5. Worksheet: Alpha Diversity

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OVERVIEW

In this exercise, we will explore aspects of local or site-specific diversity, also known as alpha (α) diversity. First we will quantify two of the fundamental components of (α) diversity: **richness** and **evenness**. From there, we will then discuss ways to integrate richness and evenness, which will include univariate metrics of diversity along with an investigation of the **species abundance distribution (SAD)**.

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. 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 exercise.
- 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 AlphaDiversity_Worskheet.Rmd and the PDF output of Knitr (AlphaDiversity_Worskheet.pdf).

1) R SETUP

In the R code chunk below, please provide the code to: 1) Clear your R environment, 2) Print your current working directory, 3) Set your working directory to your Week-2/ folder folder, and 4) Load the vegan R package (be sure to install first if you have not already).

```
rm(list = ls())
getwd()

## [1] "/cloud/project/QB2025_Huang/Week2-Alpha"
setwd("/cloud/project/QB2025_Huang/Week2-Alpha")

#install.packages("vegan")
require("vegan")
```

Loading required package: vegan
Loading required package: permute

```
## Loading required package: lattice
## This is vegan 2.6-8
```

2) LOADING DATA

In the R code chunk below, do the following: 1) Load the BCI dataset, and 2) Display the structure of the dataset (if the structure is long, use the max.level = 0 argument to show the basic information).

```
data("BCI")
print(BCI, max.levels = 0)
```

##		Abarema.macradenia	Vachellia.melanoceras	Acalypha.diversifolia
##	1	0	0	0
##	2	0	0	0
##		0	0	0
##		0	0	0
##		0	0	0
##		0	0	0
##		0	0	0
##		0	0	0
##		0	0	0
##		1	0	0
	11	0	0	0
	12	0	0	0
	13	0	0	0
	14	0	0	0
	15	0	0	0
	16 17	0	0	0
	18	0	0	0
##		0	0	0
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##		0	0	0
##		0	0	0
##		0	0	0
##		0	0	0
##	25	0	0	0
##	26	0	0	0
##	27	0	0	0
##	28	0	2	0
##	29	0	0	0
##		0	0	0
##		0	0	0
##		0	1	0
##		0	0	0
##		0	0	1
##		0	0	0
##		0	0	0
##		0	0	0
##		0	0	0
##		0	0	0
##		0	0	1
##	41 42	0	0	0
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##		0		0
##		0		0
##		0		0
##		0		0
##		Acalypha.macrostachya	Adelia.triloba	
##	1	0	0	0
##	2	0	0	0
##	3	0	0	0
##	4	0	3	0
##	5	0	1	1
##	6	0	0	0
##	7	0	0	1
##	8	0	0	0
##	9	0	5	0
	10 11	0	0	1 0
	12	0	0	1
	13	0	1	1
	14	0	0	0
	15	0	2	0
	16	0	2	0
	17	0	0	1
##	18	0	1	1
##	19	0	0	1
##	20	0	0	2
##	21	0	0	1
##	22	0	1	0
	23	0	0	0
	24	0	2	1
	25 26	0	0	1 0
	27	0	1	4
##		1	0	1
	29	0	1	0
##		0	14	2
##	31	0	5	0
##	32	0	7	0
##		0	3	1
##		0	3	0
##		0	6	0
##		0	1	0
##		0	2	0
##		0	6	0
## ##		0	9 7	0
##		0	0	1
##		0	0	0
##		0	0	1
##		0	4	0
##		0	0	0

## ##	47	0	0 2	0 0
##		0	1	0
## ##		0	0 1	0
##	50	Alchornea.costaricensis		
	1	2	0	0
##	2	1	0	0
	3	2	0	0
	4	18	0	0
##	5	3	0	0
##	6 7	2 0	1 0	0
##	8	2	0	0
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##	11	10	0	0
##	12	3	0	0
	13	1	0	1
	14	4	0	0
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	17	2	0	0
	18	0	0	0
	19	1	0	0
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##		0	0	0
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##	8		0		14		0	
##	9		0		16		0	
##	10		0		14		0	
##	11		0		14		0	
	12		2		19		0	
	13		1		8		0	
	14		0		17		0	
	15		0		15		0	
##			3		25		0	
##			2		31		0	
##			0		7		0	
## ##			1		13 10		0	
##			1		12		0	
##			4		22		0	
##			0		5		0	
##			1		14		0	
##			0		20		0	
##			0		7		0	
##	27		3		17		0	
##	28		0		16		0	
##	29		0		15		0	
##	30		0		36		0	
##			0		11		0	
##			0		21		0	
##			1		24		0	
##			0		42		0	
	35		0		93		0	
## ##			0		8 19		0	
##			1		25		0	
##			1		38		0	
##			1		65		0	
##			0		13		0	
##	42		0		13		0	
##	43		0		8		0	
##	44		0		13		0	
##	45		0		10		0	
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##		Anacardium.excelsum	and:	ira.inermis	annona	.spraguei	Apelba.	дтs

Anacardium.excelsum Andira.inermis Annona.spraguei Apeiba.glabra

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	4		0	0	0	3
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##	11		1	1	0	2
##	12		0	0	0	4
##	13		0	0	3	1
##	14		0	1	4	5
##	15		0	0	2	8
##	16		0	0	0	5
##	17		0	0	1	1
##	18		2	0	2	1
	19		0	2	1	13
##	20		0	0	2	6
##	21		2	0	0	2
##	22		0	1	0	7
##	23		2	1	0	3
##	24		1	2	0	6
##			1	0	0	6
##			0	2	0	4
	27		0	0	0	2
	28		2	1	0	6
	29		0	1	0	5
	30		0	2	0	5
	31		0	0	0	5
	32		0	0	0	4
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##			0	2	0	2
##			0	0	0	7
##			0	0	0	1
##			0	0	3	0
##			0	0	1	8
##			3	1	2	2
##			1	2	0	4
##			2	1	0	3
##		Apeiba.tibourbou	Aspidosp	oerma.desmanthum	Astrocaryum.standle	eyanum
##	1	2	_	0		0
##	2	0		0		2
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##	4	1		1	5
##	5	0		1	6
##	6	0		1	2
##	7	0		0	2
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##		0		0	2
##		0		1	1
	11	0		0	3
	12	0		0	1
	13	1		0	12
##	14	1		1	5
##	15	0		0	0
##	16	0		0	5
##	17	0		1	1
	18	1		0	6
	19	1		0	2
##		1		0	0
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##		0		0	8
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##		0		3	13
##		1		0	4
##	27	0		0	5
##	28	0		2	4
##	29	0		2	1
##	30	1		0	1
##	31	0		0	3
##		0		1	4
##		1		3	10
##		1		3	3
##		1		0	3
##		0		3	2
##		0		1	2
##		0		3	1
##				5	
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##		0		3	3
##		0		0	3
	42	1		2	13
##		0		3	1
	44	0		2	6
##	45	0		0	1
##	46	3		1	6
##	47	1		2	5
##	48	0		2	7
##	49	0		1	4
##		1		2	4
##		Astronium.graveolens	Attalea.butvracea		
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##		0	0	0
	16	0	1	0
##		2	0	0
##		0	2	0
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##		2	1	0
##		0	1	1
##		0	1	0
##		0	2	0
##		2	2	0
##		0	1	0
##		1	0	0
##		1	0	0
##		1	0	0
##		1	2	0
##		0	0	0
##		1	0	0
##		7	0	0
##		1	0	0
##		0	0	0
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##		0	1	0
##		2	0	0
##		1	0	0
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##		1	1	0
##		0	0	0
##		0	2	0
##		0	1	0
##	50	0	0	0
##		Beilschmiedia.pendula	Brosimum.alicastrum	Brosimum.guianense
##	1	4	5	0
##	2	5	2	0
##	3	7	4	0
##	4	5	3	0
##	5	8	2	0
##	6	6	2	0
##	7	5	6	0
##	8	9	4	0
##	9	11	3	0

##	10	14	6		0
	11	1	5		0
	12	2	4		0
##		0	2		0
##		3	4		0
##		9	3		0
##		4	4		0
##	17	2	5		0
##	18	0	0		0
##	19	2	4		0
##	20	1	0		0
##	21	2	2		0
##	22	0	8		0
##	23	0	2		0
##		16	4		0
##		5	5		0
##		3	3		0
##		1	5		0
##		3	4		0
##		11	2		0
##		4	5		0
##		2	2		0
##		5	8		0
##		2	3		0
## ##		5	5		0
##		1 1	1 3		0
##		2	4		0
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##		7	6		0
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##		10	2		0
##		21	2		0
##	45	42	2		0
##	46	0	5		0
##	47	1	1		1
##	48	1	6		0
##	49	11	4		0
##	50	17	4		0
##		${\tt Calophyllum.longifolium}$			
##		0	0	1	
##		2	0	1	
##		0	0	3	
##		2	0	2	
##		1	0	4	
##		2	0	1	
##		2	0	2	
##		2	1	3	
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##	13	()	1	0
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	16			0	1
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##				1	0
##				1	0
##				0	1
##				0	1
##				1	3
	26			0	1
	27			2	0
##				0	2
##				0	0
##				1	0
##				0	1
	32	(1	0
##		(0	0
##		(7	8
##		:	1	0	3
##		(1	5
##	37	<u>:</u>	1	1	1
##	38	<u>:</u>	1	0	2
##	39	() (0	2
##	40	<u>:</u>	1	1	4
##	41	()	1	1
##	42	:	1	1	1
##	43	() (0	0
##	44			1	1
##	45	3	3 (0	0
##	46	2	2	C	2
##	47	() (C	1
##	48	2	2	C	2
##	49	2	2 (C	0
##	50	()	0	1
##		${\tt Casearia.commersoniana}$	Casearia.guianens	is Casearia.	sylvestris
##	1	0		0	2
##	2	0		0	1
##	3	1		0	0
##	4	0		0	0
##	5	1		0	0
##	6	0		0	3
##	7	0		0	1
##	8	0		0	0
##	9	1		0	1
##	10	0		0	1
	11	0		0	0
	12	0		0	1
##		0		0	1
##		0		0	0
	15	0		0	0
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##	16	0	0	2
##	17	0	1	0
##	18	0	0	1
##		0	0	1
##		0	0	1
##		0	0	0
##		0	0	2
##		0	0	1
##		0	0	2
##		0	0	1
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##		0	0	1
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##		0	0	3
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##	41	0	0	2
##	42	0	0	2
##	43	0	0	0
##	44	0	0	1
##	45	0	0	0
##		0	1	3
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##	50	0	0	0
##			Cavanillesia.platanifolia	
##		2	0	
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##		9	0	
##	14	3	0	11
##		0	0	
##		1	0	
##		0	0	
##	18	6	0	0

##	19		2	0	8
##	20		3	0	11
##			1	0	2
##			2	0	1
##			6	0	2
##			1	0	3
##			2	1	10
## ##			2 0	3 1	1 3
##			3	1	3
##			3	0	5
##			3	1	14
##			0	1	3
##			1	1	4
##	33		0	1	6
##	34		1	1	2
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##			0	0	6
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## ##			0 2	1 0	2 7
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##			2	1	2
##			0	0	0
##			3	0	5
##			1	0	1
##	47		2	2	2
##	48		0	1	0
##	49		0	0	0
##	50		2	0	0
##		Cecropia.obtusifolia			
##		0	0	0	0
## ##		0	0	1	0
##		0	0	0	2
##		1	0	1	2
##		0	0	0	0
##		0	0	0	1
##	8	2	0	1	0
##	9	0	0	0	0
##		2	0	1	0
##		0	0	2	0
##		1	0	0	1
##		1	0	2	0
##		1	0	0	0
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##		0	0	2	1
##		0	0	0	0
##		3	0	0	1
##		0	0	1	3
##		4	0	2	2

	22	0	0	2
	23	3	0	2
	24	0	0	1
##		1	0	1
##		0	0	1
	27	0	0	2
##	28	0	0	0 3
##		1 1	0	1
##		0	1	0
	32	0	0	1
	33	1	0	1
	34	1	0	0
##		0	0	1
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	37	0	0	1
##	38	0	0	1
##	39	0	0	0
##	40	0	0	0
##		0	0	1
	42	0	0	0
	43	0	0	0
	44	1	0	0
##		0	0	0
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	47	0	0	0
	48	0	0	0
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	49	1	0	0
##		0	0	0 0
## ##	50	0 Cespedesia.spathulata	0 Chamguava.schippii	0 0 Chimarrhis.parviflora
## ## ##	50 1		0 Chamguava.schippii 0	0 0 Chimarrhis.parviflora 0
## ## ## ##	50 1 2	0 Cespedesia.spathulata 0 0	0 Chamguava.schippii 0 0	0 0 Chimarrhis.parviflora 0
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## ## ## ## ##	50 1 2 3 4 5	0 Cespedesia.spathulata 0 0 0	O Chamguava.schippii 0 0	0 0 Chimarrhis.parviflora 0 0
## ## ## ## ##	50 1 2 3 4 5 6	O Cespedesia.spathulata 0 0 0 0	O Chamguava.schippii 0 0 0 0	0 0 Chimarrhis.parviflora 0 0 0
## ## ## ## ## ##	50 1 2 3 4 5 6 7	O Cespedesia.spathulata 0 0 0 0 0 0 0 0 0	O Chamguava.schippii 0 0 0 0	0 0 Chimarrhis.parviflora 0 0 0 0
## ## ## ## ## ## ##	50 1 2 3 4 5 6 7 8 9	Cespedesia.spathulata 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	O Chamguava.schippii 0 0 0 0 0 0 0 0 0 0 0 0	0 0 Chimarrhis.parviflora 0 0 0 0 0 0
## ## ## ## ## ## ## ##	50 1 2 3 4 5 6 7 8 9 10	Cespedesia.spathulata 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	O Chamguava.schippii 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 Chimarrhis.parviflora 0 0 0 0 0 0 0
## ## ## ## ## ## ## ##	50 1 2 3 4 5 6 7 8 9 10 11	Cespedesia.spathulata 0 0 0 0 0 0 0 0 0 0 0 0 0	O Chamguava.schippii 0 0 0 0 0 0 0 0 0	0 0 Chimarrhis.parviflora 0 0 0 0 0 0 0 0
## ## ## ## ## ## ## ##	50 1 2 3 4 5 6 7 8 9 10 11 12	Cespedesia.spathulata 0 0 0 0 0 0 0 0 0 0 0 0 0	O Chamguava.schippii 0 0 0 0 0 0 0 0 0	0 0 Chimarrhis.parviflora 0 0 0 0 0 0 0 0
## ## ## ## ## ## ## ##	50 1 2 3 4 5 6 7 8 9 10 11 12 13	O Cespedesia.spathulata 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	O Chamguava.schippii 0 0 0 0 0 0 0 0 0 0	0 0 Chimarrhis.parviflora 0 0 0 0 0 0 0 0 0 0
## ## ## ## ## ## ## ## ##	50 1 2 3 4 5 6 7 8 9 10 11 12 13 14	O Cespedesia.spathulata 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	O Chamguava.schippii 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 Chimarrhis.parviflora 0 0 0 0 0 0 0 0 0 0
## ## ## ## ## ## ## ## ##	50 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15	O Cespedesia.spathulata 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	O Chamguava.schippii 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 Chimarrhis.parviflora 0 0 0 0 0 0 0 0 0 0 0
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## ## ## ## ## ## ## ## ## ## ## ## ##	50 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17	O Cespedesia.spathulata 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	O Chamguava.schippii 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 Chimarrhis.parviflora 0 0 0 0 0 0 0 0 0 0 0 0 0
## ## ## ## ## ## ## ## ## ## ## ## ##	50 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18	O Cespedesia.spathulata 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	O Chamguava.schippii 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 Chimarrhis.parviflora 0 0 0 0 0 0 0 0 0 0 0 0 0
## ## ## ## ## ## ## ## ## ## ## ## ##	50 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19	O Cespedesia.spathulata 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	O Chamguava.schippii 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 Chimarrhis.parviflora 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
## ## ## ## ## ## ## ## ## ## ## ## ##	50 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20	O Cespedesia.spathulata 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	O Chamguava.schippii 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 Chimarrhis.parviflora 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
## ## ## ## ## ## ## ## ## ## ## ## ##	50 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21	O Cespedesia.spathulata 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	O Chamguava.schippii 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 Chimarrhis.parviflora 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
######################################	50 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20	O Cespedesia.spathulata 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	O Chamguava.schippii 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 Chimarrhis.parviflora 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
######################################	50 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22	O Cespedesia.spathulata 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	O Chamguava.schippii 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 Chimarrhis.parviflora 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

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## ## ## ## ## ##	2 3 4 5 6 7 8 9	0 0 0 0 0 0 0	0 0 0 0 0 0 0	4 1 2 2 6 2 3 2 4 2
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######################################	2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18	0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0	4 1 2 2 6 2 3 2 4 2 2 1 4 2 1 2
######################################	2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19	0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0	4 1 2 2 6 2 3 2 4 2 2 1 4 2 1 2 1 0 0
##########################	2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	4 1 2 2 6 2 3 3 2 4 2 2 1 4 2 1 2 1 0 0 0
######################################	2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21	0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	4 1 2 2 6 2 3 3 2 4 2 2 1 4 2 1 2 1 0 0 0
##########################	2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	4 1 2 2 6 2 3 3 2 4 2 2 1 4 2 1 2 1 0 0 0 0
##########################	2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	4 1 2 2 6 2 3 3 2 4 2 2 1 4 2 1 2 1 0 0 0 0 1
###########################	2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		4 1 2 2 6 2 3 3 2 4 2 2 1 4 2 1 0 0 0 2 2
###########################	2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	4 1 2 2 6 2 3 3 2 4 2 2 1 4 2 1 0 0 0 2 2 1
###########################	2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		4 1 2 2 6 2 3 3 2 4 2 2 1 4 2 1 0 0 0 2 2

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Faramea.occidentalis Ficus.colubrinae Ficus.costaricana Ficus.insipida

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##		Ficus.maxima Ficu		Ficus.popend			
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##		0	1	0)	1
##		0	3	0)	0
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		C		0	
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		_	v	v	O

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##			0		2		0	
##			0		7		0	
##			0		4		0	
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##			0		2		0	
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## ##			0		0		0	
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##	50	Heisteria.concinna		americana		triandra		tang
##	1	4	mii cciia	0	mii coiia	21	nura.crcp.	0
##		5		0		14		0
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##	50	11	0	27	
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##		0	0	2	0
## ##		2 0	0	4 4	0 1
##			U		
##	-	O	0		0
	5	0	0	6	0 2
##		0	0	6 0	2
## ##	6			6	
	6 7	0	0	6 0 0	2 1
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## ## ## ## ##	6 7 8 9 10 11 12	0 0 0 0 1 0 0	0 0 0 0 0 0	6 0 0 1 6 4 5 0	2 1 0 1 1 2 1 0
## ## ## ## ##	6 7 8 9 10 11 12 13	0 0 0 0 1 0 0 0	0 0 0 0 0 0 0	6 0 0 1 6 4 5 0	2 1 0 1 1 2 1 0
## ## ## ## ## ##	6 7 8 9 10 11 12 13 14	0 0 0 0 1 0 0 0	0 0 0 0 0 0 0	6 0 0 1 6 4 5 0 0 2 3	2 1 0 1 1 2 1 0 1
## ## ## ## ## ##	6 7 8 9 10 11 12 13 14 15	0 0 0 1 0 0 0 1 2 0	0 0 0 0 0 0 0 0	6 0 0 1 6 4 5 0 0 2 3	2 1 0 1 1 2 1 0 1 1 2
## ## ## ## ## ## ##	6 7 8 9 10 11 12 13 14 15 16	0 0 0 1 1 0 0 0 1 2 0	0 0 0 0 0 0 0 0 0	6 0 0 1 6 4 5 0 0 2 3 2	2 1 0 1 1 2 1 0 1 1 2 0
## ## ## ## ## ## ##	6 7 8 9 10 11 12 13 14 15 16 17	0 0 0 1 0 0 0 0 1 2 0 0	0 0 0 0 0 0 0 0 0 0	6 0 0 1 6 4 5 0 0 2 3 2 0 2	2 1 0 1 1 2 1 0 1 1 2 0
## ## ## ## ## ## ##	6 7 8 9 10 11 12 13 14 15 16 17 18	0 0 0 1 1 0 0 0 1 2 0	0 0 0 0 0 0 0 0 0	6 0 0 1 6 4 5 0 0 2 3 2	2 1 0 1 1 2 1 0 1 1 2 0
## ## ## ## ## ## ##	6 7 8 9 10 11 12 13 14 15 16 17 18 19	0 0 0 1 0 0 0 1 2 0 0	0 0 0 0 0 0 0 0 0 0 0 7 2	6 0 0 1 6 4 5 0 0 2 3 2 0 2	2 1 0 1 1 2 1 0 1 1 2 0 1 2
## ## ## ## ## ## ## ##	6 7 8 9 10 11 12 13 14 15 16 17 18 19 20	0 0 0 1 0 0 0 0 1 2 0 0	0 0 0 0 0 0 0 0 0 0 0 7 2 0	6 0 0 1 6 4 5 0 0 2 3 2 0 2 1 2	2 1 0 1 1 2 1 0 1 1 2 0 1 2 0

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	32		0	0 0	0	1 2
	33 34		0	0	0	1
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	36		1	0	0	2
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##		.	0	0	0	0
## ##	50		0 Inga.semialata	0 Inga.nobilis	0 Inga.oerstediana	0 Inga.pezizifera
## ## ##	50 1	0	0 Inga.semialata 0	0 Inga.nobilis 0	0 Inga.oerstediana 0	0 Inga.pezizifera 0
## ## ## ##	50 1 2	0	0 Inga.semialata 0 0	0 Inga.nobilis 0 0	0 Inga.oerstediana 0 0	0 Inga.pezizifera 0 0
## ## ## ##	50 1 2 3	0 0 0	0 Inga.semialata 0 0 2	0 Inga.nobilis 0 0 1	0 Inga.oerstediana 0 0	0 Inga.pezizifera 0 0 0
## ## ## ## ##	50 1 2 3 4	0 0 0	0 Inga.semialata 0 0 2 4	0 Inga.nobilis 0 0 1 3	0 Inga.oerstediana 0 0 0	O Inga.pezizifera 0 0 0 0
## ## ## ##	50 1 2 3 4 5	0 0 0	0 Inga.semialata 0 0 2	0 Inga.nobilis 0 0 1 3 1	O Inga.oerstediana O O O O	O Inga.pezizifera 0 0 0 0
## ## ## ## ## ##	50 1 2 3 4 5 6	0 0 0 0	0 Inga.semialata 0 0 2 4 0	0 Inga.nobilis 0 0 1 3	0 Inga.oerstediana 0 0 0	O Inga.pezizifera 0 0 0 0
## ## ## ## ## ##	50 1 2 3 4 5 6 7	0 0 0 0 1	0 Inga.semialata 0 0 2 4 0 0	0 Inga.nobilis 0 0 1 3 1	0 Inga.oerstediana 0 0 0 0 0	O Inga.pezizifera 0 0 0 0 0
## ## ## ## ## ##	50 1 2 3 4 5 6 7 8	0 0 0 0 1 0	0 Inga.semialata 0 0 2 4 0 0	0 Inga.nobilis 0 0 1 3 1 0	O Inga.oerstediana 0 0 0 0 0 0	O Inga.pezizifera 0 0 0 0 0 0
## ## ## ## ## ## ##	50 1 2 3 4 5 6 7 8 9	0 0 0 0 1 0 0	0 Inga.semialata 0 0 2 4 0 0 0	0 Inga.nobilis 0 0 1 3 1 0 2 2	0 Inga.oerstediana 0 0 0 0 0 0 0	0 Inga.pezizifera 0 0 0 0 0 0 0
## ## ## ## ## ## ##	50 1 2 3 4 5 6 7 8 9 10	0 0 0 0 1 0 0 0	0 Inga.semialata 0 0 2 4 0 0 0 4 1	0 Inga.nobilis 0 0 1 3 1 0 2 2 2	0 Inga.oerstediana 0 0 0 0 0 0 0	0 Inga.pezizifera 0 0 0 0 0 0 0 0
## ## ## ## ## ## ## ## ## ## ## ## ##	50 1 2 3 4 5 6 7 8 9 10 11 12	0 0 0 0 1 0 0 0	0 Inga.semialata 0 0 2 4 0 0 0 4 1 1 2 1	0 Inga.nobilis 0 0 1 3 1 0 2 2 2 2 3	0 Inga.oerstediana 0 0 0 0 0 0 0 0	0 Inga.pezizifera 0 0 0 0 0 0 0 0 0
## ## ## ## ## ## ## ## ## ## ## ## ##	50 1 2 3 4 5 6 7 8 9 10 11 12 13	0 0 0 0 1 0 0 0 0 0 0	0 Inga.semialata 0 0 2 4 0 0 0 4 1 1 2 1	0 Inga.nobilis 0 0 1 3 1 0 2 2 2 2 3 0 0	0 Inga.oerstediana 0 0 0 0 0 0 0 0 0 0 0	0 Inga.pezizifera 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
######################################	50 1 2 3 4 5 6 7 8 9 10 11 12 13 14	0 0 0 0 1 0 0 0 0 0 0	0 Inga.semialata 0 0 2 4 0 0 0 4 1 1 2 1 0	0 Inga.nobilis 0 0 1 3 1 0 2 2 2 2 2 3 0 0 0	0 Inga.oerstediana 0 0 0 0 0 0 0 0 0 0 0	0 Inga.pezizifera 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
######################################	50 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15	0 0 0 0 1 0 0 0 0 0 0 1 1 1 0	0 Inga.semialata 0 0 2 4 0 0 0 4 1 1 2 1 0 1	0 Inga.nobilis 0 0 1 3 1 0 2 2 2 2 2 3 0 0 0	0 Inga.oerstediana 0 0 0 0 0 0 0 0 0 0 0 0	0 Inga.pezizifera 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
######################################	50 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16	0 0 0 0 1 0 0 0 0 0 0 1 1 1 0 0	0 Inga.semialata 0 0 2 4 0 0 0 4 1 1 2 1 0 0	0 Inga.nobilis 0 0 1 3 1 0 2 2 2 2 2 3 0 0 0 0	0 Inga.oerstediana 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 Inga.pezizifera 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
######################################	50 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17	0 0 0 0 1 0 0 0 0 0 0 1 1 1 0 0 0	0 Inga.semialata 0 0 2 4 0 0 0 4 1 1 2 1 0 1 8 6	0 Inga.nobilis 0 0 1 3 1 0 2 2 2 2 2 3 0 0 0 0 0 5 0 0 1 3 1 0 0 0 0 0 1	0 Inga.oerstediana 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 Inga.pezizifera 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
######################################	50 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18	0 0 0 0 1 0 0 0 0 0 0 0 1 1 1 0 0 0 0 0	0 Inga.semialata 0 0 2 4 0 0 0 4 1 1 2 1 0 1 8 6 0	0 Inga.nobilis 0 0 1 3 1 0 2 2 2 2 2 3 0 0 0 0 0 5 0	0 Inga.oerstediana 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 Inga.pezizifera 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
######################################	50 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19	0 0 0 0 1 0 0 0 0 0 0 1 1 1 0 0 0 0 0 0	0 Inga.semialata 0 0 2 4 0 0 0 4 1 1 2 1 0 1 8 6 0 0	0 Inga.nobilis 0 0 1 3 1 0 2 2 2 2 2 3 0 0 0 0 0 1 1 1 0 0	0 Inga.oerstediana 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 Inga.pezizifera 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
######################################	50 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20	0 0 0 0 1 1 0 0 0 0 0 1 1 1 0 0 0 0	0 Inga.semialata 0 0 0 2 4 0 0 4 1 1 2 1 0 1 8 6 0 0	0 Inga.nobilis 0 0 1 3 1 0 2 2 2 2 3 0 0 0 0 0 5 0 1 1 1	0 Inga.oerstediana 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	O Inga.pezizifera 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
################################	50 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21	0 0 0 0 1 1 0 0 0 0 0 1 1 1 0 0 0 0 0 0	0 Inga.semialata 0 0 0 2 4 0 0 0 4 1 1 2 1 0 1 8 6 0 0	0 Inga.nobilis 0 0 1 3 1 0 2 2 2 2 2 3 0 0 0 0 0 5 0 0 1 1 1 0 2 1 1 0 0 0 0 1	0 Inga.oerstediana 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	O Inga.pezizifera 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
###############################	50 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22	0 0 0 0 1 1 0 0 0 0 0 0 1 1 1 0 0 0 0 0	0 Inga.semialata 0 0 0 2 4 0 0 4 1 1 2 1 0 1 8 6 0 0 1	0 Inga.nobilis 0 0 1 3 1 0 2 2 2 2 2 3 0 0 0 0 0 5 0 1 1 1 0 2 2 2 2 1 0 0 0 0 0 0 0 0 0 0	0 Inga.oerstediana 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	O Inga.pezizifera 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
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## 5 ## 6 ## 7 ## 8 ## 10 ## 11 ## 12 ## 13 ## 14 ## 15 ## 16 ## 17	0 0 0 2 2 2 1 0 0 0 0	3 7 4 8 5 12 7 2 3 12 23 6 4	1 2 1 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 1 3 2 0 0 0 0 1 1 1 2 1 0
## 5 ## 6 ## 7 ## 8 ## 9 ## 10 ## 11 ## 12 ## 13 ## 14 ## 15 ## 16 ## 17 ## 18	0 0 0 2 2 2 1 0 0 0 0 0	3 7 4 8 5 12 7 2 3 12 23 6 4 3	1 2 1 0 0 0 0 0 0 0 1 1 1 2	2 1 3 2 0 0 0 1 1 1 2 1 0 1 3
## 5 ## 6 ## 7 ## 8 ## 9 ## 10 ## 11 ## 12 ## 13 ## 14 ## 15 ## 16 ## 17 ## 18 ## 19	0 0 0 2 2 2 1 0 0 0 0 0 1	3 7 4 8 5 12 7 2 3 12 23 6 4 3 7	1 2 1 0 0 0 0 0 0 0 0 1 1 1 2 0 0	2 1 3 2 0 0 0 1 1 1 2 1 0 1 3 4
## 5 ## 6 ## 7 ## 8 ## 9 ## 10 ## 11 ## 12 ## 13 ## 14 ## 15 ## 16 ## 17 ## 18	0 0 0 2 2 2 1 0 0 0 0 0	3 7 4 8 5 12 7 2 3 12 23 6 4 3 7	1 2 1 0 0 0 0 0 0 0 1 1 1 2	2 1 3 2 0 0 0 0 1 1 1 2 1 0 1 3 4 1
## 5 ## 6 ## 7 ## 8 ## 9 ## 10 ## 11 ## 12 ## 13 ## 14 ## 15 ## 16 ## 17 ## 18 ## 20	0 0 0 2 2 2 1 0 0 0 0 0 1 0 0	3 7 4 8 5 12 7 2 3 12 23 6 4 3 7	1 2 1 0 0 0 0 0 0 0 0 1 1 1 2 0 0	2 1 3 2 0 0 0 0 1 1 1 2 1 0 1 3 4 1 1
## 5 ## 6 ## 7 ## 8 ## 9 ## 10 ## 11 ## 12 ## 13 ## 14 ## 15 ## 16 ## 17 ## 18 ## 20 ## 21 ## 22 ## 23	0 0 0 2 2 2 1 0 0 0 0 0 1 0 0 0	3 7 4 8 5 12 7 2 3 12 23 6 4 3 7 10 8 6 4	1 2 1 0 0 0 0 0 0 0 1 1 1 2 0 0 0 0 0 0	2 1 3 2 0 0 0 1 1 1 2 1 0 1 3 4 1 1 1 0 2
## 5 ## 6 ## 7 ## 8 ## 9 ## 10 ## 11 ## 12 ## 13 ## 14 ## 15 ## 16 ## 17 ## 18 ## 20 ## 21 ## 22 ## 23 ## 24	0 0 0 2 2 2 1 0 0 0 0 1 0 0 0 0	3 7 4 8 5 12 7 2 3 12 23 6 4 3 7 10 8 6 4	1 2 1 0 0 0 0 0 0 0 1 1 1 2 0 0 0 1 1 1 0 0 0 0	2 1 3 2 0 0 0 0 1 1 1 2 1 0 1 3 4 1 1 0 2
## 5 ## 6 ## 7 ## 8 ## 9 ## 10 ## 11 ## 12 ## 15 ## 16 ## 17 ## 18 ## 20 ## 21 ## 22 ## 23 ## 24 ## 25	0 0 0 2 2 2 1 0 0 0 0 1 0 0 0 0 0 0 0 0	3 7 4 8 5 12 7 2 3 12 23 6 4 3 7 10 8 6 4 2 5	1 2 1 0 0 0 0 0 0 0 1 1 1 1 0 0 0 1 1 1 0 0 0 0 0 0 1	2 1 3 2 0 0 0 1 1 1 2 1 0 1 3 4 1 1 1 0 2
## 5 ## 6 ## 7 ## 8 ## 9 ## 10 ## 11 ## 12 ## 15 ## 16 ## 17 ## 18 ## 20 ## 21 ## 22 ## 23 ## 24 ## 25 ## 26	0 0 0 2 2 2 1 0 0 0 0 0 1 0 0 0 0 0 0 0	3 7 4 8 5 12 7 2 3 12 23 6 4 3 7 10 8 6 4 2 5	1 2 1 0 0 0 0 0 0 0 0 1 1 1 1 0 0 0 1 1 1 0 0 0 0 0 0 0 0 0 0 1 1 0	2 1 3 2 0 0 0 0 1 1 1 2 1 0 1 3 4 1 1 0 2 0 1
## 5 ## 6 ## 7 ## 8 ## 9 ## 10 ## 11 ## 12 ## 15 ## 16 ## 17 ## 18 ## 20 ## 21 ## 22 ## 23 ## 24 ## 25 ## 26	0 0 0 2 2 2 1 0 0 0 0 0 1 0 0 0 0 0 0 0	3 7 4 8 5 12 7 2 3 12 23 6 4 3 7 10 8 6 4 2 5 0 3	1 2 1 0 0 0 0 0 0 0 1 1 1 1 0 0 1 1 0 0 0 0 0 0 0 0 1 1 1 0	2 1 3 2 0 0 0 0 1 1 1 2 1 0 1 3 4 1 1 0 2 0 1
## 5 ## 6 ## 7 ## 8 ## 9 ## 10 ## 11 ## 12 ## 13 ## 15 ## 16 ## 17 ## 18 ## 20 ## 21 ## 22 ## 23 ## 24 ## 25 ## 26 ## 27 ## 28	0 0 0 2 2 2 1 1 0 0 0 0 1 1 0 0 0 0 0 0	3 7 4 8 5 12 7 2 3 12 23 6 4 3 7 10 8 6 4 2 5 0 3 3	1 2 1 0 0 0 0 0 0 0 1 1 1 1 0 0 0 1 1 0	2 1 3 2 0 0 0 0 1 1 1 2 1 0 1 3 4 1 1 0 2 0 0 1
## 5 ## 6 ## 7 ## 8 ## 9 ## 10 ## 11 ## 12 ## 15 ## 16 ## 17 ## 18 ## 20 ## 21 ## 22 ## 23 ## 24 ## 25 ## 26	0 0 0 2 2 2 1 0 0 0 0 0 1 0 0 0 0 0 0 0	3 7 4 8 5 12 7 2 3 12 23 6 4 3 7 10 8 6 4 2 5 0 3	1 2 1 0 0 0 0 0 0 0 1 1 1 1 0 0 1 1 0 0 0 0 0 0 0 0 1 1 1 0	2 1 3 2 0 0 0 0 1 1 2 1 0 1 3 4 1 1 0 2 0 1 1 0 0 1 1 0 0 1 0 1 0 0 1 0 0 1 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 1 0 0 1 0 0 1 0 1 1 0 0 1 0 1 0 0 1 0 0 1 0 0 1 0 0 1 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 1 0 0 1 0 0 1 0 1 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 1 0 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 0 1 0 0 1 0 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 1 0 0 0 0 0 1 1 1 0 1 0 1 0 1 0 1 0 0 1 1 0 0 1 0 1 0 0 1 0 1 0 1 0 1 0 1 0 1 0 0 1 0

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##		0	0	16	17
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##	50	0 Pouteria.fossicola Pouteria.reticulata	0 Dc	43	O Prioria consifora
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## 46		4	3	3
## 47		7	1	1
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## 12		0	5	
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## 16		0	2	
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"" -	1	1	∠	
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##	50	Pterocarpus.rohrii	0		0 Quassia.amara	0 Randia.armata
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## ## ## ## ## ## ##	50 1 2 3 4 5 6 7 8 9	1 0 0 2 1 1 2 2 2	0	11 12 15 14 9 3 21 7	0 Quassia.amara 0 0 0 0 0 0 0	0 Randia.armata 3 2 1 4 2 9 14 4 4
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## ###################################	50 1 2 3 4 5 6 7 8 9 10 11	1 0 0 2 1 1 2 2 1 0 2	0	11 12 15 14 9 3 21 7 4 18 25	0 Quassia.amara 0 0 0 0 0 0 0 0	0 Randia.armata 3 2 1 4 2 9 14 4 4 4 1 7
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######################################	50 1 2 3 4 5 6 7 8 9 10 11 12 13	1 0 0 2 1 1 2 2 1 0 2 2 2	0	11 12 15 14 9 3 21 7 4 18 25 11	0 Quassia.amara 0 0 0 0 0 0 0 0 0	0 Randia.armata 3 2 1 4 2 9 14 4 4 1 7 2 15
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# # # # # # # # # # # # # # # # # # #	50 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20	1 0 0 2 1 1 2 2 2 1 0 2 2 2 2 2 2 2 1 1 3 1 1 3 1 3	0	11 12 15 14 9 3 21 7 4 18 25 11 1 10 8 25 9 0 2	O Quassia.amara 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 Randia.armata 3 2 1 4 2 9 14 4 4 1 7 2 15 3 2 3 5 10 2 3
# # # # # # # # # # # # # # # # # # #	50 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21	1 0 0 2 1 1 1 2 2 2 1 0 2 2 2 2 2 2 1 1 1 3 1 3 1 3	0	11 12 15 14 9 3 21 7 4 18 25 11 1 10 8 25 9 0 2	O Quassia.amara 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 Randia.armata 3 2 1 4 2 9 14 4 4 1 7 2 15 3 2 3 5 10 2 3 1
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# # # # # # # # # # # # # # # # # # #	50 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23	1 0 0 2 1 1 1 2 2 1 0 2 2 2 2 2 2 2 2 1 1 1 3 1 1 3 1 3 1 3 1	0	11 12 15 14 9 3 21 7 4 18 25 11 1 0 8 25 9 0 2 15 12 11 6	O Quassia.amara 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 Randia.armata 3 2 1 4 2 9 14 4 4 1 7 2 15 3 2 3 5 10 2 3 1 11 1
# # # # # # # # # # # # # # # # # # #	50 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23	1 0 0 2 1 1 1 2 2 1 0 2 2 2 2 2 2 2 1 1 1 3 3 1 1 3 3 0 0 0 0 0 0 0 0 0 0 0	0	11 12 15 14 9 3 21 7 4 18 25 11 1 0 8 25 9 0 2 15 12	O Quassia.amara 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 Randia.armata 3 2 1 4 2 9 14 4 4 1 7 2 15 3 2 3 5 10 2 3 1 11

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##	1					
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######################################	2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17	0 0 0 0 0 0 0 0 0 0 0 0	0 0 1 1 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0		0 0 0 0 0 1 0 0 0 0 0 0 0	
######################################	2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18	0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 1 1 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0		0 0 0 0 0 1 0 0 0 0 0 0 0	
######################################	2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19	0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 1 1 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0		0 0 0 0 0 1 0 0 0 0 0 0 0 0	
#########################	2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20		0 0 1 1 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0		0 0 0 0 0 1 0 0 0 0 0 0 0 0	
######################################	2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21	0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 1 1 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0		0 0 0 0 0 1 0 0 0 0 0 0 0 0	
#########################	2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21		0 0 1 1 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0		0 0 0 0 0 1 0 0 0 0 0 0 0 0	
######################################	2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22		0 0 1 1 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0		0 0 0 0 1 0 0 0 0 0 0 0 0 0	
#######################################	2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23		0 0 1 1 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0		0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0	
##########################	2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24		0 0 1 1 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0		0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0	
############################	2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25		0 0 0 1 1 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0		0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0	
#############################	2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24		0 0 0 1 1 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0		0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0	

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	37	0	0		0 0	
	38	0	0		0 0	
	39	0	0		0 0	
	40	0	0		0 0	
	41 42	0	0		0 1 0	
	43	0 1	0		0 0	
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	45	1	0		0 0	
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##		Simarouba.amara Siparuna	.guianensis	Siparuna.pauciflora	Sloanea.terniflora	ì
##	1	14	3	0	1	
##	2	6	2	0	(
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##		8	2	0	2	
##		7	0	3	3	
##		7	1	0	2	
##		13	1	0	1	
## ##				0		٤.
		14	0		2	
		12	0	1	1	L
πп	10	12 17	0	1 1	1	L 2
	10 11	12 17 7	0 0 1	1 1 0	1 2 1	L 2 L
##	10 11 12	12 17 7 9	0 0 1 0	1 1 0 0	1 2 1 1	L L L
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## ## ##	10 11 12	12 17 7 9 2	0 0 1 0	1 1 0 0	1 2 1 1	l 2 1 1 1
## ## ## ##	10 11 12 13 14	12 17 7 9 2 4	0 0 1 0 0	1 1 0 0 0	1 2 1 1 1	L 2 L L L
## ## ## ##	10 11 12 13 14 15	12 17 7 9 2 4 6	0 0 1 0 0 0	1 1 0 0 0 0 0 2	1 2 1 1 1	l 2 1 1 1 1 1
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## ## ## ## ## ##	10 11 12 13 14 15 16 17 18	12 17 7 9 2 4 6 8 2 2	0 0 1 0 0 0 0 1 0	1 1 0 0 0 0 0 2 0 0 0	1 2 1 1 1 0 0 1	L 2 L L L D
## ## ## ## ## ##	10 11 12 13 14 15 16 17 18 19 20	12 17 7 9 2 4 6 8 2 2 6 8	0 0 1 0 0 0 0 1 0 1	1 1 0 0 0 0 0 2 0 0 0 0	1 2 1 1 1 0 0 1	
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## ## ## ## ## ## ##	10 11 12 13 14 15 16 17 18 19 20 21 22	12 17 7 9 2 4 6 8 2 2 2 6 8 4 5	0 0 1 0 0 0 0 1 0 1 0 0	1 0 0 0 0 0 2 0 0 0 0 0 0	1 2 1 1 1 1 0 0 1 1 0 1	
## ## ## ## ## ## ##	10 11 12 13 14 15 16 17 18 19 20 21 22 23	12 17 7 9 2 4 6 8 2 2 2 6 8 4 5	0 0 1 0 0 0 0 1 0 1 0 0 0	1 1 0 0 0 0 0 2 0 0 0 0 0 1 0 0	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	
## ## ## ## ## ## ## ##	10 11 12 13 14 15 16 17 18 19 20 21 22 23 24	12 17 7 9 2 4 6 8 2 2 2 6 8 4 5 1	0 0 1 0 0 0 0 1 0 1 0 0 0 0	1 1 0 0 0 0 0 2 2 0 0 0 0 1 0 0	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	
## ## ## ## ## ## ## ## ## ## ## ## ##	10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25	12 17 7 9 2 4 6 8 2 2 2 6 8 4 5 1 3	0 0 1 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0	1 1 0 0 0 0 2 2 0 0 0 0 1 0 0 0	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	
## ## ## ## ## ## ## ## ## ## ## ## ##	10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26	12 17 7 9 2 4 6 8 2 2 6 8 4 5 1 3	0 0 1 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0	1 1 0 0 0 0 0 2 0 0 0 0 1 0 0 0 0	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	
######################################	10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27	12 17 7 9 2 4 6 8 2 2 6 8 4 5 1 3 10 5	0 0 1 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0	1 1 0 0 0 0 0 2 0 0 0 0 1 0 0 0 0 0	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	
# # # # # # # # # # # # # # # # # # #	10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28	12 17 7 9 2 4 6 8 2 2 6 8 4 5 1 3 10 5	0 0 1 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0	1 1 0 0 0 0 0 2 0 0 0 0 1 0 0 0 0 0 0 0	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	
######################################	10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27	12 17 7 9 2 4 6 8 2 2 6 8 4 5 1 3 10 5	0 0 1 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0	1 1 0 0 0 0 0 2 0 0 0 0 1 0 0 0 0 0	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	

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	32	5	C		0	
##		2	C		0	
##		2	C)	0	
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##	36	9	C)	0	
##	37	6	C)	1	
##	38	3	C)	0	
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##		1	C		0	
##		4	C		0	
##		0	C		1	
##		0	C		0	
##		3	C		0	
##		3	C		0	
##		4	C		0	
##		0	C		0	
##		4	C		0	
##	50	3	C		1	
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##	1	15	0	1	(0
##	2	22	0	1	(0
##	3	31	0	1	(0
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##		0	0	0		0
##		8	0	2		0
##		0	1	1		0
##		0	0	0		0
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##			1 1	0
##			0 0	0
##			2 0	0
##	39		0 0	0
##	40		0 0	0
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##	45		9 0	1
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##		1	0	2
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##		1	3	0
##		1	5	0
##		0	0	1
##		0	5	1
## ##		1 0	0	0
##		2	1	0
##		0	1	0
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##		0	2	0
##		0	2	0
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##		0	3	0
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##	24	0	1	0
##	25	0	2	0
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##		0	1	0
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##		1		1
##		9		5
##		9		7
##		5		0
##		5		0
##		0		0
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##		13		13
##		2		2
##		3		3
##		1		0
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##		6		4
##		9		2
##		6		4
##		2 2		0
## ##		6		1 4
##				
##		2 4		4 3
##		2		1
##		5		2
##		6		4
##		8		1
##		6		4
##		3		0
##		0		1
##		4		3
##		13		4
##		13		2
##		4		1
##		0		3
##		8		3
##		10		2
##	38	10		2

39

##	40		1	
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##			3	
##			8	
##			3	
##			1	
##	46		0	
##	47		0	
	48		4	
##			2	
##	50		1	
##		Symphonia.globulifera Handroa		
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	2	1	0	2
	3 4	1	1	1
## ##	5	1 2	0	2 3
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	7	0	0	1
	8	1	0	0
##		1	0	0
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##	11	0	0	0
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	14	0	1	0
	15	2	1	0
	16	1	0	1
	17	0	1	1
	18 19	0	0	0
##		0	0	1
##		2	0	2
##		0	2	0
##		0	0	4
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##	25	1	0	0
##		0	0	2
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##		0	6	1
##		0	1	0
##		0	4	3
## ##		0	0	2 1
##		0	0	5
##		0	0	0
##		0	1	0
##		0	0	2
##		0	0	1
##		0	0	1
##		1	0	4
##		0	0	2
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##	42	1	0	1

##	/13	0	2	0
##		0	1	2
##		2	0	1
##		0	1	3
##	47	1	0	3
##	48	0	0	5
##	49	1	0	2
##	50	3	1	1
##		${\tt Tabernaemontana.arborea}$		Talisia.nervosa
##	1	9	6	0
##		5	1	0
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##	7	9	2	0
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	10	10	1	0
	11	4	4	0
	12	6	2	0
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	18	10	3	0
	19	9	2	0
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##		0	1	0
##		4	1	0
## ##		3 2	2	0
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## ## ## ##	47 48 49		2 1 8 2 7	1 1 0 2 2
##		Talisia.princeps	Terminalia.amazonia	Terminalia.oblonga
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	4	0	0	0
	5	0	1	0
	6 7	0	1 0	0
	8	0	0	0
	9	0	0	0
	10	0	0	0
##	11	0	0	0
##	12	0	0	0
	13	0	5	0
##	14	0	2	0
##	15	0	0	0
	16	0	0	3
	17	0	0	0
	18	0	2	0
	19	0	0	0
##		0	1	0
## ##	22	0	0	1 1
##		0	6	0
##		0	1	0
##		0	2	2
	26	1	0	5
##		0	0	10
	28	1	0	0
##	29	0	1	0
##	30	0	0	0
##		0	1	8
##		0	0	2
##		0	0	0
## ##		0	0 2	0
##		0	2	0
##		0	0	0
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##		0	0	0
##		0	1	0
##		0	0	0
##	42	0	0	0
##	43	0	0	0
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##		0	0	0
##		0	0	0
##	48	0	0	2

##		0	1	9
##	50	0	0	0 The sharement are seen
## ##	1		Tetrathylacium.johansenii	
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	11	10	0	0
	12	10	0	0
	13	6	0	0
	14	5	0	0
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	18	11	2	0
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##		4	0	0
	22	9	0	0
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	43	6	0	1
	44	4	0	0
	45	9	0	0
	46 47	20	0	0
	47	25 8	0	0
	49	4	0	0
	50	8	0	2
##			a.pittieri Trattinnickia.as	
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	47	0	1	16
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	50			
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##			0		6		0	
##			0		4		0	
##			0		5		0	
##			0		1		0	
##			0		0		0	
##			0		1		4	
##			0		6		1	
##			0		5		4	
##			0		1		0	
##			0		3		0	
##	48		0		6		3	
##	49		0		4		8	
##	50		0		4		3	
##		Trophis.racemosa	Turpinia.occ	identalis	Unonopsis	.pittieri	Virol	a.multiflora
##	1	1	•	0	-	1		0
##		1		1		5		0
##		0		1		12		0
##		1		4		3		0
##		0		2				
						4		0
##		0		1		3		2
##		1		0		3		0
##		0		1		2		0
##	9	0		1		5		0

##	10	2	1	9	1
##	11	0	1	4	0
##		0	1	0	1
##		0	0	0	0
##		1	0	3	0
##		0	5	11	0
##		2	2	1	1
##		0	0	0	0
##		2	0	0	0
##		3	0	4	0
## :		0	5	10	0
## :		0	1	6	2
## :		0	1	1	0
## :		1	0	1	0
## :		1	2	3	0
## :		2	0	3	0
## :		1	0	4	1
## :		1	7	0	0
## :		0	1	0	0
## :		0	3	5	0
##		2	1	1	1
## :		1	0	3	5
## :		2	0	4	0
## :		1	2	5	0
## :		0	1	1	0
## :		0	0	0 9	0
## :		0	2		2
## :		0	5	8 2	2
## :		0	0 2	0	0
## -		1	1	0	0
## -		0	2	4	2
##		0	0	5	3
##		1	0	5	0
##		0	0	3	0
##		0	0	4	0
##		0	0	0	0
##		2	0	0	0
##		2	0	0	1
##		0	0	2	0
##		0	1	4	1
##		Virola.sebifera Virola.sur			
##	1	17	4	0	0
##		12	3	0	0
##	3	11	2	0	0
##	4	16	2	0	0
##	5	31	6	0	0
##		19	1	0	0
##		8	1	0	0
##	8	19	1	0	0
##		16	1	0	0
##		17	2	0	0
##	11	6	4	0	0
##	12	6	2	0	2

##	13	0	0	0	3
##	14	17	1	0	1
##	15	16	4	0	0
##		24	5	0	0
##		5	0	0	1
##		0	2	0	2
##		12	1	0	0
##		15	4	0	0
##		15	10	0	0
	22	7	1	0	0
##		9	1	0	0
##	24	12	1	0	0
##	25	12	4	0	0
##	26	20	12	0	0
##	27	12	1	0	0
##		18	1	0	0
##		9	1	0	0
##		8	3	0	0
##		20	6	0	0
##		18	4	0	0
##		16	3	0	0
##		7	1		
				0	0
##		11	0	0	0
##		14	5	0	0
##		14	4	1	0
##		11	0	0	0
##		7	2	0	0
##		11	1	0	0
##	41	12	7	0	0
##	42	12	5	0	0
##	43	14	8	0	0
##	44	10	1	0	0
##	45	13	7	0	0
##		0	0	0	2
##		11	1	0	1
##		7	5	0	0
##		6	16	0	0
##		14	7	0	0
##	00		Zanthoxylum.ekmanii		
##	1	Ayropra.macrantna	Zanchoxyrum.exmanii	Zanchoxy rum. Jun.	0
##			4		0
		0			
##		0	8		1
##		0	13		1
##		0	3		0
##		0	1		0
##		0	2		0
##		0	4		0
##		0	13		1
##		4	7		10
##		1	1		0
##	12	0	0		0
##		1	5		2
##		0	12		3
##		3	5		6
	_	•	•		*

##	16	1	2	1
##	17	2	1	0
##	18	1	0	2
##	19	1	3	1
	20	1	4	2
	21	15	7	2
	22 23	0	1 0	1 0
	24	0	0	0
	25	0	4	3
	26	15	1	1
	27	8	4	1
##	28	0	0	0
##	29	0	2	0
##	30	0	1	0
	31	23	0	1
	32	4	4	0
	33	8	3	0
##		1	0	0
##		0	0 2	0
## ##		20 1	5 5	1 0
##		1	2	1
##		0	1	1
##		0	0	0
##		9	3	0
##		14	4	0
##	43	2	1	0
##	44	1	2	0
##		0	2	1
##		3	1	1
##		1	2	1
##		1	5 1	0
## ##		0	0	0
##	50		Zanthoxylum.setulosum	
##	1	2	0	0
##		2	0	0
##	3	2	0	0
##		5	0	1
##		5	0	0
##		3	0	2
##		0	0	0
##		2	0	0
##		4	0	0
## ##		1	0	0
##		0	0	0
##		0	0	0
##		1	0	0
##		2	0	0
##		0	0	0
##		1	0	1
##	18	1	0	1

```
0
## 19
                               3
                                                          0
## 20
                               1
                                                          0
                                                                                0
                               0
## 21
                                                          0
                                                                                0
                                                          0
                                                                                0
## 22
                               1
## 23
                               0
                                                          0
                                                                                0
## 24
                               0
                                                          0
                                                                                0
## 25
                               1
                                                          0
                                                                                0
                               0
                                                          0
## 26
                                                                                0
## 27
                               2
                                                          0
                                                                                0
## 28
                               0
                                                          0
                                                                                1
## 29
                               0
                                                          0
                                                                                0
                               3
                                                          0
## 30
                                                                                0
## 31
                               1
                                                          0
                                                                                0
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## 32
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                                                                                0
## 33
                               1
                                                          0
                                                                                0
## 34
                               3
                                                          0
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## 35
                               1
                                                          0
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                               0
                                                          0
## 36
                                                                                0
## 37
                               4
                                                          0
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## 38
                               1
                                                          0
                                                                                0
## 39
                               1
                                                          0
                                                                                0
## 40
                               0
                                                          0
                                                                                0
## 41
                               1
                                                          1
                                                                                0
## 42
                               1
                                                          0
                                                                                1
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## 43
## 44
                               0
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                                                                                0
## 45
                               0
                                                          0
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## 46
                               1
                                                          0
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## 47
                               0
                                                          0
                                                                                1
## 48
                               1
                                                          0
                                                                                2
## 49
                               1
                                                          0
                                                                                0
## 50
                               2
                                                          0
                                                                                0
```

3) SPECIES RICHNESS

Species richness (S) refers to the number of species in a system or the number of species observed in a sample.

Observed richness

In the R code chunk below, do the following:

- 1. Write a function called S.obs to calculate observed richness
- 2. Use your function to determine the number of species in site1 of the BCI data set, and
- 3. Compare the output of your function to the output of the specnumber() function in vegan.

```
S.obs <- function(x = ""){
   rowSums(x > 0) *1
}
S.obs(BCI[1,])
```

```
## 1
## 93
```

```
specnumber(BCI[1,])

## 1
## 93

#Species richness of the first four sites
S.obs(BCI[1:4,])

## 1 2 3 4
```

Question 1: Does specnumber() from vegan return the same value for observed richness in site1 as our function S.obs? What is the species richness of the first four sites (i.e., rows) of the BCI matrix?

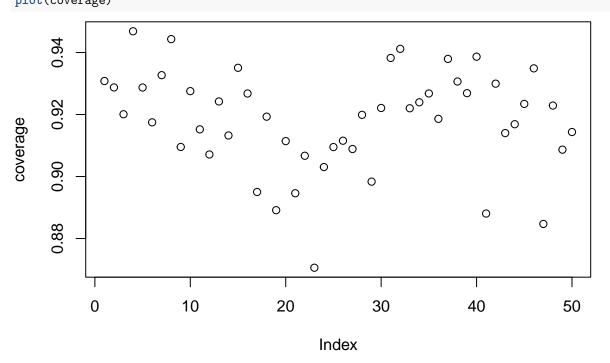
Answer 1: 'specnumber() returns the same value for observed richeness in "site 1" as 'S.obs', which is 93. The species richness of the first four sites are 93, 84, 90, 94 respectively.

Coverage: How well did you sample your site?

In the R code chunk below, do the following:

93 84 90 94

- 1. Write a function to calculate Good's Coverage, and
- 2. Use that function to calculate coverage for all sites in the BCI matrix.



range(coverage)

[1] 0.8705882 0.9468504

Question 2: Answer the following questions about coverage:

- a. What is the range of values that can be generated by Good's Coverage?
- b. What would we conclude from Good's Coverage if n_i equaled N?
- c. What portion of taxa in site1 was represented by singletons?
- d. Make some observations about coverage at the BCI plots.

Answer 2a: The range of values that can be generated by Good's Coverage is from 0 (when all species are singletons) to 1 (when no singleton exists).

Answer 2b: All species are singletons at site i

Answer 2c: The portion of singletons at site 1 is approximatly 0.0692

Answer 2d: The range of the coverage accross site is from 0.8706 to 0.9469, and according to the graph above, most coverage index are over 0.88, which is relatively high.

Estimated richness

In the R code chunk below, do the following:

- 1. Load the microbial dataset (located in the Week-2/data folder),
- 2. Transform and transpose the data as needed (see handout),
- 3. Create a new vector (soilbac1) by indexing the bacterial OTU abundances of any site in the dataset,
- 4. Calculate the observed richness at that particular site, and
- 5. Calculate coverage of that site

Question 3: Answer the following questions about the soil bacterial dataset.

- a. How many sequences did we recover from the sample soilbac1, i.e. N?
- b. What is the observed richness of soilbac1?
- c. How does coverage compare between the BCI sample (site1) and the KBS sample (soilbac1)?

Answer 3a: In total 2119 sequences.

Answer 3b: The observed richness is 1074

Answer 3c: The coverage of this site (T1_1) is 0.6479, which is even lower than the minimum coverage of the BCI samples (0.8706).

Richness estimators

In the R code chunk below, do the following:

- 1. Write a function to calculate **Chao1**,
- 2. Write a function to calculate **Chao2**,
- 3. Write a function to calculate **ACE**, and
- 4. Use these functions to estimate richness at site1 and soilbac1.

```
#function for Chao1
S.chao1 \leftarrow function(x = ""){
  S.obs(x) + (sum(x == 1)^2) / (2*sum(x == 2))
}
#function for Chao2
S.chao2 <- function(site = "", SbyS = ""){
  SbyS = as.data.frame(SbyS)
  x = SbyS[site,]
  SbyS.pa <- (SbyS > 0) * 1 # convert the Sbys to presence/absence
  Q1 = sum(colSums(SbyS.pa) == 1) # species observed once
  Q2 = sum(colSums(SbyS.pa) == 2) # species observed twice
  S.chao2 = S.obs (x) + (Q1^2) / (2 * Q2)
  return (S.chao2)
}
#function for ACE
S.ace \leftarrow function(x = "", thresh = 10){
  x \leftarrow x[x > 0] # excludes zero-abundance taxa
  S.abund <- length(which(x > thresh)) # richness of abundant taxa
  S.rare <- length(which(x <= thresh)) # richness of rare taxa</pre>
  singlt <- length(which(x == 1)) # number of singleton taxa</pre>
  N.rare <- sum(x[which (x <= thresh)]) # abundance of rare individuals
  C.ace <- 1 - (singlt / N.rare) # coverage (prop non-singlt rare inds)
  i <- c(1: thresh) # threshold abundance range
  count <- function(i, y){ # counter to go through i range</pre>
    length (y[y == i])
 a.1 <- sapply (i, count, x) # number of individuals in richness i richness classes
  f.1 \leftarrow (i * (i - 1)) * a.1 # k(k-1)kf sensu Gotelli
  G.ace <- (S.rare/C.ace) * (sum (f.1) / (N.rare* (N.rare-1)))
 S.ace <- S.abund + (S.rare/C.ace) + (singlt/C.ace) * max(G.ace, 0)
  return (S.ace)
}
#richness at site 1
S.chao1(BCI[1,])
## 119.6944
S.chao2(1, BCI)
```

```
## 1
## 104.6053
S.ace(BCI[1,])
## [1] 159.3404
#richness at soilbac1
S.chao1(soilbac1)
## T1_1
## 2628.514
S.chao2("T1_1", soilbac.t)
## T1_1
## 21055.39
S.ace(soilbac1)
## [1] 4465.983
```

Question 4: What is the difference between ACE and the Chao estimators? Do the estimators give consistent results? Which one would you choose to use and why?

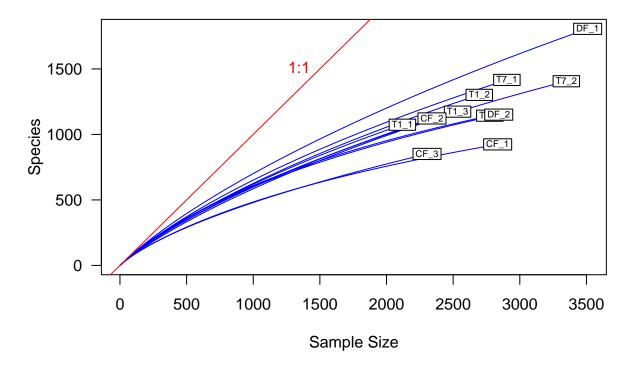
Answer 4: Instead of using the abundance or incidence of singletons and doubletons like with the Chao estimators, ACE estimator uses a threshold (conventionally 10 or fewer) to indicate whether the species is rare. ACE only looks at the richness of the taxon that are considered "rare" (ten individuals per site or fewer), while Chao estimators take into the account of all taxon. No. ACE reports the highest richness, while Chao1 the lowest for sit 1 of BCI dataset. Chao2 actually reports the highest richness for soilbac1 dataset, while Chao1 the lowest. If the site interested has a lot of "rare" taxon (observed abundance below or equal to 10) and very few "common" taxon, ACE will be a good choice since it only looks at the "rare" taxon richness. If the site taxon distribution is more even and the rare taxon are lower comparatively, Chao estimators would be a better choice. If differnt sites in a dataset can provie information for each other (that they are not entirely independent), then Chao2 is also better than Chao1.

Rarefaction

In the R code chunk below, please do the following:

- 1. Calculate observed richness for all samples in soilbac,
- 2. Determine the size of the smallest sample,
- 3. Use the rarefy() function to rarefy each sample to this level,
- 4. Plot the rarefaction results, and
- 5. Add the 1:1 line and label.

```
soilbac.S <- S.obs(soilbac.t)
min.N <- min(rowSums(soilbac.t))
S.rarefy <- rarefy(x = soilbac.t, sample = min.N, se = TRUE)
rarecurve(x = soilbac.t, step = 20, col = "blue", cex = 0.6, las = 1)
abline(0, 1, col = 'red')
text(1500, 1500, "1:1", pos = 2, col = 'red')</pre>
```



4) SPECIES EVNENNESS

Here, we consider how abundance varies among species, that is, **species evenness**.

Visualizing evenness: the rank abundance curve (RAC)

One of the most common ways to visualize evenness is in a **rank-abundance curve** (sometime referred to as a rank-abundance distribution or Whittaker plot). An RAC can be constructed by ranking species from the most abundant to the least abundant without respect to species labels (and hence no worries about 'ties' in abundance).

In the R code chunk below, do the following:

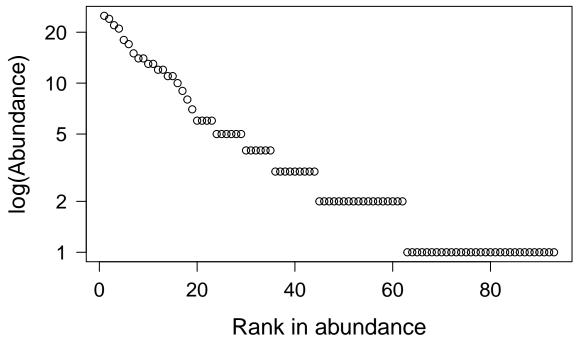
- 1. Write a function to construct a RAC,
- 2. Be sure your function removes species that have zero abundances,
- 3. Order the vector (RAC) from greatest (most abundant) to least (least abundant), and
- 4. Return the ranked vector

```
RAC <- function(x = ""){
    x.ab = x[x > 0]
    x.ab.ranked = x.ab[order(x.ab, decreasing = TRUE)]
    as.data.frame(lapply (x.ab.ranked, unlist))
    return (x.ab.ranked)
}
```

Now, let us examine the RAC for site1 of the BCI data set.

In the R code chunk below, do the following:

- 1. Create a sequence of ranks and plot the RAC with natural-log-transformed abundances,
- 2. Label the x-axis "Rank in abundance" and the y-axis "log(abundance)"



par <- opar

Question 5: What effect does visualizing species abundance data on a log-scaled axis have on how we interpret evenness in the RAC?

Answer 5: The range of y-axis (abundance) is larger if we use log-scale in this case, which makes the difference in abundance between ranks easier to visualize.

Now that we have visualized unevenness, it is time to quantify it using Simpson's evenness $(E_{1/D})$ and Smith and Wilson's evenness index (E_{var}) .

Simpson's evenness $(E_{1/D})$

In the R code chunk below, do the following:

- 1. Write the function to calculate $E_{1/D}$, and
- 2. Calculate $E_{1/D}$ for site1.

```
#function for calculating Simpson's Evenness metric
SimpE <- function(x = ""){
    S <- S.obs(x)
    x = as.data.frame(x)
    D <- diversity(x, "inv") #Simpson's diversity
    E <- (D)/S
    return(E)
}
SimpE(site1)
##    1
## 0.4238232</pre>
```

Smith and Wilson's evenness index (E_{var})

In the R code chunk below, please do the following:

- 1. Write the function to calculate E_{var} ,
- 2. Calculate E_{var} for site1, and
- 3. Compare $E_{1/D}$ and E_{var} .

```
Evar <- function(x){
    x <- as.vector(x[x>0])
    1 - (2/pi) * atan(var(log(x)))
}
Evar(site1)
```

```
## [1] 0.5067211
```

Question 6: Compare estimates of evenness for site1 of BCI using $E_{1/D}$ and E_{var} . Do they agree? If so, why? If not, why? What can you infer from the results.

Answer 6: The estimated evenness for site 1 using Simpson's Evenness Index is about 0.42, while that using Smith and Wilson's Evenness Index is 0.51. These are fairly similar, but E_{var} shows a slightly better evenness. This means E_{var} estimates the species abundance to be more even for this site than $E_{1/D}$. While $E_{1/D}$ is likely biased by the differences in the more abundant taxon, this could mean that the taxon that are more abundant are less even (i.e. there are likely some taxon that have way more observed individuals than the other taxon that are also relatively more abundant at the site).

5) INTEGRATING RICHNESS AND EVENNESS: DIVERSITY METRICS

So far, we have introduced two primary aspects of diversity, i.e., richness and evenness. Here, we will use popular indices to estimate diversity, which explicitly incorporate richness and evenness. We will write our own diversity functions and compare them against the functions in vegan.

Shannon's diversity (a.k.a., Shannon's entropy)

In the R code chunk below, please do the following:

- 1. Provide the code for calculating H' (Shannon's diversity),
- 2. Compare this estimate with the output of vegan's diversity function using method = "shannon".

```
# Function for calculating H' (Shannon's Diversity)
ShanH <- function(x = ""){
    H = 0
    for (n_i in x){
        if (n_i > 0){
            p = n_i / sum(x)
            H = H - p*log(p)
        }
    }
    return (H)
}
```

```
## [1] 4.018412
diversity(site1, index = "shannon")
```

[1] 4.018412

Simpson's diversity (or dominance)

In the R code chunk below, please do the following:

- 1. Provide the code for calculating D (Simpson's diversity),
- 2. Calculate both the inverse (1/D) and 1 D,
- 3. Compare this estimate with the output of vegan's diversity function using method = "simp".

```
#Function for calculating D (Simpson's Diversity)
SimpD <- function(x = ""){
    D = 0
    N = sum(x)
    for (n_i in x){
        D = D + (n_i^2) / (N^2)
    }
    return(D)
}

D.inv <- 1/SimpD(site1)
D.sub <- 1-SimpD(site1)
diversity(site1, index = "invsimpson")</pre>
```

```
## [1] 39.41555
diversity(site1, index = "simpson")
```

Fisher's α

[1] 0.9746293

In the R code chunk below, please do the following:

- 1. Provide the code for calculating Fisher's α ,
- 2. Calculate Fisher's α for site1 of BCI.

```
rac_f <- as.vector(site1[site1 > 0])
invD <- diversity(rac_f, index = "invsimpson")

Fisher <- fisher.alpha(rac_f)
Fisher</pre>
```

[1] 35.67297

Question 7: How is Fisher's α different from $E_{H'}$ and E_{var} ? What does Fisher's α take into account that $E_{H'}$ and E_{var} do not?

Answer 7: While $E_{H'}$ and E_{var} are both value between 0 and 1, Fisher's α is not, and α is the only fitted parameter that is estimated from the data. Both Simpson's Evenness and Smith and Wilson's Evenness Index is metrics for evenness, Fisher's α takes into account the richness as well.

6) HILL NUMBERS

Remember that we have learned about the advantages of Hill Numbers to measure and compare diversity among samples. We also learned to explore the effects of rare species in a community by examining diversity for a series of exponents q.

```
#profile <- function(com){</pre>
\# cbind(seq(0, 7, by = 0.11),
#
         unlist(lapply(seq(0, 7, by = 0.11), function(q) sum(apply(com, 1, function(x)))
#
           (x/sum(x))^q^(1/(1-q)))))))
#}
#BCI_profile <- profile(BCI)
#plot(BCI profile[, 1], BCI profile[, 2])
Hill 0 site1 <- specnumber(site1) #Hill number (q=0): richness
Hill_1_site1 <- exp(diversity(site1, index = "shannon")) #Hill (q=1): exponential Shannon's entropy
Hill_2_site1 <- diversity(site1, index = "invsimpson")</pre>
Hill_0_site1; Hill_1_site1; Hill_2_site1
## 1
## 93
## [1] 55.6127
## [1] 39.41555
```

Question 8: Using site1 of BCI and vegan package, a) calculate Hill numbers for q exponent 0, 1 and 2 (richness, exponential Shannon's entropy, and inverse Simpson's diversity). b) Interpret the effect of rare species in your community based on the response of diversity to increasing exponent q.

Answer 8a: Hill number for q = 0 (richness) is 93, for q = 1 (expoential Shannon's entropy) is 55.61, and for q = 2 (inverse Simpson's diversity) is 39.42.

Answer 8b: With decreasing importance that we treat rare species, the diversity metric seems to be decreasing at the same time. That is, the community at site 1 of BCI is considered less diverse if rare species are not considered to be important when we quantify biodiversity of the community. This also suggests that many species are rare at this site, or otherwise there will not be a huge difference between when q is 0 or 2.

##7) MOVING BEYOND UNIVARIATE METRICS OF α DIVERSITY

The diversity metrics that we just learned about attempt to integrate richness and evenness into a single, univariate metric. Although useful, information is invariably lost in this process. If we go back to the

rank-abundance curve, we can retrieve additional information – and in some cases – make inferences about the processes influencing the structure of an ecological system.

Species abundance models

plot.new()

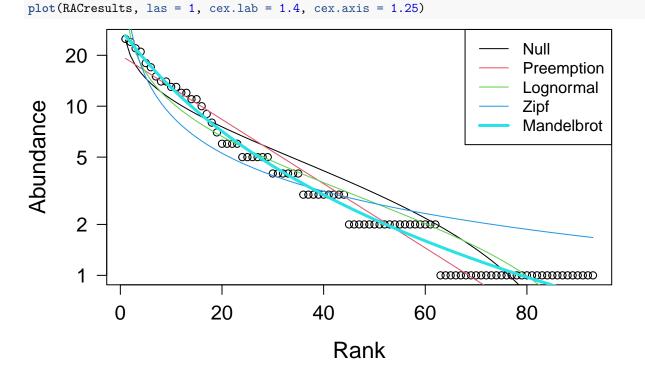
The RAC is a simple data structure that is both a vector of abundances. It is also a row in the site-by-species matrix (minus the zeros, i.e., absences).

Predicting the form of the RAC is the first test that any biodiversity theory must pass and there are no less than 20 models that have attempted to explain the uneven form of the RAC across ecological systems.

In the R code chunk below, please do the following:

- 1. Use the radfit() function in the vegan package to fit the predictions of various species abundance models to the RAC of site1 in BCI,
- 2. Display the results of the radfit() function, and
- 3. Plot the results of the radfit() function using the code provided in the handout.

```
RACresults <- radfit(site1)</pre>
RACresults
##
## RAD models, family poisson
## No. of species 93, total abundance 448
##
##
              par1
                         par2
                                  par3
                                           Deviance AIC
## Null
                                            39.5261 315.4362 315.4362
                                            21.8939 299.8041 302.3367
## Preemption
               0.042797
## Lognormal
               1.0687
                                            25.1528 305.0629 310.1281
                          1.0186
## Zipf
               0.11033
                         -0.74705
                                            61.0465 340.9567 346.0219
## Mandelbrot
               100.52
                         -2.312
                                    24.084
                                             4.2271 286.1372 293.7350
```



Question 9: Answer the following questions about the rank abundance curves: a) Based on the output of radfit() and plotting above, discuss which model best fits our rank-abundance curve for site1? b) Can we make any inferences about the forces, processes, and/or mechanisms influencing the structure of our system, e.g., an ecological community?

Answer 9a: The Mandelbrot model has the lowest AIC and BIC value among all five of the models, and its curve lines up the best with the dots, which means it is the "best" fit model to use for our rank-abundance curve for site1.

Answer 9b: First, species composition of this ecologial community is not distributed evenly. While very few species are very abundant, there is also a large number of rare species that only have a few observed individuals. This distribution is also not entirely by chance, but three different factors (paremeters) are contributing to its composition.

Question 10: Answer the following questions about the preemption model: a. What does the preemption model assume about the relationship between total abundance (N) and total resources that can be preempted? b. Why does the niche preemption model look like a straight line in the RAD plot?

Answer 10a: The total abundance depends on total resources, and rate of change is constant. In another word, if we have a fixed number of total resources for the species in this community to use, we will also have a fixed total abundance, because based on the assumption of first-come, first-serve, those who occupy the niche ealier will be more abundant as they have lengthier time to take resources.

 $Answer\ 10b$: This is because the rate of change between abundance and rank of abundance is constant.

Question 11: Why is it important to account for the number of parameters a model uses when judging how well it explains a given set of data?

Answer 11: It's self-evident that the more parameter that you use, the better fit the model is, just like the more factors that you take into consideration, the more accurately you can approximate the real world. However, with a research question in mind, a super parameterized model will distract us from getting the information we want to look at, making the model relatively "useless" even if it's more accurate.

SYNTHESIS

1. As stated by Magurran (2004) the $D=\sum p_i^2$ derivation of Simpson's Diversity only applies to communities of infinite size. For anything but an infinitely large community, Simpson's Diversity index is calculated as $D=\sum \frac{n_i(n_i-1)}{N(N-1)}$. Assuming a finite community, calculate Simpson's D, 1 - D, and Simpson's inverse (i.e. 1/D) for site 1 of the BCI site-by-species matrix.

```
D_finit <- function(x = ""){
    D = 0
    N = sum(x)
    for (n_i in x){
        D = D + (n_i * (n_i - 1)) / (N * (N - 1))
    }
    return(D)
}
SimpD_fin <- D_finit(site1)
sub_SimpD_fin <- 1-SimpD_fin
inv_SimpD_fin <- 1/SimpD_fin</pre>
SimpD_fin; sub_SimpD_fin; inv_SimpD_fin
```

```
## [1] 0.02319032
```

[1] 0.9768097

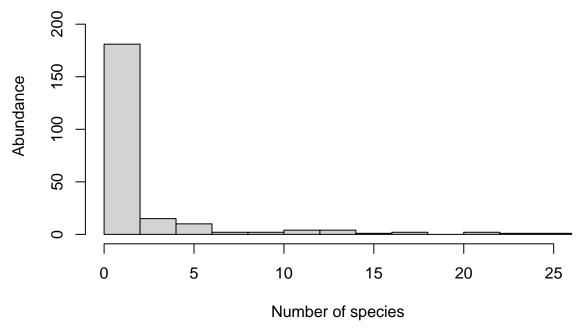
[1] 43.12145

Answer: If we assume the site 1 of BCI is finitely large, then the Simpson's Diversity Index (D) is approximately 0.022, 1-D is 0.9768, and 1/D is 43.1215

2. Along with the rank-abundance curve (RAC), another way to visualize the distribution of abundance among species is with a histogram (a.k.a., frequency distribution) that shows the frequency of different abundance classes. For example, in a given sample, there may be 10 species represented by a single individual, 8 species with two individuals, 4 species with three individuals, and so on. In fact, the rank-abundance curve and the frequency distribution are the two most common ways to visualize the species-abundance distribution (SAD) and to test species abundance models and biodiversity theories. To address this homework question, use the R function hist() to plot the frequency distribution for site 1 of the BCI site-by-species matrix, and describe the general pattern you see.

```
site1_frq <- as.vector(site1)
hist(x = as.numeric(site1), main = "Frequency distribution for site 1 in BCI",
    ylim = c(0,225), xlab = "Number of species", ylab = "Abundance")</pre>
```

Frequency distribution for site 1 in BCI



Answer: The frequency distrubtion shows that the abundance of species at site 1 of BCI is skewed to the left, which means very few species have a lot of observed individuals, while a lot of species are represented by only a few of individuals (it has a long tail).

3. We asked you to find a biodiversity dataset with your partner. This data could be one of your own or it could be something that you obtained from the literature. Load that dataset. How many sites are there? How many species are there in the entire site-by-species matrix? Any other interesting observations based on what you learned this week?

```
load("/cloud/project/QB2025_Huang/Group-project/longdataITS_objects2_datadryad.rda")
load("/cloud/project/QB2025_Huang/Group-project/longdataBac_objects2_datadryad.rda")
```

```
Bacteria <- longdataBac_datadryad</pre>
Fungi <- longdataITS_datadryad</pre>
rm(longdataBac_datadryad, longdataITS_datadryad)
# Make the species_by_site matrix
bac_by_sample <- with(Bacteria, tapply(Counts, list(ID, Sender), sum, default = 0))</pre>
fun_by_sample <- with(Fungi, tapply(Counts, list(ID, Sender), sum, default = 0))</pre>
#Bacteria diversity:
nrow(bac_by_sample)
## [1] 628
ncol(bac_by_sample)
## [1] 3142
#Fungal diversity
nrow(fun_by_sample)
## [1] 671
ncol(fun_by_sample)
## [1] 3130
#quick scan
bac_S <- specnumber(bac_by_sample)</pre>
min.N_bac <- min(rowSums(bac_by_sample))</pre>
S.rarefy_bac <- rarefy(x = bac_by_sample, sample = min.N_bac, se = TRUE)
rarecurve(x = bac_by_sample, step = 20, col = "blue", cex = 0.6, las = 1)
abline(0, 1, col = 'red')
                                                7837_4_U_oak
    200
                                               8131_3_F_spruce
                                               8243_1_G_spruce
                                               8343_4_F_spruce
                                                                                     7835 1 C coruce
8130 2 A pine
    150
                                                8343_1_F_spruce
8343_4_G_oak
                                                                                      5636_4_A_oak
Species
    100
                                                                                     5838_2_F_spruce
      50
                                                8343_4_G_pine
                                                8243_1_U_beech
                                                                                      7446_1_G_oak
                                               8343_4_G_beecl
       0
                                 200
                                                                          600
              0
                                                      400
                                              Sample Size
```

Answer: We have two datasets, one for fungal diversity and the other for bacterial diversity. For fungal diversity, there are in total 3130 species and 671 samples/sites in all communities. For

bacterial diversity, there are in total 3142 species and 628 sites. I did a quick scan for observed richness for all samples and made the rarecurve, and seems like some are way more abundant than the rest of them.

SUBMITTING YOUR ASSIGNMENT

Use Knitr to create a PDF of your completed 5.AlphaDiversity_Worksheet.Rmd document, push it to GitHub, and create a pull request. Please make sure your updated repo include both the pdf and RMarkdown files.

Unless otherwise noted, this assignment is due on Wednesday, January 29th, 2025 at 12:00 PM (noon).