

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

##	Locality	Site_name	Site	Plate	platos.analizados	Amphipoda	Anemone
## 1	AC	ACBAY	XII	66	1	0	0
## 2	AC	ACBAY	XII	67	2	0	0
## 3	AC	ACBAY	XII	68	3	0	0
## 4	AC	ACBAY	XII	69	4	0	0
## 5	AC	ACBAY	XII	70	5	0	0
## 6	AC	ACBAY	XII	71	6	0	0
##	Ascidacea	Bivalvia	Branching.coralline.algae	Branching.erect.algae			
## 1	1	0	0				1
## 2	1	0	1				1
## 3	0	0	0				0
## 4	0	1	1				1
## 5	1	0	0				1
## 6	1	0	1				0
##	Bryozoa	Coarsely.branched.algae	Crustacea	Crustose.algae	Cyanophyceae		
## 1	0		1	0	1		0
## 2	0		1	0	1		0
## 3	0		1	0	0		0
## 4	0		1	0	1		0
## 5	0		1	0	1		0
## 6	0		1	0	1		0
##	Echinoidea	Filamentous.algae	Foraminifera	Holothuroidea	Hydrozoa		
## 1	0		1	1	0		0
## 2	0		1	1	0		0
## 3	0		1	0	0		0
## 4	0		1	0	0		0
## 5	0		1	0	0		0
## 6	0		1	1	0		0
##	Jointed.calcareous.algae	Mollusca	Patellidae	Polychaeta	Porifera	Sediment	
## 1		0	0	0	1	4	1
## 2		1	0	0	1	2	1
## 3		0	0	0	1	2	1
## 4		0	0	0	1	2	1
## 5		0	0	0	1	6	1
## 6		0	0	0	1	2	0
##	Sheet.like.algae	Sipunculidae	Thick.leathery.algae	turf.algae			
## 1	0	0		0			0
## 2	0	0		0			0
## 3	0	0		0			0
## 4	0	0		0			0
## 5	0	0		0			0
## 6	0	0		0			0
##	unbranched.erect.algae	Vermetidae	Zoanthidae	Acropora.sp.	Agaricia.sp.		
## 1		0	0	0	0		0
## 2		0	1	0	0		0
## 3		0	0	0	0		0
## 4		0	1	0	0		0
## 5		0	0	0	0		0
## 6		0	1	0	0		0
##	Faviidae	Porites.spp.	Siderastrea.sp.	Unknown.Coral..broken.			
## 1	0	0	0				0
## 2	0	1	0				0

```
## 3      0      0      0      0
## 4      0      3      1      0
## 5      0      0      0      0
## 6      0      1      0      0
##   Unknown.Coral..too.small. all corales_algunos_sum
## 1      0      0      0
## 2      0      1      1
## 3      0      0      0
## 4      0      4      4
## 5      0      0      0
## 6      0      1      1
```

BoxPlot

Let see how recruitment varies per site

```
tabla2 <- as.data.frame(cbind(as.character(corales[,2]), as.numeric( corales[,43])))
colnames(tabla2) <- c("site", "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 = site, y = abund)) +
  geom_boxplot(fill = "grey80", colour = "blue") +
  scale_x_discrete() + xlab("site") +
  ylab("Recruitment (sum) of several coral genus")
```

Testing differences in ANOVA

as a poisson proces determined by site = Site name (factor)

```
glm3 <- glm (corales_algunos_sum ~ Site_name, family = poisson(), data = corales)

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

```
## Analysis of Deviance Table
##
## Model: poisson, link: log
##
## Response: corales_algunos_sum
##
## Terms added sequentially (first to last)
##
##
##          Df Deviance Resid. Df Resid. Dev  Pr(>Chi)
## NULL                104      383.40
## Site_name 11      233.88          93      149.52 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

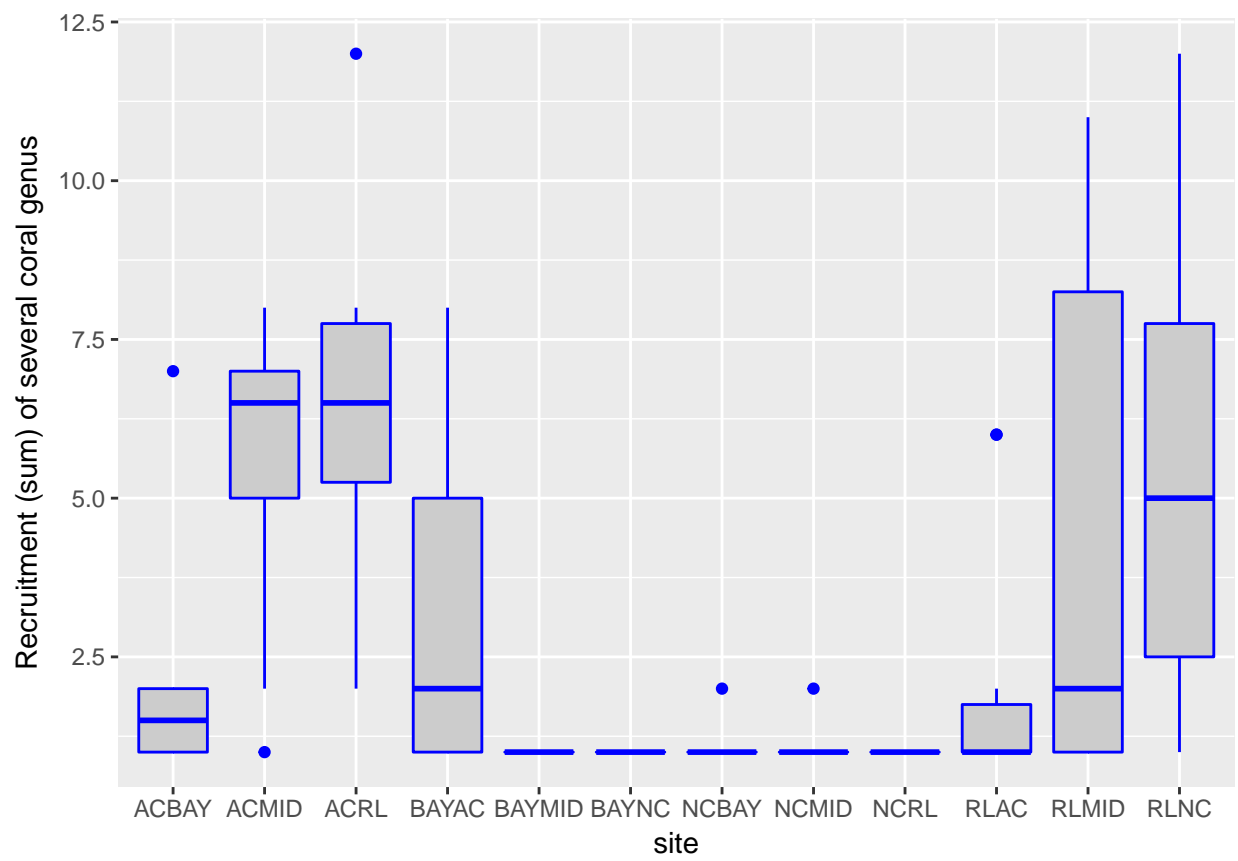


Figure 1: Sumarazing how many recruits are in the bay first agregating all corals as a sum.

```
anova1 <- aov(glm3)
(posthoc1 <- TukeyHSD(x=anova1, "Site_name", conf.level=0.95))
```

```
## Tukey multiple comparisons of means
## 95% family-wise confidence level
##
## Fit: aov(formula = glm3)
##
## $Site_name
##
```

		diff	lwr	upr	p adj
##	ACMID-ACBAY	2.000000e+00	-1.58785201	5.5878520	0.7747907
##	ACRL-ACBAY	3.000000e+00	-1.01134049	7.0113405	0.3486031
##	BAYAC-ACBAY	3.000000e-01	-3.28785201	3.8878520	1.0000000
##	BAYMID-ACBAY	-1.000000e+00	-4.58785201	2.5878520	0.9985616
##	BAYNC-ACBAY	-1.000000e+00	-4.75226544	2.7522654	0.9990455
##	NCBAY-ACBAY	-8.888889e-01	-4.55072501	2.7729472	0.9996023
##	NCMID-ACBAY	-9.000000e-01	-4.48785201	2.6878520	0.9994573
##	NCRL-ACBAY	-1.000000e+00	-4.58785201	2.5878520	0.9985616
##	RLAC-ACBAY	-3.000000e-01	-3.88785201	3.2878520	1.0000000
##	RLMID-ACBAY	1.625000e+00	-2.12726544	5.3772654	0.9493745
##	RLNC-ACBAY	5.250000e+00	1.49773456	9.0022654	0.0005511
##	ACRL-ACMID	1.000000e+00	-2.58785201	4.5878520	0.9985616
##	BAYAC-ACMID	-1.700000e+00	-4.80717098	1.4071710	0.7948034
##	BAYMID-ACMID	-3.000000e+00	-6.10717098	0.1071710	0.0685976
##	BAYNC-ACMID	-3.000000e+00	-6.29565251	0.2956525	0.1103625
##	NCBAY-ACMID	-2.888889e+00	-6.08120361	0.3034258	0.1153121
##	NCMID-ACMID	-2.900000e+00	-6.00717098	0.2071710	0.0909368
##	NCRL-ACMID	-3.000000e+00	-6.10717098	0.1071710	0.0685976
##	RLAC-ACMID	-2.300000e+00	-5.40717098	0.8071710	0.3643248
##	RLMID-ACMID	-3.750000e-01	-3.67065251	2.9206525	0.9999998
##	RLNC-ACMID	3.250000e+00	-0.04565251	6.5456525	0.0568681
##	BAYAC-ACRL	-2.700000e+00	-6.28785201	0.8878520	0.3392082
##	BAYMID-ACRL	-4.000000e+00	-7.58785201	-0.4121480	0.0158428
##	BAYNC-ACRL	-4.000000e+00	-7.75226544	-0.2477346	0.0262750
##	NCBAY-ACRL	-3.888889e+00	-7.55072501	-0.2270528	0.0273613
##	NCMID-ACRL	-3.900000e+00	-7.48785201	-0.3121480	0.0212070
##	NCRL-ACRL	-4.000000e+00	-7.58785201	-0.4121480	0.0158428
##	RLAC-ACRL	-3.300000e+00	-6.88785201	0.2878520	0.1019960
##	RLMID-ACRL	-1.375000e+00	-5.12726544	2.3772654	0.9852268
##	RLNC-ACRL	2.250000e+00	-1.50226544	6.0022654	0.6852222
##	BAYMID-BAYAC	-1.300000e+00	-4.40717098	1.8071710	0.9601819
##	BAYNC-BAYAC	-1.300000e+00	-4.59565251	1.9956525	0.9740349
##	NCBAY-BAYAC	-1.188889e+00	-4.38120361	2.0034258	0.9832350
##	NCMID-BAYAC	-1.200000e+00	-4.30717098	1.9071710	0.9778459
##	NCRL-BAYAC	-1.300000e+00	-4.40717098	1.8071710	0.9601819
##	RLAC-BAYAC	-6.000000e-01	-3.70717098	2.5071710	0.9999577
##	RLMID-BAYAC	1.325000e+00	-1.97065251	4.6206525	0.9701136
##	RLNC-BAYAC	4.950000e+00	1.65434749	8.2456525	0.0001421
##	BAYNC-BAYMID	7.993606e-15	-3.29565251	3.2956525	1.0000000
##	NCBAY-BAYMID	1.111111e-01	-3.08120361	3.3034258	1.0000000
##	NCMID-BAYMID	1.000000e-01	-3.00717098	3.2071710	1.0000000
##	NCRL-BAYMID	8.437695e-15	-3.10717098	3.1071710	1.0000000
##	RLAC-BAYMID	7.000000e-01	-2.40717098	3.8071710	0.9998059
##	RLMID-BAYMID	2.625000e+00	-0.67065251	5.9206525	0.2576398

```
## RLNC-BAYMID      6.250000e+00  2.95434749  9.5456525  0.0000005
## NCBAY-BAYNC      1.111111e-01 -3.26493498  3.4871572  1.0000000
## NCMID-BAYNC      1.000000e-01 -3.19565251  3.3956525  1.0000000
## NCRL-BAYNC       4.440892e-16 -3.29565251  3.2956525  1.0000000
## RLAC-BAYNC       7.000000e-01 -2.59565251  3.9956525  0.9998909
## RLMID-BAYNC      2.625000e+00 -0.84892277  6.0989228  0.3330517
## RLNC-BAYNC       6.250000e+00  2.77607723  9.7239228  0.0000021
## NCMID-NCBAY     -1.111111e-02 -3.20342583  3.1812036  1.0000000
## NCRL-NCBAY      -1.111111e-01 -3.30342583  3.0812036  1.0000000
## RLAC-NCBAY       5.888889e-01 -2.60342583  3.7812036  0.9999733
## RLMID-NCBAY      2.513889e+00 -0.86215720  5.8899350  0.3552433
## RLNC-NCBAY       6.138889e+00  2.76284280  9.5149350  0.0000016
## NCRL-NCMID      -1.000000e-01 -3.20717098  3.0071710  1.0000000
## RLAC-NCMID       6.000000e-01 -2.50717098  3.7071710  0.9999577
## RLMID-NCMID      2.525000e+00 -0.77065251  5.8206525  0.3125347
## RLNC-NCMID       6.150000e+00  2.85434749  9.4456525  0.0000008
## RLAC-NCRL       7.000000e-01 -2.40717098  3.8071710  0.9998059
## RLMID-NCRL       2.625000e+00 -0.67065251  5.9206525  0.2576398
## RLNC-NCRL       6.250000e+00  2.95434749  9.5456525  0.0000005
## RLMID-RLAC       1.925000e+00 -1.37065251  5.2206525  0.7194464
## RLNC-RLAC        5.550000e+00  2.25434749  8.8456525  0.0000112
## RLNC-RLMID       3.625000e+00  0.15107723  7.0989228  0.0329048

# plot(posthoc1)
```

The next graph shows how coral recruitment varies according to genus

```
library(ggplot2)

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 poisson proces 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
##
## Response: corales_algunos_sum
##
## Terms added sequentially (first to last)
```

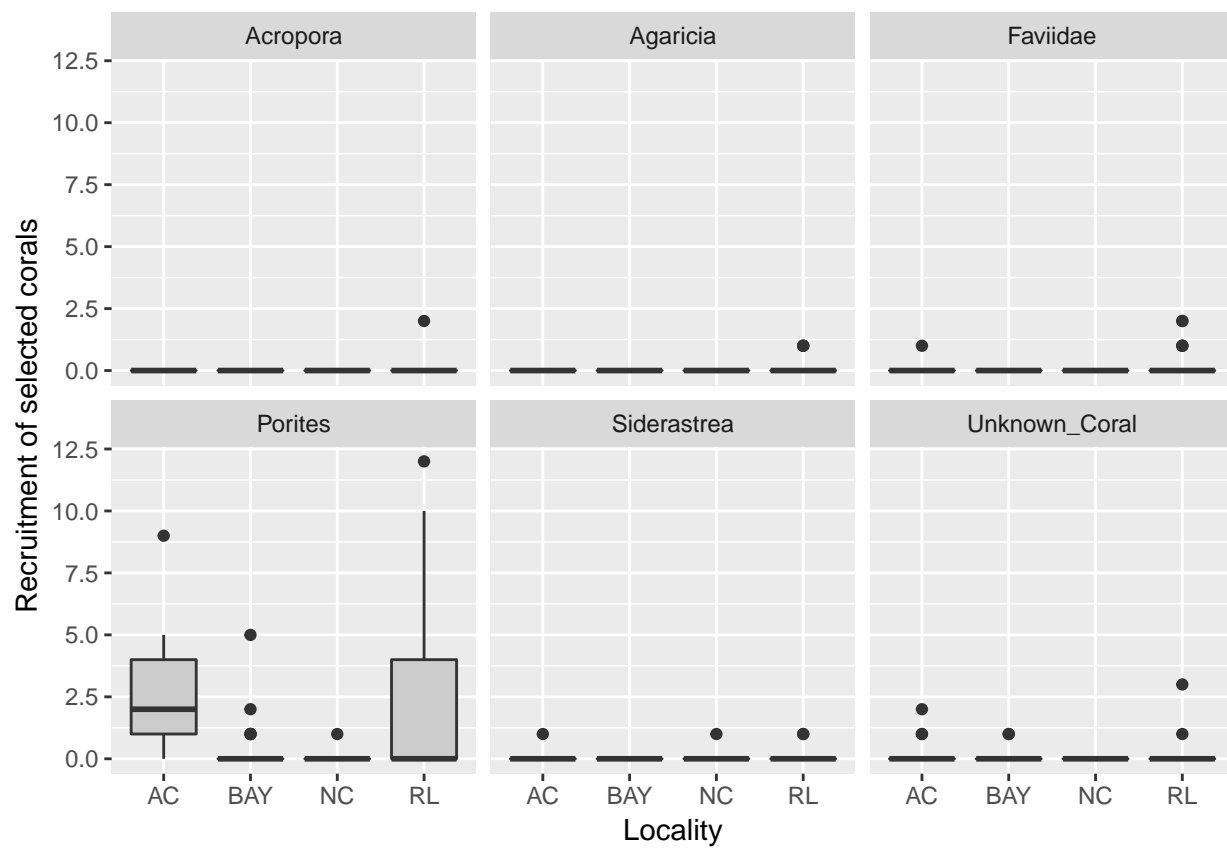


Figure 2: The second boxplot shows recruitment by locality wrapped by genus

```
##
##
##           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 ~ site + 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
## site  11    59.782      618    674.06 8.118e-10 ***
## genus  5   115.881      613    558.18 < 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
##
## Fit: aov(formula = glm5)
##
```

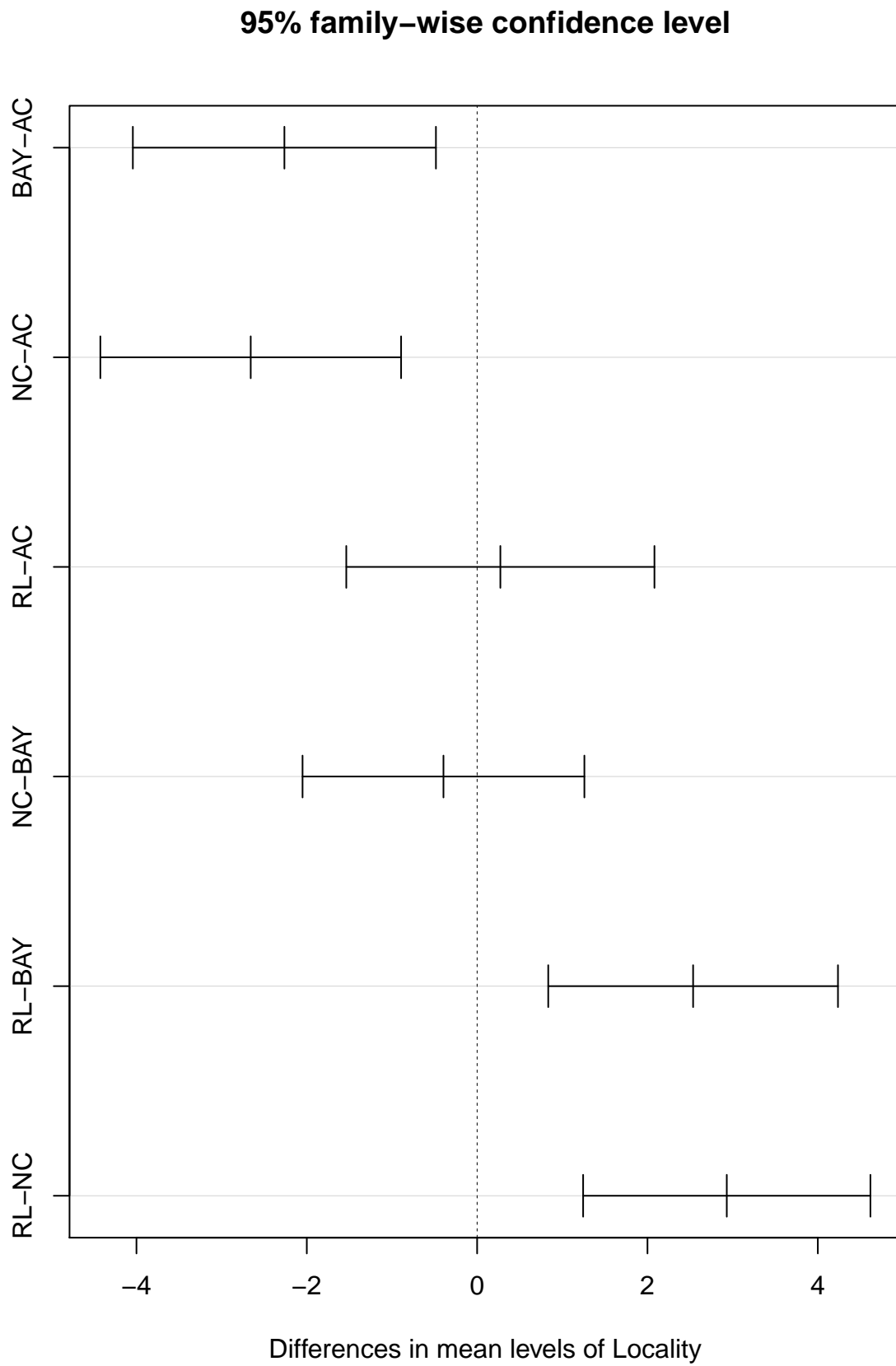



Figure 3: The graph shows the multiple comparison (Tukey test) between Localities. The pairs RL-AC and NC-BAY are not different.

```
## $genus
##
##          diff          lwr          upr          p adj
## Agaricia-Acropora      0.00952381 -0.3669669  0.3860145  0.9999997
## Faviidae-Acropora      0.05714286 -0.3193478  0.4336336  0.9980488
## Porites-Acropora       1.18095238  0.8044617  1.5574431  0.0000000
## Siderastrea-Acropora   0.01904762 -0.3574431  0.3955383  0.9999912
## Unknown_Coral-Acropora 0.07619048 -0.3003002  0.4526812  0.9924136
## Faviidae-Agaricia      0.04761905 -0.3288716  0.4241097  0.9991905
## Porites-Agaricia       1.17142857  0.7949379  1.5479193  0.0000000
## Siderastrea-Agaricia   0.00952381 -0.3669669  0.3860145  0.9999997
## Unknown_Coral-Agaricia 0.06666667 -0.3098240  0.4431574  0.9959379
## Porites-Faviidae       1.12380952  0.7473188  1.5003002  0.0000000
## Siderastrea-Faviidae   -0.03809524 -0.4145859  0.3383955  0.9997277
## Unknown_Coral-Faviidae 0.01904762 -0.3574431  0.3955383  0.9999912
## Siderastrea-Porites    -1.16190476 -1.5383955 -0.7854141  0.0000000
## Unknown_Coral-Porites  -1.10476190 -1.4812526 -0.7282712  0.0000000
## Unknown_Coral-Siderastrea 0.05714286 -0.3193478  0.4336336  0.9980488
```

```
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 plus Porifera + Polychaeta + Sediment

```
library(bootStepAIC)
```

```
## Loading required package: MASS
```

```
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 objects are masked from 'package:base':
```

```
##
```

```
##      backsolve, forwardsolve
```

```
## Loading required package: maps
```

```
glm6 <- glm (corales_algunos_sum ~ Porifera +
              Branching.coralline.algae + Branching.erect.algae +
              Sheet.like.algae +
              Coarsely.branched.algae + Filamentous.algae +
```

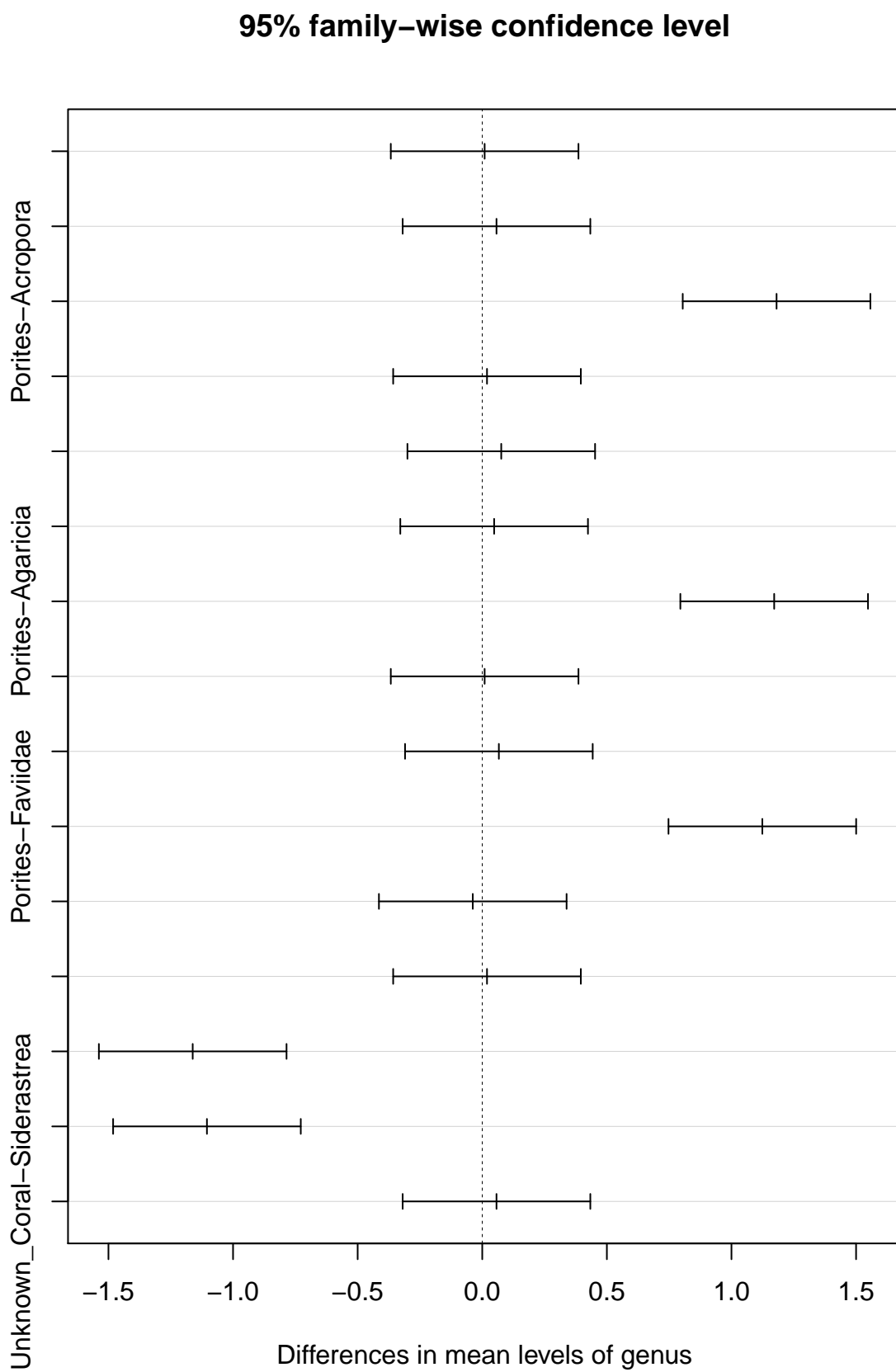


Figure 4: The graph shows the multiple comparison (Tukey test) between sites. The pairs Porites-Acropora, Porites-Agaricia, Porites-Faviidae, Siderastrea-Porites¹¹ and Unknown_Coral-Porites are different.

```

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 + Sheet.like.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
## Sheet.like.algae      0.33762    0.21835   1.546  0.1220
## 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 ***
## 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 + Sheet.like.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   82
## unbranched.erect.algae 67
## Sheet.like.algae    64
## Porifera            62
## Branching.erect.algae 57
## Branching.coralline.algae 38
## Coarsely.branched.algae 38
## Thick.leathery.algae 33
## Jointed.calcareus.algae 12
## turf.algae          2
##
## Coefficients Sign
##          + (%)  - (%)
## Crustose.algae      100.00  0.00
## turf.algae          100.00  0.00
## unbranched.erect.algae 94.03  5.97
## Sheet.like.algae    85.94 14.06
## Branching.coralline.algae 84.21 15.79
## Coarsely.branched.algae 60.53 39.47
## Branching.erect.algae 49.12 50.88
## Filamentous.algae   29.27 70.73
## Porifera            8.06 91.94
## Jointed.calcareus.algae 0.00 100.00
## Thick.leathery.algae 0.00 100.00
##
## Stat Significance
##          (%)
## Crustose.algae      100.00
## Porifera            85.48
## Filamentous.algae   85.37
## Thick.leathery.algae 81.82
## Sheet.like.algae    81.25
## unbranched.erect.algae 80.60
## Branching.coralline.algae 76.32
## Branching.erect.algae 73.68
## Coarsely.branched.algae 60.53
## turf.algae          50.00
## Jointed.calcareus.algae 16.67
##
##
## The stepAIC() for the original data-set gave
##
## Call: glm(formula = corales_algunos_sum ~ Porifera + Sheet.like.algae +
##          Filamentous.algae + Crustose.algae + Thick.leathery.algae +
##          unbranched.erect.algae, family = poisson(), data = corales)
##

```

```
## Coefficients:
##          (Intercept)          Porifera          Sheet.like.algae
##          0.2654          -0.1247          0.3893
##      Filamentous.algae      Crustose.algae      Thick.leathery.algae
##          -0.7341          1.3361          -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 + Sheet.like.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 + Sheet.like.algae + Filamentous.algae +
##      Crustose.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
```

Los porifera y las algas de tipo: - Sheet.like.algae - Filamentous.algae
- Crustose.algae - Thick.leathery.algae - unbranched.erect.algae

No son buenas predictoras del la abundancia (reclutamiento) de los corales!

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

```
library(sjPlot)
```

```
## Visit http://strengexjacke.de/sjPlot for package-vignettes.
```

```
# 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)

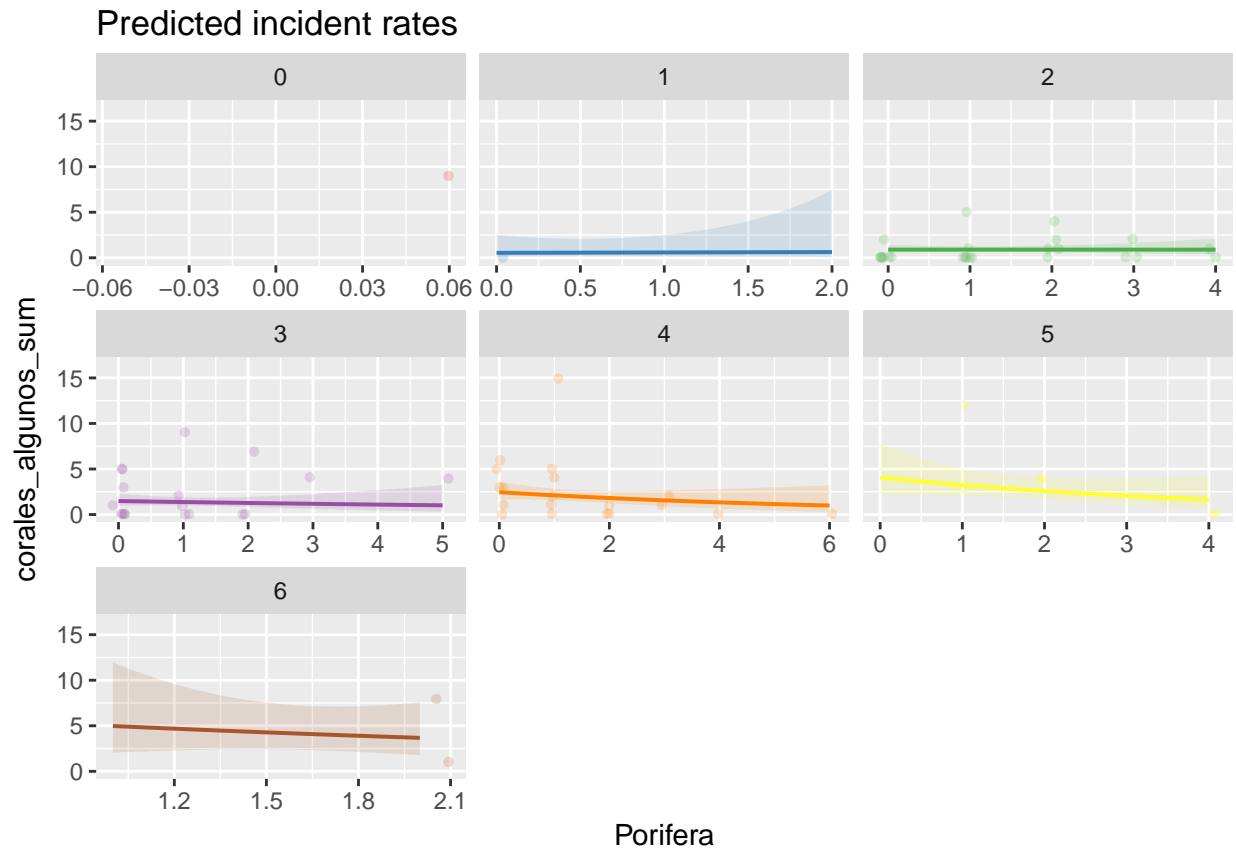
summary(glm7)

##
## 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")

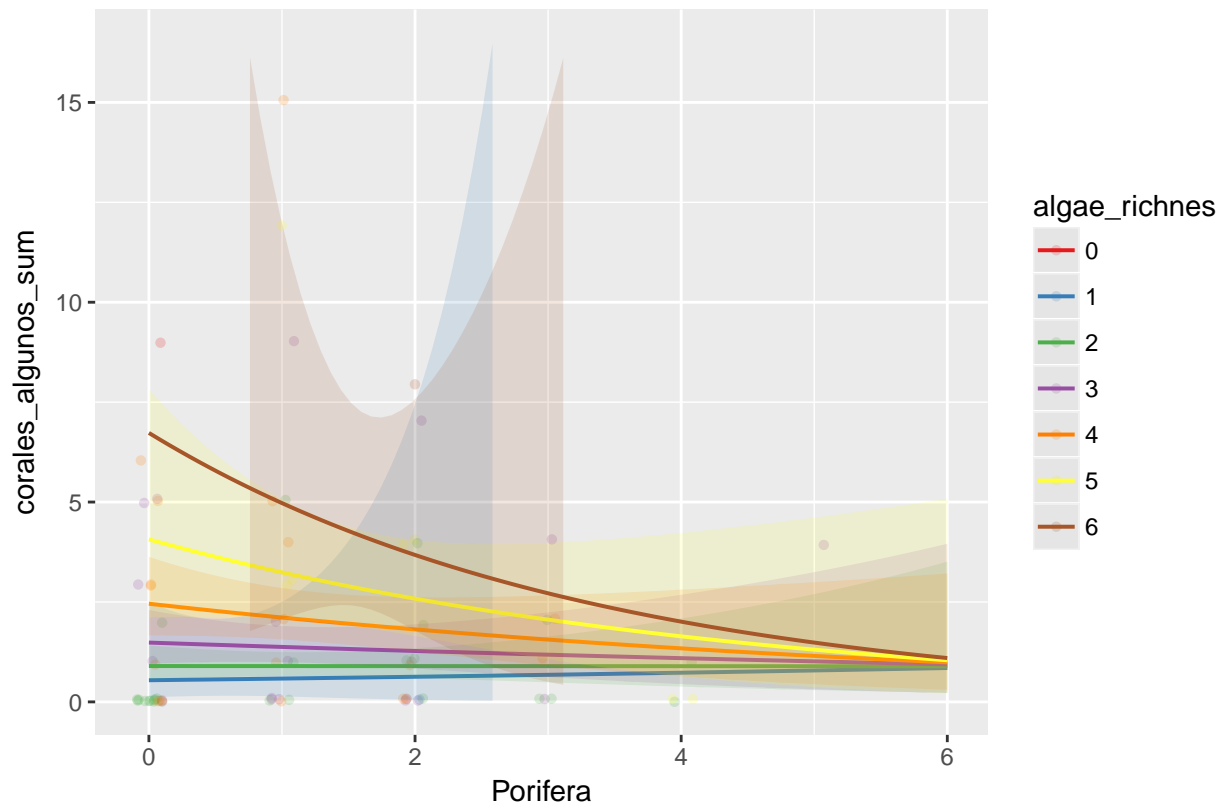
# plot predictions but not as surface
sfp.glm(glm7, type = "pred", vars = c("Porifera", "algae_richnes"), show.ci = TRUE)

```



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


Predicted incident rates



```
# sjp.glm(glm7a, type = "pred", vars = c("Polychaeta", "Crustose.algae"), show.ci = TRUE, facet.grid = FALSE)
# sjp.glm(glm7, type = "pred", vars = c("Polychaeta", "Sediment"), 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
## -----
```

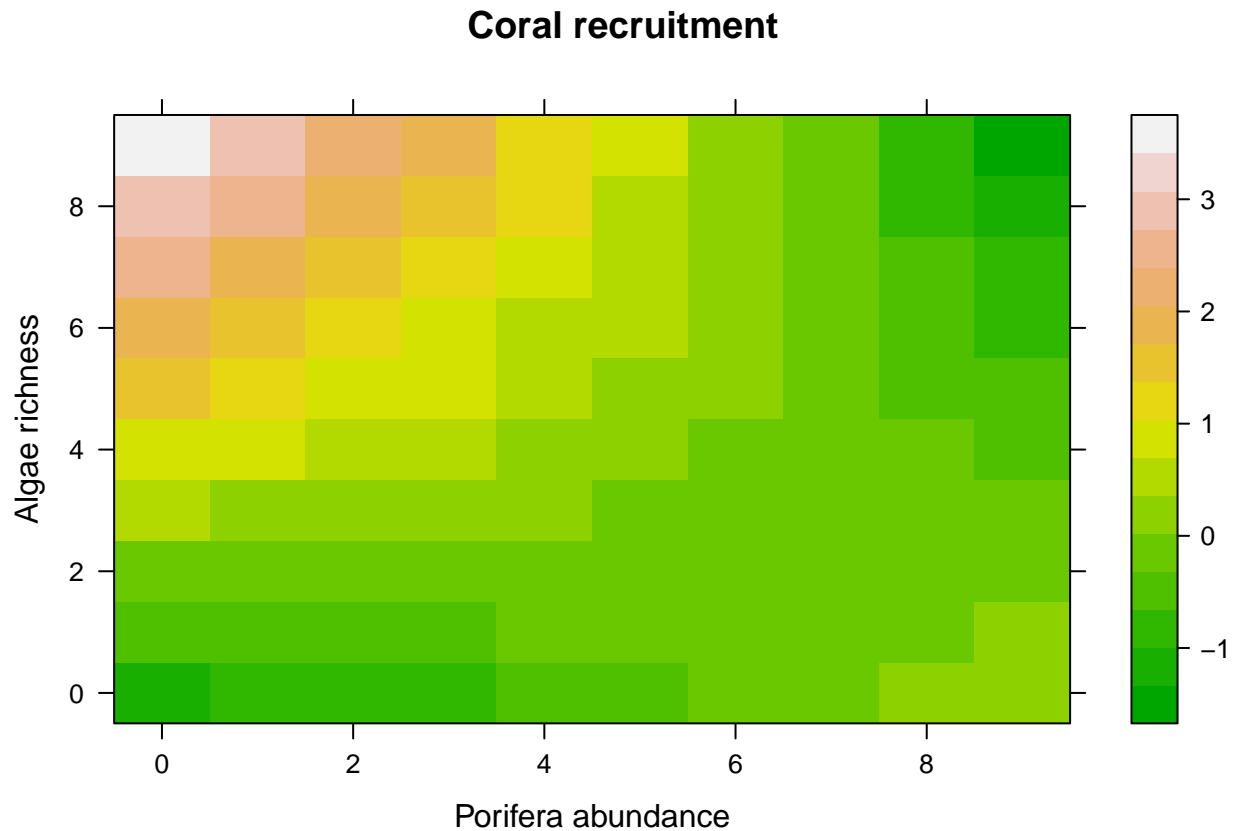
```
data(elevation)

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 recruitment",
  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("blue", "yellow", "orange", "red"))

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

##obtain original unscale values for predictors

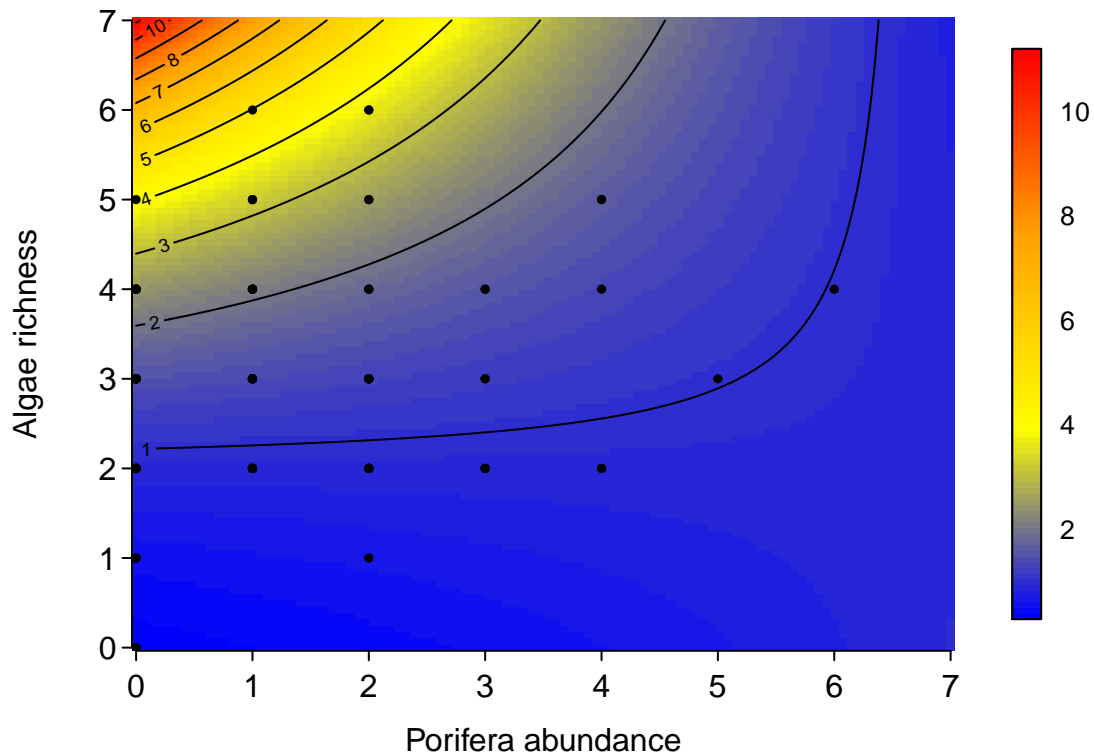
# png("BxR_FF.png", width=2000, height=1500, res=300)

#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 recruitment")
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")

```

Coral recruitment



```
# 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
```

Looking the functional groups

```
# 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)
```

```

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
# sjp.glm(glm7, type = "pred", vars = c("Sediment", "algae_richnes2"), show.ci = TRUE)
sjp.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, 6, 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

```

Explore abundance and site using mvabund package

see <http://onlinelibrary.wiley.com/doi/10.1111/j.2041-210X.2012.00190.x/full>

```
library(mvabund)
```

```
sessionInfo()
```

```

## R version 3.4.0 (2017-04-21)
## Platform: x86_64-w64-mingw32/x64 (64-bit)
## Running under: Windows 10 x64 (build 14393)
##
## Matrix products: default
##
## locale:
## [1] LC_COLLATE=Spanish_Colombia.1252 LC_CTYPE=Spanish_Colombia.1252
## [3] LC_MONETARY=Spanish_Colombia.1252 LC_NUMERIC=C
## [5] LC_TIME=Spanish_Colombia.1252
##
## attached base packages:
## [1] grid      stats      graphics  grDevices  utils      datasets  methods
## [8] base
##

```

```

## other attached packages:
## [1] mvabund_3.12.3      geoR_1.7-5.2      sjPlot_2.3.1
## [4] fields_8.15        maps_3.1.1       spam_1.4-0
## [7] lattice_0.20-35    bootStepAIC_1.2-0 MASS_7.3-47
## [10] ggplot2_2.2.1
##
## loaded via a namespace (and not attached):
## [1] tidyr_0.6.3          splines_3.4.0
## [3] merTools_0.3.0       modelr_0.1.0
## [5] shiny_1.0.3          assertthat_0.2.0
## [7] statmod_1.4.29       sp_1.2-4
## [9] highr_0.6            stats4_3.4.0
## [11] coin_1.1-3           yaml_2.1.14
## [13] backports_1.0.5      digest_0.6.12
## [15] RColorBrewer_1.1-2   minqa_1.2.4
## [17] colorspace_1.3-2     sandwich_2.3-4
## [19] htmltools_0.3.6      httpuv_1.3.3
## [21] Matrix_1.2-9         plyr_1.8.4
## [23] psych_1.7.5          broom_0.4.2
## [25] haven_1.0.0          purrr_0.2.2.2
## [27] xtable_1.8-2         mvtnorm_1.0-6
## [29] scales_0.4.1         stringdist_0.9.4.4
## [31] lme4_1.1-13          arm_1.9-3
## [33] tibble_1.3.0         effects_3.1-2
## [35] DT_0.2               TH.data_1.0-8
## [37] nnet_7.3-12          lazyeval_0.2.0
## [39] mnormt_1.5-5         survival_2.41-3
## [41] magrittr_1.5         mime_0.5
## [43] evaluate_0.10        nlme_3.1-131
## [45] foreign_0.8-67       RandomFieldsUtils_0.3.25
## [47] tools_3.4.0          multcomp_1.4-6
## [49] stringr_1.2.0        munsell_0.4.3
## [51] compiler_3.4.0       RandomFields_3.1.50
## [53] blme_1.0-4           nloptr_1.0.4
## [55] tweedie_2.2.5        htmlwidgets_0.8
## [57] tcltk_3.4.0          labeling_0.3
## [59] rmarkdown_1.5        gtable_0.2.0
## [61] codetools_0.2-15     abind_1.4-5
## [63] sjstats_0.10.0       DBI_0.6-1
## [65] reshape2_1.4.2       sjmisc_2.4.0
## [67] R6_2.2.1             splancs_2.01-40
## [69] zoo_1.8-0            knitr_1.15.1
## [71] dplyr_0.5.0          rprojroot_1.2
## [73] modeltools_0.2-21    stringi_1.1.5
## [75] parallel_3.4.0       Rcpp_0.12.10
## [77] coda_0.19-1          lmtest_0.9-35

```