Package ‘barrel’

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Title Covariance-Based Ellipses and Annotation Tools for Ordination Plots

Version 0.1.0

Description Provides tools to visualize ordination results in 'R' by adding covariance-based ellipses, centroids, vectors, and confidence regions to plots created with 'ggplot2'. The package extends the 'vegan' framework and supports Principal Component Analysis (PCA), Redundancy Analysis (RDA), and Non-metric Multidimensional Scaling (NMDS). Ellipses can represent either group dispersion (standard deviation, SD) or centroid precision (standard error, SE), following Wang et al. (2015) <doi:10.1371/journal.pone.0118537>. Robust estimators of covariance are implemented, including the Minimum Covariance Determinant (MCD) method of Hubert et al. (2018) <doi:10.1002/wics.1421>. This approach reduces the influence of outliers. barrel is particularly useful for multivariate ecological datasets, promoting reproducible, publication-quality ordination graphics with minimal effort.

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Contents

`autoplot.barrel_ord` *Autoplot method for barrel_ord objects*

Description

Generates a ggplot of site scores from a vegan ordination object with optional group ellipses, centroids, and environmental arrows. This method is designed to work with ordination objects prepared using `barrel_prepare`.

Usage

```
## S3 method for class 'barrel_ord'
autoplot(object, ...)
```

Arguments

`object`	An object of class `"barrel_ord"` (a vegan ordination object with attached metadata).
`...`	Additional arguments: **group** Character. Grouping variable in the metadata. (Required) **data** Optional species or environmental data for envfit. **kind** Type of ellipse: "se" or "sd". Default is "se". **method** Covariance method: "classic" or "robust". Default is "classic". **conf** Confidence level for ellipses. Default is 0.95. **geom_type** "polygon" or "path" for ellipse. Default is "polygon". **show_arrows** Logical; whether to show envfit vectors. Default is TRUE. **show_centroids** Logical. Default is FALSE. **show_ellipses** Logical. Default is TRUE. **show_labels** Logical. Label envfit arrows. Default is TRUE. **p_thresh** Numeric. Significance threshold for arrows. Default 0.05. **alpha** Numeric. Transparency of ellipses. Default is 0.5.

Details

If `geom_type = "polygon"`, group colors are mapped to `fill` for ellipses. If `geom_type = "path"`, group colors are mapped to `color`. The grouping variable must be present in the metadata provided to `barrel_prepare`.

Value

A ggplot2 object with ordination scores and optional graphical layers.

See Also

`barrel_prepare`, `stat_barrel`, `rda`, `metaMDS`

Examples

```
library(vegan)
data(dune)
data(dune.env)
ord <- rda(dune, scale = TRUE)
ord <- barrel_prepare(ord, dune.env)
ggplot2::autoplot(ord,
  group = "Management", data = dune,
  method = "robust", kind = "sd", geom_type = "polygon", show_arrows = TRUE
)
```

`barrel_label_axes` *Add Axis Titles with Method Name and Explained Variance*

Description

This function creates properly formatted axis titles for ordination plots. It uses the ordination method name (e.g., RDA, dbRDA, NMDS) and, when available, the percentage of variance explained by the first two axes.

Usage

```
barrel_label_axes(ord)
```

Arguments

`ord`	A vegan ordination object, such as from `rda()`, `cca()`, `capscale()`, or `metaMDS()`.

Details

The labels are retrieved using `get_ord_axis_labels` and returned as a `ggplot2::labs()` object that can be added to a plot.

Value

A `ggplot2::labs()` object with x and y axis titles.

See Also

`get_ord_axis_labels`

Examples

```
library(vegan)
library(ggplot2)
data(dune)
data(dune.env)

# Example with RDA
ord <- rda(dune)
scores_df <- as.data.frame(scores(ord, display = "sites"))
scores_df$Management <- dune.env$Management

ggplot(scores_df, aes(x = PC1, y = PC2, color = Management)) +
  geom_point() +
  barrel_label_axes(ord) +
  theme_minimal() +
  theme(axis.title = element_text(face = "bold", size = 13))
```

`barrel_ord_summary` *Summary Statistics for Ordination Objects*

Description

Computes adjusted R-squared and percentage of variance explained for constrained ordination methods (e.g., `rda`, `cca`, `capscale`, `dbrda`), or returns the stress value for non-metric multidimensional scaling (`metaMDS`).

Usage

```
barrel_ord_summary(ord)
```

Arguments

`ord`	An ordination object of class `rda`, `cca`, `capscale`, `dbrda`, or `metaMDS`.

Value

A named list with components:

method Class of the ordination object as a character string.

R2_adj Adjusted R-squared (percentage) for constrained ordinations; `NA` for NMDS.

axis_var Named numeric vector of variance explained by each axis (percentage), if available.

stress Stress value for NMDS objects.

message Message explaining output, especially for NMDS or missing R2.

Examples

```
library(vegan)
data(dune)
data(dune.env)

# PCA (unconstrained ordination)
pca <- rda(dune)
barrel_ord_summary(pca)

# RDA (constrained ordination)
rda_mod <- rda(dune ~ A1 + Moisture, data = dune.env)
barrel_ord_summary(rda_mod)

# NMDS
nmds <- metaMDS(dune, k = 2)
barrel_ord_summary(nmds)

# dbRDA
dbrda_mod <- dbrda(dune ~ A1 + Management, data = dune.env, distance = "bray")
barrel_ord_summary(dbrda_mod)
```

`barrel_prepare` *Prepare ordination object for barrel plotting*

Description

Attaches sample metadata (e.g., grouping variable) to a vegan ordination object and assigns class 'barrel_ord'.

Usage

```
barrel_prepare(ord, metadata)
```

Arguments

`ord`	A vegan ordination object (e.g., from `rda`, `cca`, `metaMDS`).
`metadata`	A data frame of sample metadata. Must have same number of rows as ordination site scores.

Value

The ordination object with metadata attached and class `"barrel_ord"`.

Examples

```
library(vegan)
data(dune)
data(dune.env)
ord <- rda(dune, scale = TRUE)
ord_prepared <- barrel_prepare(ord, dune.env)
class(ord_prepared)
```

`barrel_stats` *Comprehensive Ordination Visualization Layer*

Description

Combines ordination ellipses, centroids, environmental arrows, and annotations into a ggplot2 layer.

Usage

```
stat_barrel(
  mapping = NULL,
  data = NULL,
  geom = "path",
  position = "identity",
  kind = "se",
  conf = 0.95,
  method = c("robust", "classic"),
  show.legend = NA,
  inherit.aes = TRUE,
  geom_type = c("path", "polygon"),
  ...
)

stat_barrel_centroid(
  mapping = NULL,
  data = NULL,
  geom = "point",
  position = "identity",
  method = c("classic", "robust"),
  show.legend = NA,
  inherit.aes = TRUE,
  shape = 3,
  ...
)
```

```
stat_barrel_arrows(
  mapping = NULL,
  data = NULL,
  ord,
  matrix,
  geom = "segment",
  position = "identity",
  labels = TRUE,
  labels.color = "black",
  labels.size = 3,
  labels.fontface = "plain",
  show.significant = FALSE,
  p_thresh = 0.05,
  arrow = grid::arrow(length = grid::unit(0.25, "cm")),
  arrow.color = "grey10",
  arrow.linetype = "solid",
  arrow.size = 0.3,
  labels.max.overlaps = Inf,
  show.legend = NA,
  inherit.aes = TRUE,
  ...
)

compute_envfit_vectors(ord, matrix, p_thresh = 0.05, show.significant = FALSE)

stat_barrel_annotate(
  mapping = NULL,
  data = NULL,
  ord,
  position = "identity",
  show.legend = FALSE,
  inherit.aes = TRUE,
  xpad = 0.05,
  ypad = 0.05,
  hjust = 0,
  vjust = 1,
  ...
)
```

Arguments

`mapping`	Set of aesthetic mappings created by `aes()`.
`data`	Data frame used for plotting.
`geom`	Character; geometric object to use for ellipses, either `"path"` or `"polygon"`.
`position`	Position adjustment for ggplot2 layers (default `"identity"`).
`kind`	Character; type of ellipse: `"se"` (standard error), `"sd"` (dispersion), or `"ci"` (confidence interval).

`conf`	Numeric; confidence level for ellipses (default 0.95).
`method`	Character; covariance estimation method: `"classic"` or `"robust"`.
`show.legend`	Logical; whether to show legends (default `NA`).
`inherit.aes`	Logical; whether to inherit aesthetics (default `TRUE`).
`geom_type`	Character; geometric object to use for ellipses, either `"path"` or `"polygon"`.
`...`	Additional parameters passed to underlying geoms or stats.
`shape`	Integer; shape code for centroid points (default 3).
`ord`	Ordination object from vegan, e.g. `rda`, `cca`, `dbrda`, or `metaMDS`.
`matrix`	Optional data frame of environmental variables for arrows.
`labels`	Logical; whether to show labels on environmental arrows (default `TRUE`).
`labels.color`	Color of arrow labels (default `"black"`).
`labels.size`	Numeric size of arrow labels (default 3).
`labels.fontface`	Font face of arrow labels (default `"plain"`).
`show.significant`	Logical; whether to show only significant arrows (default `FALSE`).
`p_thresh`	Numeric; p-value threshold for significance filtering (default 0.05).
`arrow`	A grid arrow object controlling arrow appearance (default created by `grid::arrow()`).
`arrow.color`	Color of arrows (default `"grey10"`).
`arrow.linetype`	Line type of arrows (default `"solid"`).
`arrow.size`	Numeric line width of arrows (default 0.3).
`labels.max.overlaps`	Maximum number of labels in the same space (default `"Inf"`).
`xpad`	Numeric; horizontal padding for annotation text relative to x-axis range (default 0.05).
`ypad`	Numeric; vertical padding for annotation text relative to y-axis range (default 0.05).
`hjust`	Numeric; horizontal justification of annotation text (default 0).
`vjust`	Numeric; vertical justification of annotation text (default 1).

Details

Comprehensive Ordination Visualization Layer

This set of ggplot2 stats draws ellipses around groups, centroids, environmental arrows, and adds adjusted R^2 or stress annotation for ordination objects from vegan.

Value

A ggplot2 layer combining ellipses, centroids, arrows, and annotations.

Examples

```
library(ggplot2)
library(vegan)
library(robustbase)
data(dune)
data(dune.env)

pca <- vegan::rda(dune, scale = TRUE)
scores <- as.data.frame(vegan::scores(pca, display = "sites"))
scores$Management <- dune.env$Management

ggplot(scores, aes(PC1, PC2, group = Management, fill = Management)) +
  stat_barrel(
    method = "classic", kind = "se", conf = 0.95, geom_type = "polygon",
    alpha = 0.4, color = "black"
  ) +
  stat_barrel_centroid(method = "classic", shape = 3) +
  stat_barrel_arrows(
    ord = pca, matrix = dune,
    labels = TRUE, labels.color = "blue",
    arrow.color = "darkred", arrow.linetype = "solid",
    labels.fontface = "bold", show.significant = TRUE,
    labels.max.overlaps = Inf,
  ) +
  stat_barrel_annotate(ord = pca, xpad = 0.05, ypad = 0.05) +
  geom_point(aes(color = Management)) +
  theme_minimal()
```

`get_ord_axis_labels` *Internal function to get axis labels for vegan ordination objects*

Description

This function infers the ordination method used and returns proper axis labels including percentage of explained variance when applicable.

Usage

```
get_ord_axis_labels(ord)
```

Arguments

`ord`	A vegan ordination object.

Value

A list with one element `label`, a character vector for axis labels. #' @examples library(vegan) data(dune) data(dune.env) ord_pca <- rda(dune) get_ord_axis_labels(ord_pca)

`ord_compute_ellipse` *Compute coordinates for an ordination ellipse*

Description

Calculates ellipse coordinates based on a covariance matrix and center. Supports confidence ellipses (standard error, "se") or dispersion ellipses ("sd").

Usage

```
ord_compute_ellipse(
  cov,
  center = c(0, 0),
  kind = "se",
  conf = 0.95,
  npoints = 100,
  n = NULL
)
```

Arguments

`cov`	Numeric matrix (2x2) covariance matrix.
`center`	Numeric vector of length 2 specifying the ellipse center coordinates.
`kind`	Character string specifying the type of ellipse: either `"se"` for standard error/confidence ellipse or `"sd"` for standard deviation dispersion ellipse.
`conf`	Numeric confidence level or coverage (default 0.95).
`npoints`	Integer number of points to generate along ellipse perimeter (default 100).
`n`	Numeric sample size; **required** if `kind = "se"`.

Value

A numeric matrix with two columns representing x and y coordinates of the ellipse.

Examples

```
cov_mat <- matrix(c(1, 0, 0, 1), 2, 2)
center <- c(0, 0)
ell_coords <- ord_compute_ellipse(cov_mat, center, kind = "se", conf = 0.95, n = 10)
plot(ell_coords, type = "l")
```

`ord_ellipse_group` *Compute Ellipse Coordinates for a Single Group*

Description

Calculates ellipse coordinates for one group in ordination scores with robust or classic covariance.

Usage

```
ord_ellipse_group(
  scores,
  group_var,
  group_name,
  axis1,
  axis2,
  kind = "se",
  conf = 0.95,
  method = "classic"
)
```

Arguments

`scores`	Data frame of ordination scores.
`group_var`	Name of grouping column.
`group_name`	Name of the group to calculate ellipse.
`axis1`	Name of first axis column.
`axis2`	Name of second axis column.
`kind`	Type of ellipse: "se" or "sd".
`conf`	Confidence level.
`method`	Covariance method: "classic" or "robust".

Details

Compute ellipse coordinates for a specific group in ordination scores

Calculates ellipse coordinates for one group from ordination scores, supporting classical or robust covariance estimation.

Value

Data frame of ellipse coordinates with group label.

A data frame with ellipse coordinates and group label.

Examples

```
library(vegan)
data(dune)
data(dune.env)
pca <- rda(dune, scale = TRUE)
scores <- as.data.frame(scores(pca, display = "sites"))
scores$Group <- dune.env$Management
ell <- ord_ellipse_group(scores, "Group", "BF", "PC1", "PC2", kind = "se", method = "classic")
plot(ell$PC1, ell$PC2, type = "l")
```

`ord_ellipse_groups` *Compute Ellipse Coordinates for All Groups*

Description

Calculates ellipse coordinates for all groups in ordination scores.

Usage

```
ord_ellipse_groups(
  scores,
  group_var,
  axis1,
  axis2,
  kind = "se",
  conf = 0.95,
  method = "classic"
)
```

Arguments

`scores`	Data frame of ordination scores.
`group_var`	Name of grouping column.
`axis1`	Name of first axis column.
`axis2`	Name of second axis column.
`kind`	Type of ellipse: "se" or "sd".
`conf`	Confidence level.
`method`	Covariance method: "classic" or "robust".

Details

Compute ellipse coordinates for all groups in ordination scores

Calculates ellipse coordinates for all groups in ordination scores, supports classic and robust covariance estimation.

Value

Data frame of ellipse coordinates with group labels.

`ord_extract_centroids` *Extract Group Centroids from Ordination Scores*

Description

Computes centroids per group using classic mean or robust methods.

Usage

```
ord_extract_centroids(
  scores,
  group_var,
  axis1,
  axis2,
  method = c("classic", "robust")
)
```

Arguments

`scores`	Data frame of ordination scores.
`group_var`	Name of grouping column.
`axis1`	Name of first axis column.
`axis2`	Name of second axis column.
`method`	Centroid method: "classic" or "robust".

Details

Extract centroids of groups from ordination scores with classic or robust method

Computes the centroid coordinates for each group using either the classical mean or robust minimum covariance determinant.

Value

Data frame with group centroids.

`ord_extract_cov` *Extract covariance matrix from ordination scores with optional robust estimation*

Description

Computes the covariance matrix of ordination scores, optionally using robust estimation.

Usage

```
ord_extract_cov(
  scores,
  axis1,
  axis2,
  weights = NULL,
  method = c("classic", "robust")
)
```

Arguments

`scores`	Data frame of ordination scores.
`axis1`	Name of first axis column.
`axis2`	Name of second axis column.
`weights`	Optional numeric vector of weights.
`method`	Covariance method: "classic" or "robust".

Value

2x2 covariance matrix.

`ord_vectors` *Extract significant environmental vectors from vegan ordination object*

Description

Performs an envfit analysis and returns environmental vectors with p-values, filtered by significance or unfiltered.

Usage

```
ord_vectors(
  ord,
  data,
  p_thresh = 0.05,
  filter = c("significant", "nonsignificant", "all")
)
```

Arguments

`ord`	Vegan ordination object (e.g., rda, cca).
`data`	Environmental variables data frame used for envfit.
`p_thresh`	P-value threshold to determine significance (default 0.05).
`filter`	Character; one of "significant" (default), "nonsignificant", or "all".

Value

Data frame of vectors with scores, p-values, and labels.

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