

6. Worksheet: Diversity Sampling

Emmi Mueller; Z620: Quantitative Biodiversity, Indiana University

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OVERVIEW

In this worksheet, you will use the jelly bean site-by-species matrix generated from **6. Diversity Sampling**. Along with tools outlined in the **5. Local (alpha) Diversity** and **7. Control Structures** handouts, you will develop questions, visualize data, and test hypotheses related to sampling effects and its effect on estimates of within-sample biodiversity.

Directions:

1. In the Markdown version of this document in your cloned repo, change “Student Name” on line 3 (above) to your name.
2. Complete as much of the worksheet as possible during class.
3. Refer to previous handout to help with developing of questions and writing of code.
4. Answer questions in the worksheet. 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 “>”. You should notice that the answer is highlighted in green by RStudio (color may vary if you changed the editor theme).
5. Before you leave the classroom, **push** this file to your GitHub repo.
6. For the assignment portion of the worksheet, follow the directions at the bottom of this file.
7. When you are done, **Knit** the text and code into a PDF file.
8. After Knitting, submit the completed exercise by creating a **pull request** via GitHub. Your pull request should include this file `6.DiversitySampling_Worskheet.Rmd` and the PDF output of Knitr (`DiversitySampling_Worskheet.pdf`).

1) Group brainstorming

With your team partner and perhaps other students in the class, spend 15 minutes or so brainstorming questions, code, “fantasy figures”, and statistical tests that could be used to test questions with the class’s data represented in the site-by-species matrix that you have generated.

2) Code

Use the space below for code that is being used to analyze your data and test your hypotheses. Create one (and only one, although it can have multiple panels) *publication quality* figure. Make sure to annotate your code using # symbols so others (including instructors) understand what you have done and why you have done it.

```
#Clear workspace, set working directory and load packages
rm(list=ls())
getwd()
```

```
## [1] "C:/Users/emmim/GitHub/QB2019_Mueller/2.Worksheets/6.DiversitySampling"
setwd("~/GitHub/QB2019_Mueller/2.Worksheets/6.DiversitySampling")
require("vegan")
```

```
## Loading required package: vegan
```

```
## Loading required package: permute
```

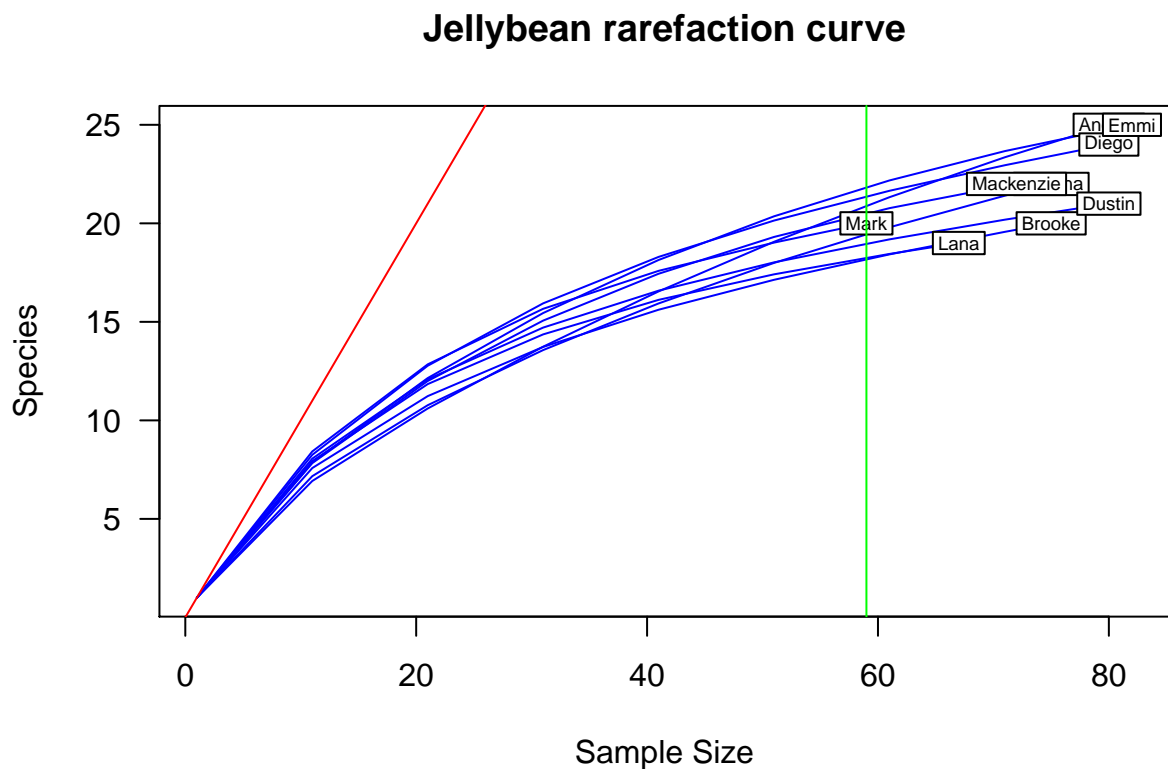
```
## Loading required package: lattice
## This is vegan 2.5-3
require("ggplot2")

## Loading required package: ggplot2
#Load Jelly Bean dataset, declare groups and remove group row from table

jellybean <- read.table("./JellyBeans_site.txt", sep = "\t", header = TRUE, row.names = 1)
jellybeangroups <- as.data.frame(jellybean["Group"])
jellybean <- jellybean[,2:29]

#Create function S.obs and print the species number found by group
S.obs <- function(x = ""){
  rowSums(x > 0) * 1
}
C <- function(x = ""){
  1 - (rowSums(x == 1) / rowSums(x))
}

#Rarefaction curve
min.N <- min(rowSums(jellybean))
jelly.rarefy <- rarefy(x = jellybean, sample = min.N, se = TRUE)
rarecurve(x = jellybean, step = 10, col = "blue", cex = 0.6, las = 1, main = "Jellybean rarefaction curve")
abline(0,1, col = 'red')
abline(v = min.N, col = 'green')
```



```

#Rarefy sample and generate Group samples
jelly.rarefied <- rrarefy(x = jellybean, sample = min.N)
x <- rep(0, ncol(jelly.rarefied))
names <- row.names(jelly.rarefied)
jelly.rarefied <- rbind(x, jelly.rarefied)
jelly.rarefied <- rbind(x, jelly.rarefied)
row.names(jelly.rarefied) <- c("GroupA", "GroupB", names)
for(column in colnames(jelly.rarefied)){
  for (row in rownames(jelly.rarefied)){
    if (row == "GroupA" || row == "GroupB"){
      else if (jellybeangroups[row,] == "A"){
        jelly.rarefied["GroupA", column] <- jelly.rarefied["GroupA", column] + jelly.rarefied[row, column]
      }
      else if (jellybeangroups[row,] == "B"){
        jelly.rarefied["GroupB", column] <- jelly.rarefied["GroupB", column] + jelly.rarefied[row, column]
      }
    }
  }
}

#Print rarefied sample individuals, species richness, and coverage
jelly.rarefied <- as.data.frame(jelly.rarefied)
for (row in row.names(jelly.rarefied)){
  if (row == "GroupA"){
    cat("\n", row)
    cat("Individuals:", as.numeric(rowSums(jelly.rarefied[row,])), " ")
    cat("Species:", as.numeric(S.obs(jelly.rarefied[row,])), " ")
    cat("Coverage:", as.numeric(C(jelly.rarefied[row,])), "\n")
  }
  else if (row != "GroupB" && jellybeangroups[row, ] == "A"){
    print(row)
    cat("Individuals:", as.numeric(rowSums(jelly.rarefied[row,])), " ")
    cat("Species:", as.numeric(S.obs(jelly.rarefied[row,])), " ")
    cat("Coverage:", as.numeric(C(jelly.rarefied[row,])), "\n")
  }
}

```

```

##
## GroupAIndividuals: 295 Species: 27 Coverage: 0.9966102
## [1] "Andrea"
## Individuals: 59 Species: 18 Coverage: 0.8474576
## [1] "Brianna"
## Individuals: 59 Species: 19 Coverage: 0.8305085
## [1] "Brooke"
## Individuals: 59 Species: 20 Coverage: 0.8305085
## [1] "Emmi"
## Individuals: 59 Species: 21 Coverage: 0.8644068
## [1] "Mackenzie"
## Individuals: 59 Species: 21 Coverage: 0.8305085

```

```

for (row in row.names(jelly.rarefied)){
  if (row == "GroupB"){
    cat("\n", row)
    cat("Individuals:", as.numeric(rowSums(jelly.rarefied[row,])), " ")
    cat("Species:", as.numeric(S.obs(jelly.rarefied[row,])), " ")

```

```

    cat("Coverage:",as.numeric(C(jelly.rarefied[row,])), "\n")
  }
  else if (row != "GroupA" && jellybeangroups[row,] == "B"){
    print(row)
    cat("Individuals:", as.numeric(rowSums(jelly.rarefied[row,])), " ")
    cat("Species:",as.numeric(S.obs(jelly.rarefied[row,])), " ")
    cat("Coverage:",as.numeric(C(jelly.rarefied[row,])), "\n")
  }
}

```

```

##
## GroupBIndividuals: 236 Species: 27 Coverage: 0.9915254
## [1] "Diego"
## Individuals: 59 Species: 22 Coverage: 0.8305085
## [1] "Dustin"
## Individuals: 59 Species: 19 Coverage: 0.8813559
## [1] "Lana"
## Individuals: 59 Species: 19 Coverage: 0.8813559
## [1] "Mark"
## Individuals: 59 Species: 20 Coverage: 0.8813559

```

```

RAC <- function(x = ""){
  x = as.vector(x)
  x.ab = x[x > 0]
  x.ab.ranked = x.ab[order(x.ab, decreasing = TRUE)]
  return(x.ab.ranked)
}
RACresultsA <- radfit(jelly.rarefied["GroupA",])
RACresultsA

```

```

##
## RAD models, family poisson
## No. of species 27, total abundance 295
##
##          par1      par2      par3      Deviance AIC      BIC
## Null                59.818  161.184  161.184
## Preemption  0.13684                64.908  168.274  169.570
## Lognormal   1.8186   1.1176                32.228  137.595  140.186
## Zipf         0.25606 -0.99745                24.045  129.411  132.003
## Mandelbrot  0.49912 -1.2365   0.84057  21.513  128.879  132.767

```

```

RACresultsB <- radfit(jelly.rarefied["GroupB",])
RACresultsB

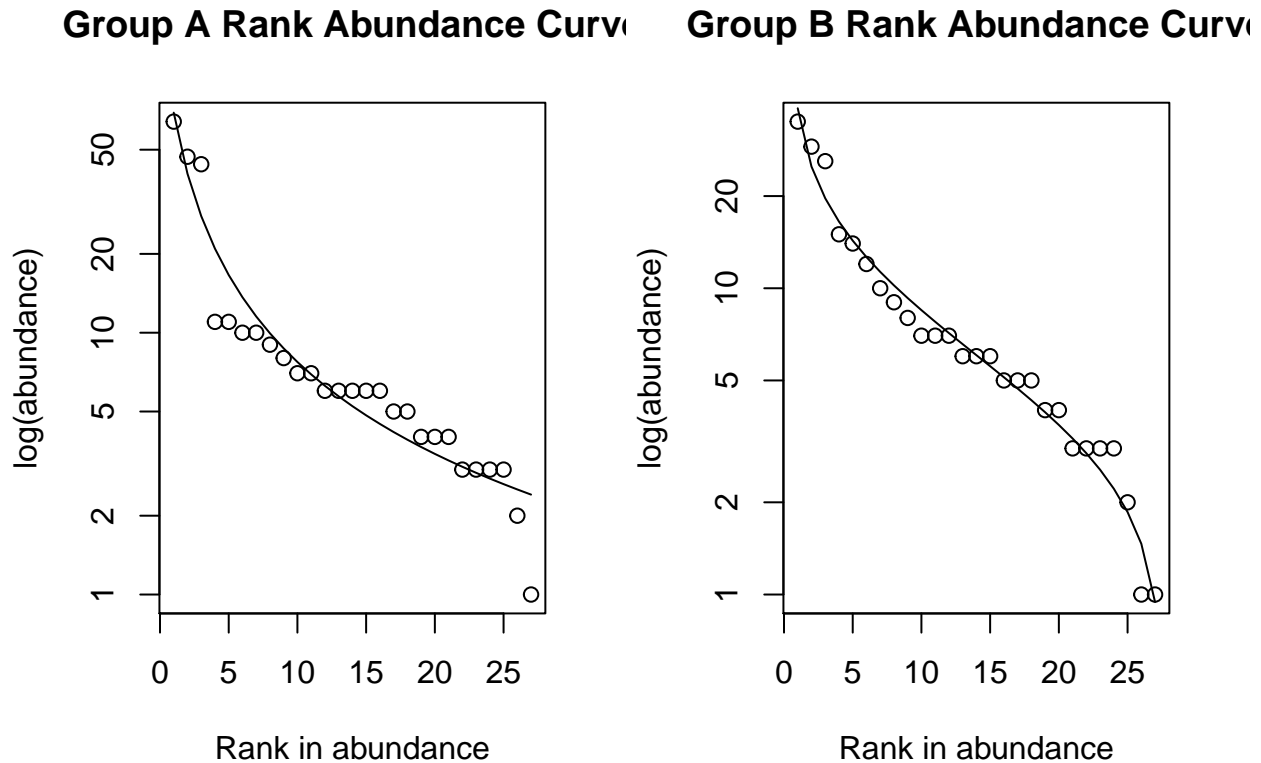
```

```

##
## RAD models, family poisson
## No. of species 27, total abundance 236
##
##          par1      par2      par3      Deviance AIC      BIC
## Null                10.5136  109.7056  109.7056
## Preemption  0.11157                12.7580  113.9500  115.2458
## Lognormal   1.7995   0.89015                4.6537  107.8457  110.4374
## Zipf         0.1907  -0.80236                11.8415  115.0335  117.6252
## Mandelbrot  2.0075  -1.5499   4.2627   5.0232  110.2152  114.1028

```

```
par(mfrow = c(1,2))
plot(rad.zipfbrot(jelly.rarefied["GroupA",]), main = "Group A Rank Abundance Curve", xlab = "Rank in ab", ylab = "log(abundance)")
plot(rad.lognormal(jelly.rarefied["GroupB",]), main = "Group B Rank Abundance Curve", xlab = "Rank in ab", ylab = "log(abundance)")
```



3) Figure caption

Write an informative yet succinct (~5 sentences) caption that creates a “stand-alone” figure. Take a peek at figures and figure captions in a paper published in your favorite journal for inspiration.

SUBMITTING YOUR ASSIGNMENT

Use Knitr to create a PDF of your completed 6.DiversitySampling_Worksheet.Rmd document, push it to GitHub, and create a pull request. Please make sure your updated repo includes both the pdf and RMarkdown files.

Unless otherwise noted, this assignment is due on **Wednesday, January 30th, 2017 at 12:00 PM (noon)**.