Brief Introduction to Vegan: Community Analysis Package

Data sets and Libraries:

You need to install and load the *vegan*, *MASS,* and *picante* packages. Also *lattice* for some graphs in vegan

## Load these libraries and datasets
```
library(vegan)
library(MASS)
library(picante)
library(lattice)
ferp<-read.csv("http://people.ucsc.edu/~ggilbert/Rclass_docs/FERP07data.csv")
data(BCI) #gets BCI community matrix form in 1-ha quadrats
##clean up FERP data and assign trees to 20x20m quadrats
ferp<-ferp[,c(1,2,4,5,6)]
ferp$qE<-trunc((ferp$east-0.001)/20,0)*20
ferp$qN<-trunc((ferp$north-0.001)/20,0)*20
ferp$Q<-paste(ferp$qE,ferp$qN,sep="_")

f<-table(ferp$Q,ferp$code) #makes a Community Matrix for the FERP
```
## end of loading libraries and datasets

The vegan package is a collection of functions that are useful for a wide variety of analyses of ecological communities. These include the kinds of multivariate analyses, measures of diversity, and more. `?vegandocs` gives a selection of helpful guides

Community data can be stored in a variety of formats. Vegan mostly uses a *Community Matrix,* where rows are samples and columns are species. Values in each cell *i,j* is the number of individuals of species *j* in sample *i*.

	species1	species2	species3
sample1	5	1	45
sample2	9	0	23
sample3	22	5	1

About the FERP data.

We'll use data from the UCSC Forest Ecology Research Plot for examples. The FERP data include 8,180 individually tagged, mapped, measured, and identified woody plants on the 6-ha UCSC Forest Ecology Research Plot (Gilbert *et al.* 2010. Beyond the tropics: forest structure in a temperate forest mapped plot. *Journal of Vegetation Science* 21:388-405.) Each tree is mapped on an East-North (x-y) coordinate system in meters from the south-west corner of the plot. There are 31 woody species.

The FERP data (FERP07data.csv) are in a data-frame form, with one line per tree. Each line includes identifying, size, and location information for that tree.

Here we create a sample by species community matrix assigning each tree to its 20x20-m quadrat, identified by the SW corner of the quadrat in meter from the SW corner of the plot. There are the 150 quadrats.

```
table(ferp$code) #number of individuals per species on the FERP
```

Simple diversity measures

There are a variety of simple measures of diversity available in picante

Function `diversity` gives Shannon, Simpson, or Inverse Simpson indices
Shannon $H' = -\Sigma(p_i * \ln(p_i))$ where p is the proportion of individuals that are species i.
Simpson's $1\text{-}D = 1 - \Sigma (p_i^2)$ using index="simpson"
Inverse Simpson $= 1/D = 1/ \Sigma (p_i^2)$ using index="invsimpson"

```
#shannon H' index for each sample in comm matrix f
diversity(x=f, index="shannon")

# Or to get the H' for the whole FERP
diversity(x=table(ferp$code),index="shannon")
```

Fisher's alpha: based on Fisher's log series: $S_n = \alpha x^n/n$, where S_n is the number of species expected with abundance of n. x and α are derived from the data

```
#for Fisher's alpha for complete FERP
fisher.alpha(x=table(ferp$code), se=TRUE)

#The number of species in each quadrat (simple richness)
specnumber(f) #or more specifically specnumber(f, MARGIN=1)
#The number of quadrats in which each species appears
specnumber(f, MARGIN=2)  #MARGIN=2 does by columns
#The total number of species on the FERP
specnumber(table(ferp$code))
```

#Pielou's evenness J' would then be H'/H'_{max}, where H'_{max}=log(S) or

```
diversity(table(ferp$code))/log(specnumber(table(ferp$code)))
```

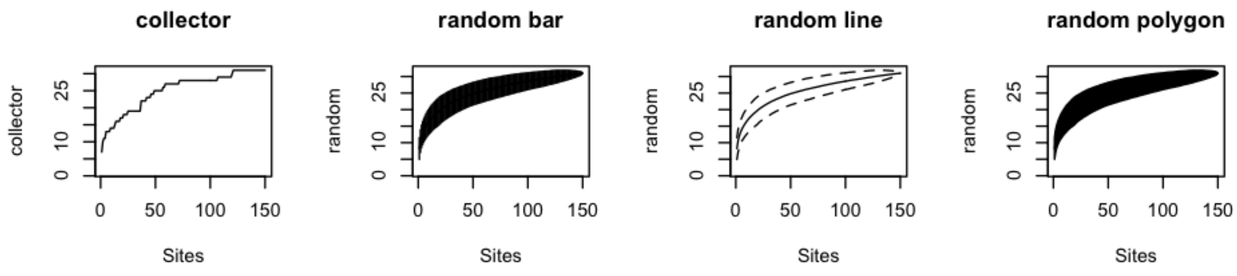
Rarefaction and species accumulation curves
You can use Hurlberts (1971) rarefaction to return the expected number of species in a given number of random individuals taken from a vector of species abundances

```
f2<-table(ferp$code) #simple vector of species counts on the ferp

#Get number of species expected in given number of individuals on FERP
rarefy(x=f2, sample=100, se=TRUE) #spp expected in 100 individs

#get species accumulation curves using specaccum
#several methods available including
#method="random" (can specify number of permutations)
#method="rarefaction" (by individuals rather than samples)
#method="collector" (in order they happen to appear)
#method="coleman"  (from Coleman 1982)
#method="exact" (expected mean species from Colwell 2004)

#method=random for sample-based rarefaction with 1000 permutations
specaccum(comm=f, method="random", permutations=1000)
sac<- specaccum(comm=f, method="random", permutations=1000)
#save to object
plot(sac) #plot the species accumulation curve with error bars
around the mean
#for various ways to display the curves
par(mfrow=c(1,4));
plot(specaccum(f,method="collector"),main="collector");
plot(sac, ci.type="bar",main="random bar"); plot(sac,
ci.type="line",ci.lty=2,main="random line"); plot(sac,
ci.type="polygon",main="random polygon");par(mfrow=c(1,1))
```



Species frequency distributions
The distribution of species in a community are often compared to Preston's lognormal (octaves) or Fisher's log series. In vegan this can be done with the `prestondistr` and `fisherfit` functions. Can also use `fitdistr` to fit to any names distribution.
Look at this using the vector of species abundances f2 where:
f2<-table(ferp$code) #simple vector of species counts on the ferp

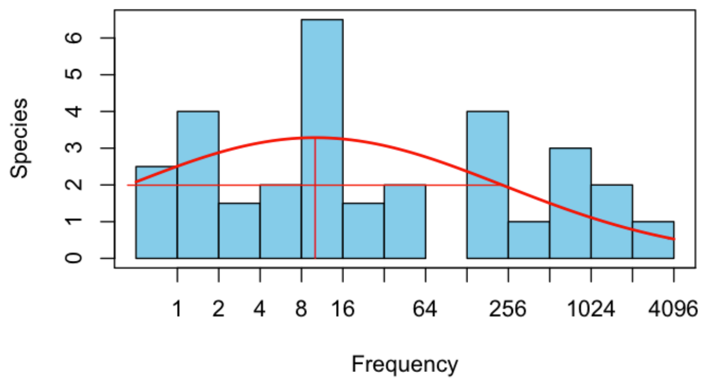
# **Preston octave (lognormal) distributions** Counts number of species of frequency by doubling octaves. Fits a left-truncated normal distribution to $\log_2$ transformed non-pooled observations with direct maximization of log-likelihood. Truncate indicates the left border for log-normal model in $\log_2$ units (default is -1 = zero). Truncation has big effect on model fit.

pd<-prestondistr(f2,truncate=-1)
#note that prestonfit takes a binning approach that does not work as well
pd #shows summary and observed and fitted frequencies per octave
plot(pd) #plot of observed (bars) and fitted (curve) frequencies
veiledspec(pd) #calculates extrapolated number of species to be expected if preston distn

```
Preston lognormal model
Method: maximized likelihood to log2 abundances
No. of species: 31

    mode    width       S0
3.330030 4.531191 3.286933
#NOTE one the log2 scale, width is the sd and S0 is the expected # spp at the mode

Frequencies by Octave
                0        1        2        3        4        5        6        8
Observed 2.500000 4.000000 1.500000 2.000000 6.500000 1.500000 2.000000 4.000000
Fitted   2.509056 2.879866 3.148341 3.278226 3.251199 3.071114 2.763095 1.932584
```



# **To Fit Fisher's log series and get Fisher's alpha**
fd<-fisherfit(f2)
fd #gives alpha, but look at str(fd) for series data
confint(fd,level=.95) #confidence interval for Fisher's alpha
plot(fd) #plots the data and Fisher's log series fit

Extrapolating Species Richness estimates from relative abundances
There are a number of ways to estimate how many species you would expect in total, based on your samples. See ?specpool help for description of how these are calculated. The estimate function is based on the functions used in Colwell's EstimateS.

From single vector of species abundances
```
f2<-table(ferp$code)  #single vector of species abundances on the FERP
veiledspec(prestondistr(f2,truncate=-1)) #Number spp expected if from Preston distn
estimateR(f2) #gives Chao1 and ACE estimates and SE as per EstimateS
```

From a community matrix of many samples
```
f<-table(ferp$Q,ferp$code) #makes a Community Matrix for the FERP
specpool(f) #bootstrapped version of estimate from samples
```

```
fea<-estaccumR(f, permutations=10)
# estaccum works like specaccum but includes Chao and ACE estimates
plot(fea) #requires lattice library
```

Beta diversity
There are at least as many ways to measure Beta diversity as alpha diversity. They are mostly different formulations of how many species are in common between two samples, and how many unique. They can be quantitative or presence/absence.

Vegan uses the function betadiver to calculate the full range of diversity measures from a community matrix.
The general form is betadiver(x=f, index = "w"). Here "f" is the FERP sample x species community matrix, and "w" refers to the Sorensen Index (w= (b+c)/(2*a+b+c), where a are shared species and b and c are unique to either sample)

To illustrate, let's use "small" – the first 5 quadrats of f.
small<-f[1:5,c(2,7,9,15,16,19,20,22,23,24,28,29,30)]

```
bdiv<-betadiver(x=small, method="w")
bdiv
0_0     0_100     0_120     0_140
0_100 0.3333333
0_120 0.2500000 0.1764706
0_140 0.2307692 0.1428571 0.2000000
0_160 0.4666667 0.2500000 0.4117647 0.2857143
```

To get the overall Beta diversity for the FERP plot, take the mean
`mean(betadiver(f,"w"))`

VARIATIONS
You can use any of the 24 beta-diversity metrics in Koleff et al. 2003 J. Animal. Ecol 72:367-382, either calling them by number or by letter (subscript of Beta). You can see the full list that are available in betadiver by typing `betadiver(help=T)`
The first 5 are:
1 "w" = (b+c)/(2*a+b+c)
2 "-1" = (b+c)/(2*a+b+c)
3 "c" = (b+c)/2
4 "wb" = b+c
5 "r" = 2*b*c/((a+b+c)^2-2*b*c)

Since most measures of Beta diversity are distance measures, you can use `vegdist` as well (See Dissimilarity matrices, below)
Note: you get exactly the same output as above from
`vegdist(small, method="bray", binary=TRUE).`

Or, if 24 distance measures from Koleff isn't enough, use `designdist` to design your own distance metric!

Dissimilarity matrices

`Vegdist` allows you to calculate the multivariate distances between pairs of samples. These dissimilarity matrices form the basis of most kinds of ordinations. There are oodles of different possible measures, set as method. The current choices include manhattan, Euclidean, Canberra, bray, kulczynski, jaccard, gower, morisita, horn, mountford, raup, binomial, and chao. See ?vegdist for details on how each is calculated, and any of many books and papers arguing vehemently about which is best. Or use `designdist` to design your own distance metric!

`vegdist` returns a matrix of pairwise distances. This is too big to look at for the full FERP data set, so let's create a subset to play with.

```
small<-f[1:5,c(2,7,9,15,16,19,20,22,23,24,28,29,30)]
vegdist(small,method="bray")
            0_0     0_100     0_120     0_140
0_100 0.6000000
0_120 0.4876033 0.2653061
0_140 0.3902439 0.5000000 0.5151515
0_160 0.3932584 0.5652174 0.5471698 0.2835821
```

Notice the default is to not include the distances along the diagonal (identities) or the upper part.

You can specify these with various arguments

```
vegdist(small, method="bray", diag=T, upper=T)
            0_0     0_100     0_120     0_140     0_160
0_0   0.0000000 0.6000000 0.4876033 0.3902439 0.3932584
0_100 0.6000000 0.0000000 0.2653061 0.5000000 0.5652174
0_120 0.4876033 0.2653061 0.0000000 0.5151515 0.5471698
0_140 0.3902439 0.5000000 0.5151515 0.0000000 0.2835821
0_160 0.3932584 0.5652174 0.5471698 0.2835821 0.0000000
```

You can first standardize quantitative data to presence/absence with argument binary

```
vegdist(small, method="bray", diag=T, upper=T, binary=T)
```

binary actually calls out to function `decostand`, which includes a broad range of **useful standardizations** for community data.

Non-metric multidimensional scaling

NMDS is the current favorite in community ordination. It avoids most of the pitfalls of the menagerie of ordination techniques of days gone by (available in vegan as cca, rda, decorana)
There are two approaches to MDS. The old (and simpler to look at) approach is called isoMDS. This picks random starting values, then iterates until convergence. It gives one solution, and is subject to getting stuck in local (rather than global) optima.
#note that because isoMDS starts with a distance matrix, it loses track of all species scores.

```
#get subset of 40 quadrats from the FERP, removing any spp not present
selQ<- expand.grid(east=seq(0,160,40),north=seq(0,280,40))
selQ$Q<-paste(selQ$east,selQ$north,sep="_")
f3<-f[rownames(f)%in%selQ$Q,]; tal<-apply(f3,MARGIN=2,FUN=sum); tal<-
tal[tal>0];
f3<-f3[,names(tal)]

f.dis<-vegdist(f3,"bray") #get bray-curtis dissimilarity matrix
f.iso<-isoMDS(d=f.dis, k=2, maxit = 50, trace=T, tol=1e-3)
#k=2 looks for 2 dimensions. Maxit sets max number of iterations
to read tolerance level tol.
#trace=T asks to print out progress every 5 steps.
```

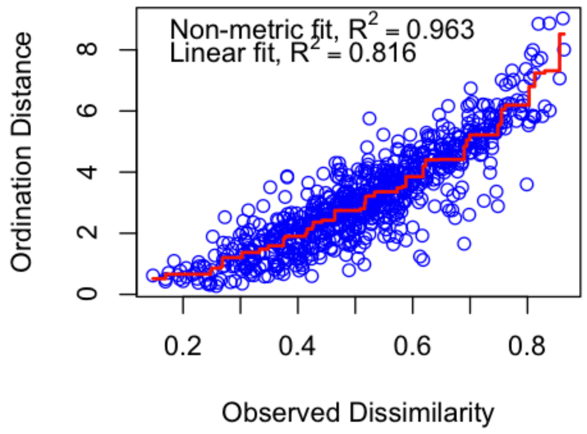
#The output object is a list with points and stress. To visualize:

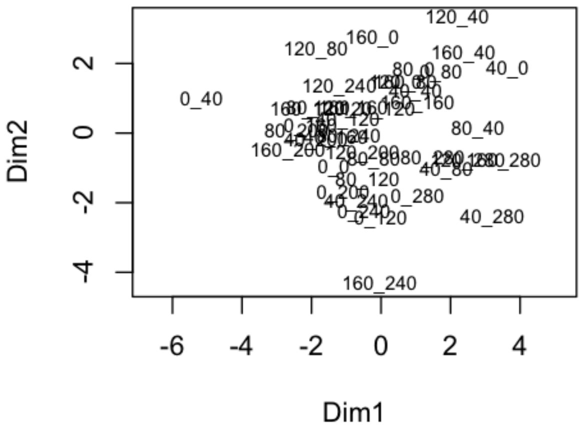
```
f.iso$stress
#strees is given in percent, the smaller the better.
#<5 is great, <10 good, >30 poor representation

stressplot(f.iso,f.dis)
#dots should be reasonably close to the line in this Shepard plot

ordiplot(f.iso, type="t",display="sites")
#plot on two ordination axes for sites
```

```
> f.iso$stress
[1] 19.35492
```



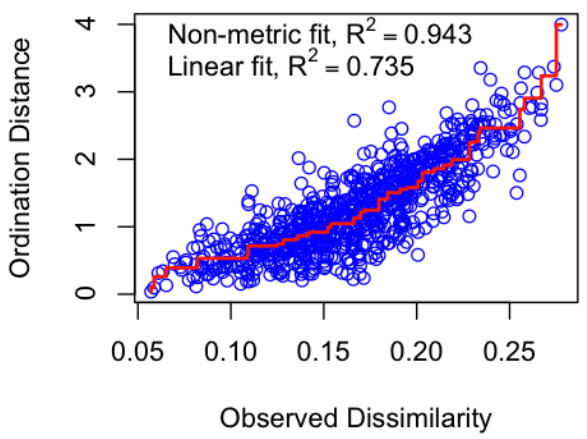


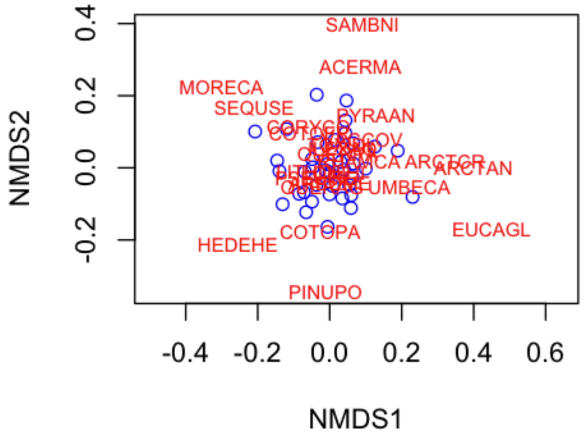
metaMDS

metaMDS uses a number of iterations through different starting configurations to avoid the pitfalls of local optima that can cause problems with isoMDS. This is the preferred approach.

```
f3.meta<-metaMDS(comm=f3,distance="gower", k=2)
#With metaMDS you can start with the community matrix and thus keep the species information
f3.meta  #note that here stress is in proportion and not percent as it is in isoMDS
stressplot(f3.meta)

fig<-ordiplot(f3.meta,type="n")  #make a blank plot
points(fig,"sites",pch=1,col="blue")  #show sites as blue circles
text(fig,"species", cex=.7, col="red") #show species as red text
identify(fig,"sites") #click on figure to identify particular sites
```



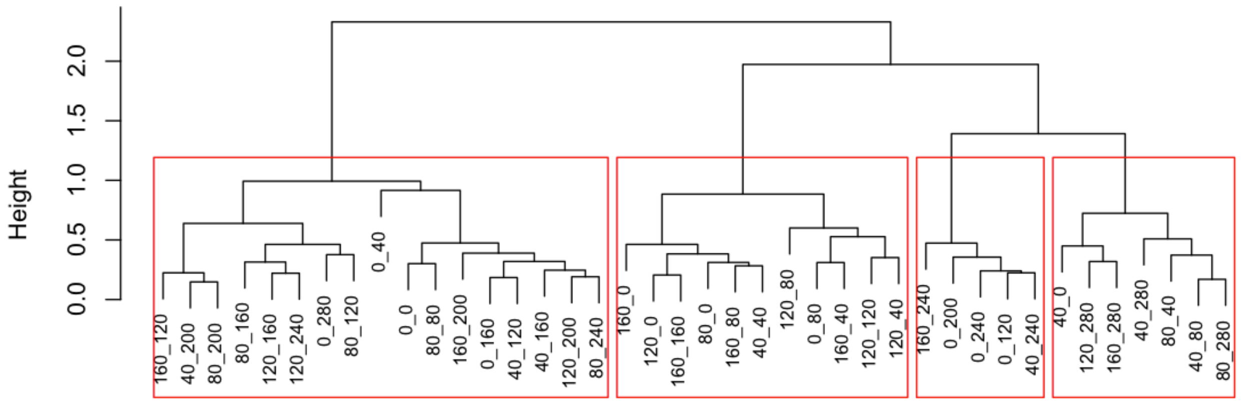


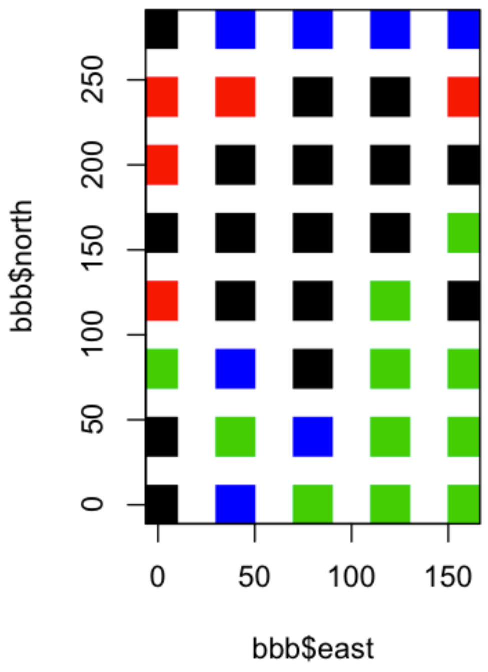
```
#note, can get basic ordination plot with
plot(f3.meta,type="t")
but ordiplot has more annotation flexibility
```

Using clustering algorithms for community classifications

Let's use the dominant species of 40 FERP quadrats (f3 – see metaMDS), and classify sites into a smaller number of vegetation types.

```
f3.dis<-vegdist(f3,method="bray")  #calculate a distance matrix
clus<-hclust(f3.dis,method="ward")  #cluster samples based on
similarity
plot(clus,cex=.75)  #look at the clusterin
rect.hclust(clus,4) #group sites into 4 groups
f3.4groups<-cutree(clus,4) #save membership in those 4 groups
#convert to a dataframe useful for plotting
bbb<-as.data.frame(f3.4groups); colnames(bbb)<-"group"
bbb$east<-unlist(strsplit(names(f3.4groups),"_"))[seq(1,79,2)]
bbb$north<-unlist(strsplit(names(f3.4groups),"_"))[seq(2,80,2)]
plot(bbb$east,bbb$north,pch=15,cex=3,col=bbb$group) #plot groups
```


Height
160_120
40_200
80_200
80_160
120_160
120_240
0_280
80_120
0_40
0_0
80_80
160_200
0_160
40_120
40_160
120_200
80_240
160_0
120_0
160_160
80_0
160_80
40_40
120_80
0_80
160_40
120_120
120_40
160_240
0_200
0_240
0_120
40_240
40_0
120_280
160_280
40_280
80_40
40_80
80_280


bbb$north
bbb$east