

bioinfo__first.R

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```
# Get current working directory
getwd()

## [1] "/Users/phanthihonghuong/Dropbox/Earlham/Spring 2019/BIOL:CS 383/Module 2"

# Set new working directory
# setwd('~/Desktop/')

data <- as.matrix(read.table('Table1.txt', header=TRUE, sep='\t', row.names = 1))
data

##      Sample1 Sample2 Sample3 Sample4
## OTU1      25      80      60      90
## OTU2      25       0       5       0
## OTU3      25       0       5       0
## OTU4      25       0       0       0
## OTU5       0      20      30      10

dim(data)

## [1] 5 4

oturichness <- rowSums(data)
oturichness

## OTU1 OTU2 OTU3 OTU4 OTU5
## 255  30  30  25  60

rowSums(data[1:2,])

## OTU1 OTU2
## 255  30

colSums(data)

## Sample1 Sample2 Sample3 Sample4
##      100      100      100      100

dataPA <- (data>0)*1
dataPA

##      Sample1 Sample2 Sample3 Sample4
## OTU1       1       1       1       1
## OTU2       1       0       1       0
## OTU3       1       0       1       0
## OTU4       1       0       0       0
## OTU5       0       1       1       1

(data>0)

##      Sample1 Sample2 Sample3 Sample4
## OTU1     TRUE     TRUE     TRUE     TRUE
## OTU2     TRUE    FALSE     TRUE    FALSE
```

```
## OTU3      TRUE    FALSE    TRUE    FALSE
## OTU4      TRUE    FALSE    FALSE   FALSE
## OTU5     FALSE     TRUE     TRUE     TRUE
```

```
TRUE*1
```

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

```
# species richness
```

```
rich <- colSums(dataPA)
```

```
rich
```

```
## Sample1 Sample2 Sample3 Sample4
```

```
##      4      2      4      2
```

```
# relative abundance
```

```
dataREL <- data
```

```
dataREL[,1] = data[,1]/sum(data[,1])
```

```
dataREL[,2] = data[,2]/sum(data[,2])
```

```
dataREL[,3] = data[,3]/sum(data[,3])
```

```
dataREL[,4] = data[,4]/sum(data[,4])
```

```
dataREL
```

```
##      Sample1 Sample2 Sample3 Sample4
```

```
## OTU1      0.25      0.8      0.60      0.9
```

```
## OTU2      0.25      0.0      0.05      0.0
```

```
## OTU3      0.25      0.0      0.05      0.0
```

```
## OTU4      0.25      0.0      0.00      0.0
```

```
## OTU5      0.00      0.2      0.30      0.1
```

```
dataREL2 <- data
```

```
for (i in 1:4) {
```

```
  dataREL2[,i] <- data[,i]/sum(data[,i])
```

```
}
```

```
dataREL2
```

```
##      Sample1 Sample2 Sample3 Sample4
```

```
## OTU1      0.25      0.8      0.60      0.9
```

```
## OTU2      0.25      0.0      0.05      0.0
```

```
## OTU3      0.25      0.0      0.05      0.0
```

```
## OTU4      0.25      0.0      0.00      0.0
```

```
## OTU5      0.00      0.2      0.30      0.1
```

```
colSums(dataREL2)
```

```
## Sample1 Sample2 Sample3 Sample4
```

```
##      1      1      1      1
```

```
# transpose matrix
```

```
t(dataREL2)
```

```
##      OTU1 OTU2 OTU3 OTU4 OTU5
```

```
## Sample1 0.25 0.25 0.25 0.25 0.0
```

```
## Sample2 0.80 0.00 0.00 0.00 0.2
```

```
## Sample3 0.60 0.05 0.05 0.00 0.3
```

```
## Sample4 0.90 0.00 0.00 0.00 0.1
```

```
library(vegan)
```

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

```
## Loading required package: lattice
## This is vegan 2.5-4
samplePA.dist <- vegdist(t(dataREL2), method='jaccard')
```