Contents

Introduction

This script reports the code to reproduce the analyses and figures presented in the second lecture of the Conservation Biology class at Stanford University (Bio 144, 2020).

Software preparation

Install `R` software (https://www.r-project.org) if you do not have it yet Then, install and load the following packages

```
install.packages('vegan')
install.packages('bipartite')
```

```
library(vegan)
library(bipartite)
```

Data import

Download data at the following link:

https://github.com/losapio/bio144_c2/blob/master/maindata.csv

Move them to your working folder, set it up as your working directory (e.g., `mydir`)

```
setwd("/mydir")
```

and import the .csv file into `R`

```
maindata <- read.csv("maindata.csv", sep=",", head=T)
```

We familiarize with the dataset and see how it looks like

```
str(maindata)
```

```
## 'data.frame':    330 obs. of  3 variables:
##  $ Transect: int  10 3 4 6 6 8 8 7 6 5 ...
##  $ Plant   : int  16 7 2 7 8 7 10 6 26 10 ...
##  $ Species : Factor w/ 80 levels "Acalypha diversifolia",..: 75 1 1 1 1 1 1 2 3 4 ...
```

```
head(maindata)
```

```
##   Transect Plant              Species
## 1       10    16           Sapranthus
## 2        3     7 Acalypha diversifolia
## 3        4     2 Acalypha diversifolia
## 4        6     7 Acalypha diversifolia
## 5        6     8 Acalypha diversifolia
## 6        8     7 Acalypha diversifolia
```

It is a `dataframe` composed of 330 observations (rows) and three variables (columns): (1) Transect is the transect number, from one to ten; (2) Plant is the count of plants occurring along each transect; (3) Species is the taxonomic name of plants.

Data preparation

To produce the Specias Accumulation Curve (SAC), we will make use of the existing function `specaccum` in `vegan` package. Take first a look at what this function does and requires.

```
?specaccum
```

This function needs data organized into a matrix with species in columns (s), transects in rows (t), and species abundance (N) as entries

$$\begin{bmatrix} N_{1,1} & \cdots & N_{1,s} \\ \vdots & \ddots & \vdots \\ N_{t,1} & \cdots & N_{t,s} \end{bmatrix} \tag{1}$$

We then convert our dataframe into such a matrix.

```
maindata$dummy <- 1
maindata$Transect <- as.character(maindata$Transect)
data_matrix <- frame2webs(maindata[,c(1,3,4)],
                 c('Transect','Species','dummy'))[[1]]
# head(data_matrix)
```

Specias Accumulation Curve

We now draw our SACs taking the whole dataset. We do so by running 10,000 permutations (all possible permutations of 10 transects are $n = 10!/(10-10)! = 3628800 $, which is computationally intense) and extrapolating richness values by means of bootstrap.

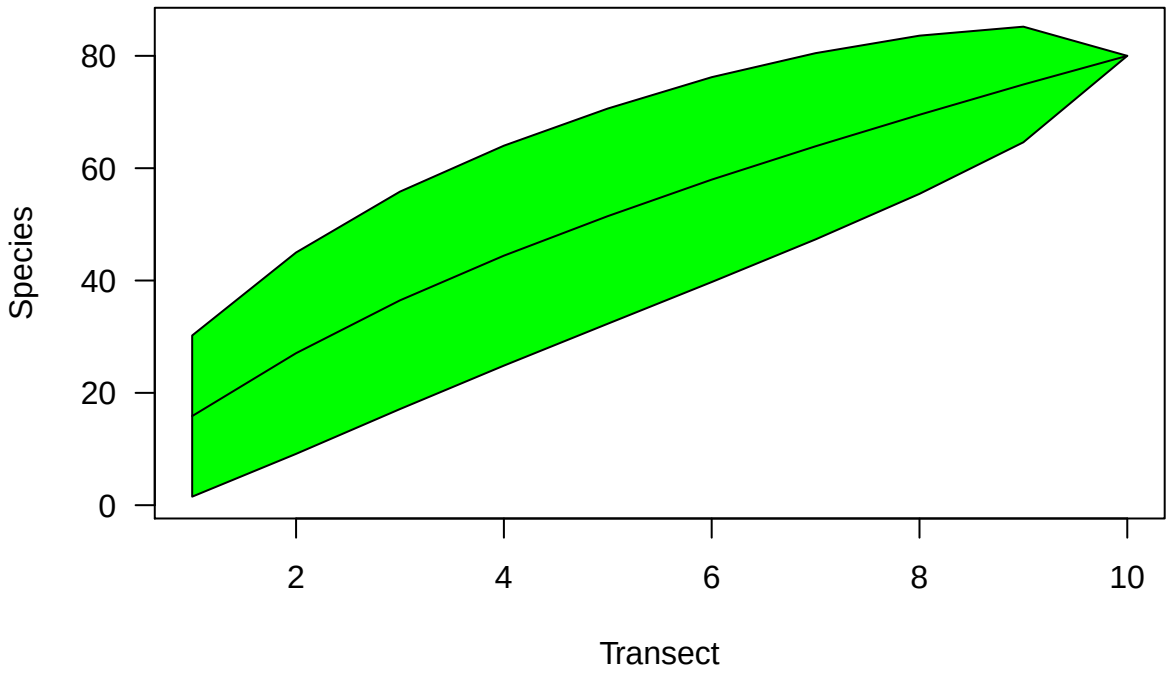
Species-based SAC

In the first case, SAC is based on adding transects (in **vegan** also called 'sites') in a random order and finding the mean SAC and its standard deviation from random permutations of the data (Gotelli & Colwell 2001).

```
sac <- specaccum(data_matrix,
                 method = 'random', permutations = 10000, gamma = 'boot')
sac
```

```
## Species Accumulation Curve
## Accumulation method: random, with 10000 permutations
## Call: specaccum(comm = data_matrix, method = "random", permutations = 10000,      gam
##
##
## Sites     1.00000  2.00000  3.00000  4.00000  5.00000  6.00000  7.00000
## Richness 15.86720 27.06400 36.46960 44.42850 51.46350 57.96360 63.90100
## sd        7.17385  8.96285  9.67827  9.78973  9.57938  9.11939  8.28997
##
## Sites     8.00000  9.00000 10
## Richness 69.51490 74.90350 80
## sd        7.04054  5.14556  0
```

```
plot(sac, ci.type='polygon', ci.col='green', las = 1,
     xlab = "Transect", ylab = "Species")
```



From the shape of the curve we can deduce our goodness of sampling. Since the curve does not reach an asymptot we need more data to have a better estimation of species richness. Indeed, there is a certain number of unseen, missing species.

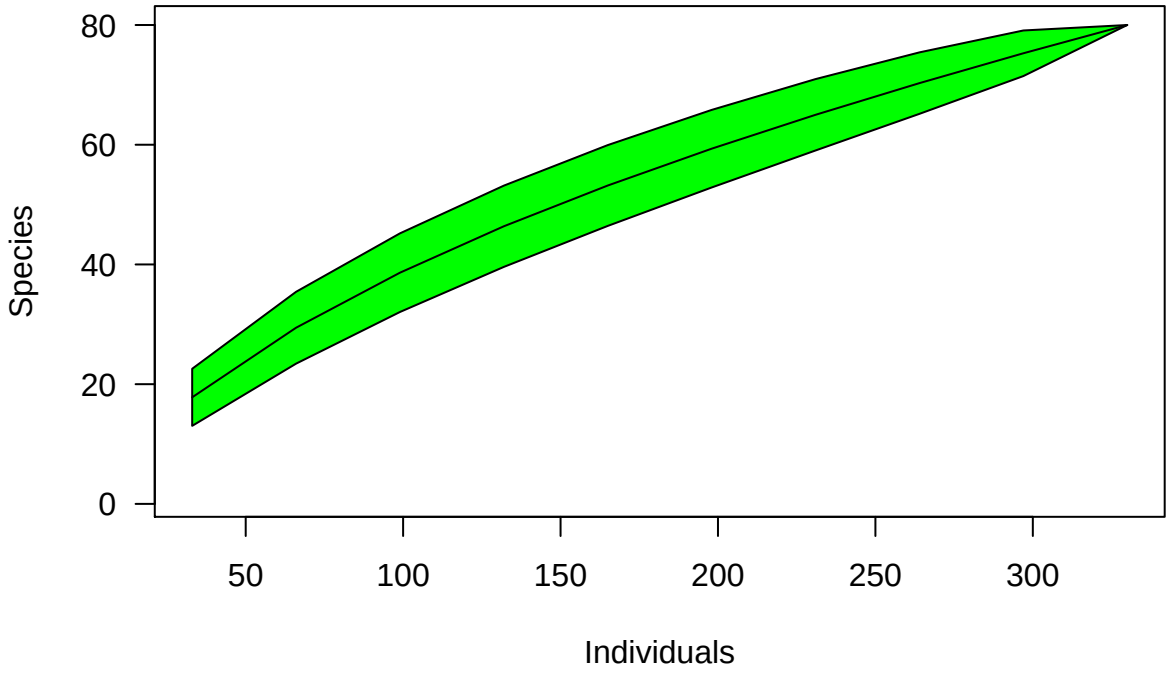
Individual-based SAC

In the second case, we will draw a SAC according to a rarefaction method that is based on sampling individuals (i.e., single plants) rather than transects (Hurlbert 1971).

```
sac <- specaccum(data_matrix,
                 method = 'rarefaction', permutations = 10000, gamma = 'boot')
sac
```

```
## Species Accumulation Curve
## Accumulation method: rarefaction
## Call: specaccum(comm = data_matrix, method = "rarefaction", permutations = 10000,
##
##
## Sites        1.0000  2.0000  3.0000   4.0000   5.0000   6.0000   7.000   8.0000
## Individuals 33.0000 66.0000 99.0000 132.0000 165.0000 198.0000 231.000 264.0000
## Richness    17.8053 29.4306 38.6249  46.3796  53.1888  59.3384  65.004  70.2952
## sd           2.3845  3.0002  3.2845   3.3941   3.3753   3.2400   2.981   2.5673
##
## Sites         9.0000  10
## Individuals 297.0000 330
## Richness     75.2801  80
## sd            1.9051   0
```

```
plot(sac, ci.type='polygon', ci.col='green', xvar = "individuals",
     las = 1, xlab = "Individuals", ylab = "Species")
```



We obtain a similar curve to the previous one. We can see how the number of observed species increases by increasing the number of transects but it does not 'saturate', indicating that species richness should continue to increase with sampling more than 10 transects.

SAC-based Predictions

Unseen species

We estimate that the number of missing species is around 99 ± 10, which corresponds to c 25% of observed species pool (i.e., 80 species).

```
?specpool
```

```
specpool(data_matrix)[,7:8]
```

```
##         boot  boot.se
## All 99.17644 10.48784
```

Notice that if we sample less than 10 transects, the estimated species number is reduced too.

```
poolaccum(data_matrix)$means[,c(2,6)]
```

```
##          S Bootstrap
## [1,] 38.07  47.10148
## [2,] 45.57  56.64035
## [3,] 52.90  65.72420
```

```
## [4,] 57.65  71.47713
## [5,] 63.27  78.31931
## [6,] 68.66  84.92757
## [7,] 74.08  91.71680
## [8,] 80.00  99.17644
```

With 3 transects we would have estimated 46 species (out of 37 observed), with 4 57, and so on, until 99 estimated species out of 80 observed over 10 transects.

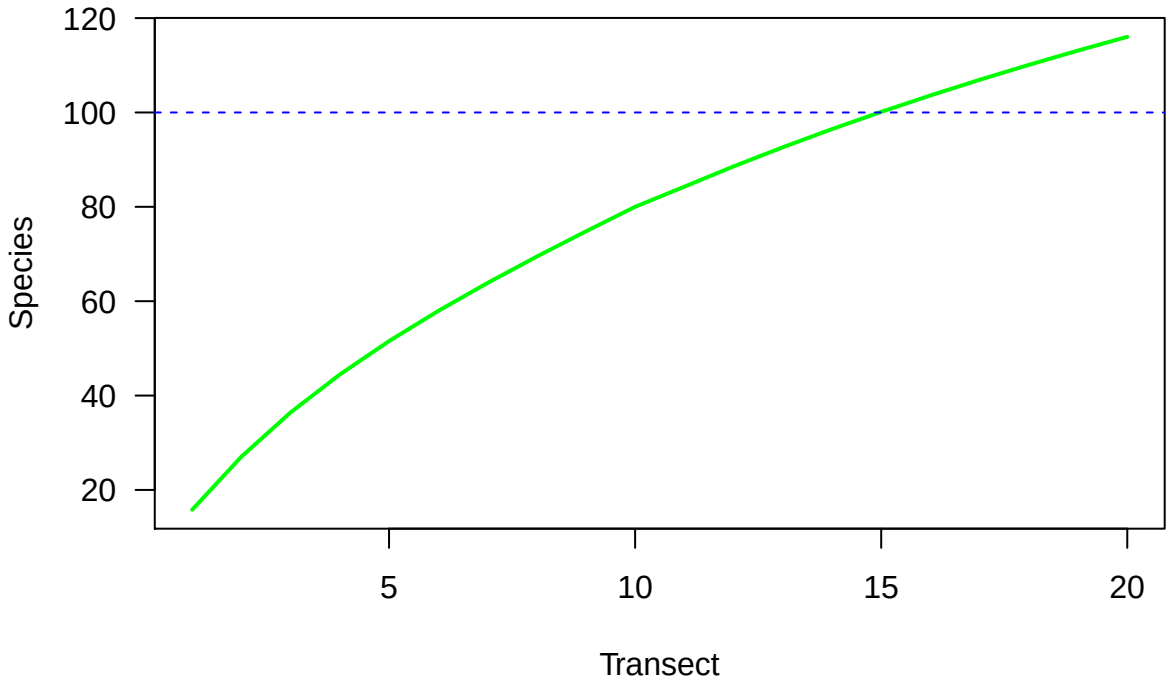
Additional sampling

Therefore, how many species can we observe by increasing the number of transects? How many new transects are needed to sample the estimated 99 species?

```
sac <- specaccum(data_matrix, method = 'exact')
sac.fit <- fitspecaccum(sac, 'lomolino')
sac.pred <- predict(sac.fit, 11:20)
names(sac.pred) <- paste('transect',11:20)
sac.pred
```

```
## transect 11 transect 12 transect 13 transect 14 transect 15 transect 16
##    84.26879    88.56517    92.62555    96.47302   100.12729   103.60535
## transect 17 transect 18 transect 19 transect 20
##   106.92201   110.09020   113.12137   116.02565
```

```
plot(c(sac.fit$richness,sac.pred), type = 'l', lwd = 2, las = 1,
     col = 'green', xlab = 'Transect', ylab = 'Species')
abline(h = 100, lty = 2, col = 'blue')
```



By sampling one more transect we observe 84 species, 89 with two more transects, 93 with three, 96 with four, and 100 with five. Thus, with fifteen total transects we may have a quite good sample of our forest.

Still, we notice that the curve does not saturate yet. Indeed, the derivate of the SAC at 20 transects is still much higher than zero.

```
specslope(sac.fit, 20)
```

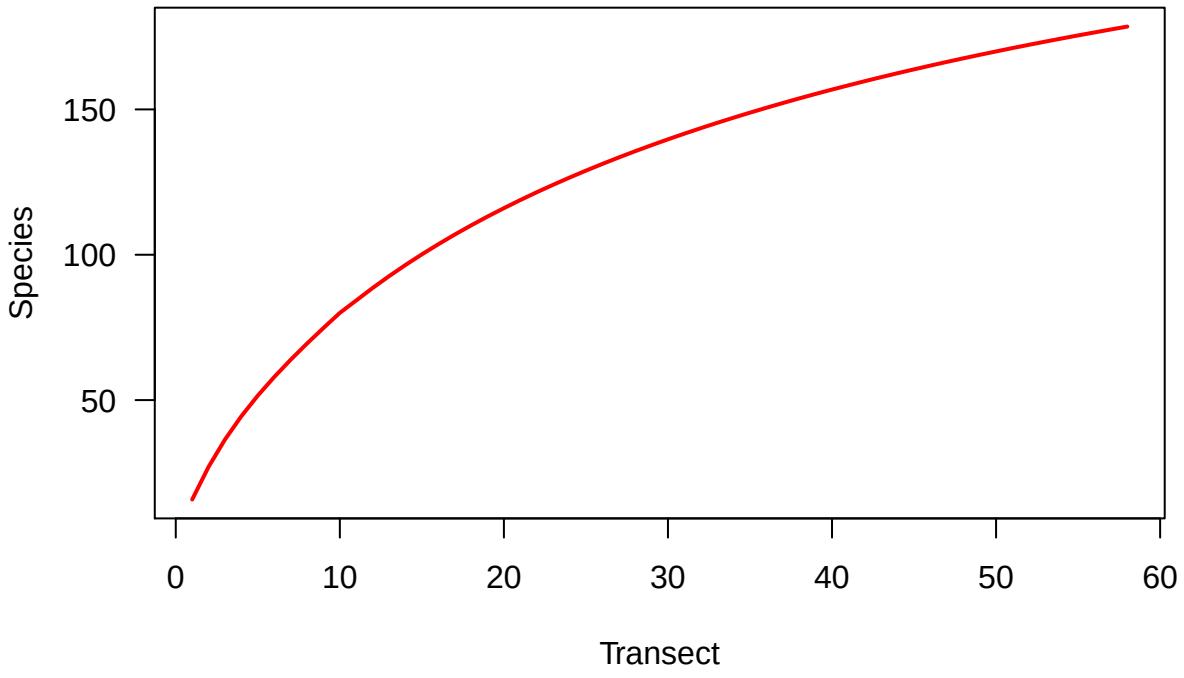
```
## [1] 2.843932
```

We estimate that the curve will start saturating (i.e., increasing rate smaller than one) with 48 additional transects.

```
specslope(sac.fit, 21:60)
```

```
##  [1] 2.7302940 2.6243435 2.5253289 2.4325955 2.3455701 2.2637486 2.1866853
##  [8] 2.1139849 2.0452949 1.9803004 1.9187187 1.8602954 1.8048010 1.7520277
## [15] 1.7017868 1.6539068 1.6082312 1.5646170 1.5229334 1.4830602 1.4448870
## [22] 1.4083120 1.3732415 1.3395887 1.3072735 1.2762214 1.2463634 1.2176355
## [29] 1.1899778 1.1633348 1.1376546 1.1128886 1.0889916 1.0659211 1.0436373
## [36] 1.0221030 1.0012831 0.9811446 0.9616566 0.9427899
```

```
sac.pred <- predict(sac.fit, 11:58)
plot(c(sac.fit$richness,sac.pred), type = 'l', lwd = 2, las = 1,
     col = 'red', xlab = 'Transect', ylab = 'Species')
```




```
sac.pred[48]
```

```
## [1] 178.4879
```

We notice how the number of newly discovered species decreases with further increasing the number of transects. With a total of 58 transects we estimate a forest richness of 178 species.

Rank–Abundance Curve

We finally examine the distribution of species abundances by means of rank–abundance curvers (RAD), also called dominance–diversity curves or Whittaker plots (Whittaker 1965, Wilson 1991). These plots show the logarithmic species abundances as a function of species rank order, that is in decreasing order from the most abundant to the least abundant species. RAD represents an important diagnostic tool for inspecting patterns of abundance distributions and diversity in communities.

We make use of the function `radfit`, which fits the following models to our abundance data: brokenstick (i.e., null model, Hurlbert 1971; Pielou 1975), niche preemption (Koleff et al. 2003), log-normal (McCune 1987), Zipf (O'Hara 2005), Zipf-Mandelbrot (Petchey & Gaston 2002). For more details, consult the help page of the function (type in `R ?radfit`), see Oksanen 2019 and references therein.

Before fitting the RAD, we pool species abundance data over the ten transects. This way, we obtain abundance data for each species at the forest site.

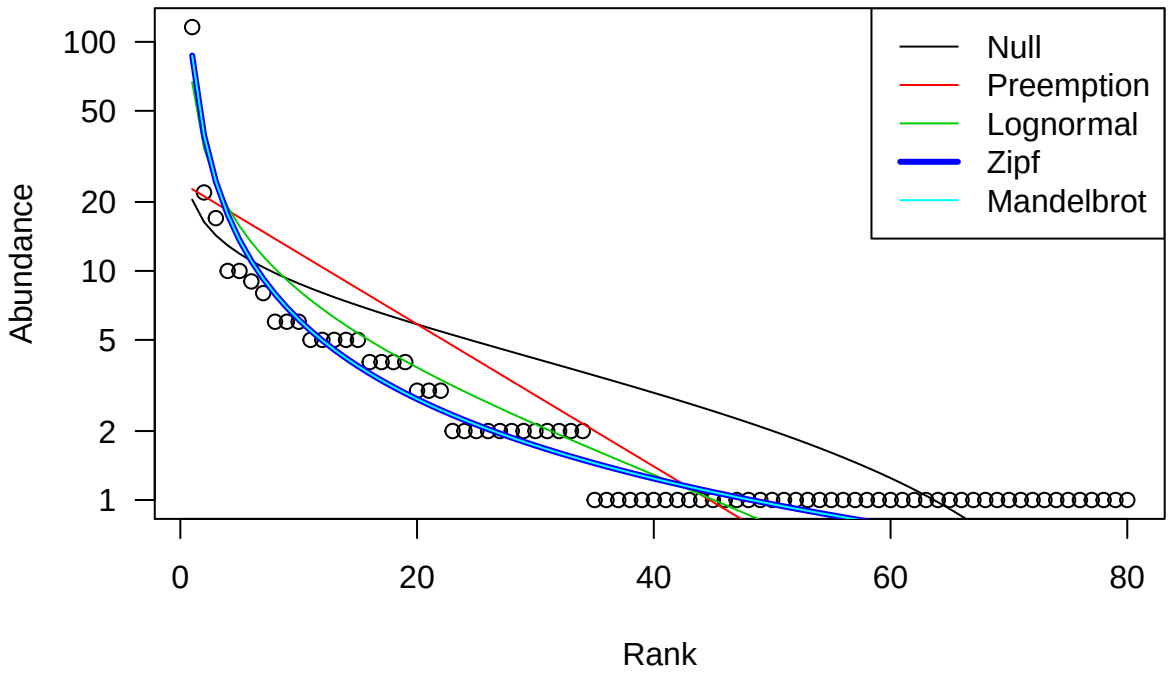
```
rad_data <- colSums(data_matrix)
rad_data
```

```
##        Acalypha diversifolia      Aegephila costaricensis
##                            6                            1
##      Allophylus campostachys        Amphitecna tuxtlensis
##                            1                            1
##               Apocynaceae 1                Apocynacee 2
##                            1                            1
##               Apoxynacaea 2          Arrabidea verrucosa
##                            1                            1
##        Astrocaryum mexicanum             Bactris mexicana
##                          116                            6
##           Bernoullia flammea          Brosimum alicastrum
##                            1                           10
##           Calatola laevigata              Capparis baduca
##                            1                            1
##        Chamaedorea alternans         Chamaedorea concolor
##                           17                            2
## Chamaedorea ernesti-augustii        Chamaedorea oblongata
##                            1                           10
##     Chamaedorea pinnatifrons              Clarisa biflora
##                            9                            1
##               Cojoba arborea                Combretum sp.
##                            1                            2
```

```
##             Cordia alliodora           Cordia megalantha
##                            1                           1
##               Costus scaber          Croton Schediarius
##                            1                           2
##           Croton schiedianus       Cymbopetalum baillonii
##                            1                           2
##         Dendropanax arboreus           Dialium guianense
##                            4                           2
##            Diospiros digyna            Eugenia mexicana
##                            2                           1
##         Faramea occidentalis                Ficus aurea
##                            2                           1
##              Flacocurtace ?    Fornsteronia viridescens
##                            1                           1
##               Guarea bijuga              Guarea glabra
##                            2                           5
##             Hampea nutricia                Inga glabra
##                            1                           1
##        Macherium floribundum                  Makania ?
##                            1                           1
## Mortoniodendron guatemalense         Myriocarpa longipes
##                            1                           3
##           Nectandra ambigens       Nectandra dendrodaphne
##                            5                           1
##        Nectandra salicifolia          Ocotea dendrodaphne
##                            1                           1
##                 Ouratea sp.               Piper sanctum
##                            1                           1
##            Pithecoctenium sp              Platimisium sp
##                            1                           1
##     Pleuratodendron lindenii         Posoqueria latifolia
##                            3                           1
##             Poulsenia armata         Pouteria campechiana
##                            6                           1
##           Pouteria durlandii          Pouteria reticulata
##                            1                           2
##              Pouteria sapota    Pseudolmedia oxyphyllaria
##                            2                          22
##        Psychotria chiapensis         Psychotria faxlucens
##                            8                           5
##             Psychotria flava        Psychotria limonensis
##                            4                           1
##      Psychotria papantlensis                Psychotria sp
##                            4                           1
##               Psychotria sp.     Psychotria veracruzensis
```

```
##                             1                             1
##           Pterocarpus rohrii          Quararibea funebris
##                             1                             3
##      Quararibea guatemalteca                   Randia sp
##                             1                             1
##               Rheedia edulis        Salacia megistophylla
##                             5                             5
##                   Sapranthus  Stemadenia donnell-smitthii
##                             1                             1
##          Tetracera volubilis           Trichilia martiana
##                             1                             2
##             Trophis mexicana            Trophis racemosa
##                             4                             2
```

```
plot(radfit(rad_data), las = 1)
```



We can see that the null model fails to represent our data, indicating the the distribution of individuals across species is not random. Indeed, we observe that few species have more individuals than expected by chance (very abundant, dominant species with low rank), while many species have less individuals than expected by chance (the majority of species with rank from 4–60). Furthermore, we can also see that the long tail of rare species with just one individuals is more pronounced that expected by chance.

The model that best represents our data is a Zipf/Zipf-Mandelbrot model, which follows a power-law distribution. This type of power-law distribution is a pattern widespread across ecological communities and many other systems, including e.g. the size distribution of river networks, the traffic volume across airports, and the occurrence of actors/actress in Hollywood movies.

References

Gotelli NJ & Colwell RK (2001). Quantifying biodiversity: procedures and pitfalls in measurement and comparison of species richness. Ecol. Lett. 4, 379–391.

Hurlbert SH (1971). The nonconcept of species diversity: a critique and alternative parameters. Ecology, 52, 577–586.

Koleff P, Gaston KJ & Lennon JJ (2003). Measuring beta diversity for presence-absence data. Journal of Animal Ecology, 72, 367–382.

McCune B (1987). Improving community ordination with the Beals smoothing function. Ecoscience, 1, 82–86.

O'Hara RB (2005). "Species richness estimators: how many species can dance on the head of a pin." Journal of Animal Ecology, 74, 375–386.

Oksanen J (2019). Vegan: ecological diversity. https://cran.r-project.org/web/packages/vegan/vignettes/diversity-vegan.pdf

Pielou EC (1975). Ecological Diversity. Wiley & Sons.

Petchey OL & Gaston KJ (2002). "Functional diver- sity (FD), species richness and community com- position." Ecology Letters, 5, 402–411.

Preston FW (1948). The commonness and rarity of species. Ecology 29, 254–283.

Whittaker RH (1965). Dominance and diversity in plant communities. Science 147, 250–260.

Wilson JB (1991). Methods for fitting dominance/diversity curves. Journal of Vegetation Science 2, 35–46.