

nMDS

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

```
## [[1]]
## [1] TRUE
##
## [[2]]
## [1] TRUE
##
## [[3]]
## [1] TRUE
```

Paso 1. LLamar a la tabla (como .csv)

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

Paso 2. Seleccionar las especies.

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

Paso 3. Vamos hacer el nMDS

```
set.seed(1) # Con este comando, siempre comenzara del mismo lugar.

moth.mds <- metaMDS(moth_sp, distance = "bray", k = 2, trymax=100) #using all the defaults

## Square root transformation
## Wisconsin double standardization
## Run 0 stress 0.2509353
## Run 1 stress 0.2595334
## Run 2 stress 0.2523396
## Run 3 stress 0.282036
## Run 4 stress 0.2509339
## ... New best solution
## ... Procrustes: rmse 0.0009701113 max resid 0.006667077
```

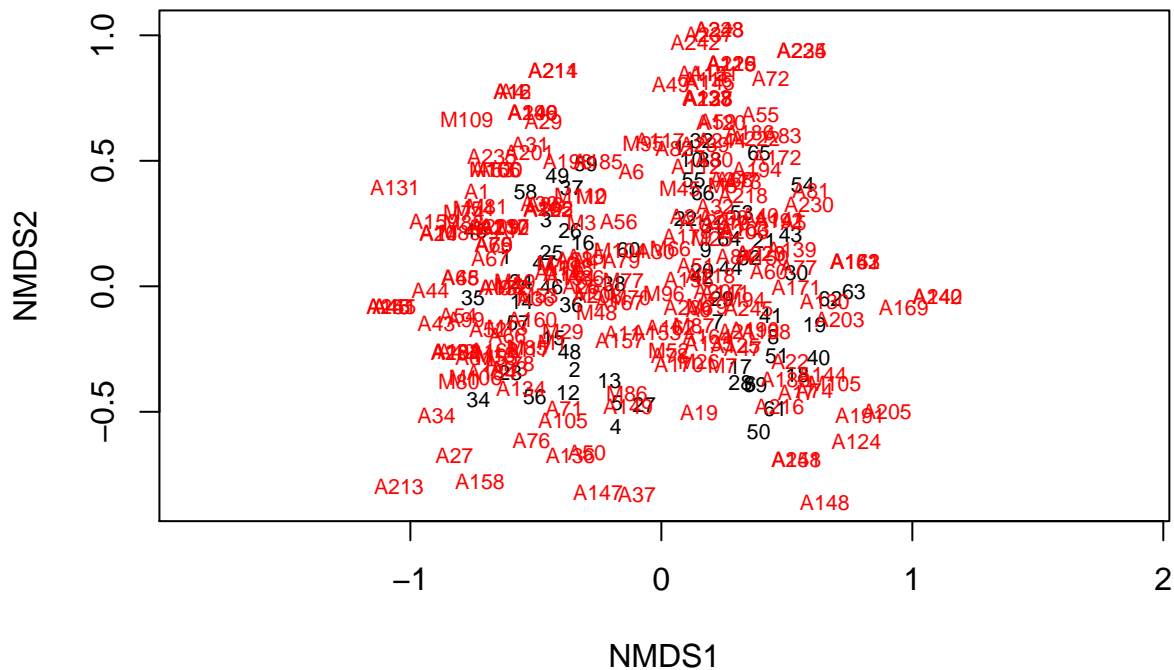
```
## ... Similar to previous best
## Run 5 stress 0.250961
## ... Procrustes: rmse 0.003294134  max resid 0.01957031
## Run 6 stress 0.2566342
## Run 7 stress 0.2510057
## ... Procrustes: rmse 0.007469064  max resid 0.04719079
## Run 8 stress 0.2530351
## Run 9 stress 0.251111
## ... Procrustes: rmse 0.01288445  max resid 0.05411702
## Run 10 stress 0.2563251
## Run 11 stress 0.2509585
## ... Procrustes: rmse 0.006726555  max resid 0.04626972
## Run 12 stress 0.2522903
## Run 13 stress 0.2509695
## ... Procrustes: rmse 0.003379292  max resid 0.02477938
## Run 14 stress 0.2523395
## Run 15 stress 0.286507
## Run 16 stress 0.2572426
## Run 17 stress 0.2566301
## Run 18 stress 0.2563038
## Run 19 stress 0.2579864
## Run 20 stress 0.2810398
## *** Solution reached
```

```
moth.mds
```

```
##
## Call:
## metaMDS(comm = moth_sp, distance = "bray", k = 2, trymax = 100)
##
## global Multidimensional Scaling using monoMDS
##
## Data:      wisconsin(sqrt(moth_sp))
## Distance: bray
##
## Dimensions: 2
## Stress:    0.2509339
## Stress type 1, weak ties
## Two convergent solutions found after 20 tries
## Scaling: centring, PC rotation, halfchange scaling
## Species: expanded scores based on 'wisconsin(sqrt(moth_sp))'
```

Paso 4. Vamos hacer el grafico. Un muy sensillo Plot

```
plot(moth.mds, type="t")
```



Paso 5. Vamos a poner Habitat, Site y Periodo en el grafico. Primer las busco en la Matrix Original

```
Habitat <- select(Moth_full, Habitat)
Site <- select(Moth_full, Site)
Period <- select(Moth_full, Period)
```

Paso 6. Extraer las coordenadas de los Axis del nmfs.

```
data.scores <- as.data.frame(scores(moth.mds)) #Using the scores function from vegan to extract the si
data.scores
```

##	NMDS1	NMDS2
## 1	-0.61922141	0.120470413
## 2	-0.34538334	-0.333130972
## 3	-0.45971354	0.264104192
## 4	-0.18201886	-0.557503052
## 5	-0.17590801	-0.464825120
## 6	0.35481540	-0.386808065
## 7	0.22592884	-0.140024092
## 8	0.44666523	-0.200156166
## 9	0.17711216	0.144021119
## 10	0.11958516	0.503172409
## 11	0.09487077	0.551938903
## 12	-0.37156920	-0.424413360
## 13	-0.20690131	-0.375013455
## 14	-0.55706899	-0.062499904

```

## 15 -0.42991704 -0.206186892
## 16 -0.31339020 0.174980913
## 17 0.31447227 -0.318507583
## 18 0.54209725 -0.351384668
## 19 0.61061747 -0.153736801
## 20 0.16198514 0.060347906
## 21 0.41066018 0.183934887
## 22 0.09682790 0.271984593
## 23 -0.60161771 -0.342357057
## 24 -0.55879744 0.019911137
## 25 -0.43636878 0.134019714
## 26 -0.36289717 0.221650212
## 27 -0.06797333 -0.472073388
## 28 0.31500121 -0.383138638
## 29 0.24237375 -0.050896154
## 30 0.53854390 0.055414562
## 31 0.20303820 0.241272327
## 32 0.16085810 0.581079898
## 33 0.19431873 0.502681123
## 34 -0.72911115 -0.453525961
## 35 -0.75026191 -0.044802339
## 36 -0.35799216 -0.074521103
## 37 -0.35700524 0.393474356
## 38 -0.18829658 0.012001047
## 39 0.37490714 -0.392733021
## 40 0.62664081 -0.282610667
## 41 0.43705481 -0.114411375
## 42 0.16265790 0.037138414
## 43 0.51508528 0.207516576
## 44 0.27622272 0.073897836
## 45 -0.73941782 0.222885589
## 46 -0.43749124 -0.003163544
## 47 -0.46597979 0.093647975
## 48 -0.36540117 -0.259838129
## 49 -0.41398258 0.441319299
## 50 0.38814421 -0.580466912
## 51 0.46084588 -0.277086944
## 52 0.35158363 0.113565102
## 53 0.32069228 0.292551847
## 54 0.56344938 0.406146054
## 55 0.12945544 0.425346242
## 56 -0.50397694 -0.441660091
## 57 -0.56920890 -0.146571940
## 58 -0.54067252 0.377662103
## 59 -0.30077513 0.487495974
## 60 -0.12962218 0.145606296
## 61 0.45381256 -0.488343932
## 62 0.67336409 -0.049121680
## 63 0.76718389 -0.022874961
## 64 0.27098802 0.188769811
## 65 0.39025161 0.533190976
## 66 0.16583030 0.371188161

```

Paso 7. Unir los datos de Habitat, Site y Periodo a mi nueva dataframe (i.e., data.scores)

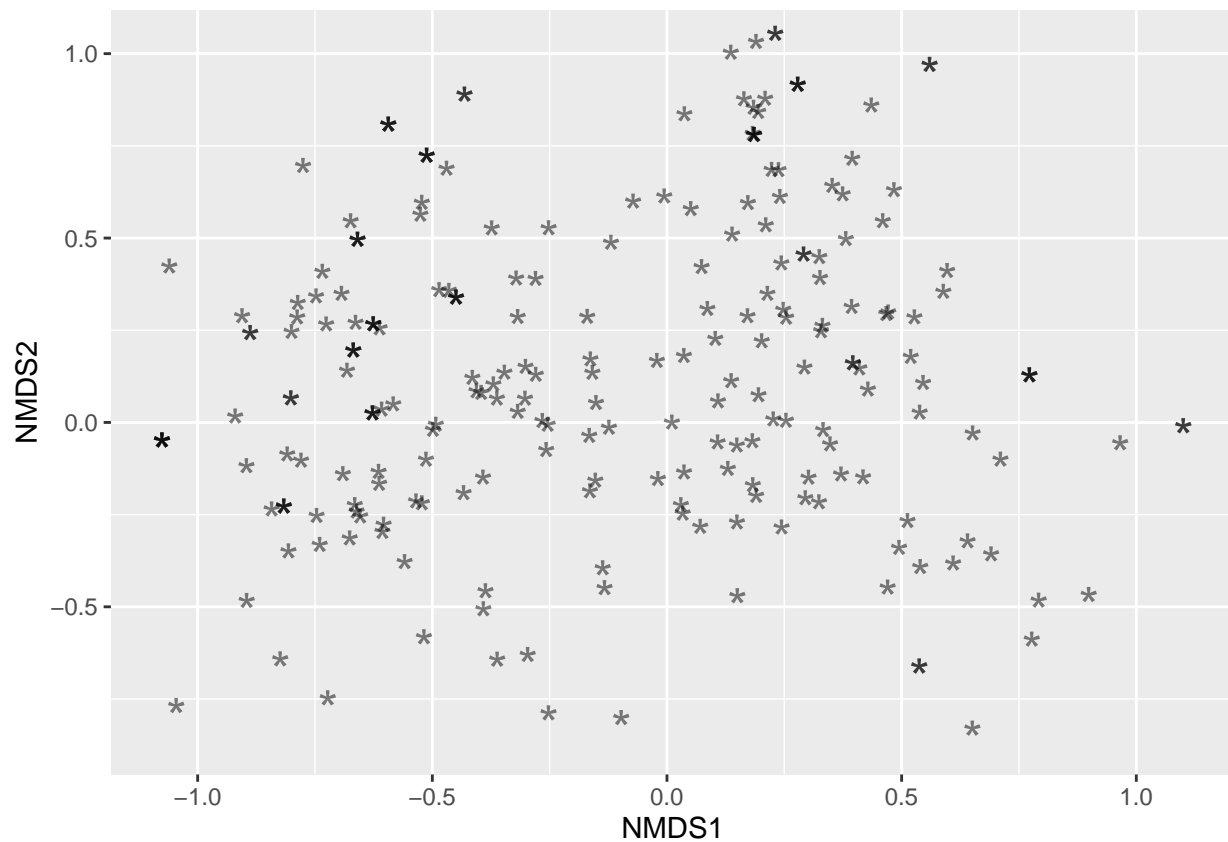
```
data.scores$Site <- unlist(Site) # create a column of site names
data.scores$Period <- unlist(Period)
data.scores$Habitat <- unlist(Habitat)
head(data.scores) #look at the data
```

```
##      NMDS1      NMDS2 Site      Period Habitat
## 1 -0.6192214  0.1204704 T1 Pre-Hurricane Tabonuco
## 2 -0.3453833 -0.3331310 T1 Pre-Hurricane Tabonuco
## 3 -0.4597135  0.2641042 T1 Pre-Hurricane Tabonuco
## 4 -0.1820189 -0.5575031 T1 Pre-Hurricane Tabonuco
## 5 -0.1759080 -0.4648251 T1 Pre-Hurricane Tabonuco
## 6  0.3548154 -0.3868081 T1 Post-Hurricane Tabonuco
```

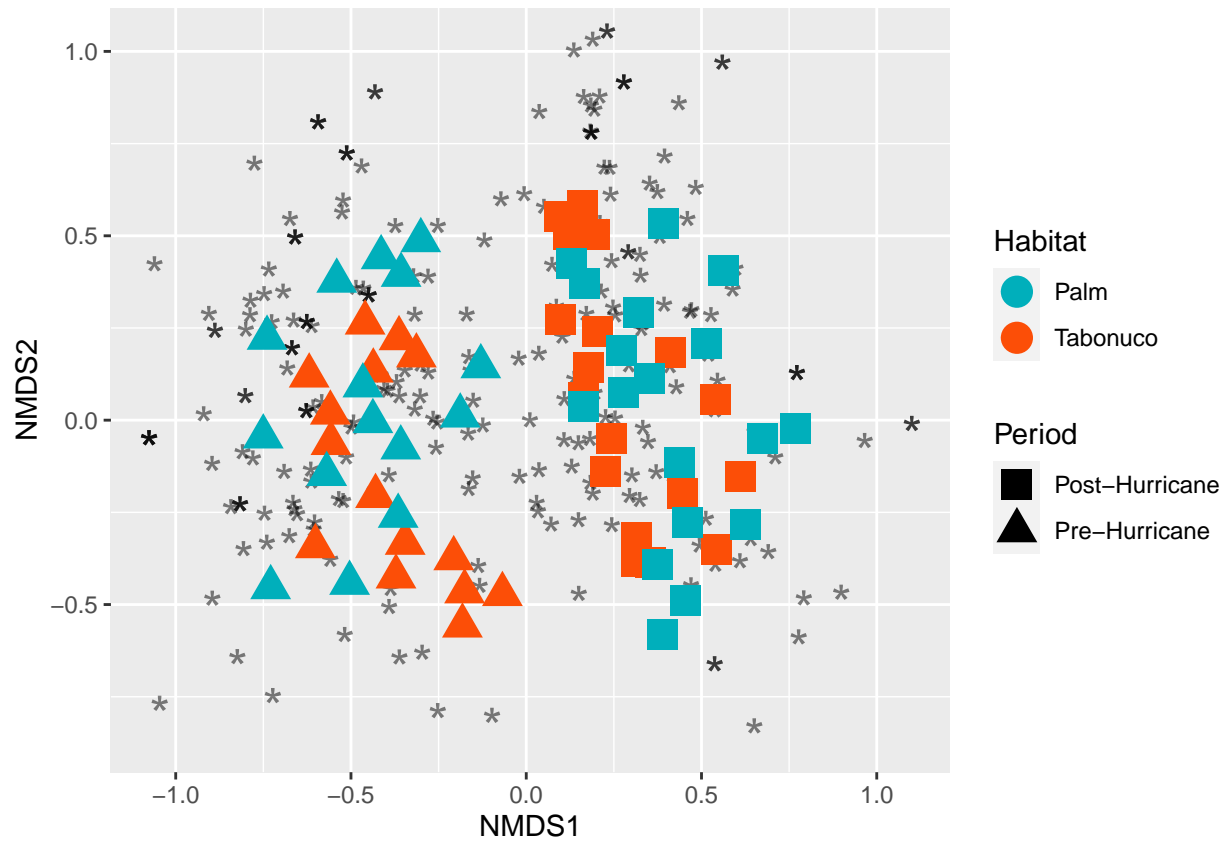
```
species.scores <- as.data.frame(scores(moth.mds, "species"))
species.scores$species <- rownames(species.scores) # create a column of species, from the rownames of .
```

```
##### nMDS Graphs #####
```

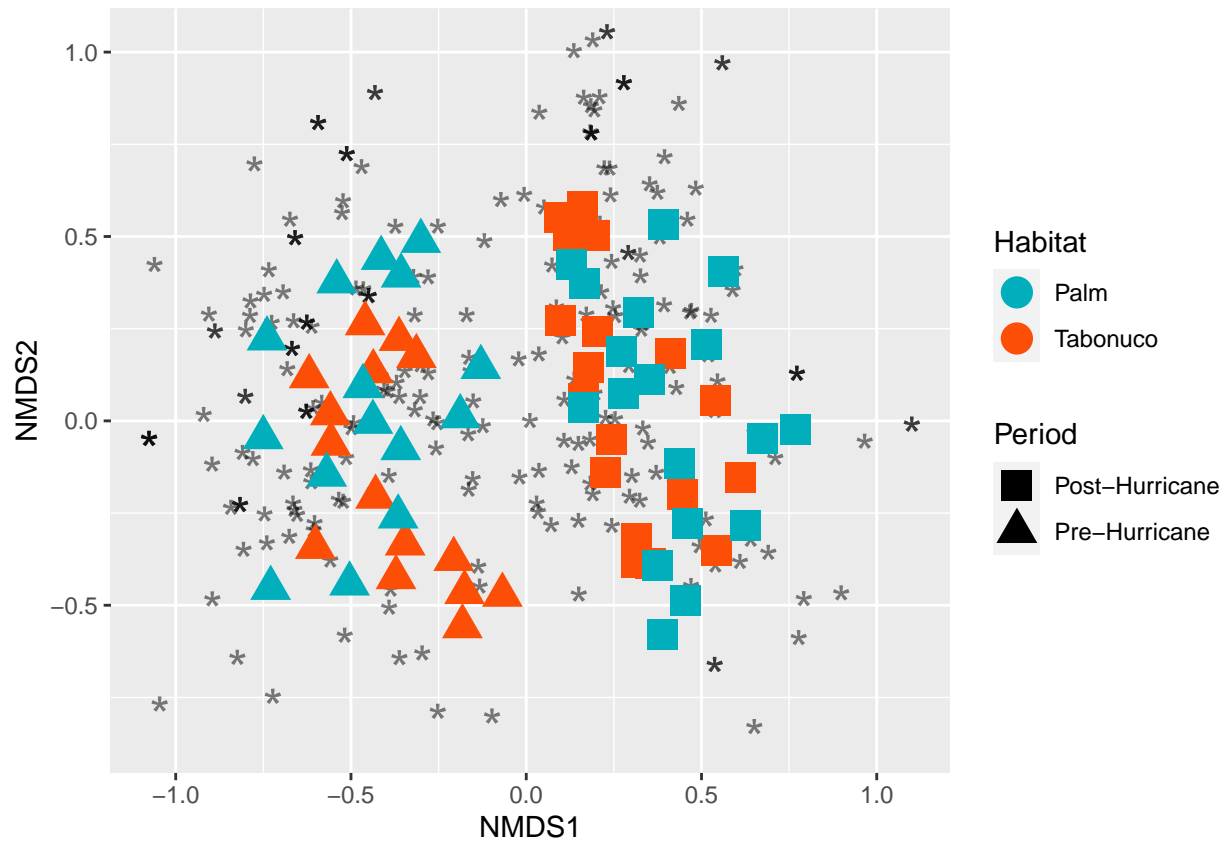
```
p <- ggplot() +
  geom_text(data=species.scores,aes(x=NMDS1,y=NMDS2, label = "*"),size=7, alpha=0.5) # add the species
p
```



```
p1 <- p + geom_point(data=data.scores,aes(x=NMDS1,y=NMDS2,
                                         shape=Period,colour=Habitat),size=5) + # add the point marker
  scale_color_manual(values=c("#00AFBB", "#FC4E07")) +
  scale_shape_manual(values=c(15, 17))
p1
```



```
p2 <- p1 + geom_text(data=data.scores,aes(x=NMDS1,y=NMDS2,label=""),size=6,vjust=0) # add the site lab
p2
```



```
p3 <- p2 + coord_equal() +
  theme_bw() +
  theme(legend.title = element_text(size=12),
        axis.text.x = element_blank(), # remove x-axis text
        axis.text.y = element_blank(), # remove y-axis text
        axis.ticks = element_blank(), # remove axis ticks
        axis.title.x = element_text(size=16), # remove x-axis labels
        axis.title.y = element_text(size=16), # remove y-axis labels
        panel.background = element_blank(),
        panel.grid.major = element_blank(), #remove major-grid labels
        panel.grid.minor = element_blank(), #remove minor-grid labels
        plot.background = element_blank()) +
  guides(color = guide_legend(override.aes = list(shape = 16, size = 4)))
p3
```

