# SJR1 Centric Diatoms Clearance Rates

## Code

File Name: MicroplanktonAnalysis/scripts/03\_calcs\_CR\_test\_cendia\_SJR1.R

library(tidyverse)

library(writexl)

load("data/MasterFiles/MasterRFiles/volbio\_all.Rdata")

load("data/Clearance Rates/taxaCen.Rdata")

source("scripts/01\_function\_clearanceRates.R")

### Using the base file taxaCen, filter out everything but SJR1

taxaCenSJR1 <- filter(taxaCen, grepl('SJR1', samp\_ev))

## Remove the esd column

taxaCenSJR1 <- select(taxaCenSJR1, samp\_ev, exp, rep, grp\_sz,

counts\_per\_ml)

### Create a df with only the controls and a df with only the

experimentals. Calculate the mean counts of the controls, then add that df to the experimentals df using left join or merge. This new df can then be used with the clearance rate function

### Controls

taxaCenSRJ1C <- taxaCenSJR1[(taxaCenSJR1$exp== "FC"),]

### Experimentals

taxaCenSRJ1E <- taxaCenSJR1[(taxaCenSJR1$exp== "T24"),]

### Calculate the mean counts of the controls

## "Cmn" in the mutate function indicates the Control (formerly FC) mean

taxaCenSRJ1Cmn <- group\_by(taxaCenSRJ1C, grp\_sz) %>%

mutate(Cmn = mean(counts\_per\_ml)) %>%

subset(select = -counts\_per\_ml) %>%

ungroup

### Remove the rep column and then remove duplicate rows

taxaCenSRJ1Cmn2 <- subset(taxaCenSRJ1Cmn, select = -rep)

duplicated(taxaCenSRJ1Cmn2) ## looks at what rows are

duplicated

taxaCenSRJ1Cmn2 <- taxaCenSRJ1Cmn2

[!duplicated(taxaCenSRJ1Cmn2), ] ## removes duplicated rows

### Join taxaCenSRJ1C and taxaCenSRJ1Cmn2

taxaCenSJR1CE <- left\_join(taxaCenSRJ1E, taxaCenSRJ1Cmn2, by = "grp\_sz")

### Remove unneeded columns

taxaCenSJR1CE <- subset(taxaCenSJR1CE, select = c(-samp\_ev.y, -exp.y))

### Rename columns

taxaCenSJR1CE <- taxaCenSJR1CE %>%

rename("event" = "samp\_ev.x",

"sample" = "exp.x",

"group" = "grp\_sz",

"cpm" = "counts\_per\_ml")

### Rename T24 to exp

taxaCenSJR1CE$sample <- replace(taxaCenSJR1CE$sample,taxaCenSJR1CE$sample=="T24","exp")

### Reorder the columns

taxaCenSJR1CE <- taxaCenSJR1CE[, c(1,4,2,3,5,6)]

### Calculate clearance rates for SJR1

source("scripts/01\_function\_clearanceRates.R")

sjr1Cr <- rowwise(taxaCenSJR1CE) %>%

mutate(CR = cr\_func(controlMnCt = Cmn, expCt = cpm))

Clearance Rate Function

cr\_func <- function(controlMnCt, expCt, numBugs=24, V=595) {

cr = V \* ((log(controlMnCt) - log(expCt))/numBugs)

if(controlMnCt == 0){

return(0)

} else{

return(cr)

}

}

### Note:

V = total volume in ml of the sample bottle;

controlMnCt = the mean count of the three replicates of the control samples;

expCt = the counts of each of the three replicates of the experimental samples;

numBugs = the number of copepods that were in the experimental sample bottles--in the Hunger Games project, it was 24 in all bottles.

## Clearance Rates Results data frame

