# Code for IR Bio All Events

### Plot the IRbio per event, take the means of the replicates for each

## taxa group per event, and sum them up, exclude from the sum any negative

## rates, also exclude the NA values

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

IRplotEvents <- CrIrCntMnTots2 %>%

group\_by(event) %>%

summarise(FRUgMnEvent = 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(trans= "log10", expand = expansion(mult = c(0, 0.1)))+

IrplotEventsRnd <- IRplotEvents %>%

mutate\_at(2, round, 3)

p <- ggplot(IrplotEventsRnd, aes(event, FRUgMnEvent))+

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

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

vjust = -.25, size = 3)+

ggtitle("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