# Site Water Plot Code and Notes

## Code

File Name 04\_plots\_siteWater.R

library(tidyverse)

library(writexl)

library(ggforce) ## for facet\_wrap\_paginate

source("scripts/01\_function\_wimGraph and Palettes.R")

load("data/SiteWater/siteBioUglTot.Rdata")

load("data/SiteWater/siteCntTot.Rdata")

### above dfs are from 03\_calcs\_SiteWaterAbund.R

### DOT PLOT of biomass, all sampling events together

p <- ggplot(siteBioUgLTot, aes(x=group\_size, tot\_bio\_ug))+

geom\_point(stat = "identity", color = "black", size = 3)+

scale\_x\_discrete ("") +

scale\_y\_continuous() +

theme(axis.text.x = element\_text(angle = 60, hjust = 0.8, vjust = 0.8, size = 12),

strip.text.x = element\_text(size = 14))+

facet\_wrap(~ samp\_ev, ncol= 2, scales="free") +

xlab("Taxa Groups with Sizes") +

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

ggtitle("Biomass Abundance, Site Water Samples")+

wimGraph()

### DOT PLOT of counts, all sampling events together

p <- ggplot(siteCntTot, aes(x=group\_size, tot\_ct))+

geom\_point(stat = "identity", color = "black", size = 1.5,)+

scale\_x\_discrete ("") +

scale\_y\_continuous() +

theme(axis.text.x = element\_text(angle = 60, hjust = 0.8, vjust = 0.8, size = 12),

strip.text.x = element\_text(size = 14))+

facet\_wrap(~ samp\_ev, ncol= 2, scales="free") +

facet\_wrap\_paginate(~ samp\_ev, ncol = 1, nrow =1, page = 1)+

xlab("Taxa Groups with Sizes") +

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

ggtitle("Cell Abundance, Site Water Samples")+

wimGraph()

### FOR PLOTTING THE INDIVIDUAL SAMPLING EVENTS

## Use the code below as a template, changing the file name, and the breaks, rescale and ylabels according to the numbers in the sampling event

## See below for the scaleBreak, rescale and ylabel settings for each of the individual sampling events

### Apply Wim's squish function

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 <- 100

rescale <- 30

ylabels <- c( 0, 5, 17, 42, 85, 1000)

brks <- scaleBreak(ylabels, Break, rescale)

siteCntTotSJR1$ySquish <- scaleBreak(siteCntTotSJR1$tot\_ct, Break=Break, rescale=30)

a <- ggplot(data=siteCntTotSJR1, 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("SJR1 Cell Abundance, Site Water Samples")+

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

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),

legend.position = "none")+

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

### The above line puts a black frame all around the plot

### Note: When saving plots as pdf, choose “Use cairo-Pdf device), and change the pdf size to 6x4.5

|  |  |  |  |
| --- | --- | --- | --- |
| Cell Abundance | | | |
| Sampling Event | Break | rescale | ylabels |
| LSZ2 | 12 | 17 | 0,3,8,60,85,300 |
| SJR1 | 20 | 20 | 0,5,10,50,1000 |
| SJR2 | 50 | 15 | 0,5,25,50,175 |
| 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 |

|  |  |  |  |
| --- | --- | --- | --- |
| Biomass, µg C L-1 | | | |
| Sampling Event | Break | rescale | ylabels |
| LSZ2 | 6 | 15 | 0,2, 4, 5, 16 |
| SJR1 | 3 | 15 | 0, 2, 3, 16, 20 |
| SJR2 | 3.5 | 15 | 0, 1, 2, 3, 0 |
| WLD2 | 5 | 10 | 0, 1, 2, 4, 6, 12 |
| YBP1 | 8 | 15 | 0,6,25,75,120 |
| YBP2 | 15 | 15 | 0,5,10,50,125,250,464 |

### Pasted below the above plot code for plotting without ySquish

a <- ggplot(data=siteCntTotSJR1, aes(group\_size, tot\_ct)) +

geom\_point(shape=16, color="navy", size = 3) +

xlab("Taxon Group") +

ggtitle("SJR1 Cell Abundance, Site Water Samples")+

scale\_y\_continuous() +

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 = 10),

legend.position = "none")