

# Package ‘PGaovR’

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**Type** Package

**Title** Analysis of Experimental Data using ANOVA and Mean Comparison

**Version** 0.1.0

**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).

**License** GPL (>= 3)

**Encoding** UTF-8

**LazyData** true

**Imports** ggplot2, grid, multcompView, stats, utils

**RoxygenNote** 7.3.3

**Depends** R (>= 3.5)

**NeedsCompilation** no

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aov_of	<i>One-Factor ANOVA for Agricultural Designs</i>
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## 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  $\pm$  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 variables
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

```

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aov\_tf

*Two-Factor ANOVA for Agricultural Experimental Designs*


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### 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  $\pm$  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

```

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fld\_layout

*Field Design Layout Plot for Agricultural Experiments*


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### 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
```

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Gnutdataset

*Groundnut Dataset*

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### 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

**Plnht** 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

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Ricedataset

*Rice Dataset*

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### 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

**DFP** 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

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Soildataset

*Soil Dataset*

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**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

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