

# Package ‘ggordiplots’

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**Type** Package

**Title** Make ggplot Versions of Vegan's Ordiplots

**Version** 0.2.8

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**Description** The vegan package includes several functions for adding features to ordination plots: ordiarrows, ordibubbles, ordiellipse, ordihull, ordispider, ordisurf. This package adds these same features to ordination plots made with ggplot2.

**License** GPL-2

**Encoding** UTF-8

**LazyData** true

**Depends** R (>= 3.2.0), ggplot2 (>= 3.0.0), vegan (>= 2.5-2),

**Suggests** formatR, permute, lattice, knitr, rmarkdown

**VignetteBuilder** knitr

**URL** <http://github.com/jfq2/ggordiplots>

**BugReports** <http://github.com/jfq2/ggordiplots/issues>

**RoxygenNote** 6.1.0

**NeedsCompilation** no

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 ggordiplots

*ggordiplots: Make ggplots with ordiplot-type features.*


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### Description

The vegan and BiodiversityR packages include several functions for adding features to ordination plots: ordiarrows, ordibubbles, ordiellipse, ordihull, ordispider, ordisurf, ordicluster. This package adds these same features to ordination plots made with ggplot2.

### Functions

gg\_enfit Fits vectors representing environmental variables to ordination plots.

gg\_ordibubble Sizes site symbols in proportion to environmental variable.

gg\_ordicluster Overlays cluster diagram on ordination plot.

gg\_ordiplot Ordination plot with options for ellipses, hulls, and spiders distinguishing treatment groups.

gg\_ordisurf Ordination plot with surface contours for environmental variable.

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 gg\_envfit

*Vegan envfit plot*


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### Description

Fits environmental parameters to an ordination plot of sites and plots them as arrows.

### Usage

```
gg_envfit(ord, env, groups = NA, scaling = 1, choices = c(1, 2),
  perm = 999, alpha = 0.05, angle = 20, len = 0.5, unit = "cm",
  arrow.col = "red", pt.size = 3, plot = TRUE)
```

### Arguments

ord	An ordination object.
env	A data frame of environmental parameters.
groups	A vector of groups.
scaling	Scaling value for plot.
choices	Axes to plot.
perm	Number of permutations.
alpha	Maximum alpha value to be included in plot.
angle	Angle of arrow tips.
len	Arrow tip length.
unit	Unit for length ("cm", "in")
arrow.col	Arrow color.
pt.size	Symbol size.
plot	A logical for plotting; defaults to TRUE.

**Value**

Silently returns the plot and data frames used for the plotting if the fit of any variable is significant at alpha. Otherwise returns a message that no variable is significant.

**Examples**

```
data("varespec")
data("varechem")
vare.dist <- vegdist(varespec)
vare.mds <- monoMDS(vare.dist)
gg_envfit(ord=vare.mds, env=varechem)
```

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gg_ordibubble	<i>Ordination Bubble Plot</i>
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**Description**

Makes a simple ordination plot of site with the symbol size scaled to an environmental variable. Result is similar to that of BiodiversityR's ordibubble function.

**Usage**

```
gg_ordibubble(ord, env.var, var.label = "Level", choices = c(1, 2),
  plot = TRUE)
```

**Arguments**

ord	An ordination object
env.var	An environmental variable.
var.label	Label for the legend; default is "Level."
choices	Axes to be plotted.
plot	A logical for plotting; defaults to TRUE.

**Value**

Silently returns the plot and data frames used for the plotting.

**Examples**

```
data(dune)
data(dune.env)
dune.bray <- vegdist(dune, method = "bray")
ord <- cmdscale(dune.bray, k=(nrow(dune)-1), eig=TRUE, add=TRUE)
gg_ordibubble(ord, env.var=dune.env$A1, var.label="A1")
```

gg\_ordicluster

*Add Dendrogram to Ordination Plot***Description**

Modeled after the ordicluster function in vegan, this function overlays an ordination object with a cluster dendrogram. Functionality has been added to include treatment groups.

**Usage**

```
gg_ordicluster(ord, cluster, treatments = NA, choices = c(1, 2),
  prune = 0, col = 1, pt.size = 3, plot = TRUE)
```

**Arguments**

ord	An ordination object.
cluster	A cluster object from 'hclust' based on the same distance as 'ord.'
treatments	A vector assigning treatments to samples.
choices	Ordination axes to be plotted.
prune	Number of upper level hierarchies removed from the dendrogram. If prune > 0, dendrogram will be disconnected.
col	A vector of cluster group memberships. Used to assign colors to line segments for each cluster group.
pt.size	Symbol size.
plot	A logical; defaults to TRUE.

**Details**

'treatments' should be a vector of class factor and length equal to the number of samples included in the ordination and cluster; integers are not coerced into factors.

**Value**

Invisibly returns a list of the data frames used to make the plot (df\_ord, df\_segments) and the plot itself (plot).

**Author(s)**

Jari Oksanen, John Quensen

**Examples**

```
data(dune)
data(dune.env)
dune.bray <- vegdist(dune, method="bray")
ord <- metaMDS(dune, k=3)
cl <- hclust(dune.bray, method="complete")
gg_ordicluster(ord, cluster=cl, treatments=dune.env$Management, prune=3, col=cutree(cl, 4))
```

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`gg_ordiplot`*Plot with Ellipses, Hulls, Spiders*

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### Description

`gg_ordiplot` uses `ggplot2` to make an ordination plot with group ellipses by default, and optionally hulls and/or spiders. It is patterned after `vegan`'s functions `ordiellipse`, `ordihull`, and `ordispider` and accepts similar parameters.

### Usage

```
gg_ordiplot(ord, groups, scaling = 1, choices = c(1, 2),
  kind = c("sd", "se", "ehull"), conf = NULL, show.groups = "all",
  ellipse = TRUE, label = FALSE, hull = FALSE, spiders = FALSE,
  pt.size = 3, plot = TRUE)
```

### Arguments

<code>ord</code>	An ordination object.
<code>groups</code>	A vector of groups.
<code>scaling</code>	Scaling for ordination plot.
<code>choices</code>	Axes to be plotted.
<code>kind</code>	Type of ellipses to show ("se", "sd", "ehull").
<code>conf</code>	Confidence value for ellipses if "se" or "sd."
<code>show.groups</code>	Subset of groups to plot.
<code>ellipse</code>	A logical for plotting ellipses; defaults to TRUE.
<code>label</code>	A logical for labeling group centroids.
<code>hull</code>	A logical for plotting group hulls.
<code>spiders</code>	A logical for plotting group spiders.
<code>pt.size</code>	Symbol size.
<code>plot</code>	A logical for plotting; defaults to TRUE.

### Value

Silently returns the plot and data frames used for the plotting.

### Examples

```
data("dune")
data("dune.env")
dune.hel <- decostand(dune, method = "hellinger")
ord <- rda(dune.hel)
gg_ordiplot(ord, groups = dune.env$Management)
```

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`gg_ordisurf`*Ordisurf with ggplot2*

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**Description**

Fits a surface (contour) plot of an environmental variable to an ordination plot.

**Usage**

```
gg_ordisurf(ord, env.var, choices = c(1, 2), var.label = "Level",  
            binwidth, pt.size = 3, plot = TRUE)
```

**Arguments**

<code>ord</code>	An ordination object.
<code>env.var</code>	Environmental variable to fit to plot.
<code>choices</code>	Axes to plot.
<code>var.label</code>	Label for the legend; default is "Level."
<code>binwidth</code>	Controls the number of contours in the plot.
<code>pt.size</code>	Symbol size.
<code>plot</code>	A logical for plotting; defaults to TRUE.

**Details**

By default, 'binwidth' is calculated as the difference between minimum and maximum values of the variable divided by 15.

**Value**

Silently returns the plot and data frames used for the plotting.

**Note**

Code for extracting plot data from the ordisurf result was taken from a blog by Olivia Rata Burge.

**Author(s)**

Olivia Rata Burge, John Quensen

**References**

<https://oliviarata.wordpress.com/2014/07/17/ordinations-in-ggplot2-v2-ordisurf/>

**Examples**

```
data(varespec)  
data(varechem)  
vare.dist <- vegdist(varespec)  
vare.mds <- monoMDS(vare.dist)  
gg_ordisurf(vare.mds, env.var = varechem$Baresoil, var.label="Bare Soil")
```

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scale_arrow	<i>Scale Arrows to Plot</i>
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**Description**

Scales envfit arrows to fit within 75

**Usage**

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

**Arguments**

arrows	A two column data frame of coordinates from envfit result.
data	A two column data frame of coordinates for ordination plot.
at	coordinates of origin (0, 0)
fill	proportion of plot area to fill with maximum arrow length

**Value**

Silently returns a data frame of scaled coordinates for adding arrows to ordination plot.

**Author(s)**

Gavin Simpson

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