Section S1. Supplemental tables

Table S1. Generalized linear model results for Caribbean gnathiids per fish. Results testing for differences in abundance among three treatments (*Reef-Bucket, Reef-Commute,* and *Reef-Seagrass*). Treatments were compared to the baseline treat (intercept) Reef-bucket treatment. **a)** analysis of deviance table and **b)** summary out; **c)** analysis of deviance table and **d)** summary out for final simplified model including fork length in model; using the Akaike Information Criterion, the full (with a non-significant interaction between treatment and fork length, P = 0.634063) and simplified model without the interaction were compared and the best model selected (i.e., the simplified model). Results testing for differences in presence/absence of gnathiids among two treatments (*Seagrass-only*; *Reef-Seagrass*)*;* **e)** analysis of deviance table and **f)** summary out. Values cited in main text are in bold.

a)

```
Analysis of Deviance Table (Type II Wald chisquare tests)

Response: Gnathiids.per.fish
          Chisq Df Pr(>Chisq)
Treatment 41.114  2  1.181e-09 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

b) Summary output

```
                       Estimate Std. Error z value Pr(>|z|)
(Intercept)              1.1378     0.2124   5.356 8.49e-08 ***
TreatmentBReef-Commute  -0.7458     0.3120  -2.390   0.0168 *
TreatmentCReef-Seagrass -2.7473     0.4288  -6.407 1.48e-10 ***
```

c) Simplified model with fork length

```
Analysis of Deviance Table (Type II Wald chisquare tests)

Response: Gnathiids.per.fish
          Chisq Df Pr(>Chisq)
Treatment 18.3994  2  0.0001011 ***
FL..cm.    3.4948  1  0.0615633 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

d) Summary output

```
Conditional model:
                       Estimate Std. Error z value Pr(>|z|)
(Intercept)             -1.6826     1.4738  -1.142   0.2536
TreatmentBReef-Commute  -0.5282     0.4303  -1.228   0.2196
TreatmentCReef-Seagrass -3.4838     0.8138  -4.281 1.86e-05 ***
FL..cm.                  0.2166     0.1159   1.869   0.0616 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

e)

```
Analysis of Deviance Table (Type II Wald chisquare tests)

Response: Gnathiidpresence1isyes
          Chisq Df Pr(>Chisq)
Treatment 0.9778  1     0.3227
```

f)

```
Conditional model:
                      Estimate Std. Error z value Pr(>|z|)
(Intercept)            -1.9924     0.4352  -4.578 4.69e-06 ***
TreatmentDSeagrass only  0.6574     0.6648   0.989    0.323
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Table S2. Linear model for fish fork length for fish used in Caribbean cage treatments. Values cited in main text are in bold. **a)** analysis of deviance table and **b)** summary out.

a)

```
Anova Table (Type II tests)

Response: FL
          Sum Sq Df F value Pr(>F)
Treatment   7.94  3  0.6175 0.6058
Residuals 325.61 76
```

b)

	Estimate	Std. Error	t value	Pr(>|t|)
(Intercept)	12.25455	0.44130	27.769	<2e-16 ***
TreatmentBReef-Commute	-0.28182	0.62409	-0.452	0.653
TreatmentCReef-Seagrass	0.03182	0.62409	0.051	0.959
TreatmentDSeagrass only	0.67403	0.70765	0.952	0.344

```
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Table S3. Virgin Islands surveys. Generalized linear model results for gnathiid abundance per fish among sites and relative to fish fork length. Values cited in main text are in bold. **a)** Initial full model, **b)** Final simplified model, and **c)** summary output for b).

a) Initial full model

```
Analysis of Deviance Table (Type II Wald chisquare tests)

Response: Gnathiids.per.fish
                        Chisq Df Pr(>Chisq)
Site                   4.5323  2     0.1037
Fork.length..cm.      16.0816  1  6.067e-05 ***
Site:Fork.length..cm.  4.0651  2     0.1310
```

b) Final simplified model

```
Analysis of Deviance Table (Type II Wald chisquare tests)

Response: Gnathiids.per.fish
                  Chisq Df Pr(>Chisq)
Site              4.236  2     0.1203
Fork.length..cm. 15.875  1  6.766e-05 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

c) Summary output for final simplified model

```
                 Estimate Std. Error z value Pr(>|z|)
(Intercept)      -2.79652    0.72952  -3.833 0.000126 ***
SiteW Lameshur    0.07371    1.21910   0.060 0.951786
SiteWhite Bay     1.47787    0.73419   2.013 0.044123 *
Fork.length..cm.  0.24520    0.06154   3.984 6.77e-05 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

**Table S4.** Gnathiid host species identified by blood meal sequencing.

| Family	Genus	Scientific Name
Acanthuridae	*Acanthurus*	*Acanthurus bahianus*
		Acanthurus chirurgus
		Acanthurus coeruleus
Albulidae	*Albula*	*Albula vulpes*
Apogonidae	*Apogon*	*Apogon binotatus*
Carangidae	*Caranx*	*Caranx bartholomaei*
		Caranx latus
		Caranx ruber
	Decapterus	*Decapterus punctatus*
	Trachinotus	*Trachinotus falcatus*
		Trachinotus goodei
Centropomidae	*Centropomus*	*Centropomus undecimalis*
Clupeidae	*Jenkinsia*	*Jenkinsia lamprotaenia*
Dactyloscopidae	*Gillellus*	*Gillellus jacksoni*
Ephippidae	*Chaetodipterus*	*Chaetodipterus faber*
Gerreidae	*Eucinostomus*	*Eucinostomus jonesii*
	Gerres	*Gerres cinereus*
Gobiidae	*Coryphopterus*	*Coryphopterus personatus*
	Nes	*Nes longus*
	Risor	*Risor* sp.
Haemulidae	*Anisotremus*	*Anisotremus surinamensis*
	Haemulon	*Haemulon aurolineatum*
		Haemulon chrysargyreum
		Haemulon flavolineatum
		Haemulon macrostomum
		Haemulon parra
		Haemulon plumierii
		Haemulon sciurus
Holocentridae	*Holocentrus*	*Holocentrus adscensionis*
		Holocentrus rufus
	Myripristis	*Myripristis jacobus*
	Neoniphon	*Neoniphon marianus*
	Sargocentron	*Sargocentron vexillarium*
Kyphosidae	*Kyphosus*	*Kyphosus bigibbus*
		Kyphosus cinerascens
		Kyphosus sectatrix
		Kyphosus vaigiensis
Labridae	*Halichoeres*	*Halichoeres bivittatus*
		Halichoeres radiatus
Labrisomidae	*Labrisomus*	*Labrisomus guppyi*
Lutjanidae	*Lutjanus*	*Lutjanus analis*
		Lutjanus apodus
		Lutjanus cyanopterus
		Lutjanus griseus
		Lutjanus jocu
		Lutjanus mahogoni
		Lutjanus purpureus
		Lutjanus synagris
	Ocyurus	*Ocyurus chrysurus*
Microdesmidae	*Microdesmus*	*Microdesmus carri*
Monacanthidae	*Monacanthus*	*Monacanthus ciliatus*

Mullidae	*Mulloidichthys*	*Mulloidichthys martinicus*
	Mullus	*Mullus argentinae*
Muraenidae	*Gymnothorax*	*Gymnothorax funebris*
		Gymnothorax moringa
Ostraciidae	*Lactophrys*	*Lactophrys trigonus*
	Rhinesomus	*Rhinesomus triqueter*
Pomacentridae	*Abudefduf*	*Abudefduf saxatilis*
		Abudefduf taurus
	Microspathodon	*Microspathodon chrysurus*
	Stegastes	*Stegastes adustus*
		Stegastes diencaeus
		Stegastes variabilis
Serranidae	*Cephalopholis*	*Cephalopholis cruentata*
	Epinephelus	*Epinephelus striatus*
	Hypoplectrus	*Hypoplectrus indigo*
Sparidae	*Archosargus*	*Archosargus rhomboidalis*
	Calamus	*Calamus bajonado*
		Calamus penna
Synodontidae	*Synodus*	*Synodus intermedius*

Section S2. Supplemental figures
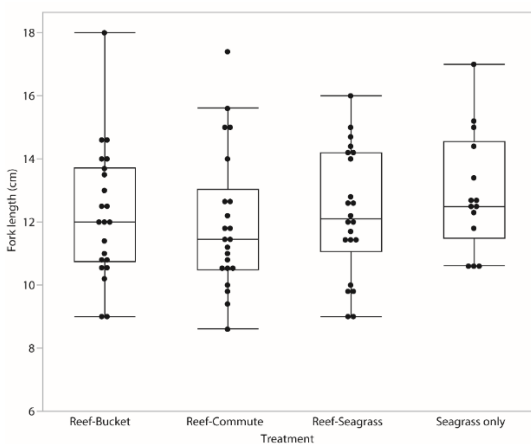
a)
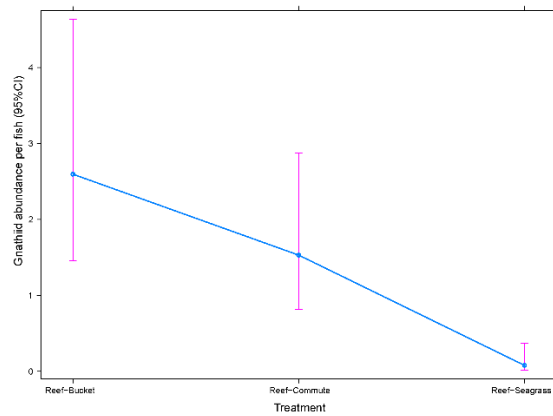
b)
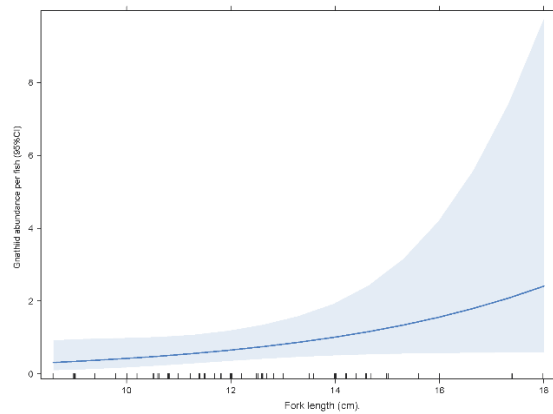
c)

Figure S1. Caribbean experiment. Effect plot of gnathiid abundance for final simplified model with fish fork length (a reduced dataset) according to **a)** three cage treatments and **b)** fish fork length. **c)** Boxplot plot for fish fork length according to four treatments. Boxplot: center line = median, box = interquartile range, error bars = 90th and 10th percentiles, and circles = outliers.

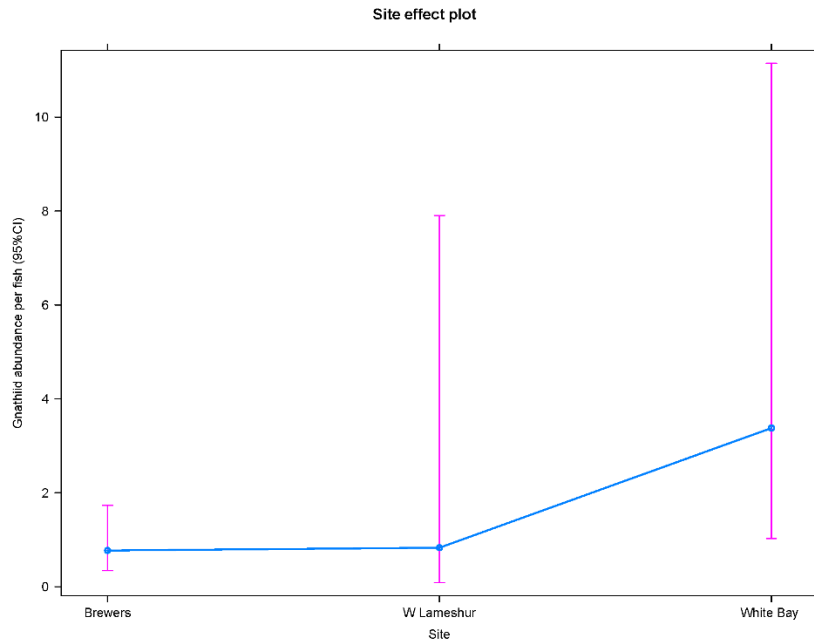**Figure S2.** Effect plot for generalized linear model of Virgin Islands gnathiids per fish for effect of sampling site.
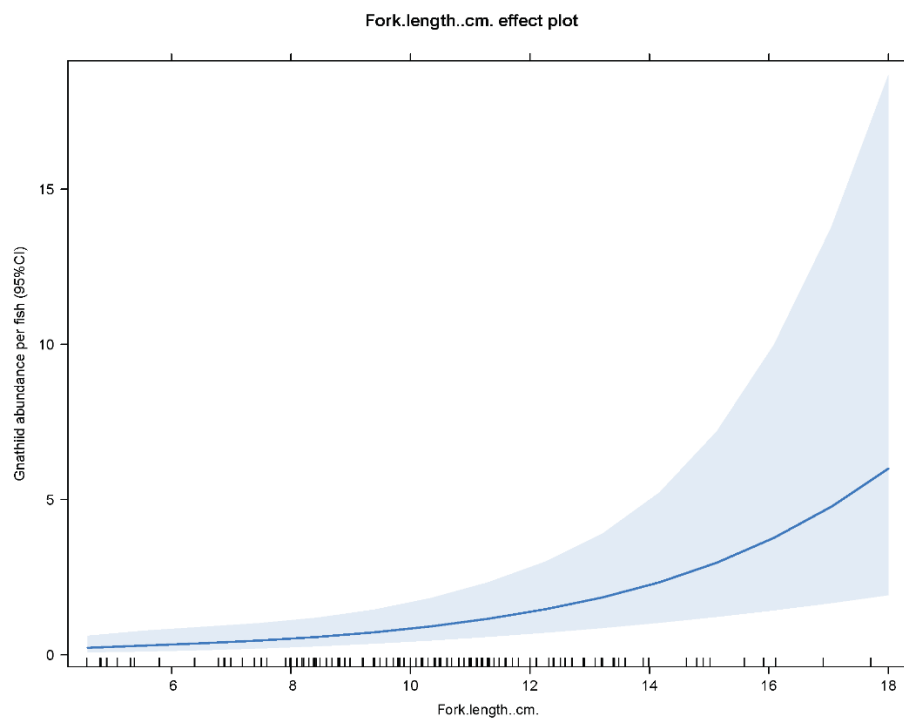

Figure S3. Effect plot for generalized linear model of Virgin Islands gnathiids per fish for effect of fish fork length.
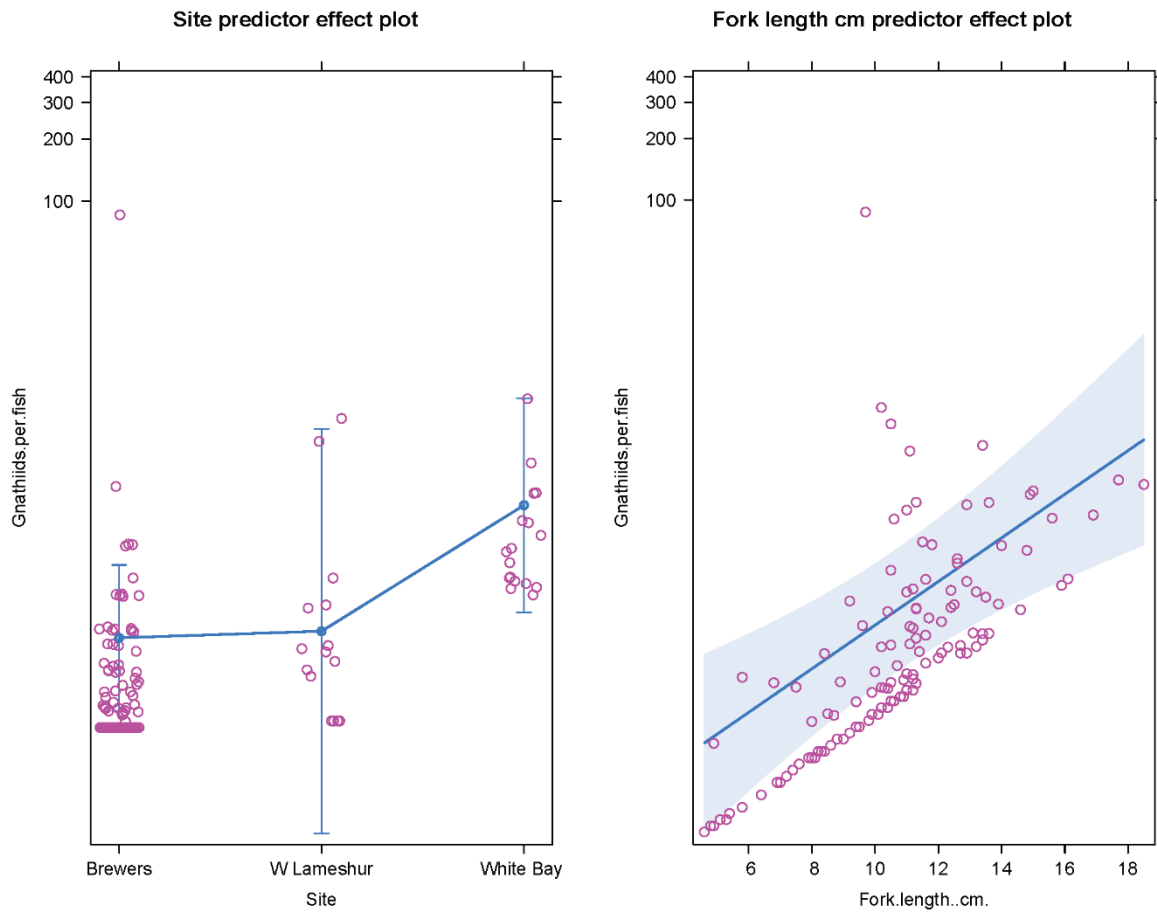
Figure S4. Effect plots for generalized linear model of Virgin Islands gnathiids per fish, showing partial residuals for effect of site and fish fork length.

Section S3. R Script Code

```
library(glmmTMB)

library(car)

library(effects)

library(DHARMa)

##################Caribbean grunt gnathiid abundance ##########################

##"Caribbean.omit.Seagrass.Only.csv"

##data with three treatments only, no seagrass only

Caribbean.omit.Seagrass.Only$Treatment<-as.factor(Caribbean.omit.Seagrass.Only$Treatment)

Caribbean.omit.Seagrass.Only$Trial.day<-as.factor(Caribbean.omit.Seagrass.Only$Trial.day)

str(Caribbean.omit.Seagrass.Only)


##negative binomial with quadratic parameterization and without zero inflation

Fit1NB2<-glmmTMB(Gnathiids.per.fish~Treatment+(1|Trial.day),
family=nbinom2(link="log"),data=Caribbean.omit.Seagrass.Only)

summary(Fit1NB2)

Anova(Fit1NB2)

plot(resid(Fit1NB2)~fitted(Fit1NB2))

##more model checking and diagnostics

Fit1NB2_simres <- simulateResiduals(Fit1NB2)

sr <- simulateResiduals(Fit1NB2)

plot(sr)

plot(sr, quantreg = TRUE)

plot(allEffects(Fit1NB2,partial.residuals=TRUE))

plot(allEffects(Fit1NB2,partial.residuals=FALSE))


##Effect plots

## effect plot for Treatment

eff.Fit1NB2<-effect("Treatment", Fit1NB2)

eff.Fit1NB2

eff.Fit1NB2$se
```

```
eff.Fit1NB2$se*1.96

eff.Fit1NB2$lower

eff.Fit1NB2$upper

summary(eff.Fit1NB2) ## output as back transformed counts (mean, upper, lower)

plot(eff.Fit1NB2,confint=list(style="auto"), multiline=TRUE, ylab="Gnathiid abundance per fish
(95%CI)",rescale.axis=FALSE)


## Redo with fork length in model, using subset of data where fork length was measured (66, instead
of 150 obs).


Fit1NB2FL<-glmmTMB(Gnathiids.per.fish~Treatment*FL..cm.+(1|Trial.day),
family=nbinom2(link="log"),data=Caribbean.omit.Seagrass.Only)

summary(Fit1NB2FL)

Anova(Fit1NB2FL) #

plot(resid(Fit1NB2FL)~fitted(Fit1NB2FL))

##more model checking and diagnostics

Fit1NB2FL_simres <- simulateResiduals(Fit1NB2FL)

sr <- simulateResiduals(Fit1NB2FL)

plot(sr) ##ALL NS

plot(sr, quantreg = TRUE)

plot(allEffects(Fit1NB2FL,partial.residuals=TRUE))

plot(allEffects(Fit1NB2FL,partial.residuals=FALSE))


##Effect plots

## effect plot for Treatment

eff.Fit1NB2FL<-effect("Treatment", Fit1NB2FL)

eff.Fit1NB2FL

eff.Fit1NB2FL$se

eff.Fit1NB2FL$se*1.96

eff.Fit1NB2FL$lower

eff.Fit1NB2FL$upper

summary(eff.Fit1NB2FL) ## output as back transformed counts (mean, upper, lower)
```

```
plot(eff.Fit1NB2FL,confint=list(style="auto"), multiline=TRUE, ylab="Gnathiid abundance per fish
(95%CI)",rescale.axis=FALSE)

plot(eff.Fit1NB2FL, confint=list(style="auto"), ylab="Gnathiid abundance per trap
(95%CI)",rescale.axis=TRUE)
```

```
##simplify model, drop non-significant 2 way
```

```
Fit1NB2FLb<-glmmTMB(Gnathiids.per.fish~Treatment+FL..cm.+(1|Trial.day),
family=nbinom2(link="log"),data=Caribbean.omit.Seagrass.Only)

summary(Fit1NB2FLb)

Anova(Fit1NB2FLb)

plot(resid(Fit1NB2FLb)~fitted(Fit1NB2FLb))

##more model checking and diagnostics

Fit1NB2FLb_simres <- simulateResiduals(Fit1NB2FLb)

sr <- simulateResiduals(Fit1NB2FLb)

plot(sr)

plot(sr, quantreg = TRUE)

plot(allEffects(Fit1NB2FLb,partial.residuals=TRUE))

plot(allEffects(Fit1NB2FLb,partial.residuals=FALSE))
```

```
##Effect plots
## effect plot for Treatment
eff.Fit1NB2FLb<-effect("Treatment", Fit1NB2FLb)

eff.Fit1NB2FLb

eff.Fit1NB2FLb$se

eff.Fit1NB2FLb$se*1.96

eff.Fit1NB2FLb$lower

eff.Fit1NB2FLb$upper

summary(eff.Fit1NB2FLb) ## output as backtransformed counts (mean, upper, lower)

plot(eff.Fit1NB2FLb,confint=list(style="auto"), multiline=TRUE, ylab="Gnathiid abundance per cage
(95%CI)",rescale.axis=FALSE)

plot(eff.Fit1NB2FLb, confint=list(style="auto"), ylab="Gnathiid abundance per cage
(95%CI)",rescale.axis=TRUE)
```

```
## effect plot for FL

eff.Fit1NB2FLbFL<-effect("FL..cm.", Fit1NB2FLb)

eff.Fit1NB2FLbFL

eff.Fit1NB2FLbFL$se

eff.Fit1NB2FLbFL$se*1.96

eff.Fit1NB2FLbFL$lower

eff.Fit1NB2FLbFL$upper

summary(eff.Fit1NB2FLbFL) ## output as backtransformed counts (mean, upper, lower)

plot(eff.Fit1NB2FLbFL,confint=list(style="auto"), multiline=TRUE, ylab="Gnathiid abundance per cage
(95%CI)",rescale.axis=FALSE)

plot(eff.Fit1NB2FLbFL, confint=list(style="auto"), ylab="Gnathiid abundance per cage
(95%CI)",rescale.axis=TRUE)


AIC(Fit1NB2FL,Fit1NB2FLb) ##simplied is lower, use it as final
```

############## Fork length by four treatments, including "Seagrass Only" treatment ##

##"Caribbean.csv"

```
library(lme4)

library(car)


Caribbean$Treatment<-as.factor(Caribbean$Treatment)

str(Caribbean)


##linear model (same output as if ANOVA)

Fit1FL<-lm(FL~Treatment,data=Caribbean)

summary(Fit1FL)

Anova(Fit1FL)

plot(resid(Fit1FL)~fitted(Fit1FL))

##more model checking and diagnostics

Fit1FL_simres <- simulateResiduals(Fit1FL)

sr <- simulateResiduals(Fit1FL)

plot(sr)

plot(sr, quantreg = TRUE)

plot(allEffects(Fit1FL,partial.residuals=TRUE))

plot(allEffects(Fit1FL,partial.residuals=FALSE))



##Effect plots

## effect plot for Treatment

eff.Fit1FL<-effect("Treatment", Fit1FL)

eff.Fit1FL

eff.Fit1FL$se

eff.Fit1FL$se*1.96

eff.Fit1FL$lower

eff.Fit1FL$upper
```

```
summary(eff.Fit1FL) ## output as back transformed counts (mean, upper, lower)
```

```
plot(eff.Fit1FL,confint=list(style="auto"), multiline=TRUE, ylab="Fork length per fish
(95%CI)",rescale.axis=F
```

#######Testing Reef Seagrass vs Seagrass only ("RSSO") as generalized linear model with binomial distribution###

```
library(glmmTMB)

library(car)

library(effects)

library(DHARMa)


## "CaribbeanReefSeagrass.Seagrassonly.csv"


CaribbeanReefSeagrass.Seagrassonly$Treatment<-
as.factor(CaribbeanReefSeagrass.Seagrassonly$Treatment)

CaribbeanReefSeagrass.Seagrassonly$Trial.day<-
as.factor(CaribbeanReefSeagrass.Seagrassonly$Trial.day)

CaribbeanReefSeagrass.Seagrassonly$GnathiidpresenceYesNo<-
as.factor(CaribbeanReefSeagrass.Seagrassonly$GnathiidpresenceYesNo)

str(CaribbeanReefSeagrass.Seagrassonly)


##binomial with Gnathiidpresence1isyes as response (yes/no gnathiids present)


##without zeroinflation and logit


Fit1RSSOBinom<-glmmTMB(Gnathiidpresence1isyes~Treatment+(1|Trial.day),
family=binomial(link="logit"),data=CaribbeanReefSeagrass.Seagrassonly)

summary(Fit1RSSOBinom)

Anova(Fit1RSSOBinom)

plot(resid(Fit1RSSOBinom)~fitted(Fit1RSSOBinom))

##more model checking and diagnostics

Fit1RSSOBinom_simres <- simulateResiduals(Fit1RSSOBinom)

sr <- simulateResiduals(Fit1RSSOBinom)

plot(sr)

plot(sr, quantreg = TRUE)

plot(allEffects(Fit1RSSOBinom,partial.residuals=TRUE))

plot(allEffects(Fit1RSSOBinom,partial.residuals=FALSE))
```

########## Virgin Island Grunts gnathiid abundance ###################################

```
## "Virgin Islands.csv"

str(Virgin.Islands)

Virgin.Islands$Site<-as.factor(Virgin.Islands$Site)

Virgin.Islands$Trial.day<-as.factor(Virgin.Islands$Trial.day)



##negative binomial full model



##Quadratic parameritization Full model

Fit1NB2VI<-glmmTMB(Gnathiids.per.fish~Site*Fork.length..cm.+(1|Trial.day),
family=nbinom2(link="log"),data=Virgin.Islands)

summary(Fit1NB2VI)

Anova(Fit1NB2VI)

plot(resid(Fit1NB2VI)~fitted(Fit1NB2VI))

##more model checking and diagnostics

Fit1NB2VI_simres <- simulateResiduals(Fit1NB2VI)

sr <- simulateResiduals(Fit1NB2VI)

plot(sr) ##ALL NS

plot(sr, quantreg = TRUE)

plot(allEffects(Fit1NB2VI,partial.residuals=TRUE))

plot(allEffects(Fit1NB2VI,partial.residuals=FALSE))



##simplify, drop twoway

##Quadratic parameritization

Fit1NB2VIb<-glmmTMB(Gnathiids.per.fish~Site+Fork.length..cm.+(1|Trial.day),
family=nbinom2(link="log"),data=Virgin.Islands)

summary(Fit1NB2VIb)

Anova(Fit1NB2VIb) ##

plot(resid(Fit1NB2VIb)~fitted(Fit1NB2VIb))

##more model checking and diagnostics

Fit1NB2VIb_simres <- simulateResiduals(Fit1NB2VIb)
```

```
sr <- simulateResiduals(Fit1NB2VIb)

plot(sr) ##ALL NS

plot(sr, quantreg = TRUE)

plot(predictorEffects(Fit1NB2VIb, residuals=TRUE), partial.residuals=list(smooth=FALSE))

plot(allEffects(Fit1NB2VIb,partial.residuals=FALSE))




AIC(Fit1NB2VI,Fit1NB2VIb)## simpler lower, use it


##Effect plots

## effect plot for SITE

eff.Fit1NB2VIbS<-effect("Site", Fit1NB2VIb)

eff.Fit1NB2VIbS

eff.Fit1NB2VIbS$se

eff.Fit1NB2VIbS$se*1.96

eff.Fit1NB2VIbS$lower

eff.Fit1NB2VIbS$upper

plot(eff.Fit1NB2VIbS)

summary(eff.Fit1NB2VIbS) ## output as backtransformed counts (mean, upper, lower)

plot(eff.Fit1NB2VIbS,confint=list(style="auto"), multiline=FALSE, ylab="Gnathiid abundance per
fish (95%CI)",rescale.axis=FALSE)

plot(eff.Fit1NB2VIbS, confint=list(style="auto"), ylab="Gnathiid abundance per trap
(95%CI)",rescale.axis=TRUE)


##Effect plots

## effect plot for FL

eff.Fit1NB2VIbF<-effect("Fork.length..cm.", Fit1NB2VIb)

eff.Fit1NB2VIbF

eff.Fit1NB2VIbF$se

eff.Fit1NB2VIbF$se*1.96

eff.Fit1NB2VIbF$lower

eff.Fit1NB2VIbF$upper
```

```
plot(eff.Fit1NB2VIbF)

summary(eff.Fit1NB2VIbF) ## output as back transformed counts (mean, upper, lower)

plot(eff.Fit1NB2VIbF,confint=list(style="auto"), multiline=FALSE, ylab="Gnathiid abundance per
fish (95%CI)",rescale.axis=FALSE)

plot(eff.Fit1NB2VIbF, confint=list(style="auto"), ylab="Gnathiid abundance per fish
(95%CI)",rescale.axis=TRUE)


## Boxplot Fig. 6 ##

habitatbox<-boxplot(RShabitat~Samples*newhabs,data=habs,

        lty=1,

        boxwex=.5,ylab="Proportion of Identified Hosts",

        xlab="Nocturnal Habitat",cex=5,

        col=c("white","lightblue"),

        xaxt="n")


my_names <- sapply(strsplit(habitatbox$names,'\\.'),function(x) x[[2]] )

my_names <- my_names[seq(1,length(my_names),2)]

axis(1,

    at = seq(1.5 , 8 ,2),

    labels = my_names ,

    tick=FALSE , cex=0.5)

legend("topleft",legend=c("Reef Sequences","Seagrass Sequences"),

     horiz = T,

     lty = 0,

     fill=c("white","lightblue"),

     inset = c(0,-.02),

     pt.cex=1,

     bty=0,

     pt.lwd = 3.0,

     cex=1.1,

     box.lty = 0)
```

```r
nfam = read.csv("famcountstrans.csv", header= TRUE)


nfam<-data.frame(nfam[1:6,-1],row.names = nfam[1:6,1])


dist<-vegdist(nfam,method = "bray") # needed to convert to distance matrix

dist<-as.matrix(dist,labels=T)


set.seed(19850816) #set.seed(1) # or any other number - this will make it reproducible

TrafficNMDS<-metaMDS(dist,autotransform = F,

        distance = "bray",

        k = 2,

        maxit = 20,

        trymax = 20,

        smin = 1e-4,

        wascores = TRUE)


kscorestibble<-scores(TrafficNMDS,display="site") %>%

  as_tibble(rownames="Count Type")

kscorestibble$Site<-Site

kscorestibble$Type<-Type


sppscores(TrafficNMDS)<-nfam

#### Basic Plots for R&SG ####

windows()

opar <- par(mfrow=c(1,1),mar = c(12,6,2,2))

stressplot(TrafficNMDS,

    cex = 1.5, cex.lab = 1.5, cex.sub = 1.5)


plot(TrafficNMDS)

ordihull(TrafficNMDS,

    kscorestibble$Site,
```

```
        display = "sites",

        draw = c("polygon"),

        col = NULL,

        lty = c(1, 2, 3),

        lwd = 3)

kscrs<-scores(TrafficNMDS, display = "sites", "species")

kcentT<-aggregate(kscrs ~ Type, data = kscorestibble, FUN = "mean")

names(kcentT) [-1] <- colnames(kscrs)


colvec <- c("orange", "black", "green3", "purple")   # Identifies colors for group assignments

pchvec <- c(21, 24, 22, 8)   # Identifies character symbols for group assignments


points(kcentT [,-1],

    pch = unique(pchvec),

    bg =c("black", "black"),

    lwd = 3.0,

    cex = 1.1)

legend(x="topright", legend = unique(Type),

    pch=unique(pchvec),

    pt.lwd = 3.0,

    pt.bg =c("black", "black"),

    lty = c(1, 2, 3, 4),

    lwd = 1.0,

    cex = 1,

    merge = F,

    inset = 0.01,

    box.lty = 0)

########## nmds by habitat ##########

#HabProps

Site<-rep(c("Cristobal","Culebra","Enrique"),2)

Site
```

```
Type<-rep(c("Reef","SG"),each=3)


HABdist<-vegdist(nfam,method = "bray") # needed to convert to distance matrix

HABdist<-as.matrix(HABdist,labels=T)


set.seed(19850816) #set.seed(1) # or any other number - this will make it reproducible

HABnmds<-metaMDS(HABdist,autotransform = F,

        distance = "bray",

        k = 2,

        maxit = 999,

        trymax = 1000,

        smin = 1e-4,

        wascores = TRUE)


Rtibble<-scores(HABnmds,display="sites") %>%

  as_tibble(rownames="Count Type")

Rtibble$Site<-Site

Rtibble$Type<-Type

sppscores(HABnmds)<-nfam


kscrs<-scores(HABnmds, display = "sites", "species")

kcentT<-aggregate(kscrs ~ Type, data = Rtibble, FUN = "mean")


windows(plot.window(xlim = c(-0.6,0.6) ,ylim = c(-0.6,0.5)))

par(cex=1.6)


plot(HABnmds)

ordihull(HABnmds,

    kscorestibble$Type,

    display = "sites",

    draw = c("polygon"),
```

```
    col = NULL,

    lty = c(1, 2, 3, 4),

    lwd = 3)
kscrs<-scores(HABnmds, display = "sites", "species")

kcentT<-aggregate(kscrs ~ Type, data = Rtibble, FUN = "mean")

names(kcentT) [-1] <- colnames(kscrs)


colvec <- c("orange", "black", "green3", "purple")   # Identifies colors for group assignments

pchvec <- c(21, 24, 22, 8)   # Identifies character symbols for group assignments


points(kcentT [,-1],

    pch = unique(pchvec),

    bg =c("black", "black"),

    lwd = 3.0,

    cex = 1.1)
legend(x="bottomright", legend = unique(Type),

    pch=unique(pchvec),

    horiz = T,

    pt.lwd = 3.0,

    pt.bg =c("black", "black"),

    lty = c(1, 2, 3, 4),

    lwd = 3.0,

    cex = 1.3,

    merge = F,

    inset = 0.01,

    box.lty = 0)


####### PERMANOVA using Adonis ########
MAIN<-data.frame(Site,Type,nfam)

#Adonis can be used to test if two or more groups have similar compositions

adonis2(nfam~Type,data=MAIN,method = "bray") # P=0.2 <- SG = R
```

#Compositions of IDed and surveyed fish are NOT statistically different

adonis2(nfam~Site,data=MAIN,method = "bray") # p=0.8

#Compositions at each site, which include all types, are the same.

test for variation within the dispersion of the data using betadisper

this needs to be a distance matrix

dist<-vegdist(nfam)

bd<-betadisper(dist,MAIN$Type,type = "centroid")

tests whether there is significant variation in betadispersion

anova(bd) # p=0.74 <-Not significant, so b-disp doesn't account for adonis significance

Dispersion across sites is homogenous; Null hyp.=no diff in disp among types

bd2<-betadisper(dist,MAIN$Site,type = "centroid")

tests whether there is significant variation in betadispersion

anova(bd2) # p=0.0001 <- significant, so b-disp does account for adonis p value

Dispersion across sites is homogenous; Null hyp.=no diff in disp among sites

permutest(bd) # p = 0.501

permutest(bd2) # p = 0.001

permutest shows that the dispersion among all types and groups are the same

the PERMANOVA shows that the centroids of ID and Day/Night are different