

Package ‘NeutroCODsAnalysis’

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Title Neutrosophic Analysis Crossover Designs

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

Description Provides methods for Neutrosophic Analysis of Variance (NANOVA) and Neutrosophic Analysis of Covariance (NANCOVA) for crossover designs, as well as NANOVA for multi-session designs with direct and residual effects using interval-valued observations. For crisp data, users can enter identical lower and upper values for the response and covariate variables to obtain results equivalent to classical Analysis of Variance (ANOVA) and Analysis of Covariance (ANCOVA), respectively. The basic concepts of neutrosophic statistics are based on Smarandache (2014) <<https://fs.unm.edu/NeutrosophicStatistics.pdf>>, while the analysis procedures implemented in this package are newly developed.

License GPL (>= 2)

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Imports MASS

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

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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	<i>Neutrosophic Analysis of Crossover Designs</i>
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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)

```

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)
```

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