Abundance Plots

# Proportion of taxa group abundance by sampling event, pgC ml-1

/Users/allisonadams/My files/Thesis/Microplankton/MicroplanktonAnalysis/Final Final/Abundance/AbundanceBiomass\_pgCmL\_plot.pdf

MicroplanktonAnalysis/Final Final/Abundance/03\_calcs\_BiomassAbundance.R

### Plot Abundance in biomass, absolute and proportionate by event, Top 5 + Other taxa groups

load("Final Final/Abundance/AI5TotProp.Rdata") # For proportions and absolute, from 03\_calcs\_BiomassAbundance.R

## ### Proportions

ggplot(AI5TotProp, aes(fill=taxaGroup, y=PropBioPgCm, x=event)) +

geom\_bar(position="fill", stat="identity")+

scale\_fill\_manual(values = c("CenDiaLg" = "cornflowerblue", "CenDiaSm" = "lightskyblue", "CilLg" = "salmon3", "CilSm" = "salmon1","FlagSm" = "#85B22C", "Other" = "peachpuff"),

limits = c("CenDiaLg", "CenDiaSm", "CilLg", "CilSm", "FlagSm", "Other"),

name = "Taxa Group")+

xlab(NULL)+

ylab(NULL)+

ggtitle("Taxa Group Relative Biomass Abundance, pgC"~mL^-1)+

theme(plot.title = element\_text(hjust = 0.5),

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

axis.text.y = element\_text(size = 6))+

wimGraph()

A graph of different colored squares

Description automatically generated

## ### Absolute

ggplot(data= AI5TotProp,aes(x = factor(taxaGroup, level = c("CenDiaLg", "CenDiaSm", "CilLg", "CilSm", "FlagSm", "Other")),

color = taxaGroup, y=BioUgL)) +

geom\_point()+

scale\_color\_manual(values = c("CenDiaLg" = "cornflowerblue", "CenDiaSm" = "lightskyblue", "CilLg" = "salmon3", "CilSm" = "salmon1", "FlagSm" = "#85B22C", "Other" = "dimgrey"))+

scale\_y\_continuous(expand=expansion(mult=c(.1,0.15)))+

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

xlab(NULL)+

ylab("Biomass, µgC"~L^-1)+

#ggtitle("Biomass")+

theme(plot.title = element\_text(hjust = 0.5),

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

axis.title.x = element\_text(size = 10),

axis.text.y = element\_text(size = 6),

axis.text.x = element\_text(angle = 60, hjust = 0.8, vjust = 0.8, size = 6),

legend.position = "none")+

wimGraph()

### saved plot as 5x5



All taxa groups, all events



Expansion of taxa groups for SJR2, WLD2, YBP1, YBP2, because their “Other” group made up >10% of biomass abundanc, ugC L-1

### Relative biomass abundance showed >10% "Other" in SJR2, WLD2, YBP1 and YBP2,

## so break them out individually

ggplot(subset(AISumAgg17, samp\_ev %in%"SJR2"),

aes(x = factor(group\_size, level = c("CenDiaLg", "CenDiaSm", "CilLg", "CilSm", "FlagSm", "ChlLg", "ChlSm","ChnDiaLg", "ChnDiaSm", "CyanoLg", "CyanoSm", "DinoLg", "FlagLg", "PenDiaLg", "PenDiaSm", "UnidLg", "UnidSm")),

y=BioUgL)) +

geom\_point( size = 2)+

scale\_y\_continuous(expand=expansion(mult=c(.1,0.15)))+

xlab("Taxa Groups")+

ylab("pgC"~ml^-1)+

ggtitle("SJR2 Biomass Abundance")+

theme(plot.title = element\_text(hjust = 0.5),

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

axis.title.x = element\_text(size = 10),

axis.text.y = element\_text(size = 9),

axis.text.x = element\_text(angle = 60, hjust = 0.8, vjust = 0.8, size = 9))+

wimGraph()









For comparison, LSZ2, which had < 5% Other



And all taxa groups, all events