

# Mothur Amplicon Analysis

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## Abstract

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## Protocol

### Step 1.

Move to directory containing Mothur:

```
cmd COMMAND
$ cd /home/c-debi/ecogeo/mothurdir
$ mothur
```

### Step 2.

Open a second terminal window.

### Step 3.

To perform rarefaction:

```
cmd COMMAND
mothur > rarefaction.single(shared=stability.an.shared, calc=sobs, freq=100)
```

### EXPECTED RESULTS

```
numsampled 0.03-F3D0 lci-F3D0 hci-F3D0 0.03-F3D1 lci-F3D1 hci-F3D1 0.03-F3D141 lci-F3D141
hci-F3D141 0.03-F3D142 lci-F3D142 hci-F3D142 0.03-F3D143 lci-F3D143 hci-F3D143 0.03-F3D144
lci-F3D144 hci-F3D144 0.03-F3D145 lci-F3D145 hci-F3D145 0.03-F3D146 lci-F3D146 hci-F3D146
0.03-F3D147 lci-F3D147 hci-F3D147 0.03-F3D148 lci-F3D148 hci-F3D148 0.03-F3D149 lci-F3D149
hci-F3D149 0.03-F3D150 lci-F3D150 hci-F3D150 0.03-F3D2 lci-F3D2 hci-F3D2 0.03-F3D3 lci-F3D3
hci-F3D3 0.03-F3Dlci-F3D5 hci-F3D5 0.03-F3D6 lci-F3D6 hci-F3D6 0.03-F3D7 lci-F3D7 hci-F3D7
0.03-F3D8 lci-F3D8 hci-F3D8 0.03-F3D9 lci-F3D9 hci-F3D9
1 1.0000 1.0000 1.0000 1.0000 1.0000 1.0000 1.0000 1.0000 1.0000 1.0000
1.0000 1.0000 1.0000 1.0000 1.0000 1.0000 1.0000 1.0000 1.0000 1.0000
1.0000 1.0000 1.0000 1.0000 1.0000 1.0000 1.0000 1.0000 1.0000 1.0000
1.0000 1.0000 1.0000 1.0000 1.0000 1.0000 1.0000 1.0000 1.0000 1.0000
1.0000 1.0000 1.0000 1.0000 1.0000 1.0000 1.0000 1.0000 1.0000 1.0000
1.0000 1.0000 1.0000 1.0000 1.0000 1.0000 1.0000 1.0000 1.0000 1.0000
```

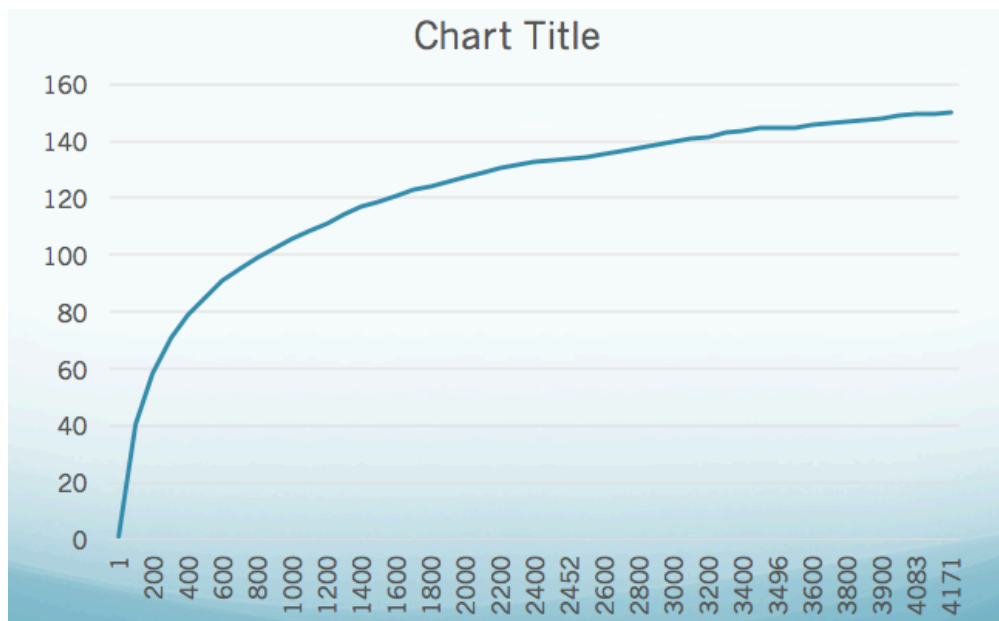
### Step 4.

We can make a rarefaction curve in Powerpoint

cmd **COMMAND**

```
$ cut -f1,2 stability.an.groups.rarefaction > sample1.rarefaction
```

📈 **EXPECTED RESULTS**



## Step 5.

Alpha diversity measures:

Sample	No. seqs used	Observed Species	Inv. Simpson	Confidence interval - L	Confidence interval - H
F3D0	2441	132.734	25.716	24.093	27.574
F3D1	2441	127.36	34.539	32.539	37.032

cmd **COMMAND**

```
$ mothur > summary.single(shared=stability.an.shared, calc=nseqs-coverage-sobs-invsimpson, subsample=2441)
```

```
$ less stability.an.groups.ave-std.summary
```

## Step 6.

What about bar graphs with relative abundance and taxonomy?

cmd **COMMAND**

```
$ less less stability.an.cons.taxonomy  
$ less stability.an.0.03.subsample.shared
```

📈 **EXPECTED RESULTS**

OTU Size Taxonomy  
Otu0001 12328

Bacteria(100);"Bacteroidetes"(100);"Bacteroidia"(100);"Bacteroidales"(100);"Porphyromonadaceae"(100);"Porphyromonadaceae"\_unclassified(100);"Porphyromonadaceae"\_unclassified(100);"Porphyromonadaceae"\_unclassified\_unclassified(100);

label	Group	numOtus	Otu0001	Otu0002	Otu0003	Otu0004	Otu0005	Otu0006	Otu0007
0.03	F3D0	296	181 116	132 201	164 132				

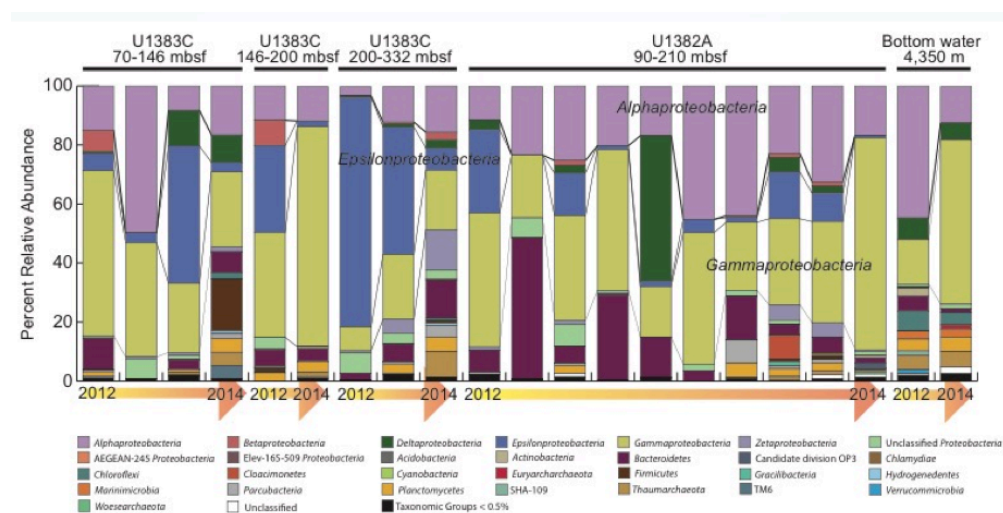
## ■ ANNOTATIONS

Elisha Wood-Charlson 03 Aug 2016

0.03.subsample.shared file missing

### Step 7.

Unrelated data:



### Step 8.

Analysis

- Beta diversity - measured differences between communities
- How related are communities to each other?
- Theta YC (community structure) - considers shared OTUs and relative abundance of OTUs
- Jaccard (community membership) - compared which OTUs are present in samples

### Step 9.

Beta diversity measures:

cmd **COMMAND**

\$ mothur > dist.shared(shared=stability.an.shared, calc=thetayc-jclass, subsample=2241)

### Step 10.

Turn distance measure output in to a dendrogram:

cmd **COMMAND**

```
$ mothur > tree.shared(phylip=stability.an.thetayc.0.03.lt.ave.dist)
$ mothur > quit()
```

```
$ Dendroscope
```

```
$ less stability.an.thetayc.0.03.lt.ave.tre
```

## Step 11.

### Statistical significance

- Involves classifying your samples in to categories → good experimental design would have classify these samples before seeing results
- E.g. surface vs deep samples or winter vs. summer
- Generate points to plot Principal Component Analysis or Non-metric Dimensional Scaling plots
- Perform AMOVA statistical tests