations = 10000,
  nboot = 1000,
  conf.level = 0.95
)
```

Value

A data frame with columns for each sample size and the proportions of significant p-values for each test (PT, NPBTT, WRST, PTT), similar to 'replext_t5_c1.1' but with variations in standard deviations and skewness.

References


Examples

```r
replext_t6_c2.1(n = c(10), n_simulations = 1)
```
Arguments

M1  Mean for the first group, default is 5.
S1  Standard deviation for the first group, default is 1.
M2  Mean for the second group, default is 7.
S2  Standard deviation for the second group, default is 1.
Sk1 Skewness parameter for the first group, default is 0.2.
Sk2 Skewness parameter for the second group, default is 0.8.
correl  Correlation between the two groups, default is 0.8.
n  Vector of sample sizes for the paired groups.
n_simulations  Number of simulations to run, default is 10,000.
nboot  Number of bootstrap samples, default is 1000.
conf.level  Confidence level for calculating p-value thresholds, default is 0.95.

Value

A data frame with columns for each sample size and the proportions of significant p-values for each test (PT, NPBTT, WRST, PTT), with a focus on differing skewness levels between the two groups.

References


Examples

replext_t6_c2.2(n = c(10), n_simulations = 1)
Usage

replext_t6_c2.3(  
  M1 = 5,  
  S1 = 1,  
  M2 = 7,  
  S2 = 3,  
  Sk1 = 0.2,  
  Sk2 = 0.8,  
  correl = 0.8,  
  n = c(3, 4, 5, 6, 7, 8, 9, 10, 15, 25, 50, 100),  
  n_simulations = 10000,  
  nboot = 1000,  
  conf.level = 0.95  
)

Arguments

- **M1**: Mean for the first group, default is 5.
- **S1**: Standard deviation for the first group, default is 1.
- **M2**: Mean for the second group, default is 7.
- **S2**: Standard deviation for the second group, default is 3.
- **Sk1**: Skewness parameter for the first group, default is 0.2.
- **Sk2**: Skewness parameter for the second group, default is 0.8.
- **correl**: Correlation between the two groups, default is 0.8.
- **n**: Vector of sample sizes for the paired groups.
- **n_simulations**: Number of simulations to run, default is 10,000.
- **nboot**: Number of bootstrap samples, default is 1000.
- **conf.level**: Confidence level for calculating p-value thresholds, default is 0.95.

Value

A data frame with columns for each sample size and the proportions of significant p-values for each test (PT, NPBT, WRST, PTT), focusing on variations in skewness and standard deviations between the groups.

References


Examples

replext_t6_c2.3(n = c(10), n_simulations = 1)
This function is a specialized wrapper around `replext_t4_c1.1` designed to replicate and extend the type I error simulation results from Table S1 cell 1.1 of the paper by Dwivedi et al. (2017).

**Usage**

```r
replext_ts1_c1.1(
  rdist = "rlnorm",
  par1_1 = 1,
  par2_1 = 0.6,
  par1_2 = 1,
  par2_2 = 0.6,
  n1 = c(5, 5, 10),
  n2 = c(5, 10, 10),
  n_simulations = 10000,
  nboot = 1000,
  conf.level = 0.95
)
```

**Arguments**

- `rdist` Distribution type, default is 'rlnorm' (lognormal). Other options are 'rpois' (Poisson), 'rchisq' (Chi-squared), and 'rcauchy' (Cauchy).
- `par1_1` First parameter for the first group's distribution, default is 1.
- `par2_1` Second parameter for the first group's distribution, default is 0.6.
- `par1_2` First parameter for the second group's distribution, default is 1.
- `par2_2` Second parameter for the second group's distribution, default is 0.6.
- `n1` Vector of sample sizes for the first group.
- `n2` Vector of sample sizes for the second group, must be the same length as n1.
- `n_simulations` Number of simulations to run, default is 10,000.
- `nboot` Number of bootstrap samples, default is 1000.
- `conf.level` Confidence level for calculating p-value thresholds, default is 0.95.

**Value**

A data frame with columns for each sample size pair (n1, n2) and the proportions of significant p-values for each test (ST, WT, NPBTT, WRST, PTTa, PTTe).
Note

When using rlnorm (lognormal distribution), 'par1' represents 'meanlog' (the mean of the logarithms) and 'par2' represents 'sdlog' (the standard deviation of the logarithms). For rpois (Poisson distribution), 'par1' is 'lambda' (the rate parameter). In the case of rchisq (Chi-squared distribution), 'par1' is 'df' (degrees of freedom) and 'par2' is 'ncp' (non-centrality parameter). Lastly, for rcauchy (Cauchy distribution), 'par1' is the 'location' parameter and 'par2' is the 'scale' parameter.

References


Examples

replext_ts1_c1.1(n1 = c(10), n2 = c(10), n_simulations = 1)

---

replext_ts1_c2.1  Replicate and Extend Simulation Results from Table S1 Cell 2.1

Description

This function is a specialized wrapper around 'replext_t4_c1.1' designed to replicate and extend the type I error simulation results from Table S1 cell 2.1 of the paper by Dwivedi et al. (2017). The default parameters are modified to align with the Poisson distribution scenarios as described in the paper. Adjusting the parameters enables the extension of these results.

Usage

replext_ts1_c2.1(  
  rdist = "rpois",  
  par1_1 = 5,  
  par2_1 = NULL,  
  par1_2 = 5,  
  par2_2 = NULL,  
  n1 = c(5, 5, 10),  
  n2 = c(5, 10, 10),  
  n_simulations = 10000,  
  nboot = 1000,  
  conf.level = 0.95  
)
Arguments

\textbf{rdist}    Distribution type, with the default set to 'rpois' (Poisson). Other options include 'rlnorm' (lognormal), 'rchisq' (Chi-squared), and 'rcauchy' (Cauchy).

\textbf{par1}    First parameter for the first group’s distribution, default is 5 for Poisson’s lambda.

\textbf{par2}    Second parameter for the first group’s distribution, typically NULL for Poisson.

\textbf{par1}    First parameter for the second group’s distribution, default is 5 for Poisson’s lambda.

\textbf{par2}    Second parameter for the second group’s distribution, typically NULL for Poisson.

\textbf{n1}    Vector of sample sizes for the first group.

\textbf{n2}    Vector of sample sizes for the second group, must be the same length as \textbf{n1}.

\textbf{n_simulations}    Number of simulations to run, default is 10,000.

\textbf{nboot}    Number of bootstrap samples, default is 1000.

\textbf{conf.level}    Confidence level for calculating p-value thresholds, default is 0.95.

Value

A data frame with columns for each sample size pair (n1, n2) and the proportions of significant p-values for each test (ST, WT, NPBTT, WRST, PTTa, PTTe).

Note

When using rlnorm (lognormal distribution), 'par1' represents 'meanlog' (the mean of the logarithms) and 'par2' represents 'sdlog' (the standard deviation of the logarithms). For rpois (Poisson distribution), 'par1' is 'lambda' (the rate parameter). In the case of rchisq (Chi-squared distribution), 'par1' is 'df' (degrees of freedom) and 'par2' is 'ncp' (non-centrality parameter). Lastly, for rcauchy (Cauchy distribution), 'par1' is the 'location' parameter and 'par2' is the 'scale' parameter.

References


Examples

replext_ts1_c2.1(n1 = c(10), n2 = c(10), n_simulations = 1)
Replext Ts1_C3.1 Replicate and Extend Simulation Results from Table S1 Cell 3.1

Description
This function is a specialized wrapper around 'replext_t4_c1.1' intended to replicate and extend the type I error simulation results from Table S1 cell 3.1 of the paper by Dwivedi et al. (2017). The default parameters are configured to match the Chi-squared distribution scenarios as detailed in the paper. Adjusting these parameters allows users to extend these results further.

Usage
replext_ts1_c3.1(
  rdist = "rchisq",
  par1_1 = 3,
  par2_1 = 0,
  par1_2 = 3,
  par2_2 = 0,
  n1 = c(5, 5, 10),
  n2 = c(5, 10, 10),
  n_simulations = 10000,
  nboot = 1000,
  conf.level = 0.95
)

Arguments
rdist Distribution type, with the default set to 'rchisq' (Chi-squared). Other options include 'rlnorm' (lognormal), 'rpois' (Poisson), and 'rcauchy' (Cauchy).
par1_1 First parameter for the first group's distribution, default is 3 for Chi-squared’s degrees of freedom (df).
par2_1 Second parameter for the first group’s distribution, typically 0 for Chi-squared.
par1_2 First parameter for the second group’s distribution, default is 3 for Chi-squared’s degrees of freedom (df).
par2_2 Second parameter for the second group’s distribution, typically 0 for Chi-squared.
n1 Vector of sample sizes for the first group.
n2 Vector of sample sizes for the second group, must be the same length as n1.
n_simulations Number of simulations to run, default is 10,000.
nboot Number of bootstrap samples, default is 1000.
conf.level Confidence level for calculating p-value thresholds, default is 0.95.

Value
A data frame with columns for each sample size pair (n1, n2) and the proportions of significant p-values for each test (ST, WT, NPBTT, WRST, PTTa, PTTe).
Note

When using rlnorm (lognormal distribution), ’par1’ represents ’meanlog’ (the mean of the logarithms) and ’par2’ represents ’sdlog’ (the standard deviation of the logarithms). For rpois (Poisson distribution), ’par1’ is ’lambda’ (the rate parameter). In the case of rchisq (Chi-squared distribution), ’par1’ is ’df’ (degrees of freedom) and ’par2’ is ’ncp’ (non-centrality parameter). Lastly, for rcauchy (Cauchy distribution), ’par1’ is the ’location’ parameter and ’par2’ is the ’scale’ parameter.

References


Examples

replext_ts1_c3.1(n1 = c(10), n2 = c(10),n_simulations = 1)

replext_ts2_c1.1 Replicate and Extend Type I Error Rates for ANOVA in a Three-Sample Setting

Description

This function aims to replicate and extend the Type I error rate analysis for ANOVA (Analysis of Variance) from the supplemental tables of the paper by Dwivedi et al. (2017). It allows for the simulation of three-sample scenarios with the option to use either normal or skew normal distributions, and performs various statistical tests to assess the Type I error rates.

Usage

replext_ts2_c1.1(  
  M1 = 5,  
  S1 = 1,  
  M2 = 5,  
  S2 = 1,  
  M3 = 5,  
  S3 = 1,  
  Sk1 = NULL,  
  Sk2 = NULL,  
  Sk3 = NULL,  
  n1 = c(2, 3, 4, 5, 6, 7, 8, 9, 10, 15),  
  n2 = c(2, 3, 4, 5, 6, 7, 8, 9, 10, 15),  
  n3 = c(2, 3, 4, 5, 6, 7, 8, 9, 10, 15),  
  n_simulations = 10000,  
  nboot = 1000,  
  conf.level = 0.95  
)
Arguments

M1
Mean for the first group, default is 5.

S1
Standard deviation for the first group, default is 1.

M2
Mean for the second group, default is 5.

S2
Standard deviation for the second group, default is 1.

M3
Mean for the third group, default is 5.

S3
Standard deviation for the third group, default is 1.

Sk1
Skewness parameter for the first group, NULL implies normal distribution.

Sk2
Skewness parameter for the second group, NULL implies normal distribution.

Sk3
Skewness parameter for the third group, NULL implies normal distribution.

n1
Vector of sample sizes for the first group.

n2
Vector of sample sizes for the second group.

n3
Vector of sample sizes for the third group, must be the same length as n1 and n2.

n_simulations
Number of simulations to run, default is 10,000.

nboot
Number of bootstrap samples for the nonparametric bootstrap test, default is 1000.

conf.level
Confidence level for calculating p-value thresholds, default is 0.95.

Value

A data frame with columns for each sample size combination (n1, n2, n3) and the proportions of significant p-values for each test (ANOVA, Kruskal-Wallis, Nonparametric Bootstrap F-test, Permutation F-test).

References


Examples

replext_ts2_c1.1(n1 = c(10), n2 = c(10), n3 = c(10), n_simulations = 1)
Description

This wrapper function is designed to reproduce or extend the Type I error rate analysis for ANOVA (Analysis of Variance) in a different setting as compared to `replext_ts2_c1.1`. It utilizes different default values for the standard deviations of the second and third groups, allowing for a different simulation setup. It is part of the analysis extending the supplemental tables of the paper by Dwivedi et al. (2017).

Usage

```r
replext_ts2_c1.2(
  M1 = 5,
  S1 = 1,
  M2 = 5,
  S2 = 2,
  M3 = 5,
  S3 = 4,
  Sk1 = NULL,
  Sk2 = NULL,
  Sk3 = NULL,
  n1 = c(2, 3, 4, 5, 6, 7, 8, 9, 10, 15),
  n2 = c(2, 3, 4, 5, 6, 7, 8, 9, 10, 15),
  n3 = c(2, 3, 4, 5, 6, 7, 8, 9, 10, 15),
  n_simulations = 10000,
  nboot = 1000,
  conf.level = 0.95
)
```

Arguments

- **M1**: Mean for the first group, default is 5.
- **S1**: Standard deviation for the first group, default is 1.
- **M2**: Mean for the second group, default is 5.
- **S2**: Standard deviation for the second group, default is 2.
- **M3**: Mean for the third group, default is 5.
- **S3**: Standard deviation for the third group, default is 4.
- **Sk1**: Skewness parameter for the first group, NULL implies normal distribution.
- **Sk2**: Skewness parameter for the second group, NULL implies normal distribution.
- **Sk3**: Skewness parameter for the third group, NULL implies normal distribution.
- **n1**: Vector of sample sizes for the first group.
This function, `replext_ts2_c2.1`, extends the `replext_ts2_c1.1` function to specifically simulate scenarios under skew normal distributions. It is tailored to explore the impact of skewness on the Type I error rates in ANOVA (Analysis of Variance), contributing to the comprehensive analysis in the context of the study by Dwivedi et al. (2017). The function allows for simulations under the assumption of skewness in all three groups.
replext_ts2_c2.1

Usage

replext_ts2_c2.1(
  M1 = 5,
  S1 = 1,
  M2 = 5,
  S2 = 1,
  M3 = 5,
  S3 = 1,
  Sk1 = 0.8,
  Sk2 = 0.8,
  Sk3 = 0.8,
  n1 = c(2, 3, 4, 5, 6, 7, 8, 9, 10, 15),
  n2 = c(2, 3, 4, 5, 6, 7, 8, 9, 10, 15),
  n3 = c(2, 3, 4, 5, 6, 7, 8, 9, 10, 15),
  n_simulations = 10000,
  nboot = 1000,
  conf.level = 0.95
)

Arguments

M1 Mean for the first group, default is 5.
S1 Standard deviation for the first group, default is 1.
M2 Mean for the second group, default is 5.
S2 Standard deviation for the second group, default is 1.
M3 Mean for the third group, default is 5.
S3 Standard deviation for the third group, default is 1.
Sk1 Skewness parameter for the first group, default is 0.8.
Sk2 Skewness parameter for the second group, default is 0.8.
Sk3 Skewness parameter for the third group, default is 0.8.
n1 Vector of sample sizes for the first group.
n2 Vector of sample sizes for the second group.
n3 Vector of sample sizes for the third group, must be the same length as n1 and n2.
n_simulations Number of simulations to run, default is 10,000.
nboot Number of bootstrap samples for the nonparametric bootstrap test, default is 1000.
conf.level Confidence level for calculating p-value thresholds, default is 0.95.

Value

A data frame with results similar to those from replext_ts2_c1.1, but with the added dimension of skewness. The data frame includes columns for each sample size combination (n1, n2, n3) and the proportions of significant p-values for each test (ANOVA, Kruskal-Wallis, Nonparametric Bootstrap F-test, Permutation F-test) under skew normal distribution.
References


See Also

replext_ts2_c1.1

Examples

replext_ts2_c2.1(n1 = c(10), n2 = c(10), n3 = c(10), n_simulations = 1)

replext_ts2_c2.2

Replicate and Extend Type I Error Rates for ANOVA with Skewness and Varied Standard Deviations

Description

The replext_ts2_c2.2 function extends the replext_ts2_c1.1 function by incorporating skewness in data distributions and utilizing different default values for standard deviations in the second and third groups. This function is specifically designed to investigate the influence of skewness combined with varying standard deviations on the Type I error rates in ANOVA (Analysis of Variance). It aligns with the broader analytical goals set in the study by Dwivedi et al. (2017), offering insights into the behavior of statistical tests under these conditions.

Usage

replext_ts2_c2.2(  
  M1 = 5,  
  S1 = 1,  
  M2 = 5,  
  S2 = 2,  
  M3 = 5,  
  S3 = 4,  
  Sk1 = 0.8,  
  Sk2 = 0.8,  
  Sk3 = 0.8,  
  n1 = c(2, 3, 4, 5, 6, 7, 8, 9, 10, 15),  
  n2 = c(2, 3, 4, 5, 6, 7, 8, 9, 10, 15),  
  n3 = c(2, 3, 4, 5, 6, 7, 8, 9, 10, 15),  
  n_simulations = 10000,  
  nboot = 1000,  
  conf.level = 0.95  
)
Arguments

- **M1**: Mean for the first group, default is 5.
- **S1**: Standard deviation for the first group, default is 1.
- **M2**: Mean for the second group, default is 5.
- **S2**: Standard deviation for the second group, default is 2.
- **M3**: Mean for the third group, default is 5.
- **S3**: Standard deviation for the third group, default is 4.
- **Sk1**: Skewness parameter for the first group, default is 0.8.
- **Sk2**: Skewness parameter for the second group, default is 0.8.
- **Sk3**: Skewness parameter for the third group, default is 0.8.
- **n1**: Vector of sample sizes for the first group.
- **n2**: Vector of sample sizes for the second group.
- **n3**: Vector of sample sizes for the third group, must be the same length as n1 and n2.
- **n_simulations**: Number of simulations to run, default is 10,000.
- **nboot**: Number of bootstrap samples for the nonparametric bootstrap test, default is 1000.
- **conf.level**: Confidence level for calculating p-value thresholds, default is 0.95.

Value

A data frame with results that extend those from `replext_ts2_c1.1`, focusing on the impact of skewness and varying standard deviations. The data frame includes columns for each sample size combination (n1, n2, n3) and the proportions of significant p-values for each test (ANOVA, Kruskal-Wallis, Nonparametric Bootstrap F-test, Permutation F-test) under these specific conditions.

References


See Also

`replext_ts2_c1.1`, `replext_ts2_c2.1`

Examples

`replext_ts2_c2.2(n1 = c(10), n2 = c(10), n3 = c(10), n_simulations = 1)`
Description

The `replext_ts2_c3.1` function is designed to replicate and extend Type I error rate analysis for ANOVA (Analysis of Variance) with a specific focus on the impact of different skewness parameters across the three groups. This function is a variation of `replext_ts2_c1.1`, providing an opportunity to explore how varying degrees of skewness in each group affect the statistical inferences in ANOVA, as part of the extended analysis in the context of the study by Dwivedi et al. (2017).

Usage

```r
replext_ts2_c3.1(
  M1 = 5,
  S1 = 1,
  M2 = 5,
  S2 = 1,
  M3 = 5,
  S3 = 1,
  Sk1 = 0.8,
  Sk2 = 0.8,
  Sk3 = 1,
  n1 = c(2, 3, 4, 5, 6, 7, 8, 9, 10, 15),
  n2 = c(2, 3, 4, 5, 6, 7, 8, 9, 10, 15),
  n3 = c(2, 3, 4, 5, 6, 7, 8, 9, 10, 15),
  n_simulations = 10000,
  nboot = 1000,
  conf.level = 0.95
)
```

Arguments

- **M1**: Mean for the first group, default is 5.
- **S1**: Standard deviation for the first group, default is 1.
- **M2**: Mean for the second group, default is 5.
- **S2**: Standard deviation for the second group, default is 1.
- **M3**: Mean for the third group, default is 5.
- **S3**: Standard deviation for the third group, default is 1.
- **Sk1**: Skewness parameter for the first group, default is 0.8.
- **Sk2**: Skewness parameter for the second group, default is 0.8.
- **Sk3**: Skewness parameter for the third group, default is 1.
- **n1**: Vector of sample sizes for the first group.
Vector of sample sizes for the second group.

Vector of sample sizes for the third group, must be the same length as n1 and n2.

Number of simulations to run, default is 10,000.

Number of bootstrap samples for the nonparametric bootstrap test, default is 1000.

Confidence level for calculating p-value thresholds, default is 0.95.

Value

A data frame with results that build upon those from `replext_ts2_c1.1`. The data frame includes columns for each sample size combination (n1, n2, n3) and the proportions of significant p-values for each test (ANOVA, Kruskal-Wallis, Nonparametric Bootstrap F-test, Permutation F-test) under the specified skewness conditions for each group.

References


See Also

`replext_ts2_c1.1`

Examples

```r
replext_ts2_c3.1(n1 = c(10), n2 = c(10), n3 = c(10), n_simulations = 1)
```

Description

The `replext_ts2_c3.2` function is a modification of the `replext_ts2_c1.1` function, designed to explore the impact of both skewness and different standard deviations in a three-sample ANOVA setting. This variant maintains skewness in all groups but changes the default standard deviations for the second and third groups. It contributes to a more comprehensive understanding of Type I error rates in the context of the study by Dwivedi et al. (2017), especially under conditions of non-normality.
Usage

replext_ts2_c3.2(
    M1 = 5,
    S1 = 1,
    M2 = 5,
    S2 = 2,
    M3 = 5,
    S3 = 4,
    Sk1 = 0.8,
    Sk2 = 0.8,
    Sk3 = 1,
    n1 = c(2, 3, 4, 5, 6, 7, 8, 9, 10, 15),
    n2 = c(2, 3, 4, 5, 6, 7, 8, 9, 10, 15),
    n3 = c(2, 3, 4, 5, 6, 7, 8, 9, 10, 15),
    n_simulations = 10000,
    nboot = 1000,
    conf.level = 0.95
)

Arguments

M1  Mean for the first group, default is 5.
S1  Standard deviation for the first group, default is 1.
M2  Mean for the second group, default is 5.
S2  Standard deviation for the second group, default is 2.
M3  Mean for the third group, default is 5.
S3  Standard deviation for the third group, default is 4.
Sk1 Skewness parameter for the first group, default is 0.8.
Sk2 Skewness parameter for the second group, default is 0.8.
Sk3 Skewness parameter for the third group, default is 1.
n1  Vector of sample sizes for the first group.
n2  Vector of sample sizes for the second group.
n3  Vector of sample sizes for the third group, must be the same length as n1 and n2.
n_simulations Number of simulations to run, default is 10,000.
nboot Number of bootstrap samples for the nonparametric bootstrap test, default is 1000.
conf.level Confidence level for calculating p-value thresholds, default is 0.95.

Value

A data frame with results that extend those from replext_ts2_c1.1. This data frame includes columns for each sample size combination (n1, n2, n3) and the proportions of significant p-values for each test (ANOVA, Kruskal-Wallis, Nonparametric Bootstrap F-test, Permutation F-test), under the specific conditions of varying skewness and standard deviations.
References


See Also

replext_ts2_c1.1, replext_ts2_c3.1

Examples

replext_ts2_c3.2(n1 = c(10), n2 = c(10), n3 = c(10), n_simulations = 1)

---

replext_ts2_c4.1

Replicate and Extend Type I Error Rates for ANOVA with Skewness in Specific Sample Size Combinations

Description

The replext_ts2_c4.1 function is a specialized version of replext_ts2_c1.1, designed to analyze Type I error rates in ANOVA settings with skewness in data distributions and tailored combinations of sample sizes for each group. This function explores the impact of non-normality (skewness) and varying group sizes, thereby extending the analysis framework of the study by Dwivedi et al. (2017).

Usage

replext_ts2_c4.1(
  M1 = 5,
  S1 = 1,
  M2 = 5,
  S2 = 1,
  M3 = 5,
  S3 = 1,
  Sk1 = 0.8,
  Sk2 = 0.8,
  Sk3 = 0.8,
  n1 = c(2, 2, 2, 3, 2, 2, 3, 2, 2, 3, 2),
  n2 = c(2, 3, 3, 4, 2, 3, 4, 2, 4, 2),
  n3 = c(3, 3, 4, 3, 6, 6, 4, 7, 5, 8),
  n_simulations = 10000,
  nboot = 1000,
  conf.level = 0.95
)
Arguments

M1  Mean for the first group, default is 5.
S1  Standard deviation for the first group, default is 1.
M2  Mean for the second group, default is 5.
S2  Standard deviation for the second group, default is 1.
M3  Mean for the third group, default is 5.
S3  Standard deviation for the third group, default is 1.
Sk1 Skewness parameter for the first group, default is 0.8.
Sk2 Skewness parameter for the second group, default is 0.8.
Sk3 Skewness parameter for the third group, default is 0.8.
n1  Vector of specific sample sizes for the first group.
n2  Vector of specific sample sizes for the second group.
n3  Vector of specific sample sizes for the third group, not necessarily the same length as n1 and n2.
n_simulations Number of simulations to run, default is 10,000.
nboot Number of bootstrap samples for the nonparametric bootstrap test, default is 1000.
conf.level Confidence level for calculating p-value thresholds, default is 0.95.

Value

A data frame with results extending those from replext_ts2_c1.1, focusing on the combined effects of skewness and specific sample size configurations. The data frame includes columns for each unique sample size combination (n1, n2, n3) and the proportions of significant p-values for each test (ANOVA, Kruskal-Wallis, Nonparametric Bootstrap F-test, Permutation F-test) in these particular scenarios.

References


See Also

replext_ts2_c1.1

Examples

replext_ts2_c4.1(n1 = c(10), n2 = c(10), n3 = c(10), n_simulations = 1)
Description

replext_ts2_c4.2 is designed to explore the impact of specific combinations of sample sizes on the Type I error rates in ANOVA (Analysis of Variance) under conditions of skewness and varying standard deviations. This function extends replext_ts2_c1.1 by utilizing unique sample size combinations along with altered default standard deviations and skewness parameters. It is part of a broader analysis aimed at understanding statistical behavior in skewed and heteroscedastic scenarios, aligning with the research context provided by Dwivedi et al. (2017).

Usage

replext_ts2_c4.2(
  M1 = 5,
  S1 = 1,
  M2 = 5,
  S2 = 2,
  M3 = 5,
  S3 = 4,
  Sk1 = 0.8,
  Sk2 = 0.8,
  Sk3 = 0.8,
  n1 = c(2, 2, 2, 3, 2, 3, 2, 3, 2),
  n2 = c(2, 3, 4, 2, 3, 4, 2, 4, 2),
  n3 = c(3, 3, 6, 6, 4, 7, 5, 8),
  n_simulations = 10000,
  nboot = 1000,
  conf.level = 0.95
)

Arguments

M1  Mean for the first group, default is 5.
S1  Standard deviation for the first group, default is 1.
M2  Mean for the second group, default is 5.
S2  Standard deviation for the second group, default is 2.
M3  Mean for the third group, default is 5.
S3  Standard deviation for the third group, default is 4.
Sk1 Skewness parameter for the first group, default is 0.8.
Sk2 Skewness parameter for the second group, default is 0.8.
Sk3 Skewness parameter for the third group, default is 0.8.
n1 Vector of sample sizes for the first group, with specific combinations.
n2 Vector of sample sizes for the second group, with specific combinations.
n3 Vector of sample sizes for the third group, with specific combinations.
n_simulations Number of simulations to run, default is 10,000.
nboot Number of bootstrap samples for the nonparametric bootstrap test, default is 1000.
conf.level Confidence level for calculating p-value thresholds, default is 0.95.

Value
A data frame with results extending those from replext_ts2_c1.1. This data frame provides insights into the Type I error rates for each test (ANOVA, Kruskal-Wallis, Nonparametric Bootstrap F-test, Permutation F-test) under the conditions of skewness, varying sample sizes, and varying standard deviations.

References

See Also
replext_ts2_c1.1

Examples
replext_ts2_c4.2(n1 = c(10), n2 = c(10), n3 = c(10), n_simulations = 1)

This function aims to replicate and extend the statistical power analysis for ANOVA (Analysis of Variance) from the supplemental tables of the paper by Dwivedi et al. (2017). It allows for the simulation of three-sample scenarios with the option to use either normal or skew normal distributions, and performs various statistical tests to assess the statistical power. The function is a wrapper around replext_ts2_c1.1.
Usage

replext_ts3_c1.1(
  M1 = 5,
  S1 = 1,
  M2 = 6,
  S2 = 1,
  M3 = 7,
  S3 = 1,
  Sk1 = NULL,
  Sk2 = NULL,
  Sk3 = NULL,
  n1 = c(2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 25, 50, 100),
  n2 = c(2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 25, 50, 100),
  n3 = c(2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 25, 50, 100),
  n_simulations = 10000,
  nboot = 1000,
  conf.level = 0.95
)

Arguments

M1  Mean for the first group, default is 5.
S1  Standard deviation for the first group, default is 1.
M2  Mean for the second group, default is 6.
S2  Standard deviation for the second group, default is 1.
M3  Mean for the third group, default is 7.
S3  Standard deviation for the third group, default is 1.
Sk1 Skewness parameter for the first group, NULL implies normal distribution.
Sk2 Skewness parameter for the second group, NULL implies normal distribution.
Sk3 Skewness parameter for the third group, NULL implies normal distribution.
n1  Vector of sample sizes for the first group.
n2  Vector of sample sizes for the second group.
n3  Vector of sample sizes for the third group, must be the same length as n1 and n2.
n_simulations  Number of simulations to run, default is 10,000.
nboot Number of bootstrap samples for the nonparametric bootstrap test, default is 1000.
conf.level Confidence level for calculating p-value thresholds, default is 0.95.

Value

A data frame with columns for each sample size combination (n1, n2, n3) and the proportions of significant p-values for each test (ANOVA, Kruskal-Wallis, Nonparametric Bootstrap F-test, Permutation F-test).
**References**


**Examples**

replext_ts3_c1.1(n1 = c(10), n2 = c(10), n3 = c(10), n_simulations = 1)

replext_ts3_c1.2

Replicate and Extend Statistical Power Analysis for ANOVA

**Description**

This function is a wrapper around replext_ts2_c1.1. The function is designed to reproduce or extend the statistical power analysis for ANOVA (Analysis of Variance) from Dwivedi et al. (2017) supplemental table 3, cell 1.2.

**Usage**

replext_ts3_c1.2(
  M1 = 5,
  S1 = 1,
  M2 = 6,
  S2 = 2,
  M3 = 7,
  S3 = 4,
  Sk1 = NULL,
  Sk2 = NULL,
  Sk3 = NULL,
  n1 = c(2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 25, 50, 100),
  n2 = c(2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 25, 50, 100),
  n3 = c(2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 25, 50, 100),
  n_simulations = 10000,
  nboot = 1000,
  conf.level = 0.95
)

**Arguments**

- **M1**: Mean for the first group, default is 5.
- **S1**: Standard deviation for the first group, default is 1.
- **M2**: Mean for the second group, default is 6.
- **S2**: Standard deviation for the second group, default is 2.
- **M3**: Mean for the third group, default is 7.
Skewness parameter for the first group, NULL implies normal distribution.

Sk2
Skewness parameter for the second group, NULL implies normal distribution.

Sk3
Skewness parameter for the third group, NULL implies normal distribution.

n1
Vector of sample sizes for the first group.

n2
Vector of sample sizes for the second group.

n3
Vector of sample sizes for the third group, must be the same length as n1 and n2.

n_simulations
Number of simulations to run, default is 10,000.

nboot
Number of bootstrap samples for the nonparametric bootstrap test, default is 1000.

conf.level
Confidence level for calculating p-value thresholds, default is 0.95.

Value
A data frame with columns for each sample size combination (n1, n2, n3) and the proportions of significant p-values for each test (ANOVA, Kruskal-Wallis, Nonparametric Bootstrap F-test, Permutation F-test).

References

See Also
replext_ts2_c1.1

Examples
replext_ts3_c1.2(n1 = c(10), n2 = c(10), n3 = c(10), n_simulations = 1)
**Usage**

```r
replext_ts3_c2.1(
    M1 = 5,
    S1 = 1,
    M2 = 6,
    S2 = 1,
    M3 = 7,
    S3 = 1,
    Sk1 = 0.8,
    Sk2 = 0.8,
    Sk3 = 0.8,
    n1 = c(2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 25, 50, 100),
    n2 = c(2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 25, 50, 100),
    n3 = c(2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 25, 50, 100),
    n_simulations = 10000,
    nboot = 1000,
    conf.level = 0.95
)
```

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>M1</code></td>
<td>Mean for the first group, default is 5.</td>
</tr>
<tr>
<td><code>S1</code></td>
<td>Standard deviation for the first group, default is 1.</td>
</tr>
<tr>
<td><code>M2</code></td>
<td>Mean for the second group, default is 6.</td>
</tr>
<tr>
<td><code>S2</code></td>
<td>Standard deviation for the second group, default is 1.</td>
</tr>
<tr>
<td><code>M3</code></td>
<td>Mean for the third group, default is 7.</td>
</tr>
<tr>
<td><code>S3</code></td>
<td>Standard deviation for the third group, default is 1.</td>
</tr>
<tr>
<td><code>Sk1</code></td>
<td>Skewness parameter for the first group, default is 0.8.</td>
</tr>
<tr>
<td><code>Sk2</code></td>
<td>Skewness parameter for the second group, default is 0.8.</td>
</tr>
<tr>
<td><code>Sk3</code></td>
<td>Skewness parameter for the third group, default is 0.8.</td>
</tr>
<tr>
<td><code>n1</code></td>
<td>Vector of sample sizes for the first group.</td>
</tr>
<tr>
<td><code>n2</code></td>
<td>Vector of sample sizes for the second group.</td>
</tr>
<tr>
<td><code>n3</code></td>
<td>Vector of sample sizes for the third group, must be the same length as <code>n1</code> and <code>n2</code>.</td>
</tr>
<tr>
<td><code>n_simulations</code></td>
<td>Number of simulations to run, default is 10,000.</td>
</tr>
<tr>
<td><code>nboot</code></td>
<td>Number of bootstrap samples for the nonparametric bootstrap test, default is 1000.</td>
</tr>
<tr>
<td><code>conf.level</code></td>
<td>Confidence level for calculating p-value thresholds, default is 0.95.</td>
</tr>
</tbody>
</table>

**Value**

A data frame with columns for each sample size combination (`n1`, `n2`, `n3`) and the proportions of significant p-values for each test (ANOVA, Kruskal-Wallis, Nonparametric Bootstrap F-test, Permutation F-test).
References


See Also

replext_ts2_c1.1

Examples

replext_ts3_c2.1(n1 = c(10), n2 = c(10), n3 = c(10), n_simulations = 1)

---

replext_ts3_c2.2 Replicate and Extend Statistical Power Analysis for ANOVA with Skewness and Varied Standard Deviations

Description

This function is a wrapper around replext_ts2_c1.1. The function is designed to reproduce or extend the statistical power analysis for ANOVA (Analysis of Variance) from Dwivedi et al. (2017) supplemental table 3, cell 2.2.

Usage

replext_ts3_c2.2(
  M1 = 5,
  S1 = 1,
  M2 = 6,
  S2 = 2,
  M3 = 7,
  S3 = 4,
  Sk1 = 0.8,
  Sk2 = 0.8,
  Sk3 = 0.8,
  n1 = c(2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 25, 50, 100),
  n2 = c(2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 25, 50, 100),
  n3 = c(2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 25, 50, 100),
  n_simulations = 10000,
  nboot = 1000,
  conf.level = 0.95
)
Arguments

- **M1**: Mean for the first group, default is 5.
- **S1**: Standard deviation for the first group, default is 1.
- **M2**: Mean for the second group, default is 6.
- **S2**: Standard deviation for the second group, default is 2.
- **M3**: Mean for the third group, default is 7.
- **S3**: Standard deviation for the third group, default is 4.
- **Sk1**: Skewness parameter for the first group, default is 0.8.
- **Sk2**: Skewness parameter for the second group, default is 0.8.
- **Sk3**: Skewness parameter for the third group, default is 0.8.
- **n1**: Vector of sample sizes for the first group.
- **n2**: Vector of sample sizes for the second group.
- **n3**: Vector of sample sizes for the third group, must be the same length as `n1` and `n2`.
- **n_simulations**: Number of simulations to run, default is 10,000.
- **nboot**: Number of bootstrap samples for the nonparametric bootstrap test, default is 1000.
- **conf.level**: Confidence level for calculating p-value thresholds, default is 0.95.

Value

A data frame with columns for each sample size combination (n1, n2, n3) and the proportions of significant p-values for each test (ANOVA, Kruskal-Wallis, Nonparametric Bootstrap F-test, Permutation F-test).

References


See Also

- replext_ts2_c1.1

Examples

```r
replext_ts3_c2.2(n1 = c(10), n2 = c(10), n3 = c(10), n_simulations = 1)
```
Replicate and Extend Statistical Power Analysis for ANOVA with diverse Skewness Parameters

Description

This function is a wrapper around replex_t2_s2_c1.1. The function is designed to reproduce or extend the statistical power analysis for ANOVA (Analysis of Variance) from Dwivedi et al. (2017) supplemental table 3, cell 3.1.

Usage

```r
replext_ts3_c3.1( 
  M1 = 5,
  S1 = 1,
  M2 = 6,
  S2 = 1,
  M3 = 7,
  S3 = 1,
  Sk1 = 0.8,
  Sk2 = 0.8,
  Sk3 = 1,
  n1 = c(2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 25, 50, 100),
  n2 = c(2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 25, 50, 100),
  n3 = c(2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 25, 50, 100),
  n_simulations = 10000,
  nboot = 1000,
  conf.level = 0.95
)
```

Arguments

- `M1`: Mean for the first group, default is 5.
- `S1`: Standard deviation for the first group, default is 1.
- `M2`: Mean for the second group, default is 6.
- `S2`: Standard deviation for the second group, default is 1.
- `M3`: Mean for the third group, default is 7.
- `S3`: Standard deviation for the third group, default is 1.
- `Sk1`: Skewness parameter for the first group, default is 0.8.
- `Sk2`: Skewness parameter for the second group, default is 0.8.
- `Sk3`: Skewness parameter for the third group, default is 1.
- `n1`: Vector of sample sizes for the first group.
- `n2`: Vector of sample sizes for the second group.
n3           Vector of sample sizes for the third group, must be the same length as n1 and n2.
n_simulations Number of simulations to run, default is 10,000.
nboot         Number of bootstrap samples for the nonparametric bootstrap test, default is 1000.
conf.level    Confidence level for calculating p-value thresholds, default is 0.95.

Value
A data frame with columns for each sample size combination (n1, n2, n3) and the proportions of significant p-values for each test (ANOVA, Kruskal-Wallis, Nonparametric Bootstrap F-test, Permutation F-test).

References

See Also
replext_ts2_c1.1

Examples

replext_ts3_c3.1(n1 = c(10), n2 = c(10), n3 = c(10), n_simulations = 1)

replext_ts3_c3.2
Replicate and Extend Statistical Power Analysis for ANOVA with Varied Skewness and Standard Deviations

Description
This function is a wrapper around replext_ts2_c1.1. The function is designed to reproduce or extend the statistical power analysis for ANOVA (Analysis of Variance) from Dwivedi et al. (2017) supplemental table 3, cell 3.2.

Usage

replext_ts3_c3.2(
    M1 = 5,
    S1 = 1,
    M2 = 6,
    S2 = 2,
    M3 = 7,
    S3 = 4,
replext_ts3_c3.2

\[
\begin{align*}
\text{Sk1} &= 0.8, \\
\text{Sk2} &= 0.8, \\
\text{Sk3} &= 1, \\
\text{n1} &= c(2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 25, 50, 100), \\
\text{n2} &= c(2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 25, 50, 100), \\
\text{n3} &= c(2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 25, 50, 100), \\
\text{n\_simulations} &= 10000, \\
\text{n\_boot} &= 1000, \\
\text{conf\_level} &= 0.95
\end{align*}
\]

Arguments

- **M1**: Mean for the first group, default is 5.
- **S1**: Standard deviation for the first group, default is 1.
- **M2**: Mean for the second group, default is 6.
- **S2**: Standard deviation for the second group, default is 2.
- **M3**: Mean for the third group, default is 7.
- **S3**: Standard deviation for the third group, default is 4.
- **Sk1**: Skewness parameter for the first group, default is 0.8.
- **Sk2**: Skewness parameter for the second group, default is 0.8.
- **Sk3**: Skewness parameter for the third group, default is 1.
- **n1**: Vector of sample sizes for the first group.
- **n2**: Vector of sample sizes for the second group.
- **n3**: Vector of sample sizes for the third group, must be the same length as n1 and n2.
- **n\_simulations**: Number of simulations to run, default is 10,000.
- **n\_boot**: Number of bootstrap samples for the nonparametric bootstrap test, default is 1000.
- **conf\_level**: Confidence level for calculating p-value thresholds, default is 0.95.

Value

A data frame with columns for each sample size combination (n1, n2, n3) and the proportions of significant p-values for each test (ANOVA, Kruskal-Wallis, Nonparametric Bootstrap F-test, Permutation F-test).

References


See Also

replext_ts2_c1.1
Examples

```r
replext_ts3_c3.2(n1 = c(10), n2 = c(10), n3 = c(10), n_simulations = 1)
```

**Description**

This function is a wrapper around `replext_ts2_c1.1`. The function is designed to reproduce or extend the statistical power analysis for ANOVA (Analysis of Variance) from Dwivedi et al. (2017) supplemental table 3, cell 4.1.

**Usage**

```r
replext_ts3_c4.1(M1 = 5, S1 = 1, M2 = 6, S2 = 1, M3 = 7, S3 = 1, Sk1 = 0.8, Sk2 = 0.8, n1 = c(2, 2, 2, 3, 2, 3, 2, 3, 2), n2 = c(2, 3, 3, 4, 2, 3, 4, 2, 4), n3 = c(3, 3, 4, 3, 6, 6, 4, 7, 5, 8), n_simulations = 10000, nboot = 1000, conf.level = 0.95)
```

**Arguments**

- `M1` Mean for the first group, default is 5.
- `S1` Standard deviation for the first group, default is 1.
- `M2` Mean for the second group, default is 6.
- `S2` Standard deviation for the second group, default is 1.
- `M3` Mean for the third group, default is 7.
- `S3` Standard deviation for the third group, default is 1.
- `Sk1` Skewness parameter for the first group, default is 0.8.
- `Sk2` Skewness parameter for the second group, default is 0.8.
Sk3  Skewness parameter for the third group, default is 0.8.
n1  Vector of specific sample sizes for the first group.
n2  Vector of specific sample sizes for the second group.
n3  Vector of specific sample sizes for the third group, not necessarily the same length as n1 and n2.
n_simulations  Number of simulations to run, default is 10,000.
nboot  Number of bootstrap samples for the nonparametric bootstrap test, default is 1000.
conf.level  Confidence level for calculating p-value thresholds, default is 0.95.

Value

A data frame with columns for each sample size combination (n1, n2, n3) and the proportions of significant p-values for each test (ANOVA, Kruskal-Wallis, Nonparametric Bootstrap F-test, Permutation F-test).

References


See Also

replext_ts2_c1.1

Examples

replext_ts3_c4.1(n1 = c(10), n2 = c(10), n3 = c(10), n_simulations = 1)
Usage

replext_ts3_c4.2(
    M1 = 5,
    S1 = 1,
    M2 = 6,
    S2 = 2,
    M3 = 7,
    S3 = 4,
    Sk1 = 0.8,
    Sk2 = 0.8,
    Sk3 = 0.8,
    n1 = c(2, 2, 2, 3, 2, 3, 2, 3, 2, 3, 2),
    n2 = c(2, 3, 3, 4, 2, 3, 4, 2, 4, 2, 4),
    n3 = c(3, 3, 4, 3, 6, 6, 4, 7, 5, 8),
    n_simulations = 10000,
    nboot = 1000,
    conf.level = 0.95
)

Arguments

M1  Mean for the first group, default is 5.
S1  Standard deviation for the first group, default is 1.
M2  Mean for the second group, default is 6.
S2  Standard deviation for the second group, default is 2.
M3  Mean for the third group, default is 7.
S3  Standard deviation for the third group, default is 4.
Sk1 Skewness parameter for the first group, default is 0.8.
Sk2 Skewness parameter for the second group, default is 0.8.
Sk3 Skewness parameter for the third group, default is 0.8.
n1  Vector of sample sizes for the first group, with specific combinations.
n2  Vector of sample sizes for the second group, with specific combinations.
n3  Vector of sample sizes for the third group, with specific combinations.
n_simulations Number of simulations to run, default is 10,000.
nboot Number of bootstrap samples for the nonparametric bootstrap test, default is 1000.
conf.level Confidence level for calculating p-value thresholds, default is 0.95.

Value

A data frame with columns for each sample size combination (n1, n2, n3) and the proportions of significant p-values for each test (ANOVA, Kruskal-Wallis, Nonparametric Bootstrap F-test, Permutation F-test).
References


See Also

replext_ts2_c1.1

Examples

replext_ts3_c4.2(n1 = c(10), n2 = c(10), n3 = c(10), n_simulations = 1)