

Package ‘aanova’

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Type Package

Title Robust Ecological and Fisheries Data Analysis and Visualization

Version 1.0.1

Description A comprehensive statistical and visualization toolkit tailored for fisheries science, stock assessment workflows, and aquatic ecology. It provides streamlined wrappers for univariate and factorial ANOVA, ANCOVA, MANOVA, generalized linear models (GLMs) for count data, non-linear morphometric regressions, custom correlation heatmaps, and integrated Mantel test network linkages.

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ancova_analysis	<i>Analysis of Covariance (ANCOVA) with Adjusted Means Visualization</i>
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Description

This function performs an Analysis of Covariance to test group differences in a continuous response variable while controlling for a continuous covariate. It extracts the ANCOVA table, estimated marginal means (EMMs), and generates a publication-ready regression scatter plot with parallel trend lines.

Usage

```
ancova_analysis(  
  data,  
  response_var,  
  factor_var,  
  covariate_var,  
  factor_levels = NULL,  
  color_palette = "Set1"  
)
```

Arguments

- data A data frame in long format.
- response_var Character; the name of the continuous numeric response variable.
- factor_var Character; the name of the categorical independent variable (groups).
- covariate_var Character; the name of the continuous covariate variable.
- factor_levels Optional character vector; custom order for the factor levels.
- color_palette Character; name of a color palette from RColorBrewer. Default is "Set1".

Value

A list containing the ANCOVA model summary, EMMs, and the ggplot object.

Description

Computes correlation matrices (Pearson, Spearman, or Kendall) and generates publication-ready heatmaps with customizable shapes (circles, squares), layout views (full, lower, upper), and optional text labels.

Usage

```
correlation_heatmap(  
  data,  
  numeric_vars = NULL,  
  method = "pearson",  
  shape = "circle",  
  view = "lower",  
  show_text = NULL,  
  color_palette = "RdBu"  
)
```

Arguments

data	A data frame containing numeric variables.
numeric_vars	Optional character vector of numeric column names to include. If NULL, all numeric columns are used.
method	Character; correlation method: "pearson", "spearman", or "kendall". Default is "pearson".
shape	Character; marker shape for the heatmap: "circle" or "square". Default is "circle".
view	Character; matrix display layout: "full", "lower", or "upper". Default is "lower".
show_text	Logical; whether to display numeric correlation values inside markers. Default is FALSE for circles and TRUE for squares.
color_palette	Character; name of a diverging color palette from RColorBrewer. Default is "RdBu".

Value

A list containing the correlation matrix, p-value matrix, and the ggplot object.

glm_analysis	<i>Generalized Linear Models (GLMs) for Fisheries Count and Binary Data</i>
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Description

This function fits Generalized Linear Models (e.g., Poisson, Quasipoisson, Binomial) to non-normal ecological data, extracts model summaries, incident rate ratios (IRR) or odds ratios, and generates a publication-ready forest plot visualizing effect sizes.

Usage

```
glm_analysis(
  data,
  response_var,
  predictor_vars,
  family_type = "poisson",
  color_palette = "Set1"
)
```

Arguments

data	A data frame containing the variables.
response_var	Character; the name of the numeric count or binary response variable.
predictor_vars	Character vector; the names of the independent predictor variables.
family_type	Character; distribution family: "poisson", "quasipoisson", or "binomial". Default is "poisson".
color_palette	Character; name of a color palette from RColorBrewer. Default is "Set1".

Value

A list containing the model summary, coefficient table, and the ggplot object.

hilsa_ancova	<i>Length-Weight ANCOVA Dataset for Hilsa Shad</i>
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Description

A simulated dataset containing body weight, total length, and habitat types of Hilsa shad (*Tenualosa ilisha*) to demonstrate Analysis of Covariance (ANCOVA).

Usage

```
hilsa_ancova
```

Format

A data frame with 90 rows and 3 variables:

- Habitat** A factor representing the environment (Marine, Estuary, River).
- Total_Length_cm** A numeric vector representing total fish length in centimeters (covariate).
- Weight_g** A numeric vector representing fish body weight in grams (response).

hilsa_catch	<i>Catch Count Dataset for Hilsa Shad GLMs</i>
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Description

A simulated dataset containing catch counts, fishing effort, and environmental variables for Hilsa shad (*Tenualosa ilisha*) to demonstrate Generalized Linear Models (GLMs).

Usage

hilsa_catch

Format

A data frame with 120 rows and 4 variables:

- Habitat** A factor representing the environment (Marine, Estuary, River).
- Season** A factor representing the season (Monsoon, Dry).
- Fishing_Hours** A numeric vector representing fishing effort in hours.
- Catch_Count** An integer vector representing the number of fish caught (count response).

hilsa_env	<i>Environmental and Catch Parameters for Correlation Analysis</i>
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Description

A simulated dataset containing oceanographic measurements and catch weights to demonstrate customizable correlation matrix heatmaps.

Usage

hilsa_env

Format

A data frame with 100 rows and 6 variables:

SST_C Sea Surface Temperature in degrees Celsius.

Salinity_ppt Water salinity in parts per thousand.

Depth_m Water depth in meters.

DO_mgL Dissolved oxygen in milligrams per liter.

Chlorophyll_a Chlorophyll-a concentration.

Catch_kg Total fish catch in kilograms.

hilsa_morphology	<i>Morphometric Measurements of Hilsa Shad</i>
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Description

A simulated dataset containing multiple continuous morphological traits of Hilsa shad (*Tenualosa ilisha*) across different aquatic habitats to demonstrate Multivariate Analysis of Variance (MANOVA).

Usage

hilsa_morphology

Format

A data frame with 90 rows and 4 variables:

Habitat A factor representing the environment (Marine, Estuary, River).

Body_Depth_cm A numeric vector representing maximum body depth in centimeters.

Head_Length_cm A numeric vector representing head length in centimeters.

Fin_Length_cm A numeric vector representing pectoral fin length in centimeters.

hilsa_regression	<i>Morphometric Regression Dataset for Hilsa Shad</i>
------------------	---

Description

A simulated dataset containing length and weight measurements of Hilsa shad (*Tenualosa ilisha*) across various habitats for evaluating linear, logarithmic, and polynomial regression models.

Usage

hilsa_regression

Format

- A data frame with 100 rows and 3 variables:
- Total_Length_cm** A numeric vector representing total fish length in centimeters.
- Weight_g** A numeric vector representing fish body weight in grams.
- Habitat** A factor representing the environment (River, Estuary, Marine).

hilsa_three_way	<i>Comprehensive Body Weights of Hilsa Shad (Three-Way)</i>
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Description

A simulated dataset containing body weights of Hilsa shad (*Tenualosa ilisha*) across multiple habitats, fishing seasons, and size classes to demonstrate three-way ANOVA interaction models and faceted visualization.

Usage

hilsa_three_way

Format

- A data frame with 120 rows and 4 variables:
- Habitat** A factor representing the environment (Marine, Estuary, River).
- Season** A factor representing the season (Monsoon, Dry).
- Size_Class** A factor representing growth stage (Juvenile, Adult).
- Weight_g** A numeric vector representing fish body weight in grams.

hilsa_two_way	<i>Multi-Factor Body Weights of Hilsa Shad</i>
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Description

A simulated dataset containing the body weights of Hilsa shad (*Tenualosa ilisha*) across different habitats and fishing seasons to demonstrate two-way ANOVA interaction effects.

Usage

hilsa_two_way

Format

- A data frame with 90 rows and 3 variables:
- Habitat** A factor representing the environment (Marine, Estuary, River).
- Season** A factor representing the season (Monsoon, Dry).
- Weight_g** A numeric vector representing fish body weight in grams.

hilsa_weight	<i>Body Weights of Hilsa Shad Across Habitats</i>
--------------	---

Description

A simulated dataset containing the body weights of Hilsa shad (*Tenualosa ilisha*) sampled from three distinct ecological environments: Marine, Estuary, and River. This dataset is designed to demonstrate one-way ANOVA and variance visualization.

Usage

hilsa_weight

Format

A data frame with 90 rows and 2 variables:

Habitat A factor representing the sampling environment (Marine, Estuary, River).

Weight_g A numeric vector representing the body weight of the fish in grams.

manova_analysis	<i>Multivariate Analysis of Variance (MANOVA) with Alternative Visualizations</i>
-----------------	---

Description

This function performs a one-way MANOVA across multiple continuous response variables grouped by a categorical factor, extracts multivariate test statistics, univariate ANOVA breakdowns, and generates either faceted boxplots or a Canonical Discriminant Analysis (LDA) multivariate scatter plot.

Usage

```
manova_analysis(  
  data,  
  response_vars,  
  factor_var,  
  factor_levels = NULL,  
  plot_type = "boxplot",  
  color_palette = "Set1"  
)
```

Arguments

<code>data</code>	A data frame in long format.
<code>response_vars</code>	Character vector; the names of the continuous numeric response variables.
<code>factor_var</code>	Character; the name of the categorical independent variable.
<code>factor_levels</code>	Optional character vector; custom order for the factor levels.
<code>plot_type</code>	Character; type of visualization: "boxplot" or "lda". Default is "boxplot".
<code>color_palette</code>	Character; name of a color palette from RColorBrewer. Default is "Set1".

Value

A list containing the MANOVA test summary, univariate ANOVA summaries, and the ggplot object.

`mantel_heatmap_analysis`

Integrated Mantel Test and Correlation Heatmap

Description

Computes internal correlations among environmental variables and performs Mantel tests linking community composition to environmental parameters using base `vegan` and `ggplot2`.

Usage

```
mantel_heatmap_analysis(
  comm_data,
  env_data,
  method = "pearson",
  spec_dist = "bray",
  env_dist = "euclidean",
  color_palette = "RdBu"
)
```

Arguments

<code>comm_data</code>	A data frame containing community or species abundance data.
<code>env_data</code>	A data frame containing numeric environmental variables.
<code>method</code>	Character; correlation method: "pearson" or "spearman". Default is "pearson".
<code>spec_dist</code>	Character; distance metric for community data (e.g., "bray", "euclidean"). Default is "bray".
<code>env_dist</code>	Character; distance metric for environmental data. Default is "euclidean".
<code>color_palette</code>	Character; color palette for heatmap. Default is "RdBu".

Value

A list containing the correlation matrix, Mantel test results, and the ggplot object.

one_way_anova

One-Way Analysis of Variance (ANOVA) with Visualization

Description

This function performs a one-way ANOVA, calculates Tukey's HSD post-hoc test, extracts Estimated Marginal Means (EMMs), and generates a publication-ready plot.

Usage

```
one_way_anova(
  data,
  factor_var,
  numeric_var,
  factor_levels = NULL,
  plot_type = "boxplot",
  error_type = "se",
  sig_display = "letters",
  y_limits = NULL,
  add_jitter = TRUE,
  show_mean = TRUE,
  mean_color = "darkred",
  color_palette = "Set1"
)
```

Arguments

data	A data frame in long format.
factor_var	Character; the name of the categorical independent variable.
numeric_var	Character; the name of the continuous response variable.
factor_levels	Optional character vector; specifies the exact order of the categorical levels on the x-axis.
plot_type	Character; type of plot: "boxplot", "barplot", or "pointrange". Default is "boxplot".
error_type	Character; error bar type for bar/pointrange plots: "se" (Standard Error) or "sd" (Standard Deviation).
sig_display	Character; display significance via "letters" (compact letter display) or "stars" (p-value brackets).
y_limits	Optional numeric vector of length 2; explicitly sets the Y-axis limits (e.g., c(0, 150)).
add_jitter	Logical; if TRUE, adds jittered points to the boxplot.
show_mean	Logical; if TRUE, displays a mean point inside the boxplot.
mean_color	Character; color for the mean point in the boxplot.
color_palette	Character; name of a color palette from RColorBrewer.

Value

A list containing the ANOVA summary, Tukey HSD results, EMMs, a clean summary table, and the ggplot object.

regression_analysis	<i>Flexible Regression Analysis with Shaded Confidence Intervals and Statistics</i>
---------------------	---

Description

This function fits linear, logarithmic, or polynomial regression models to data, calculates coefficients, R-squared, and p-values, and generates a publication-ready plot with confidence interval shading and equation annotations.

Usage

```
regression_analysis(  
  data,  
  x_var,  
  y_var,  
  fit_type = "linear",  
  group_var = NULL,  
  color_palette = "Set1"  
)
```

Arguments

data	A data frame containing the variables.
x_var	Character; the name of the independent variable (x-axis).
y_var	Character; the name of the dependent response variable (y-axis).
fit_type	Character; type of model: "linear", "logarithmic", or "polynomial". Default is "linear".
group_var	Optional character; the name of a categorical variable to group/color regressions by.
color_palette	Character; name of a color palette from RColorBrewer. Default is "Set1".

Value

A list containing model summaries, regression parameters, and the ggplot object.

three_way_anova	<i>Three-Way Analysis of Variance (ANOVA) with Faceted Interaction Visualization</i>
-----------------	--

Description

This function performs a three-way ANOVA with full interaction effects, calculates Tukey's HSD post-hoc tests, extracts Estimated Marginal Means (EMMs), and generates faceted publication-ready interaction plots with compact letter displays.

Usage

```
three_way_anova(
  data,
  factor1_var,
  factor2_var,
  factor3_var,
  numeric_var,
  factor1_levels = NULL,
  factor2_levels = NULL,
  factor3_levels = NULL,
  plot_type = "boxplot",
  error_type = "se",
  y_limits = NULL,
  add_jitter = TRUE,
  show_mean = TRUE,
  mean_color = "darkred",
  color_palette = "Set1"
)
```

Arguments

data	A data frame in long format.
factor1_var	Character; the name of the first categorical independent variable (x-axis).
factor2_var	Character; the name of the second categorical independent variable (groups/fill).
factor3_var	Character; the name of the third categorical independent variable (facets).
numeric_var	Character; the name of the continuous response variable.
factor1_levels	Optional character vector; custom order for the first factor.
factor2_levels	Optional character vector; custom order for the second factor.
factor3_levels	Optional character vector; custom order for the third factor.
plot_type	Character; type of interaction plot: "boxplot", "barplot", or "pointrange". Default is "boxplot".
error_type	Character; error bar type for bar/pointrange plots: "se" or "sd". Default is "se".
y_limits	Optional numeric vector of length 2; explicitly sets the Y-axis limits.

add_jitter	Logical; if TRUE, adds jittered points to the boxplot. Default is TRUE.
show_mean	Logical; if TRUE, displays a mean point inside the boxplot. Default is TRUE.
mean_color	Character; color for the mean point in the boxplot. Default is "darkred".
color_palette	Character; name of a color palette from RColorBrewer. Default is "Set1".

Value

A list containing the ANOVA summary, Tukey HSD results, EMMs, summary statistics table, and the ggplot object.

two_way_anova	<i>Two-Way Analysis of Variance (ANOVA) with Interaction Visualization</i>
---------------	--

Description

This function performs a two-way ANOVA with interaction effects, calculates Tukey's HSD post-hoc tests, extracts Estimated Marginal Means (EMMs), and generates publication-ready interaction plots with compact letter displays.

Usage

```
two_way_anova(
  data,
  factor1_var,
  factor2_var,
  numeric_var,
  factor1_levels = NULL,
  factor2_levels = NULL,
  plot_type = "boxplot",
  error_type = "se",
  y_limits = NULL,
  add_jitter = TRUE,
  show_mean = TRUE,
  mean_color = "darkred",
  color_palette = "Set1"
)
```

Arguments

data	A data frame in long format.
factor1_var	Character; the name of the first categorical independent variable (x-axis).
factor2_var	Character; the name of the second categorical independent variable (groups/fill).
numeric_var	Character; the name of the continuous response variable.
factor1_levels	Optional character vector; custom order for the first factor levels.
factor2_levels	Optional character vector; custom order for the second factor levels.

<code>plot_type</code>	Character; type of interaction plot: "boxplot", "barplot", or "pointrange". Default is "boxplot".
<code>error_type</code>	Character; error bar type for bar/pointrange plots: "se" or "sd". Default is "se".
<code>y_limits</code>	Optional numeric vector of length 2; explicitly sets the Y-axis limits.
<code>add_jitter</code>	Logical; if TRUE, adds jittered points to the boxplot. Default is TRUE.
<code>show_mean</code>	Logical; if TRUE, displays a mean point inside the boxplot. Default is TRUE.
<code>mean_color</code>	Character; color for the mean point in the boxplot. Default is "darkred".
<code>color_palette</code>	Character; name of a color palette from RColorBrewer. Default is "Set1".

Value

A list containing the ANOVA summary, Tukey HSD results, EMMs, summary statistics table, and the ggplot object.

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