Modifying Plots Made with ggordiplots

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Introduction

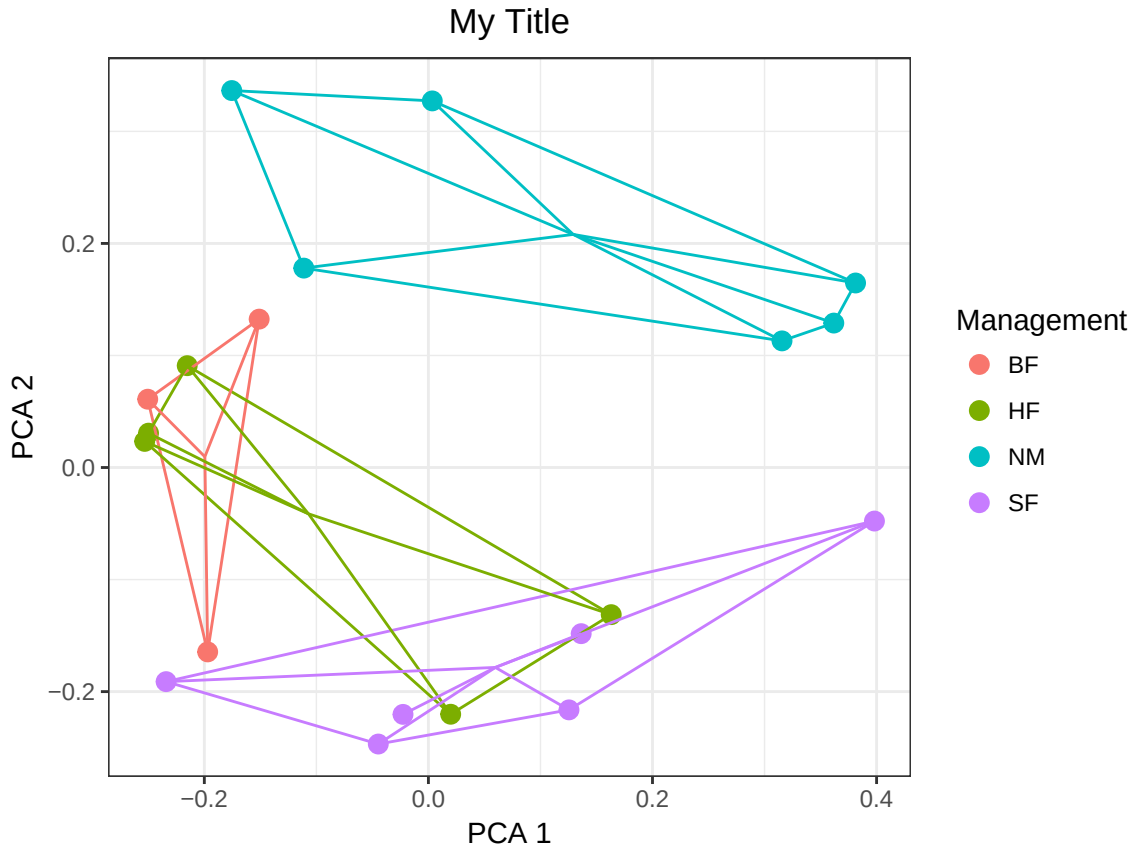
To enable further customization, all functions in this package return silently a list of the data frames used for the plots and the plots themselves These may be captured by assigning the function result to a variable. For `gg_ordiplot`, for example, get a list of the names of the items returned:

```
suppressPackageStartupMessages(library(vegan))
suppressPackageStartupMessages(library(ggplot2))
suppressPackageStartupMessages(library(ggordiplots))
data("dune")
data("dune.env")
dune.hel <- decostand(dune, method = "hellinger")
ord <- rda(dune.hel)
my.plot <- gg_ordiplot(ord, groups = dune.env$Management, hull = TRUE, spiders = TRUE,
    ellipse = FALSE, plot = FALSE)
names(my.plot)
```

```
## [1] "df_ord"      "df_mean.ord" "df_ellipse"  "df_hull"     "df_spiders"
## [6] "plot"
```

The last object in the list is the plot itself. You can capture the plot and make modifications by adding `ggplot2` labels and themes:

```
a.plot <- my.plot$plot
a.plot + theme_bw() + labs(color = "Management", x = "PCA 1", y = "PCA 2", title = "My Title") +
    theme(plot.title = element_text(hjust = 0.5))  # centers main title, ggplot2 version 2.2+
```



The other items in the list are the data frames used for the plot layers:

Item	Description
df_ord	Point coordinates for ordination with Group variable
df_mean.ord	Label coordinates
df_ellipse	Data for plotting ellipses
df_hull	Data for plotting hulls
df_spiders	Data for plotting spiders

You can check the first few lines of each data frame thus:

```
head(my.plot$df_spiders)
```

```
##    Group     cntr.x       cntr.y          x           y
## 2     BF -0.1995202  0.009619176 -0.1970059 -0.16455540
## 10    BF -0.1995202  0.009619176 -0.2505024  0.06096196
## 11    BF -0.1995202  0.009619176 -0.1510522  0.13245097
## 5     HF -0.1070437 -0.041316511 -0.2532165  0.02333147
## 6     HF -0.1070437 -0.041316511 -0.2152557  0.09089893
## 7     HF -0.1070437 -0.041316511 -0.2497939  0.03067965
```

The ggplot2 statements I used for each layer are:

```
# Basic ordination plot:
xlab <- paste("Axis", choices[1], sep = " ")
ylab <- paste("Axis", choices[2], sep = " ")
```

```
geom_point(data = df_ord, aes(x = x, y = y, color = Group), size = 3) + xlab(xlab) +
    ylab(ylab)

# Plot ellispes:
geom_path(data = df_ellipse, aes(x = x, y = y, color = Group), show.legend = FALSE)

# Plot centroid labels:
geom_text(data = df_mean.ord, aes(x = x, y = y, label = Group, color = Group),
    show.legend = FALSE)

# Plot hulls:
geom_path(data = df_hull, aes(x = x, y = y, color = Group), show.legend = FALSE)

# Plot spiders:
geom_segment(data = df_spiders, aes(x = cntr.x, xend = x, y = cntr.y, yend = y,
    color = Group), show.legend = FALSE)

# Plot cluster segments:
geom_segment(data = df_segments, aes(x = x, y = y, xend = xend, yend = yend))
```

With the above information and some knowledge of `ggplot2` you can modify the plots however you wish. And to learn more, you can inspect the code by entering `gg_ordiplot` or any other function written in R (i.e. not compiled) without parentheses. As a short example, the hidden function in `vegan` for generating data for an ellipse is:

```
vegan:::veganCovEllipse
```

```
## function (cov, center = c(0, 0), scale = 1, npoints = 100)
## {
##     theta <- (0:npoints) * 2 * pi/npoints
##     Circle <- cbind(cos(theta), sin(theta))
##     Q <- chol(cov, pivot = TRUE)
##     o <- attr(Q, "pivot")
##     t(center + scale * t(Circle %*% Q[, o]))
## }
## <environment: namespace:vegan>
```

Examples

Say you want to make an ordination plot with points distinguished by two variables assigned to symbol shape and symbol color. You can do this by extracting `df_ord` from a plot result and adding a second grouping variable. Continuing with the example from above:

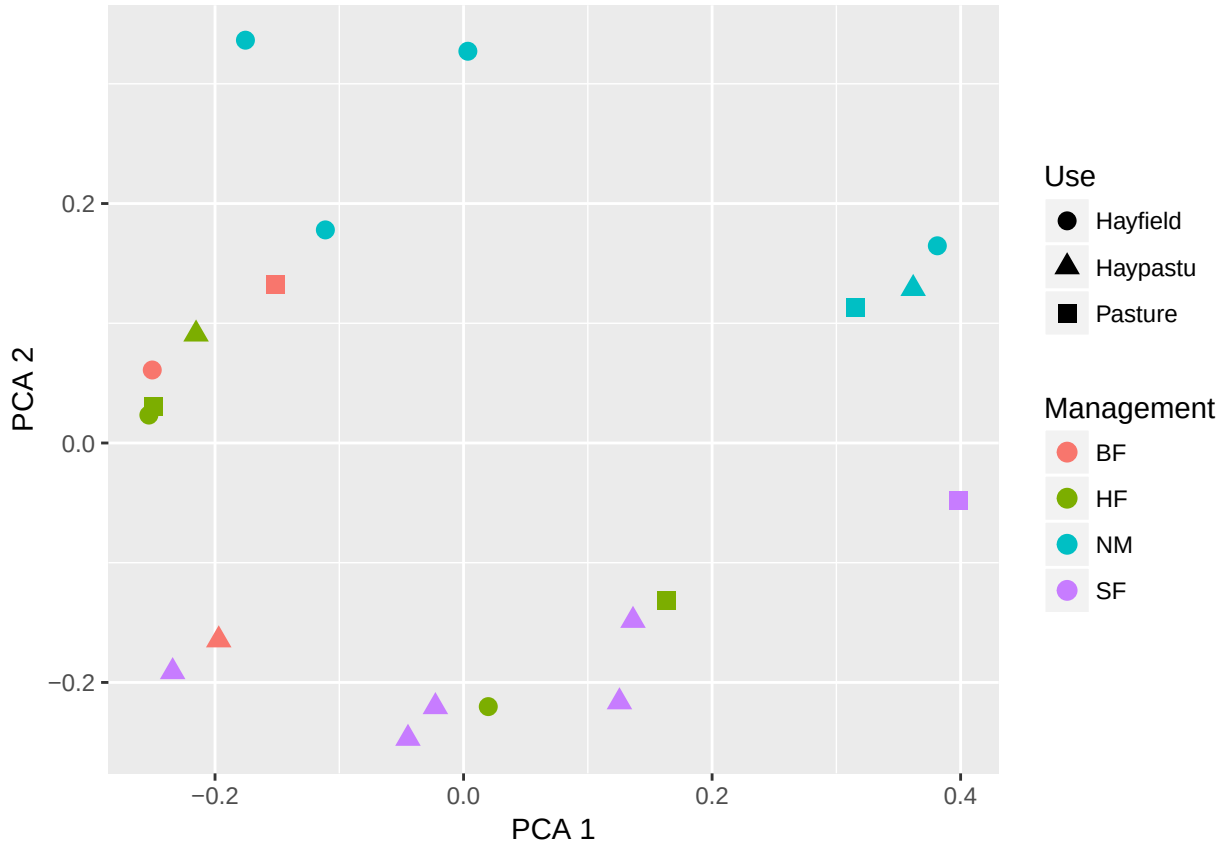
```
ord.data <- my.plot$df_ord
head(ord.data)
```

```
##             x           y Group
## 1 -0.23409791 -0.19110003    SF
## 2 -0.19700590 -0.16455540    BF
## 3 -0.04472727 -0.24679380    SF
## 4 -0.02267027 -0.22032168    SF
## 5 -0.25321647  0.02333147    HF
## 6 -0.21525573  0.09089893    HF
```

```
ord.data$Use <- dune.env$Use
colnames(ord.data) <- c("x", "y", "Management", "Use")
head(ord.data)
```

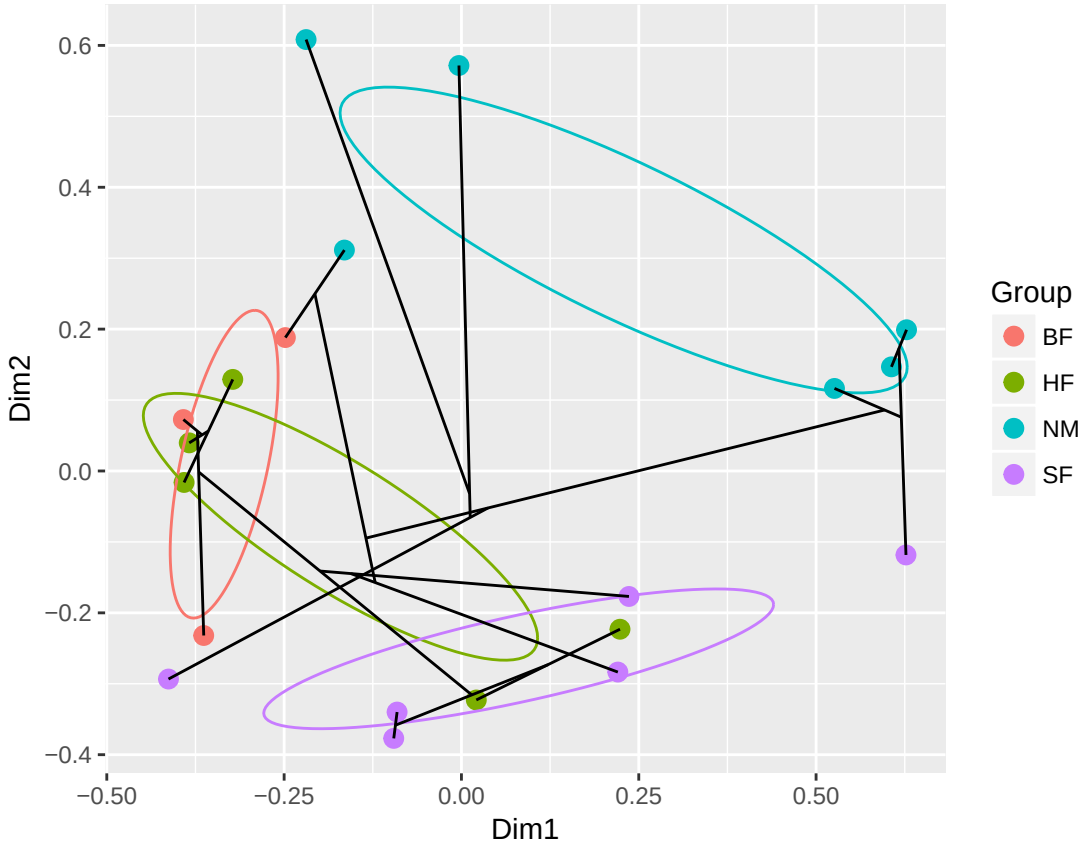
```
##             x           y Management      Use
## 1 -0.23409791 -0.19110003         SF Haypastu
## 2 -0.19700590 -0.16455540         BF Haypastu
## 3 -0.04472727 -0.24679380         SF Haypastu
## 4 -0.02267027 -0.22032168         SF Haypastu
## 5 -0.25321647  0.02333147         HF Hayfield
## 6 -0.21525573  0.09089893         HF Haypastu
```

```
ggplot(data = ord.data, aes(x = x, y = y, color = Management, shape = Use)) +
    geom_point(size = 3) + xlab("PCA 1") + ylab("PCA 2")
```



As long as you start from the same data, you can take plots and data frames generated with different functions and combine them in new ways. For example, add a dendrogram to an ellipse plot.

```
data("dune")
data("dune.env")
dune.bray <- vegdist(dune, method = "bray")
ord <- cmdscale(dune.bray, k = nrow(dune) - 1, eig = TRUE, add = TRUE)
cl <- hclust(dune.bray, method = "single")
clstr.plot <- gg_ordicluster(ord, cluster = cl, plot = FALSE)
ellipse.plot <- gg_ordiplot(ord, groups = dune.env$Management, plot = FALSE)
ellipse.plot$plot + geom_segment(data = clstr.plot$df_segments, aes(x = x, y = y,
    xend = xend, yend = yend))
```



Enjoy!