Order of operations for Clearance Rate and Ingestion Rate calculations in R

and how to combine them

## Clearance Rate, ml copepod-1 day-1

(ml of water with that organism in it; i.e., concentration of that organism)

V /T \* ( lnC -lnE)/n

V= volume of sample settled \* preservative factor

T= time of experiment, in our case, 1 day

C = means of control samples, either counts ml-1, or biomass in pgC ml-1 or µgC L-1

E = experimental samples, either counts ml-1, or biomass in pgC ml-1 or µgC L-1

## Ingestion Rate (aka feeding rate or consumption rate), quantity (biomass pgC or µgC, or cell counts) copepod-1 day-1

CR x mean I

CR = Clearance rate, either in ml copepod-1 day-1, or in

I = initial samples

Clearance Rate:

1. Create the base data frame with only the C and E columns, the control samples and the experimental samples
2. Create a data frame from the above with only the control samples and another one with only the experimental samples
3. Using the control samples data frame, apply the mean function to counts per ml, or biomass per ml, to get the contro means across the three replicates. When writing the group\_by argument, leave out the rep column so that what remains in the data frame is one row for each individiual organism/size and the mean of the control sample counts per ml or biomass per ml.
4. Since clearance rate needs the mean control samples and the three replicates experimental samples, join those two data frames into one. This will necessarily include the rep column, since we need the experimental samples individucal replicate counts or biomass for the calculation.
5. Then, with the joined data frame, remove the unneeded columns and rename as needed.
6. Calculate the clearance rate with the clearance rate function
7. The resulting data frame includes all the replicates since the clearance rate was calculated for each replicate.

Ingestion Rate

1. Create a data frame with only the I column, the initial samples
2. As in #3, using the initial samples data frame, apply the mean function to counts per ml, or biomass per ml, to get the control means across the three replicates. When writing the group\_by argument, leave out the rep column so that what remains in the data frame is one row for each individiual organism/size and the mean of the control sample counts per ml or biomass per ml.
3. Remove unneeded columns and rename as needed. Main columns needed are:
   1. event, group, type, Imn, CR
   2. Other columns may be added as desired, but the above are required for the FR calculations
4. Join the intial means data frame with the clearance rate data frame
5. Remove unneeded columns and rename as needed.
6. Calculate ingestion rate with the feeding rate function