Lionfish Cluster Plot

GG

1/28/2019

library(vegan)

## Warning: package 'vegan' was built under R version 3.4.4

## Loading required package: permute

## Loading required package: lattice

## This is vegan 2.5-1

library(dbplyr)  
library(tidyverse)

## ── Attaching packages ────────────────────────────────────────────────────────────────────────────────────────── tidyverse 1.2.1 ──

## ✔ ggplot2 2.2.1 ✔ purrr 0.2.4  
## ✔ tibble 1.4.2 ✔ dplyr 0.7.4  
## ✔ tidyr 0.8.0 ✔ stringr 1.3.0  
## ✔ readr 1.1.1 ✔ forcats 0.3.0

## ── Conflicts ───────────────────────────────────────────────────────────────────────────────────────────── tidyverse\_conflicts() ──  
## ✖ dplyr::filter() masks stats::filter()  
## ✖ dplyr::ident() masks dbplyr::ident()  
## ✖ dplyr::lag() masks stats::lag()  
## ✖ dplyr::sql() masks dbplyr::sql()

PCA\_fish <- read\_csv("~/Desktop/Lionfish/Darwin\_matrix.csv")

## Warning: Missing column names filled in: 'X1' [1]

## Parsed with column specification:  
## cols(  
## .default = col\_double(),  
## X1 = col\_character()  
## )

## See spec(...) for full column specifications.

library(tidyverse)  
row.names(PCA\_fish) <- PCA\_fish$X1

## Warning: Setting row names on a tibble is deprecated.

PCA\_fish[1] = NULL

K means cluster analysis

library(tidyverse) # data manipulation  
library(cluster) # clustering algorithms  
library(factoextra)

## Welcome! Related Books: `Practical Guide To Cluster Analysis in R` at https://goo.gl/13EFCZ

library(ggplot2)  
cluster2 <- kmeans(PCA\_fish, centers = 2, nstart = 25)  
str(cluster2)

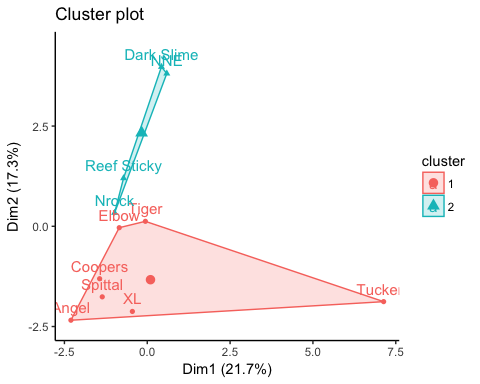
## List of 9  
## $ cluster : Named int [1:11] 1 1 1 1 1 2 2 2 1 2 ...  
## ..- attr(\*, "names")= chr [1:11] "Elbow" "Tiger" "XL" "Spittal" ...  
## $ centers : num [1:2, 1:29] 0.0773 0.4283 0.3028 0.0669 0.1872 ...  
## ..- attr(\*, "dimnames")=List of 2  
## .. ..$ : chr [1:2] "1" "2"  
## .. ..$ : chr [1:29] "Chromis bermudae" "Chromis insolata" "Paranthia furcifer" "Chaetodon sedentarius" ...  
## $ totss : num 1.56  
## $ withinss : num [1:2] 0.851 0.171  
## $ tot.withinss: num 1.02  
## $ betweenss : num 0.539  
## $ size : int [1:2] 7 4  
## $ iter : int 1  
## $ ifault : int 0  
## - attr(\*, "class")= chr "kmeans"

pcaplot <- fviz\_cluster(cluster2, data = PCA\_fish, fill = "darkblue") + ylim(-2.5,4.5) + theme\_classic()  
ggsave(PCA\_fish, plot = pcaplot, device = "eps")

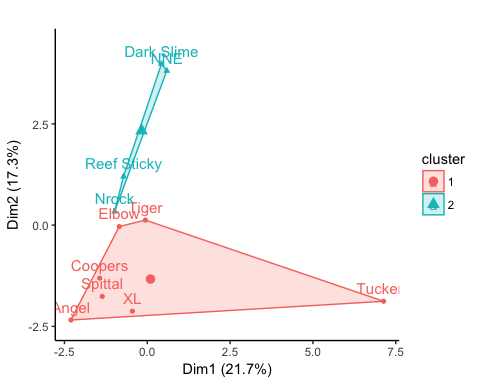
## Saving 5 x 4 in image

## Warning in grid.Call.graphics(C\_polygon, x$x, x$y, index): semi-  
## transparency is not supported on this device: reported only once per page

pcaplot



ggpcaplot <- pcaplot + theme\_classic() + labs(title="")  
ggpcaplot



ggsave(PCA\_fish, plot = ggpcaplot, device = "eps")

## Saving 5 x 4 in image

## Warning in grid.Call.graphics(C\_polygon, x$x, x$y, index): semi-  
## transparency is not supported on this device: reported only once per page