# **Table of all the ways I can look at the data**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | Clearance Rate | Ingestion Rate, biomass | Ingestion Rate, cell counts | Abundance, initial samples | Plots to make |
| All taxa 17 groups, individually | Shows the copepod’s ability to capture prey items . Also a measure of selectivity (not to be labeled “preference”) | How much carbon nutrition copepods got from all the taxa groups | How much food they ate in terms of numbers of cells, but not as informative as biomass | What was found in the water they live in. Compare what was there to what they ate and didn’t eat |  |
| Top 5 taxa groups and “Other” | Shows the copepod’s ability to capture prey items, in broader taxa groups | Which taxa were most important to their carbon nutrition, and which were so low that alone they didn’t impact the copepod much | Which taxa were most important to their ingestion, and which were so low that alone they didn’t impact the copepod much | What was found in the water they live in in broader taxa groups. Compare what was there to what they ate and didn’t eat | IR biomass  IRbio with CR  IRcells? with CR?  All this with abundance? |
| Cell Size,  15 µm esd  >=15 µm esd | Determine how much the clearance rate is higher for the larger than the smaller cells. | What amount of carbon nutrition did they get from smaller or larger cells, and was there a big difference between the two size groups?  How does cell size contribute, or not, to their nutrition? | How many prey item cells did they eat in each size group, and and was there a big difference between the two size groups?  How does cell size contribute, or not, to the cells they ate? | How many prey items of each of the two size groups were found in the water they live in. Compare what was there to what they ate and didn’t eat. | IR biomass  IRbio with CR  IRcells? with CR?  All this with abundance? |
| Subsets of key taxa(e.g., large centric diatoms, ciliates, maybe others | Is CR the same for each subset? |  |  |  |  |

From Wim’s email 4/26/23 Re Q2 good question.  Yes you could add up the IR but not the CR. You will have to go back to the count data you used for this and add up the counts and the biomasses across the Other category, then run your subsequent code again. You should expect to do this more than once as we go over the results. For example at some point yousill want to do the calculations by cell size since we already know that clearance rates are low on small cells.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | Done | Calculation | File name and location | Results Notes/  What it tells me | Keep as Final |
| Ingestion Rate  Biomass | ü | All taxa 17 groups, individually, reps and means | 03\_calcs\_CR\_FR.R  FRBio\_Rep\_Mn.Rdata  BugFRMn\_GrpSz.Rdata (means only)  CR\_IRbio\_mn.Rdata |  |  |
| ü | Top 5 taxa groups and “Other” | 03\_calcs\_IRtop5..R  FRBio5\_Rep\_Mn.Rdata  BugFRMn5\_GrpSz.Rdata  CR5\_IRbio\_mn.Rdata  CrIrAb5Cell.Rdata  IRbio\_top5Other.pdf, reps & mns  IRbio\_top5.pdf, top 5 only, reps and means |  |  |
| ü | Cell Size,  15 µm esd  >=15 µm esd | 03\_calcs\_CR\_FR.R, line 418  Frbio\_allEvents.Rdata  04\_plots\_IR\_Various.R, line 210  IRbio\_allEvents.pdf, plot |  |  |
| ? | Taxa totals by Sampling Event |  |  |  |
| ü | Taxa totals combined across all sampling events | 03\_calcs\_BiomassEtc.R  IRbioOverall.Rdata  IRbio\_AllEventsCombined\_plot.pdf, this has a dot for each event  IRbio\_allEvents.pdf, this has means  This is essentially the same as the cell size plot above |  |  |
| ü | Totals by Sampling Event | 03\_calcs\_CR\_FR.R, line 310  IRbio\_eventsOnly.Rdata  04\_plots\_IR\_Top5.R, line 179  IRcells\_eventsOnly\_plot.pdf, bar plot |  |  |
| ü | Taxa group percentages of total per sampling event | 04\_plots\_IR\_Various.R IR\_bio\_percentTot.Rdata |  |  |
| ü | Taxa that contributed at least 10% of total | 04\_plots\_IR\_Various.R IRbio\_topPercent.Rdata |  |  |
| Ingestion Rate  Cell counts | ü | All taxa 17 groups, individually | 03\_calcs\_CR\_FR.R  sumCpm\_FR.Rdata  CpmFRMn\_GrpSz.Rdata, line 355  04\_plots\_IRcells\_bio\_all.R  IRcells\_all\_plot.pdf |  |  |
| ü | Top 5 taxa groups and “Other” | 03\_calcs\_IRtop5.R  sum5Cpm\_FR.Rdata, reps & mns  CpmFRMn5\_txGp.Rdata, mns  Plot, IRcells\_Top5.pdf  04\_plots\_IR\_Top5.R |  |  |
| ü | Cell Size,  15 µm esd  >=15 µm esd | 04\_plots\_IR\_Various.R, line 185  03\_calcs\_CR\_FR.R  FR\_cell\_Size.Rdata  IRcells\_SmLg.pdf, this one has all samp\_ev IR separately |  |  |
| ü | Taxa totals combined across all sampling events | 03\_calcs\_CR\_FR.R, line 429  IR\_cells\_allEvents.Rdata  04\_plots\_IR\_Various.R, line 289  IRcells\_taxaOnly.pdf, plot  This is essentially the same as the cell size plot above, but takes the means of the taxa by samp\_ev |  |  |
| ü | Totals by Sampling Event | 03\_calcs\_CR\_FR.R, line 392  IRcells\_eventsOnly.Rdata  04\_plots\_IR\_Top5.R, line 169  IRcells\_eventsOnly\_plot.pdf |  |  |
|  | Taxa group percentages of total per sampling event |  |  |  |
|  |  |  |  |  |  |
| Clearance Rate | ü | All taxa 17 groups, individually | 03\_calcs\_CR\_FR.R  sumCpm\_cr.Rdata  sumCpm\_CRmn.Rdata  CR\_IRbio\_mn.Rdata, line 305  04\_plots\_IR\_Top5.R, line 139  CR\_All\_plot.pdf |  |  |
| ü | Top 5 taxa groups and “Other” | 03\_calcs\_IRtop5..R  sum5Cpm\_cr.Rdata  sum5Cpm\_CRmn.Rdata  CR5\_IRbio\_mn.Rdata, line 235  CrIrAb5Cell.Rdata  04\_plots\_IR\_Top5.R, line 96  CR\_Top5\_plot.pdf |  |  |
| ü | Cell Size,  15 µm esd  >=15 µm esd | 03\_calcs\_CR\_FR.R, line 152  CR\_allEvents.Rdata  CR\_taxaOnly.pdf, plot  04\_plots\_IR\_Various.R, line 252 |  |  |
| ü | Totals by Sampling Event | 03\_calcs\_CR\_FR.R, line 140  sumCRmnEventsOnly.Rdata  CR\_eventsOnly.pdf, plot  04\_plots\_IR\_Top5.R |  |  |
| ü | Taxa totals combined across all sampling events | This is essentially the same as the cell size plots  03\_calcs\_CR\_FR.R, line 152  CR\_allEvents.Rdata  CR\_taxaOnly.pdf, plot  04\_plots\_IR\_Various.R, line 265 |  |  |
|  | Taxa group percentages of total per sampling event |  |  |  |
| Cell Abundance | ü | All taxa 17 groups, individually | 03\_calcs\_Abun\_Other.R  abundance.Rdata, line 36 or so  04\_plots\_Abundance.R, line 75  Abundance\_allEvents.pdf, plot |  |  |
| ü | Top 5 taxa groups and “Other” | 03\_calcs\_Abun\_Other.R, line 105  abundance5.Rdata  CrIrAb5Cell.Rdata  04\_plots\_Abundance.R, line 121  Abundance\_top5.pdf, plot |  |  |
| ü | Cell Size,  15 µm esd  >=15 µm esd | 03\_calcs\_Abun\_Other.R, line 131  AB\_allEvents.Rdata  04\_plots\_Abundance.R, line 97  Ab\_SmLg.pdf, plot |  |  |
| ü | Totals by Sampling Event | 03\_calcs\_Abun\_Other.R  AbEventsOnly.Rdata, line 140  04\_plots\_Abundance.R, line 175  Ab\_eventsOnly.pdf |  |  |
|  | Taxa group percentages of total per sampling event |  |  |  |

**Note:** The data below are from before I calculated everything with the NAs, so while the concepts are still correct, the numbers will be slightly off, so don’t use the numbers for anything

# How I decided on which taxa groups were the top to focus on (top 5)

1. Looking at the Ingestion Rates, biomass, from highest to lowest table, in all sampling events, except for YBP2, the ingestion rates were at or below zero or very close in only a few sampling events, for the bottom 12 out of 17 taxa groups.

|  |  |  |
| --- | --- | --- |
| Sampling Event | # of taxa > 0 | IR µg C d-1 |
| SJR1 | 12 out of 12 | 0 |
| LSZ2 | 11 | 0.01 |
| SJR2 | 10 | 0.01-0.02 |
| YBP1 | 12 | 0 |
| WLD2 | 9 | 0.01, 0.02, 0.05 |

1. YBP2 had the highest ingestion rate, clearance rate and abundance of all sampling events, far higher than the other 5, with large ciliates 3.75 µg C d-1. The next highest after that was large centric diatoms in SJR1 and LSZ2, at 1.2 µg C d-1.
2. Clearance Rates had a similar story, with all top 5 IR biomass ranked taxa groups in the top 7 CR groups. The remaining 10 taxa groups had inconsistent, varying CR among sampling events.

# Results Summary

* Ingestion Rates, biomass and cells
* Clearance Rates
* Abundance, by taxa and by sampling event
* Growth Rates
* Compare Rates and abundance
  + Highest taxa
  + Highest sampling events

## Abundance by Sampling Event, high to low Abundance by Taxa Group

|  |  |
| --- | --- |
| Sampling Event | Cells mL-1 |
| YBP2 | 2877.26 |
| LSZ2 | 1950.39 |
| YBP1 | 1933.20 |
| WLD2 | 1522.97 |
| SJR2 | 667.97 |
| SJR1 | 663.78 |

|  |  |
| --- | --- |
| Taxa Group | Cells mL-1 |
| FlagSm | 864.88 |
| CenDiaSm | 267.17 |
| UnidSm | 225.93 |
| CenDiaLg | 76.44 |
| PenDiaSm | 44.71 |
| ChlSm | 38.40 |
| CilSm | 34.04 |
| CilLg | 19.89 |
| CyanoLg | 11.05 |
| PenDiaLg | 5.20 |
| UnidLg | 4.22 |
| FlagLg | 3.86 |
| CyanoSm | 2.33 |
| ChlLg | 2.01 |
| ChnDiaLg | 1.56 |
| DinoLg | 0.86 |
| ChnDiaSm | 0.04 |

## Ingestion Rates

|  |  |
| --- | --- |
| Taxa Group | total  µg C d-1 |
| CilLg | 4.08 |
| CenDiaLg | 2.93 |
| CenDiaSm | 0.95 |
| CilSm | 0.30 |
| FlagLg | 0.25 |
| FlagSm | 0.19 |
| PenDiaLg | 0.15 |
| ChnDiaLg | 0.07 |
| UnidSm | 0.05 |
| PenDiaSm | 0.02 |
| DinoLg | 0.01 |
| ChlSm | 0.01 |
| ChlLg | 0.00 |
| CyanoSm | 0.00 |
| ChnDiaSm | 0.00 |
| UnidLg | -0.08 |
| CyanoLg | -0.25 |

## 

|  |  |
| --- | --- |
| Sampling Event | IRbioMn  totals |
| YBP2 | 5.12 |
| LSZ2 | 1.73 |
| SJR1 | 1.38 |
| SJR2 | 0.20 |
| WLD2 | 0.14 |
| YBP1 | 0.12 |

# 6/11/23

Notes on taxa with NA CR, and whether or not and why to exclude those groups from the analysis

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Taxa** | **CR NA?** | **cpmE** | **Cmn** |  | **Exclude?** |
|  |  |  |  |  |  |
| CenDiaLg | only in YBP1 | 0 in one rep | 0 in 2 reps | Re-distri | No |
|  |  |  |  |  |  |
|  |  |  |  |  |  |
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