Package: NeutroDOE (via r-universe)

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Title Neutrosophic Analysis of Experimental Designs

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Description Provides methods for neutrosophic analysis of interval-valued observations from a range of experimental designs. The package combines methods for completely randomized designs, randomized complete block designs, incomplete block designs, Latin square designs, Youden square designs, crossover designs, multi-session designs, split-plot designs, strip-plot designs, and pooled analyses. Available procedures include analysis of variance, analysis of covariance, multivariate analysis of variance, treatment comparisons, Levene's test, and Aitken transformation. When lower and upper bounds are equal, supported procedures provide corresponding analyses for crisp data. The component methods are consolidated from the five source CRAN packages listed in the package merge notes.

License GPL-3

Encoding UTF-8

Depends R (>= 4.1.0)

Imports MASS, stats

NeedsCompilation no

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`CODnsANCOVA` *Neutrosophic Analysis of Covariance for Crossover Designs*

Description

Performs neutrosophic ANCOVA for crossover designs with direct treatment, residual, unit, period, and covariate effects. For crisp data, provide identical lower and upper matrices ('Lower_y = Upper_y' and 'Lower_z = Upper_z'); the function then yields classical ANCOVA results.

Usage

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

Arguments

Lower_y	Matrix of lower response values.
Upper_y	Matrix of upper response values.
Lower_z	Matrix of lower covariate values.
Upper_z	Matrix of upper covariate values.
design	Treatment-allocation matrix.
alpha	Significance level. Default is 0.05.
verbose	Logical; print the ANCOVA table when 'TRUE'.

Value

A list containing the neutrosophic ANCOVA table and calculated sums of squares, mean sums of squares, and F statistics.

Examples

```
Lower_y <- matrix(c(
13.14, 9.40, 12.73, 6.72, 6.32,
7.00, 11.47, 5.78, 16.06, 4.69,
5.60, 20.22, 9.57, 5.00, 9.73,
5.53, 6.64, 17.39, 9.57, 14.54,
14.46, 9.99, 8.87, 15.12, 10.45,
7.88, 6.62, 15.98, 10.29, 14.20,
4.83, 18.34, 9.70, 5.00, 9.89,
10.01, 13.20, 8.36, 17.94, 5.50,
16.17, 9.40, 12.96, 6.34, 7.19
), nrow = 9, byrow = TRUE)

Upper_y <- matrix(c(
18.24, 12.08, 15.67, 11.56, 11.94,
12.38, 15.29, 11.10, 21.90, 9.99,
10.62, 22.32, 12.11, 10.22, 13.05,
10.43, 9.44, 20.71, 13.47, 16.58,
17.48, 15.77, 13.49, 20.80, 16.13,
11.80, 9.72, 21.38, 15.57, 18.02,
9.77, 21.50, 13.98, 10.92, 15.05,
12.03, 16.24, 11.06, 23.32, 11.26,
18.93, 12.46, 16.34, 11.72, 12.15
), nrow = 9, byrow = TRUE)

Lower_z <- matrix(c(
195.89, 96.89, 257.23, 261.07, 254.25,
145.95, 117.95, 387.43, 105.70, 215.71,
163.26, 248.84, 235.63, 307.45, 246.18,
130.16, 195.21, 285.14, 307.71, 209.24,
138.38, 260.36, 310.74, 249.52, 98.62,
151.72, 226.72, 257.21, 205.90, 196.29,
251.63, 225.61, 207.61, 217.33, 261.98,
37.32, 96.61, 287.98, 241.99, 307.31,
```

```
304.91, 306.46, 405.96, 348.47, 307.91
), nrow = 9, byrow = TRUE)

Upper_z <- matrix(c(
204.11, 103.11, 262.77, 264.93, 263.75,
154.05, 122.05, 392.57, 112.30, 220.29,
166.74, 251.16, 242.37, 310.55, 251.82,
133.84, 200.79, 292.86, 312.29, 218.76,
141.62, 267.64, 313.26, 254.48, 101.38,
160.28, 233.28, 264.79, 214.10, 203.71,
260.37, 234.39, 212.39, 226.67, 266.02,
46.68, 103.39, 292.02, 248.01, 312.69,
311.09, 313.54, 414.04, 351.53, 316.09
), nrow = 9, byrow = TRUE)

design <- matrix(c(
  1, 2, 3, 4, 5,
  5, 1, 2, 3, 4,
  2, 3, 4, 5, 1,
  4, 5, 1, 2, 3,
  3, 4, 5, 1, 2,
  4, 5, 1, 2, 3,
  2, 3, 4, 5, 1,
  5, 1, 2, 3, 4,
  1, 2, 3, 4, 5
), nrow = 9, byrow = TRUE)

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

CODnsANOVA *Neutrosophic Analysis of Crossover Designs*

Description

Performs neutrosophic analysis of variance for crossover designs with direct and residual effects using interval-valued observations.

Usage

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

Arguments

Lower_y	Matrix of lower response values.
Upper_y	Matrix of upper response values.
design	Treatment-allocation matrix. Rows represent periods and columns represent experimental units or panelists.
alpha	Significance level for F-tests and LSD comparisons. Default is 0.05.
verbose	Logical; print ANOVA tables and LSD comparisons when 'TRUE'.

Details

For crisp data, provide identical lower and upper matrices ('Lower_y = Upper_y'); the function then yields classical ANOVA results.

Value

A list containing neutrosophic ANOVA tables, test statistics, treatment means, and LSD comparison results.

Examples

```
Lower_y <- matrix(c(
13.14, 9.40, 12.73, 6.72, 6.32, 18.24, 12.08, 15.67,
7.00, 11.47, 5.78, 16.06, 4.69, 12.38, 15.29, 11.10,
5.60, 20.22, 9.57, 5.00, 9.73, 10.62, 22.32, 12.11,
5.53, 6.64, 17.39, 9.57, 14.54, 10.43, 9.44, 20.71,
14.46, 9.99, 8.87, 15.12, 10.45, 17.48, 15.77, 13.49,
7.88, 6.62, 15.98, 10.29, 14.20, 11.80, 9.72, 21.38,
4.83, 18.34, 9.70, 5.00, 9.89, 9.77, 21.50, 13.98,
10.01, 13.20, 8.36, 17.94, 5.50, 12.03, 16.24, 11.06
), nrow = 8, byrow = TRUE)

Upper_y <- matrix(c(
18.24, 12.08, 15.67, 11.56, 11.94, 20.24, 16.08, 20.67,
12.38, 15.29, 11.10, 21.90, 9.99, 17.38, 20.29, 15.10,
10.62, 22.32, 12.11, 10.22, 13.05, 15.62, 27.32, 17.11,
10.43, 9.44, 20.71, 13.47, 16.58, 15.43, 14.44, 25.71,
17.48, 15.77, 13.49, 20.80, 16.13, 22.48, 20.77, 18.49,
11.80, 9.72, 21.38, 15.57, 18.02, 16.80, 14.72, 25.38,
9.77, 21.50, 13.98, 10.92, 15.05, 14.77, 26.50, 18.98,
12.03, 16.24, 11.06, 23.32, 11.26, 17.03, 21.24, 16.06
), nrow = 8, byrow = TRUE)

design <- matrix(c(
1,2,3,4,5,6,7,8,
8,1,2,3,4,5,6,7,
2,3,4,5,6,7,8,1,
7,8,1,2,3,4,5,6,
3,4,5,6,7,8,1,2,
6,7,8,1,2,3,4,5,
4,5,6,7,8,1,2,3,
```

```
5,6,7,8,1,2,3,4
), nrow = 8, byrow = TRUE)

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

CRDnsANCOVA *Neutrosophic Analysis of Covariance for Completely Randomized Design*

Description

Performs Neutrosophic Analysis of Covariance (NANCOVA) for interval-valued response and covariate data from a Completely Randomized Design (CRD).

Usage

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

Arguments

Lower_y	Numeric matrix of lower bounds of the response variable.
Upper_y	Numeric matrix of upper bounds of the response variable.
Lower_z	Numeric matrix of lower bounds of the covariate.
Upper_z	Numeric matrix of upper bounds of the covariate.
design	Numeric matrix representing the CRD treatment layout.
alpha	Significance level for interval-based LSD comparisons. Default is 0.05.
verbose	Logical. If TRUE, prints the NANCOVA table and LSD comparisons.

Value

A list containing the Neutrosophic ANCOVA table, interval LSD comparisons (if treatment effects are significant), and the interval LSD value.

Examples

```
Lower_y <- matrix(c(
  20,25,30,35,
  21,26,31,36,
  19,24,29,34,
  20,25,30,35,
  21,26,31,36
), nrow = 5, byrow = TRUE)

Upper_y <- matrix(c(
  22,27,32,37,
  23,28,33,38,
  21,26,31,36,
  22,27,32,37,
  23,28,33,38
), nrow = 5, byrow = TRUE)

Lower_z <- matrix(c(
  8,9,10,11,
  9,10,11,12,
  8,9,10,11,
  9,10,11,12,
  8,9,10,11
), nrow = 5, byrow = TRUE)

Upper_z <- matrix(c(
  9,10,11,12,
  10,11,12,13,
  9,10,11,12,
  10,11,12,13,
  9,10,11,12
), nrow = 5, byrow = TRUE)

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

CRDnsANCOVA(Lower_y, Upper_y, Lower_z, Upper_z, design)
```

CRDnsANOVA *Neutrosophic Analysis of Variance for Completely Randomized Design*

Description

Performs neutrosophic analysis of variance (NANOVA) for a completely randomized design using interval-valued observations.

Usage

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

Arguments

Lower_y	Matrix of lower bounds of the response variable.
Upper_y	Matrix of upper bounds of the response variable.
design	Matrix specifying treatment allocation.
alpha	Significance level for LSD test.
verbose	Logical. If TRUE, prints the analysis.

Value

A list containing the NANOVA table, treatment means, pairwise comparisons, and LSD interval.

Examples

```
Lower_y <- matrix(c(
  9.5, 19.5, 29.5, 39.5,
  10.0, 20.0, 30.0, 40.0,
  10.5, 20.5, 30.5, 40.5,
  9.8, 19.8, 29.8, 39.8,
  10.2, 20.2, 30.2, 40.2
), nrow = 5, byrow = TRUE)

Upper_y <- matrix(c(
  10.5, 20.5, 30.5, 40.5,
  11.0, 21.0, 31.0, 41.0,
  11.5, 21.5, 31.5, 41.5,
  10.8, 20.8, 30.8, 40.8,
  11.2, 21.2, 31.2, 41.2
), nrow = 5, byrow = TRUE)

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

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

CRDnsMANOVA *Neutrosophic MANOVA for a Completely Randomized Design*

Description

Performs neutrosophic multivariate analysis of variance (MANOVA) for interval-valued multivariate observations under a completely randomized design using Wilks' Lambda as the multivariate test criterion.

Usage

```
CRDnsMANOVA(Lower_y, Upper_y, group, alpha = 0.05, verbose = TRUE)
```

Arguments

`Lower_y`	A numeric matrix containing the lower bounds of the response variables. Rows represent observations and columns represent response variables.
`Upper_y`	A numeric matrix containing the upper bounds of the response variables. Must have the same dimensions as `Lower_y`.
`group`	A vector or factor identifying the treatment group for each observation. Its length must equal `nrow(Lower_y)`.
`alpha`	Significance level used to obtain the critical F value. Defaults to `0.05`.
`verbose`	Logical; if `TRUE`, prints the neutrosophic MANOVA table. Defaults to `TRUE`.

Value

A list containing the results of the neutrosophic MANOVA with the following components:

MANOVA.table A data frame containing the neutrosophic MANOVA table, including the source of variation, degrees of freedom, Wilks' Lambda interval, approximate F-statistic interval, and decision.

Wilks.Lambda A named numeric vector containing the lower and upper bounds of Wilks' Lambda.

Approx.F A named numeric vector containing the lower and upper bounds of the approximate F-statistic.

F.critical The critical F value at the specified significance level.

Decision The hypothesis testing decision ("Significant", "Not Significant", or "Indeterminate").

treatment_ss A list containing the lower, upper, determinate, and indeterminate treatment sum of squares matrices.

total_ss A list containing the lower, upper, determinate, and indeterminate total sum of squares matrices.

residual_ss A list containing the lower, upper, determinate, and indeterminate residual sum of squares matrices.

Examples

```
YL <- matrix(c(8.27, 2.50, 5.30, 1.41,
               8.40, 6.27, 0.00, 3.42),
             ncol = 2, byrow = TRUE)

YU <- matrix(c(9.73, 3.50, 6.70, 2.59,
               9.60, 7.73, 0.00, 4.58),
             ncol = 2, byrow = TRUE)

g <- c(1, 1, 2, 2)

fit <- CRDnsMANOVA(
  Lower_y = YL,
  Upper_y = YU,
  group = g
)

fit$MANOVA.table
fit$Decision
```

IBDnsANCOVA *Neutrosophic ANCOVA for Incomplete Block Designs*

Description

Performs neutrosophic analysis of covariance for incomplete block designs using interval-valued responses and covariates.

Usage

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

Arguments

Lower_y	Matrix of lower interval responses.
Upper_y	Matrix of upper interval responses.
Lower_z	Matrix of lower interval covariates.
Upper_z	Matrix of upper interval covariates.
design	Incomplete block design matrix.

alpha	Significance level for LSD test and F-test (default = 0.05).
verbose	Logical. If TRUE, prints the neutrosophic ANCOVA table, significance codes, LSD interval and pairwise treatment comparisons. Default = FALSE.

Details

The rows of the response and design arrays represent blocks, while the columns represent treatment allocations within blocks.

Value

A list containing:

- STAR_NANCOVA : Neutrosophic ANCOVA table.
- LSD : Neutrosophic LSD interval.
- Comparison : Pairwise treatment comparison table.

Examples

```
Lower_y <- matrix(c(
  46.46436719,49.56056768,47.21541951,
  47.41402083,51.24762662,50.95734839,
  50.7492564,51.250892,50.01772519,
  51.72202304,53.83285904,54.53288749,
  53.71983091,55.3957797,53.85646279,
  55.29951886,57.48888886,56.81959243,
  56.01454397,57.64266115,56.15643552
), nrow = 7, byrow = TRUE)

Upper_y <- matrix(c(
  49.53563281,52.43943232,52.78458049,
  52.58597917,54.75237338,53.04265161,
  53.2507436,56.749108,55.98227481,
  54.27797696,58.16714096,59.46711251,
  56.28016909,60.6042203,58.14353721,
  58.70048114,60.51111114,59.18040757,
  59.98545603,62.35733885,61.84356448
), nrow = 7, byrow = TRUE)

Lower_z <- matrix(c(
  87.6024962,49.87728481,21.20537996,
  74.19109283,70.90050743,69.79918837,
  118.3567216,84.52944492,87.2387685,
  116.5444728,127.5038727,122.3890764,
  104.4945972,117.9310944,126.206537,
  101.9435439,91.18240208,81.56378309,
  92.28882349,86.13485988,83.04950126
), nrow = 7, byrow = TRUE)

Upper_z <- matrix(c(
  90.3975038,60.12271519,32.79462004,
```

```
  81.80890717,73.09949257,72.20081163,
  127.6432784,97.47055508,102.7612315,
  131.4555272,136.4961273,135.6109236,
  119.5054028,122.0689056,133.793463,
  116.0564561,102.8175979,96.43621691,
  99.71117651,93.86514012,92.95049874
), nrow = 7, byrow = TRUE)

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

IBDnsANCOVA(
  Lower_y = Lower_y,
  Upper_y = Upper_y,
  Lower_z = Lower_z,
  Upper_z = Upper_z,
  design = design,
  verbose = TRUE
)
```

`IBDnsANOVA` *Neutrosophic ANOVA for Incomplete Block Designs*

Description

Performs neutrosophic analysis of variance for incomplete block designs using interval-valued observations.

Usage

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

Arguments

`Lower_y`	Matrix of lower interval responses.
`Upper_y`	Matrix of upper interval responses.
`design`	Incomplete block design matrix.
`alpha`	Significance level for LSD test and F-test (default = 0.05).
`verbose`	Logical. If TRUE, prints the neutrosophic ANOVA table, LSD interval, significance codes and pairwise treatment comparisons. Default = FALSE.

Details

The rows of the response and design arrays represent blocks, while the columns represent treatment allocations within blocks.

Value

A list containing:

- STAR_NANOVA : Neutrosophic ANOVA table.
- LSD : Neutrosophic LSD interval.
- Comparison : Pairwise treatment comparison table.

Examples

```
Lower_y <- matrix(c(
  46.46436719,49.56056768,47.21541951,
  47.41402083,51.24762662,50.95734839,
  50.74925640,51.25089200,50.01772519,
  51.72202304,53.83285904,54.53288749,
  53.71983091,55.39577970,53.85646279,
  55.29951886,57.48888886,56.81959243,
  56.01454397,57.64266115,56.15643552
), nrow = 7, byrow = TRUE)

Upper_y <- matrix(c(
  49.53563281,52.43943232,52.78458049,
  52.58597917,54.75237338,53.04265161,
  53.25074360,56.74910800,55.98227481,
  54.27797696,58.16714096,59.46711251,
  56.28016909,60.60422030,58.14353721,
  58.70048114,60.51111114,59.18040757,
  59.98545603,62.35733885,61.84356448
), nrow = 7, byrow = TRUE)

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

IBDnsANOVA( Lower_y,  Upper_y,  design,  verbose = TRUE )
```

LDnsANCOVA *Neutrosophic ANCOVA for Lattice Designs*

Description

Performs neutrosophic analysis of covariance for lattice designs using interval-valued responses and covariates.

Usage

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

Arguments

Lower_y	Matrix of lower interval responses.
Upper_y	Matrix of upper interval responses.
Lower_z	Matrix of lower interval covariates.
Upper_z	Matrix of upper interval covariates.
design	Lattice design matrix.
alpha	Significance level for LSD test and F-test (default = 0.05).
verbose	Logical. If TRUE, prints the neutrosophic ANCOVA table, significance codes, LSD interval and pairwise treatment comparisons. Default = FALSE.

Details

The rows of the response and design arrays represent blocks, while the columns represent treatment allocations within blocks.

Value

A list containing:

- STAR_NANCOVA : Neutrosophic ANCOVA table.
- LSD : Neutrosophic LSD interval.
- Comparison : Pairwise treatment comparison table.

Examples

```
Lower_y <- matrix(c(
  86.81,81.44,89.83,
  76.14,72.77,72.93,
  92.17,58.56,70.48,
  111.43,78.95,56.87,
  84.71,74.19,98.10,
  78.91,90.49,87.52,
  99.76,80.10,94.54,
  62.05,86.81,63.06,
  67.52,70.05,68.24
), nrow = 9, byrow = TRUE)

Upper_y <- matrix(c(
  89.19,88.56,94.17,
  79.86,79.23,79.07,
  95.83,65.44,79.52,
  118.57,85.05,63.13,
  89.29,77.81,105.90,
  85.09,99.51,92.48,
  104.24,87.90,99.46,
  65.95,91.19,70.94,
  72.48,79.95,75.76
), nrow = 9, byrow = TRUE)

Lower_z <- matrix(c(
  27.04,24.47,20.28,
  32.31,37.02,23.16,
  12.58,8.35,22.37,
  7.31,20.02,25.12,
  9.93,33.58,12.50,
  17.74,37.01,24.99,
  22.28,4.65,22.52,
  21.71,18.47,20.41,
  35.65,17.27,23.22
), nrow = 9, byrow = TRUE)

Upper_z <- matrix(c(
  36.96,27.53,26.72,
  37.69,40.98,26.84,
  17.42,15.65,32.03,
  16.69,29.78,28.28,
  16.07,36.42,21.50,
  22.26,40.99,30.01,
  25.72,13.35,30.08,
  25.49,27.53,29.19,
  44.35,24.73,30.98
), nrow = 9, byrow = TRUE)

design <- matrix(c(
  1,2,3,
  7,9,8,
```

```
  6,4,5,
  1,7,4,
  8,5,2,
  3,6,9,
  1,8,6,
  4,2,9,
  3,5,7
), nrow = 9, byrow = TRUE)

LDnsANCOVA(
  Lower_y = Lower_y,
  Upper_y = Upper_y,
  Lower_z = Lower_z,
  Upper_z = Upper_z,
  design = design,
  verbose = TRUE
)
```

`LDnsANOVA` *Neutrosophic ANOVA for Lattice Designs*

Description

Performs neutrosophic analysis of variance for lattice designs using interval-valued observations.

Usage

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

Arguments

`Lower_y`	Matrix of lower interval responses.
`Upper_y`	Matrix of upper interval responses.
`design`	Lattice design matrix.
`alpha`	Significance level for LSD test and F-test (default = 0.05).
`verbose`	Logical. If TRUE, prints the neutrosophic ANOVA table, significance codes, LSD interval and pairwise treatment comparisons. Default = FALSE.

Details

The rows of the response and design arrays represent blocks, while the columns represent treatment allocations within blocks.

Value

A list containing:

- STAR_NANOVA : Neutrosophic ANOVA table.
- LSD : Neutrosophic LSD interval.
- Comparison : Pairwise treatment comparison table.

Examples

```
Lower_y <- matrix(c(
  86.81,81.44,89.83,
  76.14,72.77,72.93,
  92.17,58.56,70.48,
  111.43,78.95,56.87,
  84.71,74.19,98.10,
  78.91,90.49,87.52,
  99.76,80.10,94.54,
  62.05,86.81,63.06,
  67.52,70.05,68.24
), nrow=9, byrow=TRUE)

Upper_y <- matrix(c(
  89.19,88.56,94.17,
  79.86,79.23,79.07,
  95.83,65.44,79.52,
  118.57,85.05,63.13,
  89.29,77.81,105.90,
  85.09,99.51,92.48,
  104.24,87.90,99.46,
  65.95,91.19,70.94,
  72.48,79.95,75.76
), nrow=9, byrow=TRUE)

design <- matrix(c(
  1,2,3,
  7,9,8,
  6,4,5,
  1,7,4,
  8,5,2,
  3,6,9,
  1,8,6,
  4,2,9,
  3,5,7
), nrow=9, byrow=TRUE)

LDnsANOVA(Lower_y, Upper_y,design,verbose = TRUE )
```

LSDnsANCOVA *Neutrosophic Analysis of Covariance for Latin Square Design*

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)
```

LSDnsANOVA *Neutrosophic Analysis of Variance for Latin Square Design*

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)
```

MSDnsANOVA *Neutrosophic Analysis of Multi-Session Designs*

Description

Performs determinate–indeterminate neutrosophic ANOVA for the revised two-session crossover design methodology.

Usage

```
MSDnsANOVA(design, D, I, verbose = TRUE)
```

Arguments

design	Square treatment-allocation matrix. Rows are periods and columns are panelists.
D	Matrix of determinate observations, with the same dimensions as ‘design‘.
I	Matrix of indeterminate observations, with the same dimensions as ‘design‘.
verbose	Logical; print the ANOVA table when ‘TRUE‘.

Details

For crisp data, provide an indeterminate matrix containing only zeros (‘I = 0‘); the function then yields classical ANOVA results.

Value

A list containing the ANOVA table, information matrices, canonical efficiency factors, sums of squares, mean square error, and degrees of freedom.

Examples

```
design <- matrix(c(
  1,2,3,4,5,6,7,8,
  8,1,2,3,4,5,6,7,
  2,3,4,5,6,7,8,1,
  7,8,1,2,3,4,5,6,
  3,4,5,6,7,8,1,2,
  6,7,8,1,2,3,4,5,
```

```
  4,5,6,7,8,1,2,3,
  5,6,7,8,1,2,3,4
), nrow = 8, byrow = TRUE)

D <- matrix(c(
  61.56,63.38,65.20,67.00,68.80,70.55,71.20,70.11,
  62.82,60.94,65.26,69.234,68.10,68.21,71.60,73.20,
  72.10,67.21,68.60,70.50,72.30,74.10,75.90,63.50,
  66.21,67.52,68.90,69.20,67.10,70.80,68.90,72.60,
  65.76,62.10,72.00,72.80,73.20,76.50,64.10,65.90,
  65.20,64.40,65.00,65.80,71.00,73.26,71.65,68.30,
  68.10,72.30,74.10,74.20,76.20,65.00,66.80,68.60,
  68.60,66.90,72.20,68.00,66.00,73.00,65.80,71.30
), nrow = 8, byrow = TRUE)

I <- matrix(c(
  2.41,3.02,2.40,4.96,2.90,2.53,4.90,3.23,
  1.92,4.75,4.35,2.63,1.87,4.52,2.29,2.88,
  1.43,3.45,2.60,2.83,1.25,1.39,1.70,4.96,
  4.88,1.55,1.16,4.44,4.58,3.15,4.58,2.30,
  4.34,4.63,2.67,1.15,2.22,1.14,2.78,4.30,
  3.22,4.54,4.34,1.46,2.99,2.46,3.57,2.69,
  4.63,1.62,1.12,3.67,2.64,3.91,4.34,4.17,
  2.11,3.33,4.75,4.68,2.50,3.50,2.89,1.19
), nrow = 8, byrow = TRUE)

result <- MSDnsANOVA(design, D, I, verbose = TRUE)
```

`nsAitkenTransform` *Aitken Transformation for Neutrosophic Interval Data*

Description

Applies an Aitken variance-stabilizing transformation to interval-valued observations using group-specific interval MSE values.

Usage

```
nsAitkenTransform(Lower_y, Upper_y, group, MSE_lower, MSE_upper)
```

Arguments

`Lower_y`	Numeric matrix of lower interval bounds.
`Upper_y`	Numeric matrix of upper interval bounds.
`group`	Vector identifying the group/year for every row of the input.
`MSE_lower`	Numeric vector of lower MSE bounds, one per group.
`MSE_upper`	Numeric vector of upper MSE bounds, one per group.

Value

A list containing transformed lower/upper matrices and their determinate and indeterminate components.

Examples

```
Lower_y <- matrix(
  c(8.2, 5.1,
    7.9, 5.4,
    9.0, 6.2,
    8.8, 6.0,
    7.5, 4.8,
    7.8, 5.0,
    8.6, 5.8,
    8.4, 5.6),
  ncol = 2,
  byrow = TRUE
)

Upper_y <- matrix(
  c(8.8, 5.7,
    8.5, 6.0,
    9.6, 6.8,
    9.4, 6.6,
    8.1, 5.4,
    8.4, 5.6,
    9.2, 6.4,
    9.0, 6.2),
  ncol = 2,
  byrow = TRUE
)

group <- rep(1:4, each = 2)

transformed <- nsAitkenTransform(
  Lower_y = Lower_y,
  Upper_y = Upper_y,
  group = group,
  MSE_lower = c(29.83, 16.30, 21.21, 3.62),
  MSE_upper = c(30.02, 16.43, 21.24, 3.89)
)

transformed$weights
```

---

nsLeveneTest *Neutrosophic Levene's Test for Interval-Valued Data*

Description

Tests homogeneity of variances for interval-valued observations using neutrosophic lower and upper test-statistic bounds.

Usage

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

Arguments

Lower_y	Numeric matrix of lower interval bounds.
Upper_y	Numeric matrix of upper interval bounds; same dimensions as Lower_y.
design	Treatment-design matrix. Treatment labels in each row must be arranged in consecutive year blocks.
alpha	Significance level. Default is 0.05.
verbose	Logical; print the test table when TRUE.

Value

An invisible list containing the Levene statistic interval, critical F value, homogeneity decision, and ANOVA table.

Examples

```
# Two replications, three treatments, and two years.
# Columns are ordered as:
# Year 1 (T1, T2, T3), Year 2 (T1, T2, T3).

Lower_y <- matrix(c(
  10, 12, 11, 13, 14, 12,
   9, 11, 10, 12, 13, 11
), nrow = 2, byrow = TRUE)

Upper_y <- matrix(c(
  12, 14, 13, 15, 16, 14,
  11, 13, 12, 14, 15, 13
), nrow = 2, byrow = TRUE)

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

levene_result <- nsLeveneTest(
  Lower_y = Lower_y,
  Upper_y = Upper_y,
  design = design,
  alpha = 0.05,
  verbose = TRUE
)

levene_result$Homogeneity
```

`PooledCRDnsANOVA` *Pooled Neutrosophic ANOVA for a Completely Randomized Design*

Description

Performs pooled neutrosophic analysis of variance for a completely randomized design.

Usage

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

Arguments

`Lower_y`	Numeric matrix of lower response bounds. Columns must be arranged in consecutive year or location blocks, each containing all treatments.
`Upper_y`	Numeric matrix of upper response bounds.
`design`	Numeric treatment-layout matrix with the same dimensions as `Lower_y`.
`alpha`	Significance level. Default is `0.05`.
`verbose`	Logical; print results when `TRUE`.

Value

A list containing the initial and final NANOVA tables, interaction test, decision, and pooled MSE when applicable.

Examples

```
# Three replications, three treatments, and two years.
# Columns 1-3 are Year 1; columns 4-6 are Year 2.

Lower_y <- matrix(c(
  20, 25, 30, 21, 26, 31,
  22, 27, 32, 23, 28, 33,
  21, 26, 31, 22, 27, 32
), nrow = 3, byrow = TRUE)

Upper_y <- matrix(c(
  22, 27, 32, 23, 28, 33,
  24, 29, 34, 25, 30, 35,
  23, 28, 33, 24, 29, 34
), nrow = 3, byrow = TRUE)

# Treatment layout:
# Year 1 = Treatments 1, 2, 3
# Year 2 = Treatments 1, 2, 3
design <- matrix(c(
  1, 2, 3, 1, 2, 3,
  1, 2, 3, 1, 2, 3,
```

```
  1, 2, 3, 1, 2, 3
), nrow = 3, byrow = TRUE)

result <- PooledCRDnsANOVA(
  Lower_y = Lower_y,
  Upper_y = Upper_y,
  design = design,
  alpha = 0.05,
  verbose = TRUE
)

result$NANOVA.table
```

`PooledRBDnsANOVA` *Pooled Neutrosophic Analysis of Variance for a Randomized Block Design*

Description

Performs the pooled neutrosophic ANOVA calculation for interval-valued observations measured in a Randomized Block Design over multiple years or locations or seasons.

Usage

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

Arguments

`Lower_y`	Numeric matrix of lower response bounds. Columns must be ordered in consecutive year blocks, each containing all treatments.
`Upper_y`	Numeric matrix of upper response bounds, with the same dimensions as `Lower_y`.
`design`	Numeric matrix giving the treatment labels for `Lower_y`.
`alpha`	Significance level for the treatment-by-year interaction test.
`verbose`	Logical; print the neutrosophic ANOVA table when `TRUE`.

Value

An invisible list containing the neutrosophic ANOVA table, interaction F interval and critical value, interaction decision, and the mean-square interval used for subsequent F intervals.

Examples

```
# Three blocks, three treatments, and two years.
# Columns 1-3 are Year 1; columns 4-6 are Year 2.
# Each block contains every treatment once in each year.

Lower_y <- matrix(c(
  20, 25, 30, 22, 28, 23,
```

```
  27, 32, 21, 33, 24, 29,
  31, 22, 26, 25, 30, 34
), nrow = 3, byrow = TRUE)

Upper_y <- matrix(c(
  22, 27, 32, 24, 30, 25,
  29, 34, 23, 35, 26, 31,
  33, 24, 28, 27, 32, 36
), nrow = 3, byrow = TRUE)

# Treatment layout for each block:
# Year 1 occupies columns 1-3.
# Year 2 occupies columns 4-6.
design <- matrix(c(
  1, 2, 3, 2, 3, 1,
  2, 3, 1, 3, 1, 2,
  3, 1, 2, 1, 2, 3
), nrow = 3, byrow = TRUE)

result <- PooledRBDnsANOVA(
  Lower_y = Lower_y,
  Upper_y = Upper_y,
  design = design,
  alpha = 0.05,
  verbose = TRUE
)

result$NANOVA.table
```

RCBDnsANCOVA *Neutrosophic Analysis of Covariance for RCBD*

Description

Performs neutrosophic analysis of covariance for a Randomized Complete Block Design using interval-valued response and covariate data.

Usage

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

Arguments

`Lower_y`	Numeric matrix of lower response values.
`Upper_y`	Numeric matrix of upper response values.
`Lower_z`	Numeric matrix of lower covariate values.
`Upper_z`	Numeric matrix of upper covariate values.
`design`	Numeric matrix representing the RCBD layout.
`alpha`	Significance level for LSD test. Default is `0.05`.
`verbose`	Logical; if `TRUE`, prints the analysis. Default is `FALSE`.

Value

A list containing the NANCOVA table, LSD interval, and treatment comparisons (if treatment effect is significant).

Examples

```
Lower_y <- matrix(c(
  46.84, 97.69, 39.30, 49.20,
  51.52, 83.38, 56.48, 42.15,
  44.42, 49.64, 44.21, 35.79,
  32.77, 74.30, 55.72, 70.55
), nrow = 4, byrow = TRUE)

Upper_y <- matrix(c(
  49.66,101.31,47.70,55.80,
  60.98,87.62,60.52,44.85,
  52.26,59.36,52.79,44.61,
  42.23,82.70,59.28,75.45
), nrow = 4, byrow = TRUE)

Lower_z <- matrix(c(
  224.95,245.87,245.19,259.41,
  222.06,213.83,253.10,247.51,
  255.67,230.55,265.05,246.67,
  137.98,214.68,251.49,257.70
), nrow = 4, byrow = TRUE)

Upper_z <- matrix(c(
  229.05,250.13,252.81,268.59,
  229.94,222.17,258.90,256.49,
  262.33,237.45,274.95,249.33,
  142.02,219.32,260.51,264.30
), nrow = 4, byrow = TRUE)

design <- matrix(c(
  1,2,3,4,
  1,2,3,4,
  1,2,3,4,
  1,2,3,4
```

```
), nrow = 4, byrow = TRUE)

result <- RCBDnsANCOVA(
  Lower_y,
  Upper_y,
  Lower_z,
  Upper_z,
  design,
  alpha = 0.05,
  verbose = TRUE
)
```

RCBDnsANOVA *Neutrosophic Analysis of Variance for Randomized Complete Block Design*

Description

Performs Neutrosophic Analysis of Variance (NANOVA) for interval-valued response data from a Randomized Complete Block Design (RCBD).

Usage

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

Arguments

Lower_y	Numeric matrix of lower bounds of the response variable.
Upper_y	Numeric matrix of upper bounds of the response variable.
design	Numeric matrix representing the RCBD layout.
alpha	Significance level for interval-based LSD test. Default is 0.05.
verbose	Logical. If TRUE, prints the NANOVA table and LSD comparisons.

Value

A list containing the Neutrosophic ANOVA table, interval-based LSD comparisons (if applicable), and the interval LSD.

Examples

```
Lower_y <- matrix(c(
  120.230,125.488,132.987,127.086,127.672,128.013,
  122.594,121.009,123.969,120.358,120.424,122.197,
  121.183,130.671,128.794,114.863,122.595,122.073,
  127.620,124.532,132.893,125.528,125.850,127.550
), nrow = 4, byrow = TRUE)

Upper_y <- matrix(c(
```

```
  127.6967536,131.2116955,141.2127373,136.1540904,130.6884772,136.8474149,
  129.8264289,130.3314544,133.3113414,126.5063118,128.4362999,130.2714433,
  124.5068016,139.3287297,134.1060197,124.2774447,127.2248520,130.3948469,
  131.0638721,129.8884785,135.5666716,127.7580663,132.0178679,133.3903886
), nrow = 4, byrow = TRUE)

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

RCBDnsANOVA(Lower_y, Upper_y, design)
```

`SplitPlotDnsANOVA` *Neutrosophic Analysis of Variance for Split-Plot Designs*

Description

Performs Neutrosophic Analysis of Variance (NANOVA) for split-plot designs using interval-valued observations. The function provides neutrosophic ANOVA tables, interval-valued F-tests, significance tests, and Least Significant Difference (LSD) based multiple comparisons. For crisp data, users may provide identical lower and upper response values to obtain results equivalent to classical split-plot ANOVA.

Usage

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

Arguments

`Lower_y`	A matrix containing the lower values of the response variable.
`Upper_y`	A matrix containing the upper values of the response variable.
`design`	A data frame containing three columns corresponding to replication, main plot treatments, and sub plot treatments, respectively.
`alpha`	Significance level used for hypothesis testing and LSD-based multiple comparisons. Default is 0.05.
`verbose`	Logical. If TRUE, the neutrosophic ANOVA table, significance tests, LSD values, and multiple comparison results are displayed. Default is FALSE.

Value

A list containing:

Split_Plot_NANOVA Neutrosophic ANOVA table containing sources of variation, degrees of freedom, neutrosophic sums of squares, mean squares, F-statistics, and significance levels.

LSD_MainPlot Neutrosophic LSD interval for main plot effects, returned only when the main plot effect is significant.

LSD_SubPlot Neutrosophic LSD interval for sub plot effects, returned only when the sub plot effect is significant.

LSD_Interaction Neutrosophic LSD interval for interaction effects, returned only when the interaction effect is significant.

Comparison_MainPlot Pairwise neutrosophic comparisons among main plot treatment means.

Comparison_SubPlot Pairwise neutrosophic comparisons among sub plot treatment means.

Comparison_Interaction Pairwise neutrosophic comparisons among interaction treatment means.

Examples

```
Lower_y <- matrix(c(
  13.81,13.11,18.16,
  18.54,19.84,28.43,
  11.48,14.33,14.29,
  14.50,15.99,21.19,
  11.65,18.08,17.37,
  11.78,12.46,17.21,
  11.67,11.28,8.65,
  18.81,16.27,21.46,
  11.96,16.15,18.19,
  10.34,11.28,16.91,
  9.08,14.91,11.95,
  11.04,10.80,6.48
), ncol = 3, byrow = TRUE)

Upper_y <- matrix(c(
  17.19,21.89,23.44,
  22.46,29.16,31.97,
  19.72,22.07,22.71,
  23.30,24.41,27.81,
  18.35,22.92,20.43,
  20.22,19.14,19.39,
  14.13,17.72,18.35,
  21.59,20.73,29.34,
  19.84,24.85,26.81,
  15.46,15.72,20.09,
  17.92,20.09,17.85,
  13.96,13.00,14.52
), ncol = 3, byrow = TRUE)

Rep <- factor(rep(paste0("R",1:4), each = 9))
MainPlot <- factor(rep(rep(paste0("M",1:3), each = 3), 4))
SubPlot <- factor(rep(paste0("S",1:3), 12))
design <- data.frame(Rep, MainPlot, SubPlot)

result <- SplitPlotDnsANOVA(Lower_y = Lower_y, Upper_y = Upper_y, design = design,
 alpha = 0.05, verbose = TRUE)
```

`StripPlotDnsANOVA` *Neutrosophic Analysis of Variance for Strip-Plot Designs*

Description

Performs Neutrosophic Analysis of Variance (NANOVA) for strip-plot designs using interval-valued observations. The function provides neutrosophic ANOVA tables, interval-valued F-tests, significance tests, and Least Significant Difference (LSD) based multiple comparisons for horizontal factors, vertical factors, and their interaction effects. For crisp data, users may provide identical lower and upper response values to obtain results equivalent to classical strip-plot ANOVA.

Usage

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

Arguments

`Lower_y`	A matrix containing the lower values of the response variable.
`Upper_y`	A matrix containing the upper values of the response variable.
`design`	A data frame containing three columns corresponding to replication, horizontal factor treatments, and vertical factor treatments, respectively.
`alpha`	Significance level used for hypothesis testing and LSD-based multiple comparisons. Default is 0.05.
`verbose`	Logical. If TRUE, the neutrosophic ANOVA table, significance tests, LSD values, and multiple comparison results are displayed. Default is FALSE.

Value

A list containing:

Strip_Plot_NANOVA Neutrosophic ANOVA table containing sources of variation, degrees of freedom, neutrosophic sums of squares, mean squares, F-statistics, and significance levels.

LSD_Horizontal Neutrosophic LSD interval for horizontal factor effects, returned only when the horizontal factor effect is significant.

LSD_Vertical Neutrosophic LSD interval for vertical factor effects, returned only when the vertical factor effect is significant.

LSD_Interaction Neutrosophic LSD interval for horizontal x vertical interaction effects, returned only when the interaction effect is significant.

Comparison_Horizontal Pairwise neutrosophic comparisons among horizontal factor treatment means.

Comparison_Vertical Pairwise neutrosophic comparisons among vertical factor treatment means.

Comparison_Interaction Pairwise neutrosophic comparisons among horizontal x vertical treatment combinations.

Examples

```
Lower_y <- matrix(c(
  10,12,
  11,13,
  12,14,
  13,15,
  11,12,
  12,13
), nrow = 6, byrow = TRUE)

Upper_y <- matrix(c(
  12,14,
  13,15,
  14,16,
  15,17,
  13,14,
  14,15
), nrow = 6, byrow = TRUE)

# Strip-plot design
# 2 Replications x 3 Horizontal Factors x 2 Vertical Factors
Rep <- factor(rep(c("R1","R2"), each = 6))
Horizontal <- factor(rep(c("H1","H2","H3"), each = 2, times = 2))
Vertical <- factor(rep(c("S1","S2"), times = 6))
design <- data.frame(Rep, Horizontal, Vertical)

result <- StripPlotDnsANOVA(
  Lower_y = Lower_y,
  Upper_y = Upper_y,
  design = 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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