

# Module “4”: Assignment 1

Ellen Bledsoe

2025-05-05

## Assignment Details

### Purpose

The goal of this assignment is to work with community data to calculate observed and estimated species richness and plot species accumulation curves.

### 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

May 12 at midnight MST

---

## Assignment Questions

All questions are worth 1 point unless otherwise specified.

We are going to compare two different communities in this assignment.

### Set-Up

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

```
library(vegan)
```

## Community 1

For our first community in this assignment, we are going to use a site x species matrix for trail cameras along the Santa Cruz River.

2. Use the `read.csv()` function to bring in the SCR trail camera data (called `SCR_camera_data.csv`)

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

3. First, use the `head()` function to take a look at the dataset.

```
head(scr)
```

```
## homo_sapien canis_familiaris felis_catus canis_latrans
## 1          3                0          0          18
## 2         10                5          1         103
## 3         47                2          1          21
## 4         28               10          0          41
## 5        114               16          0          40
## 6         14                0          2           2
## geococcyx_californianus pecari_tajacu spermophilus_tereticaudus
## 1                0                0                0
## 2                3                2                0
## 3                1                2                0
## 4                0                0                0
## 5                8                4                0
## 6                0               10                0
## sylvilagus_audubonii lepus_californicus haemorhous_mexicanus lynx_rufus
## 1                47                3                0                0
## 2                77                0                0                0
## 3                48                0                0                0
## 4                 6                0                0                0
## 5               55                0                2                2
## 6               67                0                0                4
## procyon_lotor equus_caballus pipilo_aberti otospermophilus_variegatus
## 1                0                0                0                0
## 2                0                0                0                0
## 3                0                1                0                0
## 4                0                3                0                0
## 5                2                0                0                0
## 6                0                0                8               32
## spilogale_putorius butorides_virescens zonotrichia_leucophrys ardea_herodias
## 1                0                0                0                0
## 2                0                0                0                0
## 3                0                0                0                0
## 4                0                0                0                0
## 5                0                1                0                0
## 6                0                0                2                0
## anas_platyrhynchos sayornis_nigricans accipiter_cooperii neotoma_sp
```

```
## 1      0      0      0      0
## 2      0      0      0      0
## 3      0      0      0      0
## 4      0      0      0      0
## 5      0      0      0      0
## 6      0      1      0      1
##  junco_hyemalis campylorhynchus_brunneicapillus
## 1      0      0
## 2      0      0
## 3      0      0
## 4      0      0
## 5      0      0
## 6      1      0
```

4. How many sites were surveyed? How many species were seen?

*Sites: 15 Species: 25*

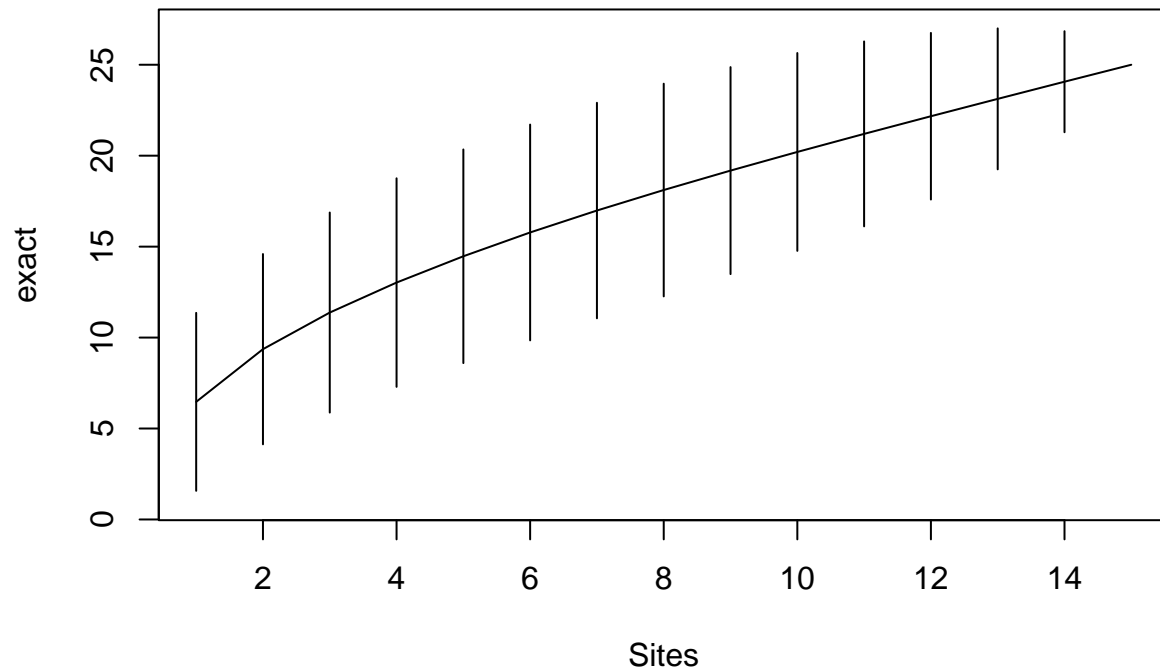
5. Use the `specaccum()` function to prep the data for the species accumulation curve.

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

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

6. Next, plot the species accumulation curve based on our observed data.

```
plot(scr_sac)
```



7. Use the `specpool()` function to calculate the estimated species richness.

```
scr_richness <- specpool(scr)
scr_richness
```

```
##      Species      chao  chao.se    jack1 jack1.se    jack2      boot boot.se  n
## All         25 116.4667 104.1535 38.06667 6.191033 49.39524 30.15487 2.9969 15
```

8. Save the observed species richness and estimated species richness values as objects. You the `$` operator to reference specific named values from the `scr_richness` object.

```
scr_observed <- scr_richness$Species
scr_observed
```

```
## [1] 25
```

```
scr_estimated <- scr_richness$chao
scr_estimated
```

```
## [1] 116.4667
```

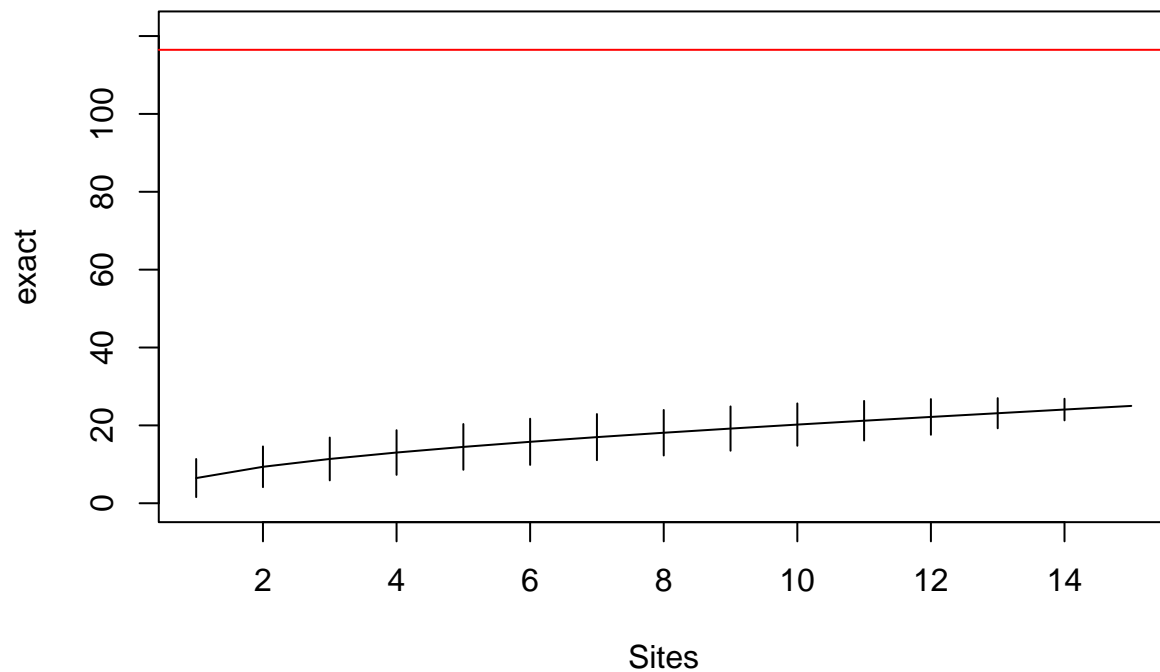
9. Based on the Chao estimator, how many species are present but we did not observe?

```
scr_estimated - scr_observed
```

```
## [1] 91.46667
```

10. Now, let's add our estimated species richness to our species accumulation curve. Remember to set the y-axis range appropriately and to run the `plot()` and `abline()` functions together.

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



11. Interpret the plot you just made. What is the predicted asymptote value? How does it relate to our species accumulation curve? What does that mean?

*Answer:* With an estimated species richness of >116 compared to an observed richness of 25, it appears we have not sampled nearly enough to see all of the possible species in the community.

## Community 2

12. Now, bring in the data for our second community, fish species from the Doubs River in France.

```
fish <- read.csv("../data_raw/Doubs_fish.csv")
```

13. Use the `head()` function to take a look at the dataset.

```
head(fish)
```

```
##   CHA TRU VAI LOC OMB BLA HOT TOX VAN CHE BAR SPI GOU BRO PER BOU PSO ROT CAR
## 1   0   3   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0
## 2   0   5   4   3   0   0   0   0   0   0   0   0   0   0   0   0   0   0
## 3   0   5   5   5   0   0   0   0   0   0   0   0   0   1   0   0   0   0
## 4   0   4   5   5   0   0   0   0   0   1   0   0   1   2   2   0   0   0
## 5   0   2   3   2   0   0   0   0   5   2   0   0   2   4   4   0   0   2
## 6   0   3   4   5   0   0   0   0   1   2   0   0   1   1   1   0   0   0
##   TAN BCO PCH GRE GAR BBO ABL ANG
## 1   0   0   0   0   0   0   0   0
## 2   0   0   0   0   0   0   0   0
## 3   0   0   0   0   0   0   0   0
## 4   1   0   0   0   0   0   0   0
## 5   3   0   0   0   5   0   0   0
## 6   2   0   0   0   1   0   0   0
```

In this dataset, each row represents a survey occasion rather than a site.

14. Use the `specaccum()` function to prep the data for the species accumulation curve.

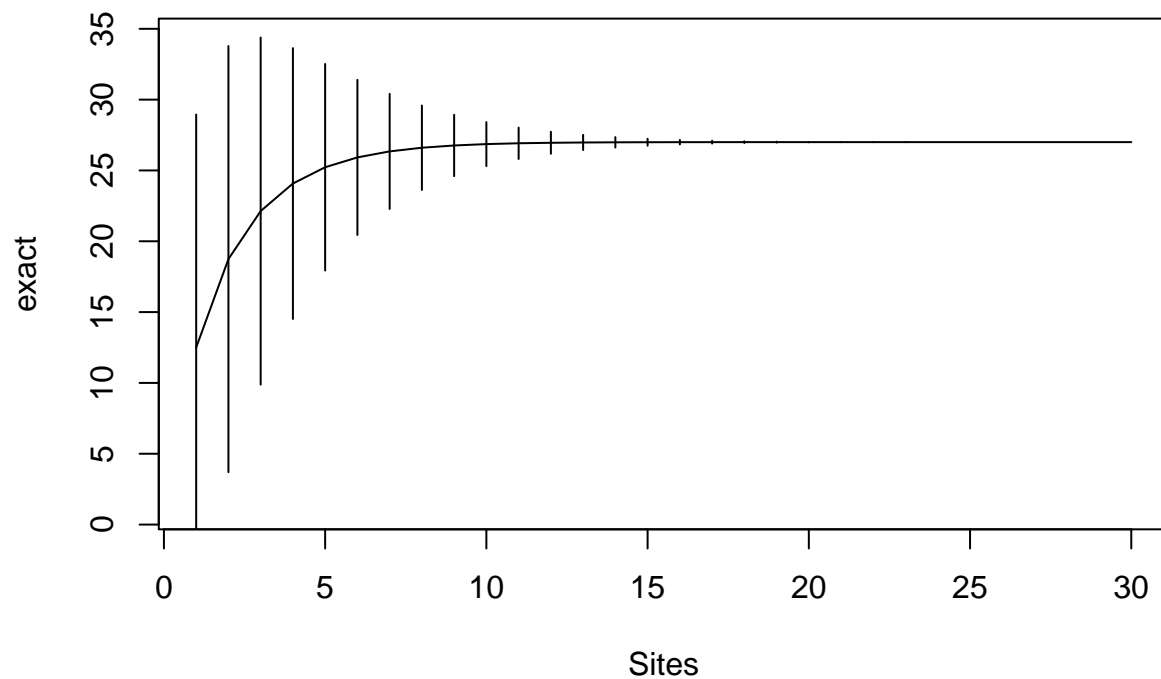
```
# A warning is fine!
fish_sac <- specaccum(fish)
fish_sac
```

```
## Species Accumulation Curve
## Accumulation method: exact
## Call: specaccum(comm = fish)
##
##
## Sites      1.000000  2.000000  3.000000  4.000000  5.000000  6.000000  7.000000
## Richness 12.500000 18.742529 22.133498 24.076665 25.226910 25.921113 26.344608
## sd        8.224962  7.521837  6.125741  4.780134  3.645886  2.738364  2.032045
##
## Sites      8.000000  9.000000 10.000000 11.000000 12.000000 13.000000 14.000000
## Richness 26.604116 26.763081 26.860035 26.918697 26.953776 26.974418 26.986307
```

```
## sd      1.491678  1.083656  0.778985  0.553784  0.388989  0.269569  0.183966
##
## Sites    15.000000 16.00000 17.000000 18.000000 19.000000 20.000000 21.000000
## Richness 26.992969 26.99657 26.998432 26.999339 26.999749 26.999917 26.999978
## sd      0.123247  0.08070  0.051322  0.031424  0.018253  0.009885  0.004868
##
## Sites    22.000000 2.30e+01 24 25 26 27 28 29 30
## Richness 26.999996 2.70e+01 27 27 27 27 27 27 27
## sd      0.002031 7.01e-04 0 0 0 0 0 0 0
```

15. Next, plot the species accumulation curve based on our observed data.

```
plot(fish_sac)
```



16.

Use the `specpool()` function to calculate the estimated species richness.

```
fish_richness <- specpool(fish)
fish_richness
```

```
##      Species chao chao.se jack1 jack1.se jack2      boot      boot.se n
## All      27    27        0    27        0    27 27.00065 0.02849795 30
```

17. Save the observed species richness and estimated species richness values as objects. You the `$` operator to reference specific named values from the `scr_richness` object.

```
fish_observed <- fish_richness$Species
fish_observed
```

```
## [1] 27
```

```
fish_estimated <- fish_richness$chao
fish_estimated
```

```
## [1] 27
```

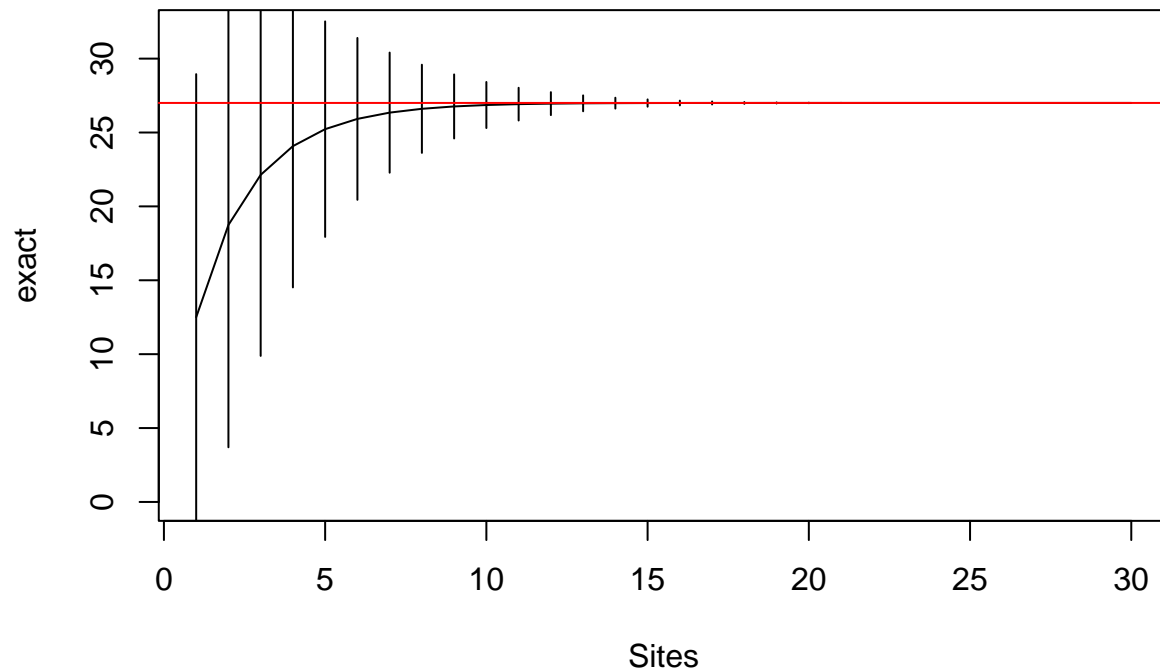
18. Based on the Chao estimator, how many species are present but we did not observe?

```
fish_estimated - fish_observed
```

```
## [1] 0
```

19. Now, let's add our estimated species richness to our species accumulation curve. Remember to set the y-axis range appropriately and to run the `plot()` and `abline()` functions together.

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



20. Interpret the plot you just made. How does community 2 differ from community 1? How does our sampling differ between community 1 and community 2?

*Answer:* This community likely does not have any species which we have not observed, because the species accumulation curve has hit an asymptote and the estimated richness is the same as the observed. This is in complete contrast to community 1, which would require much more sampling to observe all of the species estimated.