

Diversity indexes

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Loading packages

```
library(pacman)
pacman::p_load(tidyverse, vegan, iNEXT, nlme, readxl, writexl)
```

Loading Data

```
df <- readxl::read_excel("uniao.xlsx")
```

Getting only the necessary variables

```
df <- df[, c("Kingdom", "Phylum", "Diabasadden", "Longyearbyen")]
df <- df %>%
  filter(Kingdom != "Unknown")
```

Creating the results data frame

```
index <- data.frame(
  Kingdom = character(0),
  Phylum = character(0),
  Local = character(0),
  Margalef = numeric(0),
  Shannon = numeric(0),
  Simpson = numeric(0),
  Evenness = numeric(0),
  Falpha = numeric(0)
)
```

getting all indices in automatized way

```
for(i in unique(df$Kingdom)){
  filo <- df %>%
    filter(Kingdom == i)

  for(j in unique(filo$Phylum)){
    species <- filo %>%
      filter(Phylum == j)

    #matrix treatment

    dados <- t(species[, c("Diabasadden", "Longyearbyen")])
    matriz_dados <- data.matrix(dados)

    #margalef
    riqueza <- specnumber(matriz_dados)
    abundancia <- apply(matriz_dados, 1, sum)
```

```

Margalef <- round( (riqueza - 1) / log(abundancia) , 2)

#shannon
shannon <- diversity(matriz_datos, index="shannon", MARGIN = 1)
if(length(shannon) < 2){
  shannon[[2]] <- NA
}

#simpson
simpson <- diversity(matriz_datos, index="simpson", MARGIN = 1)
if(length(simpson) < 2){
  simpson[[2]] <- NA
}

#evenness
J <- (diversity(matriz_datos)) / (log(specnumber(matriz_datos)))

#fisher's Alpha
alpha <- fisher.alpha(matriz_datos)
if(length(alpha) < 2){
  alpha[[2]] <- NA
}

index <- rbind(index, data.frame(
  Kingdom = i,
  Phylum = j,
  Local = names(Margalef)[1],
  Margalef = Margalef[[1]],
  Shannon = shannon[[1]],
  Simpson = simpson[[1]],
  Evenness = J[[1]],
  Falpha = alpha[[1]]
))

index <- rbind(index, data.frame(
  Kingdom = i,
  Phylum = j,
  Local = names(Margalef)[[2]],
  Margalef = Margalef[[2]],
  Shannon = shannon[[2]],
  Simpson = simpson[[2]],
  Evenness = J[[2]],
  Falpha = alpha[[2]]
))
}
}

```

writing an excel file

```
write_xlsx(index, "indices.xlsx")
```