

Package ‘NeutroBasicDesignsAnalysis’

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

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

Description Provides neutrosophic statistical methods for interval-valued data from completely randomized and randomized complete block designs. Methods include neutrosophic analysis of variance, analysis of covariance, multivariate analysis of variance, pooled analysis of variance, Levene's test, and Aitken transformation. When the lower and upper bounds are equal (crisp data), the methods reduce to their corresponding classical statistical analyses. The basic concept of neutrosophic statistics is based on Smarandache (2014) <<https://fs.unm.edu/NeutrosophicStatistics.pdf>>, while the statistical analysis procedures implemented in this package are newly developed.

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

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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)
```

```

), 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
```

nsAitkenTransform	<i>Aitken Transformation for Neutrosophic Interval Data</i>
-------------------	---

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)
```

```

), nrow = 4, byrow = TRUE)

result <- RCBAnsANCOVA(
  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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