library(car)

library(lme4)

library(emmeans)

library(multcomp)

library("glmmTMB")

library("bbmle")## for AIC

library(ggplot2)

library(DHARMa) # check model fit

**For oyster stats**

#######################oyster stats ###########################################################

dat6<-read.csv("dir/oyster\_in\_cages.csv" , sep=",")

fit\_pois<- glmmTMB(Num\_spat~Site\*Cage\_type\*Sample\_dat +

(1|Site/Mound\_ID/Cage\_ID), data=dat6, ziformula=~0, family=poisson) # exclude zero-inflated - ziformula~0 summary(fit\_pois)

###

fit\_zipois <- glmmTMB(Num\_spat~Site\*Cage\_type\*Sample\_dat +

(1|Site/Mound\_ID/Cage\_ID), data=dat6, ziformula=~1,family=poisson)

fit\_zinbinom <- update(fit\_zipois,family=nbinom2)

fit\_nbinom <- update(fit\_zinbinom,ziformula=~0) ### best !!!!!!!!!!!

fit\_zinbinom1 <- update(fit\_zipois,family=nbinom1)

AICtab(fit\_pois,fit\_zipois,fit\_zinbinom,fit\_zinbinom1,fit\_nbinom)

summary(fit\_nbinom)

Anova(fit\_nbinom) # Anova(fit\_zinbinom1)

## check fit

ff <- simulateResiduals(fit\_nbinom)

plot(ff)

# mult comp

comp<-emmeans(fit\_nbinom, list(pairwise ~ Sample\_dat\*Site\*Cage\_type), adjust = "tukey") # from emmeans

#comp<-emmeans(fit\_nbinom, list(pairwise ~ Site\*Cage\_type), adjust = "tukey", by="Sample\_dat") # type-repsonse backtransforms

comp<-emmeans(fit\_nbinom, list(pairwise ~ Cage\_type\*Sample\_dat), adjust = "tukey", by=c("Site") )

########################################################################

### oyster juvi stats

fit\_pois<- glmmTMB(Num\_spat\_25~Site\*Cage\_type\*Sample\_dat + (1|Site/Mound\_ID/Cage\_ID), data=dat6, ziformula=~0, family=poisson)

fit\_zipois <- glmmTMB(Num\_spat\_25~Site\*Cage\_type\*Sample\_dat +

(1|Site/Mound\_ID/Cage\_ID),data=dat6,ziformula=~1,family=poisson)

fit\_zinbinom <- update(fit\_zipois,family=nbinom2)

fit\_nbinom <- update(fit\_zinbinom,ziformula=~0)

fit\_zinbinom1 <- update(fit\_zipois,family=nbinom1) ### best !!!

AICtab(fit\_pois,fit\_zipois,fit\_zinbinom,fit\_zinbinom1,fit\_nbinom)

summary(fit\_zinbinom)

Anova(fit\_zinbinom)

## check fit

ff <- simulateResiduals(fit\_zinbinom)

plot(ff)

#

## mult comp

comp<-emmeans(fit\_zinbinom1, list(pairwise ~ Cage\_type\*Sample\_dat\*Site), adjust = "tukey") # from emmeans - adjust use tukey or mvt

comp<-emmeans(fit\_zinbinom1, list(pairwise ~ Cage\_type\*Sample\_dat), adjust = "tukey", by=c("Site") )

comp\_plot<-plot(comp, comparisons = TRUE, horizontal = TRUE, ylab= "Factor combination")

### get easily read dataframe from emmeans

emmeans::pwpp(comp)

mes<- data.frame(comp[2]) %>% # names(comp) names(mes)

rename(contrast="pairwise.differences.of.Sample\_dat..Site..Cage\_type.contrast", p="pairwise.differences.of.Sample\_dat..Site..Cage\_type.p.value") %>%

select(contrast,p) %>%

separate(contrast, into=c("one", "two"), sep="-") %>%

separate(one, into = c("dat\_1", "other"), sep = "\\s", extra = "merge") %>%

separate(other, into = c("site\_1", "cage\_1"), sep = "\\s", extra = "merge") %>%

mutate(cage\_1 = str\_replace(cage\_1, "^\\S\* ", "")) %>%

separate(two, into = c("dat\_2", "cage\_2"), sep = "\\s", extra = "merge") %>%

separate(cage\_2, into = c("dat\_2", "other"), sep = "\\s", extra = "merge") %>%

separate(other, into = c("site\_2", "cage\_2"), sep = "\\s", extra = "merge") %>%

mutate(cage\_2 = str\_replace(cage\_2, "^\\S\* ", "")) %>%

filter(p <= 0.3) %>%

filter\_(~dat\_1 == dat\_2) %>%

filter(site\_1 != "Clam") %>%

filter(site\_2 != "Clam") %>%

arrange(dat\_1,site\_1,cage\_1)

########################################################################

########################################################################

**##### plot for osyters in cage**

dat<-dat6 # this is oyster\_in\_cage csv

dat$Sample\_dat<-factor(dat$Sample\_dat,levels=c("initial","Summer\_2010" ,"FAll\_2010","Spring\_2011","Fall\_2011" ))

dat$Site<-factor(dat$Site,levels=c("Crab Hole","Gibbs Shoal","Clam Shoal"))

dat$Cage\_type<-factor(dat$Cage\_type,levels=c("Open","Control","Roof","Large Mesh","Small Mesh"))

f<-aggregate(cbind(Num\_spat,Num\_spat\_25)~Site+Sample\_dat+Cage\_type+Cage\_ID,data=dat,FUN=function(x) x=mean(x))

######################### plot oy and juv oyster at each sample####################

Si<-c('Crab Hole','Gibbs Shoal','Clam Shoal')

Ca<-c("Open","Control","Roof","Large Mesh","Small Mesh")

cl<-c("gray90","gray70","gray45")

le<-levels(dat$Sample\_dat)

z<-2+3.5\*4

tt<-seq(2,z,by=3.5)

ss<-c(0,rep(c(.1,.1,.5),4),.1,.1)

alp<-c("A","B","C","D","E","F","G","H","I","J")

par(mfcol=c(5,2),oma=c(2,3,.5,.5),mar=c(.5,.5,.5,.5))###(bottom,left,top,right

k<-0

for (j in 5:6) {

for (i in 1:length(le)) {

k<-k+1

z<-f[f$Sample\_dat==le[i],]

resp<-z[,j]

fac1<-factor(z$Site, levels=c('Crab Hole','Gibbs Shoal','Clam Shoal'))

fac2<-factor(z$Cage\_type,levels=c("Open","Control","Roof","Large Mesh","Small Mesh"))

me<-aggregate(resp~fac1+fac2,data=z,FUN=function(x) x=mean(x))

y.means <-me[,3]

sd <- aggregate(resp~fac1+fac2,data=z,FUN=function(x) x=sd(x))

y.sd<-sd[,3]

co<-aggregate(resp~fac1+fac2,data=z,FUN=function(x) x=length(x))

y.count<- co[,3]

y.se<-y.sd/(sqrt(y.count))

barx <- barplot(y.means,axes=FALSE,border = NA,

ylim=c(0,26), space=ss,col=cl)

#axis(side=1,labels=FALSE,tck=0)

abline(0,0)

error.bar(barx,y.means, y.se)

text(.1,24.5,alp[k],cex=1)

if(j==5){

axis(side=2)

}

if(j==6){

axis(side=2,labels=FALSE)

}

if(j==5 && i==4){

legend(1,27,Si,fill=cl,bty="n")

}

}

}

ex<-.8

lin<--.2

mtext("Open", SOUTH<-1,line=lin, cex=ex, at=.56,outer=TRUE)

mtext("Control", SOUTH<-1,line=lin, cex=ex, at=.66,outer=TRUE)

mtext("Roof", SOUTH<-1,line=lin, cex=ex, at=.75 ,outer=TRUE)

mtext("Large", SOUTH<-1,line=lin, cex=ex, at=.84 ,outer=TRUE)

mtext("Small", SOUTH<-1,line=lin, cex=ex, at=.93 ,outer=TRUE)

mtext("Open", SOUTH<-1,line=lin, cex=ex, at=.07,outer=TRUE)

mtext("Control", SOUTH<-1,line=lin, cex=ex, at=.16,outer=TRUE)

mtext("Roof", SOUTH<-1,line=lin, cex=ex, at=.25 ,outer=TRUE)

mtext("Large", SOUTH<-1,line=lin, cex=ex, at=.34 ,outer=TRUE)

mtext("Small", SOUTH<-1,line=lin, cex=ex, at=.43 ,outer=TRUE)

mtext(expression(paste("Oysters per shell")), WEST<-2,line=1.5, cex=ex, at=.50,outer=TRUE)

########################################################################

########################################################################

**##### Stats for crab and drills in cage**

dat1<-read.csv("dir/crab\_in\_cages.csv" , sep=",")

dat1.5<-read.csv("dir/ drill\_in\_cages.csv" , sep=",")

## stats

#### crabs####################

# modc6<-glmer(Crabs~Site\*Cage\_type+(Sample\_dat|Site/Mound\_ID),data=dat1,family='poisson')##

fit\_zipois <- glmmTMB(Crabs~Site+Cage\_type+Sample\_dat+Site:Cage\_type+Site:Sample\_dat+Cage\_type:Sample\_dat +

(1|Site/Mound\_ID),data=dat1,ziformula=~1,family=poisson)

fit\_zipois <- glmmTMB(Crabs~Site\*Cage\_type\*Sample\_dat +

(1|Site/Mound\_ID),data=dat1,ziformula=~1,family=poisson)

fit\_pois<-update(fit\_zipois,ziformula=~0) # exclude zero-inflated - ziformula~0

fit\_zinbinom <- update(fit\_zipois,family=nbinom2)

fit\_nbinom <- update(fit\_zinbinom,ziformula=~0)

fit\_zinbinom1 <- update(fit\_zipois,family=nbinom1) ### best !!!

AICtab(fit\_pois,fit\_zipois,fit\_zinbinom,fit\_zinbinom1,fit\_nbinom)

summary(fit\_zinbinom1)

Anova(fit\_zinbinom1)

## check fit

ff <- simulateResiduals(fit\_zinbinom1)

plot(ff)

# mult comp

g1 <- glht(fit\_nbinom, linfct = mcp(Site\*Cage\_type = "Tukey"))

summary(g1)

## mult comp

comp<-emmeans(fit\_zinbinom1, list(pairwise ~ Cage\_type\*Sample\_dat), adjust = "tukey", by=c("Site") )

comp\_plot<-plot(comp, comparisons = TRUE, horizontal = TRUE, ylab= "Factor combination")

###. Drill stats

fit\_zipois <- glmmTMB(Drills~Cage\_type+Sample\_dat++

(1|Mound\_ID),data=dat1.5,ziformula=~1,family=poisson)

fit\_pois<-update(fit\_zipois,ziformula=~0) # exclude zero-inflated - ziformula~0

fit\_zinbinom <- update(fit\_zipois,family=nbinom2)

fit\_nbinom <- update(fit\_zinbinom,ziformula=~0)

fit\_zinbinom1 <- update(fit\_zipois,family=nbinom1) ### best !!!, but didn't converge - no p value zipois second best

AICtab(fit\_pois,fit\_zipois,fit\_zinbinom,fit\_zinbinom1,fit\_nbinom)

summary(fit\_zipois)

Anova(fit\_zipois)

## check fit

ff <- simulateResiduals(fit\_zipois)

plot(ff)

####################################################################

#################################################################

####################################################################

#################################################################

**####. For fauna on reefs**

#############################################################

## set catchfile to folder were datasheets are!!!!!!!!!!!!!!!!

#################mud crab bins############

dat<-read.table(paste(catchfile,"/binall.csv", sep=""), header=T,sep=',')

Binmult<-19.24

#head(dat)

dat$sizecount<-apply(dat[,12:61],1,function(x) length(which(!is.na(x))))

#colnames(dat)

#dim(dat)

####abundance

ab<-dat[,c(1,3:11,63)]

caab<-cast(ab,Id+Year+Season+Site+Mound+treatment+Depth~Species,mean,value='Tot.num')

###convert NAN to 0's

caab[is.na(caab)] <- 0

###conver tto per m2

caab$MCall<-caab$E.Depressus+caab$P.Herbstii+caab$MudCrab

caab$MCallm2<-caab$MCall\*Binmult

###biomass

bio<-dat[,c(1,3:10,62,63)]

cabio<-cast(bio,Id+Year+Season+Site+Mound+treatment+Depth~Species,mean,value='Weight')

cabio[is.na(cabio)] <- 0

####corrections

cabio[5,8]<-3.2

cabio[153,8]<-42.25

cabio$MCbio<-cabio$E.Depressus+cabio$P.Herbstii+cabio$MudCrab

cabio$MCbiom2<-cabio$MCbio\*Binmult

###new data frame with abund and biomass########

caab1<-caab[,c(1:7,37:38)]

cabio1<-cabio[,c(1,37:38)]

mc<-merge(caab1,cabio1)

mc$treatbi<-"New"

mc$treatbi[which(mc$treatment=="Old")]<-"Old"

#####

mc<-mc[!mc$Year==2009,]####remove 2009

mc<-mc[mc$Site=='Crab Hole' | mc$Site=='Gibbs Shoal'| mc$Site=='Clam Shoal',]####keep 3

mcse <- summarySE(mc, measurevar="MCall", groupvars=c("Site"))

mcbse<- summarySE(mc, measurevar="MCbio", groupvars=c("Site"))

##calculations for >10mm###############################################################

SW<-read.table(paste0(catchfile,"mudcrabStoW.csv"), header=T,sep=',')

#unique(dat$Species)

mcc<-dat[dat$Species=="E.Depressus" | dat$Species=="P.Herbstii" | dat$Species=="MudCrab",]

mcc<-mcc[mcc$Site=='Crab Hole' | mcc$Site=='Gibbs Shoal'| mcc$Site=='Clam Shoal',]####keep 3

mcc<-mcc[!mcc$Year==2009,]####remove 2009

######correct bad number

mcc[79,24]<-6.3

mcc$crabsgr10<-rowSums(mcc[,c(12:61)]>9.9,na.rm = TRUE)##sum # >9.9

mcc4<-aggregate(crabsgr10~Id+Date+Year+Season+Mound.ID+Site+Mound+Depth,data=mcc,FUN=function(x)x=sum(x))###poo

mcc2<-mcc[,1:61]##?

mcc33<-mcc[is.na(mcc$X2),]

###fit curve from only 1 in bin n=22

x<-mcc33$X1

y<-mcc33$Weight

x1<-x^2

x2<-x^2.6

x3<-x^2.8##

x4<-x^2.7#####best.979

#plot(x4,y)

fit1 <- lm(y~x1+0)

fit2 <- lm(y~x2+0)

fit3 <- lm(y~x3+0)

fit4 <- lm(y~x4+0)

###fit curve form MHC mud crabs n>300

#plot(SW$mm,SW$g)

x<-SW$mm

y<-SW$g

x3<-x^2.8#####best fit r2 .9623

fit3 <- lm(y~x3+0)

#summary(fit4)

#plot(SW$mm,sqrt(SW$g))

#pr<-((mcc[,12:61])^2.8\*.0007356)###from MHC mud crabs

pr<-((mcc[,12:61])^2.7\*.000903)###from lone crabs in bins

pr<-data.frame(pr)

#pred<-predict(mod,pr,type="response",na.action = na.omit)

mccb<-cbind(mcc[,1:11],pr[,1:50])

#colnames(mcc)

###sum biomass for crabs >9.9mm########################

cb<-melt(mccb,id=c(1:11))##move length # into one column

cb1<-cb[!is.na(cb$value),]##remove na's in value

cn<-melt(mcc2,id=c(1:11))##move length # into one column

cn1<-cn[!is.na(cn$value),]##remove na's in value

cb2<-cb1[cn1$value>9.9,]##keep only crab bio that bigger than 9.9mm cw

cb3<-cb2[,c(1,3:9,13)]###

cb4<-aggregate(value~Id+Date+Year+Season+Mound.ID+Site+Mound+Depth,data=cb3,FUN=function(x)x=sum(x))###poo

####merge >10 with origial Mc data############################

##########################################################################3

cb5<-cb4[,c(1,9)]

mcc5<-mcc4[,c(1,9)]

mc1<-merge(mc,cb5,by.x = "Id", by.y = "Id", all = TRUE)

mc1<-merge(mc1,mcc5,by.x = "Id", by.y = "Id", all = TRUE)

names(mc1)[13]<-paste("crabsgr10bio")

mc1$crabsgr10bio[is.na(mc1$crabsgr10bio)]<-0

mc1$crabsgr10biom2<-mc1$crabsgr10bio\*Binmult

mc1$crabsgr10[is.na(mc1$crabsgr10)]<-0

mc1$crabsgr10m2<-mc1$crabsgr10\*Binmult

##################################################################

###DRills################################################

od<-caab[,1:8]

od$odm2<-od$AtlanticOysterDrill\*Binmult

od$odbio<-cabio[,8]

od$odbiom2<-od$odbio\*Binmult

od<-od[od$Site=='Crab Hole' | od$Site=='Gibbs Shoal'| od$Site=='Clam Shoal',]####keep 3

od<-od[!od$Year==2009,]####remove 2009

###snap shimp####none in these three sites-Ocra and West's

ss<-caab[,c(1:7,32)]

ss$ssm2<-ss$SnappingShrimp\*Binmult

ss$ssbio<-cabio[,32]

ss$ssbiom2<-ss$ssbio\*Binmult

###################predators#######################################

pred<-read.table(paste(catchfile,"/catch.csv", sep=""), header=T,sep=',')

colnames(pred)

pred<-pred[!pred$Year==2009,]##remove 2009

pred<-pred[!pred$Season=="Winter",]##remove winter

pred<-pred[pred$Site=='Crab Hole' | pred$Site=='Gibbs Shoal'| pred$Site=='Clam Shoal',]

###GN

predgn<-pred[pred$Gear=="Net",]

gn<-cast(predgn,Year+Season+Site+rep~Species,length,value='Weight')

gnbi<-cast(predgn,Year+Season+Site+rep~Species,mean,value='Weight')

gn1<-aggregate(cbind(Bluefish,Sheepshead)~Year+Season+Site,data=gn,

FUN=function(x)x=mean(x))###biomass of each speces per set

####CT

predct<-pred[pred$Gear=="CT",]

ct<-cast(predct,Year+Season+Site+rep~Species,length,value='Weight')##num of individs

bcw<-predct[predct$Species=="Blue\_crab",]

bcw1<-aggregate(cbind(S..Length..cm.)~Site,data=bcw,FUN=function(x)x=mean(x))##weight nt label right for ct bimoass is s length

bcwcount<-aggregate(cbind(S..Length..cm.)~Site,data=bcw,FUN=function(x)x=count(x))##weight nt label right

ct1<-aggregate(cbind(Blue\_crab)~Year+Season+Site,data=ct,FUN=function(x)x=mean(x))###count of each speces per set

ctse <- summarySE(ct1, measurevar="Blue\_crab", groupvars=c("Site"))

##average per sampling day

###average per site

###count of samplings

###############vis surveys SL=0.817\*TL

##log(W)=-4.5287+3.0446\*log(SL) both from schwartz 1990 or W=.0296L^3.045

vis1<-read.table(paste(catchfile,"/vissurvey.csv", sep=""), header=T,sep=',')

colnames(vis1)

vis1$SH.1bio<-((vis1$SH.size.1\*0.817)^3.045)\*.0296

vis1$SH.2bio<-((vis1$SH.size.2\*0.817)^3.045)\*.0296

vis1$SH.3bio<-((vis1$SH.size.3\*0.817)^3.045)\*.0296

vis1$SH.bio<-rowSums(vis1[,25:27],na.rm = TRUE)

vis1$SH.bioperm2<-vis1$SH.bio/10

vis<-vis1#[,1:14]

vis<-vis[!vis$Year==2009,]##remove 2009

vis<-vis[vis$Site=='Crab Hole' | vis$Site=='Gibbs Shoal'| vis$Site=='Clam Shoal',]

vi<-vis

vi1<-aggregate(cbind(Sheepshead,Black\_seabass)~Year+Yearrep+Site+Mound,data=vi,

FUN=function(x)x=mean(x))###count of each speces per set

#vish <- summarySE(vi1, measurevar="Sheepshead", groupvars=c("Site","Year"))

vise <- summarySE(vi, measurevar="Sheepshead", groupvars=c("Site"))

#####quads##########################################################################

quad<-read.table(paste(catchfile,"/quadrat.csv", sep=""), header=T,sep=',')

stod<-read.table("/Users/geraldn/Dropbox/Documents/NC Research/CRFL/Data/R/Sample\_dat\_to\_num.csv", header=T,sep=',')

##bcw1 has bc biomass from traps

quad$Date<-as.Date(quad$Date,format='%d-%m-%Y')###format date from excel

tmp <- as.POSIXlt(quad$Date)

tmp$year <- tmp$year+2000

quad$Date<- as.Date(tmp)

quad$Month<-as.numeric(format(quad$Date,"%m"))###extract month

quad$Year<-as.numeric(format(quad$Date,"%Y"))

quad<-join(quad,stod)#add in sample dat to num

quad$stonem2<-quad$stone\*4

quad$blue.crabm2<-quad$blue.crab\*4

quad<-join(quad,bcw1)#####

quad$bcbio<-quad$blue.crab\*quad$S..Length..cm.###biomass for ct bimoass is s length

quad$stbio<-quad$stone\*mean(mean(bcw1[,2])\*2)###biomass

quad$bcbiom2<-quad$blue.crabm2\*quad$S..Length..cm.###biomass

quad$stbiom2<-quad$stonem2\*(mean(bcw1[,2])\*2)###biomass

qu<-quad[quad$Site=='Crab Hole' | quad$Site=='Gibbs Shoal'| quad$Site=='Clam Shoal',]

#qu1<-aggregate(cbind(stonem2,blue.crabm2)~Year+Yearrep+Site+Mound,data=qu,

# FUN=function(x)x=mean(x))###count of each speces per set

qustse <- summarySE(qu, measurevar="stonem2", groupvars=c("Site"))

qubcse <- summarySE(qu, measurevar="blue.crabm2", groupvars=c("Site"))

qustbise <- summarySE(qu, measurevar="stbiom2", groupvars=c("Site"))

qubcbise <- summarySE(qu, measurevar="bcbiom2", groupvars=c("Site"))

######################################################################################

error.bar <- function(x, y, upper, lower=upper, length=0.1,...){

if(length(x) != length(y) | length(y) !=length(lower) | length(lower) != length(upper))

stop("vectors must be same length")

arrows(x,y+upper, x, y-lower, angle=90, code=3, length=length, ...)

}

#########################################################################

##############################################################################

######### graph all predators #########

#################################################################################

c<-.75#cex of sample size

qq<-.2##x for letter of plot

a<--.5

space<-c(1:3)

space2<-c(seq(2,18,by=4))

cl<-c("gray90","gray70","gray45")

Si<-c('Crab Hole','Gibbs Shoal','Clam Shoal')

let<-c("A","B","C","D")

setwd(figfile)

setEPS()

postscript("predplot.eps", width = 6.6, height = 6.5,colormodel="rgb" )

par(mfrow=c(6,2),oma=c(2,3,1,2), mar=c(.5,4,.5,1))

###########################################################################

############allmc

datp<-mc#################################################3

fac2<-factor(datp$Site, levels=c('Crab Hole','Gibbs Shoal','Clam Shoal'))

# datp$Site<-factor(datp$Site, levels=c('Crab Hole','Gibbs Shoal','Clam Shoal'))

####goood stats

datp$resp<-datp$MCall

me<-aggregate(resp~Site\*Mound\*Season,data=datp,FUN=function(x) x=mean(x))

#kruskal.test(resp~ Site, data = me) ##sig

#DunnTest(resp~ Site,data=me,method="fdr")

fit\_zipois <- glmmTMB(resp~Site\*Season +

(1|Site/Mound),data=me,ziformula=~1,family=poisson)

fit\_pois<-update(fit\_zipois,ziformula=~0) # exclude zero-inflated - ziformula~0

fit\_zinbinom <- update(fit\_zipois,family=nbinom2)

fit\_nbinom <- update(fit\_zinbinom,ziformula=~0)

fit\_zinbinom1 <- update(fit\_zipois,family=nbinom1) ### best !!!, but didn't converge - no p value fit\_nbinom second best

AICtab(fit\_pois,fit\_zipois,fit\_zinbinom,fit\_zinbinom1,fit\_nbinom)

summary(fit\_nbinom)

Anova(fit\_nbinom)

## check fit

# ff <- simulateResiduals(fit\_pois)

# plot(ff)

datp$resp<-datp$MCallm2

me1<-aggregate(resp~Site\*Mound,data=datp,FUN=function(x) x=mean(x))

fac2<-factor(me1$Site, levels=c('Crab Hole','Gibbs Shoal','Clam Shoal'))

me<-aggregate(resp~fac2,data=me1,FUN=function(x) x=mean(x))

y.means <-me[,2]

sd <- aggregate(resp~fac2,data=me1,FUN=function(x) x=sd(x))

y.sd<-sd[,2]

co<-aggregate(resp~fac2,data=me1,FUN=function(x) x=length(x))

y.count<- co[,2]

y.se<-y.sd/(sqrt(y.count))

barx <- barplot(y.means,axes=FALSE,border = NA,ylim=c(0,600), col=cl,ylab='')

axis(side=2)

abline(0,0)

error.bar(barx,y.means, y.se)

## number of samples

we<-50

f<-aggregate(me1$resp~fac2,FUN=function(x) x=length(x))

text(barx, we, labels = f[,2],cex=c,co='black')

#add letter to plots

text(qq,570,labels="A")

qqq<-c("a","a","b")

brr<-barx

text(brr,550,qqq,cex=1)

#add.image(3.1, 300, mcp, adj.x = 0.5, adj.y = 0.5,

# image.width = 0.3, image.height = .34,col=grey( (0:256)/256))

#######bio########################

datp<-mc#################################################3

#fac2<-factor(datp$Site, levels=c('Crab Hole','Gibbs Shoal','Clam Shoal'))

#datp$resp<-datp$MCbio

#me<-aggregate(resp~Site\*Mound,data=datp,FUN=function(x) x=mean(x))

####goood stats

datp$resp<-datp$MCall # hist(datp$resp)

me<-aggregate(resp~Site\*Mound\*Season,data=datp,FUN=function(x) x=mean(x))

fit\_zipois <- glmmTMB(resp~Site\*Season + (1|Site/Mound),data=me,ziformula=~1,family=poisson)

fit\_pois<-update(fit\_zipois,ziformula=~0) # exclude zero-inflated - ziformula~0

fit\_zinbinom <- update(fit\_zipois,family=nbinom2)

fit\_nbinom <- update(fit\_zinbinom,ziformula=~0)

fit\_zinbinom1 <- update(fit\_zipois,family=nbinom1) ### best !!!, but didn't converge - no p value fit\_nbinom second best

AICtab(fit\_pois,fit\_zipois,fit\_zinbinom,fit\_zinbinom1,fit\_nbinom)

summary(fit\_nbinom)

Anova(fit\_nbinom)

## check fit

ff <- simulateResiduals(fit\_nbinom )

plot(ff)

##### biomass

datp$resp<-datp$MCbiom2

me<-aggregate(resp~Site\*Mound\*Season,data=datp,FUN=function(x) x=mean(x))

fit\_zig <- glmmTMB(resp~Site\*Season +

(1|Site/Mound),data=me,ziformula=~1,family=gaussian(link = "identity"))

fit\_g<-update(fit\_zig,ziformula=~0) # exclude zero-inflated - ziformula~0

fit\_g\_log <- glmmTMB(resp+1~Site\*Season +

(1|Site/Mound),data=me,ziformula=~0,family=gaussian(link = "log") )

fit\_g\_inv <- glmmTMB(resp+1~Site\*Season +

(1|Site/Mound),data=me,ziformula=~0,family=gaussian(link = "inverse") )

AICtab(fit\_zig,fit\_g,fit\_g\_log,fit\_g\_inv)

summary(fit\_zig)

Anova(fit\_zig)

## check fit

# ff <- simulateResiduals(fit\_zig)

# plot(ff)

fac2<-factor(me1$Site, levels=c('Crab Hole','Gibbs Shoal','Clam Shoal'))

me<-aggregate(resp~fac2,data=me1,FUN=function(x) x=mean(x))

y.means <-me[,2]

sd <- aggregate(resp~fac2,data=me1,FUN=function(x) x=sd(x))

y.sd<-sd[,2]

co<-aggregate(resp~fac2,data=me1,FUN=function(x) x=length(x))

y.count<- co[,2]

y.se<-y.sd/(sqrt(y.count))

barx <- barplot(y.means,axes=FALSE,border = NA,ylim=c(0,200), col=cl,ylab='')

axis(side=2)

abline(0,0)

error.bar(barx,y.means, y.se)

## number of samples

we<-20

f<-aggregate(me1$resp~fac2,FUN=function(x) x=length(x))

text(barx, we, labels = f[,2],cex=c,co='black')

#add letter to plots

text(qq,190,labels="G")

qqq<-c("a","a","a")

text(brr,170,qqq,cex=1)

#add.image(4.1, 100, mcp, adj.x = 0.5, adj.y = 0.5,

# image.width = 0.3, image.height = .34,col=grey( (0:256)/256))

#big mc###############################################################

datp<-mc1#####################

datp$resp<-datp$crabsgr10

me<-aggregate(resp~Site\*Mound\*Season,data=datp,FUN=function(x) x=mean(x))

fit\_zipois <- glmmTMB(resp~Site\*Season + (1|Site/Mound),data=me,ziformula=~1,family=poisson)

fit\_pois<-update(fit\_zipois,ziformula=~0) # exclude zero-inflated - ziformula~0

fit\_zinbinom <- update(fit\_zipois,family=nbinom2)

fit\_nbinom <- update(fit\_zinbinom,ziformula=~0)

fit\_zinbinom1 <- update(fit\_zipois,family=nbinom1) ### best !!!, but didn't converge - no p value fit\_nbinom second best

AICtab(fit\_pois,fit\_zipois,fit\_zinbinom,fit\_zinbinom1,fit\_nbinom)

summary(fit\_pois)

Anova(fit\_pois)

## check fit

# ff <- simulateResiduals(fit\_pois)

# plot(ff)

datp$resp<-datp$crabsgr10m2

me1<-aggregate(resp~Site\*Mound,data=datp,FUN=function(x) x=mean(x))

fac2<-factor(me1$Site, levels=c('Crab Hole','Gibbs Shoal','Clam Shoal'))

me<-aggregate(resp~fac2,data=me1,FUN=function(x) x=mean(x))

y.means <-me[,2]

sd <- aggregate(resp~fac2,data=me1,FUN=function(x) x=sd(x))

y.sd<-sd[,2]

co<-aggregate(resp~fac2,data=dme1,FUN=function(x) x=length(x))

y.count<- co[,2]

y.se<-y.sd/(sqrt(y.count))

barx <- barplot(y.means,axes=FALSE,border = NA,ylim=c(0,140), col=cl,ylab='')

axis(side=2)

abline(0,0)

error.bar(barx,y.means, y.se)

## number of samples

we<-10

f<-aggregate(me1$resp~fac2,FUN=function(x) x=length(x))

text(barx, we, labels = f[,2],cex=c,co='black')

#add letter to plots

text(qq,133,labels="B")

qqq<-c("a","a","b")

text(brr,130,qqq,cex=1)

#add.image(3.1, 100, mcp, adj.x = 0.5, adj.y = 0.5,

# image.width = 0.46, image.height = .57,col=grey( (0:256)/256))

#######bio########################

datp<-mc1#################################################3

#datp$resp<-datp$crabsgr10bio

#me<-aggregate(resp~Site\*Mound,data=datp,FUN=function(x) x=mean(x))

#kruskal.test(resp~ Site, data = me) ##sig

#DunnTest(resp~ Site,data=me,method="fdr")

datp$resp<-datp$crabsgr10biom2

me1<-aggregate(resp~Site\*Mound,data=datp,FUN=function(x) x=mean(x))

fac2<-factor(me1$Site, levels=c('Crab Hole','Gibbs Shoal','Clam Shoal'))

me<-aggregate(resp~fac2,data=me1,FUN=function(x) x=mean(x))

y.means <-me[,2]

sd <- aggregate(resp~fac2,data=me1,FUN=function(x) x=sd(x))

y.sd<-sd[,2]

co<-aggregate(resp~fac2,data=me1,FUN=function(x) x=length(x))

y.count<- co[,2]

y.se<-y.sd/(sqrt(y.count))

barx <- barplot(y.means,axes=FALSE,border = NA,ylim=c(0,150), col=cl,ylab='')

axis(side=2)

abline(0,0)

error.bar(barx,y.means, y.se)

## number of samples

we<-13

f<-aggregate(me1$resp~fac2,FUN=function(x) x=length(x))

text(barx, we, labels = f[,2],cex=c,co='black')

#add letter to plots

text(qq,137,labels="H")

qqq<-c("a","a","a")

text(brr,140,qqq,cex=1)

###############################################################################

#drills

datp<-od#####################

datp$resp<-datp$AtlanticOysterDrill

me<-aggregate(resp~Site\*Mound\*Season,data=datp,FUN=function(x) x=mean(x))

fit\_zipois <- glmmTMB(resp~Site\*Season + (1|Site/Mound),data=me,ziformula=~1,family=poisson)

fit\_pois<-update(fit\_zipois,ziformula=~0) # exclude zero-inflated - ziformula~0

fit\_zinbinom <- update(fit\_zipois,family=nbinom2)

fit\_nbinom <- update(fit\_zinbinom,ziformula=~0)

fit\_zinbinom1 <- update(fit\_zipois,family=nbinom1) ###

AICtab(fit\_pois,fit\_zipois,fit\_zinbinom,fit\_zinbinom1,fit\_nbinom)

summary(fit\_zinbinom)

Anova(fit\_zinbinom)

## check fit

# ff <- simulateResiduals(fit\_zinbinom)

# plot(ff)

datp$resp<-datp$odm2

me1<-aggregate(resp~Site\*Mound,data=datp,FUN=function(x) x=mean(x))

fac2<-factor(me1$Site, levels=c('Crab Hole','Gibbs Shoal','Clam Shoal'))

me<-aggregate(resp~fac2,data=me1,FUN=function(x) x=mean(x))

y.means <-me[,2]

sd <- aggregate(resp~fac2,data=me1,FUN=function(x) x=sd(x))

y.sd<-sd[,2]

co<-aggregate(resp~fac2,data=me1,FUN=function(x) x=length(x))

y.count<- co[,2]

y.se<-y.sd/(sqrt(y.count))

barx <- barplot(y.means,axes=FALSE,border = NA,ylim=c(0,20), col=cl,ylab='')

axis(side=2)

abline(0,0)

error.bar(barx,y.means, y.se)

## number of samples

we<-1

f<-aggregate(me1$resp~fac2,FUN=function(x) x=length(x))

text(barx, we, labels = f[,2],cex=c,co='black')

#add letter to plots

text(qq,19.2,labels="C")

qqq<-c("a","a","b")

text(brr,19,qqq,cex=1)

#add.image(.9, 12, odp, adj.x = 0.5, adj.y = 0.5,

# image.width = 0.4, image.height = .28,col=grey( (0:256)/256))

#######bio########################

datp<-od############

#datp$resp<-datp$odbio

#me<-aggregate(resp~Site\*Mound,data=datp,FUN=function(x) x=mean(x))

#kruskal.test(resp~ Site, data = me) ##sig

#DunnTest(resp~ Site,data=me,method="fdr")

datp$resp<-datp$odbiom2

me1<-aggregate(resp~Site\*Mound,data=datp,FUN=function(x) x=mean(x))

fac2<-factor(me1$Site, levels=c('Crab Hole','Gibbs Shoal','Clam Shoal'))

me<-aggregate(resp~fac2,data=me1,FUN=function(x) x=mean(x))

y.means <-me[,2]

sd <- aggregate(resp~fac2,data=me1,FUN=function(x) x=sd(x))

y.sd<-sd[,2]

co<-aggregate(resp~fac2,data=me1,FUN=function(x) x=length(x))

y.count<- co[,2]

y.se<-y.sd/(sqrt(y.count))

barx <- barplot(y.means,axes=FALSE,border = NA,ylim=c(0,15), col=cl,ylab='')

axis(side=2)

abline(0,0)

error.bar(barx,y.means, y.se)

## number of samples

we<-.75

f<-aggregate(me1$resp~fac2,FUN=function(x) x=length(x))

text(barx, we, labels = f[,2],cex=c,co='black')

#add letter to plots

text(qq,14.4,labels="I")

qqq<-c("a","a","b")

text(brr,13.5,qqq,cex=1)

###############################################################################

#blue crab

datp<-qu#####################

datp$resp<-datp$blue.crab

me<-aggregate(resp~Site\*Mound\*Season,data=datp,FUN=function(x) x=mean(x))

#

fit\_zipois <- glmmTMB(resp~Site\*Season + (1|Site/Mound),data=me,ziformula=~1,family=poisson)

fit\_pois<-update(fit\_zipois,ziformula=~0) # exclude zero-inflated - ziformula~0

fit\_zinbinom <- update(fit\_zipois,family=nbinom2)

fit\_nbinom <- update(fit\_zinbinom,ziformula=~0)

fit\_zinbinom1 <- update(fit\_zipois,family=nbinom1) ### best

AICtab(fit\_pois,fit\_zipois,fit\_zinbinom,fit\_zinbinom1,fit\_nbinom)

#

fit\_zig <- glmmTMB(resp~Site\*Season + (1|Site/Mound),data=me,ziformula=~1,family=gaussian(link = "identity"))

fit\_g<-update(fit\_zig,ziformula=~0) # exclude zero-inflated - ziformula~0

fit\_g\_log <- glmmTMB(resp+1~Site\*Season + (1|Site/Mound),data=me,ziformula=~0,family=gaussian(link = "log") )

fit\_g\_inv <- glmmTMB(resp+1~Site\*Season + (1|Site/Mound),data=me,ziformula=~0,family=gaussian(link = "inverse") )

AICtab(fit\_zig,fit\_g,fit\_g\_log,fit\_g\_inv) # fit\_g\_inv

summary(fit\_zig)

Anova(fit\_zig)

## check fit

# ff <- simulateResiduals(fit\_g\_inv)

# plot(ff)

datp$resp<-datp$blue.crabm2

me1<-aggregate(resp~Site\*Mound,data=datp,FUN=function(x) x=mean(x))

fac2<-factor(me1$Site, levels=c('Crab Hole','Gibbs Shoal','Clam Shoal'))

me<-aggregate(resp~fac2,data=me1,FUN=function(x) x=mean(x))

y.means <-me[,2]

sd <- aggregate(resp~fac2,data=me1,FUN=function(x) x=sd(x))

y.sd<-sd[,2]

co<-aggregate(resp~fac2,data=me1,FUN=function(x) x=length(x))

y.count<- co[,2]

y.se<-y.sd/(sqrt(y.count))

barx <- barplot(y.means,axes=FALSE,border = NA,ylim=c(0,.1), col=cl,ylab='')

axis(side=2,labels=c(0,0.05,0.1),at=c(0,0.05,0.1))

abline(0,0)

error.bar(barx,y.means, y.se)

## number of samples

we<-.006

f<-aggregate(me1$resp~fac2,FUN=function(x) x=length(x))

barxx<-c(.7,2.1,3.1)

text(barxx, we, labels = f[,2],cex=c,co='black')

#add letter to plots

text(qq,.095,labels="D")

qqq<-c("a","a","a")

text(brr,.09,qqq,cex=1)

#add.image(.9, 12, odp, adj.x = 0.5, adj.y = 0.5,

# image.width = 0.4, image.height = .28,col=grey( (0:256)/256))

#######bio########################bc

datp<-qu#####################

datp$resp<-datp$bcbio

me<-aggregate(resp~Site\*Season\*Mound,data=datp,FUN=function(x) x=mean(x))

#

fit\_zig <- glmmTMB(resp~Site\*Season + (1|Site/Mound),data=me,ziformula=~1,family=gaussian(link = "identity"))

fit\_g<-update(fit\_zig,ziformula=~0) # exclude zero-inflated - ziformula~0

fit\_g\_log <- glmmTMB(resp+1~Site\*Season + (1|Site/Mound),data=me,ziformula=~0,family=gaussian(link = "log") )

fit\_g\_inv <- glmmTMB(resp+1~Site\*Season + (1|Site/Mound),data=me,ziformula=~0,family=gaussian(link = "inverse") )

AICtab(fit\_zig,fit\_g,fit\_g\_log,fit\_g\_inv) # fit\_g\_inv

summary(fit\_g\_inv)

Anova(fit\_g\_inv)

## check fit

# ff <- simulateResiduals(fit\_g\_inv)

# plot(ff)

datp$resp<-datp$bcbiom2

me1<-aggregate(resp~Site\*Mound,data=datp,FUN=function(x) x=mean(x))

fac2<-factor(me1$Site, levels=c('Crab Hole','Gibbs Shoal','Clam Shoal'))

me<-aggregate(resp~fac2,data=me1,FUN=function(x) x=mean(x))

y.means <-me[,2]

sd <- aggregate(resp~fac2,data=me1,FUN=function(x) x=sd(x))

y.sd<-sd[,2]

co<-aggregate(resp~fac2,data=me1,FUN=function(x) x=length(x))

y.count<- co[,2]

y.se<-y.sd/(sqrt(y.count))

barx <- barplot(y.means,axes=FALSE,border = NA,ylim=c(0,10), col=cl,ylab='')

axis(side=2)

abline(0,0)

error.bar(barx,y.means, y.se)

## number of samples

we<-.75

f<-aggregate(me1$resp~fac2,FUN=function(x) x=length(x))

text(barxx, we, labels = f[,2],cex=c,co='black')

#add letter to plots

text(qq,9.3,labels="J")

text(brr,8.5,qqq,cex=1)

###############################################################################

#Stone

datp<-qu#####################

datp$resp<-datp$stone

me<-aggregate(resp~Site\*Mound\*Season,data=datp,FUN=function(x) x=mean(x))

#

fit\_zipois <- glmmTMB(resp~Site + (1|Site/Mound),data=me,ziformula=~1,family=poisson)

fit\_pois<-update(fit\_zipois,ziformula=~0) # exclude zero-inflated - ziformula~0

fit\_zinbinom <- update(fit\_zipois,family=nbinom2)

fit\_nbinom <- update(fit\_zinbinom,ziformula=~0)

fit\_zinbinom1 <- update(fit\_zipois,family=nbinom1) ### best

AICtab(fit\_pois,fit\_zipois,fit\_zinbinom,fit\_zinbinom1,fit\_nbinom)

#bio stat

datp$resp<-datp$stbio

me<-aggregate(resp~Site\*Mound\*Season,data=datp,FUN=function(x) x=mean(x))

fit\_zig <- glmmTMB(resp~Site\*Season +

(1|Site/Mound),data=me,ziformula=~1,family=gaussian(link = "identity"))

fit\_g<-update(fit\_zig,ziformula=~0) # exclude zero-inflated - ziformula~0

fit\_g\_log <- glmmTMB(resp+1~Site\*Season +

(1|Site/Mound),data=me,ziformula=~0,family=gaussian(link = "log") )

fit\_g\_inv <- glmmTMB(resp+1~Site\*Season +

(1|Site/Mound),data=me,ziformula=~0,family=gaussian(link = "inverse") )

AICtab(fit\_zig,fit\_g,fit\_g\_log,fit\_g\_inv) # fit\_g\_inv

summary(fit\_g)

Anova(fit\_g)

## check fit

# ff <- simulateResiduals(fit\_g)

# plot(ff)

fac2<-factor(datp$Site, levels=c('Crab Hole','Gibbs Shoal','Clam Shoal'))

datp$resp<-datp$stonem2

me1<-aggregate(resp~Site\*Mound,data=datp,FUN=function(x) x=mean(x))

fac2<-factor(me1$Site, levels=c('Crab Hole','Gibbs Shoal','Clam Shoal'))

me<-aggregate(resp~fac2,data=me1,FUN=function(x) x=mean(x))

y.means <-me[,2]

sd <- aggregate(resp~fac2,data=me1,FUN=function(x) x=sd(x))

y.sd<-sd[,2]

co<-aggregate(resp~fac2,data=me1,FUN=function(x) x=length(x))

y.count<- co[,2]

y.se<-y.sd/(sqrt(y.count))

barx <- barplot(y.means,axes=FALSE,border = NA,ylim=c(0,.2), col=cl,ylab='')

axis(side=2,labels=c(0,0.1,0.2), at=c(0,0.1,0.2))

abline(0,0)

error.bar(barx,y.means, y.se)

## number of samples

we<-.015

f<-aggregate(me1$resp~fac2,FUN=function(x) x=length(x))

text(barxx, we, labels = f[,2],cex=c,co='black')

#add letter to plots

text(qq,.192,labels="E")

text(brr,.19,qqq,cex=1)

#add.image(.9, 12, odp, adj.x = 0.5, adj.y = 0.5,

# image.width = 0.4, image.height = .28,col=grey( (0:256)/256))

#######bio########################

datp<-qu############

#datp$resp<-datp$stbio

#me<-aggregate(resp~Site\*Mound,data=datp,FUN=function(x) x=mean(x))

#kruskal.test(resp~ Site, data = me) ##sig

#DunnTest(resp~ Site,data=me,method="fdr")

fac2<-factor(datp$Site, levels=c('Crab Hole','Gibbs Shoal','Clam Shoal'))

datp$resp<-datp$stbiom2

me1<-aggregate(resp~Site\*Mound,data=datp,FUN=function(x) x=mean(x))

fac2<-factor(me1$Site, levels=c('Crab Hole','Gibbs Shoal','Clam Shoal'))

me<-aggregate(resp~fac2,data=me1,FUN=function(x) x=mean(x))

y.means <-me[,2]

sd <- aggregate(resp~fac2,data=me1,FUN=function(x) x=sd(x))

y.sd<-sd[,2]

co<-aggregate(resp~fac2,data=me1,FUN=function(x) x=length(x))

y.count<- co[,2]

y.se<-y.sd/(sqrt(y.count))

barx <- barplot(y.means,axes=FALSE,border = NA,ylim=c(0,30), col=cl,ylab='')

axis(side=2)

abline(0,0)

error.bar(barx,y.means, y.se)

## number of samples

we<-3

f<-aggregate(me1$resp~fac2,FUN=function(x) x=length(x))

text(barxx, we, labels = f[,2],cex=c,co='black')

#add letter to plots

text(qq,29,labels="K")

text(brr,28,qqq,cex=1)

######################################################################3

#SH

vis\_d<- vis %>%

mutate(Date=gsub("-", "/", Date)) %>% # ,"-"

tidyr::separate(col=Date, c("month", "date", "year"), sep=c("/") , remove=F) %>%

mutate(Season=if\_else(month>6,"summer", "spring"))

datp<-vis\_d#####################

datp$resp<-datp$Sheepshead

#me<-aggregate(resp~Site\*Mound,data=datp,FUN=function(x) x=mean(x))

#mec<-aggregate(resp~Site\*Mound,data=datp,FUN=function(x) x=length(x))###mean(mec$resp)

#mec<-aggregate(resp~Site,data=datp,FUN=function(x) x=length(x))###mea

me<-aggregate(resp~Site\*Mound\*Season,data=datp,FUN=function(x) x=mean(x))

#

fit\_zipois <- glmmTMB(resp~Site + (1|Site/Mound),data=me,ziformula=~1,family=poisson)

fit\_pois<-update(fit\_zipois,ziformula=~0) # exclude zero-inflated - ziformula~0

fit\_zinbinom <- update(fit\_zipois,family=nbinom2)

fit\_nbinom <- update(fit\_zinbinom,ziformula=~0)

fit\_zinbinom1 <- update(fit\_zipois,family=nbinom1) ### best

AICtab(fit\_pois,fit\_zipois,fit\_zinbinom,fit\_zinbinom1,fit\_nbinom)

summary(fit\_zinbinom1)

Anova(fit\_zinbinom1)

# bio

datp$resp<-datp$SH.bio

me<-aggregate(resp~Site\*Mound\*Season,data=datp,FUN=function(x) x=mean(x))

fit\_zig <- glmmTMB(resp~Site +

(1|Site/Mound),data=me,ziformula=~1,family=gaussian(link = "identity"))

fit\_g<-update(fit\_zig,ziformula=~0) # exclude zero-inflated - ziformula~0

fit\_g\_log <- glmmTMB(resp+1~Site +

(1|Site/Mound),data=me,ziformula=~0,family=gaussian(link = "log") )

fit\_g\_inv <- glmmTMB(resp+1~Site +

(1|Site/Mound),data=me,ziformula=~0,family=gaussian(link = "inverse") )

AICtab(fit\_zig,fit\_g,fit\_g\_log,fit\_g\_inv) # abund fit\_zipois,

summary(fit\_pois)

Anova(fit\_pois)

## check fit

# ff <- simulateResiduals(fit\_zinbinom1)

# plot(ff)

fac2<-factor(datp$Site, levels=c('Crab Hole','Gibbs Shoal','Clam Shoal'))

datp$resp<-datp$Sheepshead/10

me1<-aggregate(resp~Site\*Mound,data=datp,FUN=function(x) x=mean(x))

fac2<-factor(me1$Site, levels=c('Crab Hole','Gibbs Shoal','Clam Shoal'))

me<-aggregate(resp~fac2,data=me1,FUN=function(x) x=mean(x))

y.means <-me[,2]

sd <- aggregate(resp~fac2,data=me1,FUN=function(x) x=sd(x))

y.sd<-sd[,2]

co<-aggregate(resp~fac2,data=me1,FUN=function(x) x=length(x))

y.count<- co[,2]

y.se<-y.sd/(sqrt(y.count))

barx <- barplot(y.means,axes=FALSE,border = NA,ylim=c(0,.12), col=cl,ylab='')

axis(side=2)

abline(0,0)

error.bar(barx,y.means, y.se)

## number of samples

we<-.006

f<-aggregate(me1$resp~fac2,FUN=function(x) x=length(x))

text(barx, we, labels = f[,2],cex=c,co='black')

#add letter to plots

text(qq,.115,labels="F")

text(brr,.105,qqq,cex=1)

axis(side=1,at=barx,labels=Si,tick=FALSE,pos=.009)

#######bio########################

datp<-vis#################################################3

#datp$resp<-datp$SH.bio

#me<-aggregate(resp~Site\*Mound,data=datp,FUN=function(x) x=mean(x))

#kruskal.test(resp~ Site, data = me) ##sig

#DunnTest(resp~ Site,data=me,method="fdr")

fac2<-factor(datp$Site, levels=c('Crab Hole','Gibbs Shoal','Clam Shoal'))

datp$resp<-datp$SH.bioperm2

me1<-aggregate(resp~Site\*Mound,data=datp,FUN=function(x) x=mean(x))

fac2<-factor(me1$Site, levels=c('Crab Hole','Gibbs Shoal','Clam Shoal'))

me<-aggregate(resp~fac2,data=me1,FUN=function(x) x=mean(x))

y.means <-me[,2]

sd <- aggregate(resp~fac2,data=me1,FUN=function(x) x=sd(x))

y.sd<-sd[,2]

co<-aggregate(resp~fac2,data=me1,FUN=function(x) x=length(x))

y.count<- co[,2]

y.se<-y.sd/(sqrt(y.count))

barx <- barplot(y.means,axes=FALSE,border = NA,ylim=c(0,60), col=cl,ylab='')

axis(side=2)

abline(0,0)

error.bar(barx,y.means, y.se)

## number of samples

we<-4

f<-aggregate(me1$resp~fac2,FUN=function(x) x=length(x))

text(barxx, we, labels = f[,2],cex=c,co='black')

#add letter to plots

text(qq,57,labels="L")

text(brr,57,qqq,cex=1)

axis(side=1,at=barx,labels=Si,tick=FALSE,pos=5)

#add.image(2.5, 45, SHp, adj.x = 0.5, adj.y = 0.5,

# image.width = 0.5, image.height = .75,col=grey( (0:256)/256))

mtext(expression(paste("Abundance (m"^{-2},")")), side=2,line=-1.7, adj=.5,cex=.8, outer=TRUE)

mtext(expression(paste("Biomass (g\*m"^{-2},")")), side=2,line=-24.5, adj=.5,cex=.8, outer=TRUE)

ll<-1

mtext("Mud crab", side=2,line=ll, adj=.97,cex=.8, outer=TRUE)

mtext("Mud crab", side=2,line=ll, adj=.79,cex=.8, outer=TRUE)

mtext("(>=10mm)", side=2,line=-.3, adj=.79,cex=.8, outer=TRUE)

mtext("Drill", side=2,line=ll, adj=.60,cex=.8, outer=TRUE)

mtext("Blue crab", side=2,line=ll, adj=.41,cex=.8, outer=TRUE)

mtext("Stone crab", side=2,line=ll, adj=.22,cex=.8, outer=TRUE)

mtext("Sheepshead", side=2,line=ll, adj=.01,cex=.8, outer=TRUE)

dev.off()

#############