# Clearance Rates Experimental Medians Code and Plots

## Code

1/24/23

Updated 1/25/23

library(tidyverse)

library(writexl)

load("data/Clearance Rates/crAllCR.Rdata")

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

### Plot which taxa have CR > 0

### Prepare the data for preliminary look

## Per notes from discussion with Wim 1/20/23:

## Take median CR of the 3 E reps

## Have one panel per sampling event

## Get rid of CR near 0, or NA, but keep the negative values

### Use the split apply combine method as for the control means

### Use crAllCR.Rdata as the base, as it already has only the E samples and the CR

### Apply the median function to the CR across the three replicates

crMedE1 <- crAllCR %>%

group\_by(event, sample, group) %>%

summarize(CRmed = median(CR))

### Remove all taxa with NA in the CRmed

crMedE\_noNA <- drop\_na(crMedE1)

### Pass crMedE\_noNA to the name “x” for easier code writing

x <- crMedE\_noNA

head(x) # shows first six rows

### Make abbreviations in the x axis labels so they fit better on the plot. I chose minlength = 12 so that enough info would be in the abbreviations that I would know what they are.

x$seq <- factor(1:nrow(x), ordered=T, labels=abbreviate(x$group, minlength = 12))

### Plot it

p <- ggplot(x, aes(x=seq, CRmed)) +

geom\_point(size=2, color="coral") +

scale\_x\_discrete ("") +

scale\_y\_continuous(breaks = seq(-35, 70, by=10))+

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

strip.text.x = element\_text(size = 10))+

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

xlab("Taxa Groups with Sizes") +

ylab("Median Clearance Rate, Experimental Samples") +

geom\_hline(yintercept = 0, color = "blue")+

geom\_hline(yintercept = 5, color = "cyan")+

wimGraph(textSize = 6)

### Run it

p

## Plots

Notes:

Plot below shows a dark blue line at 0 on the y-axis and a light blue line at 5. I chose 5 since we discussed eliminating taxon groups that had an experimental sample clearance rate near 0, just so we can see the low ones more easily.

The plots cannot show all taxon groups in each plot since there are 77 total. Instead, they show the ones that are present in those sampling events, so I will have to do my comparison on paper or some other way.

