

Module “4”: Assignment 1

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Assignment Details

Purpose

The goal of this assignment is to understand, apply, and interpret detection probability in estimating densities through distance sampling.

Task

Write R code to successfully answer each question below or write text to successfully answer the question.

Criteria for Success

- Code is within the provided code chunks
- Code chunks run without errors
- Code produces the correct result
 - Code attempts will get half points
 - Code that produces the correct answer will receive full points
- Text answers correctly address the question asked

Due Date

December 5 at midnight MST

Assignment Questions

All questions are worth 1 point unless otherwise specified.

Set-Up

We are going to need to load the community ecology package, **vegan**.

```
library(vegan)
```

Species Accumulation Curves

For this section of the assignment, we are going to use a survey x species matrix for trail cameras along the Santa Cruz River.

```
scr <- read.csv("../data_raw/SCR_camera_data.csv")
```

1. First, use the `specaccum()` function to prep the data for the species accumulation curve model.

```
# A warning is fine!  
scr_sac <- specaccum(scr)
```

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

2. Next, fit a species accumulation model to the data.

```
scr_sac_fit <- fitspecaccum(scr_sac, model = "asympt")
```

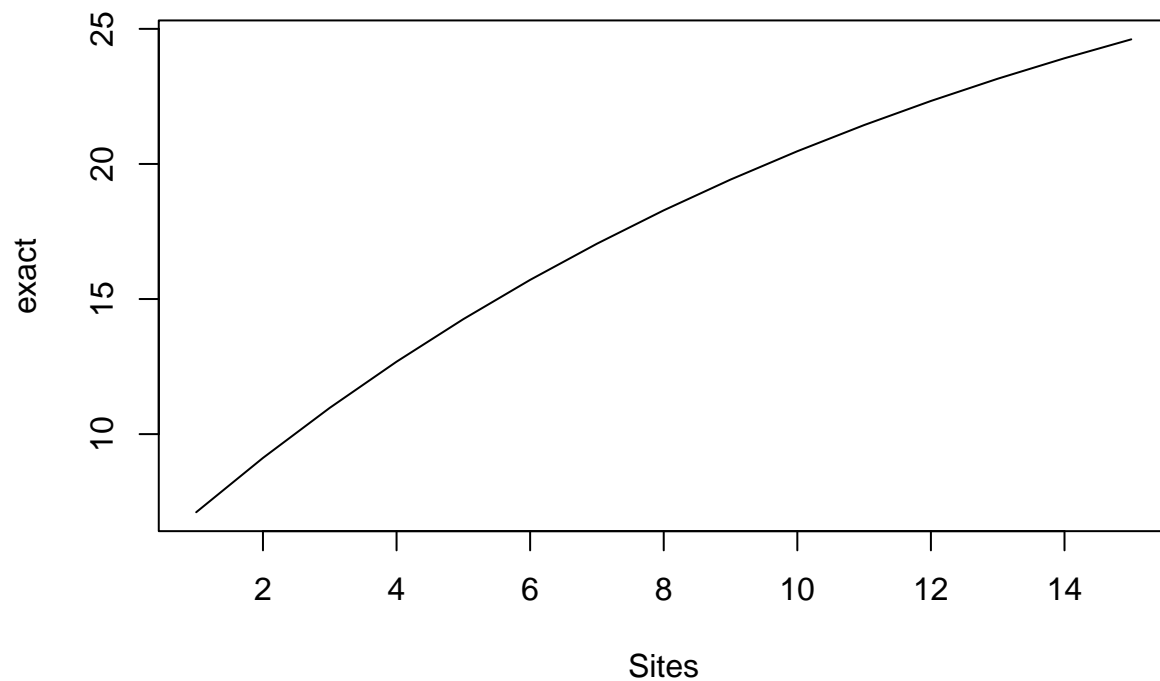
3. What is the predicted asymptote for this data?

```
coef(scr_sac_fit)
```

```
##      Asym      R0      lrc  
## 32.879079  4.928119 -2.510697
```

4. Let's plot species accumulation curve model.

```
plot(scr_sac_fit)
```



5. Based on the predicted asymptote, the number of species we have in the dataset, and the plot you just made, what can we conclude? (2 points)

Answer: We have not done enough sampling to find all of the species likely present in the community, since our dataset only has 25 species and our curve has not yet reached the asymptote (32.8)

Species Richness and Diversity Indices

For the rest of our calculations, we are going to compare 2 communities. I've written code below to create those communities.

```
comm1 <- data.frame(species = c("DO", "DM", "SO", "SH", "SF", "PP", "PB", "BA"),
                    individuals = c(14, 89, 30, 12, 3, 3, 8, 23))
comm2 <- data.frame(species = c("DO", "DM", "SO", "SH", "SF"),
                    individuals = c(37, 32, 30, 44, 39))
```

Species Richness

6. Use code to calculate the species richness of each community. Which community is more species rich?

```
nrow(comm1)
```

```
## [1] 8
```

```
nrow(comm2)
```

```
## [1] 5
```

Shannon Diversity Index

We are going to start with `comm1`.

7. Write a line of code to calculate the number of individuals in the first community. Use this to create the object `total_comm1`.

```
total_comm1 <- sum(comm1$individuals)
total_comm1
```

```
## [1] 182
```

8. Add a column to the `comm1` data frame with each species' proportion of the community.

```
comm1$prop <- comm1$individuals / total_comm1
```

9. Now add a column with the natural logs of the proportions.

```
comm1$ln_prop <- log(comm1$prop)
```

10. Add a column with the result of the proportion of the community multiplied by the natural log.

```
comm1$prop_lnprop <- comm1$prop * comm1$ln_prop
```

11. Calculate the Shannon Index for this community.

```
H_comm1 <- sum(comm1$prop_lnprop * -1)
H_comm1
```

```
## [1] 1.557667
```

12. Now that you've worked your way through calculating the Shannon Index for community 1, calculate it for community 2.

```
total_comm2 <- sum(comm2$individuals)
comm2$prop <- comm2$individuals / total_comm2
comm2$ln_prop <- log(comm2$prop)
comm2$prop_lnprop <- comm2$prop * comm2$ln_prop
H_comm2 <- sum(comm2$prop_lnprop) * -1
H_comm2
```

```
## [1] 1.600014
```

13. Which community is more diverse, according to the Shannon Diversity Index? How do you know? (2 points)

Answer: Community 2 has the higher value and is therefore considered more diverse

Simpson Diversity Index

Fortunately, a lot of the work has already been done to calculate the Simpson Diversity Index. We only need to add a little bit more to get there.

14. Add another column to the `comm1` data frame that has the squared proportion.

```
comm1$prop_sq <- comm1$prop * comm1$prop
```

15. Calculate the Simpson Diversity Index for community 1

```
D1 = 1 - sum(comm1$prop_sq)
D1
```

```
## [1] 0.7049873
```

16. Now calculate the Simpson Index for community 2

```
comm2$prop_sq <- comm2$prop * comm2$prop
D2 = 1 - sum(comm2$prop_sq)
D2
```

```
## [1] 0.7962203
```

17. Do the values you've calculated for the Simpson Index corroborate your answer for which community is more diverse? Why or why not? Does this correspond to the community to the highest richness? (2 points)

Answer: Yes, the Simpson's index corroborates the Shannon index in terms of diversity—Community 2 has the higher value in both cases, meaning it is the more diverse. This is different from species richness, however, in that Community 1 has higher richness.