**Plots of Ingestion Rates and Clearance Rates:**

## Across All Sampling Events

## Individual Sampling Events

# Ingestion Rates, Biomass µg C L-1

### Across All Sampling Events

File Name: Plot test Bpm dots.R

### Wim's scale break code

scaleBreak <- function(xvalue, Break, rescale) {

# Function to set up plotting an axis with a single scale break

# This is an actual change of scale, unlike what ggplot has

# Input:

# xvalue The raw data (for either axis)

# Break The value at the break in raw data units

# rescale The divisor (>1 usually) to reduce the scale

# Use:

# Run this for the data to be plotted

# Run it again for the axis tick locations

# Then plot the rescaled data with the rescaled tick locations

# and the original tick locations for the tick labels

ifelse(xvalue < Break, xvalue, (xvalue-Break)/rescale + Break)

}

Break <- 60

rescale <- 20

ylabels <- c(-34, 0, 10, 20, 55, 150,500)

brks <- scaleBreak(ylabels, Break, rescale)

FrAllOverall\_ug$ySquish <- scaleBreak(FrAllOverall\_ug$FrBpm\_ug, Break=Break, rescale=20)

ggplot(data=FrAllOverall\_ug, aes(group\_size, ySquish)) +

#geom\_point(shape=16, color="navy", size = 4) +

geom\_point(aes(color = FrBpm\_ug>0), size = 4)+

scale\_color\_manual(values=c("FALSE"="maroon","TRUE"="navy"))+

geom\_hline(yintercept= Break, color="green4", linewidth=1, linetype=2) +

xlab("Taxon Group") +

scale\_y\_continuous("Ingestion rate, µgC L^-1", breaks=brks, labels=ylabels) +

theme(axis.text.x = element\_text(angle = 60, hjust = 0.8, vjust = 0.8, size = 10),legend.position = "none")+

wimGraph()



### Ingestion Rates, Individual Sampling Events

File name: 04\_plots\_CRFR\_Samp\_Ev.R

(Same as the code for the site water individual sampling events plots)

For each plot, replace the data file with the individual sampling event df, and change the ggtitle andy labels

a <- ggplot(data=FrGrpsLSZ2, aes(group\_size, ySquish)) +

geom\_point(shape=16, color="navy", size = 4) +

geom\_hline(yintercept= Break, color="green4", linewidth=1, linetype=2) +

xlab("Taxon Group") +

ggtitle("LSZ2 Biomass Ingestion Rates")+

scale\_y\_continuous(breaks=brks, labels=ylabels) +

ylab(bquote('Biomass, \u00b5gC L'^-1))+

#ylab(bquote('Cells L'^-1))+

wimGraph()+

theme(plot.title = element\_text(face = "bold", size = (16)), axis.text.x = element\_text(angle = 60, hjust = 0.8, vjust = 0.8, size = 12), axis.text.y = element\_text(size = 12), .position = "none")+

theme(panel.background = element\_rect(colour = "black", size=1.5))

|  |  |  |  |
| --- | --- | --- | --- |
| Ingestion Rates Plots, Biomass, µg C copepod-1 d-1 | | | |
| Sampling Event | Break | rescale | ylabels |
| LSZ2 | 0.1 | 20 | 0, 0.05, 0.1, 0.3, 1.3 |
| SJR1 | 0.2 | 25 | -0.08,0, 0.05, 0.1, 1.2 |
| SJR2 | No breaks or rescale needed | | -7, 0, 5, 20, 45 |
| WLD2 | No breaks or rescale needed | | 0.00, 0.01, 0.02, 0.03, 0.04, 0.05 |
| YBP1 | 0.01 | 25 | 0, 0.003, 0.008, 0.04, 0.05 |
| YBP2 | 0.6 | 25 | -0.3, 0, 0.2, 0.5, 3.8 |

# Ingestion Rates, Cells copepod-1 d-1

### Across All Sampling Events

See Wim’s Scale Break code above

Break <- 200

rescale <- 20

ylabels <- c(-60, 0, 150, 600, 1300, 4000)

brks <- scaleBreak(ylabels, Break, rescale)

FrCpmOverall$ySquish <- scaleBreak(FrCpmOverall$FrCpmAllEvents,

Break=Break, rescale=20)

### Notes: point colores for < or > 0;

Plot outlined in a black box

a <- ggplot(data=FrCpmOverall, aes(group\_size, ySquish)) +

geom\_point(aes(color = FrCpmAllEvents>0), size = 4) + scale\_color\_manual(values=c("FALSE"="maroon","TRUE"="navy") )+

geom\_hline(yintercept= Break, color="green4", linewidth=1, linetype=2) +

xlab("Taxon Group") +

ggtitle("Ingestion Rates Across All Sampling Events")+

scale\_y\_continuous(breaks=brks, labels=ylabels) +

ylab(bquote('Ingestion rate, cells mL'^-1))+

wimGraph()+

theme(plot.title = element\_text(face = "bold", size = (20)),

axis.text.x = element\_text(angle = 60, hjust = 0.8, vjust = 0.8, size = 10),

legend.position = "none")+

theme(panel.background = element\_rect(colour = "black", size=1.5))



# Ingestion Rates, Individual Sampling Events, Cells copepod-1 d-1

File name: 04\_plots\_CRFR\_Samp\_Ev.R

(Same as the code for the site water individual sampling events plots)

|  |  |  |  |
| --- | --- | --- | --- |
| Ingestion Rates Plots, Cell Abundance | | | |
| Sampling Event | Break | rescale | ylabels |
| LSZ2 | 150 | 100 | 0,10, 56, 100, 150, 3120, 4890, 6832 |
| SJR1 | 600 | 70 | -180, -78, 3, 175, 300, 537, 600, 1900, 2720 |
| SJR2 | 750 | 100 | 0,45, 150, 422, 708, 750, 1690 |
| WLD2-Crazy! | -300 | 1.5 | -360,-300, -42, 0, 20, 45, 65, 192 |
| YBP1 | 200 | 300 | 0, 10, 25,50, 180,200, 5100 |
| YBP2 | 500 | 100 | -400, 0, 50, 300, 1900,14300 |

# Ingestion Rates, Individual Sampling Events, Reps with Means, Cells copepod-1 d-1

File name: 04\_plots IR Rep Means.R

(Same as the code for the clearance rates reps and means plots, but file name changed accordingly.)

Can’t use the Scale Break Function since there are two data sets (reps and means) in one plot and it messes up the scale change.

|  |  |  |
| --- | --- | --- |
| Ingestion Rates Plots, Cells | | |
| Sampling Event | limits | breaks |
| LSZ2 | -11, 66 | -10,-3, 0, 5, 10, 14, 30, 40, 53, 64 |
|  |  |  |
| SJR1 | -39, 62 | -38, -15, 0, 5, 10, 20, 30, 40, 50, 61 |
|  |  |  |
| SJR2-with means | -1400, 25100 | -1345, -13, 0, 200, 400, 700, 1500, 2500, 9000, 14311, 25000 |
| SJR2 w/o CenDiaSm |  |  |
| WLD2-Crazy! | -32, 56 | -31, -15, 0, 5, 20, 30, 40, 55 |
|  |  |  |
| YBP1 | -37, 72 | -36, 0, 5, 9, 15, 20, 30, 42, 71 |
|  |  |  |
| YBP2 | -38, 94 | -37, -13, 0, 5, 20, 27, 38, 50, 80, 93 |
|  |  |  |

# Clearance Rates Rates, mL-1 copepod-1 d-1

### Across All Sampling Events

## Clearance Rates, Individual Sampling Events

These plots didn’t need the Scale Break function

\*\* When saving plot to pdf, choose Use cairo\_pdf device, and change pdf size to 6 x 4.5 inches

a <- geom\_point(aes(color = crMnCpm>0), size = 4)+

scale\_color\_manual(values=c("FALSE"="maroon",

"TRUE"="navy"))+

xlab("Taxon Group") +

ggtitle("YBP2 Clearance Rates")+

scale\_y\_continuous(limits = c(-33, 63), breaks = c(-32, 0, 5, 27, 38, 50, 62)) +

ylab("mL"~copepod^-1~d^-1)+

wimGraph()+

theme(plot.title = element\_text(face = "bold", size = (16)),

axis.text.x = element\_text(angle = 60, hjust = 0.8, vjust = 0.8, size = 10),

axis.text.y = element\_text(size = 10),

legend.position = "none")+

theme(panel.background = element\_rect(colour = "black", size=1.5))

# Clearance Rates Rates, mL-1 copepod-1 d-1

### Across All Sampling Events

## Clearance Rates, Individual Sampling Events

|  |  |  |  |
| --- | --- | --- | --- |
| Clearance Rates Plots | | | |
| Sampling Event | Break | rescale | ylabel breaks |
| LSZ2 | limits -3, 54: breaks -3, 0, 5, 10, 14, 30, 40, 53 | | |
| SJR1 | limits -31, 50: breaks -30, -5, 0, 10, 27, 43, 49 | | |
| SJR2 | limits -8, 40: breaks -7, 0, 10, 18, 25, 30, 39 | | |
| WLD2 | limits -14, 46: breaks -13, -3, 0, 5, 17, 30, 45 | | |
| YBP1 | limits -1, 43: breaks 0, 5, 9, 15, 20, 30, 42 | | |
| YBP2 | limits -33, 63: breaks -32, 0, 5, 27, 38, 50, 62 | | |

# Clearance Rates Rates, mL-1 copepod-1 d-1, reps and means

From 04\_plots RepMeans.R

### These files are from 03\_calcs\_CrFr\_bySizeSmLg.R

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

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

Example with LSZ2; replace with other sampling event names for individual plots

### LSZ2

## Use this data frame to plot the means

CrGrpsLSZ2 <- CrGrps %>%

filter(event =="LSZ2")

## Use this data frame to plot the reps

CrGrpsRepsLSZ2 <- CrGrpsReps %>%

filter(event =="LSZ2")

a <- ggplot(data=CrGrpsLSZ2, aes(group\_size, crMnCpm)) +

geom\_hline(yintercept=0, color="gray",

linewidth=1) +

geom\_point(aes(color = crMnCpm>0), size = 4)+

scale\_color\_manual(values=c("FALSE"="maroon",

"TRUE"="navy"))+

geom\_point(data = CrGrpsRepsLSZ2, aes(y=CR), color="orange", size=2)+

xlab("Taxon Group") +

ggtitle("LSZ2 Clearance Rates")+

scale\_y\_continuous(limits = c(-11, 66),

breaks=c(-10,-3, 0, 5, 10, 14, 30, 40, 53, 64)) +

ylab("mL"~copepod^-1~d^-1)+

wimGraph()+

theme(plot.title = element\_text(face = "bold", size = (16)),

axis.text.x = element\_text(angle = 60, hjust = 0.8, vjust = 0.8, size = 10),

axis.text.y = element\_text(size = 10),

legend.position = "none")+

theme(panel.background = element\_rect(colour = "black", size=1.5))

|  |  |  |
| --- | --- | --- |
| Clearance Rates Plots | | |
| Sampling Event | limits | breaks |
| LSZ2 | -11, 66 | -10,-3, 0, 5, 10, 14, 30, 40, 53, 64 |
| SJR1 | -39, 62 | -38, -15, 0, 5, 10, 20, 30, 40, 50, 61 |
| SJR2 | -11, 59 | -10, 0, 5, 10, 15, 20, 25, 30,35,40,45,58 |
| WLD2 | -32, 56 | -31, -15, 0, 5, 20, 30, 40, 55 |
| YBP1 | -37, 72 | -36, 0, 5, 9, 15, 20, 30, 42, 71 |
| YBP2 | -38, 94 | -37, -13, 0, 5, 20, 27, 38, 50, 80, 93 |