

MOB Relative Abundance

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Overview

Following code written by Kevin Webster to estimate MOB relative abundance from qPCR data

Set working directory

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

```
## [1] "/Users/lennonj/GitHub/radiolyticCH4/code/caves/qPCR"
```

```
setwd("~/GitHub/radiolyticCH4")
```

Read Microbial data

```
mob <- read.delim("~/GitHub/radiolyticCH4/data/caves/qPCR/mob.661.out.txt", sep = " ",  
  stringsAsFactors = FALSE)  
eub <- read.delim("~/GitHub/radiolyticCH4/data/caves/qPCR/20150813_VN_EUB_qPCR.txt",  
  stringsAsFactors = FALSE)
```

Calculate the relative abundance of methanotrophs

```
mob[,4] <- as.numeric(mob[,4]) # change data type of mob column 4  
eub[,4] <- as.numeric(eub[,4]) # change data type of eub column 4  
mob[,2] <- as.numeric(mob[,2]) # change data type of mob column 2
```

```
## Warning: NAs introduced by coercion
```

```
n.mob <- mob[1:51,4] # names the mob copy number vector  
n.eub <- eub[1:51,4] # names the 16S copy number vector  
  
# mass of the soil used to extract DNA from  
mass <- c(0.25, 0.25, 0.25, 0.23, 0.23, 0.23, 0.25, 0.25, 0.25,  
  0.25, 0.25, 0.25, 0.19, 0.19, 0.19, 0.25, 0.25, 0.25,  
  0.245, 0.245, 0.245, 0.235, 0.235, 0.235, 0.25, 0.25, 0.25,  
  0.25, 0.25, 0.25, 0.24, 0.24, 0.24, 0.24, 0.24, 0.24,  
  0.23, 0.23, 0.23, 0.25, 0.25, 0.25, 0.245, 0.245, 0.245,  
  0.25, 0.25, 0.25, 0.24, 0.24, 0.24)
```

```

# dilution of template used for qPCR
dil <- c(1.49, 1.49, 1.49, 24, 24, 24, 20, 20, 20,
        10, 10, 10, 18.75, 18.75, 18.75, 7.2, 7.2, 7.2,
        8.4, 8.4, 8.4, 16.4, 16.4, 16.4, 4.4, 4.4, 4.4,
        20.4, 20.4, 20.4, 12, 12, 12, 1, 1, 1,
        1, 1, 1, 30, 30, 30, 6.8, 6.8, 6.8,
        2.8, 2.8, 2.8, 5.2, 5.2, 5.2)

# correct for the dilution of template
n.mob.cor <- n.mob*dil

mob.rabund <- n.mob/n.eub # calculates the relative abundance of MOB

# calculate the number of pmoA genes per gram of soil
mob.p.mass <- n.mob.cor/mass

name <- mob[1:51,2] # generates a labeling vector
t.m.rabund <- cbind(name, mass, n.mob.cor, mob.rabund, mob.p.mass) # summary table

write.table(t.m.rabund, file = "~/GitHub/radiolyticCH4/data/caves/qPCR/mob.rabund.txt")

```