Package ‘npboottprm’

July 22, 2025

Title Nonparametric Bootstrap Test with Pooled Resampling

Version 0.3.2

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 'npboottprm' 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, 'npboottprm' incorporates an interactive 'shiny' web application, nonparboot_app(), offering intuitive, user-friendly data exploration.

License MIT + file LICENSE

Encoding UTF-8

RoxygenNote 7.3.2

URL `https://github.com/mightymetrika/npboottprm`

BugReports `https://github.com/mightymetrika/npboottprm/issues`

Suggests testthat (>= 3.0.0)

Config/testthat/edition 3

Depends R (>= 2.10)

LazyData true

Imports DT, fGarch, ggplot2, lmPerm, MASS, MKinfer, mmints, shiny, shinythemes, sn

NeedsCompilation no

Author Mackson Ncube [aut, cre],
mightymetrika, LLC [cph, fnd]

Maintainer Mackson Ncube <`macksonncube.stats@gmail.com`>

Repository CRAN

Date/Publication 2024-09-13 16:10:02 UTC

Contents

`data_f` *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

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

```
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

```
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

Dwivedi AK, Mallawaarachchi I, Alvarado LA (2017). "Analysis of small sample size studies using nonparametric bootstrap test with pooled resampling method." Statistics in Medicine, 36 (14), 2187-2205. https://doi.org/10.1002/sim.7263

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

Dwivedi AK, Mallawaarachchi I, Alvarado LA (2017). 'Analysis of small sample size studies using nonparametric bootstrap test with pooled resampling method.' Statistics in Medicine, 36 (14), 2187-2205. https://doi.org/10.1002/sim.7263

Examples

```
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 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.

Value

A Shiny app object which can be run to start the application.

References

Dwivedi AK, Mallawaarachchi I, Alvarado LA. Analysis of small sample size studies using nonparametric bootstrap test with pooled resampling method. Stat Med. 2017 Jun 30;36(14):2187-2205. doi: 10.1002/sim.7263. Epub 2017 Mar 9. PMID: 28276584.

Examples

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

`replext_pgsql` *Replext Simulation Shiny App with Database Integration*

Description

This application replicates and extends the simulation results from the paper by Dwivedi et al. (2017), now with added functionality to interact with a PostgreSQL database. The app includes a user interface for selecting simulation parameters and a server logic to process the simulation and handle user interactions, including saving and retrieving data from a database.

Usage

```
replext_pgsql(dbname, datatable, host, port, user, password)
```

Arguments

`dbname`	The name of the PostgreSQL database to connect to.
`datatable`	The name of the table in the database where the simulation results will be stored and retrieved.
`host`	The host address of the PostgreSQL database.
`port`	The port number for the PostgreSQL database connection.
`user`	The username for accessing the PostgreSQL database.
`password`	The password for the specified user to access the PostgreSQL database.

Details

The app's user interface consists of:

- 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.
- Buttons to run the simulation and submit the results to a PostgreSQL database.
- A table to display the simulation results and previously saved responses.
- A download button to export all responses as a CSV file.

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 submission of results and storing them in a PostgreSQL database.
- Loading existing responses from the database.
- Downloading responses as a CSV file.

Value

A Shiny app object which can be run to start the application.

References

Dwivedi AK, Mallawaarachchi I, Alvarado LA. Analysis of small sample size studies using nonparametric bootstrap test with pooled resampling method. Stat Med. 2017 Jun 30;36(14):2187-2205. doi: 10.1002/sim.7263. Epub 2017 Mar 9. PMID: 28276584.

Examples

```
if (interactive()) {
  replext_pgsql(
    dbname = "your_db_name",
    datatable = "your_data_table",
    host = "localhost",
    port = 5432,
    user = "your_username",
    password = "your_password"
  )
}
```

`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

Dwivedi AK, Mallawaarachchi I, Alvarado LA. Analysis of small sample size studies using nonparametric bootstrap test with pooled resampling method. Stat Med. 2017 Jun 30;36(14):2187-2205. doi: 10.1002/sim.7263. Epub 2017 Mar 9. PMID: 28276584.

Examples

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

`replext_t2_c1.2` *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 (`S2`) to 3 by default.

Usage

```
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 (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 nonparametric bootstrap test with pooled resampling method. Stat Med. 2017 Jun 30;36(14):2187-2205. doi: 10.1002/sim.7263. Epub 2017 Mar 9. PMID: 28276584.

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.
`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

Dwivedi AK, Mallawaarachchi I, Alvarado LA. Analysis of small sample size studies using nonparametric bootstrap test with pooled resampling method. Stat Med. 2017 Jun 30;36(14):2187-2205. doi: 10.1002/sim.7263. Epub 2017 Mar 9. PMID: 28276584.

See Also

`replext_t2_c1.1`

Examples

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

`replext_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 `replext_t2_c1.1`, setting specific skewness and variance parameters as per the cell's requirements.

Usage

```
replext_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

Dwivedi AK, Mallawaarachchi I, Alvarado LA. Analysis of small sample size studies using nonparametric bootstrap test with pooled resampling method. Stat Med. 2017 Jun 30;36(14):2187-2205. doi: 10.1002/sim.7263. Epub 2017 Mar 9. PMID: 28276584.

See Also

`replext_t2_c1.1`

Examples

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

`replext_t2_c3.1` *Replicate and Extend Simulation Results from Table 2 Cell 3.1*

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_c1.1`, setting specific skewness parameters as per the cell's requirements.

Usage

```
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

Dwivedi AK, Mallawaarachchi I, Alvarado LA. Analysis of small sample size studies using nonparametric bootstrap test with pooled resampling method. Stat Med. 2017 Jun 30;36(14):2187-2205. doi: 10.1002/sim.7263. Epub 2017 Mar 9. PMID: 28276584.

See Also

`replext_t2_c1.1`

Examples

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

`replext_t2_c3.2` *Replicate and Extend Simulation Results from Table 2 Cell 3.2*

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

Dwivedi AK, Mallawaarachchi I, Alvarado LA. Analysis of small sample size studies using nonparametric bootstrap test with pooled resampling method. Stat Med. 2017 Jun 30;36(14):2187-2205. doi: 10.1002/sim.7263. Epub 2017 Mar 9. PMID: 28276584.

See Also

`replext_t2_c1.1`

Examples

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

`replext_t2_c4.1` *Replicate and Extend Simulation Results from Table 2 Cell 4.1*

Description

This function is designed to replicate and extend the simulation results from Table 2 cell block 4.1 of the paper by Dwivedi et al. (2017). It addresses scenarios with unequal sample sizes but the same skewed distribution and equal variance in both groups. The function acts as a wrapper around `replext_t2_c1.1`, setting specific skewness parameters and sample sizes as per the cell's requirements.

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, 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 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 nonparametric bootstrap test with pooled resampling method. Stat Med. 2017 Jun 30;36(14):2187-2205. doi: 10.1002/sim.7263. Epub 2017 Mar 9. PMID: 28276584.

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

Dwivedi AK, Mallawaarachchi I, Alvarado LA. Analysis of small sample size studies using nonparametric bootstrap test with pooled resampling method. Stat Med. 2017 Jun 30;36(14):2187-2205. doi: 10.1002/sim.7263. Epub 2017 Mar 9. PMID: 28276584.

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

Dwivedi AK, Mallawaarachchi I, Alvarado LA. Analysis of small sample size studies using nonparametric bootstrap test with pooled resampling method. Stat Med. 2017 Jun 30;36(14):2187-2205. doi: 10.1002/sim.7263. Epub 2017 Mar 9. PMID: 28276584.

See Also

`replext_t2_c1.1`

Examples

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

`replext_t3_c1.2` *Replicate and Extend Statistical Power Analysis from Table 3 Cell 1.2*

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

Dwivedi AK, Mallawaarachchi I, Alvarado LA. Analysis of small sample size studies using nonparametric bootstrap test with pooled resampling method. Stat Med. 2017 Jun 30;36(14):2187-2205. doi: 10.1002/sim.7263. Epub 2017 Mar 9. PMID: 28276584.

See Also

`replext_t2_c1.1`

Examples

```
replext_t3_c1.2(n1 = c(10), n2 = c(10), n_simulations = 1)
```

`replext_t3_c2.1` *Replicate and Extend Statistical Power Analysis from Table 3 Cell 2.1*

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 (n1, n2) and the proportions of significant p-values for each test (ST, WT, NPBTT, WRST, PTT), reflecting the power analysis.

References

Dwivedi AK, Mallawaarachchi I, Alvarado LA. Analysis of small sample size studies using nonparametric bootstrap test with pooled resampling method. Stat Med. 2017 Jun 30;36(14):2187-2205. doi: 10.1002/sim.7263. Epub 2017 Mar 9. PMID: 28276584.

See Also

`replext_t2_c1.1`

Examples

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

`replext_t3_c2.2` *Replicate and Extend Statistical Power Analysis from Table 3 Cell 2.2*

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

```
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

Dwivedi AK, Mallawaarachchi I, Alvarado LA. Analysis of small sample size studies using nonparametric bootstrap test with pooled resampling method. Stat Med. 2017 Jun 30;36(14):2187-2205. doi: 10.1002/sim.7263. Epub 2017 Mar 9. PMID: 28276584.

See Also

`replext_t2_c1.1`

Examples

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

`replext_t3_c3.1` *Replicate and Extend Statistical Power Analysis from Table 3 Cell 3.1*

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

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):2187-2205. doi: 10.1002/sim.7263. Epub 2017 Mar 9. PMID: 28276584.

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

`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 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

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):2187-2205. doi: 10.1002/sim.7263. Epub 2017 Mar 9. PMID: 28276584.

See Also

`replext_t2_c1.1`

Examples

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

`replext_t3_c4.1` *Replicate and Extend Statistical Power Analysis from Table 3 Cell 4.1*

Description

This function is crafted to replicate and extend the statistical power analysis from Table 3 cell block 4.1 in the paper by Dwivedi et al. (2017). It focuses on scenarios with unequal sample sizes, same skewed distribution, and equal variance between the two groups. It utilizes `replext_t2_c1.1` with adjusted skewness parameters, means, and specific sample sizes.

Usage

```
replext_t3_c4.1(
  M1 = 5,
  S1 = 1,
  M2 = 7,
  S2 = 1,
  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 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

Dwivedi AK, Mallawaarachchi I, Alvarado LA. Analysis of small sample size studies using nonparametric bootstrap test with pooled resampling method. Stat Med. 2017 Jun 30;36(14):2187-2205. doi: 10.1002/sim.7263. Epub 2017 Mar 9. PMID: 28276584.

See Also

`replext_t2_c1.1`

Examples

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

`replext_t3_c4.2` *Replicate and Extend Statistical Power Analysis from Table 3 Cell 4.2*

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

Dwivedi AK, Mallawaarachchi I, Alvarado LA. Analysis of small sample size studies using nonparametric bootstrap test with pooled resampling method. Stat Med. 2017 Jun 30;36(14):2187-2205. doi: 10.1002/sim.7263. Epub 2017 Mar 9. PMID: 28276584.

See Also

`replext_t2_c1.1`

Examples

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

`replext_t3_c5.1` *Replicate and Extend Statistical Power Analysis from Table 3 Cell 5.1*

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.

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

Dwivedi AK, Mallawaarachchi I, Alvarado LA. Analysis of small sample size studies using nonparametric bootstrap test with pooled resampling method. Stat Med. 2017 Jun 30;36(14):2187-2205. doi: 10.1002/sim.7263. Epub 2017 Mar 9. PMID: 28276584.

See Also

`replext_t2_c1.1`

Examples

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

`replext_t3_c5.2` *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

```
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
)
```

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

Dwivedi AK, Mallawaarachchi I, Alvarado LA. Analysis of small sample size studies using nonparametric bootstrap test with pooled resampling method. Stat Med. 2017 Jun 30;36(14):2187-2205. doi: 10.1002/sim.7263. Epub 2017 Mar 9. PMID: 28276584.

See Also

`replext_t2_c1.1`

Examples

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

`replext_t4_c1.1` *Replicate and Extend Simulation Results from Table 4 Cell 1.1*

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

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):2187-2205. doi: 10.1002/sim.7263. Epub 2017 Mar 9. PMID: 28276584.

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

Dwivedi AK, Mallawaarachchi I, Alvarado LA. Analysis of small sample size studies using nonparametric bootstrap test with pooled resampling method. Stat Med. 2017 Jun 30;36(14):2187-2205. doi: 10.1002/sim.7263. Epub 2017 Mar 9. PMID: 28276584.

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

Dwivedi AK, Mallawaarachchi I, Alvarado LA. Analysis of small sample size studies using nonparametric bootstrap test with pooled resampling method. Stat Med. 2017 Jun 30;36(14):2187-2205. doi: 10.1002/sim.7263. Epub 2017 Mar 9. PMID: 28276584.

Examples

```
replext_t4_c3.1(n1 = c(10), n2 = c(10),n_simulations = 1)
```

`replext_t4_c4.1` *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

Dwivedi AK, Mallawaarachchi I, Alvarado LA. Analysis of small sample size studies using nonparametric bootstrap test with pooled resampling method. Stat Med. 2017 Jun 30;36(14):2187-2205. doi: 10.1002/sim.7263. Epub 2017 Mar 9. PMID: 28276584.

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_c1.1', 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

Dwivedi AK, Mallawaarachchi I, Alvarado LA. Analysis of small sample size studies using nonparametric bootstrap test with pooled resampling method. Stat Med. 2017 Jun 30;36(14):2187-2205. doi: 10.1002/sim.7263. Epub 2017 Mar 9. PMID: 28276584.

Examples

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

`replext_t4_c6.1` *Replicate and Extend Simulation Results from Table 4 Cell 6.1*

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

```
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.

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

Dwivedi AK, Mallawaarachchi I, Alvarado LA. Analysis of small sample size studies using nonparametric bootstrap test with pooled resampling method. Stat Med. 2017 Jun 30;36(14):2187-2205. doi: 10.1002/sim.7263. Epub 2017 Mar 9. PMID: 28276584.

Examples

```
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

```
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

Dwivedi AK, Mallawaarachchi I, Alvarado LA. Analysis of small sample size studies using nonparametric bootstrap test with pooled resampling method. Stat Med. 2017 Jun 30;36(14):2187-2205. doi: 10.1002/sim.7263. Epub 2017 Mar 9. PMID: 28276584.

Examples

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

`replext_t5_c1.1` *Replicate and Extend Simulation Results for Paired Distributions*

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

```
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

Dwivedi AK, Mallawaarachchi I, Alvarado LA. Analysis of small sample size studies using nonparametric bootstrap test with pooled resampling method. Stat Med. 2017 Jun 30;36(14):2187-2205. doi: 10.1002/sim.7263. Epub 2017 Mar 9. PMID: 28276584.

Examples

```
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

```
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

Dwivedi AK, Mallawaarachchi I, Alvarado LA. Analysis of small sample size studies using nonparametric bootstrap test with pooled resampling method. Stat Med. 2017 Jun 30;36(14):2187-2205. doi: 10.1002/sim.7263. Epub 2017 Mar 9. PMID: 28276584.

Examples

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

`replext_t5_c1.3` *Replicate 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

```
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

Dwivedi AK, Mallawaarachchi I, Alvarado LA. Analysis of small sample size studies using nonparametric bootstrap test with pooled resampling method. Stat Med. 2017 Jun 30;36(14):2187-2205. doi: 10.1002/sim.7263. Epub 2017 Mar 9. PMID: 28276584.

Examples

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

`replext_t5_c2.1` *Replicate and Extend 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 simulation results from Table 5 cell 2.1 of the paper by Dwivedi et al. (2017). It focuses on paired distributions that combine normal and skew normal behaviors with different standard deviations and specified skewness parameters for each group.

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

Dwivedi AK, Mallawaarachchi I, Alvarado LA. Analysis of small sample size studies using nonparametric bootstrap test with pooled resampling method. Stat Med. 2017 Jun 30;36(14):2187-2205. doi: 10.1002/sim.7263. Epub 2017 Mar 9. PMID: 28276584.

Examples

```
replext_t5_c2.1(n = c(10), n_simulations = 1)
```

`replext_t5_c2.2` *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

```
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

Dwivedi AK, Mallawaarachchi I, Alvarado LA. Analysis of small sample size studies using nonparametric bootstrap test with pooled resampling method. Stat Med. 2017 Jun 30;36(14):2187-2205. doi: 10.1002/sim.7263. Epub 2017 Mar 9. PMID: 28276584.

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

```
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

Dwivedi AK, Mallawaarachchi I, Alvarado LA. Analysis of small sample size studies using nonparametric bootstrap test with pooled resampling method. Stat Med. 2017 Jun 30;36(14):2187-2205. doi: 10.1002/sim.7263. Epub 2017 Mar 9. PMID: 28276584.

Examples

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

`replext_t6_c1.1` *Replicate and Extend Statistical Power Simulation Results for Paired Distributions*

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 1.1 of the paper by Dwivedi et al. (2017).

Usage

```
replext_t6_c1.1(
  M1 = 5,
  S1 = 1,
  M2 = 7,
  S2 = 1,
  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 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

Dwivedi AK, Mallawaarachchi I, Alvarado LA. Analysis of small sample size studies using nonparametric bootstrap test with pooled resampling method. Stat Med. 2017 Jun 30;36(14):2187-2205. doi: 10.1002/sim.7263. Epub 2017 Mar 9. PMID: 28276584.

Examples

```
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

Dwivedi AK, Mallawaarachchi I, Alvarado LA. Analysis of small sample size studies using nonparametric bootstrap test with pooled resampling method. Stat Med. 2017 Jun 30;36(14):2187-2205. doi: 10.1002/sim.7263. Epub 2017 Mar 9. PMID: 28276584.

Examples

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

`replext_t6_c1.3` *Replicate and Extend Statistical Power 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 statistical power simulation results from Table 6 cell 1.3 of the paper by Dwivedi et al. (2017).

Usage

```
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

Dwivedi AK, Mallawaarachchi I, Alvarado LA. Analysis of small sample size studies using nonparametric bootstrap test with pooled resampling method. Stat Med. 2017 Jun 30;36(14):2187-2205. doi: 10.1002/sim.7263. Epub 2017 Mar 9. PMID: 28276584.

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).
`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

Dwivedi AK, Mallawaarachchi I, Alvarado LA. Analysis of small sample size studies using nonparametric bootstrap test with pooled resampling method. Stat Med. 2017 Jun 30;36(14):2187-2205. doi: 10.1002/sim.7263. Epub 2017 Mar 9. PMID: 28276584.

Examples

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

`replext_t6_c2.2` *Replicate and Extend Statistical Power 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 statistical power simulation results from Table 6 cell 2.2 of the paper by Dwivedi et al. (2017).

Usage

```
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
)
```

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

Dwivedi AK, Mallawaarachchi I, Alvarado LA. Analysis of small sample size studies using nonparametric bootstrap test with pooled resampling method. Stat Med. 2017 Jun 30;36(14):2187-2205. doi: 10.1002/sim.7263. Epub 2017 Mar 9. PMID: 28276584.

Examples

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

`replext_t6_c2.3` *Replicate and Extend Statistical Power Simulation Results for Paired Distributions with Varied Skewness and Standard Deviations*

Description

`replext_t6_c2.3` is a wrapper function around `replext_t5_c1.1`, specifically designed to replicate and extend the statistical power simulation results from Table 6 cell 2.3 of the paper by Dwivedi et al. (2017).

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, NPBTT, WRST, PTT), focusing on variations in skewness and standard deviations between the groups.

References

Dwivedi AK, Mallawaarachchi I, Alvarado LA. Analysis of small sample size studies using nonparametric bootstrap test with pooled resampling method. Stat Med. 2017 Jun 30;36(14):2187-2205. doi: 10.1002/sim.7263. Epub 2017 Mar 9. PMID: 28276584.

Examples

```
replext_t6_c2.3(n = c(10), n_simulations = 1)
```

`replext_ts1_c1.1` *Replicate and Extend Simulation Results from Table S1 Cell 1.1*

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 1.1 of the paper by Dwivedi et al. (2017).

Usage

```
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

Dwivedi AK, Mallawaarachchi I, Alvarado LA. Analysis of small sample size studies using nonparametric bootstrap test with pooled resampling method. Stat Med. 2017 Jun 30;36(14):2187-2205. doi: 10.1002/sim.7263. Epub 2017 Mar 9. PMID: 28276584.

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

`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 5 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

Dwivedi AK, Mallawaarachchi I, Alvarado LA. Analysis of small sample size studies using nonparametric bootstrap test with pooled resampling method. Stat Med. 2017 Jun 30;36(14):2187-2205. doi: 10.1002/sim.7263. Epub 2017 Mar 9. PMID: 28276584.

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

Dwivedi AK, Mallawaarachchi I, Alvarado LA. Analysis of small sample size studies using nonparametric bootstrap test with pooled resampling method. Stat Med. 2017 Jun 30;36(14):2187-2205. doi: 10.1002/sim.7263. Epub 2017 Mar 9. PMID: 28276584.

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

Dwivedi AK, Mallawaarachchi I, Alvarado LA. Analysis of small sample size studies using nonparametric bootstrap test with pooled resampling method. Stat Med. 2017 Jun 30;36(14):2187-2205. doi: 10.1002/sim.7263. Epub 2017 Mar 9. PMID: 28276584.

Examples

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

`replext_ts2_c1.2` *Replicate and Extend Type I Error Rates for ANOVA in a Different Setting*

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

```
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.
`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 similar to `replext_ts2_c1.1` 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), but with the modified default parameters.

References

Dwivedi AK, Mallawaarachchi I, Alvarado LA. Analysis of small sample size studies using nonparametric bootstrap test with pooled resampling method. Stat Med. 2017 Jun 30;36(14):2187-2205. doi: 10.1002/sim.7263. Epub 2017 Mar 9. PMID: 28276584.

See Also

`replext_ts2_c1.1`

Examples

```
replext_ts2_c1.2(n1 = c(10), n2 = c(10), n3 = c(10), n_simulations = 1)
```

`replext_ts2_c2.1` *Replicate and Extend Type I Error Rates for ANOVA with Skewness*

Description

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.

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

Dwivedi AK, Mallawaarachchi I, Alvarado LA. Analysis of small sample size studies using nonparametric bootstrap test with pooled resampling method. Stat Med. 2017 Jun 30;36(14):2187-2205. doi: 10.1002/sim.7263. Epub 2017 Mar 9. PMID: 28276584.

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

Dwivedi AK, Mallawaarachchi I, Alvarado LA. Analysis of small sample size studies using nonparametric bootstrap test with pooled resampling method. Stat Med. 2017 Jun 30;36(14):2187-2205. doi: 10.1002/sim.7263. Epub 2017 Mar 9. PMID: 28276584.

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)
```

`replext_ts2_c3.1` *Replicate and Extend Type I Error Rates for ANOVA with Diverse Skewness Parameters*

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

```
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.
`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 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

Dwivedi AK, Mallawaarachchi I, Alvarado LA. Analysis of small sample size studies using nonparametric bootstrap test with pooled resampling method. Stat Med. 2017 Jun 30;36(14):2187-2205. doi: 10.1002/sim.7263. Epub 2017 Mar 9. PMID: 28276584.

See Also

`replext_ts2_c1.1`

Examples

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

`replext_ts2_c3.2` *Replicate and Extend Type I Error Rates for ANOVA with Varied Skewness and Standard Deviations*

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

Dwivedi AK, Mallawaarachchi I, Alvarado LA. Analysis of small sample size studies using nonparametric bootstrap test with pooled resampling method. Stat Med. 2017 Jun 30;36(14):2187-2205. doi: 10.1002/sim.7263. Epub 2017 Mar 9. PMID: 28276584.

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, 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

Dwivedi AK, Mallawaarachchi I, Alvarado LA. Analysis of small sample size studies using nonparametric bootstrap test with pooled resampling method. Stat Med. 2017 Jun 30;36(14):2187-2205. doi: 10.1002/sim.7263. Epub 2017 Mar 9. PMID: 28276584.

See Also

`replext_ts2_c1.1`

Examples

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

`replext_ts2_c4.2` *Replicate and Extend Type I Error Rates for ANOVA with Specific Sample Size Combinations*

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, 2, 3, 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 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 standrd deviations.

References

Dwivedi AK, Mallawaarachchi I, Alvarado LA. Analysis of small sample size studies using nonparametric bootstrap test with pooled resampling method. Stat Med. 2017 Jun 30;36(14):2187-2205. doi: 10.1002/sim.7263. Epub 2017 Mar 9. PMID: 28276584.

See Also

`replext_ts2_c1.1`

Examples

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

`replext_ts3_c1.1` *Replicate and Extend Statistical Power Analysis for ANOVA in a Three-Sample Setting*

Description

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

Dwivedi AK, Mallawaarachchi I, Alvarado LA. Analysis of small sample size studies using nonparametric bootstrap test with pooled resampling method. Stat Med. 2017 Jun 30;36(14):2187-2205. doi: 10.1002/sim.7263. Epub 2017 Mar 9. PMID: 28276584.

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.
`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.
`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

Dwivedi AK, Mallawaarachchi I, Alvarado LA. Analysis of small sample size studies using nonparametric bootstrap test with pooled resampling method. Stat Med. 2017 Jun 30;36(14):2187-2205. doi: 10.1002/sim.7263. Epub 2017 Mar 9. PMID: 28276584.

See Also

`replext_ts2_c1.1`

Examples

```
replext_ts3_c1.2(n1 = c(10), n2 = c(10), n3 = c(10), n_simulations = 1)
```

`replext_ts3_c2.1` *Replicate and Extend Statistical Power Analysis for ANOVA with Skewness*

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 2.1.

Usage

```
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

`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 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

Dwivedi AK, Mallawaarachchi I, Alvarado LA. Analysis of small sample size studies using nonparametric bootstrap test with pooled resampling method. Stat Med. 2017 Jun 30;36(14):2187-2205. doi: 10.1002/sim.7263. Epub 2017 Mar 9. PMID: 28276584.

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

Dwivedi AK, Mallawaarachchi I, Alvarado LA. Analysis of small sample size studies using nonparametric bootstrap test with pooled resampling method. Stat Med. 2017 Jun 30;36(14):2187-2205. doi: 10.1002/sim.7263. Epub 2017 Mar 9. PMID: 28276584.

See Also

`replext_ts2_c1.1`

Examples

```
replext_ts3_c2.2(n1 = c(10), n2 = c(10), n3 = c(10), n_simulations = 1)
```

`replext_ts3_c3.1` *Replicate and Extend Statistical Power Analysis for ANOVA with Diverse Skewness Parameters*

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 3.1.

Usage

```
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

Dwivedi AK, Mallawaarachchi I, Alvarado LA. Analysis of small sample size studies using nonparametric bootstrap test with pooled resampling method. Stat Med. 2017 Jun 30;36(14):2187-2205. doi: 10.1002/sim.7263. Epub 2017 Mar 9. PMID: 28276584.

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,
  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 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.
`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

Dwivedi AK, Mallawaarachchi I, Alvarado LA. Analysis of small sample size studies using nonparametric bootstrap test with pooled resampling method. Stat Med. 2017 Jun 30;36(14):2187-2205. doi: 10.1002/sim.7263. Epub 2017 Mar 9. PMID: 28276584.

See Also

`replext_ts2_c1.1`

Examples

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

`replext_ts3_c4.1` *Replicate and Extend Statistical Power Analysis for ANOVA with Skewness in Specific Sample Size Combinations*

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

```
replext_ts3_c4.1(
  M1 = 5,
  S1 = 1,
  M2 = 6,
  S2 = 1,
  M3 = 7,
  S3 = 1,
```

```
  Sk1 = 0.8,
  Sk2 = 0.8,
  Sk3 = 0.8,
  n1 = c(2, 2, 2, 3, 2, 2, 3, 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 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

Dwivedi AK, Mallawaarachchi I, Alvarado LA. Analysis of small sample size studies using nonparametric bootstrap test with pooled resampling method. Stat Med. 2017 Jun 30;36(14):2187-2205. doi: 10.1002/sim.7263. Epub 2017 Mar 9. PMID: 28276584.

See Also

`replext_ts2_c1.1`

Examples

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

`replext_ts3_c4.2` *Replicate and Extend Statistical Power Analysis for ANOVA with Specific Sample Size Combinations*

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 4.2.

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, 2, 3, 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 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

Dwivedi AK, Mallawaarachchi I, Alvarado LA. Analysis of small sample size studies using nonparametric bootstrap test with pooled resampling method. Stat Med. 2017 Jun 30;36(14):2187-2205. doi: 10.1002/sim.7263. Epub 2017 Mar 9. PMID: 28276584.

See Also

`replext_ts2_c1.1`

Examples

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

Index