

# Rarefaction

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Cargamos librerías y datos de las dos minas Pmt y S1.

```
library("phyloseq")
library("ggplot2")
library("RColorBrewer")
library("patchwork")
library(vegan)
```

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

```
## Loading required package: lattice
```

```
## This is vegan 2.6-2
```

```
setwd("~/metagenomas")
```

```
raw_metagenomes <- import_biom("metagenomes_Pmt_S1.biom")
raw_metagenomes@tax_table@.Data <- substring(raw_metagenomes@tax_table@.Data, 4)
colnames(raw_metagenomes@tax_table@.Data) <- c("Kingdom", "Phylum", "Class", "Order", "Family", "Genus",
unique(raw_metagenomes@tax_table@.Data[, "Kingdom"])
```

```
## [1] "Bacteria" "Archaea" "Eukaryota" "Viruses"
```

```
raw_metagenomes <- subset_taxa(raw_metagenomes, Kingdom == "Bacteria")
```

Extraemos los OTUs y calculamos el número máximo de conteos.

```
otu <- otu_table(raw_metagenomes)
otu <- as.data.frame(t(otu))
sample_names <- rownames(otu)

S <- specnumber(otu)
S
```

```
## Pmt2_S287 S1_S286
##      7887      7981
```

```
raremax <- min(rowSums(otu))
raremax
```

```
## [1] 2184595
```

Aplicamos rarefy con los OTUs, número máximo de conteos y el paso para aplicar el rarefy.

```
rare1 <- rarefy(t(otu), sample= c(seq(100000,2000000 , by = 100000), raremax) , se = T, MARG = 2)
rare_t <- t(rare1)
```

Guardamos los datos en una base de datos, calculamos las desviaciones estándar.

```
site <- c(rep("Pmt2_S287",21), rep("S1_S286",21))

reads <- c(c(seq(100000,2000000 , by = 100000), raremax), c(seq(100000,2000000 , by = 100000), raremax))

Pmt2_S <- rare_t[,1]
Pmt2_se <- rare_t[,2]
S1_S <- rare_t[,3]
S1_se <- rare_t[,4]

Svalues <- c(Pmt2_S, S1_S)
sevalues <- c(Pmt2_se, S1_se)

data <- data.frame(Site= site,
                   reads = reads,
                   S = Svalues,
                   se = sevalues)
```

Realizamos el plot.

```
rare_plot <- ggplot(data, aes(x= reads, y=S, col=Site)) +
  geom_point()+
  geom_errorbar(aes(ymin=S-se, ymax=S+se), width=.3,
               position=position_dodge(0.001))+
  ylab("OTUs")

rare_plot
```

