Clearance Rates Code and Plots

## **Calculations** 03\_calcs\_CR\_IR\_New\_06\_03.R

## **Plots** 04\_plots\_CR\_IR\_New.R

### \_\_\_\_\_\_\_\_\_\_\_\_ CREATE THE BASE DATA FRAME \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

base <- volbio\_all\_cr %>%

select(samp\_ev, exp, rep, esd, group\_size, cpm, bio\_pgC\_ml)

save(base, file = "data7\_24/Clearance Rates 2/base.Rdata")

###### \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_CLEARANCE RATE \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_###

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### Sum up the cpm for the 15 group\_size groups, adding all cpm for organisms

## that fall into those 15 categories, such as, all the small centric diatoms

## in a sampling event, experimental bottle

sumCpm <- base %>%

group\_by(samp\_ev, group\_size, exp, rep) %>%

summarise(TotalCpm=sum(cpm),

.groups = 'drop') %>%

as.data.frame()

## Create the base data frame that has only the control and experimental cpm

sumCpm\_CE <- sumCpm %>%

filter( str\_detect(exp, "C|E"))

### Create another df from the above, with only the control samples

sumCpm\_C <- sumCpm\_CE%>%

filter(exp == "C") %>%

rename(cpmC = TotalCpm)

### Create a df with only experimental samples

sumCpm\_E <- sumCpm\_CE%>%

filter(exp == "E")%>%

rename(cpmE = TotalCpm)

### Create a df with only initial samples (for the ingestion rates)

sumCpm\_I <- sumCpm%>%

filter(exp == "I")%>%

rename(cpmI = TotalCpm)

### Apply the mean function to the controls df to get control mean counts

## per ml across the three replicates. Leave out the rep column so

## that what remains in the df is one row for each individual organism/size

## and the mean of the control sample counts per ml or biomass per ml

sumCpm\_Cmn <- sumCpm\_C %>%

group\_by(samp\_ev, group\_size, exp) %>%

summarise(Cmn=mean(cpmC),

.groups = 'drop') %>%

as.data.frame()

### Since CR needs the mean control samples and the three replicates experimental

## samples, join the experimental sample df with the control means df. This will

## necessarily include the rep column, since we need the experimental samples

## individual replicate counts or biomass for the calculation.

sumCpmE\_Cmn <- left\_join(sumCpm\_E, sumCpm\_Cmn,

by = c("samp\_ev", "group\_size"))

### Remove unneeded columns, and rename and re-order remaining columns

## Do I need the exp column?--Can't keep it since E is one column and C

## is another column

names(sumCpmE\_Cmn)

sumCpmE\_Cmn <- select(sumCpmE\_Cmn,

event = samp\_ev,

group\_size, rep, cpmE,

Cmn)

### Calculate clearance rates. The resulting data frame includes all the replicates

## since the CR was calculated for each replicate.

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

sumCpm\_cr <- rowwise(sumCpmE\_Cmn) %>%

mutate(CRmlcd = cr\_func(controlMnCt = Cmn, expCt = cpmE))

save(sumCpm\_cr, file = "data7\_24/Clearance Rates 2/sumCpm\_cr.Rdata")

write\_xlsx(sumCpm\_cr, "data7\_24/Clearance Rates 2/sumCpm\_cr.xlsx")

### Take the mean of the CR per taxa group (group\_size)

sumCpm\_CRmn <- sumCpm\_cr %>%

group\_by(event, group\_size) %>%

summarize(CrMNmlcd = mean(CRmlcd, na.rm = TRUE))

## Create the base data frame that has only the biomass, sum the bio\_pgC\_ml

## for all same-sized group\_size organsims, per event, per exp, per rep

load("data7\_24/Clearance Rates 2/base.Rdata")

sumBpm <- base %>%

group\_by(samp\_ev, exp, rep, group\_size) %>%

summarise(TotalBpm=sum(bio\_pgC\_ml),

.groups = 'drop') %>%

as.data.frame()

###data frame that has only the initial samples

sumBpm\_I <- sumBpm %>%

filter(exp == "I")%>%

select(samp\_ev, exp, rep, group\_size, TotalBpm)

### Apply the mean function to the initial mean biomass pgC per ml across

## the three replicates, as done in the CR

sumBpm\_Imn <- sumBpm\_I %>%

group\_by(samp\_ev, exp, group\_size) %>%

summarise(ImnBpm = mean(TotalBpm),

.groups = 'drop') %>%

as.data.frame()

### Remove unneeded columns, and rename and re-order remaining columns

names(sumBpm\_Imn)

sumBpm\_Imn <- select(sumBpm\_Imn,

event = samp\_ev, exp,

group\_size, ImnBpm)

### Join sumBpm\_Imn with the df that has clearance rates, sumCpm\_cr

load("data7\_24/Clearance Rates 2/sumCpm\_cr.Rdata")

sumBpm\_cr\_Imn <- left\_join(sumCpm\_cr, sumBpm\_Imn,

by = c("event", "group\_size"))

### Remove unneeded columns, and rename and re-order remaining columns

names(sumBpm\_cr\_Imn)

sumBpm\_cr\_Imn <- select(sumBpm\_cr\_Imn,

event, rep, group\_size, ImnBpm, CRmlcd)

### Calculate ingestion (feeding) rate

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

sumBpm\_FR <- rowwise(sumBpm\_cr\_Imn) %>%

mutate(FR = fr\_func(CR=CRmlcd, initialMnCt = ImnBpm))

### Rename the FR column to FRpgCmL so I remember it's in those units

sumBpm\_FR <- sumBpm\_FR %>%

rename("FRpgCcd" = "FR")