

Package ‘NeutroCrdRcbdAnalysis’

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Type Package

Title Neutrosophic Analysis of Completely Randomized Designs and
Randomized Complete Block Designs

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Description Provides neutrosophic analysis of variance (NANOVA) and
analysis of covariance (NANCOVA) for Completely Randomized Designs
(CRD) and Randomized Complete Block Designs (RCBD) using
interval-valued observations. Computes interval sums of squares,
mean squares, F-statistics, significance tests, and interval-based
least significant difference (LSD) comparisons. When lower and
upper observations are identical (crisp data), the methods reduce to the
corresponding classical ANOVA and ANCOVA.

License GPL-3

Encoding UTF-8

Imports MASS, stats

RoxygenNote 7.3.3

NeedsCompilation no

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CRDnsANCOVA	<i>Neutrosophic Analysis of Covariance for Completely Randomized Design</i>
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Description

Performs Neutrosophic Analysis of Covariance (NANCOVA) for interval-valued response and co-variate 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)

```

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
)
```

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)
```

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