ANOSIM, PERMANOVA, SIMPER, Indicator Value

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```
libraries <- c("vegan", "ggplot2", "dplyr")
lapply(libraries, require, character.only = TRUE)

## [[1]]
## [1] TRUE
##
## [[2]]
## [1] TRUE
##
## [[3]]
## [1] TRUE</pre>
```

Paso 1. LLamar de nuevo a las tablas.

```
Moth_full <- read.csv("data/fullmatrix.csv")
head(Moth_full)</pre>
```

##		${\tt TimeCode}$		Y	ear	r Site		Habitat			Month			Period					Abundance			Richness		M1	M2
##	1	T1Apr17		2	2017	T1		Tabonuco		April		1	Pre-Hurricane						73	3		25	1	0	
##	2	T1May17		2	2017 T1		T1	Tabonuco		May		ıy	Pre-Hurricane						6:	1		25	0	0	
##	3	T1Jun17		2	2017		T1	Tabonuco		June		ie	Pre-Hurricane						68	3		33	6	1	
##	4	T1Jul17		2	2017		T1	Tabonuco		July		У	Pre-Hurricane						73	3		17	3	0	
##	5	T1Aug17		2	2017		T1	Tabonuco		uco	August		t	Pre-Hurricane						46	6		19	2	0
##	6	T10ct17		2	2017		T1	Tabonuco		October		r I	Post-Hurricane				е		124	4		15	0	0	
##		M3 N	M5 M7	M	18 M	10	M13	3 M:	15	M17	M19	M2	25 1	M26	M29	M4	5 M	48	M50	M52	M5	3 M	54 M	55 N	166
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##		M70	M74	M7	7 M	79	M80) Ma	31	M85	M86	M8	37 I	88N	M89	M94	4 M	95	M96	M100	M C	104	M10	5 M:	106
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```

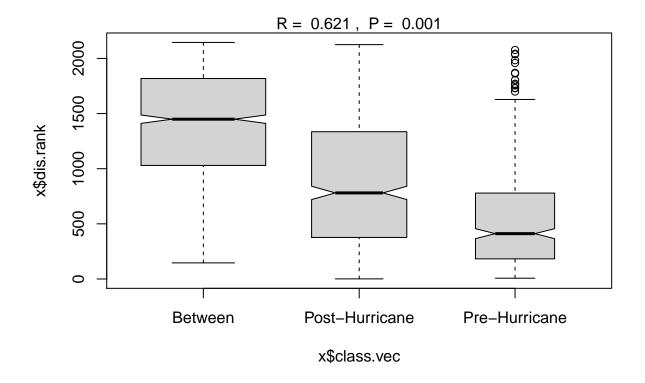
```
moth_sp <- select(Moth_full, M1:A248)
```

Paso 2. Vamos a comparar entre grupos. Son los grupos propuestos (e identificados en el nMDS) significativamente diferente? Vamos hacer un ANOSIM

```
##
## Call:
   anosim(x = moth.dist, grouping = Moth_full$Period)
## Dissimilarity: bray
##
## ANOSIM statistic R: 0.6206
         Significance: 0.001
##
##
## Permutation: free
## Number of permutations: 999
##
## Upper quantiles of permutations (null model):
##
      90%
             95% 97.5%
                           99%
```

```
## 0.0305 0.0434 0.0619 0.0772
##
## Dissimilarity ranks between and within classes:
##
                   0%
                           25%
                                  50%
                                           75%
                                                 100%
                                                         N
## Between
                  146 1029.75 1449.0 1817.375 2145.0 1080
## Post-Hurricane
                       376.50
                               780.5 1334.875 2125.0
## Pre-Hurricane
                       182.50
                               411.0 779.000 2076.5
```

plot(moth.ano)



SIMPER

(sim <- with(Moth.frm, simper(moth, Hurricane))) summary(sim)

(sim <- with(Moth.frm, simper(moth, Habitat))) summary(sim)

Indicator Value

install.packages("labdsv") install.packages("indicspecies") library("indicspecies") library("labdsv")

library(vegan) library(MASS) library(labdsv) library(cluster) library(indicspecies)

 $ind_species < -multipatt(moth,Moth.frm\$Hurricane,max.order=2, \\duleg = TRUE,func = "IndVal.g",control = how(nperm=5000 \\ind_species \\summary(ind_species)$

other things to do

Berger-Parker dominance

graficos de canopy cover

https://rpubs.com/Roeland-KINDT/694021

```
install.packages("BiodiversityR") library(BiodiversityR)

speciespreH <- select(Moth.frm, M1:A248) Period <- select(Moth.frm, Period)

Accum.2 <- accumcomp(speciespreH, y=Period, factor='Period', method='exact', conditioned=FALSE, plotit=FALSE) Accum.2

accum.long1 <- accumcomp.long(Accum.2, ci=NA, label.freq=5) accum.long1

plotgg1 <- ggplot(data=accum.long1, aes(x = Sites, y = Richness, ymax = UPR, ymin = LWR)) + scale_x_continuous(expand=c(0, 1), sec.axis = dup_axis(labels=NULL, name=NULL)) + scale_y_continuous(sec.axis = dup_axis(labels=NULL, name=NULL)) + geom_line(aes(colour=Grouping), size=2) + geom_point(data=subset(accum.labelit==TRUE), aes(colour=Grouping, shape=Grouping), size=5) + geom_ribbon(aes(colour=Grouping), alpha=0.2, show.legend=FALSE) + labs(x = "Month", y = "Species diversity", colour = "Period", shape = "Period")+ theme_classic()

plotgg1
```