Assignment: Spatial Diversity

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OVERVIEW

This assignment will emphasize primary concepts and patterns associated with spatial diversity, while using R as a Geographic Information Systems (GIS) environment. Complete the assignment by refering to examples in the handout.

After completing this assignment you will be able to:
1. Begin using R as a geographical information systems (GIS) environment.
2. Identify primary concepts and patterns of spatial diversity.
3. Examine effects of geographic distance on community similarity.
4. Generate simulated spatial data.

Directions:

1. Change "Student Name" on line 3 (above) with your name.
2. Complete as much of the assignment as possible during class; what you do not complete in class will need to be done on your own outside of class.
3. Use the handout as a guide; it contains a more complete description of data sets along with the proper scripting needed to carry out the assignment.
4. Be sure to **answer the questions** in this assignment document. Space for your answer is provided in this document and indicated by the ">" character. If you need a second paragraph be sure to start the first line with ">".
5. Before you leave the classroom, **push** this file to your GitHub repo.
6. When you are done wit the assignment, **Knit** the text and code into an html file.
7. After Knitting, please submit the completed assignment by creating a **pull request** via GitHub. Your pull request should include this file *spatial_assignment.Rmd* and the html output of `Knitr` (*spatial_assignment.html*).

1) R SETUP

In the R code chunk below, provide the code to:

1. Clear your R environment
2. Print your current working directory,
3. Set your working directory to your "*/Week4-Spatial*" folder, and

```
rm(list=ls())
getwd()
setwd("C:/Users/Savannah/GitHub/QB2017_Bennett/Week4-Spatial")
```

2) LOADING R PACKAGES

In the R code chunk below, do the following:

1. Install and/or load the following packages: `vegan`, `sp`, `gstat`, `raster`, `RgoogleMaps`, `maptools`, `rgdal`, `simba`, `gplots`, `rgeos`

```r
require(vegan)

# Classes and methods for handling spatial data
require(sp)

# Methods for geostatistical analyses
require(gstat)

# Methods to create a RasterLayer object
require(raster)

# For querying the Google server for static maps.
require(RgoogleMaps)

# Tools for manipulating and reading geospatial data
require(maptools)

# Geospatial Data Abstraction Library
require(rgdal)

# Similarity measures for community data
require(simba)

# Programming tools for plotting data
require(gplots)


# Geostatistical package, used here for semivariograms
require(rgeos)
```

Question 1: What are the packages `simba`, `sp`, and `rgdal` used for?

> ***Answer 1***: 'simba' is used to generate similarity measures for community data, while 'sp' is used for geostatistical analyses.

3) LOADING DATA

In the R code chunk below, use the example in the handout to do the following:

1. Load the Site-by-Species matrix for the Indiana ponds datasets: BrownCoData/SiteBySpecies.csv
2. Load the Environmental data matrix: BrownCoData/20130801_PondDataMod.csv
3. Assign the operational taxonomic units (OTUs) to a variable 'otu.names'
4. Remove the first column (i.e., site names) from the OTU matrix.

```r
Ponds <- read.table(file = "BrownCoData/20130801_PondDataMod.csv", head = TRUE, sep = ",")

OTUs <- read.csv(file = "BrownCoData/SiteBySpecies.csv", head = TRUE, sep = ",")

otu.names <- names(OTUs) # Get the names of the OTUs

OTUs <- as.data.frame(OTUs[-1]) # remove first column (site names)

rich <- specnumber(OTUs)
```

```r
max(rich)
```

Question 2a: How many sites and OTUs are in the SiteBySpecies matrix?

> ***Answer 2a***: There are 51 sites, and a total of 16,383 OTUs observed, which comprised of 100 different OTUs in this dataset.

Question 2b: What is the greatest species richness found among sites?

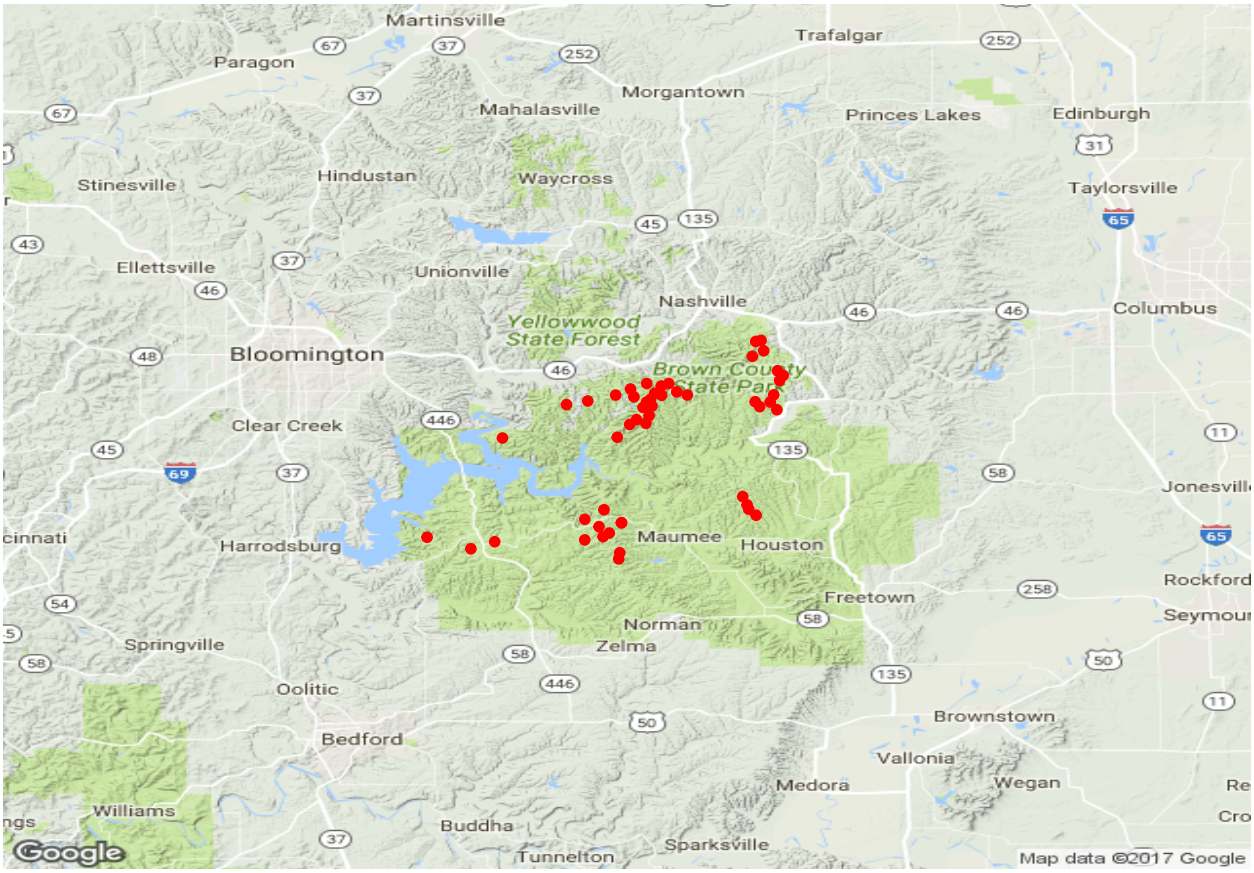
> ***Answer 2b***: The highest richness is 3659 OTUs.

4) GENERATE MAPS

In the R code chunk below, do the following:

1. Using the example in the handout, visualize the spatial distribution of our samples with a basic map in RStudio using the `GetMap` function in the package `RgoogleMaps`. This map will be centered on Brown County, Indiana (39.1 latitude, -86.3 longitude).

```r
lats <- as.numeric(Ponds[, 3]) # latitudes (north and south)

lons <- as.numeric(Ponds[, 4]) # longitudes (east and west)

newmap <- GetMap(center = c(39.1,-86.3), zoom = 10,
destfile = "PondsMap.png", maptype="terrain")

PlotOnStaticMap(newmap, zoom = 10, cex = 2, col = 'blue') # Plot map in RStudio

PlotOnStaticMap(newmap, lats, lons, cex = 1, pch = 20, col = 'red', add = TRUE)
```



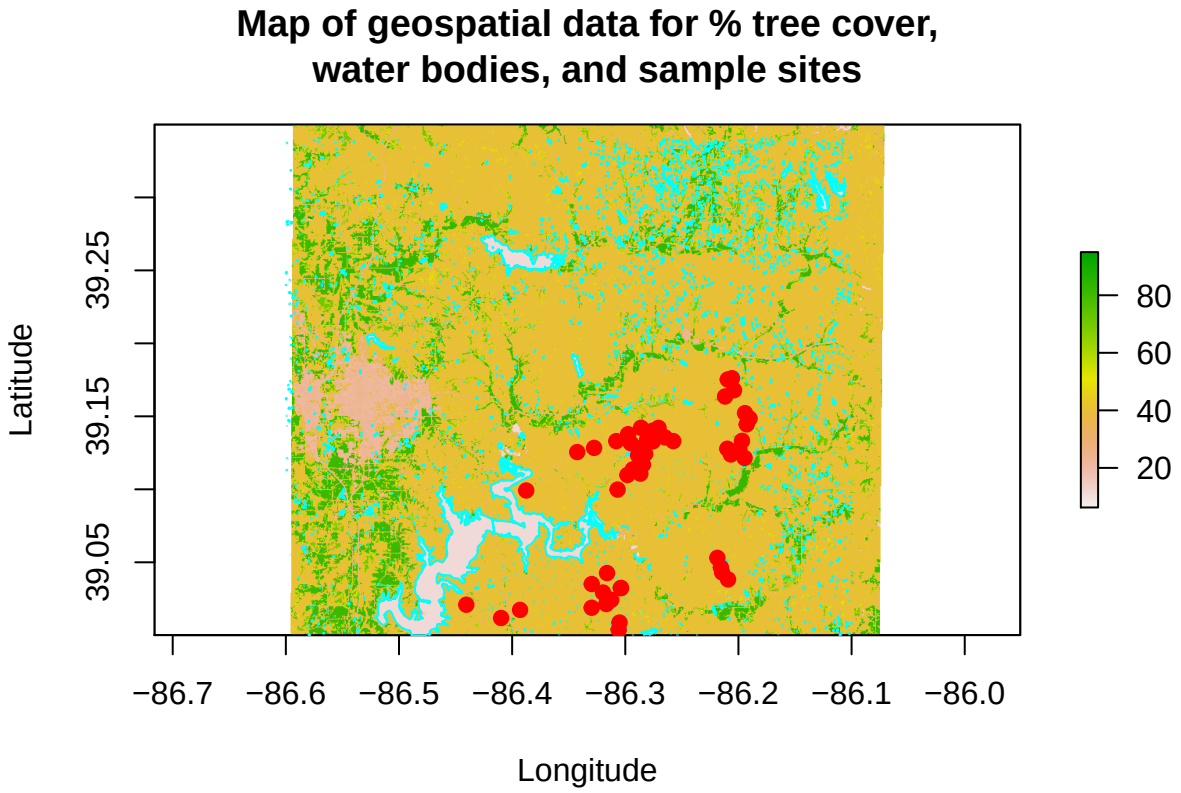
Question 3: Briefly describe the geographical layout of our sites.

> ***Answer 3***: According to this map, the sampling sites are clustered into about five groups. It seems like three of those clusters are around Lake Monroe.The other two clusters are located west of Lake Monroe.

In the R code chunk below, do the following:

1. Using the example in the handout, build a map by combining lat-long data from our ponds with land cover data and data on the locations and shapes of surrounding water bodies.

```
# 1. Import TreeCover.tif as a raster file.
# 2. Plot the % tree cover data
# 3. Import water bodies as a shapefile.
# 4. Plot the water bodies around our study area, i.e., Monroe County.
# 5. Convert lat-long data for ponds to georeferenced points.
# 6. Plot the refuge pond locations

Tree.Cover <- raster("TreeCover/TreeCover.tif") # import TreeCover.tif as a raster file.
plot(Tree.Cover, xlab = 'Longitude', ylab = 'Latitude',
main = 'Map of geospatial data for % tree cover,\nwater bodies, and sample sites')

Water.Bodies <- readShapeSpatial("water/water.shp") # import water bodies as a shapefile.
plot(Water.Bodies, border='cyan', axes = TRUE, add = TRUE)
Refuge.Ponds <- SpatialPoints(cbind(lons, lats)) # convert lat-long data for ponds to georeferenced poi
plot(Refuge.Ponds, line='r', col='red', pch = 20, cex = 1.5, add = TRUE)
```



Question 4a: What are datums and projections?

> ***Answer 4a***: Datum refers to a model for Earth's shape, while a projection is the way in which coordinates on a sphere are projected onto a 2-D surface.

5) UNDERSTANDING SPATIAL AUTOCORRELATION

Question 5: In your own words, explain the concept of spatial autocorrelation.

> ***Answer 5***:Spatial autocorrelation refers to how points can be grouped together or dispersed from each other, which depicts biodiversity over spatial scales. Its is used to determine whether differences in biodiversity among separate areas is due to geographic separation.

6) EXAMINING DISTANCE-DECAY

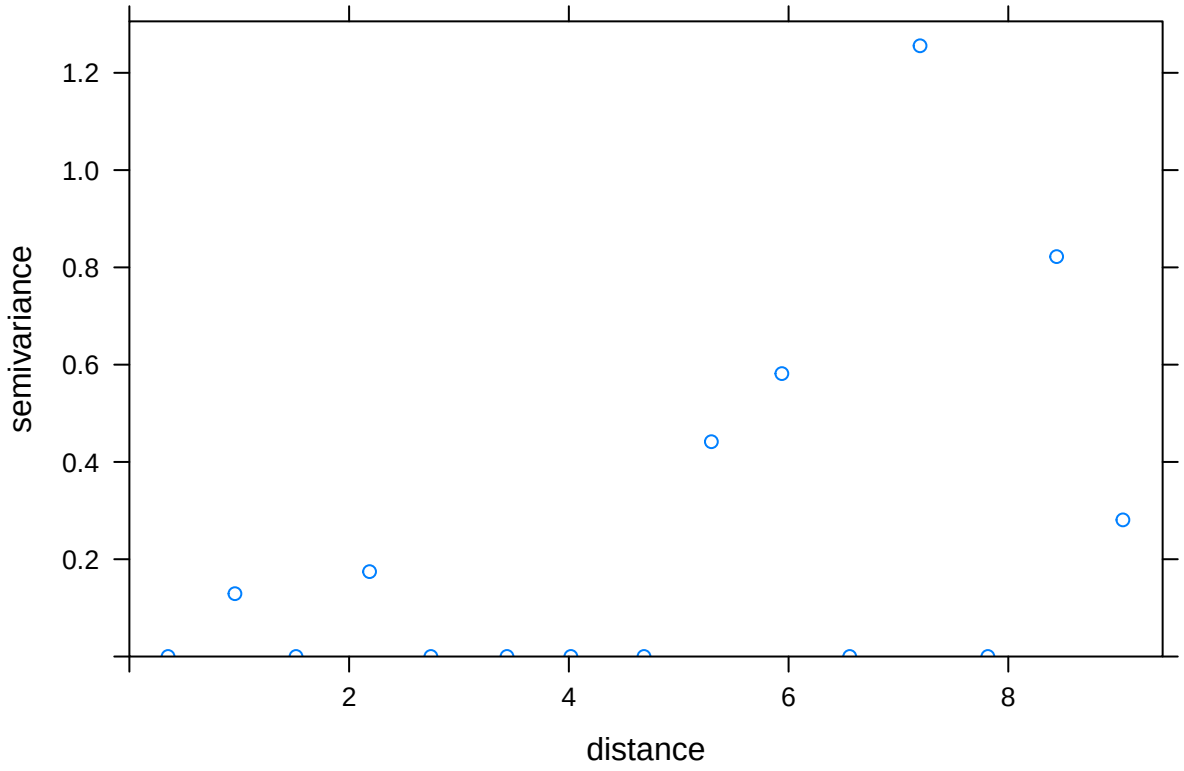
Question 6: In your own words, explain what a distance decay pattern is and what it reveals.

> ***Answer 6***: A distance decay pattern is a plot that shows Bray-Curtis similarity by geographic distance. It shows how similar sites are to one another with relation to distance among sites. For example, a distance decay plot might show that similarity among sites decreases when the distance between sites increases.

In the R code chunk below, do the following:

1. Generate the distance decay relationship for bacterial communities of our refuge ponds and for some of the environmental variables that were measured. Note: You will need to use some of the data transformations within the *semivariogram* section of the handout.

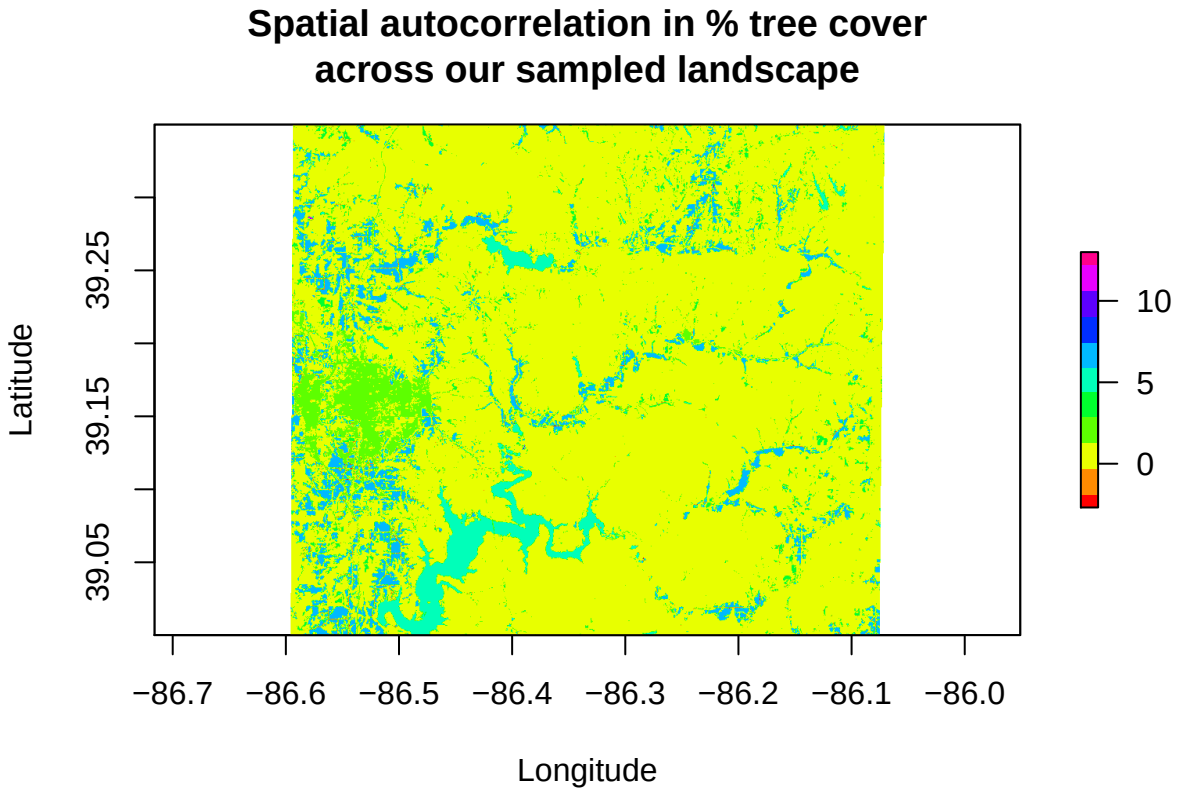
```r
# 1) Calculate Bray-Curtis similarity between plots using the `vegdist()` function
# 2) Assign UTM lattitude and longitude data to 'lats' and 'lons' variables
# 3) Calculate geographic distance between plots and assign to the variable 'coord.dist'
# 4) Transform environmental data to numeric type, and assign to variable 'x1'
# 5) Using the `vegdist()` function in `simba`, calculate the Euclidean distance between the plots for
# 6) Transform all distance matrices into database format using the `liste()` function in `simba`:
# 7) Create a data frame containing similarity of the environment and similarity of community.
# 8) Attach the columns labels 'env' and 'struc' to the dataframe you just made.
# 9) After setting the plot parameters, plot the distance-decay relationships, with regression lines in
# 10) Use `simba` to calculates the difference in slope or intercept of two regression lines

#Construct a new dataframe for coordinates
xy <- data.frame(env = Ponds$TDS, pond.name = Ponds$Sample_ID, lats = Ponds$lat, longs = Ponds$long)
coordinates(xy) <- ~lats+longs # Transform 'xy' into a spatial points dataframe

# Identify the current projection (i.e., lat-long) and datum (NAD83).
proj4string(xy) <- CRS("+proj=longlat +datum=NAD83")
# coordinate reference system (CRS)
# Then, transform the projection and data so we can get meaningful georeferenced distances
UTM <- spTransform(xy, CRS("+proj=utm +zone=51 +ellps=WGS84"))
UTM <- as.data.frame(UTM)
# coordinate reference

xy$lats_utm <- UTM[,2] # lattitude data according to UTM

xy$lons_utm <- UTM[,3] # longitude data according to UTM

#coordinates(xy) = ~lats_utm+lons_utm # Step required by the variogram function
# Examine the semivariance with regards to one of our environmental variables
env.vgm <- variogram(env~1, data=xy)
plot(env.vgm)
```




```
#Moran's I

Moran(Tree.Cover)
```

```
## [1] 0.8378045
```

```
TC.Moran <- MoranLocal(Tree.Cover)

plot(TC.Moran,xlab="Longitude",ylab="Latitude",
main="Spatial autocorrelation in % tree cover\nacross our sampled landscape",
col=rainbow(11,alpha=1))
```




```
#Distance-decay Relationship

comm.dist <-1- vegdist(OTUs) # Bray-Curtis similarity between the plots

lats <- as.numeric(xy$lats_utm) # lattitude data
lons <- as.numeric(xy$lons_utm) # longitude data
coord.dist <- dist(as.matrix(lats, lons)) # geographical distance between plots

# transform environmental data to numeric types
x1 <- as.numeric(Ponds$"SpC")
# calculate the distance (Euclidean) between the plots regarding environmental variables
env.dist <- vegdist(x1,"euclidean") # using the vegdist function in vegan

# transform all distance matrices into database format using the liste function in simba:
comm.dist.ls <- liste(comm.dist,entry="comm")
env.dist.ls <- liste(env.dist,entry="env")
coord.dist.ls <- liste(coord.dist,entry="dist")

#Now, create a data frame containing similarity of the environment and similarity of community.
df <- data.frame(coord.dist.ls, env.dist.ls[,3], comm.dist.ls[,3])

names(df)[4:5] <- c("env","struc")

attach(df)

#Finally, let's plot the Distance-decay relationships, with regression lines in red.
```

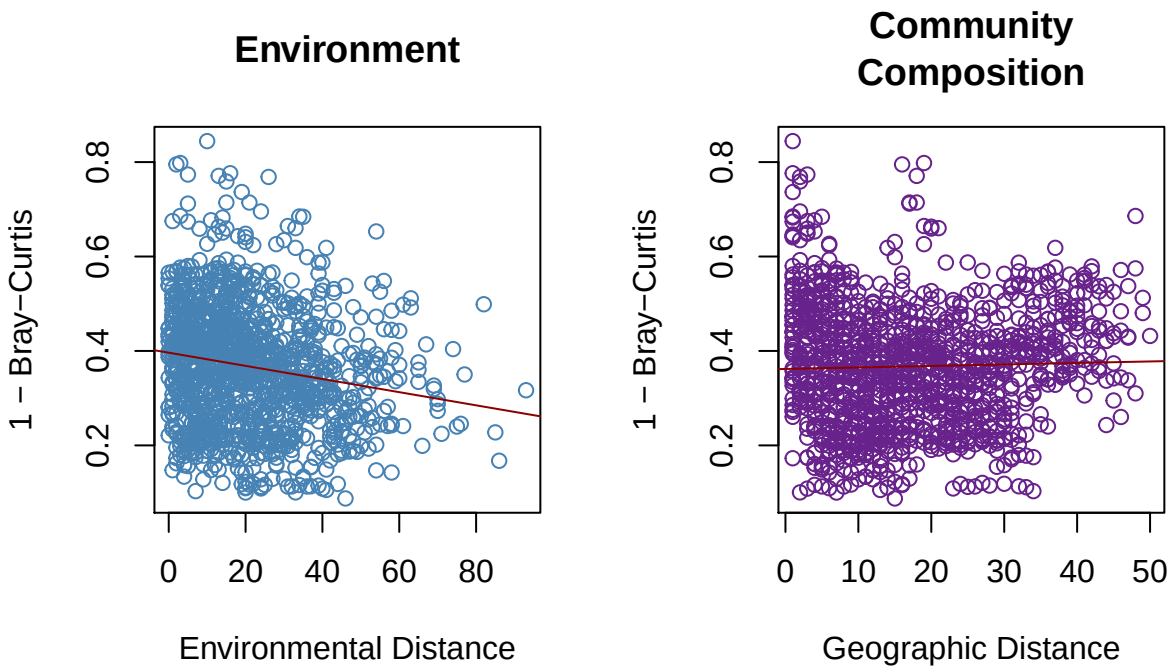
```
par(mfrow=c(1,2),pty="s")
plot(env, struc,xlab="Environmental Distance",ylab="1 - Bray-Curtis",
main ="Environment",col='SteelBlue')

OLS <- lm(struc ~env)

OLS # print regression results to the screen
```

```
##
## Call:
## lm(formula = struc ~ env)
##
## Coefficients:
## (Intercept)          env
##    0.396314    -0.001394
```

```
abline(OLS,col="red4")

plot(dist, struc,xlab="Geographic Distance",ylab="1 - Bray-Curtis",
main="Community\nComposition",col='darkorchid4')

OLS <- lm(struc ~dist)

OLS # print regression results to the screen
```

```
##
## Call:
## lm(formula = struc ~ dist)
##
## Coefficients:
## (Intercept)         dist
##   0.3618550    0.0003184
```

```
abline(OLS,col="red4")
```




```
diffslope(env, struc, dist, struc) # a function in simba that calculates the difference in slope or int
```

```
##
## Is difference in slope significant?
## Significance is based on 1000 permutations
##
## Call:
## diffslope(x1 = env, y1 = struc, x2 = dist, y2 = struc)
##
## Difference in Slope: -0.001712
## Significance: 0.001
##
## Empirical upper confidence limits of r:
##      90%      95%    97.5%      99%
## 0.000425 0.000541 0.000624 0.000697
```

Question 7: What can you conclude about community similarity with regars to environmental distance and geographic distance?

> ***Answer 7***: Community similarity appears to decrease with environmental distance, and increase with geographic distance. Therefore, community similarity is higher with lower environmental distance, and greater geographic distance. The slope of the regression lines for environmental and geographic distances were significantly different as well (p=0.001).

7) EXAMINING SPECIES SPATIAL ABUNDANCE DISTRIBUTIONS

Question 8: In your own words, explain the species spatial abundance distribution and what it reveals.

Answer 8: Spatial abundance distribution shows how species are distributed across a particular site or geographic location. It shows how abundant certain species are in a specific area. Spatial abundance distributions can show the distribution of all species, or specific species of interest.

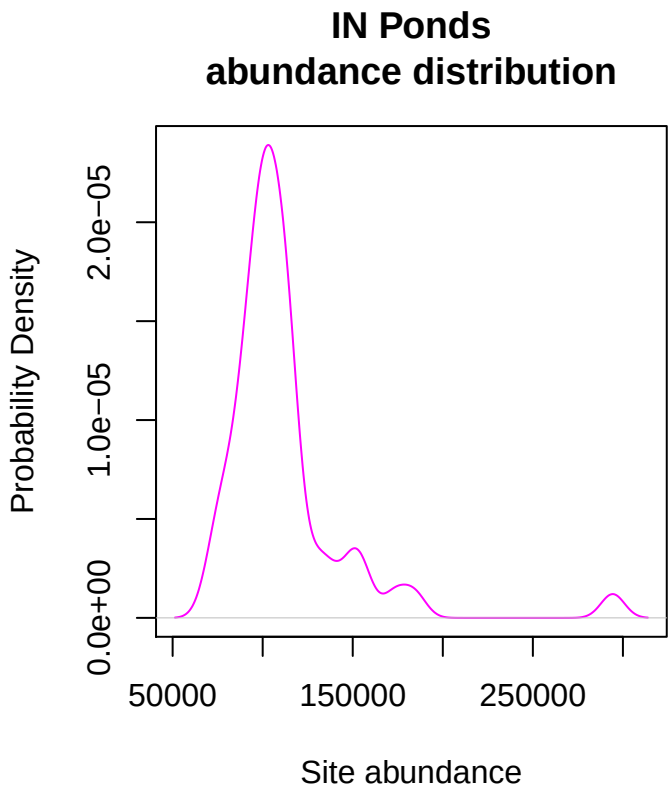
In the R code chunk below, do the following:

1. Define a function that will generate the SSAD for a given OTU.
2. Draw six OTUs at random from the IN ponds dataset and and plot their SSADs as kernel density curves. Use **while loops** and **if** statements to accomplish this.

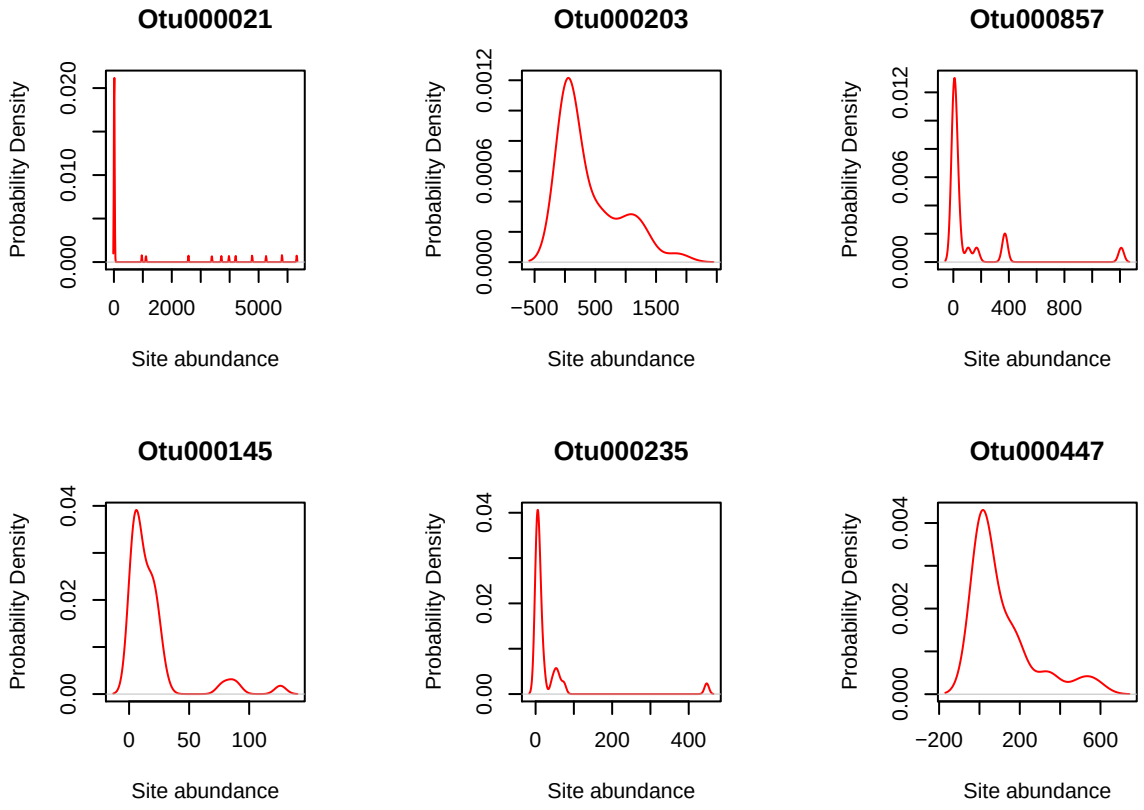
```
# 1. Define an SSAD function
# 2. Set plot parameters
# 3. Declare a counter variable
# 4. Write a while loop to plot the SSADs of six species chosen at random

siteN <- rowSums(OTUs) # Abundances in each plot
siteN
```

```
##  [1] 173194  91490 100595 100306 109561  94396 101579  90070 107097 114167
## [11] 101843 115108 151746  98495 109220 184225 149383  95476 108600 294346
## [21]  82508 108550  99190  78281 109876  91989 100153  85429 106245 117809
## [31] 101640  94125 115895 113251 132327 129936 156408 110889 102649  85770
## [41] 117904 139882 117278 101096  77124  70786  75233 107828 101166  93045
## [51]  89874
```

```
par(mfrow=c(1,1),pty="s")
plot(density(siteN),col = 'magenta',xlab='Site abundance',
ylab='Probability Density',main = 'IN Ponds\nabundance distribution')
```



```
ssad <-function(x){
ad <- c(2,3)
ad <-OTUs[, otu]
ad = as.vector(t(x =ad))
ad =ad[ad >0]
}

par(mfrow=c(2,3))

ct <-0 # a counter variable
while (ct <6){# While the ct variable is less than 4, do ...
otu <- sample(1:length(OTUs),1) # choose 1 random OTU (i.e., a random column of the site-by-species mat
ad <- ssad(otu) # find the OTU's SSAD
if (length(ad) >10& sum(ad >100)){ # if the species is present in at least 10 sites and has an overall
ct <-ct +1
plot(density(ad),col = 'red',xlab='Site abundance',
ylab='Probability Density',main =otu.names[otu])
}
}
```



8) UNDERSTANDING SPATIAL SCALE

Many patterns of biodiversity relate to spatial scale.

Question 9: List, describe, and give examples of the two main aspects of spatial scale

Answer 9: The two main aspects of spatial scale are extent and grain. Extent is the greatest distance/area used in a study, whereas grain refers to the smallest unit of distance measured in a study. An example of extent would be a study site with an area of 50ha, and an example of grain would be a study that used multiple plots, each being 1ha.

9) CONSTRUCTING THE SPECIES-AREA RELATIONSHIP

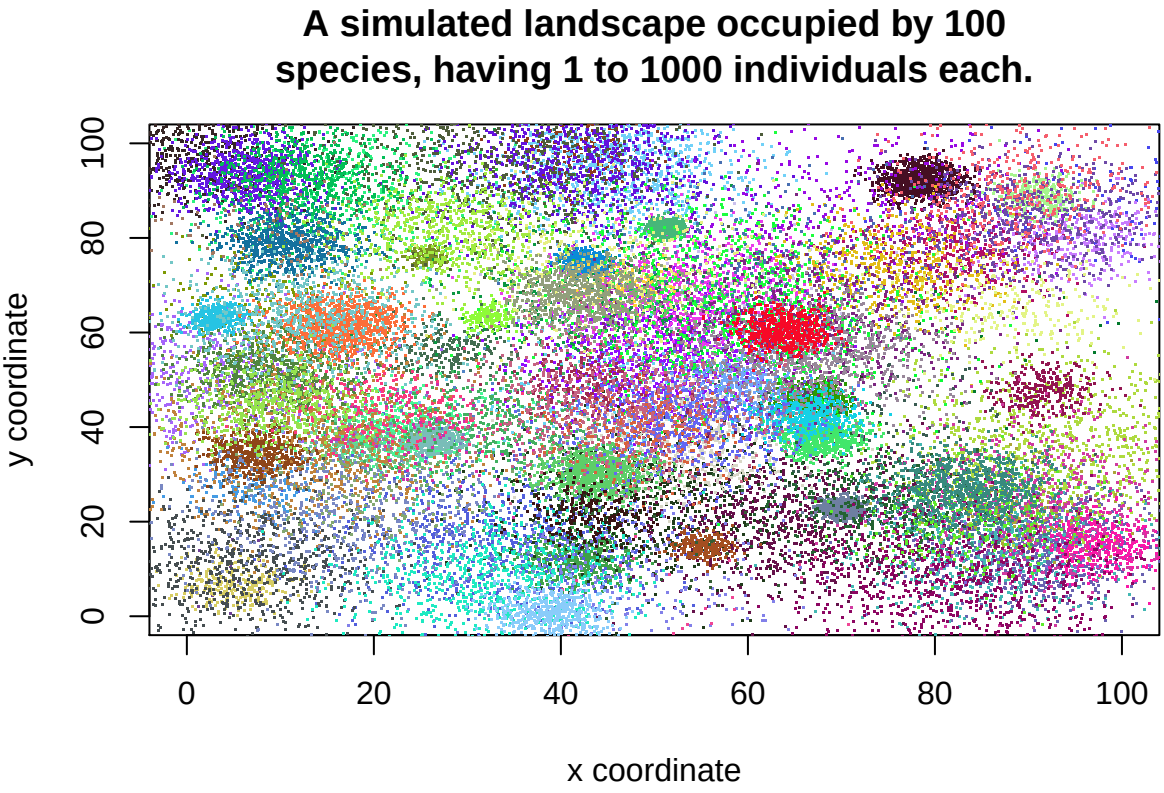
Question 10: In your own words, describe the species-area relationship.

Answer 10: The species-area relationship shows how often a specific species will be found as the sampling area increases.

In the R code chunk below, provide the code to:

1. Simulate the spatial distribution of a community with 100 species, letting each species have between 1 and 1,000 individuals.

```
# 1. Declare variables to hold simulated community and species information
# 2. Populate the simulated landscape

community <- c() # an initiall empty community
species <- c() # with zero species

# initiate the plot, i.e., landscape
plot(0,0,col='white',xlim = c(0,100),ylim = c(0,100),
xlab='x coordinate',ylab='y coordinate',
main='A simulated landscape occupied by 100
species, having 1 to 1000 individuals each.')

while (length(community) <100){ # while the community has less than 100 species
# choose the mean, standard deviation, and species color at random
std <- runif(1,1,10) # random sample from a uniform distribution
ab <- sample(1000,1) # random number between 1 and 1000
x <- rnorm(ab,mean = runif(1,0,100),sd =std) # 1000 random numbers from a Normal distribution
y <- rnorm(ab,mean = runif(1,0,100),sd =std) # 1000 random numbers from a Normal distribution
color <- c(rgb(runif(1),runif(1),runif(1))) # Let each species have a randomly chosen color

points(x, y,pch=".",col=color) # Add points to a plot
species <- list(x, y, color) # The species color, x-coords, and y-coords
community[[length(community)+1]] <-species # Add the species info to the community
}
```



While consult the handout for assistance, in the R chunk below, provide the code to:

1. Use a nested design to examine the SAR of our simulated community.
2. Plot the SAR and regression line.

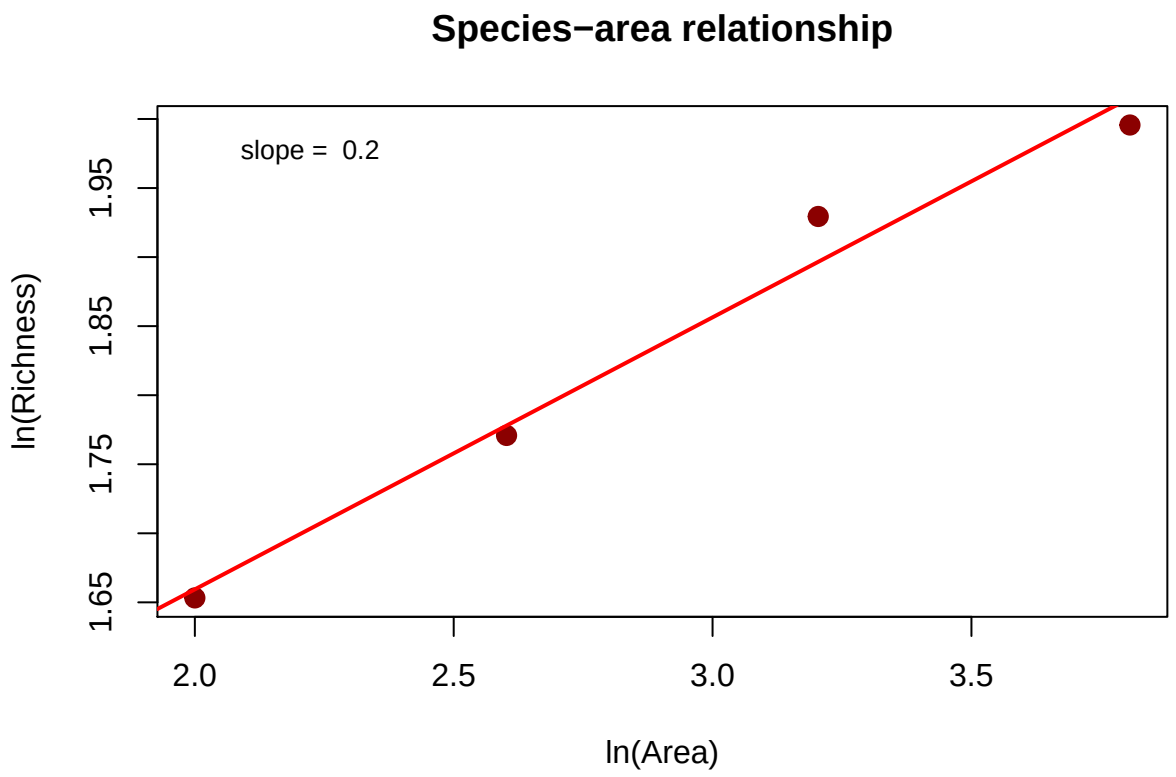
```
# 1. Declare the spatial extent and lists to hold species richness and area data
# 2. Construct a 'while' loop and 'for' loop combination to quantify the numbers of species for progres
# 3. Be sure to log10-transform the richness and area data

lim <-10 # smallest spatial extent. This also equals the spatial grain.
S.list <- c() # holds the number of species
A.list <- c() # holds the spatial scales

while (lim <=100){ # while the spatial extent is less than or equal to 100...
  S <-0 # initiate richness at zero
  for (sp in community){ # for each species in the community
    xs <-sp[[1]] # assign the x coordinates
    ys <-sp[[2]] # assign the y coordinates
    sp.name <-sp[[3]] # assign the species name
    xy.coords <- cbind(xs, ys) # combine the columns for x and y coordinates
    for (xy in xy.coords){ # for each pair of xy coordinates
      if (max(xy) <=lim){ # if the individual is within our current spatial extent...
        S <-S +1 # then the species occurs there
        break
        }
      }
  }
```

```
   # break out of the last for loop because we now know the species occurs inside our samplign }
  S.list <- c(S.list, log10(S))
  A.list <- c(A.list, log10(lim^2))
  lim <-lim *2 # increase the extent multiplicatively
}
```

In the R code chunk below, provide the code to:

1. Plot the richness and area data as a scatter plot.
2. Calculate and plot the regression line
3. Add a legend for the z-value (i.e., slope of the SAR)

```
results <- lm(S.list ~A.list)
plot(A.list, S.list,col="dark red",pch=20,cex=2,
     main="Species-area relationship",
     xlab='ln(Area)',ylab='ln(Richness)')

abline(results,col="red",lwd=2)

int <- round(results[[1]][[1]],2)

z <- round(results[[1]][[2]],2)
legend(x=2,y=2, paste(c('slope = ', z),collapse =" "),cex=0.8,
box.lty=0)
```



Question 10a: Describe how richness relates to area in our simulated data by interpreting the slope of the SAR.

Answer 10a: The slope of the SAR in our simulated model is 0.19, which shows you the degree to which richness will increase with area. It allows you to determine how much richness will increase as area increases.

Question 10b: What does the y-intercept of the SAR represent?

Answer 10b: The y-intercept of the SAR would represent the richness value at the smallest area unit in the study. It would have the smallest richness value as well.

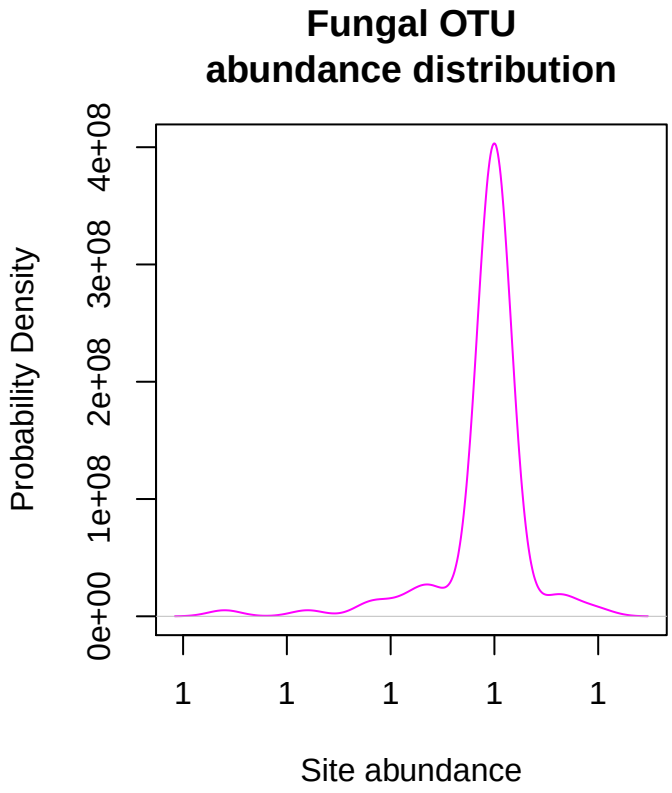
SYNTHESIS

Load the dataset you are using for your project. Plot and discuss either the geogrpahic Distance-Decay relationship, the SSADs for at least four species, or any variant of the SAR (e.g., random accumulation of plots or areas, accumulation of contiguous plots or areas, nested design).

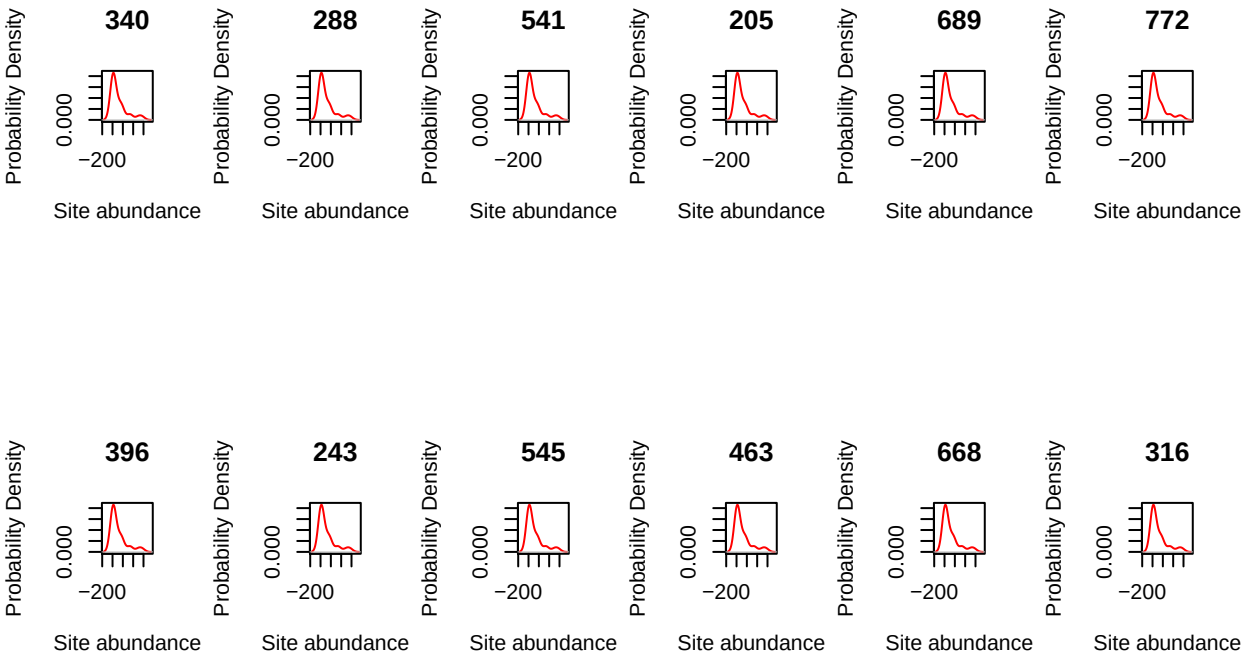
```
#Spatial Abundance Distribution
fungi.data <- read.csv("finalprojectdata1csv.csv", sep = ",", header = TRUE)
fungi.data <- fungi.data[,-1]

siteN1 <- rowSums(fungi.data) # Abundances in each plot
siteN1
```

```
##  [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 1 1 1 1 1 1 1 1 1 1 1
## [36] 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 1 1 1 1 1 1 1 1 1 1
## [71] 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 1 1 1 1
```

```
par(mfrow=c(1,1),pty="s")
plot(density(siteN1),col = 'magenta',xlab='Site abundance',
ylab='Probability Density',main = 'Fungal OTU\nabundance distribution')
```




```
ssad1 <-function(x){
ad <- c(2,3)
ad <-fungi.data
ad = as.vector(t(x =ad))
ad =ad[ad >0]
}

par(mfrow=c(2,6))

ct <-0 # a counter variable
while (ct <12){# While the ct variable is less than 4, do ...
fungi.otu <- sample(1:length(fungi.data),1) # choose 1 random OTU (i.e., a random column of the site-by
ad <- ssad(fungal.otu) # find the OTU's SSAD
if (length(ad) >10& sum(ad >100)){ # if the species is present in at least 10 sites and has an overall
ct <-ct +1
plot(density(ad),col = 'red',xlab='Site abundance',
ylab='Probability Density',main =fungi.otu)
}
}
```



The species spatial distribution curve with all OTUs from our data set is not very helpful because the data is presesnted as relative abundances. Therefore, all of the x-axis values are 1. I also selected various random OTUs from the dataset, an dplotted their spatial distribution curves. All of the OTUs that I randomly sampled seem to be have a higher probability of being sampled when total site abundance is relatively low (50-100). This might indicate that these OTUs are relatively rare.