# Loading Microbiome Data

**Install biom package**

```
install.packages('biom',repo='http://cran.wustl.edu')
```

**Load biom package**

```
library('biom')
```

**Load global gut data using biom package**

```
gg.otus.biom <- read_biom('../data/globalgut/otutable.biom')
```

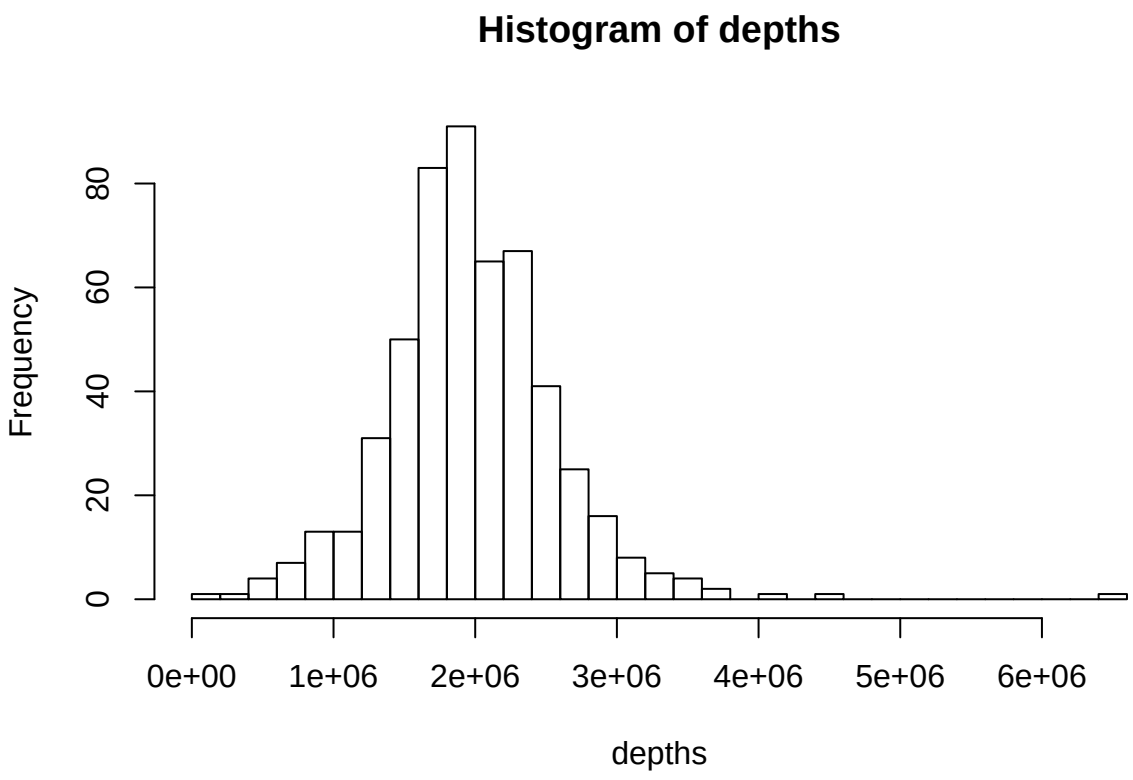
**Extract data matrix (OTU counts) from biom table**

```
gg.otus <- as.matrix(biom_data(gg.otus.biom))

# transpose so that rows are samples and columns are OTUs
gg.otus <- t(gg.otus)
```

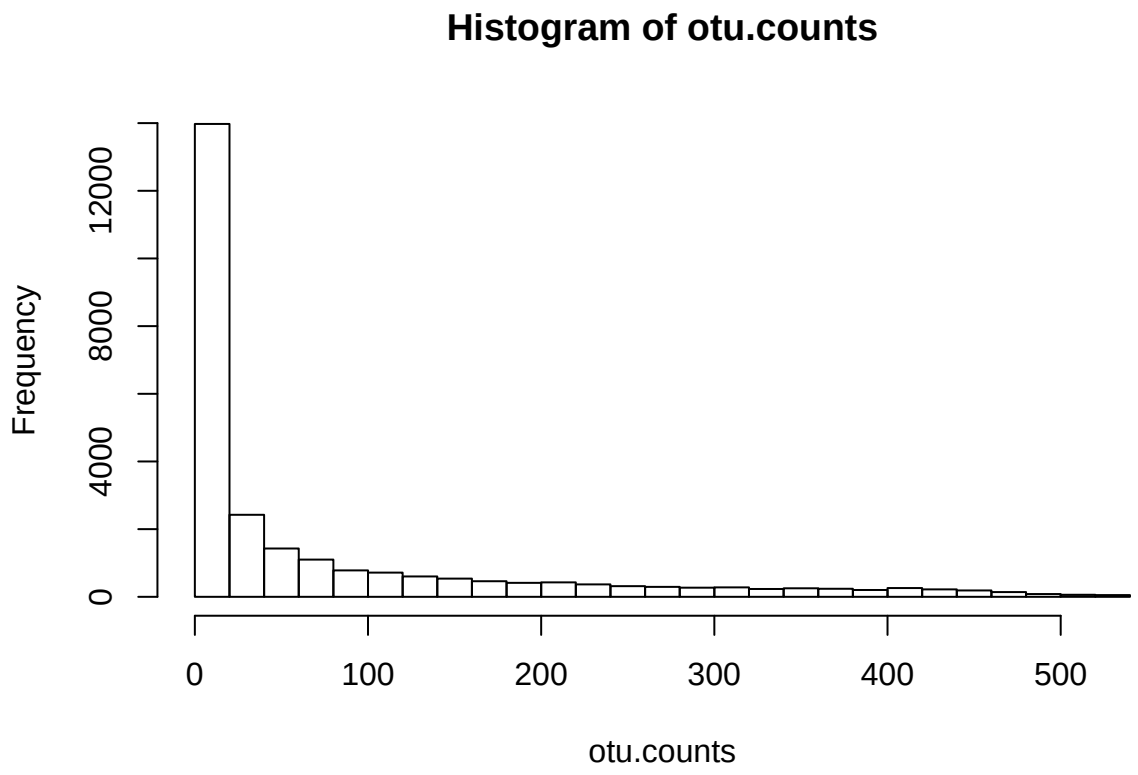
**Plot histogram of sample depths**

```
depths <- rowSums(gg.otus)
hist(depths,breaks=30)
```



**Plot histogram of OTU frequencies**

```
otu.counts <- colSums(gg.otus > 0)
hist(otu.counts,breaks=30)
```



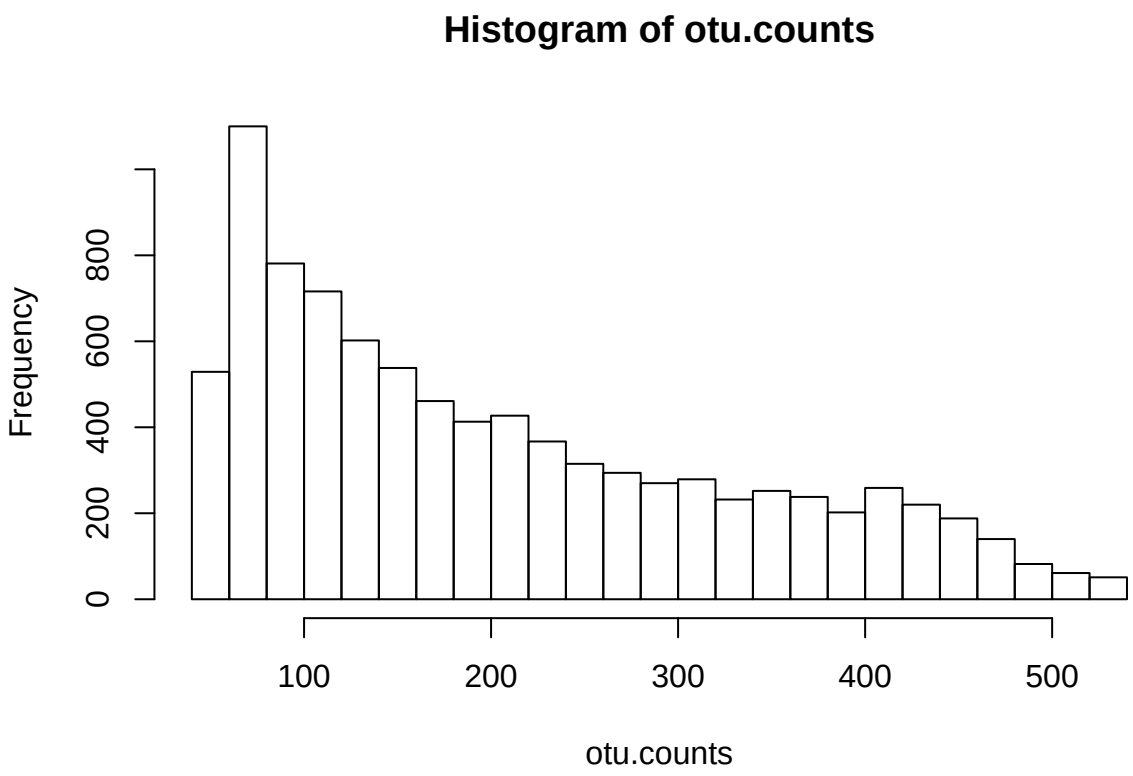

**Remove OTUs present in $< 10\%$ of samples**

```
gg.otus <- gg.otus[,colMeans(gg.otus > 0) >= .1]
depths <- rowSums(gg.otus)
dim(gg.otus)
```

```
## [1]  530 9017
```

**Re-plot histogram of OTU frequencies now that we removed singletons**

```
otu.counts <- colSums(gg.otus > 0)
hist(otu.counts,breaks=30)
```




**Remove any samples with very low depth**

```
sort(depths)[1:10]
```

```
##  USygt34.T2.418554   USygt25.M.418835  AmzC3adltM.418849
##                  1             309608             405006
##    USygt3.M.418496    Amz33eld.418866  USinfTw1.2.418491
##             420719             504968             576975
## AmzC30adltF.418737  AmzC9adltM.418480 AmzC22chldM.418704
##             595770             631957             646988
##   USygt12.F.418502
##             679153
```

```
gg.otus <- gg.otus[depths >= 1000,]
dim(gg.otus)
```

```
## [1]  529 9017
```

**Load mapping file**

```
gg.map <- read.table('../data/globalgut/map.txt',sep='\t',head=T,row=1,check=F,comment='')
```

**Ensure that mapping file and OTU table contain the sample samples in the same order**

```
sample.ids <- intersect(rownames(gg.otus), rownames(gg.map))

# might as well put the samples in alphabetical order
sample.ids <- sort(sample.ids)

# in R you can subset using sample IDs or numerical indices. Most languages only use indices.
gg.otus <- gg.otus[sample.ids,]
gg.map <- gg.map[sample.ids,]
dim(gg.otus)
```

```
## [1]  529 9017
```

```
dim(gg.map)
```

```
## [1] 529  63
```