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

As a rule of thumb literature has identified the following cut-off values for stress-level:

Higher than 0.2 is poor (risks for false interpretation). 0.1 - 0.2 is fair (some distances can be misleading for interpretation). 0.05 - 0.1 is good (can be confident in inferences from plot). Less than 0.05 is excellent (this can be rare).

An important number to note is the stress, which is roughly the "goodness of fit" of your NMDS ordination. For a good representation of your data, the stress value should ideally be less than 0.2.

```
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
```

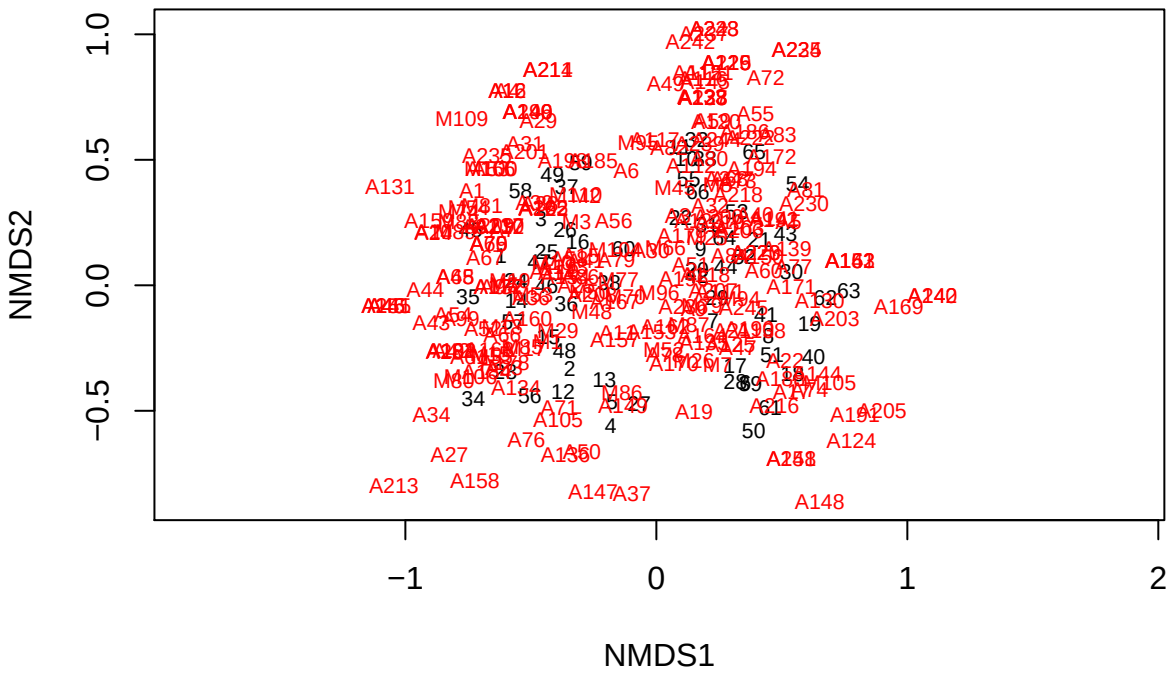
```
## Run 0 stress 0.2509353
## Run 1 stress 0.2595334
## Run 2 stress 0.2523396
## Run 3 stress 0.282036
## Run 4 stress 0.2509339
## ... New best solution
## ... Procrustes: rmse 0.0009701113  max resid 0.006667077
## ... Similar to previous best
## Run 5 stress 0.250961
## ... Procrustes: rmse 0.003294134  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))'
```

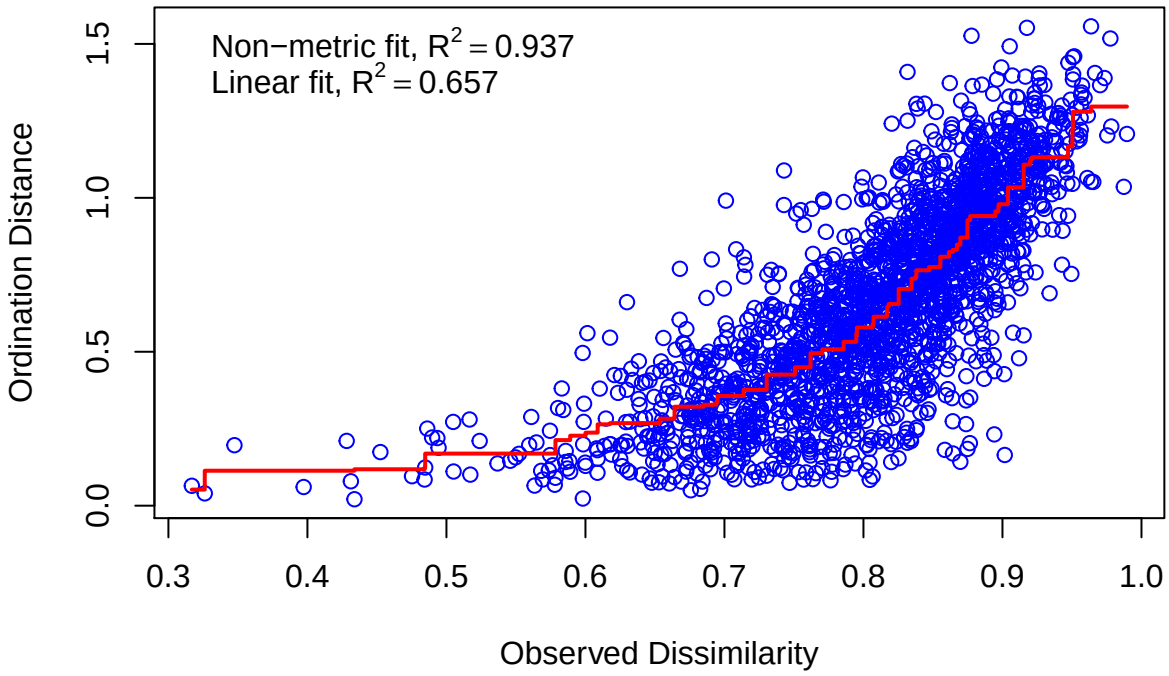
Paso 4. Vamos hacer el grafico. Un muy sensillo Plot

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



Paso 5. Mirar el stressplot Large scatter around the line suggests that original dissimilarities are not well preserved in the reduced number of dimensions. Looks pretty good in this case.

```
stressplot(moth.mds)
```



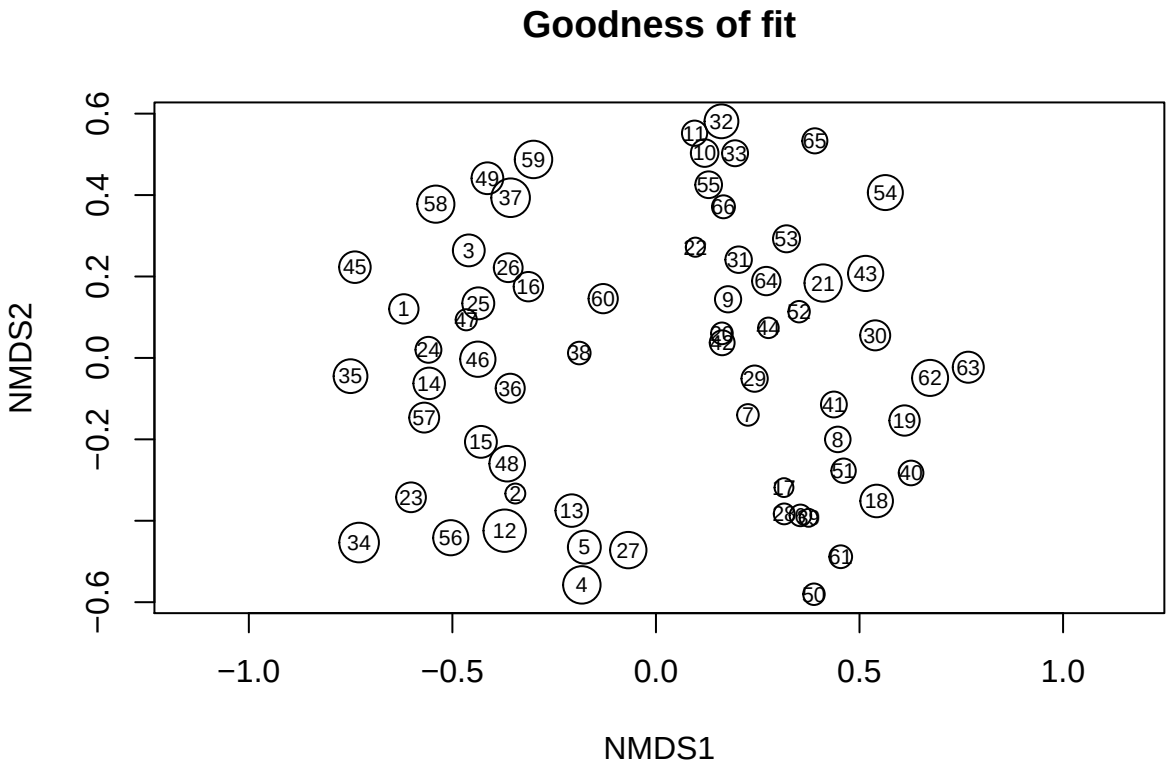
Paso 6. Otra metrica para evaluar el ajuste (buen desempeno) del nMDS es mirar el "Goodness of fit".

Visitar esta pagina para mas informacion: https://rdrr.io/rforge/vegan/man/goodness.metaMDS.html

```
gof <- goodness(moth.mds)
gof
```

```
##  [1] 0.03081585 0.02092671 0.03345693 0.03934151 0.03456932 0.02270405
##  [7] 0.02267995 0.02680810 0.02753120 0.02897304 0.02650191 0.04450752
## [13] 0.03412675 0.03305425 0.03345389 0.03087429 0.01976678 0.03423633
## [19] 0.03182412 0.02277720 0.03916362 0.02009878 0.03125329 0.02720130
## [25] 0.03354618 0.03025820 0.03822878 0.02183686 0.02757183 0.03151484
## [31] 0.02780051 0.03553918 0.02725503 0.04161688 0.03548390 0.03050237
## [37] 0.04057359 0.02372956 0.01882180 0.02589446 0.02716969 0.02614204
## [43] 0.03696792 0.02157502 0.03311220 0.03707901 0.02217101 0.03736177
## [49] 0.03334138 0.02258202 0.02564067 0.02251966 0.02835295 0.03679571
## [55] 0.02805723 0.03691240 0.03143149 0.03904002 0.03934138 0.03073778
## [61] 0.02391046 0.03786065 0.03260026 0.02980762 0.02637525 0.02409839
```

```
{plot (moth.mds, display = 'sites', type = 't', main = 'Goodness of fit') # this function draws NMDS or
points (moth.mds, display = 'sites', cex = 2*gof/mean(gof))} # and this adds the points with size refle
```



Paso 7. Vamos a poner Habitat, Site y Periodo en el grafico. Primer las busco en la Matrix Orignal

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

Paso 8. Extraer las cordenadas de los Axis del nmds.

```
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 9. 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
```

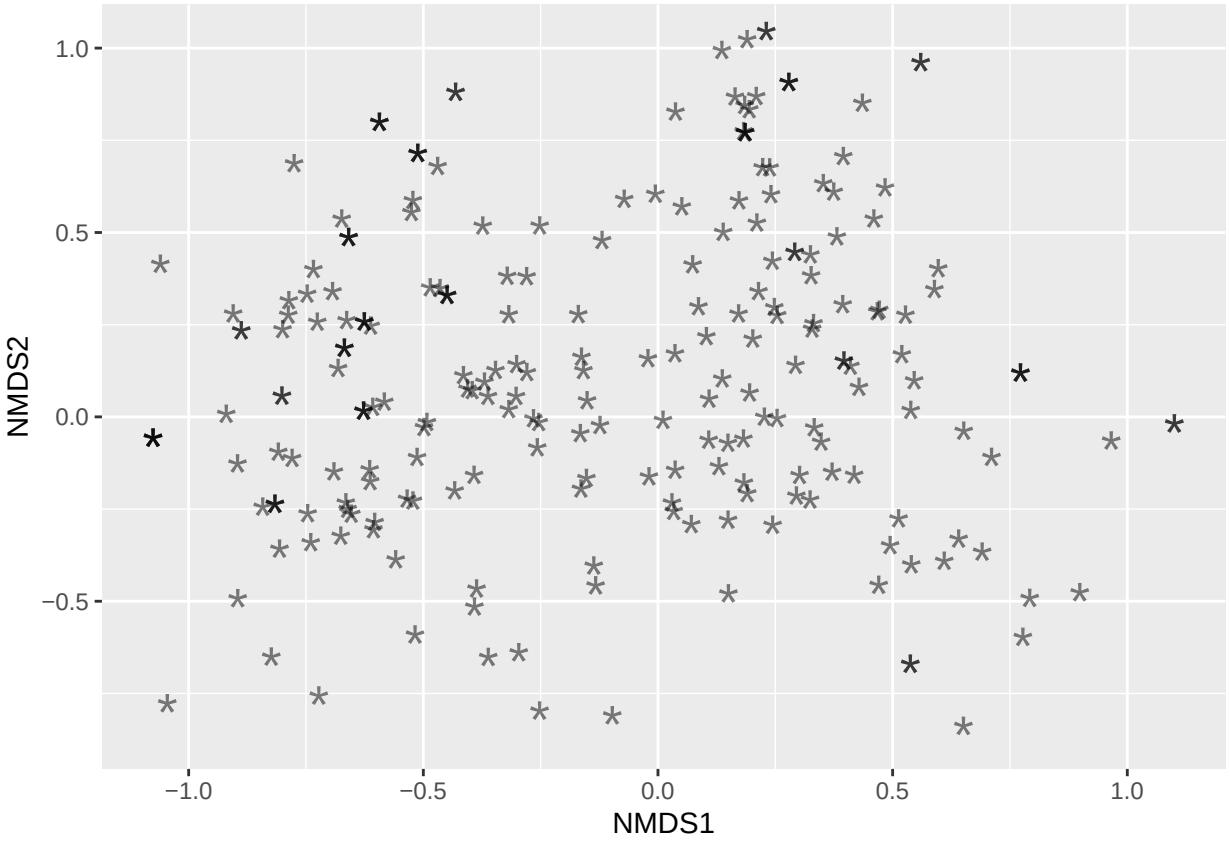
Paso 10. Extraer las cordenadas de las especies y ponerlas en una nueva matrix.

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

Paso 11. Vamos hacer graficos bonitos en ggplot2. Solo Especies.

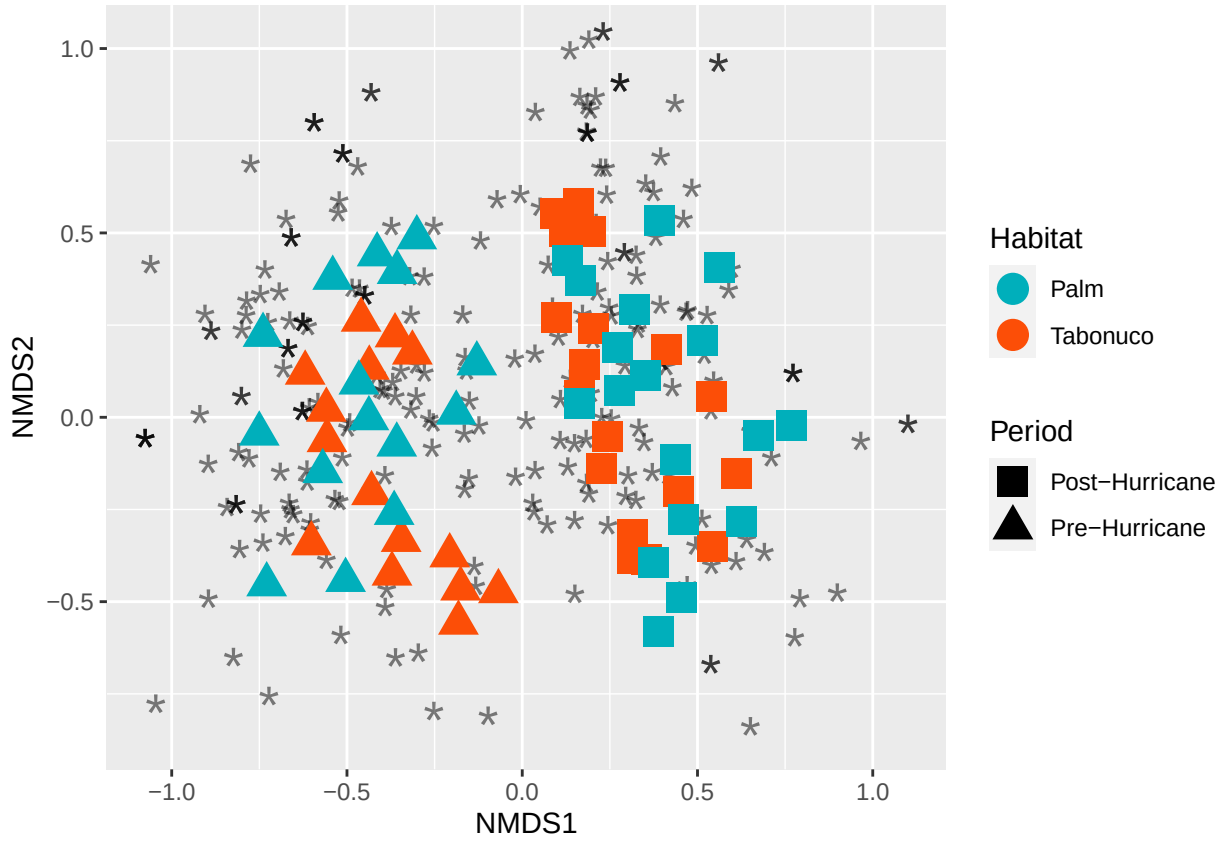
```
p <- ggplot() +
  geom_text(data=species.scores, aes(x=NMDS1,y=NMDS2, label = "*"),size=7, alpha=0.5) # add the species

p
```



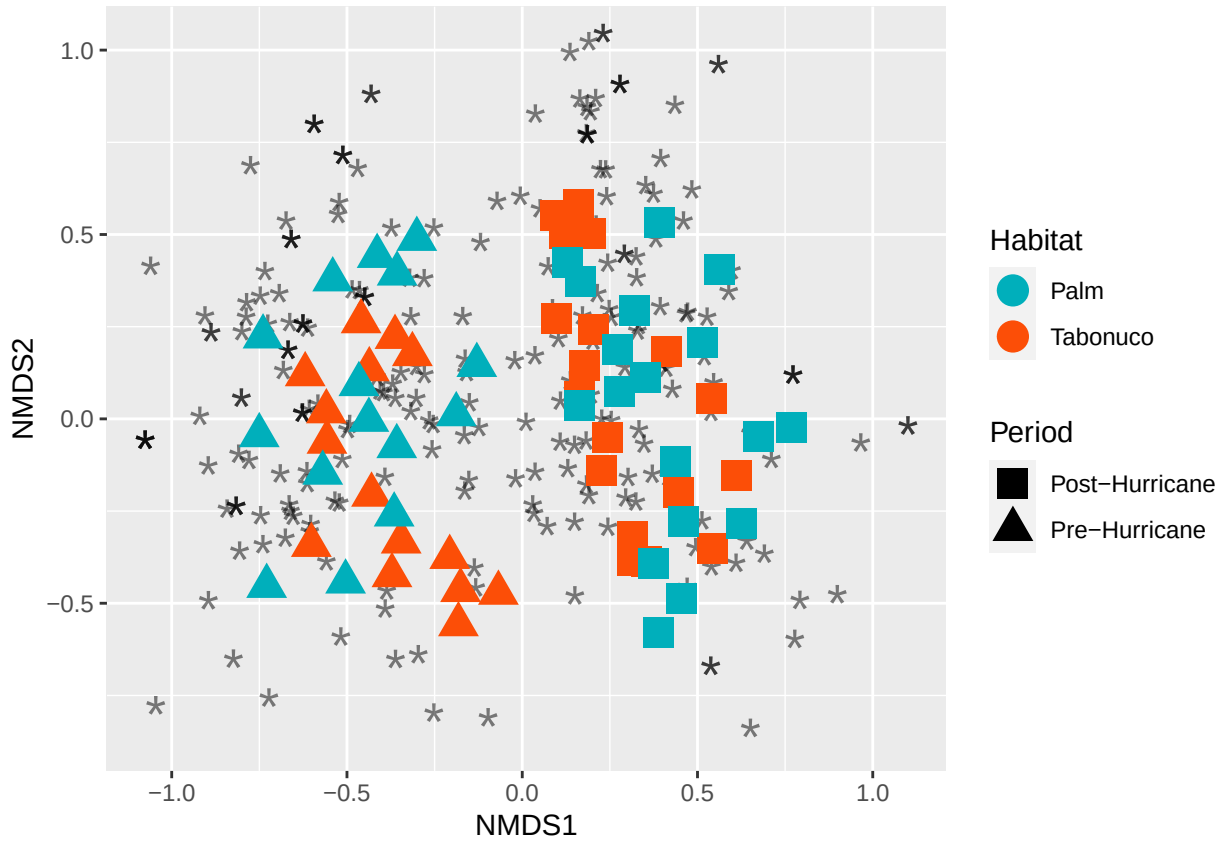
Paso 12. Vamos a poner etiquetas. En este caso solo Habitats y Periordo

```
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
```



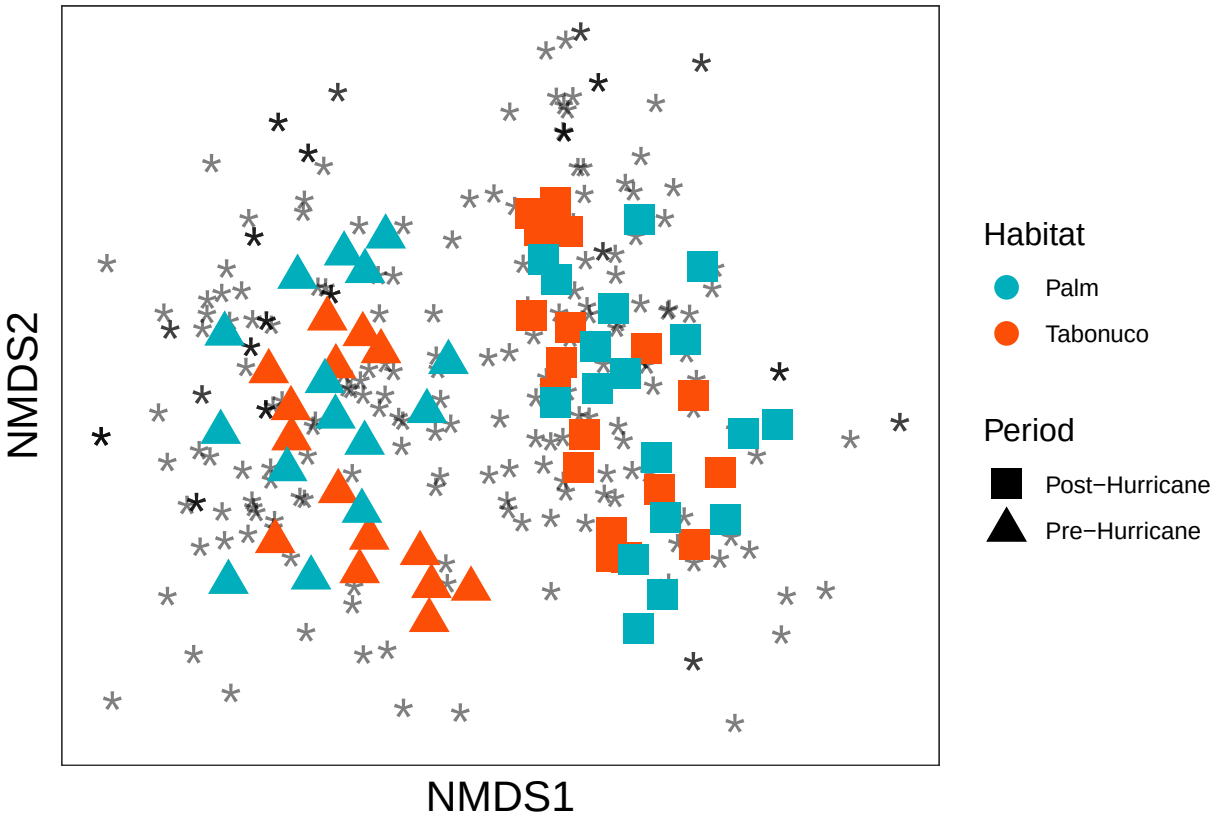
Paso 13. Agrerar sitios.

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



Paso 14. Graficos de Publicacion.

```
p3 <- p1 + 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
```


NMDS2
NMDS1
Habitat
Palm
Tabonuco
Period
Post−Hurricane
Pre−Hurricane