

Package ‘NeutroRCDsAnalysis’

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Type Package

Title Neutrosophic Analysis of Row Column Designs

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Maintainer Vinaykumar L.N. <vinaymandya123@gmail.com>

Description Description: Provides methods for Neutrosophic Analysis of Variance (NANOVA) and Neutrosophic Analysis of Covariance (NANCOVA) for row-column designs, including Latin square designs and Youden square designs, using interval-valued observations. The package computes neutrosophic sums of squares, mean squares, interval-valued F-statistics, significance tests, and multiple comparisons using Least Significant Difference (LSD) procedures. For crisp data, users may enter identical lower and upper values of responses to obtain classical Analysis of Variance (ANOVA) results. Similarly, users may enter identical lower and upper values for both responses and covariates to obtain classical Analysis of Covariance (ANCOVA) results.

License GPL-3

Encoding UTF-8

Depends R (>= 4.0.0)

Imports MASS

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NeedsCompilation no

Author Neethu R.S. [aut, ctb],
Boyina Devi Priyanka [aut, ctb],
Cini Varghese [aut, ctb],
Mohd Harun [aut, ctb],
Anindita Datta [aut, ctb],
Vinaykumar L.N. [aut, cre]

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| LSDnsANCOVA | <i>Neutrosophic Analysis of Covariance for Latin Square Design</i> |
|-------------|--|

Description

Performs Neutrosophic Analysis of Covariance (NANCOVA) for Latin square designs using interval-valued response and covariate observations. The function computes neutrosophic sums of squares, mean squares, interval-valued F-statistics, significance tests, and Least Significant Difference (LSD)-based treatment comparisons. For crisp data, enter identical lower and upper values to obtain the corresponding classical ANCOVA results.

Usage

```
LSDnsANCOVA(Lower_y, Upper_y, Lower_z, Upper_z, design, alpha = 0.05, verbose = FALSE)
```

Arguments

| | |
|---------|--|
| Lower_y | Matrix containing lower bounds of response observations. |
| Upper_y | Matrix containing upper bounds of response observations. |
| Lower_z | Matrix containing lower bounds of covariate observations. |
| Upper_z | Matrix containing upper bounds of covariate observations. |
| design | Matrix representing Latin square treatment allocation. |
| alpha | Significance level for the F-test and LSD test. Default is 0.05. |
| verbose | Logical. If TRUE, displays the ANCOVA table, LSD interval, treatment comparisons and significance codes. Default is FALSE. |

Details

Input matrix structure:

- Rows represent blocks (or rows of the design).
- Columns represent treatment positions within each block.
- ‘Lower_y’ and ‘Upper_y’ must have the same dimensions as the design matrix.
- ‘Lower_z’ and ‘Upper_z’ must have the same dimensions as the design matrix.

Value

A list containing:

- `nancova_table`: Neutrosophic ANCOVA table.
- `comparison`: LSD treatment comparisons, if applicable.
- `LSD`: Lower and upper limits of the LSD interval.

Examples

```
Lower_y <- matrix(c(
  18.86,15.49,18.62,16.37,12.04,
  18.23,26.80,26.70,15.89,16.96,
  26.26,12.16,27.15,18.30,22.93,
  25.31,26.71,18.36,9.98,28.34,
  29.78,21.20,21.99,18.97,18.71
), nrow = 5, byrow = TRUE)
```

```
Upper_y <- matrix(c(
  21.14,22.51,25.38,21.63,19.96,
  27.77,29.20,33.30,18.11,25.04,
  29.74,19.84,36.85,25.70,31.07,
  34.69,29.29,21.64,18.02,33.66,
  32.22,28.80,24.01,25.03,21.29
), nrow = 5, byrow = TRUE)
```

```
Lower_z <- matrix(c(
  9.11,7.39,7.09,4.10,5.92,
  6.91,4.26,13.10,5.86,12.54,
  8.89,4.98,4.32,8.80,9.77,
  6.40,7.28,3.29,3.81,4.45,
  6.42,2.51,6.06,3.25,5.73
), nrow = 5, byrow = TRUE)
```

```
Upper_z <- matrix(c(
  16.89,10.61,14.91,9.90,8.08,
  11.09,9.74,16.90,12.14,17.46,
  13.11,11.02,11.68,11.20,18.23,
  9.60,12.72,10.71,8.19,7.55,
  15.58,7.49,9.94,12.75,14.27
), nrow = 5, byrow = TRUE)
```

```
design <- matrix(c(
  2,1,5,4,3,
  1,4,3,5,2,
  3,2,4,1,5,
  5,3,1,2,4,
  4,5,2,3,1
), nrow = 5, byrow = TRUE)
```

```
LSDnsANCOVA(Lower_y, Upper_y, Lower_z, Upper_z, design, alpha = 0.05, verbose = TRUE)
```

Description

Performs Neutrosophic Analysis of Variance (NANOVA) for Latin square designs using interval-valued observations. The function computes neutrosophic sums of squares, mean squares, interval-valued F-statistics, significance tests, and Least Significant Difference (LSD)-based treatment comparisons. When the data are crisp, identical lower and upper values may be entered to obtain the corresponding classical ANOVA results.

Usage

```
LSDnsANOVA(Lower_y, Upper_y, design, alpha = 0.05, verbose = FALSE)
```

Arguments

| | |
|---------|---|
| Lower_y | Matrix containing lower bounds of observations. |
| Upper_y | Matrix containing upper bounds of observations. |
| design | Matrix representing Latin square treatment allocation. |
| alpha | Significance level (default is 0.05.) for the F-test and LSD test. |
| verbose | Logical. If TRUE, displays the NANOVA table, LSD interval, treatment comparisons, and significance codes. Default is FALSE. |

Details

Input matrix structure:

- Rows represent blocks (or rows of the design).
- Columns represent treatment positions within each block.
- ‘Lower_y’ and ‘Upper_y’ must have the same dimensions as the design matrix.

Value

A list containing:

- `nanova_table`: Neutrosophic ANOVA table.
- `comparison`: LSD treatment comparisons, if applicable.
- `LSD`: Lower and upper limits of the LSD interval.

Examples

```

Lower_y <- matrix(c(
  243.28,233.45,232.41,239.27,
  237.38,223.30,240.86,240.33,
  232.12,234.67,230.45,220.81,
  219.26,231.43,248.44,227.88
), nrow = 4, byrow = TRUE)

Upper_y <- matrix(c(
  246.72,238.55,237.59,242.73,
  242.62,226.70,245.14,245.67,
  235.88,239.33,233.55,223.19,
  224.74,236.57,253.57,230.12
), nrow = 4, byrow = TRUE)

design <- matrix(c(
  3,4,2,1,
  1,2,4,3,
  4,3,1,2,
  2,1,3,4
), nrow = 4, byrow = TRUE)

LSDnsANOVA(Lower_y, Upper_y, design, alpha = 0.05, verbose = TRUE)

```

YSDnsANCOVA

*Neutrosophic Analysis of Covariance for Youden Square Design***Description**

Performs Neutrosophic Analysis of Covariance (NANCOVA) for Youden square designs using interval-valued observations and covariates. The function computes neutrosophic sums of squares, mean squares, interval-valued F-statistics, significance tests, and Least Significant Difference (LSD)-based treatment comparisons. For crisp data, enter identical lower and upper values to obtain the corresponding classical ANCOVA results.

Usage

```
YSDnsANCOVA(Lower_y, Upper_y, Lower_z, Upper_z, design, alpha = 0.05, verbose = FALSE)
```

Arguments

| | |
|---------|---|
| Lower_y | Matrix containing lower bounds of response observations. |
| Upper_y | Matrix containing upper bounds of response observations. |
| Lower_z | Matrix containing lower bounds of covariate observations. |
| Upper_z | Matrix containing upper bounds of covariate observations. |
| design | Matrix representing Youden square treatment allocation. |

| | |
|---------|--|
| alpha | Significance level for the F-test and LSD test. Default is 0.05. |
| verbose | Logical. If TRUE, prints the ANCOVA table, LSD interval, treatment comparisons and significance codes. Default is FALSE. |

Details

Input matrix structure:

- Rows represent blocks of the design.
- Columns represent treatment positions within each row.
- ‘Lower_y’ and ‘Upper_y’ must have the same dimensions as the design matrix.
- ‘Lower_z’ and ‘Upper_z’ must have the same dimensions as the design matrix.

Value

A list containing:

- nancova_table: Neutrosophic ANCOVA table.
- comparison: LSD treatment comparisons, if performed.
- LSD: Lower and upper limits of the LSD interval.

Examples

```
Lower_y <- matrix(c(
  2.06, 2.34, 0.13, 15.63, 15.72, 8.18, 292.48,
  15.39, 218.67, 10.02, 13.67, 8.90, 25.23, 24.86,
  35.78, 24.90, 308.36, 19.96, 22.01, 20.17, 28.99,
  45.05, 42.44, 33.19, 280.58, 31.40, 31.82, 28.41
), nrow = 4, byrow = TRUE)
```

```
Upper_y <- matrix(c(
  5.94, 8.26, 2.33, 18.17, 18.08, 12.42, 295.52,
  19.61, 221.33, 14.38, 17.33, 13.10, 27.77, 29.54,
  38.22, 27.10, 311.64, 25.44, 26.39, 22.63, 33.60,
  48.55, 45.96, 35.41, 283.42, 36.00, 35.58, 32.59
), nrow = 4, byrow = TRUE)
```

```
Lower_z <- matrix(c(
  10.57, 269.93, 224.08, 260.05, 257.81, 257.58, 13.76,
  246.72, 7.42, 216.00, 257.15, 232.38, 237.91, 215.32,
  246.50, 215.17, 2.63, 257.26, 267.90, 212.10, 254.15,
  262.67, 250.51, 250.45, 6.09, 245.01, 228.31, 258.90
), nrow = 4, byrow = TRUE)
```

```
Upper_z <- matrix(c(
  13.43, 272.07, 227.92, 265.95, 260.19, 260.42, 18.24,
  249.28, 12.58, 220.00, 262.85, 235.62, 240.09, 218.68,
  251.50, 220.83, 7.37, 260.74, 272.10, 215.90, 257.85,
  265.33, 253.49, 253.55, 11.91, 250.99, 231.69, 263.10
), nrow = 4, byrow = TRUE)
```

```

design <- matrix(c(
  2,3,4,5,6,7,1,
  7,1,2,3,4,5,6,
  6,7,1,2,3,4,5,
  5,6,7,1,2,3,4
), nrow = 4, byrow = TRUE)

YSDnsANCOVA(Lower_y, Upper_y, Lower_z, Upper_z, design, alpha = 0.05, verbose = TRUE)

```

YSDnsANOVA

Neutrosophic Analysis of Variance for Youden Square Design

Description

Performs Neutrosophic Analysis of Variance (NANOVA) for Youden square designs using interval-valued observations. The function computes neutrosophic sums of squares, mean squares, interval-valued F-statistics, significance tests, and Least Significant Difference (LSD)-based treatment comparisons. For crisp data, enter identical lower and upper values to obtain the corresponding classical ANOVA results.

Usage

```
YSDnsANOVA(Lower_y, Upper_y, design, alpha = 0.05, verbose = FALSE)
```

Arguments

| | |
|---------|--|
| Lower_y | Matrix containing lower bounds of observations. |
| Upper_y | Matrix containing upper bounds of observations. |
| design | Matrix representing Youden square treatment allocation. |
| alpha | Significance level for the F-test and LSD test. Default is 0.05. |
| verbose | Logical. If TRUE, displays the NANOVA table, LSD interval, treatment comparisons and significance codes. Default is FALSE. |

Details

Input matrix structure:

- Rows represent blocks of the design.
- Columns represent treatment positions within each row.
- ‘Lower_y’ and ‘Upper_y’ must have the same dimensions as the design matrix.

Value

A list containing:

- `nanova_table`: Neutrosophic ANOVA table.
- `comparison`: LSD treatment comparisons, if applicable.
- `LSD`: Lower and upper limits of the LSD interval.

Examples

```
Lower_y <- matrix(c(
  4.51,7.77,3.53,7.92,5.97,7.42,6.37,
  6.37,4.36,4.68,8.19,6.08,6.80,4.86,
  4.88,4.64,8.69,7.81,9.50,9.60,9.10,
  8.05,7.92,5.61,8.41,6.53,11.36,5.94
), nrow = 4, byrow = TRUE)
```

```
Upper_y <- matrix(c(
  8.12,11.06,6.44,11.16,8.30,10.17,9.81,
  10.31,7.50,8.01,10.82,8.49,10.69,7.77,
  7.76,7.24,10.82,11.04,13.20,11.63,11.59,
  11.66,10.45,8.92,12.03,8.95,14.64,9.14
), nrow = 4, byrow = TRUE)
```

```
design <- matrix(c(
  2,3,4,5,6,7,1,
  7,1,2,3,4,5,6,
  6,7,1,2,3,4,5,
  5,6,7,1,2,3,4
), nrow = 4, byrow = TRUE)
```

```
YSDnsANOVA(Lower_y, Upper_y, design, alpha = 0.05, verbose = TRUE)
```

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