# Code for Mean IR bio per taxa group

### Plot the mean IRbio per taxa group, take the means of the replicates for each taxa group across all events, and average them, exclude from the sum any negative rates, also exclude the NA values

load("data/Clearance Rates 2/CrIrCntRepMnTots.Rdata")

MeanIRplotTaxa <- CrIrCntMnTots2 %>%

group\_by(group\_size) %>%

summarise(FRUgMnTaxa = mean(FRUgMn[FRUgMn >= 0 ], na.rm = TRUE))

### Put numbers on top of bars

#geom\_text(aes(label=TotalCpmI), position = position\_dodge(width = 0.9), vjust = -.25, size = 3)

### Make it so numbers on highest bars don't get cut off

# scale\_y\_continuous(expand = expansion(mult = c(0, 0.1)))+

### Round the numbers to 3 decimal places so they can be read on the plot

MeanIRplotTaxaRnd <- MeanIRplotTaxa %>%

mutate\_at(2, round, 3)

p <- ggplot(MeanIRplotTaxaRnd, aes(group\_size, FRUgMnTaxa))+

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

geom\_text(aes(label=FRUgMnTaxa), position = position\_dodge(width = 0.9),

vjust = -.25, size = 2.5)+

ggtitle("Mean Biomass Ingestion Rates")+

scale\_x\_discrete ("", expand=expansion(mult=c(0.07,0.07))) +

scale\_y\_continuous (expand=expansion(mult=c(0,0.15))) +

wimGraph()+

theme(axis.text.x = element\_text(angle = 60, hjust = 0.8, vjust = 0.8, size = 9.5),

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

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

axis.title.y = element\_text(size = 11),

title = element\_text(size = 11))+

ylab("µg C"~d^-1) +

xlab(NULL)

p