Cave Rock Values

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Overview

Code written by Kevin Webster to calcuate copy number abundance (expressed as MOB per gram rock bifoilm) and relative abundance (MOB / 16S rRNA gene)

Set working directory

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

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

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

Read in relevant data

```r
mob <- read.delim("~/GitHub/radiolyticCH4/data/caves/qPCR/mob.rabund.txt", sep =" ",
                  stringsAsFactors = FALSE)
rock.names <- read.delim("~/GitHub/radiolyticCH4/data/caves/qPCR/sample.by.rock.txt",
                  stringsAsFactors = FALSE, header = FALSE)

mob[is.na(mob)] <- 0
```

Calculate the average pmoA copy numbers on each rock per gram

```r
mob[,5] <- as.numeric(mob[,5]) # change data type of mob column 3

n.mob <- mob[,5] # names the mob copy number vector

#Calculate the arverage copy numbers on each rock

# Minh Chou Cave Bag 1 ROck 1
MC1R1 = mean(mob[1:3,5])

# Minh Chou Cave Bag 1 Rock 2
MC1R2 = mean(mob[7:9,5])

# Minh Chou Cave Bag 1 Rock 3
MC1R3 = mean(mob[19:21,5])
```

```r
# Minh Chou Cave Bag 2 Rock 1
MC2R1 = mean(mob[16:18,5])

# Minh Chou Cave Bag 2 Rock 2
MC2R2 = mean(mob[13:15,5])

# Minh Chou Cave Bag 2 Rock 3
MC2R3 = mean(mob[25:27,5])

# Minh Chou Cave Bag 3 Rock 1
MC3R1 = mean(mob[10:12,5])

# Minh Chou Cave Bag 3 Rock 2
MC3R2 = mean(mob[4:6,5])

# Minh Chou Cave Bag 3 Rock 3
MC3R3 = mean(mob[22:24,5])

# Hoa Cuong Cave Bag 1 Rock 1
HC1R1 = mean(mob[40:42,5])

# Hoa Cuong Cave Bag 1 Rock 2
HC1R2 = mean(mob[49:51,5])

# Hoa Cuong Cave Bag 1 Rock 3
HC1R3 = mean(mob[46:48,5])

# Hoa Cuong Cave Bag 2 Rock 1
HC2R1 = mean(mob[28:30,5])

# Hoa Cuong Cave Bag 2 Rock 2
HC2R2 = mean(mob[43:45,5])

# Hoa Cuong Cave Bag 2 Rock 3
HC2R3 = mean(mob[37:39,5])

# Hoa Cuong Cave Bag 3 Rock 1
HC3R1 = mean(mob[34:36,5])

# Hoa Cuong Cave Bag 3 Rock 2
HC3R2 = mean(0,0,0)

# Hoa Cuong Cave Bag 3 Rock 3
HC3R3 = mean(mob[31:33,5])
```

Calculate average copy number per gram of soil per bag

```r
# Minh Chou Cave Bag 1
MC1 <- (MC1R1+MC1R3)/2 # removed MC1R2; no amplification

# Minh Chou Cave Bag 2
MC2 <- (MC2R1+MC2R2+MC2R3)/3
```

```r
# Minh Chou Cave Bag 3
MC3 <- (MC3R1+MC3R2+MC3R3)/3

# Hoa Cuong Cave Bag 1
HC1 <- (HC1R1+HC1R2)/2 # removed HC1R3; no amplificaiton

# Hoa Cuong Cave Bag 2
HC2 <- (HC2R1+HC2R2+HC2R3)/3

# Hoa Cuong Cave Bag 3
HC3 <- (HC3R1+HC3R2+HC3R3)/3

sem <- function(x) sqrt(var(x)/length(x))
meanMC.gram <- mean(c(MC1, MC2, MC3))
min(c(MC1, MC2, MC3))
```

```
## [1] 10314
```

```r
max(c(MC1, MC2, MC3))
```

```
## [1] 26371
```

```r
semMC.gram <- sem((c(MC1, MC2, MC3)))
meanHC.gram <- mean(c(HC1, HC2, HC3))
semHC.gram <- sem(c(HC1, HC2, HC3))
min(c(HC1, HC2, HC3))
```

```
## [1] 34896
```

```r
max(c(HC1, HC2, HC3))
```

```
## [1] 152673
```

Calculate the average relative abundance

```r
mob[,4] <- as.numeric(mob[,4]) # change data type of mob column 3

n.mob <- mob[,4] # names the mob copy number vector

#Calculate the arverage copy numbers on each rock

# Minh Chou Cave Bag 1 ROck 1
relMC1R1 = mean(mob[1:3,4])

# Minh Chou Cave Bag 1 Rock 2
# relMC1R2 = mean(mob[7:9,4]) # no MOB amplificaiton on entire sample

# Minh Chou Cave Bag 1 Rock 3
```

```r
relMC1R3 = mean(mob[19:21,4])

# Minh Chou Cave Bag 2 Rock 1
relMC2R1 = mean(mob[16:17,4]) # no MOB amplifcition on 269 tech rep 3

# Minh Chou Cave Bag 2 Rock 2
relMC2R2 = mean(mob[13,4]) # no amplificaiton on 268 tech rep 2 and 3

# Minh Chou Cave Bag 2 Rock 3
relMC2R3 = mean(mob[c(25,27),4]) # no amplificaiton on 272 tech rep 2

# Minh Chou Cave Bag 3 Rock 1
#relMC3R1 = mean(mob[10:12,4]) # no MOB amplificaiton on entire sample

# Minh Chou Cave Bag 3 Rock 2
relMC3R2 = mean(mob[5:6,4]) # outlier on 265 tech rep 1

# Minh Chou Cave Bag 3 Rock 3
#relMC3R3 = mean(mob[22:24,4]) # no MOB amplificaiton on entire sample

# Hoa Cuong Cave Bag 1 Rock 1
relHC1R1 = mean(mob[40:42,4])

# Hoa Cuong Cave Bag 1 Rock 2
relHC1R2 = mean(mob[49:51,4])

# Hoa Cuong Cave Bag 1 Rock 3
relHC1R3 = mean(mob[46:48,4])

# Hoa Cuong Cave Bag 2 Rock 1
relHC2R1 = mean(mob[28:30,4])

# Hoa Cuong Cave Bag 2 Rock 2
relHC2R2 = mean(mob[43:45,4])

# Hoa Cuong Cave Bag 2 Rock 3
#relHC2R3 = mean(mob[37:39,4]) # no MOB amplificaiton on entire sample

# Hoa Cuong Cave Bag 3 Rock 1
relHC3R1 = mean(mob[c(34,36),4]) # no amplificaiton on 272 tech rep 2

# Hoa Cuong Cave Bag 3 Rock 2
relHC3R2 = mean(0,0,0)

# Hoa Cuong Cave Bag 3 Rock 3
relHC3R3 = mean(mob[31:33,4])
```

Calculate average rel abund per bag

```r
# Minh Chou Cave Bag 1
relMC1 <- (relMC1R1+relMC1R3)/2 # removed MC1R2; no amplification
```

```r
# Minh Chou Cave Bag 2
relMC2 <- (relMC2R1+relMC2R2+relMC2R3)/3

# Minh Chou Cave Bag 3
relMC3 <- (relMC3R2)

# Hoa Cuong Cave Bag 1
relHC1 <- (relHC1R1+relHC1R2+relHC1R3)/3

# Hoa Cuong Cave Bag 2
relHC2 <- (relHC2R1+relHC2R2)/2

# Hoa Cuong Cave Bag 3
relHC3 <- (relHC3R1+relHC3R3)/2

sem <- function(x) sqrt(var(x)/length(x))
rel.meanMC.gram <- mean(c(relMC1, relMC2, relMC3))
min(c(relMC1, relMC2, relMC3))*100
```

```
## [1] 0.1078
```

```r
max(c(relMC1, relMC2, relMC3))*100
```

```
## [1] 0.5646
```

```r
semMC.gram <- sem((c(relMC1, relMC2, relMC3)))

rel.meanHC.gram <- mean(c(relHC1, relHC2, relHC3))
rel.semHC.gram <- sem(c(relHC1, relHC2, relHC3))
min(c(relHC1, relHC2, relHC3))*100
```

```
## [1] 0.951
```

```r
max(c(relHC1, relHC2, relHC3))*100
```

```
## [1] 1.477
```