Package: PGaovR (via r-universe)

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Type Package

Title Analysis of Experimental Data using ANOVA and Mean Comparison

Version 0.1.1

Description Provides tools for designing and analyzing agricultural experiments. It includes functions for generating randomized treatment layouts for standard experimental designs such as Completely Randomized Design (CRD), Randomized Block Design (RBD), Latin Square Design (LSD), Factorial Randomized Block Design (FRBD), split-plot design, and strip-plot design. The package implements one-factor and two-factor analysis of variance (ANOVA) and offers multiple comparison procedures, including Least Significant Difference (lsd), Tukey, and Duncan tests, to compare treatment means in single-factor and factorial experiments. The methods follow classical experimental design principles described in Gomez and Gomez (1984, Statistical Procedures for Agricultural Research, John Wiley & Sons, New York).

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Contents

`aov_of` *One-Factor ANOVA for Agricultural Designs*

Description

Performs analysis of variance for one-factor experiments under Completely Randomized Design (CRD), Randomized Block Design (RBD), and Latin Square Design (LSD). Supports multiple response variables, data transformation, and mean comparison tests.

Usage

```
aov_of(
  data,
  design = c("CRD", "RBD", "LSD"),
  treatment,
  replication = NULL,
  row = NULL,
  column = NULL,
  responsevar = "all",
  test = c("lsd", "tukey", "duncan"),
  transform = NULL,
  narc = 1,
  alpha = 0.05
)
```

Arguments

`data`	A data frame containing experimental data.
`design`	Type of design. One of "CRD", "RBD", or "LSD".
`treatment`	Name of treatment column in the dataset.
`replication`	Name of replication/block column (required for RBD).
`row`	Name of row factor (required for LSD).

`column`	Name of column factor (required for LSD).
`responsevar`	Specific variables c("v1" ,"v2", "v3") or "all".
`test`	Mean comparison test. Options include "lsd", "tukey", or "duncan".
`transform`	List specifying transformations for variables. Options include "log", "sqrt", and "arcsine".
`narc`	Numeric or list specifying denominator for arcsine transformation.
`alpha`	Significance level (e.g., 0.05).

Details

This function supports:

- Analysis for CRD, RBD, and LSD designs
- Multiple response variables
- Data transformations (log, square root, arcsine)
- Mean separation tests (LSD, Tukey, Duncan)
- Combined summary table output

Value

A list containing:

Individual outputs Analysis results for each response variable separately.

Summary statistics Arithmetic mean, standard deviation, minimum, and maximum values for each variable.

Shapiro-Wilk test Results of the Shapiro-Wilk test for normality.

ANOVA and mean comparison ANOVA table along with mean comparison based on the selected test for each response variable.

Combined table A summary table including mean ± SD, grouping letters, SEm, SEd, CD, and CV values for all variables.

Examples

```
# Example
data(Gnutdataset)
head(Gnutdataset)
Out_rbd <- aov_of(
           Gnutdataset,
           design = "RBD",
           treatment = "Trt",
           replication = "Rep",
           responsevar = "all",
           transform = list(Noflwr="sqrt", Germ="arcsine", Disease="arcsine"),
           narc = list(Germ=10, Disease=5),
           alpha = 0.05 )

# Single variable result
```

```
Out_rbd$Germ

# Combined table for all varaibles
Out_rbd$Combined_table

# Entire output
Out_rbd

#Example without transformation
Out_rbd2 <- aov_of(
  Soildataset,
  design = "RBD",
  treatment = "TRT",
  replication = "REP",
  responsevar = "all",
  test = "lsd",
  alpha = 0.05
)

Out_rbd2$Combined_table
```

`aov_tf` *Two-Factor ANOVA for Agricultural Experimental Designs*

Description

Performs analysis of variance for two-factor experiments Factorial CRD (FCRD), Factorial RBD (FRBD), Split-Plot, and Strip-Plot designs.

Usage

```
aov_tf(
  data,
  design = c("FCRD", "FRBD", "SPLIT", "STRIP"),
  factor_A,
  factor_B,
  replication = NULL,
  responsevar = "all",
  test = c("lsd", "tukey", "duncan"),
  transform = NULL,
  narc = 1,
  alpha = 0.05
)
```

Arguments

`data`	A data frame containing experimental data.
`design`	Type of design "FCRD", "FRBD", "SPLIT" or "STRIP".

`factor_A`	Name of Factor A column in the dataset.
`factor_B`	Name of Factor B column in the dataset.
`replication`	Name of replication/block column (required for FRBD, SPLIT, STRIP).
`responsevar`	Specific variables c("v1" ,"v2", "v3") or "all".
`test`	Mean comparison test. Options include"lsd", "tukey", or "duncan".
`transform`	List or character specifying transformations ("log", "sqrt", "arcsine").
`narc`	Numeric or list specifying denominator for arcsine transformation.
`alpha`	Significance level (default 0.05).

Value

A list containing:

Individual outputs Analysis results for each response variable separately.

Summary statistics Arithmetic mean, standard deviation, minimum, and maximum values for each variable.

Shapiro-Wilk test Results of the Shapiro-Wilk test for normality.

ANOVA and mean comparison ANOVA table along with mean comparison based on the selected test for each response variable.

Combined table A summary table -two way including mean ± SD, grouping letters, SEm, SEd, CD, and CV values for all variables.

#’

Examples

```
#Rice dataset with Factor A as TRT and Factor B as SPACE and replications in "BLOCK" column
data("Gnutdataset")
"head(Ricedataset)"

#Example: Factorial CRD
out <- aov_tf(
  Ricedataset,
  design = "FCRD",
  factor_A = "TRT",
  factor_B = "SPACE",
  replication = "BLOCK",
  responsevar = "all",
  test = "lsd",
  transform = NULL,
  narc = 1,
  alpha = 0.05
)

#Example: Split-plot with transformation
out2 <- aov_tf(
  Ricedataset,
  design = "SPLIT",
```

```
    factor_A = "TRT",
    factor_B = "SPACE",
    replication = "BLOCK",
    responsevar = "all",
    test = "lsd",
    transform = list(GPP = "log", Disease = "arcsine"),
    narc = list(Disease = 5),
    alpha = 0.05
  )

  out2$PH
  out2$GPP
```

`fld_layout` *Field Design Layout Plot for Agricultural Experiments*

Description

Generates randomized field layouts for agricultural experimental designs including Completely Randomized Design (CRD), Randomized Block Design (RBD), and Latin Square Design (LSD), factorial designs, split-plot, and strip-plot.

Usage

```
fld_layout(
  design = "RBD",
  treatments = paste0("T", 1:5),
  A = c("A1", "A2"),
  B = c("B1", "B2", "B3"),
  blocks = 3,
  replications = 3,
  plot_length = 2,
  plot_width = 1,
  alley = 0.3,
  block_gap = 0.6,
  border = NULL,
  treatment_label_size = NULL,
  block_label_size = NULL,
  show_field_dimensions = TRUE,
  show_plot_dimensions = TRUE,
  seed = NULL
)
```

Arguments

`design`	Type of design. Options include" "CRD", "RBD", "LSD", "FCRD","FRBD", "SPLIT", or "STRIP".

`treatments`	Vector of treatment labels (used in CRD, RBD, LSD).
`A`	Vector of Factor A levels (for factorial, split, strip designs).
`B`	Vector of Factor B levels (for factorial, split, strip designs).
`blocks`	Number of blocks (required for RBD, SPLIT, STRIP).
`replications`	Number of replications. Can be a single number (equal replication) or a vector (unequal replication, e.g., c(2,3,4,2)).
`plot_length`	Length of each plot
`plot_width`	Width of each plot
`alley`	Spacing between adjacent plots.
`block_gap`	Gap between blocks.
`border`	Border area around the field layout.
`treatment_label_size`	Size of treatment labels in the layout
`block_label_size`	Size of block labels
`show_field_dimensions`	Logical; display field dimensions
`show_plot_dimensions`	Logical; display plot dimensions
`seed`	Random seed for reproducibility. Optional random seed to ensure reproducibility of randomization; same seed gives the same layout/results across runs.

Details

This function supports:

- Completely Randomized Design (CRD)
- Randomized Block Design (RBD)
- Latin Square Design (LSD)
- Factorial CRD and RBD (FCRD, FRBD)
- Split-plot and strip-plot designs
- Unequal and equal replication structures in CRD
- Custom plot dimensions and spacing

Value

A list containing:

plot A ggplot object showing field layout

layout Data frame containing plot arrangement

Examples

```
layout_crd <- fld_layout(
    design = "CRD",
    treatments = paste0("T", 1:7),
    replications = c(2,3,4,2,1,5,4),
    plot_length = 2.5,
  plot_width = 1.8,
  alley = 0.3,
  border = 1.5,
  seed = 123
  )
  layout_crd$plot


# RBD example
layout_rbd <- fld_layout(
  design = "RBD",
  treatments = paste0("T",1:7),
  blocks = 4,
  seed = 123
)
layout_rbd$plot

layout_rbd <- fld_layout(
  design = "RBD",
  treatments = paste0("T",1:7),
  blocks = 4,
   treatment_label_size = 4,
   block_label_size = 3,
  show_field_dimensions = FALSE,
  show_plot_dimensions = FALSE,
  seed = 123
)
layout_rbd$plot

# Latin Square Design
layout_lsd <- fld_layout(
  design = "LSD",
  treatments = paste0("T", 1:6),
  seed = 123
)
layout_lsd$plot

# Factorial CRD
result <- fld_layout(
  design = "FCRD",
  A = c("A1", "A2", "A3"),
  B = c("B1", "B2", "B3", "B4"),
  replications = 3,
  seed = 101
)
result$plot
```

```
# Split plot
result2 <- fld_layout(
  design = "SPLIT",
  A = c("A1", "A2", "A3"),
  B = c("B1", "B2", "B3", "B4"),
  blocks = 3,
  seed = 101 )
result2$plot
```

`Gnutdataset` *Groundnut Dataset*

Description

Hypothetical dataset for single-factor groundnut experiment.

Usage

```
Gnutdataset
```

Format

A data frame with 24 observations and 10 variables:

Trt	Treatment levels
Rep	Replication
Germ	Germination percentage
Plntht	Plant height (cm)
Noflwr	Number of flowers per plant
Spread	Plant spread (cm)
Leaflnth	Leaf length (cm)
Nopodplnt	Number of pods per plant
Wt	Pod weight per plant (g)
Disease	Disease incidence

Details

Used for demonstration of one-factor ANOVA.

Source

Simulated data

`Ricedataset` *Rice Dataset*

Description

Hypothetical dataset for two-factor experiment (treatment and spacing).

Usage

```
Ricedataset
```

Format

A data frame with 96 observations and 11 variables:

TRT Treatment

SPACE Spacing

BLOCK Block

DFF Days to flowering

PH Plant height

TTP Tillers per plant

PL Panicle length

GPP Grains per panicle

HSW Hundred seed weight

GYP Grain yield

Disease Disease incidence

Details

Used for two-factor ANOVA demonstration.

Source

Simulated data

`Soildataset` *Soil Dataset*

Description

Hypothetical dataset for single-factor soil experiment.

Usage

```
Soildataset
```

Format

A data frame with 33 observations and 15 variables:

TRT Treatment

REP Replication

BD Bulk density

PD Particle density

POR Porosity

HC Hydraulic conductivity

pH Soil pH

CEC Cation exchange capacity

N Nitrogen

P Phosphorus

K Potassium

S Sulfur

OC Organic carbon

MBN Microbial biomass nitrogen

MBC Microbial biomass carbon

Details

Used for soil analysis demonstration.

Source

Simulated data

Index