#Figures for Manuscript 1

```{r}

#choice

par(mfrow=c(2,2))

abplot

tegplot

pachyplot

pagurusplot

LabAssayWholeTissue <- read.csv("LabAssaysWholeTissue.csv",header=T)

View(LabAssayWholeTissue)

choice <- LabAssayWholeTissue[1:232,]

fig1<- ggplot(choice, aes(x=algae\_spp., y= algae\_Wd, fill = algae\_spp.)) + geom\_boxplot(show.legend = FALSE) + theme\_bw() + xlab("") + ylab("Algae Mass Consumed (g)") + ggtitle("Food Choice Assay") + theme(axis.text=element\_text(size=12),

axis.title=element\_text(size=12),plot.title =element\_text(hjust = 0.5)) +

facet\_grid(grazer\_spp. ~., scales = "free\_y", labeller = as\_labeller(c("Haliotis cracherodii" = "H. cracherodii", "Tegula" = "T. funebralis", "Pachy" = "P. crassipes", "Pagurus" = "P. samuelis")),)

fig1

view(choice)

#performance

#this figure only shows final dry mass of non-shell tissue for tegula and red abalone. All other tissue will be in the appendix

fig2<- ggplot(performance, aes(x=diet, y= terminal\_dry\_mass, fill= diet)) + geom\_boxplot(show.legend = FALSE) + theme\_bw() + xlab("Diet") + ylab("Dry Tissue Mass (g)") + ggtitle("Final herbivore tissue mass by diet") + theme(axis.text=element\_text(size=12),

axis.title=element\_text(size=12),plot.title =element\_text(hjust = 0.5)) +

facet\_grid(grazer\_spp. ~ , scales = "free\_y", labeller = as\_labeller(c("red abalone" = "H. rufescence", "tegula" = "T. funebralis")),) +

#facet\_grid allows you to separate the graph by category (grazer type), scales allows thee y axis to have different scales since total grazing is different by grazer species

geom\_vline(xintercept=c(1.5),linetype="dotted") +

#adds a dotted vertical line at position x

scale\_x\_discrete(limits = c("starved", "macro", "mixed", "sargassum"), labels=c("starved" = "Starved", "macro" = "M. pyrifera",

"mixed" = "Mixed","sargassum" = "S. horneri")) + #limits changes the order of categories on the x axis

#labels renames the tick marks

theme(axis.text.x = element\_text(face="italic",

size=10)) #italisizes the tick marks in the x axis

fig2

```

#Analysis for manuscript 1

```{r}

#load data

performanceassay<-read.csv("PerformanceAssays2020.csv", header=TRUE,)

view(performanceassay)

na.omit(performanceassay)

#R decided to add phantom rows of NA at the bottom. Subset the dataframe to only keep the rows with actual information

performance <- performanceassay[1:160,]

#performance assay

performance2 <- subset(performance, diet != "starved" ) #filter out the starved treatment for the model

view(performance2)

#check normality

qqnorm(performance2$terminal\_dry\_mass)

plot(performance2$terminal\_dry\_mass)

#look at them individually

redabs<-subset(performance2, grazer\_spp.== "red abalone")

hist(redabs$terminal\_dry\_mass)

tegs<-subset(performance2, grazer\_spp.== "tegula")

hist(tegs$terminal\_dry\_mass)

#create simple model

m <- lm(terminal\_dry\_mass ~ diet, performance2)

summary(m)

par(mfrow = c(2, 2))

plot(m)

anova(m)

m2<-lm(terminal\_dry\_mass ~ diet\*grazer\_spp., performance2)

summary(m2)

par(mfrow = c(2, 2))

plot(m2)

anova(m2)

m3<-glmer(terminal\_dry\_mass ~ diet\*grazer\_spp. + (1| est\_total\_dry\_mass\_i) , family = gaussian, performance2)

summary(m3)

par(mfrow = c(2, 2))

plot(m3)

anova(m3)

#Tukeys post hoc test

hsd <- HSD.test(m3, trt = 'diet')

print(m3)

plot(m3)

#check assumptions of ANOVA

# check Levene's test for constant variance

leveneTest(m)

## null hypothesis is that we have constant variance

### P=0.43, do not reject the hypothesis

#check the normality of the residuals

qqnorm(m$residuals)

shapiro.test(m$residuals)

##resuduals are normally distributed

#Tukeys post hoc test

hsd <- HSD.test(m2, trt = 'diet')

print(hsd)

plot(hsd)

#does differnt diet affect weight of grazers

m3<- glmer(terminal\_dry\_mass ~ diet\*grazer\_spp. + (1| est\_total\_dry\_mass\_i), data = performance2, family = binomial)

anova(m3)

model2<- aov(terminal\_dry\_mass ~ diet + est\_total\_dry\_mass\_i, data = tegs)

Anova(model2,type="III")

hsd2 <- HSD.test(model2, trt = 'diet')

print(hsd2)

plot(hsd2)

test<- aov(terminal\_dry\_mass ~ diet, data = redabs)

Anova(test)

hsd1 <- HSD.test(test, trt = 'diet')

print(hsd1)

plot(hsd1)

model1<- aov(terminal\_dry\_mass ~ diet + est\_total\_dry\_mass\_i, data = redabs)

Anova(model1,type="III")

hsd <- HSD.test(model1, trt = 'diet')

print(hsd)

plot(hsd)

test<- aov(terminal\_dry\_mass ~ diet, data = redabs)

Anova(test)

hsd1 <- HSD.test(test, trt = 'diet')

print(hsd1)

plot(hsd1)

```