RDA

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1. Primer paso: cargar las librerias que necesitas.

```
library(BiodiversityR)
library(ggrepel)
library(ggplot2)
library(readxl)
library(ggsci)
library(ggforce)
library(dplyr)
```

2. Segundo paso: cargar los datos.

```
species=read.csv("data/RDA_species.csv", header=T, row.names=NULL, sep=",")
env=read.csv("data/RDA_environmetal.csv", header=T, row.names=NULL, sep=",")
```

3. Before we can use this explanatory matrix we need to check that its rows are in the same order as our response matrix all.equal(rownames(species), rownames(env))

```
all.equal(rownames(species), rownames(env))
```

```
## [1] TRUE
```

4. Remover la columna de sitos.

```
species_1 <- select(species, -site)
env_1 <- select(env, -site)
```

5. Transformar datos. # Apply log+1 transformation to your species occurrences data (spe matrix) # in order to correct for possible statistical errors associated to rare or very #common species

```
species_2 <- decostand(species_1, method = "hellinger")
```