

Module “4”: Lab 1

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Species Richness

Today, we will be working with community data to calculate species richness, plot species accumulation curves, and calculate our estimate of species richness.

Set-Up

For today’s lab and assignment, we will need to load a new package called **vegan**. I’ve already installed the package on Posit Cloud, so we only need to load it into our work space.

```
library(vegan)
```

The **vegan** package is one of the most popular packages available for working with community-level data. It includes functions for many multivariate analyses commonly used in the analysis of ecological communities. We will be using it today for its species accumulation curve functions.

Community Data

For this example, we are going to use a dataset that is included with R already called BCI. This dataset is from a long-term research site in Panama run by the Smithsonian called Barro Colorado Island set up to monitor forest dynamics.

We can use the **data()** function to bring it into our environment.

In your assignment, you will use the **read.csv()** function, as usual.

```
data(BCI)
```

We can use the **head()** function to take a look at the data frame.

```
# 50 rows, each corresponding to a different plot  
# 225 column, each for a different species  
# head(BCI)
```

The concepts of spatial and temporal replication apply not only to “capture-recapture” analyses of species richness, but also for species accumulation curves. Would we consider this spatial or temporal replication?

First, let’s run our plot by species matrix through the **specaccum()** function to prepare the data to be put into a species accumulation curve model.

You will get a warning; no need to be concerned.

```
BCI_sac <- specaccum(BCI)
```

```
## Warning in cor(x > 0): the standard deviation is zero
```

```
BCI_sac
```

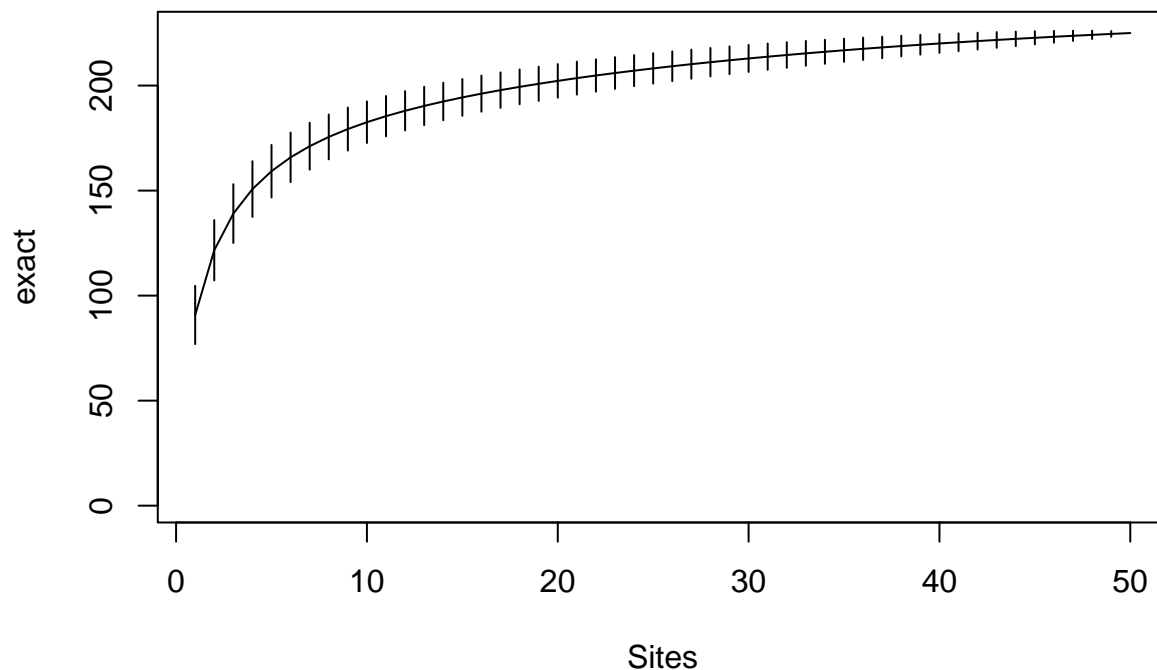
```
## Species Accumulation Curve
## Accumulation method: exact
## Call: specaccum(comm = BCI)
##
##
## Sites      1.00000  2.00000  3.00000  4.00000  5.00000  6.00000  7.00000
## Richness 90.78000 121.60980 139.04587 150.71157 159.23634 165.83062 171.14214
## sd       6.93481  7.19336  7.00199  6.63577  6.24812  5.89474  5.59124
##
## Sites      8.00000  9.00000 10.00000 11.00000 12.00000 13.00000 14.00000
## Richness 175.55318 179.30561 182.56044 185.42917 187.99142 190.30560 192.4155
## sd       5.33703  5.12587  4.95014  4.80256  4.67674  4.56741  4.4703
##
## Sites      15.00000 16.00000 17.00000 18.00000 19.00000 20.00000 21.00000
## Richness 194.35454 196.14879 197.81879 199.38098 200.84871 202.23287 203.54250
## sd       4.38202  4.29995  4.22206  4.14681  4.07304  3.99989  3.92675
##
## Sites      22.00000 23.00000 24.00000 25.00000 26.00000 27.00000 28.00000
## Richness 204.78512 205.96707 207.09370 208.16959 209.19868 210.18438 211.12965
## sd       3.85313  3.77873  3.70328  3.62663  3.54864  3.46921  3.38823
##
## Sites      29.00000 30.00000 31.00000 32.00000 33.00000 34.00000 35.00000
## Richness 212.03708 212.9090 213.74738 214.55410 215.33078 216.07889 216.79978
## sd       3.30563  3.2213  3.13514  3.04702  2.95678  2.86426  2.76922
##
## Sites      36.00000 37.00000 38.00000 39.00000 40.00000 41.00000 42.00000
## Richness 217.49467 218.16469 218.81087 219.43418 220.03550 220.61567 221.17546
## sd       2.67142  2.57053  2.46617  2.35786  2.24501  2.12687  2.00249
##
## Sites      43.00000 44.00000 45.00000 46.00000 47.00000 48.00000 49.00000
## Richness 221.71561 222.23680 222.73968 223.22488 223.69296 224.1445 224.58000
## sd       1.87058  1.72938  1.57635  1.40765  1.21639  0.9916  0.69541
##
## Sites      50
## Richness 225
## sd       0
```

How do we interpret this output?

Plot the Species Abundance Curve

Plot the species abundance curve based on the *observed* data.

```
plot(BCI_sac)
```



What does this plot tell us?

Estimating Species Richness

While the `specaccum()` function gives us the data site by site so we can plot the species accumulation curve, we can use the `specpool()` function to find our overall values, both for *observed* species richness and our estimated species richness.

The output of `specpool()` will give us the estimates from several different estimators. We are going to use the *chao* estimator.

```
BCI_richness <- specpool(BCI)
BCI_richness
```

```
##      Species      chao chao.se jack1 jack1.se   jack2      boot boot.se  n
## All      225 236.3732 6.54361 245.58 5.650522 247.8722 235.6862 3.468888 50
```

Let's save our observed species richness and estimated species richness as objects to reference later. We can use the `$` operator to reference each value by name.

```
BCI_observed <- BCI_richness$Species
BCI_observed
```

```
## [1] 225
```

```
BCI_estimated <- BCI_richness$chao
BCI_estimated
```

```
## [1] 236.3732
```

Based on our estimated and observed richness values, how many species does the model think are present but we failed to observe?

```
BCI_estimated - BCI_observed
```

```
## [1] 11.37316
```

Plotting the Estimate

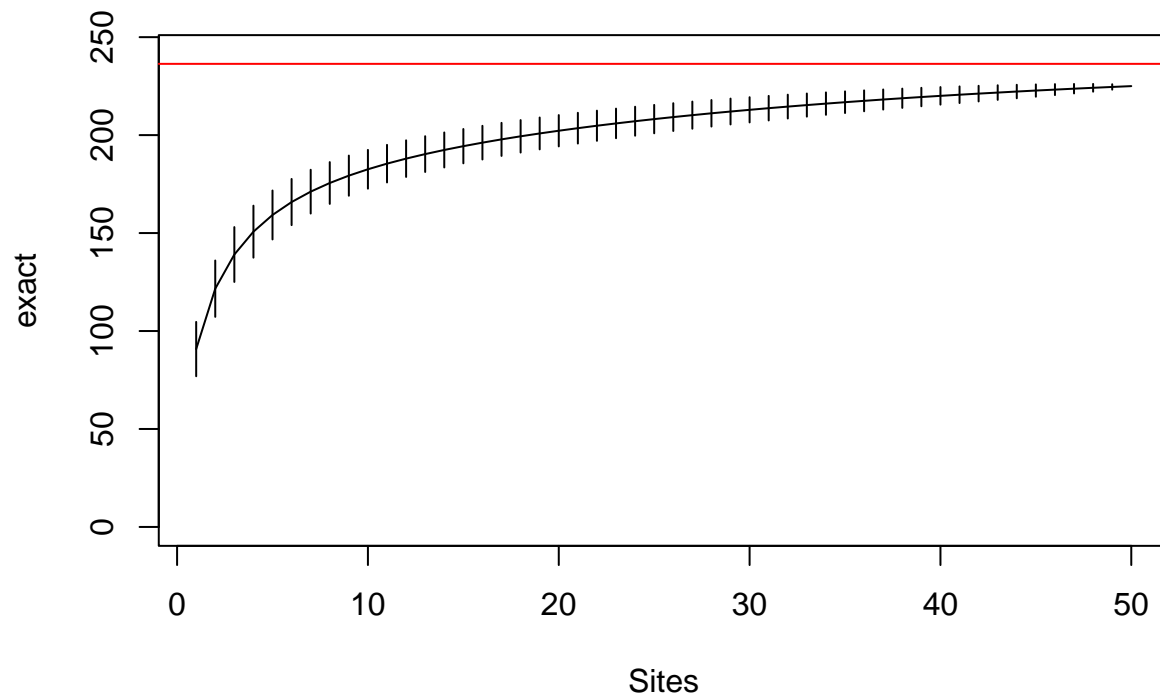
Let's add a horizontal line in our species accumulation curve plot to compare against our curve.

First, we will need to make sure that the range of the y-axis on the plot goes high enough to show our estimated richness line. We can do this by setting the `ylim` argument to run from 0 to the estimated richness plus a few extra for good measure.

We can then use the `abline()` function to add a horizontal line. We set the `h` argument equal to the estimated richness value. We can also change the color of this line by setting the `col` argument.

One quirky thing about plotting this way is that both lines of code have to be run together for the plot to successfully be created. The easiest way to do this is by hitting the green run arrow on the code chunk.

```
plot(BCI_sac, ylim = c(0, BCI_estimated + 5))  
abline(h = BCI_estimated, col = "red")
```



How do we interpret this plot?