# Plots of All Taxon Groups Ingestion Rates and

# Plots of Individual Sampling Events Ingestion Rates

# Biomass µg C L-1

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))

|  |  |  |  |
| --- | --- | --- | --- |
| Biomass, µg C L-1 | | | |
| Sampling Event | Break | rescale | ylabels |
| LSZ2 | 30 | 100 | 0, 4, 10, 25, 30, 378, 1360 |
| SJR1 | 30 | 50 | -28, 0, 2, 20, 100, 1255 |
| SJR2 | No breaks or rescale needed | | -7, 0, 5, 20, 45 |
| WLD2 | No breaks or rescale needed | | -1, 0, 3,5,8, 12 |
| YBP1 | 103 | 20 | 0, 0.5,1,4, 12, 17 |
| YBP2 | 500 | 100 | -212, 0,25,77, 300, 5200 |

# Cells mL-1

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

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

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

|  |  |  |  |
| --- | --- | --- | --- |
| Cell Abundance | | | |
| Sampling Event | Break | rescale | ylabels |
| LSZ2 | 50 | 100 | 0,8,30,50, 1270, 3120, 6800 |
| SJR1 | 85 | 70 | -37,0,25,76,180, 1900, 2720 |
| SJR2 | 2.5 | 100 | -2,0,2, 12,40,190, 630, 708 |
| WLD2 | 20 | 15 | 0,8,15,50,150,290 |
| YBP1 | 8 | 15 | 0,6,25,75,120 |
| YBP2 | 15 | 15 | 0,5,10,50,125,250,464 |