

Package ‘ggvegan’

February 27, 2026

Type Package

Title 'ggplot2' Plots for the 'vegan' Package

Version 0.2.1

Depends R (>= 4.1.0)

Imports vegan (>= 2.3-0), dplyr, tibble, vctrs, ggplot2, grid, tidyr,
ggrepel, generics

Suggests testthat (>= 3.0.0), vdiffR (>= 1.0.0), permute, withr

Description Functions to produce 'ggplot2'-based plots of objects produced by functions in the 'vegan' package. Provides 'fortify()', 'autoplot()', and 'tidy()' methods for many of 'vegan's functions. The aim of 'ggvegan' is to make it easier to work within the 'tidyverse' with 'vegan'.

License GPL-2

ByteCompile true

RoxygenNote 7.3.3

Encoding UTF-8

Config/testthat/edition 3

Language en-GB

NeedsCompilation no

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Repository CRAN

Date/Publication 2026-02-27 20:30:02 UTC

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add_biplot_arrows *Adds a biplot arrow layer to an existing plot*

Description

Adds a biplot arrow layer to an existing plot

Usage

```
add_biplot_arrows(object, plt, vars, arrow.col = "navy")
```

Arguments

object	an ordination object.
plt	a ggplot object.
vars	character; length 2 vector of dimension names.
arrow.col	colour specification for biplot arrows and their labels.

add_biplot_centroids *Adds a biplot arrow layer to an existing plot*

Description

Adds a biplot arrow layer to an existing plot

Usage

```
add_biplot_centroids(object, plt, vars, arrow.col = "navy")
```

Arguments

object	an ordination object.
plt	a ggplot object.
vars	character; length 2 vector of dimension names.
arrow.col	colour specification for biplot arrows and their labels.

`add_spp_site_scores` *Adds species and site score layers to an existing plot*

Description

Adds species and site score layers to an existing plot

Usage

```
add_spp_site_scores(object, plt, vars, geom, draw_list, arrows)
```

Arguments

<code>object</code>	an ordination object.
<code>plt</code>	a ggplot object.
<code>vars</code>	character; length 2 vector of dimension names.
<code>geom</code>	character; vector of length 1 or 2 indicating which geom will be used for the species or site scores.
<code>draw_list</code>	logical; vector of types of scores indicating which are available and requested for plotting.
<code>arrows</code>	logical; length 1 vector indicating if species scores should be drawn using arrows.

`arrow_mul` *Scale Vectors to Data*

Description

Scale vector arrows to fill proportion of the data.

Usage

```
arrow_mul(arrows, data, at = c(0, 0), fill = 0.75)
```

Arguments

<code>arrows</code>	a two-column matrix-like object containing coordinates for the arrows/vectors on x and y axes.
<code>data</code>	a two-column matrix-like object containing coordinates of the data on the x and y axes.
<code>at</code>	numeric vector of length 2; location of the origin of the arrows.
<code>fill</code>	numeric; what proportion of the range of the data to fill

Value

a numeric multiplier that will scale the arrows

Author(s)

Gavin L. Simpson

autoplot.anosim *ggplot-based plot for objects of class "anosim"*

Description

Produces a multi-layer ggplot object representing the output of objects produced by `vegan::anosim()`.

Usage

```
## S3 method for class 'anosim'
autoplot(
  object,
  notch = TRUE,
  varwidth = TRUE,
  xlab = NULL,
  ylab = NULL,
  title = "Analysis of similarities",
  subtitle = NULL,
  caption = bquote(R == .(r) * ", " ~ P == .(p)),
  ...
)
```

Arguments

object	an object of class "anosim", the result of a call to <code>vegan::anosim()</code> .
notch	logical; make notched (default) or standard box plot?
varwidth	logical; make box width proportional to the square-root of the number of observations in the group (default)?
xlab	character; label for the x-axis.
ylab	character; label for the y-axis.
title	character; title for the plot.
subtitle	character; subtitle for the plot.
caption	character; caption for the plot.
...	additional arguments passed to other methods.

Value

A ggplot object.

Author(s)

Didzis Elferts. Modifications by Gavin L. Simpson.

Examples

```
library("vegan")

data(dune)
data(dune.env)
dune.dist <- vegdist(dune)
dune.ano <- with(dune.env, anosim(dune.dist, Management))

autoplot(dune.ano, notch = FALSE)
```

autoplot.cca

ggplot-based plot for objects of class "cca"

Description

Produces a multi-layer ggplot object representing the output of objects produced by `vegan::cca()` or `vegan::capscale()`.

Usage

```
## S3 method for class 'cca'
autoplot(
  object,
  axes = c(1, 2),
  geom = c("point", "text"),
  layers = c("species", "sites", "biplot", "centroids"),
  legend.position = "right",
  title = NULL,
  subtitle = NULL,
  caption = NULL,
  ylab = NULL,
  xlab = NULL,
  arrow.col = "navy",
  ...
)
```

Arguments

object	an object of class "cca", the result of a call to <code>vegan::cca()</code> or <code>vegan::capscale()</code> .
axes	numeric; which axes to plot, given as a vector of length 2.
geom	character; which geom to use for the species (variables) and sites (samples) layers. A vector of length 2; if a vector of length 1, geom is extended to the required length.

layers	character; which scores to plot as layers
legend.position	character or two-element numeric vector; where to position the legend. See ggplot2::theme() for details. Use "none" to not draw the legend.
title	character; subtitle for the plot.
subtitle	character; subtitle for the plot.
caption	character; caption for the plot.
ylab	character; label for the y-axis.
xlab	character; label for the x-axis.
arrow.col	colour specification for biplot arrows and their labels.
...	Additional arguments passed to the fortify() method.

Details

TODO

Value

Returns a ggplot object.

Author(s)

Gavin L. Simpson

Examples

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

sol <- cca(dune ~ A1 + Management, data = dune.env)
autoplot(sol)
```

autoplot.dbrda *ggplot-based plot for objects of class "dbrda"*

Description

Produces a multi-layer ggplot object representing the output of objects produced by [vegan::dbrda\(\)](#).

Usage

```
## S3 method for class 'dbrda'
autoplot(
  object,
  axes = c(1, 2),
  geom = c("point", "text"),
  layers = c("sites", "biplot", "centroids"),
  legend.position = "none",
  title = NULL,
  subtitle = NULL,
  caption = NULL,
  ylab = NULL,
  xlab = NULL,
  const = NULL,
  arrow.col = "navy",
  ...
)
```

Arguments

object	an object of class "dbrda", the result of a call to vegan::dbrda()
axes	numeric; which axes to plot, given as a vector of length 2.
geom	character; which geom to use for the site (sample) scores. One of "point", or "text".
layers	character; which scores to plot as layers
legend.position	character or two-element numeric vector; where to position the legend. See ggplot2::theme() for details. Use "none" to not draw the legend.
title	character; subtitle for the plot.
subtitle	character; subtitle for the plot.
caption	character; caption for the plot.
ylab	character; label for the y-axis.
xlab	character; label for the x-axis.
const	General scaling constant to dbrda scores. See vegan::scores.rda() for details.
arrow.col	colour specification for biplot arrows and their labels.
...	Additional arguments passed to the fortify() method.

Details

TODO

Value

Returns a ggplot object.

Author(s)

Gavin L. Simpson

Examples

```
library("vegan")

data(dune, dune.env)

dune_dbrda <- dbrda(
  dune ~ A1 + Moisture + Use + Management,
  data = dune.env
)
autoplot(dune_dbrda)
```

autoplot.decorana *ggplot-based plot for objects of class "decorana"*

Description

Produces a multi-layer ggplot object representing the output of objects produced by [vegan::decorana\(\)](#).

Usage

```
## S3 method for class 'decorana'
autoplot(
  object,
  axes = c(1, 2),
  geom = c("point", "text"),
  layers = c("sites", "species"),
  legend.position = "right",
  title = NULL,
  subtitle = NULL,
  caption = NULL,
  ylab,
  xlab,
  ...
)
```

Arguments

object	an object of class "decorana", the result of a call to vegan::decorana() .
axes	numeric; which axes to plot, given as a vector of length 2.
geom	character; which geom to use for the species (variables) and sites (samples) layers. A vector of length 2; if a vector of length 1, geom is extended to the required length.
layers	character; which scores to plot as layers

legend.position	character or two-element numeric vector; where to position the legend. See ggplot2::theme() for details. Use "none" to not draw the legend.
title	character; subtitle for the plot.
subtitle	character; subtitle for the plot.
caption	character; caption for the plot.
ylab	character; label for the y-axis.
xlab	character; label for the x-axis.
...	Additional arguments passed to fortify.decorana() .

Details

TODO

Value

Returns a ggplot object.

Author(s)

Gavin L. Simpson

Examples

```
library("vegan")
data(dune)

sol <- decorana(dune)
autoplot(sol)
autoplot(sol, layers = "species", geom = "text")
```

autoplot.envfit *ggplot-based plot for envfit objects*

Description

Produces a multi-layer ggplot object representing the output of objects produced by [vegan::envfit\(\)](#).

Usage

```
## S3 method for class 'envfit'
autoplot(
  object,
  geom = c("label", "text", "label_repel", "text_repel"),
  line.col = "black",
  xlab = NULL,
  ylab = NULL,
```

```
  title = NULL,  
  subtitle = NULL,  
  caption = NULL,  
  ...  
)
```

Arguments

object	an object of class "envfit", the result of a call to <code>vegan::envfit()</code> .
geom	character; which geom to use to label vectors and factor centroids.
line.col	colour with which to draw vectors.
xlab	character; label for the x-axis.
ylab	character; label for the y-axis.
title	character; subtitle for the plot.
subtitle	character; subtitle for the plot.
caption	character; caption for the plot.
...	additional arguments passed to <code>ggplot2::fortify()</code> .

Value

A ggplot object.

Author(s)

Gavin L. Simpson

Examples

```
library("vegan")  
data(varespec, varechem)  
ord1 <- metaMDS(varespec)  
fit1 <- envfit(ord1, varechem, perm = 199)  
  
autoplot(fit1, geom = 'label_repel')  
  
data(dune, dune.env)  
ord2 <- cca(dune)  
fit2 <- envfit(ord2 ~ Moisture + A1, dune.env, perm = 199)  
  
autoplot(fit2)
```

autoplot.fisherfit *Plot Fisher's log-series*

Description

Draws a bar plot of species rank abundance with Fisher's log-series superimposed.

Usage

```
## S3 method for class 'fisherfit'
autoplot(
  object,
  show.fitted = TRUE,
  xlab = "Abundance",
  ylab = "Number of Species",
  title = "Fisher's log-series distribution",
  bar.col = NA,
  bar.fill = "grey35",
  line.col = "red",
  linewidth = 0.7,
  subtitle = NULL,
  caption = NULL,
  ...
)
```

Arguments

object	an object of class <code>vegan::fisherfit()</code> .
show.fitted	logical; should the estimated distribution also be plotted?
xlab	character; label for the x axis.
ylab	character; label for the y axis.
title	character; subtitle for the plot.
bar.col	colour for the bar outlines. The default, NA, does not draw outlines around bars.
bar.fill	fill colour for the bars.
line.col	colour for Fisher's log-series curve.
linewidth	numeric; linewidth aesthetic for the log-series curve.
subtitle	character; subtitle for the plot.
caption	character; caption for the plot.
...	additional arguments passed to other methods.

Value

A ggplot object.

Author(s)

Gavin L. Simpson

Examples

```
library("vegan")

data(BCI)
mod <- fisherfit(BCI[5,])
autoplot(mod)
```

autoplot.isomap *ggplot-based plot for objects of class "isomap"*

Description

Produces a multi-layer ggplot object representing the output of objects produced by [vegan::isomap\(\)](#).

Usage

```
## S3 method for class 'isomap'
autoplot(
  object,
  axes = c(1, 2),
  geom = c("point", "text"),
  network = TRUE,
  line.col = "grey85",
  linewidth = 0.7,
  xlab = NULL,
  ylab = NULL,
  title = "Isometric feature mapping",
  subtitle = NULL,
  caption = NULL,
  ...
)
```

Arguments

object	an object of class "isomap", the result of a call to vegan::isomap() .
axes	numeric; which axes to plot, given as a vector of length 2.
geom	character; which geom to use for the MDS scores layer.
network	logical; should the edges of the ISOMAP network be drawn?
line.col	colour with which to draw the network edges.
linewidth	numeric; linewidth aesthetic for the log-series curve.
xlab	character; label for the x-axis.

ylab	character; label for the y-axis.
title	character; subtitle for the plot.
subtitle	character; subtitle for the plot.
caption	character; caption for the plot.
...	additional arguments passed to other methods.

Value

A ggplot object.

Author(s)

Gavin L. Simpson

Examples

```
library("vegan")

data(BCI)
dis <- vegdist(BCI)
ord <- isomap(dis, k = 3)

autoplot(ord)

autoplot(ord, geom = "text")
```

autoplot.metaMDS *ggplot-based plot for objects of class "metaMDS"*

Description

Produces a multi-layer ggplot object representing the output of objects produced by `vegan::metaMDS()`.

Usage

```
## S3 method for class 'metaMDS'
autoplot(
  object,
  geom = c("point", "text"),
  layers = c("species", "sites"),
  legend.position = "right",
  title = NULL,
  subtitle = NULL,
  caption = NULL,
  ylab,
  xlab,
  ...
)
```

Arguments

object	an object of class "metaMDS", the result of a call to <code>vegan::metaMDS()</code> .
geom	character; which geom to use for the species (variables) and sites (samples) layers. A vector of length 2; if a vector of length 1, geom is extended to the required length.
layers	character; which scores to plot as layers
legend.position	character or two-element numeric vector; where to position the legend. See <code>ggplot2::theme()</code> for details. Use "none" to not draw the legend.
title	character; subtitle for the plot.
subtitle	character; subtitle for the plot.
caption	character; caption for the plot.
ylab	character; label for the y-axis.
xlab	character; label for the x-axis.
...	Additional arguments passed to <code>\link{fortify.metaMDS}</code> .

Details

TODO

Value

Returns a ggplot object.

Author(s)

Gavin L. Simpson

Examples

```
library("vegan")  
  
data(dune)  
  
sol <- metaMDS(dune)  
autoplot(sol)
```

autoplot.permustats *Autoplot Graphics for vegan permustats Objects*

Description

Alternatives for **lattice** graphics functions `vegan::densityplot.permustats()`, `vegan::densityplot.permustats()` and `vegan::boxplot.permustats()`.

Usage

```
## S3 method for class 'permustats'
autoplot(
  object,
  plot = c("box", "violin", "density", "qqnorm"),
  scale = FALSE,
  facet = FALSE,
  gg.params = list(),
  ...
)
```

Arguments

object	object from <code>vegan::permustats()</code> .
plot	character; the type of plot, or a geom from ggplot2 .
scale	logical; use standardized effect sizes (SES)?
facet	logical; should the plot be faceted by term?
gg.params	list; arguments passed to function drawing the box-like object. Depending on argument plot the parameters are passed to <code>ggplot2::geom_boxplot()</code> , <code>ggplot2::geom_violin()</code> , <code>ggplot2::geom_density()</code> or <code>ggplot2::geom_qq()</code> .
...	Other parameters passed to functions (ignored).

Details

Function `fortify()` returns a data frame with variables `permutations` (numeric) and `term` (factor labelling the permutation). The result of `fortify()` can be used to custom build diagnostic plots. `autoplot()` provides basic plots of `vegan::permustats()` objects with limited flexibility.

Value

Returns a ggplot object.

Examples

```

library("vegan")

data(dune, dune.env)
mod <- cca(dune ~ A1 + Management + Moisture, dune.env)
(ano <- anova(mod, by = "onedf"))
pstat <- permustats(ano)
head(fortify(pstat))
autoplot(pstat, "box")

if (requireNamespace("ggplot2")) {
  library("ggplot2")

  # avoid overplotting x-axis text
  autoplot(pstat, "violin") +
    scale_x_discrete(guide = guide_axis(n.dodge = 2))

  autoplot(pstat, "qqnorm", facet = TRUE) +
    geom_qq_line()
}

autoplot(pstat, "density", facet = TRUE)

```

autoplot.poolaccum *ggplot-based plot for objects of class "poolaccum"*

Description

Produces a multi-layer ggplot object representing the output of objects produced by `vegan::poolaccum()`.

Usage

```

## S3 method for class 'poolaccum'
autoplot(
  object,
  facet = TRUE,
  ribbon = facet,
  ncol = NULL,
  ribbon.alpha = 0.3,
  xlab = "Size",
  ylab = "Richness",
  title = "Accumulated species richness",
  subtitle = NULL,
  caption = NULL,
  ...
)

```

Arguments

object	an object of class "poolaccum", the result of a call to <code>vegan::poolaccum()</code> .
facet	logical; should extrapolated richness estimators be shown in separate facets?
ribbon	logical; show the quantile-based uncertainty interval? Uses <code>ggplot2::geom_ribbon()</code> for plot.
ncol	numeric; if faceting the plot, how many columns to use. Default arguments will result in three columns.
ribbon.alpha	numeric; alpha transparency used for the uncertainty interval. Passed to the alpha aesthetic of <code>ggplot2::geom_ribbon()</code> .
xlab	character; label for the x axis.
ylab	character; label for the y axis.
title	character; title for the plot.
subtitle	character; subtitle for the plot.
caption	character; caption for the plot.
...	additional arguments passed to <code>fortify.poolaccum()</code> .

Value

A ggplot object.

Author(s)

Didzis Elferts & Gavin L. Simpson

Examples

```
library("vegan")

data(BCI)
pool <- poolaccum(BCI)

autoplot(pool)

## Turn off facetting; turns off ribbon too
autoplot(pool, facet = FALSE)
```

autoplot.prc

ggplot-based plot for objects of class "prc"

Description

Produces a multi-layer ggplot object representing the output of objects produced by `vegan::prc()`.

Usage

```
## S3 method for class 'prc'
autoplot(
  object,
  select,
  xlab,
  ylab,
  title = NULL,
  subtitle = NULL,
  caption = NULL,
  legend.position = "top",
  ...
)
```

Arguments

object	an object inheriting from class "prc", the result of a call to vegan::prc() .
select	a logical vector where TRUE selects and FALSE deselects species. Alternatively a numeric vector that contains the indices selecting species. Note that these are with respect to the original species matrix, not the fortified object.
xlab	character; label for the x-axis
ylab	character; label for the y-axis
title	character; subtitle for the plot
subtitle	character; subtitle for the plot
caption	character; caption for the plot
legend.position	character; position for the legend grob. See argument legend.position in function ggplot2::theme() .
...	Additional arguments passed to <code>\link{fortify.prc}</code> .

Details

TODO

Value

Returns a ggplot object.

Author(s)

Gavin L. Simpson

Examples

```

library("vegan")

data(pyrifos)
week <- gl(11, 12, labels=c(-4, -1, 0.1, 1, 2, 4, 8, 12, 15, 19, 24))
dose <- factor(rep(c(0.1, 0, 0, 0.9, 0, 44, 6, 0.1, 44, 0.9, 0, 6), 11))

## Fit PRC model
mod <- prc(pyrifos, dose, week)

## plot
want <- colSums(pyrifos) >= 300
autoplot(mod, select = want)

```

autoplot.prestonfit *Plot Preston's log-normal model of species abundance*

Description

Draws a bar plot of species rank abundance with Preston's log-normal model superimposed.

Usage

```

## S3 method for class 'prestonfit'
autoplot(
  object,
  show.fitted = TRUE,
  xlab = "Abundance",
  ylab = "Number of Species",
  title = "Preston's lognormal distribution",
  subtitle = NULL,
  caption = NULL,
  bar.col = NA,
  bar.fill = "grey35",
  line.col = "red",
  linewidth = 0.7,
  ...
)

```

Arguments

object	an object of class <code>vegan::prestonfit()</code> .
show.fitted	logical; should the estimated distribution also be plotted?
xlab	character; label for the x axis.
ylab	character; label for the y axis.
title	character; title for the plot.

subtitle	character; subtitle for the plot.
caption	character; caption for the plot.
bar.col	colour for the bar outlines. The default, 'NA', does not draw outlines around bars.
bar.fill	fill colour for the bars.
line.col	colour for Preston's log-normal curve.
linewidth	numeric; size aesthetic for the log-normal curve.
...	additional arguments passed to other methods.

Value

A ggplot object.

Author(s)

Gavin L. Simpson

Examples

```
library("vegan")

data(BCI)
pfit <- prestonfit(colSums(BCI))
autoplot(pfit)
```

autoplot.rda

ggplot-based plot for objects of class 'rda'

Description

Produces a multi-layer ggplot object representing the output of objects produced by `vegan::rda()`.

Usage

```
## S3 method for class 'rda'
autoplot(
  object,
  axes = c(1, 2),
  geom = c("point", "text"),
  layers = c("species", "sites", "biplot", "centroids"),
  arrows = TRUE,
  legend.position = "none",
  title = NULL,
  subtitle = NULL,
  caption = NULL,
  ylab = NULL,
```

```

xlab = NULL,
const = NULL,
arrow.col = "navy",
...
)

```

Arguments

object	an object of class "rda", the result of a call to vegan::rda()
axes	numeric; which axes to plot, given as a vector of length 2.
geom	character; which geom to use for the species (variables) and sites (samples) layers. A vector of length 2; if a vector of length 1, geom is extended to the required length.
layers	character; which scores to plot as layers
arrows	logical; represent species (variables) using vectors?
legend.position	character or two-element numeric vector; where to position the legend. See ggplot2::theme() for details. Use "none" to not draw the legend.
title	character; subtitle for the plot.
subtitle	character; subtitle for the plot.
caption	character; caption for the plot.
ylab	character; label for the y-axis.
xlab	character; label for the x-axis.
const	General scaling constant to rda scores. See vegan::scores.rda() for details.
arrow.col	colour specification for biplot arrows and their labels.
...	Additional arguments passed to the fortify() method.

Details

TODO

Value

Returns a ggplot object.

Author(s)

Gavin L. Simpson

Examples

```

library("vegan")

data(dune)

pca <- rda(dune)

```

```
autoplot(pca)

## Just the species scores
autoplot(pca, layers = "species")
```

```
autoplot.vegan_pco    ggplot-based plot for objects of class "vegan_pco"
```

Description

Produces a multi-layer ggplot object representing the output of objects produced by `vegan::pco()`.

Usage

```
## S3 method for class 'vegan_pco'
autoplot(
  object,
  geom = "point",
  legend.position = "right",
  title = NULL,
  subtitle = NULL,
  caption = NULL,
  ylab = NULL,
  xlab = NULL,
  ...
)
```

Arguments

<code>object</code>	an object of class "vegan_pco", the result of a call to <code>vegan::pco()</code> .
<code>geom</code>	character; which geom to use for the site (sample) scores. One of "point", or "text".
<code>legend.position</code>	character or two-element numeric vector; where to position the legend. See <code>ggplot2::theme()</code> for details. Use "none" to not draw the legend.
<code>title</code>	character; subtitle for the plot.
<code>subtitle</code>	character; subtitle for the plot.
<code>caption</code>	character; caption for the plot.
<code>ylab</code>	character; label for the y-axis.
<code>xlab</code>	character; label for the x-axis.
<code>...</code>	Additional arguments passed to the <code>fortify()</code> method.

Details

TODO

Value

Returns a ggplot object.

Author(s)

Gavin L. Simpson

Examples

```
library("vegan")  
  
data(dune)  
  
sol <- pco(dune)  
autoplot(sol)
```

check_user_layers	<i>Check user-supplied layers against list of valid layers</i>
-------------------	--

Description

Check user-supplied layers against list of valid layers

Usage

```
check_user_layers(user, valid, message = FALSE)
```

Arguments

user	character; vector of user supplied layer names.
valid	character; vector of valid layer names.
message	logical; should a message be raised in the case of invalid user-supplied layer names.

fortify.anosim	<i>Fortify analysis of similarities (ANOSIM) results</i>
----------------	--

Description

Prepares a fortified version of results from `vegan::anosim()` objects.

Usage

```
## S3 method for class 'anosim'  
fortify(model, data, ...)  
  
## S3 method for class 'anosim'  
tidy(x, data, ...)
```

Arguments

model, x	an object of class <code>vegan::anosim()</code> .
data	original data set. Currently ignored.
...	additional arguments for other methods. Currently ignored.

Value

A data frame with columns Rank and Class with ranks of dissimilarity.

Author(s)

Original implementation by Didzis Elferts. Modification to tibbles by Gavin L. Simpson.

Examples

```
library("vegan")  
  
library("ggplot2")  
data(dune, dune.env)  
dune.dist <- vegdist(dune)  
dune.ano <- with(dune.env, anosim(dune.dist, Management))  
  
df <- fortify(dune.ano)  
  
ggplot(df, aes(x = class, y = rank)) +  
  geom_boxplot(notch = FALSE, varwidth = TRUE)
```

fortify.cca

Fortify a "cca" object.

Description

Fortifies an object of class "cca" to produce a data frame of the selected axis scores in long format, suitable for plotting with `ggplot2::ggplot()`.

Usage

```
## S3 method for class 'cca'  
fortify(model, data, axes = 1:6, layers = c("sp", "wa", "lc", "bp", "cn"), ...)  
  
## S3 method for class 'cca'  
tidy(x, data, axes = 1:6, layers = c("sp", "wa", "lc", "bp", "cn"), ...)
```

Arguments

model, x	an object of class "cca", the result of a call to <code>vegan::cca()</code> , <code>vegan::rda()</code> , or <code>vegan::capscale()</code> .
data	currently ignored.
axes	numeric; which axes to extract scores for.
layers	character; the scores to extract in the fortified object. Passed to <code>display</code> in the respective <code>vegan::scores()</code> method.
...	additional arguments passed to <code>vegan::scores.cca()</code> .

Details

TODO

Value

A data frame (tibble) in long format containing the ordination scores. The first two components are score (the type of score in each row) and label (the text label to use on plots for this row). The remaining columns are the extracted ordination axis scores.

Author(s)

Gavin L. Simpson

Examples

```
library("vegan")  
  
data(dune)  
data(dune.env)  
  
sol <- cca(dune ~ A1 + Management, data = dune.env)  
head(fortify(sol))
```

fortify.dbrda	<i>Fortify a "dbrda" object.</i>
---------------	----------------------------------

Description

Fortifies an object of class "dbrda" to produce a data frame of the selected axis scores in long format, suitable for plotting with `ggplot2::ggplot()`.

Usage

```
## S3 method for class 'dbrda'
fortify(
  model,
  data = NULL,
  axes = 1:6,
  layers = c("wa", "lc", "bp", "reg", "cn"),
  const = NULL,
  ...
)
```

```
## S3 method for class 'dbrda'
tidy(
  x,
  data = NULL,
  axes = 1:6,
  layers = c("wa", "lc", "bp", "reg", "cn"),
  const = NULL,
  ...
)
```

Arguments

<code>model, x</code>	an object of class "dbrda", the result of a call to <code>vegan::dbrda()</code> .
<code>data</code>	currently ignored.
<code>axes</code>	numeric; which axes to extract scores for.
<code>layers</code>	character; the scores to extract in the fortified object. Passed to display in the respective <code>vegan::scores()</code> method.
<code>const</code>	NULL; General scaling constant to RDA scores. See <code>vegan::scores.rda()</code> for the details.
<code>...</code>	additional arguments passed to <code>vegan::scores.rda()</code> .

Details

TODO

Value

A data frame (tibble) in long format containing the ordination scores. The first two components are score (the type of score in each row) and label (the text label to use on plots for this row). The remaining columns are the extracted ordination axis scores.

Author(s)

Gavin L. Simpson

Examples

```
library("vegan")

data(dune)
data(dune.env)

sol <- dbrda(dune ~ A1 + Management, data = dune.env)
head(fortify(sol))
```

fortify.decorana	<i>Fortify a "decorana" object.</i>
------------------	-------------------------------------

Description

Fortifies an object of class "decorana" to produce a data frame of the selected axis scores in long format, suitable for plotting with `ggplot2::ggplot()`.

Usage

```
## S3 method for class 'decorana'
fortify(model, data, axes = 1:4, layers = c("sites", "species"), ...)

## S3 method for class 'decorana'
tidy(x, data, axes = 1:4, layers = c("sites", "species"), ...)
```

Arguments

model, x	an object of class "decorana", the result of a call to <code>vegan::decorana()</code> .
data	currently ignored.
axes	numeric; which axis scores are required?
layers	character; the scores to extract in the fortified object.
...	additional arguments passed to <code>vegan::scores.decorana()</code> .

Details

TODO

Value

A data frame in long format containing the ordination scores. The first two components are the axis scores.

Author(s)

Gavin L. Simpson

Examples

```
library("vegan")

data(dune)

sol <- decorana(dune)
head(fortify(sol))
head(fortify(sol, layers = "species"))
```

fortify.envfit	<i>Fortify method for envfit objects</i>
----------------	--

Description

Produces a tidy data frame from the results of an `vegan::envfit()` object.

Usage

```
## S3 method for class 'envfit'
fortify(model, data, ...)

## S3 method for class 'envfit'
tidy(x, data, ...)
```

Arguments

model, x	an object of class <code>envfit</code> , the result of a call to <code>vegan::envfit()</code> .
data	additional data to augment the <code>envfit</code> results. Currently ignored.
...	arguments passed to <code>vegan::scores.envfit()</code> .

Value

A data frame with columns `label`, `type`, containing the label for, and whether each row refers to, the fitted vector or factor. Remaining variables are coordinates on the respective ordination axes returned by `vegan::scores.envfit()`.

Author(s)

Gavin L. Simpson

Examples

```
library("vegan")

data(varespec, varechem)
ord <- metaMDS(varespec)
fit <- envfit(ord, varechem, perm = 199)

fortify(fit)

data(dune, dune.env)
ord <- ca(dune)
fit <- envfit(ord ~ Moisture + A1, dune.env, perm = 199)

fortify(fit)
```

fortify.fisherfit *Tidied species rank abundance data and estimated Fisher's log-series*

Description

Prepares a data frame of results from a `vegan::fisherfit()` object suitable for plotting with `ggplot2::ggplot()`.

Usage

```
## S3 method for class 'fisherfit'
fortify(model, data, ...)

## S3 method for class 'fisherfit'
tidy(x, data, ...)
```

Arguments

`model, x` an object of class `vegan::fisherfit()`.
`data` original data set. Currently ignored.
`...` other arguments pass to methods. Currently ignored.

Value

A data frame with columns 'Rank' and 'Abundance'. Additionally, Fisher's α and the nuisance parameter are returned as attributes 'alpha' and 'k' respectively.

Author(s)

Gavin L. Simpson

Examples

```
library("vegan")

data(BCI)
mod <- fisherfit(BCI[5,])
head(fortify(mod))
```

fortify.isomap	<i>Fortify isometric feature mapping results</i>
----------------	--

Description

Prepares fortified versions of results from `vegan::isomap()` objects.

Usage

```
## S3 method for class 'isomap'
fortify(model, data = NULL, axes = NULL, what = c("sites", "network"), ...)

## S3 method for class 'isomap'
tidy(x, data = NULL, axes = NULL, what = c("sites", "network"), ...)
```

Arguments

<code>model, x</code>	an object of class <code>vegan::isomap()</code> .
<code>data</code>	data.frame; additional data to be added to the fortified object.
<code>axes</code>	numeric; which axes to return. For <code>what = "network"</code> this must be of length two only.
<code>what</code>	character; what aspect of the results should be fortified? <code>"sites"</code> returns to ordination scores from the multidimensional scaling part of the model. <code>"network"</code> returns the coordinates for edges joining points.
<code>...</code>	additional arguments for other methods. Currently ignored.

Details

Two different objects can be created from the results of an `vegan::isomap()` object. The first is the standard scores representation of fortified ordinations in `vegan`, which results in a wide data frame where rows contain observations and column the coordinates of observations on the MDS axes. Because ISOMAP also produces a network or sorts, the coordinates of the edges of the network can also be returned in a tidy format using `what = "network"`.

Value

A data frame. For `what = "sites"`, the data frame contains one variable per dimension of the multidimensional scaling embedding of the dissimilarities. Variables are named `"DimX"` with `"X"` being an integer. An additional variable is `label`, containing a label for each observation. For `what = "network"`, the data frame contains four variables containing the coordinates in the chosen MDS axes for the start and end points of the network edges.

Author(s)

Gavin L. Simpson

Examples

```
library("vegan")

library("ggplot2")
data(BCI)
dis <- vegdist(BCI)
ord <- isomap(dis, k = 3)

df <- fortify(ord, data = data.frame(Richness = specnumber(BCI)))
net <- fortify(ord, what = "network", axes = 1:2)

ggplot(df, aes(x = dim1, y = dim2)) +
  geom_segment(data = net,
              aes(x = xfrom, y = yfrom,
                  xend = xto, yend = yto),
              colour = "grey85", size = 0.8) +
  geom_point(aes(size = Richness)) +
  coord_fixed()
```

fortify.metaMDS

Fortify a "metaMDS" object.

Description

Fortifies an object of class "metaMDS" to produce a data frame of the selected axis scores in long format, suitable for plotting with `ggplot2::ggplot()`.

Usage

```
## S3 method for class 'metaMDS'
fortify(model, data, axes = 1:2, layers = c("sites", "species"), ...)

## S3 method for class 'metaMDS'
tidy(x, data, layers = c("sites", "species"), ...)
```

Arguments

model, x	an object of class "metaMDS", the result of a call to <code>vegan::metaMDS()</code> .
data	currently ignored.
axes	numeric; which axes to extract scores for.
layers	character; the scores to extract in the fortified object. Passed to display in the respective <code>vegan::scores()</code> method.
...	additional arguments passed to <code>vegan::scores.metaMDS()</code> . Note you can't use display.

Details

TODO

Value

A data frame in long format containing the ordination scores. The first two components are the axis scores.

Author(s)

Gavin L. Simpson

Examples

```
library("vegan")

data(dune)

ord <- metaMDS(dune)
head(fortify(ord))
```

fortify.permustats *Fortify permutation statistics*

Description

Fortify permutation statistics

Usage

```
## S3 method for class 'permustats'
fortify(model, data, scale = FALSE, ...)

## S3 method for class 'permustats'
tidy(x, data, scale = FALSE, ...)
```

Arguments

model, x	an object of created by <code>vegan::permustats()</code> .
data	original data set. Currently ignored.
scale	logical; return standardized effect sizes (SES)?
...	Other parameters passed to functions (ignored).

Value

A tibble with columns `permutations`, and `terms` containing the values of tests statistics under the null hypothesis, and a factor labelling the permutation, respectively.

Examples

```
library("vegan")
data(dune, dune.env, package = "vegan")
mod <- adonis2(dune ~ Management + A1, data = dune.env)
## use permustats
perm <- permustats(mod)
```

fortify.poolaccum *Fortify extrapolated species richness of a species pool*

Description

Prepares a fortified version of results from `vegan::poolaccum()` objects.

Usage

```
## S3 method for class 'poolaccum'
fortify(model, data, alpha = 0.05, ...)

## S3 method for class 'poolaccum'
tidy(x, data, alpha = 0.05, ...)
```

Arguments

<code>model, x</code>	an object of class <code>vegan::poolaccum()</code> .
<code>data</code>	original data set. Currently ignored.
<code>alpha</code>	level of quantiles for envelopes shown (default 0.05).
<code>...</code>	additional arguments passed to <code>vegan::summary.poolaccum()</code> , notably <code>display</code> to control which indices should be computed.

Value

A data frame with columns `index`, `size`, `richness`, `lower`, `upper`, and `std_dev`, containing the richness index, permutation richness estimator, sample size, upper and lower $1 - \alpha$ quantile interval, and standard deviation of permutation estimates, respectively.

Author(s)

Gavin L. Simpson & Didzis Elferts

Examples

```

library("vegan")
library("ggplot2")
data(BCI)
pool <- poolaccum(BCI)
df <- fortify(pool)
df

ggplot(df, aes(x = size, y = richness, colour = index)) +
  geom_ribbon(aes(ymin = lower, ymax = upper, x = size, fill = index),
            alpha = 0.3, inherit.aes = FALSE) +
  geom_line() +
  facet_wrap(~ index)

```

fortify.prc

*Fortify a "prc" object***Description**

Fortifies an object of class "prc" to produce a data frame of the selected axis scores in long format, suitable for plotting with `ggplot2::ggplot()`.

Usage

```

## S3 method for class 'prc'
fortify(model, data, scaling = "symmetric", axis = 1, ...)

## S3 method for class 'prc'
tidy(x, data, scaling = "symmetric", axis = 1, ...)

```

Arguments

model, x	an object of class "prc", the result of a call to <code>vegan::prc()</code> .
data	currently ignored.
scaling	the desired scaling. See <code>vegan::scores.cca()</code> for details.
axis	numeric; which PRC axis to extract. Default is axis = 1, which is the most generally useful choice.
...	additional arguments currently ignored.

Details

TODO

Value

A data frame in long format containing the ordination scores. The first three components are the Time, Treatment, and associated Response. The last two components, score and label are an indicator factor and a label for the rows for use in plotting.

Author(s)

Gavin L. Simpson

Examples

```
library("vegan")
data(pyrifos)
week <- gl(11, 12, labels=c(-4, -1, 0.1, 1, 2, 4, 8, 12, 15, 19, 24))
dose <- factor(rep(c(0.1, 0, 0, 0.9, 0, 44, 6, 0.1, 44, 0.9, 0, 6), 11))
ditch <- gl(12, 1, length=132)

pyrifos_prc <- prc(pyrifos, dose, week)
fortify(pyrifos_prc)
```

fortify.prestonfit *Tidied species octave abundance data*

Description

Prepares a data frame of results from a `vegan::prestonfit()` object suitable for plotting with `ggplot2::ggplot()`.

Usage

```
## S3 method for class 'prestonfit'
fortify(model, data, ...)
```

```
## S3 method for class 'prestonfit'
tidy(x, data, ...)
```

Arguments

`model, x` an object of class `vegan::prestonfit()`.
`data` original data set. Currently ignored.
`...` other arguments pass to methods. Currently ignored.

Value

A data frame with columns 'Octave' and 'Abundance'.

Author(s)

Gavin L. Simpson

Examples

```
library("vegan")

data(BCI)
pfit <- prestonfit(colSums(BCI))
fortify(pfit)
```

fortify.rda

Fortify a "rda" object.

Description

Fortifies an object of class "rda" to produce a data frame of the selected axis scores in long format, suitable for plotting with `ggplot2::ggplot()`.

Usage

```
## S3 method for class 'rda'
fortify(
  model,
  data = NULL,
  axes = 1:6,
  layers = c("sp", "wa", "lc", "bp", "cn"),
  const = NULL,
  ...
)

## S3 method for class 'rda'
tidy(
  x,
  data = NULL,
  axes = 1:6,
  layers = c("sp", "wa", "lc", "bp", "reg", "cn"),
  const = NULL,
  ...
)
```

Arguments

<code>model, x</code>	an object of class "rda", the result of a call to <code>vegan::rda()</code> .
<code>data</code>	currently ignored.
<code>axes</code>	numeric; which axes to extract scores for.
<code>layers</code>	character; the scores to extract in the fortified object. Passed to display in the respective <code>vegan::scores()</code> method.
<code>const</code>	NULL; General scaling constant to RDA scores. See <code>vegan::scores.rda()</code> for the details.
<code>...</code>	additional arguments passed to <code>vegan::scores.rda()</code> .

Details

TODO

Value

A data frame (tibble) in long format containing the ordination scores. The first two components are score (the type of score in each row) and label (the text label to use on plots for this row). The remaining columns are the extracted ordination axis scores.

Author(s)

Gavin L. Simpson

Examples

```
library("vegan")

data(dune)
data(dune.env)

sol <- rda(dune ~ A1 + Management, data = dune.env)
head(fortify(sol))
```

fortify.renyiaccum *Fortify Rényi accumulation curves*

Description

Prepares a fortified version of results from `vegan::renyiaccum()` objects.

Usage

```
## S3 method for class 'renyiaccum'
fortify(model, data, ...)

## S3 method for class 'renyiaccum'
tidy(x, data, ...)
```

Arguments

<code>model, x</code>	an object of class <code>vegan::renyiaccum()</code> .
<code>data</code>	original data set. Currently ignored.
<code>...</code>	additional arguments passed to other methods. Ignored in this method.

Value

A data frame (tibble) is returned. What is returned depends on how `vegan::renyiaccum()` was called. If `raw = FALSE`, then a data frame with columns `site`, `scale`, `mean`, `std_dev`, `min`, `max`, `q2.5`, and `q97.5`, containing the accumulated sites, the Rényi scale, and summary statistics of the Rényi accumulation curves. An additional column `collector` will be present if `collector = TRUE` was used in the `vegan::renyiaccum()` call. If `raw = TRUE`, then a data frame with columns `site`, `permutation`, `scale`, and `diversity`, containing the site and permutation identifiers, Rényi scale, and the Rényi diversity, respectively.

Author(s)

Gavin L. Simpson much rewritten from an original by Didzis Elferts.

Examples

```
library("vegan")
library("ggplot2")
data(BCI)
pool <- renyiaccum(BCI)
df <- fortify(pool)
df

ggplot(df, aes(x = site, y = mean)) +
  geom_ribbon(aes(ymin = q2.5, ymax = q97.5, x = site),
            alpha = 0.2, inherit.aes = FALSE) +
  geom_line() +
  facet_wrap(~ scale)
```

fortify.vegan_pco *Fortify a "vegan_pco" object.*

Description

Fortifies an object of class "vegan_pco" to produce a data frame of the selected axis scores in long format, suitable for plotting with `ggplot2::ggplot()`.

Usage

```
## S3 method for class 'vegan_pco'
fortify(model, data = NULL, axes = 1:6, ...)

## S3 method for class 'vegan_pco'
tidy(x, data = NULL, axes = 1:6, const = NULL, ...)
```

Arguments

model, x	an object of class "vegan_pco", the result of a call to <code>vegan::pco()</code> .
data	currently ignored.
axes	numeric; which axes to extract scores for.
...	additional arguments passed to <code>vegan::scores.rda()</code> .
const	NULL; General scaling constant to RDA scores. See <code>vegan::scores.rda()</code> for the details.

Details

TODO

Value

A data frame (tibble) in long format containing the ordination scores. The first two components are score (the type of score in each row) and label (the text label to use on plots for this row). The remaining columns are the extracted ordination axis scores.

Author(s)

Gavin L. Simpson

Examples

```
library("vegan")

data(dune)

sol <- pco(dune)
head(fortify(sol))
```

geom_ordi_arrow *Add a biplot arrow layer to an ordiggplot*

Description

Add a biplot arrow layer to an ordiggplot

Usage

```
geom_ordi_arrow(
  score,
  data,
  text = TRUE,
  box = FALSE,
  arrow.params = list(),
  text.params = list(),
  ...
)
```

Arguments

score	Ordination score to be added to the plot.
data	Alternative data to the function that will be used instead of score.
text	Add text labels to the plot.
box	Draw a box behind the text (logical).
arrow.params, text.params	Parameters to modify arrows or their text labels.
...	other arguments passed to <code>ggplot2::geom_segment()</code> , <code>ggplot2::geom_label()</code> , or <code>ggplot2::geom_text()</code>

Value

Returns a ggplot2 layer or a list of such layers: a "LayerInstance" object that inherits from classes "Layer", "ggproto", and "gg".

geom_ordi_axis	<i>Crosshair for axes in eigenvector methods</i>
----------------	--

Description

Crosshair for axes in eigenvector methods

Usage

```
geom_ordi_axis(lty = 3, ...)
```

Arguments

lty	Linetype.
...	other arguments passed to <code>ggplot2::geom_hline()</code> and <code>ggplot2::geom_vline()</code>

Value

Returns a ggplot2 layer or a list of such layers: a "LayerInstance" object that inherits from classes "Layer", "ggproto", and "gg".

geom_ordi_label *Add a label layer to an ordiggplot*

Description

Add a label layer to an ordiggplot

Usage

```
geom_ordi_label(score, data, ...)
```

Arguments

score	Ordination score to be added to the plot.
data	Alternative data to the function that will be used instead of score.
...	other arguments passed to ggplot2::geom_label()

Value

Returns a ggplot2 layer or a list of such layers: a "LayerInstance" object that inherits from classes "Layer", "ggproto", and "gg".

geom_ordi_point *Add a point layer to an ordiggplot*

Description

Add a point layer to an ordiggplot

Usage

```
geom_ordi_point(score, data, ...)
```

Arguments

score	Ordination score to be added to the plot.
data	Alternative data to the function that will be used instead of score.
...	other arguments passed to ggplot2::geom_point()

Value

Returns a ggplot2 layer or a list of such layers: a "LayerInstance" object that inherits from classes "Layer", "ggproto", and "gg".

geom_ordi_text	<i>Add a text layer to an ordiggplot</i>
----------------	--

Description

Add a text layer to an ordiggplot

Usage

```
geom_ordi_text(score, data, ...)
```

Arguments

score	Ordination score to be added to the plot.
data	Alternative data to the function that will be used instead of score.
...	other arguments passed to <code>ggplot2::geom_text()</code>

Value

Returns a ggplot2 layer or a list of such layers: a "LayerInstance" object that inherits from classes "Layer", "ggproto", and "gg".

get_dimension_names	<i>Extract the names of the dimensions to plot as a character vector</i>
---------------------	--

Description

Find the character vector of names for the two dimensions of data to be plotted.

Usage

```
get_dimension_names(object)
```

Arguments

object	a fortified ordination object.
--------	--------------------------------

Value

A length 2 character vector of dimension names.

Author(s)

Gavin L. Simpson

label_fun	<i>Adds a label layer using one of a set of common geoms</i>
-----------	--

Description

Adds labels to a plot using one of `ggplot2::geom_label()`, `ggplot2::geom_text()`, `ggrepel::geom_label_repel()` or `ggrepel::geom_text_repel()`.

Usage

```
label_fun(data, geom = c("label", "text", "label_repel", "text_repel"), vars)
```

Arguments

data	data frame; data set to use for the label layer. Must contain a variable label containing the strings to use as labels.
geom	character; which geom to use for labelling.
vars	character; vector of names of variables to pass to the x and y aesthetics of the chosen geom.

Author(s)

Gavin L. Simpson

layer_draw_list	<i>List of layers to draw for a given vegan object</i>
-----------------	--

Description

List of layers to draw for a given vegan object

Usage

```
layer_draw_list(valid, layers = NULL, available = NULL)
```

Arguments

valid	character; vector of valid layer names
layers	character; a vector of layer names for object that has already been filtered for validity.
available	character; what layers are actually available

`ordiggplot`*Create a ggplot Object*

Description

Function `ordiggplot` sets up an ordination graph but draws no result. You can add new graphical elements to this plot with `geom_ordi_*` function of this package, or you can use standard **ggplot2** `geom_*` functions and use `ggscores` as their data argument.

Usage

```
ordiggplot(model, axes = c(1, 2), arrow.mul, ...)
```

```
ggscores(score)
```

Arguments

<code>model</code>	An ordination result object from vegan .
<code>axes</code>	Two axes to be plotted
<code>arrow.mul</code>	Multiplier to arrow length. If missing, the arrow length are adjusted to fit to other scores, but if some score types are not displayed, the arrows may be badly scaled, and manual adjustment can be useful.
<code>...</code>	Parameters passed to underlying functions.
<code>score</code>	Ordination score to be added to the plot.

Details

The **ggvegan** package has two contrasting approaches to draw ordination plots. The `autoplot` functions (e.g. `autoplot.rda()`, `autoplot.cca()`, and `autoplot.metaMDS`) draw a complete plot with one command, but the design is hard-coded in the function. However, you can add new elements to the graph.

In contrast, function `ordiggplot()` only sets up an ordination plot, and does not draw anything. It allows you to add layers to the plot one by one with full flexibility of the **ggplot2** functions. There are some specific functions `geom_ordi_*` functions that are similar as similarly named `geom_*` functions. For these you need to give the type of ordination scores to be added, and in addition, you can give any `geom_*` function arguments to modify the plot. Alternatively, you can use any **ggplot2** function and in its data argument use `ggscores()` function to select the data elements for the function.

The `ordiggplot()` function extracts results using `fortify()` functions of this package, and it accepts the arguments of those functions. This allows setting, e.g., the scaling of ordination axes.

Value

Returns a ggplot object.

Examples

```

library("vegan")
library("ggplot2")
data(dune, dune.env, varespec, varechem)
m <- cca(dune ~ Management + A1, dune.env)

## use geom_ordi_* functions
orddigplot(m) + geom_ordi_axis() +
  geom_ordi_point("sites") +
  geom_ordi_text("species", col = "darkblue",
                mapping = aes(fontface = "italic")) +
  geom_ordi_label("centroids") +
  geom_ordi_arrow("biplot")

## use ggscores + standard geom_* functions
orddigplot(m, scaling = "sites") +
  geom_point(data = ggcores("sites")) +
  geom_text(data = ggcores("species"),
            mapping = aes(fontface = "italic")) +
  geom_label(data = ggcores("centroids"), fill = "yellow") +
  geom_ordi_arrow("biplot")

## Messy arrow biplot for PCA
m <- rda(dune)
orddigplot(m) +
  geom_ordi_axis() +
  geom_ordi_point("sites") +
  geom_ordi_arrow("species")

```

scores_length	<i>Number of scores</i>
---------------	-------------------------

Description

Returns the number of scores returns in object 'x'.

Usage

```
scores_length(x)
```

Arguments

x The object whose number of scores is required.

Value

a numeric vector of length 1 with the number of scores.

Author(s)

Gavin L. Simpson

StatVectorfit*Add Fitted Vectors to Ordination plots*

Description

Fits arrows to show the direction of fastest increase in continuous environmental variables in ordination space. The arrows are scaled relative to their correlation coefficient, and they can be added to an ordination plot with `geom_ordi_arrow()`.

Usage

```
stat_vectorfit(  
  mapping = NULL,  
  data = NULL,  
  geom = "text",  
  position = "identity",  
  na.rm = FALSE,  
  show.legend = FALSE,  
  inherit.aes = TRUE,  
  edata = NULL,  
  formula = NULL,  
  arrow.mul = NULL,  
  ...  
)
```

Arguments

mapping	Set of aesthetic mappings created by <code>aes()</code> . If specified and <code>inherit.aes = TRUE</code> (the default), it is combined with the default mapping at the top level of the plot. You must supply mapping if there is no plot mapping.
data	The data to be displayed in this layer. There are three options: If <code>NULL</code> , the default, the data is inherited from the plot data as specified in the call to <code>ggplot()</code> . A <code>data.frame</code> , or other object, will override the plot data. All objects will be fortified to produce a data frame. See <code>fortify()</code> for which variables will be created. A function will be called with a single argument, the plot data. The return value must be a <code>data.frame</code> , and will be used as the layer data. A function can be created from a formula (e.g. <code>~ head(.x, 10)</code>).
geom	The geometric object to use to display the data for this layer. When using a <code>stat_*()</code> function to construct a layer, the <code>geom</code> argument can be used to override the default coupling between stats and geoms. The <code>geom</code> argument accepts the following:

	<ul style="list-style-type: none"> • A Geom ggproto subclass, for example <code>GeomPoint</code>. • A string naming the geom. To give the geom as a string, strip the function name of the <code>geom_</code> prefix. For example, to use <code>geom_point()</code>, give the geom as "point". • For more information and other ways to specify the geom, see the layer geom documentation.
<code>position</code>	<p>A position adjustment to use on the data for this layer. This can be used in various ways, including to prevent overplotting and improving the display. The <code>position</code> argument accepts the following:</p> <ul style="list-style-type: none"> • The result of calling a position function, such as <code>position_jitter()</code>. This method allows for passing extra arguments to the position. • A string naming the position adjustment. To give the position as a string, strip the function name of the <code>position_</code> prefix. For example, to use <code>position_jitter()</code>, give the position as "jitter". • For more information and other ways to specify the position, see the layer position documentation.
<code>na.rm</code>	Remove missing values (Not Yet Implemented).
<code>show.legend</code>	logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display. To include legend keys for all levels, even when no data exists, use TRUE. If NA, all levels are shown in legend, but unobserved levels are omitted.
<code>inherit.aes</code>	If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn't inherit behaviour from the default plot specification, e.g. annotation_borders() .
<code>edata</code>	Environmental data where the continuous variables are found.
<code>formula</code>	Formula to select variables from edata. If missing, all continuous variables of edata are used.
<code>arrow.mul</code>	Multiplier to arrow length. If missing, the multiplier is selected automatically so that arrows fit the current graph.
<code>...</code>	Other arguments passed to the functions.

Value

Returns a ggplot2 layer or a list of such layers: a "LayerInstance" object that inherits from classes "Layer", "ggproto", and "gg".

Examples

```
library("vegan")
library("ggplot2")

data(mite, mite.env)
m <- metaMDS(mite, trace = FALSE, trymax = 100)

## add fitted vectors for continuous variables
```

```
ordiggplot(m) +
  geom_ordi_point("sites") +
  geom_ordi_arrow("sites", stat = "vectorfit", edata = mite.env)

## can be faceted
ordiggplot(m) + geom_ordi_point("sites") +
  geom_ordi_arrow("sites", stat = "vectorfit", edata = mite.env) +
  facet_wrap(mite.env$Topo)
```

valid_layers

Valid layers for vegan objects

Description

Valid layers for vegan objects

Usage

```
valid_layers(object, ...)
```

S3 method for class 'rda'

```
valid_layers(object, ...)
```

S3 method for class 'cca'

```
valid_layers(object, ...)
```

S3 method for class 'dbrda'

```
valid_layers(object, ...)
```

Arguments

object An R object.

... Additional arguments passed to methods.

Value

A character vector of valid ordination layers for the provided object.

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