

Corales reclutamiento

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Coral and recruitment

The main questions to be addressed in this investigation are:

1. Are there any coral recruits coming through the channels to colonize the bay?.
2. How high is the abundance level of coral recruitment in the reef lagoon, the channels and the bay?.
3. Are the natural and the artificial channel act differently for coral recruitment?.
4. Further we want to know the differences in salinity and temperature in the channels, the lagoon compared to the bay as well as water exchange and near surface water currents close to the channels to get an idea of the local water movement in the area.

Study area

“SE Chetumal Bay” (BAY) is surrounded by cays and channels connecting it to the rest of the bay.

The artificial channel (AC), called “Zaragoza Channel” is a man made channel built in the 19 th century, closed because of sedimentation and has been reopened from 1996-2000 by the Mexican army.

The natural channel (NC), called “Bacalar Chico” is a historical old, meandered, mangrove channel.

The reef lagoon (RL) which influences the Chetumal Bay through the channels is part of the national park “Xcalak Reefs”.

Answering the questions

The main questions to be addressed in this investigation are:

1. Are there any coral recruits coming through the channels to colonize the bay?.

Very hard to answer taking in to account that you are not tracking coral or larvae movement through the channels. We can answer how many recruits are in the bay by genus in a boxplot

2. How high is the abundance level of coral recruitment in the reef lagoon, the channels and the bay?

We can see the abundance of corals by plotting how many recruits are in the bay by genus in a boxplot (same graph as previous question)

3. Are the natural and the artificial channel act differently for coral recruitment?

We can see if there are statistically significant differences between Localities by an ANOVA (1) and also between sites by ANOVA (2).

4. Further we want to know the differences in salinity and temperature in the channels, the lagoon compared to the bay as well as water exchange and near surface water currents close to the channels to get an idea of the local water movement in the area.

We need the salinity data!

Load the data set and put together tables

```
library(lme4)
library(nlme)
library(arm)
library(sjPlot)
library(dplyr)
library(ggplot2)

# read data set
library(readr)
# Qcual cambio a 1
corales <- read.csv("C:/Users/diego.lizcano/Box Sync/CodigoR/Nancy2/data/corales3.csv",
                    sep = ";", header = T)

corales$all <- apply(corales[,35:41], 1, sum) # suma de todos los corales

# tabla de Acropora sp. Agaricia sp. Faviidae Porites spp. Siderastrea sp
corales_algunos1 <- cbind(corales$Acropora.sp. , corales$Agaricia.sp. ,
                        corales$Faviidae , corales$Porites.spp. ,
                        corales$Siderastrea.sp. , corales$Unknown.Coral..too.small.)

# here in the same column
corales_algunos2 <- as.data.frame(rbind(cbind(corales$Acropora.sp. , "Acropora"),
                                          cbind(corales$Agaricia.sp. , "Agaricia"),
                                          cbind(corales$Faviidae , "Faviidae"),
                                          cbind(corales$Porites.spp. , "Porites" ),
                                          cbind(corales$Siderastrea.sp. , "Siderastrea"),
                                          cbind(corales$Unknown.Coral..too.small. , "Unknown_Coral") ))

corales_algunos2$V1 <- as.numeric(levels(corales_algunos2$V1)[corales_algunos2$V1]) # convert from fact

corales_algunos3 <- cbind(corales_algunos2, c(as.character(rep(corales$Locality, 6) )))
colnames(corales_algunos3) <- c("recruitment", "genus", "Locality")
corales_algunos3 <- as.data.frame(corales_algunos3) # make data frame

# suma de las abundancias de los corales seleccionados
corales$corales_algunos_sum <- apply(corales_algunos1, 1, sum)
```

BoxPlot

```
tabla2 <- as.data.frame(cbind(as.character(corales[,1]), as.numeric( corales[,43])))
colnames(tabla2) <- c("Locality", "abund")
tabla2$abund <- as.numeric(tabla2$abund)
tabla3 <- table(tabla2) # abundancia de selected corales and locality
tabla4 <- apply(tabla3, 1, mean) # suma selected corales by locality
# barplot(tabla4)

ggplot(tabla2, aes(x = Locality, y = abund)) +
  geom_boxplot(fill = "grey80", colour = "blue") +
```

```
scale_x_discrete() + xlab("Locality") +
ylab("Recruitment (sum) of several coral genus")
```

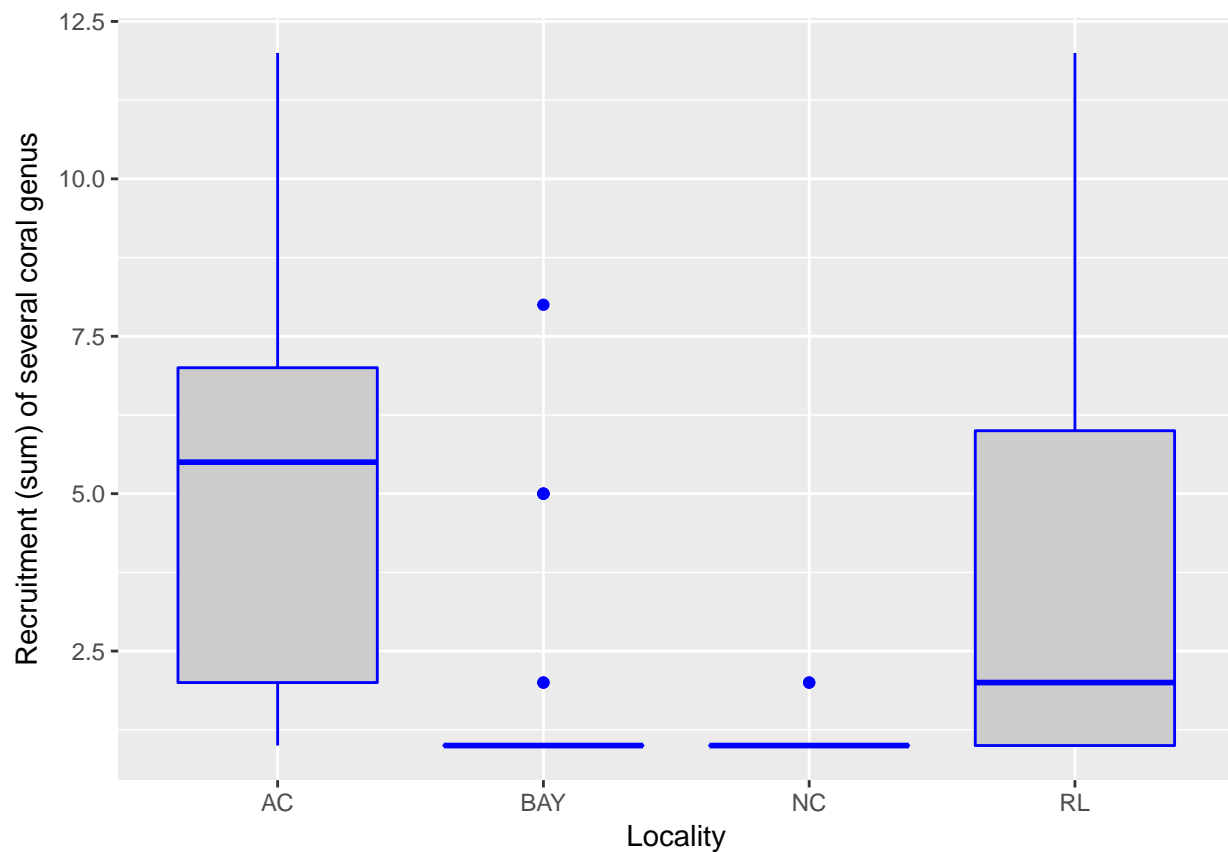


Figure 1: Sumarazing how many recuits are in the bay first agregating all corals as a sum.

```
ggplot(corales_algunos3, aes(x = Locality , y = recruitment)) +
  geom_boxplot(fill = "grey80") + facet_wrap(~genus) +
  scale_x_discrete() + xlab("Locality") +
  ylab("Recruitment of selected corals")
```

Testing differences in ANOVA

as a piosson procces determined by site = locality name (factor)

```
glm4 <- glm (corales_algunos_sum ~ Locality, family = poisson(), data = corales)
```

```
# summary(glm1)
# summary(glm2)
# summary(glm3)
anova(glm4, test = "Chisq")
```

```
## Analysis of Deviance Table
##
## Model: poisson, link: log
##
```

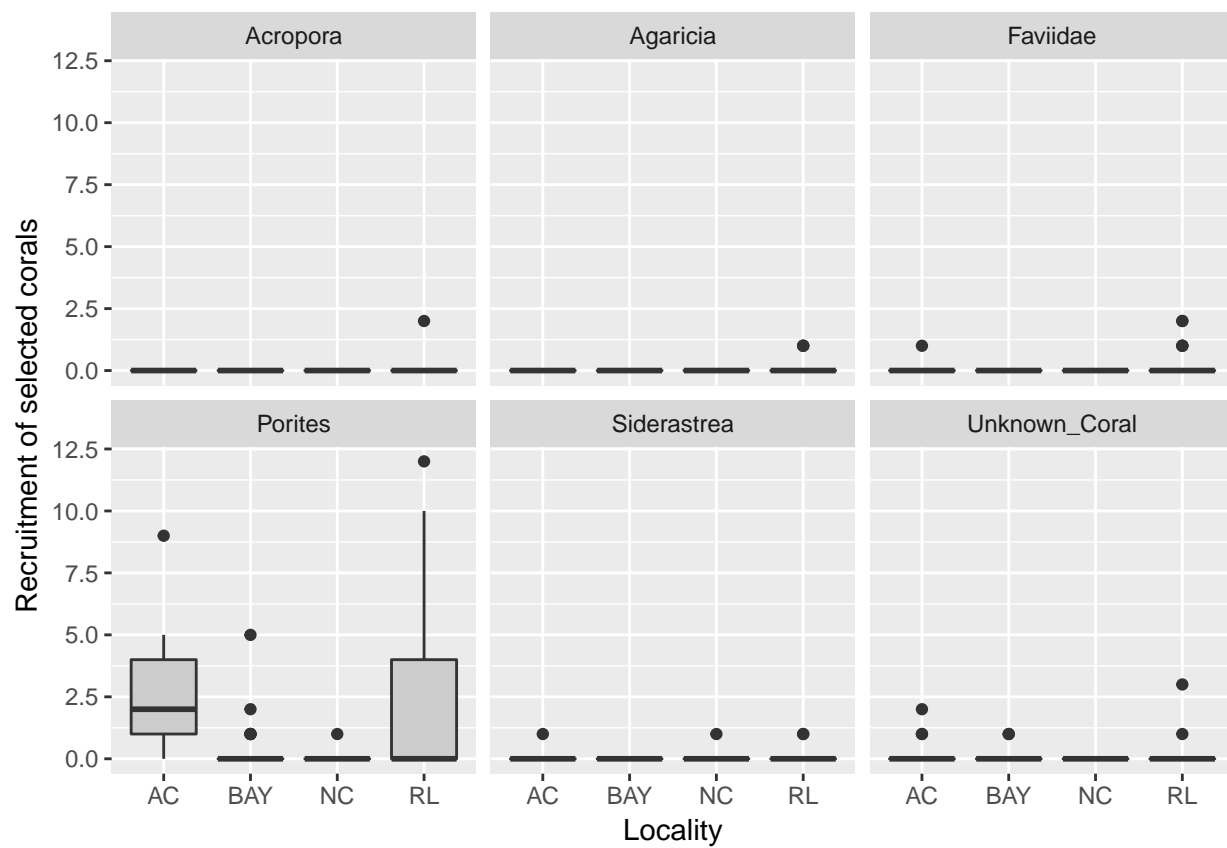


Figure 2: The second boxplot shows recruitment by locality wrapped by genus

```
## Response: corales_algunos_sum
##
## Terms added sequentially (first to last)
##
##
##           Df Deviance Resid. Df Resid. Dev  Pr(>Chi)
## NULL                104      383.40
## Locality  3    145.93      101    237.47 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

anova1 <- aov(glm4)
(posthoc1 <- TukeyHSD(x=anova1, "Locality", conf.level=0.95))

## Tukey multiple comparisons of means
## 95% family-wise confidence level
##
## Fit: aov(formula = glm4)
##
## $Locality
##           diff           lwr           upr       p adj
## BAY-AC -2.2629870 -4.0421683 -0.4838057 0.0067119
## NC-AC  -2.6583072 -4.4239397 -0.8926748 0.0008750
## RL-AC   0.2727273 -1.5363127  2.0817672 0.9791740
## NC-BAY -0.3953202 -2.0498895  1.2592491 0.9241044
## RL-BAY  2.5357143  0.8349006  4.2365280 0.0010022
## RL-NC   2.9310345  1.2443990  4.6176699 0.0000910

plot(posthoc1)
```

Las localidades BAY y NC son significativamente diferentes a AC y RL. Y como se aprecia en el boxplot (Fig. 1) tienen menor reclutamiento de coral.

```
glm5 <- glm (recruitment ~ Locality + genus, data = corales_algunos3)
anova(glm5, test = "Chisq")

## Analysis of Deviance Table
##
## Model: gaussian, link: identity
##
## Response: recruitment
##
## Terms added sequentially (first to last)
##
##
##           Df Deviance Resid. Df Resid. Dev  Pr(>Chi)
## NULL                629      733.84
## Locality  3    30.145      626      703.70 5.639e-07 ***
## genus     5   115.881      621      587.82 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

anova2 <- aov(glm5)
(posthoc2 <- TukeyHSD(x=anova2, "genus", conf.level=0.95))

## Tukey multiple comparisons of means
## 95% family-wise confidence level
```

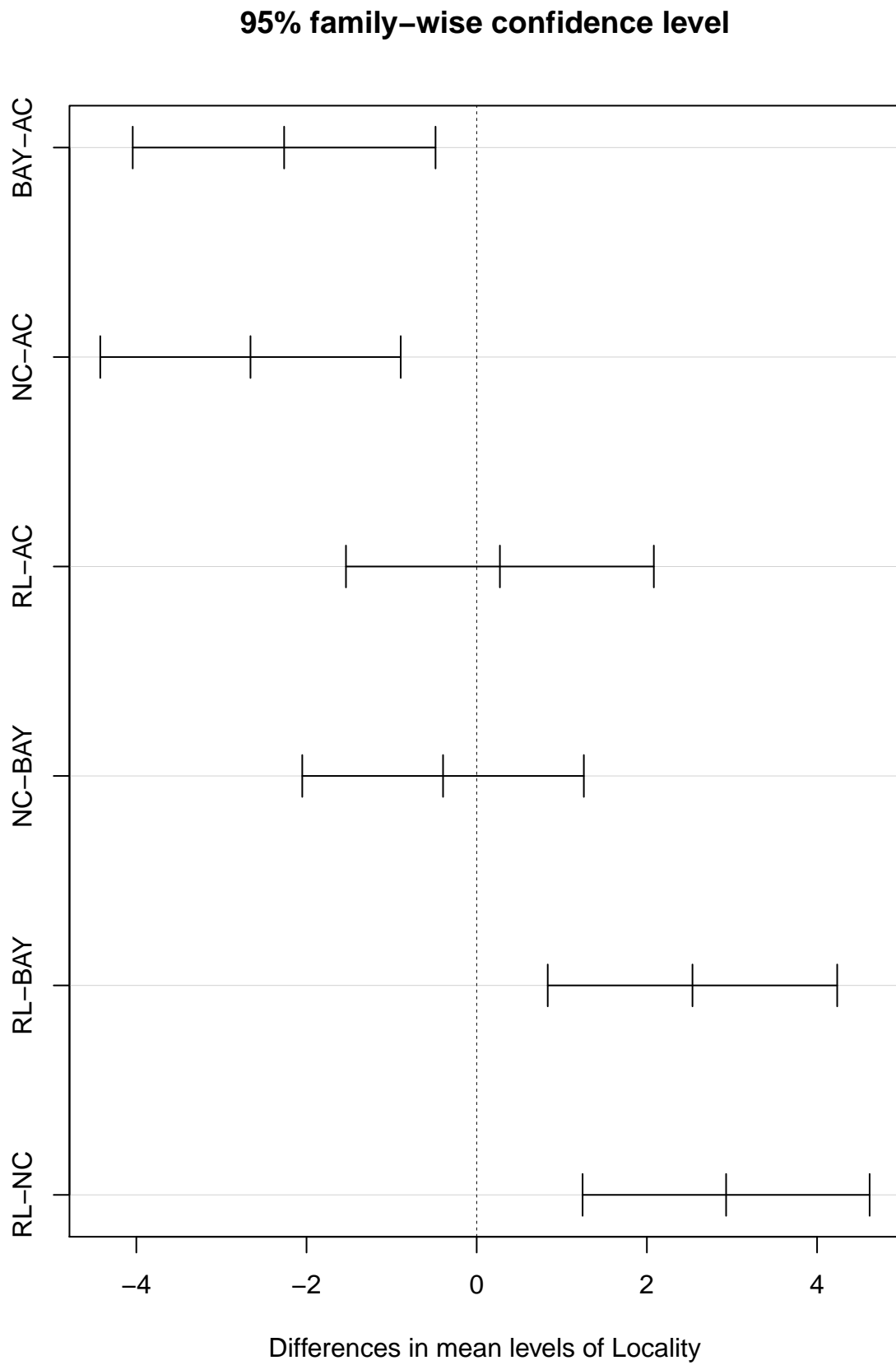


Figure 3: The graph shows the multiple comparison (Tukey test) between Localities. The pairs RL-AC and NC-BAY are not different.

```
##
## Fit: aov(formula = glm5)
##
## $genus
##               diff      lwr      upr      p adj
## Agaricia-Acropora  0.00952381 -0.3743205  0.3933681 0.9999997
## Faviidae-Acropora  0.05714286 -0.3267015  0.4409872 0.9982222
## Porites-Acropora   1.18095238  0.7971080  1.5647967 0.0000000
## Siderastrea-Acropora 0.01904762 -0.3647967  0.4028920 0.9999920
## Unknown_Coral-Acropora 0.07619048 -0.3076539  0.4600348 0.9930667
## Faviidae-Agaricia  0.04761905 -0.3362253  0.4314634 0.9992633
## Porites-Agaricia   1.17142857  0.7875842  1.5552729 0.0000000
## Siderastrea-Agaricia 0.00952381 -0.3743205  0.3933681 0.9999997
## Unknown_Coral-Agaricia 0.06666667 -0.3171777  0.4505110 0.9962935
## Porites-Faviidae   1.12380952  0.7399652  1.5076539 0.0000000
## Siderastrea-Faviidae -0.03809524 -0.4219396  0.3457491 0.9997524
## Unknown_Coral-Faviidae 0.01904762 -0.3647967  0.4028920 0.9999920
## Siderastrea-Porites -1.16190476 -1.5457491 -0.7780604 0.0000000
## Unknown_Coral-Porites -1.10476190 -1.4886062 -0.7209176 0.0000000
## Unknown_Coral-Siderastrea 0.05714286 -0.3267015  0.4409872 0.9982222
```

```
plot(posthoc2)
```

In most of the comparisons where Porites is included produces a statistically significant difference. As we can see in the Boxplot (Fig. 2) Porites recruitment is bigger than other genus.

Stepwise regression procedure for all algae

```
library(bootStepAIC)
library(lattice)
library(fields)

## Loading required package: spam

## Loading required package: grid

## Spam version 1.4-0 (2016-08-29) is loaded.
## Type 'help( Spam)' or 'demo( spam)' for a short introduction
## and overview of this package.
## Help for individual functions is also obtained by adding the
## suffix '.spam' to the function name, e.g. 'help( chol.spam)'.

##
## Attaching package: 'spam'

## The following object is masked from 'package:arm':
##
##      display

## The following objects are masked from 'package:base':
##
##      backsolve, forwardsolve

## Loading required package: maps
```

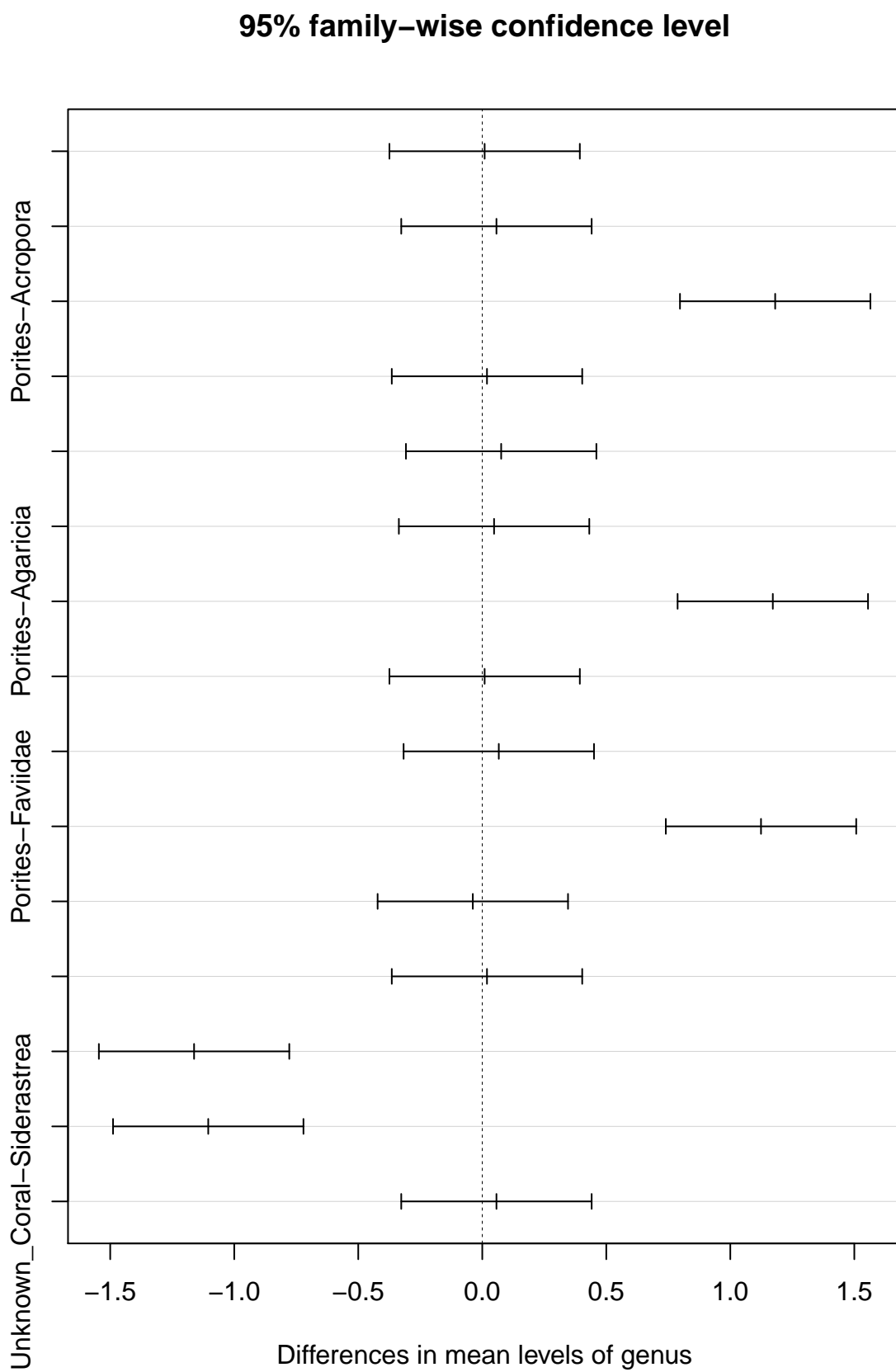


Figure 4: The graph shows the multiple comparison (Tukey test) between sites. The pairs Porites-Acropora, Porites-Agaricia, Porites-Faviidae, Siderastrea-Porites and Unknown_Coral-Porites are different.


```
glm6 <- glm (corales_algunos_sum ~ Porifera + Branching.coralline.algae + Branching.erect.algae +
Coarsely.branched.algae + Filamentous.algae +
Jointed.calcareus.algae + Crustose.algae +
Sheet.like.algae + Thick.leathery.algae +
turf.algae + unbranched.erect.algae , family = poisson(), data = corales)
summary(glm6)
```

```
##
## Call:
## glm(formula = corales_algunos_sum ~ Porifera + Branching.coralline.algae +
##      Branching.erect.algae + Coarsely.branched.algae + Filamentous.algae +
##      Jointed.calcareus.algae + Crustose.algae + Sheet.like.algae +
##      Thick.leathery.algae + turf.algae + unbranched.erect.algae,
##      family = poisson(), data = corales)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -2.952  -1.115  -1.034   0.000   5.789
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)      0.22263    0.37939   0.587  0.5573
## Porifera         -0.12934    0.06965  -1.857  0.0633 .
## Branching.coralline.algae  0.15250    0.20301   0.751  0.4525
## Branching.erect.algae    0.02190    0.18913   0.116  0.9078
## Coarsely.branched.algae   0.08391    0.20507   0.409  0.6824
## Filamentous.algae    -0.80304    0.36200  -2.218  0.0265 *
## Jointed.calcareus.algae  -0.77573    1.03090  -0.752  0.4518
## Crustose.algae        1.35651    0.23036   5.889 3.89e-09 ***
## Sheet.like.algae       0.33762    0.21835   1.546  0.1220
## Thick.leathery.algae   -2.06925    1.08144  -1.913  0.0557 .
## turf.algae           0.47334    1.03073   0.459  0.6461
## unbranched.erect.algae  0.60029    0.26483   2.267  0.0234 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##      Null deviance: 383.4  on 104  degrees of freedom
## Residual deviance: 290.1  on  93  degrees of freedom
## AIC: 432.14
##
## Number of Fisher Scoring iterations: 6
fit.boot <- boot.stepAIC(glm6, data = corales, B = 100) # That's it !
fit.boot
```

```
##
## Summary of Bootstrapping the 'stepAIC()' procedure for
##
## Call:
## glm(formula = corales_algunos_sum ~ Porifera + Branching.coralline.algae +
##      Branching.erect.algae + Coarsely.branched.algae + Filamentous.algae +
##      Jointed.calcareus.algae + Crustose.algae + Sheet.like.algae +
##      Thick.leathery.algae + turf.algae + unbranched.erect.algae,
```

```

##      family = poisson(), data = corales)
##
## Bootstrap samples: 100
## Direction: backward
## Penalty: 2 * df
##
## Covariates selected
##
##              (%)
## Crustose.algae      100
## Filamentous.algae   89
## unbranched.erect.algae 67
## Porifera            62
## Sheet.like.algae    62
## Coarsely.branched.algae 56
## Branching.erect.algae 55
## Thick.leathery.algae 39
## Branching.coralline.algae 35
## Jointed.calcareus.algae 20
## turf.algae          4
##
## Coefficients Sign
##              + (%)  - (%)
## Crustose.algae      100.00  0.00
## turf.algae          100.00  0.00
## unbranched.erect.algae 91.04  8.96
## Branching.coralline.algae 88.57 11.43
## Sheet.like.algae    80.65 19.35
## Coarsely.branched.algae 64.29 35.71
## Branching.erect.algae 56.36 43.64
## Filamentous.algae   31.46 68.54
## Porifera            8.06 91.94
## Thick.leathery.algae 7.69 92.31
## Jointed.calcareus.algae 0.00 100.00
##
## Stat Significance
##              (%)
## Crustose.algae      100.00
## Thick.leathery.algae 84.62
## Sheet.like.algae    82.26
## Filamentous.algae   78.65
## turf.algae          75.00
## unbranched.erect.algae 74.63
## Branching.erect.algae 74.55
## Porifera            72.58
## Coarsely.branched.algae 67.86
## Branching.coralline.algae 65.71
## Jointed.calcareus.algae 5.00
##
##
## The stepAIC() for the original data-set gave
##
## Call:  glm(formula = corales_algunos_sum ~ Porifera + Filamentous.algae +
##           Crustose.algae + Sheet.like.algae + Thick.leathery.algae +
##           unbranched.erect.algae, family = poisson(), data = corales)

```

```
##
## Coefficients:
##          (Intercept)          Porifera          Filamentous.algae
##          0.2654          -0.1247          -0.7341
##          Crustose.algae          Sheet.like.algae          Thick.leathery.algae
##          1.3361          0.3893          -1.9908
## unbranched.erect.algae
##          0.5671
##
## Degrees of Freedom: 104 Total (i.e. Null);  98 Residual
## Null Deviance:          383.4
## Residual Deviance: 291.5          AIC: 423.6
##
## Stepwise Model Path
## Analysis of Deviance Table
##
## Initial Model:
## corales_algunos_sum ~ Porifera + Branching.coralline.algae +
##   Branching.erect.algae + Coarsely.branched.algae + Filamentous.algae +
##   Jointed.calcareus.algae + Crustose.algae + Sheet.like.algae +
##   Thick.leathery.algae + turf.algae + unbranched.erect.algae
##
## Final Model:
## corales_algunos_sum ~ Porifera + Filamentous.algae + Crustose.algae +
##   Sheet.like.algae + Thick.leathery.algae + unbranched.erect.algae
##
##
##          Step Df   Deviance Resid. Df Resid. Dev      AIC
## 1
## 2   - Branching.erect.algae  1 0.01338634      94   290.1117 430.1547
## 3   - Coarsely.branched.algae  1 0.16861492      95   290.2803 428.3233
## 4           - turf.algae  1 0.20177300      96   290.4821 426.5251
## 5 - Branching.coralline.algae  1 0.53745281      97   291.0195 425.0626
## 6   - Jointed.calcareus.algae  1 0.49083957      98   291.5104 423.5534
```

Las algas de tipo: - Branching.erect - Coarsely.branched - turf - Branching.coralline - Jointed.calcareus

No son buenas predictoras de la abundancia de los corales!

Predicting recruitment of all corals as a function of porifera and algae (several). No matter stepwise procedure

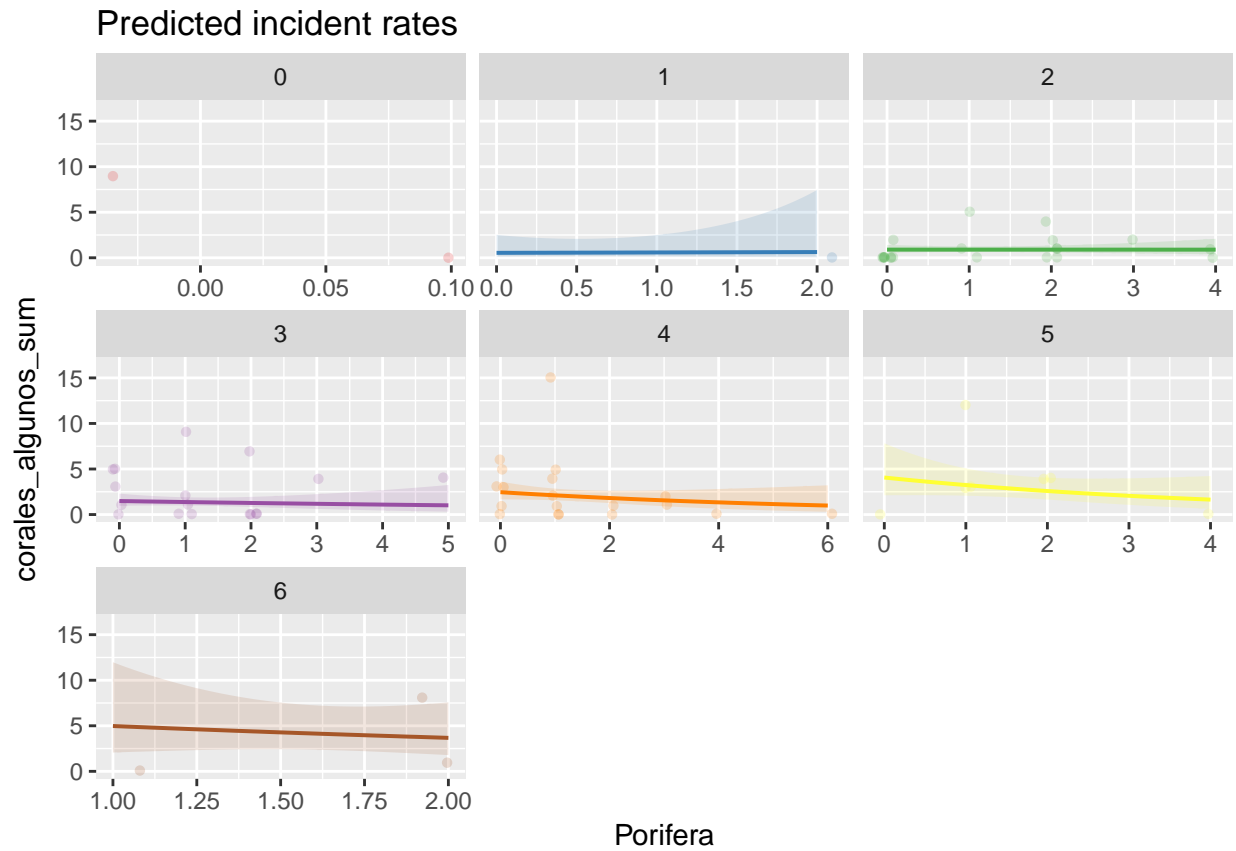
```
# algae richness
corales$algae_richnes <- apply(cbind(corales$Branching.coralline.algae , corales$Branching.erect.algae ,
corales$Coarsely.branched.algae , corales$Filamentous.algae ,
corales$Jointed.calcareus.algae , corales$Crustose.algae ,
corales$Sheet.like.algae + corales$Thick.leathery.algae ,
corales$turf.algae , corales$unbranched.erect.algae),1,sum)

glm7 <- glm(corales_algunos_sum ~ Porifera * algae_richnes, family = poisson(), data = corales)
glm8 <- glm(corales_algunos_sum ~ Porifera * algae_richnes + I(algae_richnes)^2, family = poisson(), data = corales)
```

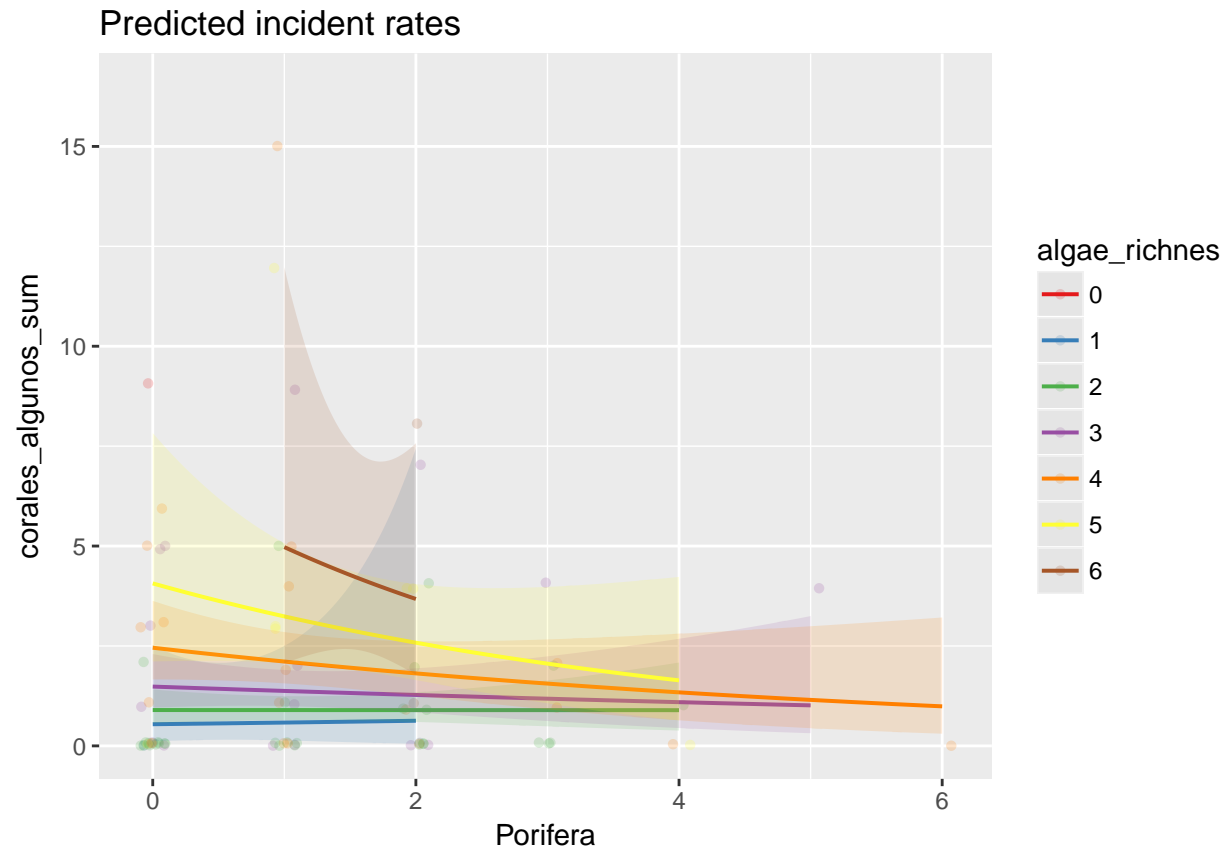
```
summary(glm7)
```

```
##
## Call:
## glm(formula = corales_algunos_sum ~ Porifera * algae_richnes,
##      family = poisson(), data = corales)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -3.1540  -1.5963  -1.3384   0.1105   6.5051
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    -1.11731    0.35162  -3.178  0.00148 **
## Porifera         0.14997    0.21851   0.686  0.49250
## algae_richnes    0.50398    0.10018   5.031 4.89e-07 ***
## Porifera:algae_richnes -0.07539    0.06023  -1.252  0.21062
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##      Null deviance: 383.40  on 104  degrees of freedom
## Residual deviance: 341.93  on 101  degrees of freedom
## AIC: 467.97
##
## Number of Fisher Scoring iterations: 6
newdato <- as.data.frame(cbind(Porifera=rep(1:10, each = 10), algae_richnes=rep(1:10, 10)) )
predichos <- predict(glm7, newdata = newdato, type = "response")

# plot predictions but not as surface
sjp.glm(glm7, type = "pred", vars = c("Porifera", "algae_richnes"), show.ci = TRUE)
```



```
sjp.glm(glm7, type = "pred", vars = c("Porifera", "algae_richnes"), show.ci = TRUE, facet.grid = FALSE)
```



```
require(geoR)
```

```
## Loading required package: geoR
```

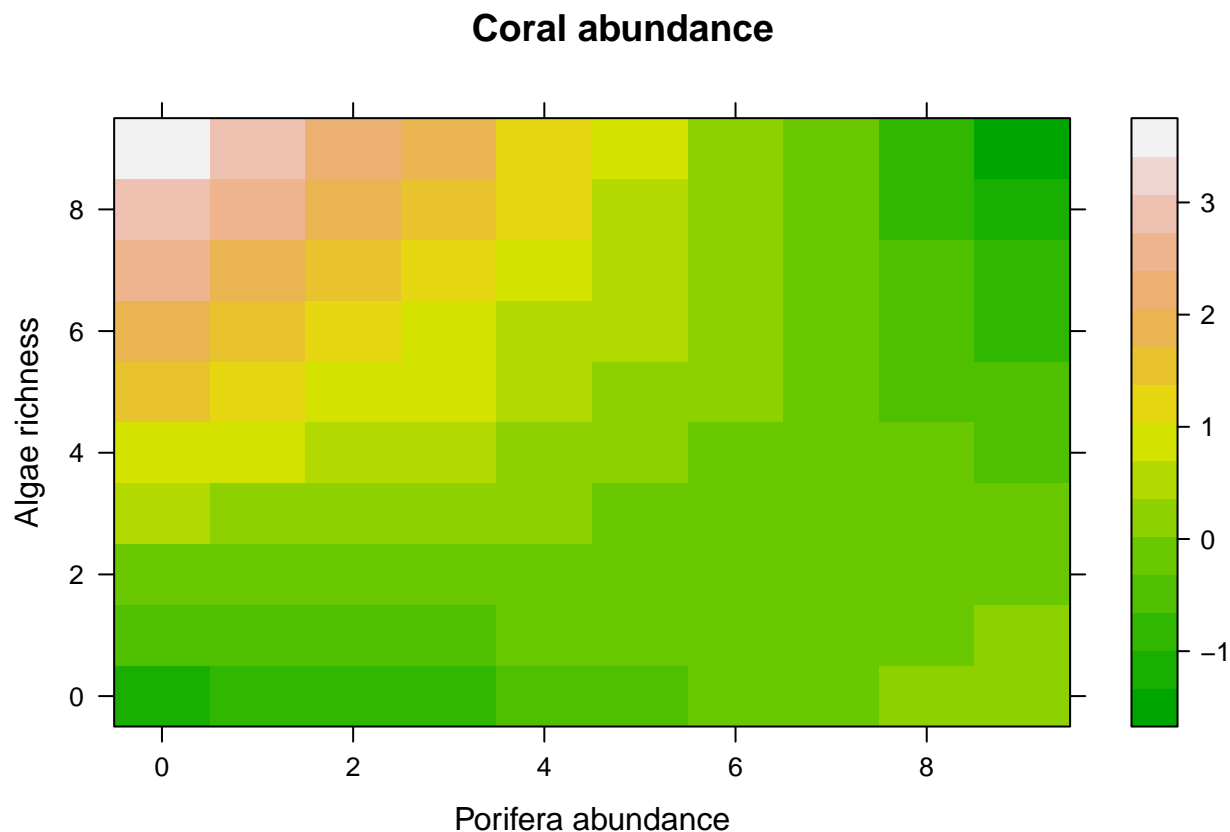
```
## -----
## Analysis of Geostatistical Data
## For an Introduction to geoR go to http://www.leg.ufpr.br/geoR
## geoR version 1.7-5.2 (built on 2016-05-02) is now loaded
## -----
```

```
data(elevation)
```

```
grid = expand.grid(list(Porifera = seq(0, 9, 1), algae_richnes = seq(0, 9, 1)))
```

```
z = predict(glm7, newdata = grid)
grid$Height = as.numeric(z)
```

```
levelplot(Height ~ Porifera*algae_richnes, data = grid,
  xlab = "Porifera abundance", ylab = "Algae richness",
  main = "Coral abundance",
  col.regions = terrain.colors(100)
)
```



```
#####

#### with image for predictors with interaction terms####
psi.matrix <- array(NA, dim = c(100, 100)) # Prediction matrix, for every

# combination of values of two interacting predictors
pr.mat<-data.frame(Porifera=seq(0,
                                7,
                                length.out=100),
                  algae_richnes=seq(0, 7,
                                     length.out=100))

for(i in 1:100){
  for(j in 1:100){
    psi.matrix[i, j]<-predict(glm7, newdata=data.frame(
      Porifera=pr.mat$Porifera[i],
      # mean=pr.mat$mean[j]),
      # range=pr.mat$range[j]),
      algae_richnes=pr.mat$algae_richnes[j]),
      type="response")
  }
}

mapPalette <- colorRampPalette(c("grey", "yellow", "orange", "red"))
```

```

#plot.par<-par() #save default graphics parameters

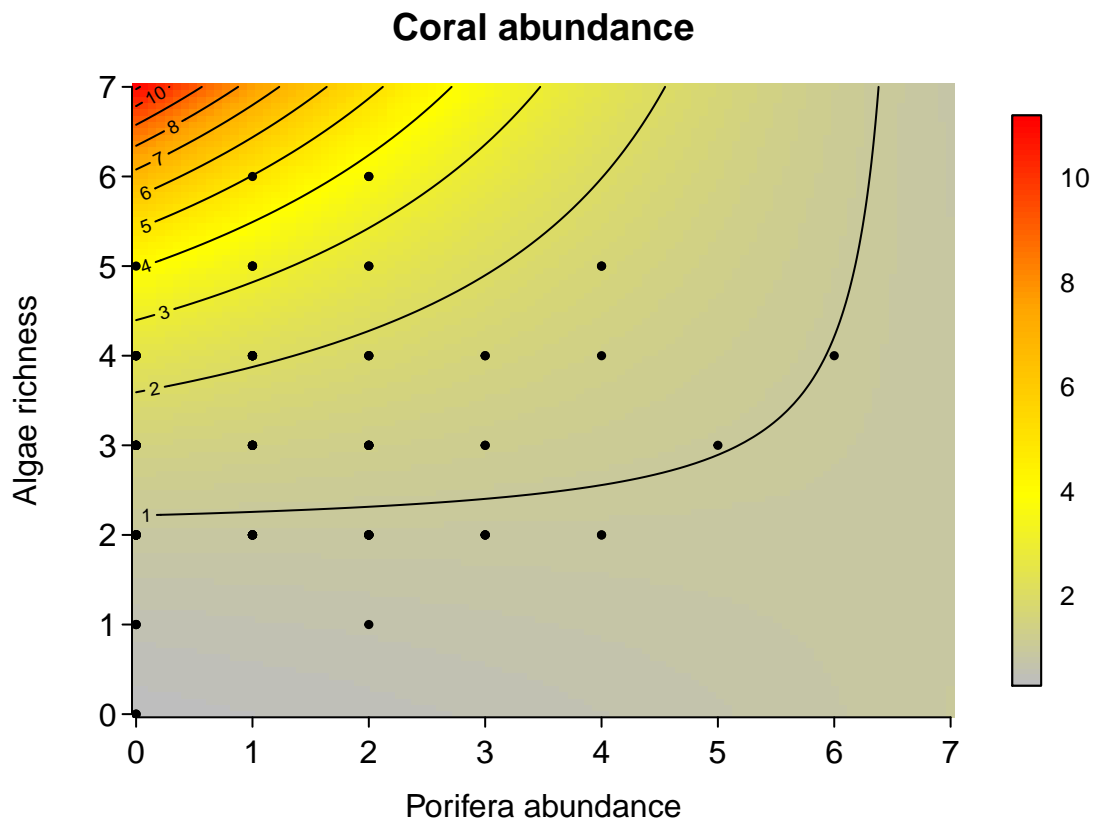
##obtain original unscale values for predictors

# png("BxR_FF.png", width=2000, height=1500, res=300)

#fig<-layout(matrix(c(1:12), 6,2, byrow=F))
par(mar=c(3,5,3,2))
image.plot(x = pr.mat$Porifera, y = pr.mat$algae_richnes , z = psi.matrix,
          col = mapPalette(100), axes=F,xlab = NA ,ylab = NA,
          legend.width=1, axis.args=list(cex.axis=0.8, lwd=0,
          line=-0.5), main="Coral abundance")
contour(x = pr.mat$Porifera, y = pr.mat$algae_richnes, z = psi.matrix,
        add = TRUE, lwd = 1)
axis(side = 1, tck = -.015, labels = NA)
axis(side = 2, tck = -.015, labels = NA)
axis(side = 1, lwd = 0, line = -.6)
axis(side = 2, lwd = 0, line = -.6, las = 1)
mtext(side = 1, "Porifera abundance", line = 1.8)
mtext(side = 2, "Algae richness", line = 2.3)

points(corales$Porifera, corales$algae_richnes, pch=19, cex=0.5,
       col="black")

```




```
# dev.off()
```

```
# glm6 <- glm (corales_algunos_sum ~ Porifera + Filamentous.algae + Crustose.algae +  
#   Sheet.like.algae + Thick.leathery.algae + unbranched.erect.algae, family = poisson(), data = corales)  
# fit.boot2 <- boot.stepAIC(glm6, data = corales, B = 100) # That's it !  
# fit.boot2
```

Predicting recruitment of all corals as a function of porifera and algae (just “good” predictors). Taking in to account the stepwise procedure

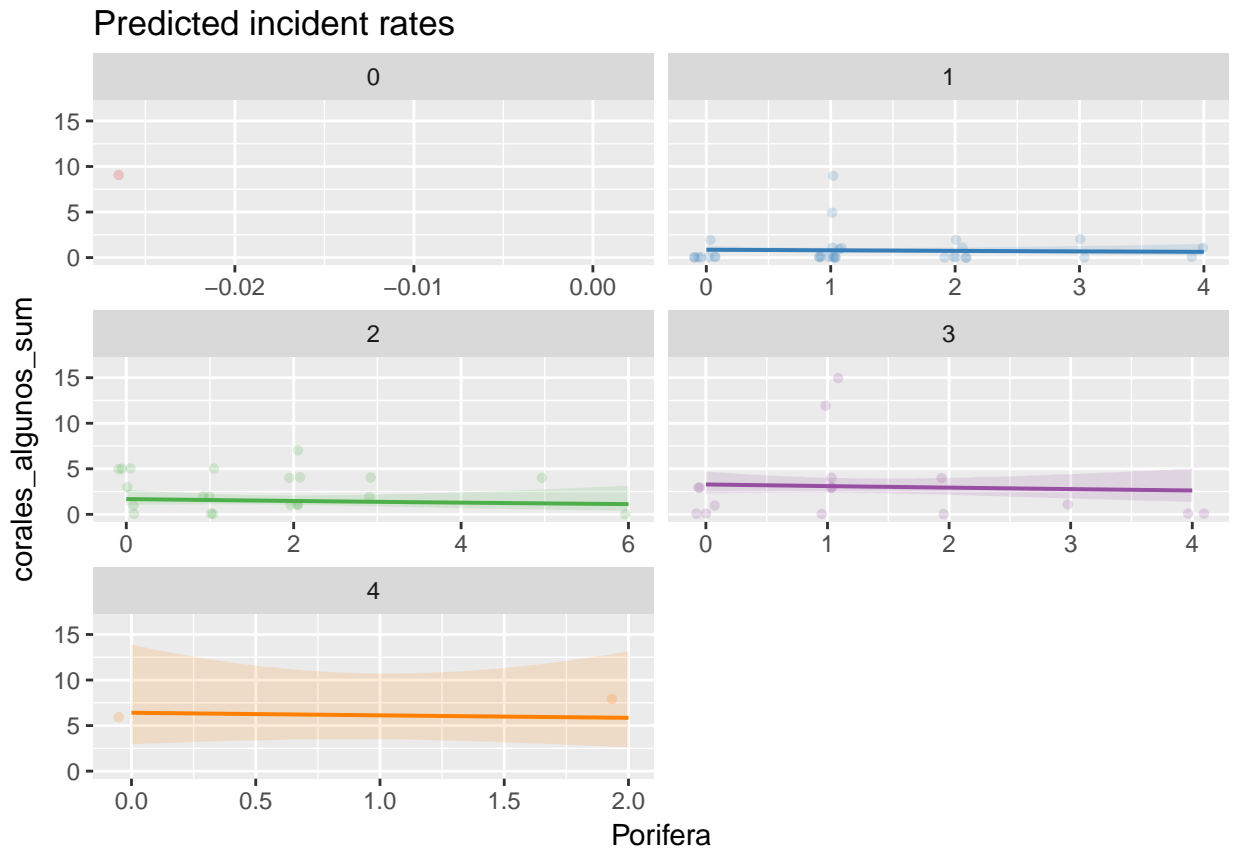
```
# algae richness  
corales$algae_richnes2 <- apply(cbind(corales$Filamentous.algae ,  
                                     corales$Crustose.algae ,  
                                     corales$Sheet.like.algae + corales$Thick.leathery.algae ,  
                                     corales$unbranched.erect.algae),1,sum)  
  
glm7 <- glm(corales_algunos_sum ~ Porifera * algae_richnes2, family = poisson(), data = corales)  
glm8 <- glm(corales_algunos_sum ~ Porifera * algae_richnes2 + I(algae_richnes)^2, family = poisson(), data = corales)
```

```
summary(glm7)
```

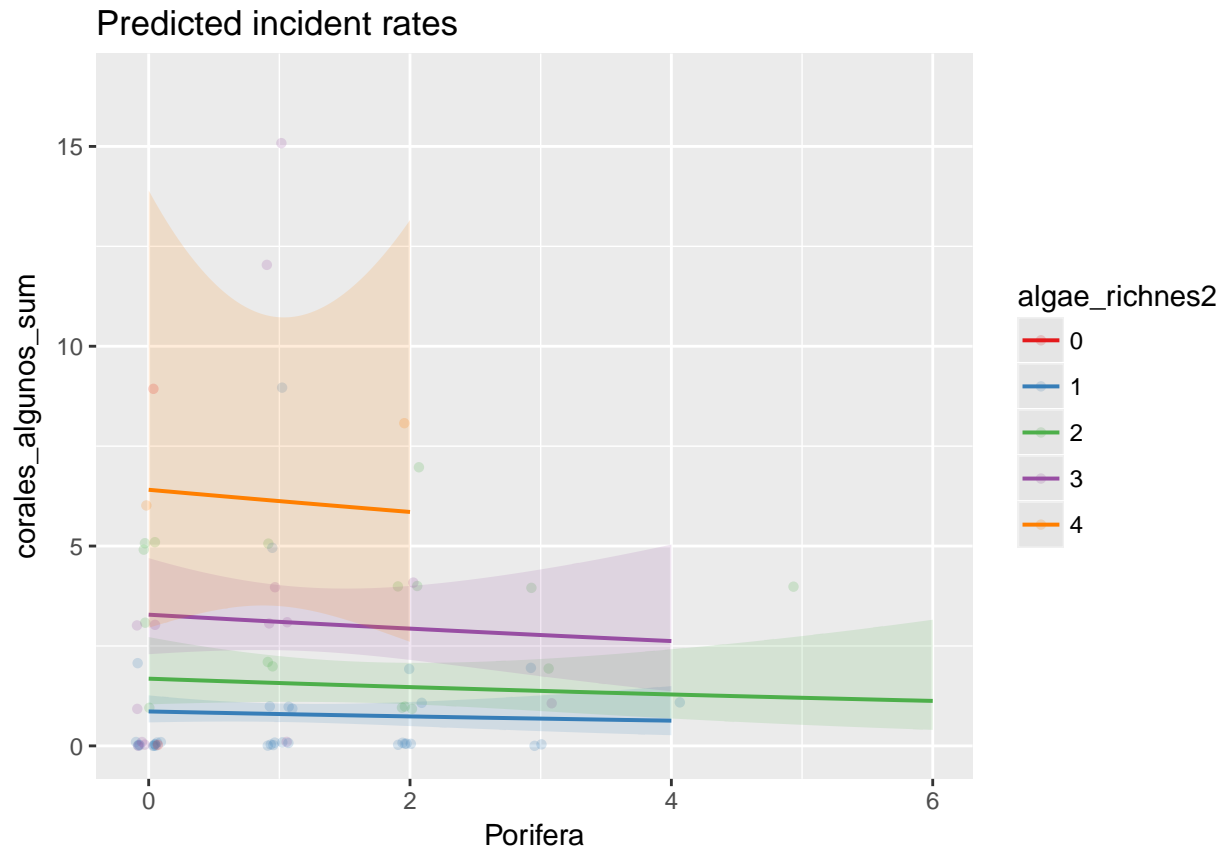
```
##  
## Call:  
## glm(formula = corales_algunos_sum ~ Porifera * algae_richnes2,  
##      family = poisson(), data = corales)  
##  
## Deviance Residuals:  
##      Min       1Q   Median       3Q      Max   
## -2.5623  -1.3125  -1.2143   0.2188   6.0959   
##  
## Coefficients:  
##              Estimate Std. Error z value Pr(>|z|)      
## (Intercept)    -0.81822    0.26445  -3.094  0.00197 **   
## Porifera       -0.08863    0.17790  -0.498  0.61832      
## algae_richnes2  0.66896    0.10994   6.085 1.17e-09 ***  
## Porifera:algae_richnes2  0.01083    0.07452   0.145  0.88442      
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
##  
## (Dispersion parameter for poisson family taken to be 1)  
##  
##      Null deviance: 383.40  on 104  degrees of freedom  
## Residual deviance: 317.17  on 101  degrees of freedom  
## AIC: 443.22  
##
```

```
## Number of Fisher Scoring iterations: 6
newdato <- as.data.frame(cbind(Porifera=rep(1:10, each = 10), algae_richnes2=rep(1:10, 10)) )
predichos <- predict(glm7, newdata = newdato, type = "response")

# plot predictions but not as surface
sjp.glm(glm7, type = "pred", vars = c("Porifera", "algae_richnes2"), show.ci = TRUE)
```



```
sjp.glm(glm7, type = "pred", vars = c("Porifera", "algae_richnes2"), show.ci = TRUE, facet.grid = FALSE)
```

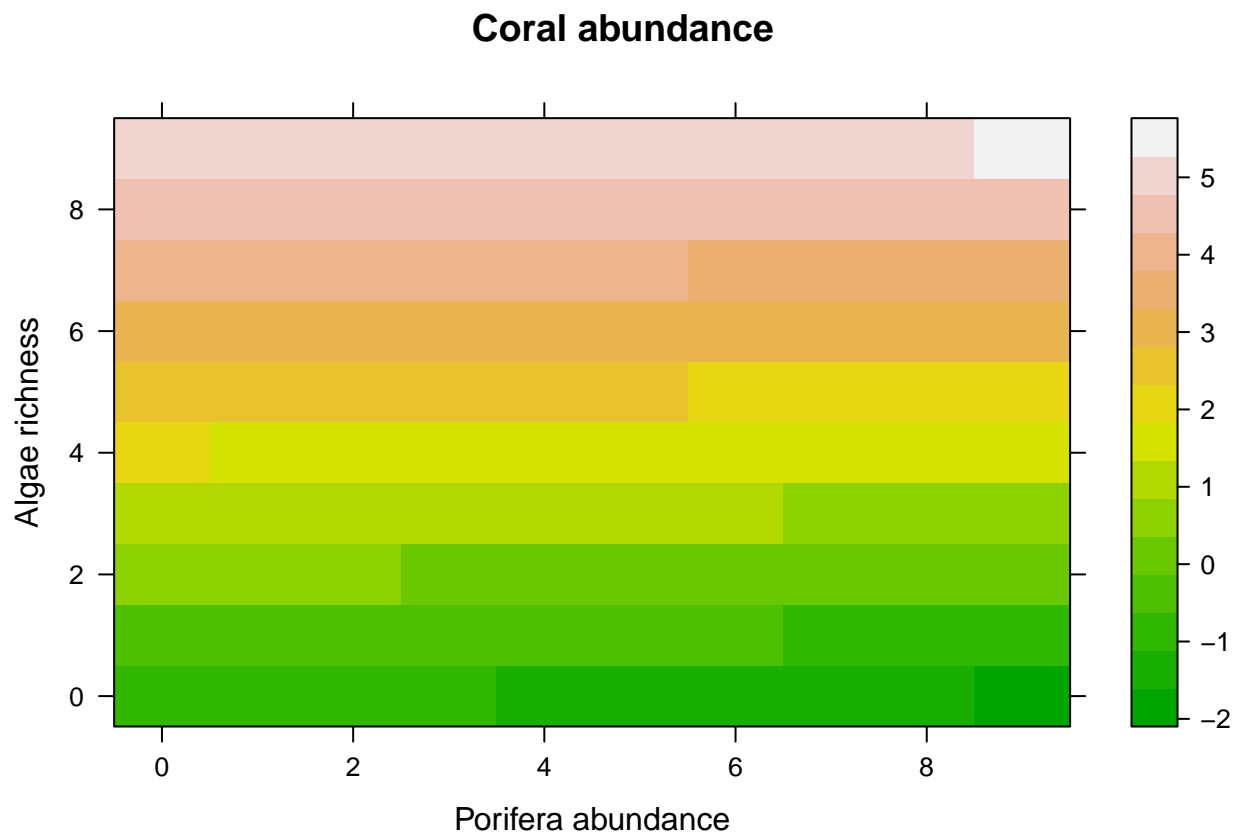


```
require(geoR)
data(elevation)

grid = expand.grid(list(Porifera = seq(0, 9, 1), algae_richnes2 = seq(0, 9, 1)))

z = predict(glm7, newdata = grid)
grid$Height = as.numeric(z)

levelplot(Height ~ Porifera*algae_richnes2, data = grid,
  xlab = "Porifera abundance", ylab = "Algae richness",
  main = "Coral abundance",
  col.regions = terrain.colors(100)
)
```



```
#####

#### with image for predictors with interaction terms####
psi.matrix <- array(NA, dim = c(100, 100)) # Prediction matrix, for every

# combination of values of two interacting predictors
pr.mat<-data.frame(Porifera=seq(0,
                                7,
                                length.out=100),
                   algae_richnes2=seq(0, 7,
                                       length.out=100))

for(i in 1:100){
  for(j in 1:100){
    psi.matrix[i, j]<-predict(glm7, newdata=data.frame(
      Porifera=pr.mat$Porifera[i],
      # mean=pr.mat$mean[j]),
      # range=pr.mat$range[j]),
      algae_richnes2=pr.mat$algae_richnes2[j]),
      type="response")
  }
}

mapPalette <- colorRampPalette(c("grey", "yellow", "orange", "red"))
```

```

#plot.par<-par() #save default graphics parameters

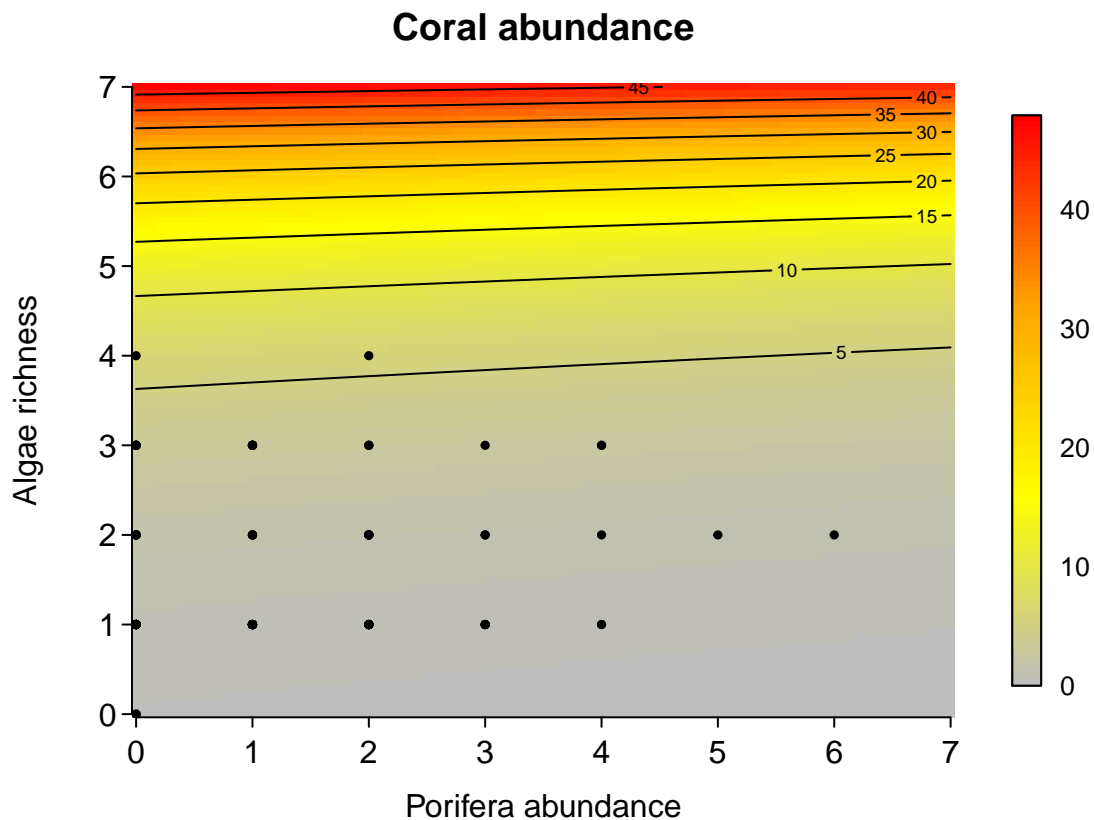
##obtain original unscale values for predictors

# png("BxR_FF.png", width=2000, height=1500, res=300)

#fig<-layout(matrix(c(1:12), 6,2, byrow=F))
par(mar=c(3,5,3,2))
image.plot(x = pr.mat$Porifera, y = pr.mat$algae_richnes2, z = psi.matrix,
          col = mapPalette(100), axes=F,xlab = NA,ylab = NA,
          legend.width=1, axis.args=list(cex.axis=0.8, lwd=0,
          line=-0.5), main="Coral abundance")
contour(x = pr.mat$Porifera, y = pr.mat$algae_richnes2, z = psi.matrix,
        add = TRUE, lwd = 1)
axis(side = 1, tck = -.015, labels = NA)
axis(side = 2, tck = -.015, labels = NA)
axis(side = 1, lwd = 0, line = -.6)
axis(side = 2, lwd = 0, line = -.6, las = 1)
mtext(side = 1, "Porifera abundance", line = 1.8)
mtext(side = 2, "Algae richness", line = 2.3)

points(corales$Porifera, corales$algae_richnes2, pch=19, cex=0.5,
       col="black")

```



```
# dev.off()
```

```
# glm6 <- glm (corales_algunos_sum ~ Porifera + Filamentous.algae + Crustose.algae +  
#   Sheet.like.algae + Thick.leathery.algae + unbranched.erect.algae, family = poisson(), data = corales)  
# fit.boot2 <- boot.stepAIC(glm6, data = corales, B = 100) # That's it !  
# fit.boot2
```

En este caso los Porifera dejan de ser significativos y las algas (seleccionadas) son mucho mas importantes en la relacion. Al final el modelo podria ser solo lineal.

Con cual nos quedamos???? yo pensaria que el primer modelo es mas bonito en la grafica... pero al final lo importante es la explicacion biologica.

Adicionalmente que otro grupo aparte de Porifera podemos probar? que tal si juntamos algunos corales como Porites y Acropora... tendria sentido???

Predicting recruitment of coral abundance as a function of sediment and algae (just “good” predictors). Taking into account the stepwise procedure

```
# algae richness  
corales$algae_richnes2 <- apply(cbind(corales$Filamentous.algae ,  
                                     corales$Crustose.algae ,  
                                     corales$Sheet.like.algae + corales$Thick.leathery.algae ,  
                                     corales$unbranched.erect.algae),1,sum)  
  
glm7 <- glm(corales_algunos_sum ~ Sediment * algae_richnes2, family = poisson(), data = corales)  
glm8 <- glm(corales_algunos_sum ~ Sediment * algae_richnes2 + I(algae_richnes)^2, family = poisson(), data = corales)
```

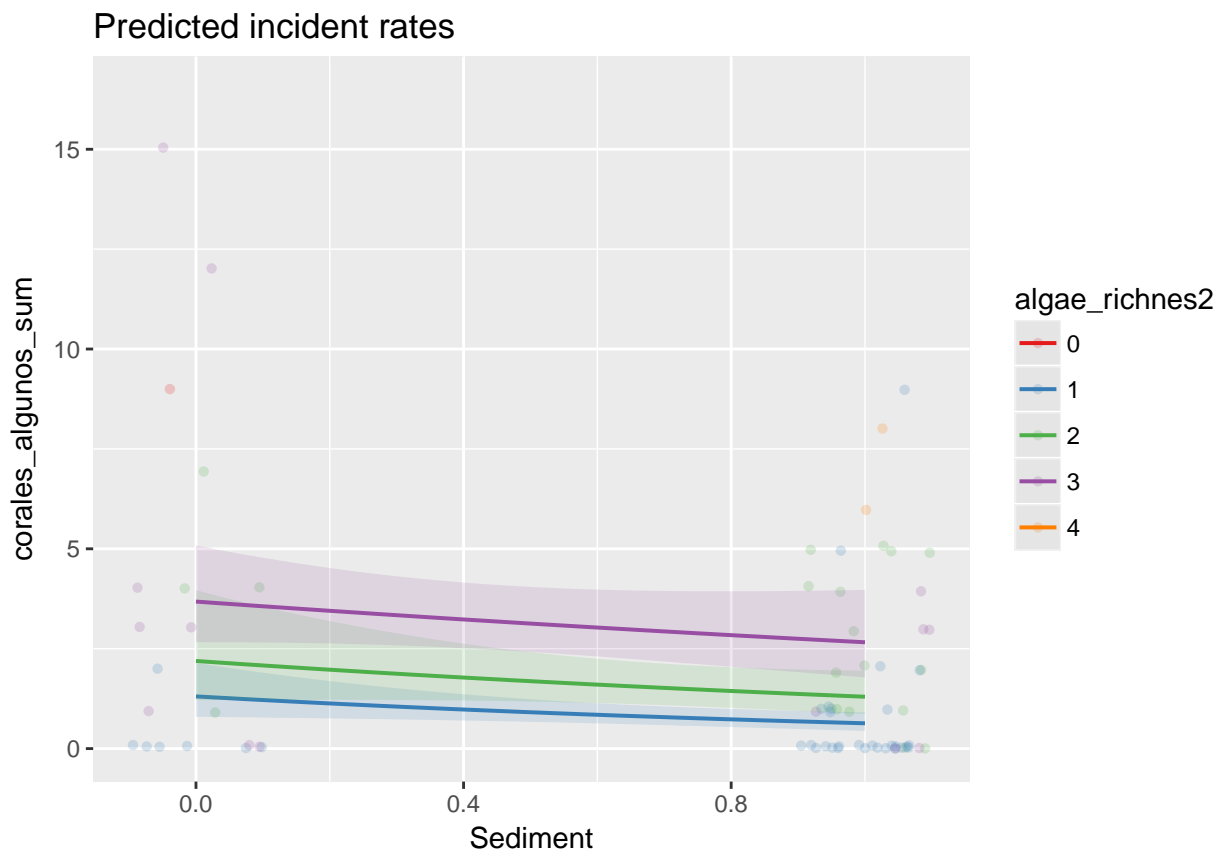
```
summary(glm7)
```

```
##  
## Call:  
## glm(formula = corales_algunos_sum ~ Sediment * algae_richnes2,  
##      family = poisson(), data = corales)  
##  
## Deviance Residuals:  
##      Min       1Q   Median       3Q      Max   
## -2.7128  -1.6114  -1.1255   0.4244   5.5710   
##  
## Coefficients:  
##              Estimate Std. Error z value Pr(>|z|)      
## (Intercept)    -0.2500     0.3345  -0.748  0.454732      
## Sediment       -0.9243     0.4167  -2.218  0.026543 *      
## algae_richnes2    0.5176     0.1364   3.794  0.000148 ***     
## Sediment:algae_richnes2  0.2001     0.1709   1.171  0.241621      
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## (Dispersion parameter for poisson family taken to be 1)
##
## Null deviance: 383.40 on 104 degrees of freedom
## Residual deviance: 308.98 on 101 degrees of freedom
## AIC: 435.02
##
## Number of Fisher Scoring iterations: 6

newdatao <- as.data.frame(cbind(Sediment=rep(0:1, each = 10), algae_richnes2=rep(1:10, 10)) )
predichos <- predict(glm7, newdata = newdatao, type = "response")

# plot predictions but not as surface
# sgp.glm(glm7, type = "pred", vars = c("Sediment", "algae_richnes2"), show.ci = TRUE)
sgp.glm(glm7, type = "pred", vars = c("Sediment", "algae_richnes2"), show.ci = TRUE, facet.grid = FALSE)
```



```
require(geoR)
data(elevation)

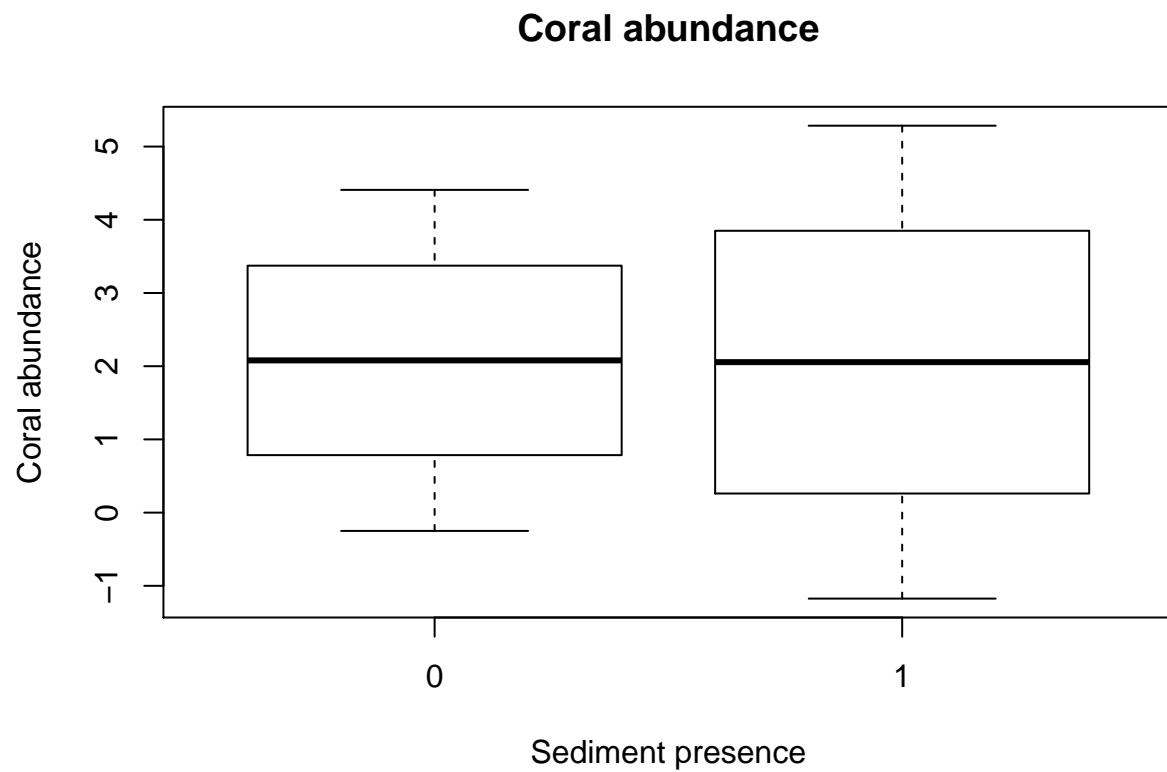
grid = expand.grid(list(Sediment = rep(c(0, 1), 10), algae_richnes2 = seq(0, 9, 1)))

z = predict(glm7, newdata = grid)
grid$Height = as.numeric(z)
```

```

boxplot(Height ~ Sediment , data=grid,
        xlab = "Sediment presence", ylab = "Coral abundance",
        main = "Coral abundance",
        col.regions = terrain.colors(100)
)

```



```

# glm6 <- glm (corales_algunos_sum ~ Porifera + Filamentous.algae + Crustose.algae +
#   Sheet.like.algae + Thick.leathery.algae + unbranched.erect.algae, family = poisson(), data = cora
# fit.boot2 <- boot.stepAIC(glm6, data = corales, B = 100) # That's it !
# fit.boot2

```