Week 2 Exercise

Z620: Quantitative Biodiversity, Indiana University

November 8, 2014

In this exercise, we will conduct exercises on alpha diversity

RETRIEVE AND SET YOUR WORKING DIRECTORY

```
getwd()
```

```
## [1] "C:/Users/Mario Muscarella/Documents/GitHub/QuantitativeBiodiversity/Assignments/Week2"
```

```
#setwd("~/GitHub/Quantitative_Biodiversity/Assignments/Week2")
```

INSTALL PACKAGES

People develop different packages for certain tasks that can be carried out in the R enviornment. Use the 'help'funciton to learn about package installation and add-ons. install.packages("vegan")

```
require("vegan") #Both of these are not needed
```

```
## Loading required package: vegan
## Loading required package: permute
## This is vegan 2.0-10
```

```
library("vegan")
```

In the library of vegan, there is a data set that we will be using called BCI. BCI stands for Barro Colorado Island, which is a located in Panama. The BCI data frame has 50 plots (rows) of 1 hectare with counts of trees on each plot with total of 225 species (columns)

```
data(BCI)
```

Let's look at the data in the first few plots

```
head(BCI)[,1:3] # MEM: Added column selection so that it didn't print everything.
```

```
##   Abarema.macradenium Acacia.melanoceras Acalypha.diversifolia
## 1                   0                   0                     0
## 2                   0                   0                     0
## 3                   0                   0                     0
## 4                   0                   0                     0
## 5                   0                   0                     0
## 6                   0                   0                     0
```

Calculate Shannon index. 'Margin = 1' means diversity is calculated row-wise; 'Margin = 2' means diversity is calcualted column-wise.With base = exp(1), we are esimating Shannon's index using the natural logrithm of each taxon's relative abundance using the equation; $H' = -\sum(p_i \times ln(p_i))$

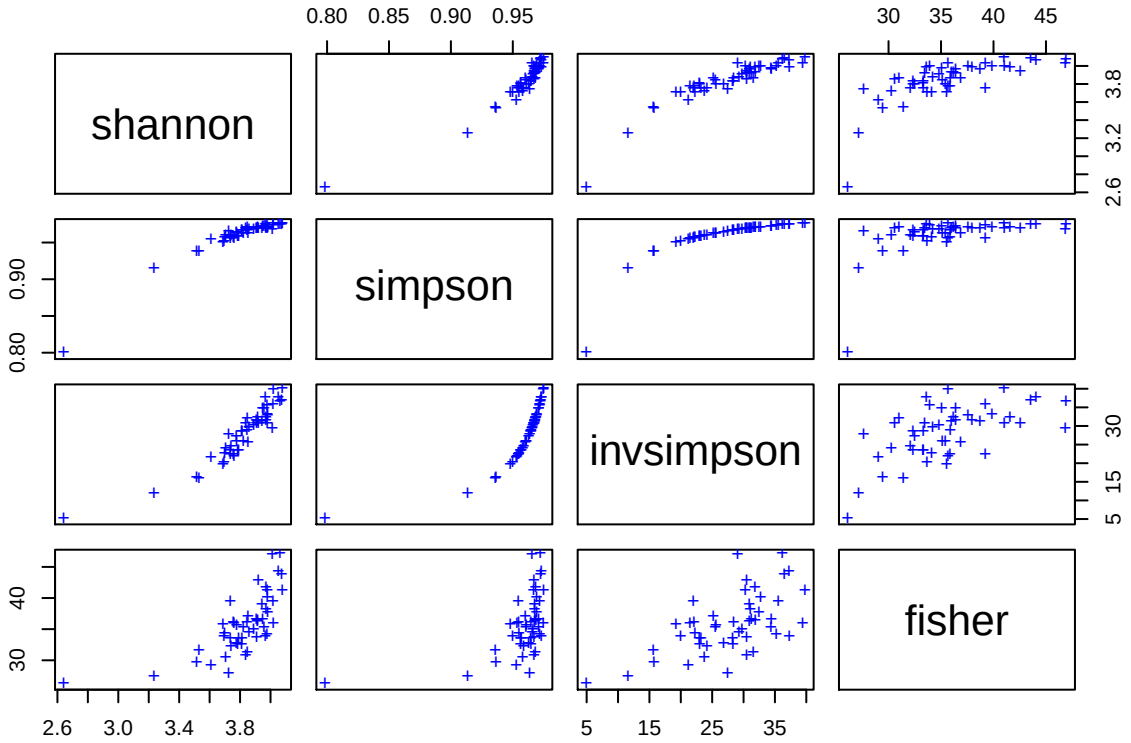
```
shannon <- diversity(BCI, index="shannon", MARGIN = 1, base=exp(1))
```

Can also calculate other diversity metrics

```
simpson <- diversity(BCI, "simpson")
invsimpson <- diversity(BCI, "inv")
fisher <- fisher.alpha(BCI)
```

Let's plot ***Pairs is not a normal plotting tool, introduce first***

```
pairs(cbind(shannon, simpson, invsimpson, fisher), pch="+", col="blue")
```



Species richness

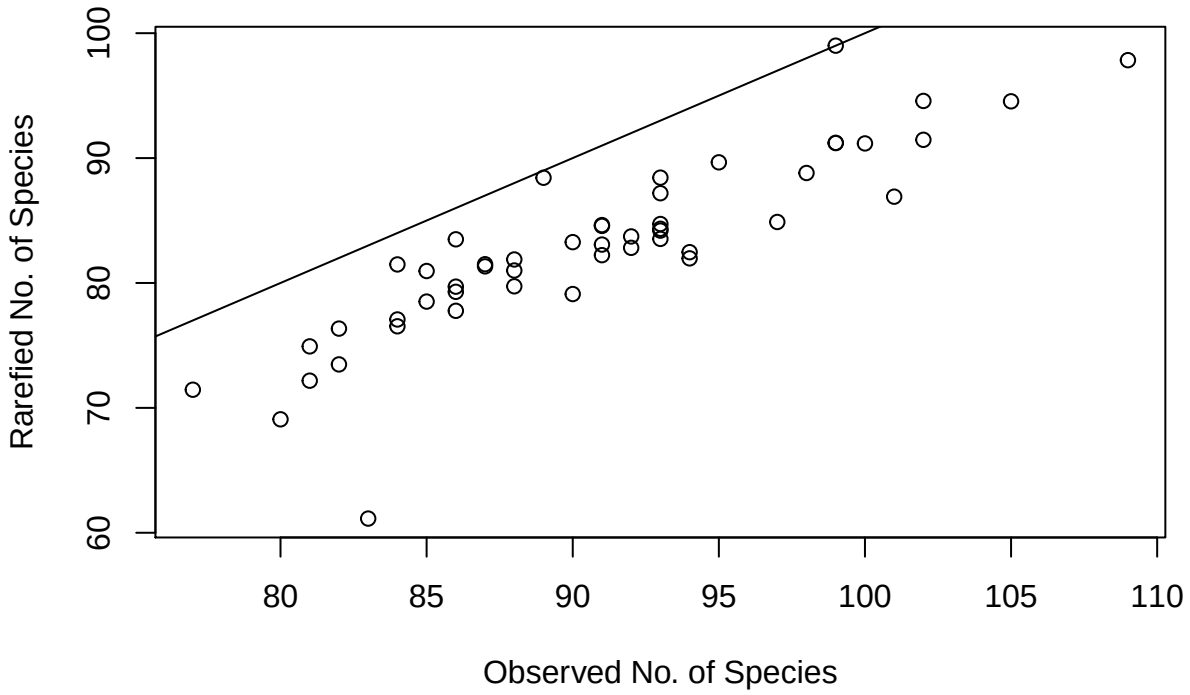
```
S <- specnumber(BCI)
```

Rarefaction

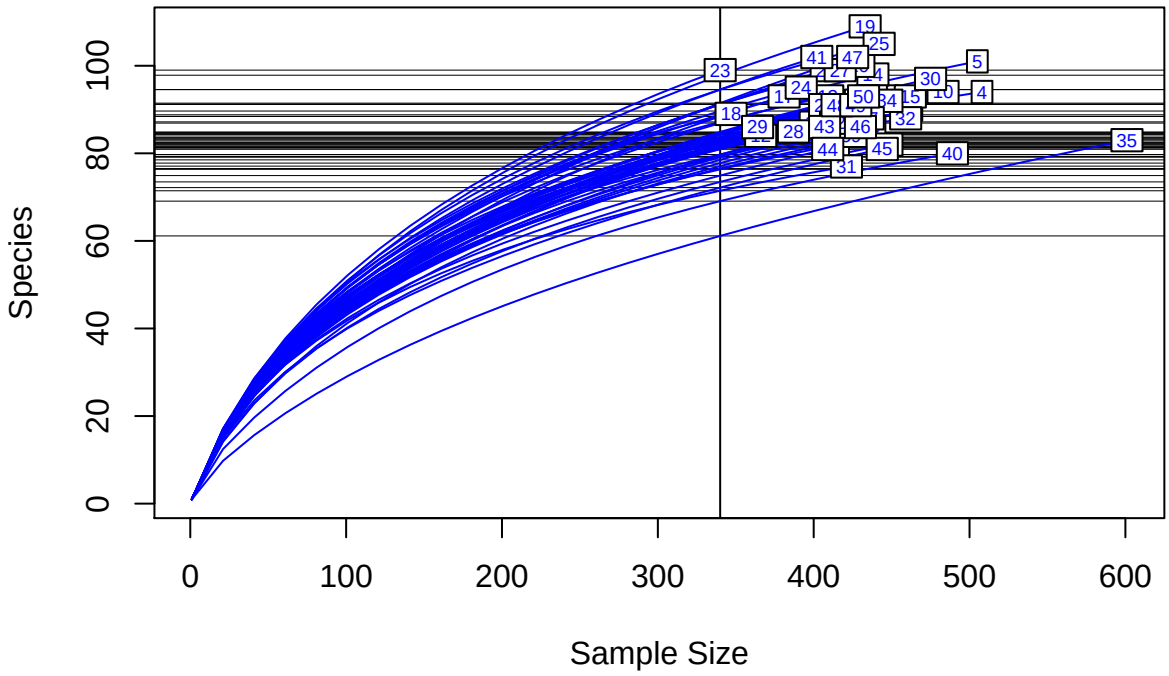
```
(raremax <- min(rowSums(BCI)))
```

```
## [1] 340
```

```
Srare <- rarefy(BCI, raremax)
plot(S, Srare, xlab = "Observed No. of Species", ylab = "Rarefied No. of Species")
abline(0, 1)
```




```
rarecurve(BCI, step = 20, sample = raremax, col = "blue", cex = 0.6)
```



Example: http://www.jennajacobs.org/R/rarefaction.html

Calculating relative abundances

```
BCI_t <- t(BCI)

BCIrel <- BCI_t
for(i in 1:ncol(BCI_t)){
  BCIrel[,i] = BCI_t[,i] / sum(BCI_t[,i])
  }
```

What's one way to test that this worked?

```
colSums(BCIrel)
```

```
##  1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25
##  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1
## 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50
##  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1
```

Now let's create a rank abundance curve. First, let's rank taxa within a sample (site 1) by relative abundance

```
rad <- BCIrel[order(BCIrel[,1], decreasing=TRUE), ]
head(rad)
```

```
##                              1       2       3        4       5       6
## Alseis.blackiana      0.05580 0.05977 0.03888 0.045276 0.03168 0.03398
## Poulsenia.armata      0.05357 0.03678 0.06048 0.029528 0.04950 0.03641
## Oenocarpus.mapora     0.04911 0.04828 0.03024 0.045276 0.03366 0.04612
## Hirtella.triandra     0.04688 0.03218 0.01080 0.007874 0.01188 0.01456
## Trichilia.tuberculata 0.04018 0.06207 0.06048 0.068898 0.02970 0.07524
## Virola.sebifera       0.03795 0.02759 0.02376 0.031496 0.06139 0.04612
##                              7       8       9      10      11      12
## Alseis.blackiana      0.04327 0.03248 0.03912 0.02899 0.03491 0.05191
## Poulsenia.armata      0.01923 0.03016 0.01222 0.04969 0.05486 0.02186
## Oenocarpus.mapora     0.04808 0.04640 0.04401 0.04141 0.04239 0.05191
## Hirtella.triandra     0.01683 0.03248 0.01956 0.01449 0.02993 0.01639
## Trichilia.tuberculata 0.06490 0.08353 0.15892 0.09524 0.10224 0.12568
## Virola.sebifera       0.01923 0.04408 0.03912 0.03520 0.01496 0.01639
##                             13      14       15       16       17      18
## Alseis.blackiana      0.01956 0.03881 0.032468 0.057208 0.081365 0.02017
## Poulsenia.armata      0.00000 0.02968 0.034632 0.073227 0.005249 0.00000
## Oenocarpus.mapora     0.04156 0.05023 0.023810 0.034325 0.081365 0.06916
## Hirtella.triandra     0.02689 0.02968 0.008658 0.009153 0.010499 0.03458
## Trichilia.tuberculata 0.08557 0.07534 0.071429 0.057208 0.094488 0.06628
## Virola.sebifera       0.00000 0.03881 0.034632 0.054920 0.013123 0.00000
##                             19      20      21      22       23      24
## Alseis.blackiana      0.030023 0.02331 0.02941 0.05263 0.014706 0.03571
## Poulsenia.armata      0.009238 0.03497 0.10784 0.01196 0.002941 0.01531
## Oenocarpus.mapora     0.055427 0.04429 0.02696 0.05742 0.064706 0.06122
## Hirtella.triandra     0.055427 0.02797 0.04167 0.01435 0.029412 0.03827
## Trichilia.tuberculata 0.101617 0.07692 0.05637 0.10048 0.067647 0.09694
## Virola.sebifera       0.027714 0.03497 0.03676 0.01675 0.026471 0.03061
##                             25      26      27       28       29       30
## Alseis.blackiana      0.04525 0.01720 0.04077 0.041344 0.041209 0.075789
## Poulsenia.armata      0.00905 0.05405 0.02158 0.002584 0.005495 0.016842
## Oenocarpus.mapora     0.03167 0.01474 0.02638 0.025840 0.043956 0.025263
## Hirtella.triandra     0.05882 0.05897 0.01918 0.023256 0.019231 0.006316
## Trichilia.tuberculata 0.05882 0.03686 0.04796 0.111111 0.129121 0.069474
## Virola.sebifera       0.02715 0.04914 0.02878 0.046512 0.024725 0.016842
##                             31       32       33       34       35      36
## Alseis.blackiana      0.02613 0.045752 0.055046 0.093960 0.154742 0.01860
## Poulsenia.armata      0.05701 0.004357 0.009174 0.002237 0.000000 0.03256
## Oenocarpus.mapora     0.01663 0.010893 0.022936 0.020134 0.006656 0.05581
## Hirtella.triandra     0.03325 0.017429 0.020642 0.008949 0.001664 0.05581
## Trichilia.tuberculata 0.07838 0.108932 0.084862 0.069351 0.049917 0.06512
## Virola.sebifera       0.04751 0.039216 0.036697 0.015660 0.018303 0.03256
##                             37       38       39      40      41      42
## Alseis.blackiana      0.04368 0.055928 0.089623 0.13292 0.03234 0.03140
## Poulsenia.armata      0.01379 0.002237 0.002358 0.00409 0.02736 0.06280
## Oenocarpus.mapora     0.03448 0.024609 0.009434 0.00409 0.02736 0.04589
## Hirtella.triandra     0.01609 0.006711 0.007075 0.01431 0.07711 0.04348
## Trichilia.tuberculata 0.07586 0.131991 0.186321 0.19836 0.04726 0.03623
## Virola.sebifera       0.03218 0.024609 0.016509 0.02249 0.02985 0.02899
##                             43      44      45      46       47      48
## Alseis.blackiana      0.01966 0.03178 0.02252 0.06744 0.040000 0.02892
## Poulsenia.armata      0.13514 0.13447 0.12838 0.00000 0.009412 0.05542
## Oenocarpus.mapora     0.02703 0.02445 0.01802 0.08372 0.065882 0.03614
## Hirtella.triandra     0.05651 0.04401 0.05856 0.05116 0.077647 0.09880
```

```
## Trichilia.tuberculata 0.08845 0.06357 0.05856 0.03721 0.037647 0.04578
## Virola.sebifera       0.03440 0.02445 0.02928 0.00000 0.025882 0.01687
##                            49      50
## Alseis.blackiana      0.014052 0.02083
## Poulsenia.armata      0.091335 0.09954
## Oenocarpus.mapora     0.009368 0.02778
## Hirtella.triandra     0.100703 0.06250
## Trichilia.tuberculata 0.060890 0.04167
## Virola.sebifera       0.014052 0.03241
```

Let's make a ranking now that species abundances are ordered/sorted

```
ranks <- seq(1,nrow(rad))
```

Let's create RAD plot

```
plot(ranks,rad[,1],type='l',col="black",xlab="Rank",lwd=8,ylab="Relative Abundance",xlim=range(ranks))
```