Overview of Allison’s Thesis

Project:

* Location: Sacramento River Delta, four different habitat types
* Study organism: the copepod, *Pseudodiaptomus forbesi*
* Purpose: A study on copepod production and the things that can affect it. Specifically, my part of the project is to analyze the food available to them in the four different habitat types and analyze it in comparison to copepod growth rates at each habitat location
* Reason: copepods are a main food source for imperiled larval fishes in the Delta, and their numbers are low; and most studies only use chlorophyll as a proxy for food availability, but it has been a poor predictor of copepod production, as it leaves out other food sources, such as microzooplankton.
* Water samples taken from four different habitat types in the Sacramento River Delta
  + Sampling event names as seen in the R files, are:
    - SJR1 or 2: San Joaquin River 1 or 2
    - YBP1 or 2 : Yolo Bypass 1 or 2
    - WLD2: Wildlands 2
    - LSZ2: Low Salinity Zone 2
* Copepods collected and incubated for 24 and 48 hours; then preserved and measured to determine growth rates
* Water samples taken for microplankton content:
  + Site water (site)
  + Initial Samples (IC), preserved immediately
  + Experimental samples (T24), that had copepods added to them to see how much and what they ate, and incubated for 24 hours
  + Final samples (FC), also called controls, incubated for 24 hours, with no copepods to compare with what was present after 24 hours
* Counted and identified microplankton present in the water samples at two magnification levels, 100x, and 400x, since smaller organisms could not be identified at 100x magnification.
* Microplankton analysis done by calculating the biomass in carbon content of all the different types of microplankton found in the samples, and comparing it with the growth rates of the copepods and the habitat types, to determine if a certain organism and a certain habitat type provides better food for the copepods.

Analysis:

* Microplankton ambient analysis
  + Counts and biomass by groups
  + Counts and biomass by groups by sampling event
  + Counts and biomass by groups by sampling event by experimental sample
  + Counts and biomass by groups by sampling event by experimental sample by replicate
  + Counts and biomass per volume
  + Aggregate organism categories
  + Counts and biomass per volume aggregated
* What I have so far
  + Counts
    - Totals 100x, 400x, and Combined
    - Per Organism Group
  + Biomass
  + Some breakdowns of biomass per organism type and size
* What I need R help with
  + Graph controls (IC and FC) and experimentals (T24) so I can look at them and see what types of particles differ between them consistently among the replicates (3 each) for a given experiment.
  + Consolidate size categories
  + Eventually create graphs that compare microplankton presence with growth rates, feeding rates, clearance rates, reproduction rates?
* Clean up growth rate results, including the growth rate and the confidence intervals

**Here’s what I would like Dylan to to:**

* General idea:
  + Graph one sampling event at a time, so a separate graph for each sampling event, SJR1, SJR2, YBP1, YBP2, WLD2, LSZ2
  + Graph the organisms (grp\_typ) and their counts (tot\_ct)
  + **BUT!!** I just realized I need to make two changes to the data:
    - For the organisms, I need to combine the grp\_typ with the dimensions (sa, la, wi), which I did in another script, but not in the ctbm\_grptyp.Rdata file. Can you do it? This is the line of code I wrote in the other script:   
      ## Combine group, type, sa, la, wi, into one column and call it "category"

ct\_bmn\_fin$category <- paste(ct\_bmn\_fin$group, ct\_bmn\_fin$type,

ct\_bmn\_fin$sa, ct\_bmn\_fin$la)

* + - And for the counts, I need the mean counts, and what I have in the file is the total counts. Can you do the means? There are three replicates for each experiment, so counts (tot\_ct) divided by 3.
* One graph will have
  + X axis: grp\_typ (the new one that includes the dimensions in the name) in decreasing order of abundance, with vertical labels, because the names are so long, or something that looks nice and readable
  + Y axis: log scale of mean counts in FC (controls), overlayed with log scale of counts in T24 and IC, in different colors to distinguish them.
* I attached below a really rough whiteboard drawing from a zoom meeting as a rough example. But ignore the numbers on the x-axis. They should be the name labels. And I didn’t draw in the IC data.
* A second graph will
  + take the first graph above and select only those organisms whose mean counts are 3 and above (I might change this number later)
  + X axis: log of mean counts of FC
  + Y axis: log of mean counts of T24
  + Make the sizes and colors of the symbols different to distinguish the sizes of the cells
  + Draw a 1 to 1 line (maybe geom ab line in R) ??? My advisor said this, and I don’t remember what he meant

Chart, scatter chart

Description automatically generated