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 recuits 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 ploting how many recuits 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 diferences between Localityes by an ANOVA (1) and also between sites by ANOVA (2).

Load the data set and put together tables

```
## Warning: package 'Matrix' was built under R version 3.4.1

## Warning: package 'sjPlot' was built under R version 3.4.1

## Warning: package 'dplyr' was built under R version 3.4.1

##   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
##   Ascidiacea 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 Cyanophycea
## 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.calcareus.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")
```

```
tabla_sitio <- corales %>%
     group_by(Site) %>%
     summarise (Amphipoda = as.numeric(sum(Amphipoda)),
                Anemone= as.numeric(sum(Anemone)),
                Ascidiacea = as.numeric(sum(Ascidiacea)),
                Bivalvia= as.numeric(sum(Bivalvia)),
                Branching_coralline_algae =as.numeric(sum(Branching.coralline.algae)),
                Branching_erect_algae= as.numeric(sum(Branching.erect.algae)),
                Bryozoa = as.numeric(sum(Bryozoa)),
                Coarsely.branched.algae= as.numeric(sum(Coarsely.branched.algae)),
                Crustacea= as.numeric(sum(Crustacea)),
                Crustose.algae=as.numeric(sum(Crustose.algae)),
                Cyanophycea= as.numeric(sum(Cyanophycea)),
                Echinoidea= as.numeric(sum(Echinoidea)),
                Filamentous.algae= as.numeric(sum(Filamentous.algae)),
                Foraminifera= as.numeric(sum(Foraminifera)),
                Holothuroidea= as.numeric(sum(Holothuroidea)),
                Hydrozoa= as.numeric(sum(Hydrozoa)),
                Jointed.calcareus.algae= as.numeric(sum(Jointed.calcareus.algae)),
                Mollusca= as.numeric(sum(Mollusca)),
```

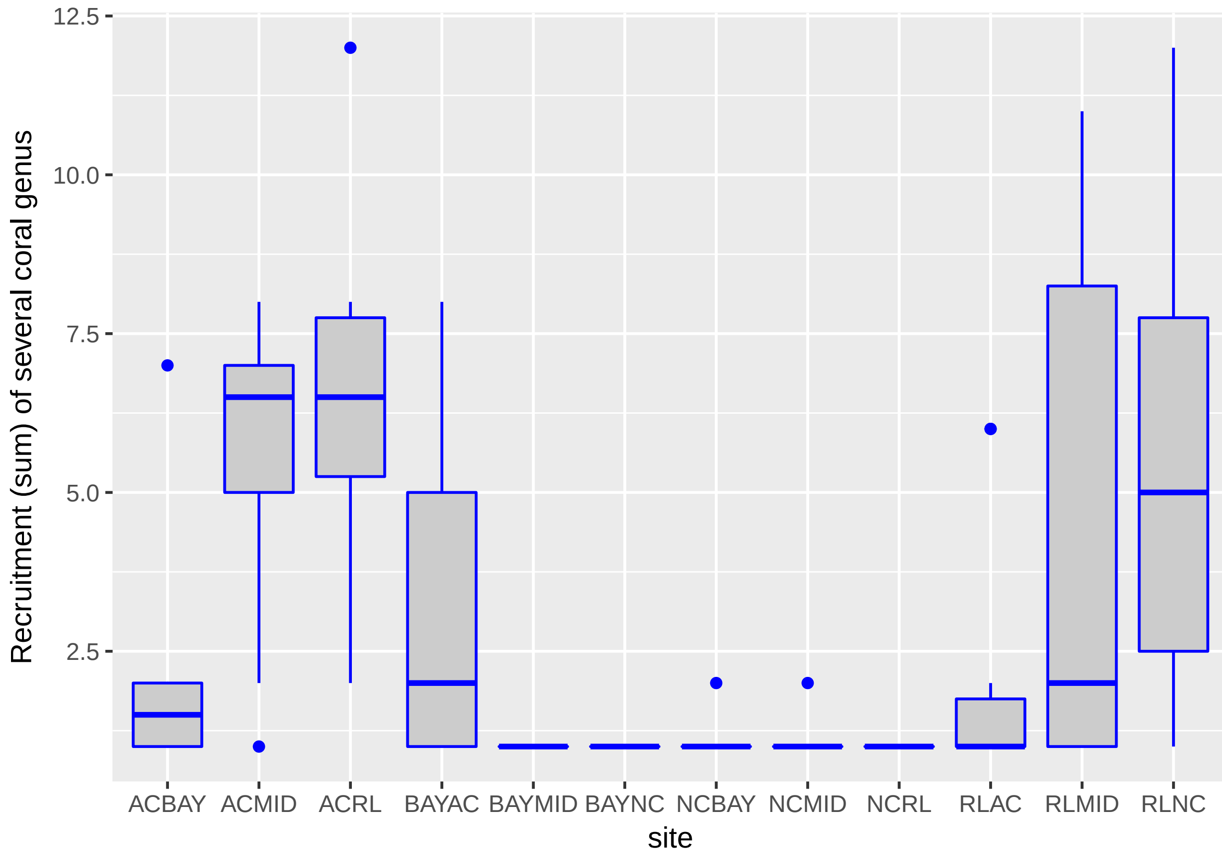


Figure 1: Sumarazing how many recuits are in the bay first agregating all corals as a sum.

```
                Patellidae=as.numeric(sum(Patellidae)),
                Polychaeta= as.numeric(sum(Polychaeta)),
                Porifera=as.numeric(sum(Porifera)),
                Sheet.like.algae= as.numeric(sum(Sheet.like.algae)),
                Sipunculidae=as.numeric(sum(Sipunculidae)),
                Thick.leathery.alga=as.numeric(sum(Thick.leathery.algae)),
                turf.algae= as.numeric(sum(turf.algae)),
                unbranched.erect.algae = as.numeric(sum(unbranched.erect.algae)),
                Vermetidae=as.numeric(sum(Vermetidae)),
                Zoanthidae = as.numeric(sum(Zoanthidae)),
                Acropora.sp.=as.numeric(sum(Acropora.sp.)),
                Agaricia.sp.=as.numeric(sum(Agaricia.sp.)),
                Faviidae=as.numeric(sum(Faviidae)),
                Porites.spp.=as.numeric(sum(Porites.spp.)),
                Siderastrea.sp.=as.numeric(sum(Siderastrea.sp.)),
                Unknown.Coral..broken.=as.numeric(sum(Unknown.Coral..broken.)),
                Unknown.Coral..too.small.=as.numeric(sum(Unknown.Coral..too.small.)))

tabla_sitio$suma <- apply(tabla_sitio[,2:32], 1, sum)
tabla_sitio[,c(1,37)]
```

```
## # A tibble: 12 x 2
##      Site  suma
##    <fctr> <dbl>
##  1      I    59
##  2     II    42
##  3    III    27
##  4     IV    56
##  5     IX    92
##  6      V    79
##  7     VI    58
##  8    VII    67
##  9   VIII    56
## 10      X    42
## 11     XI    77
## 12    XII    60
```

Testing diferences in ANOVA

as a piosson procces 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
```

```
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
```

```r
# plot(posthoc1)
```

The next graph shows how coral recruitment varies according to genus

```r
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 diferences in ANOVA

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

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

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

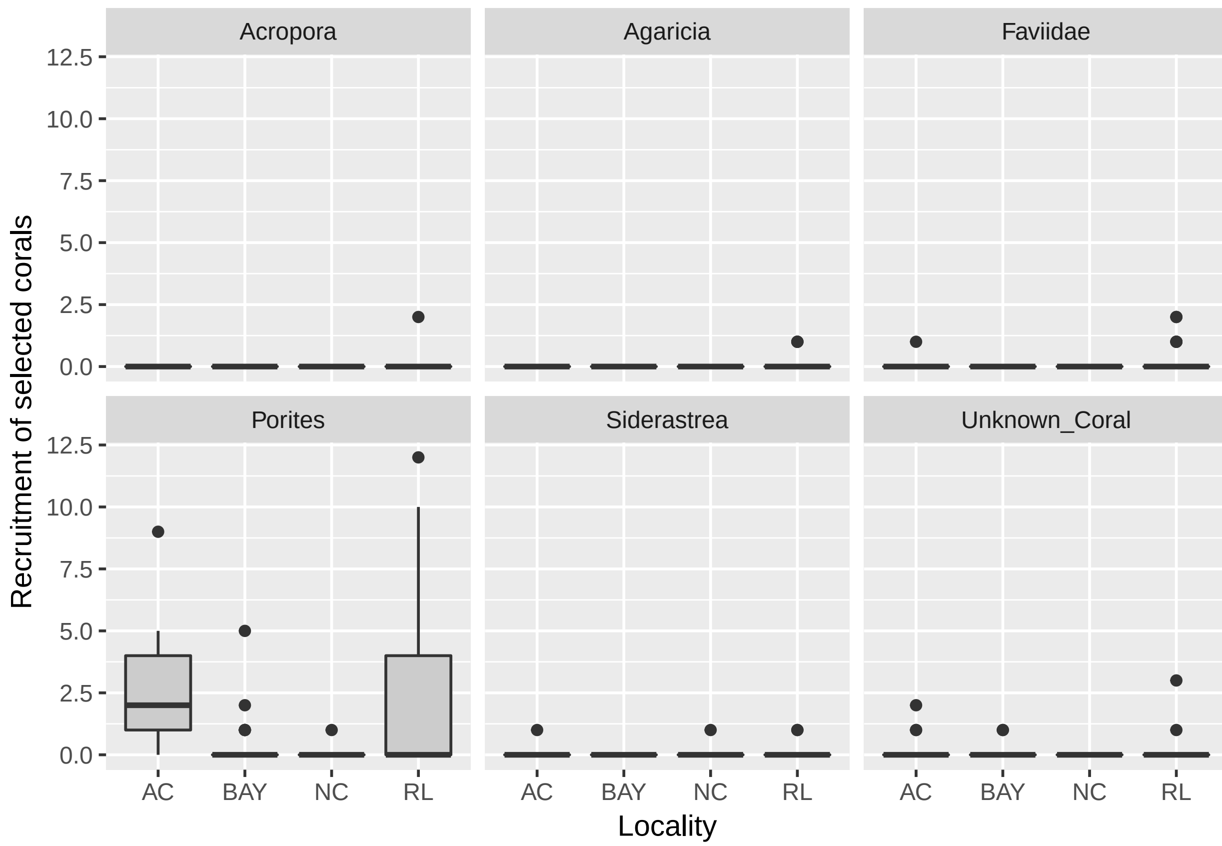


Figure 2: The second boxplot shows recruitment by locality wraped by genus

```
## 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
## Locality  3   145.93       101     237.47 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
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
```

```r
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.

```r
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
```

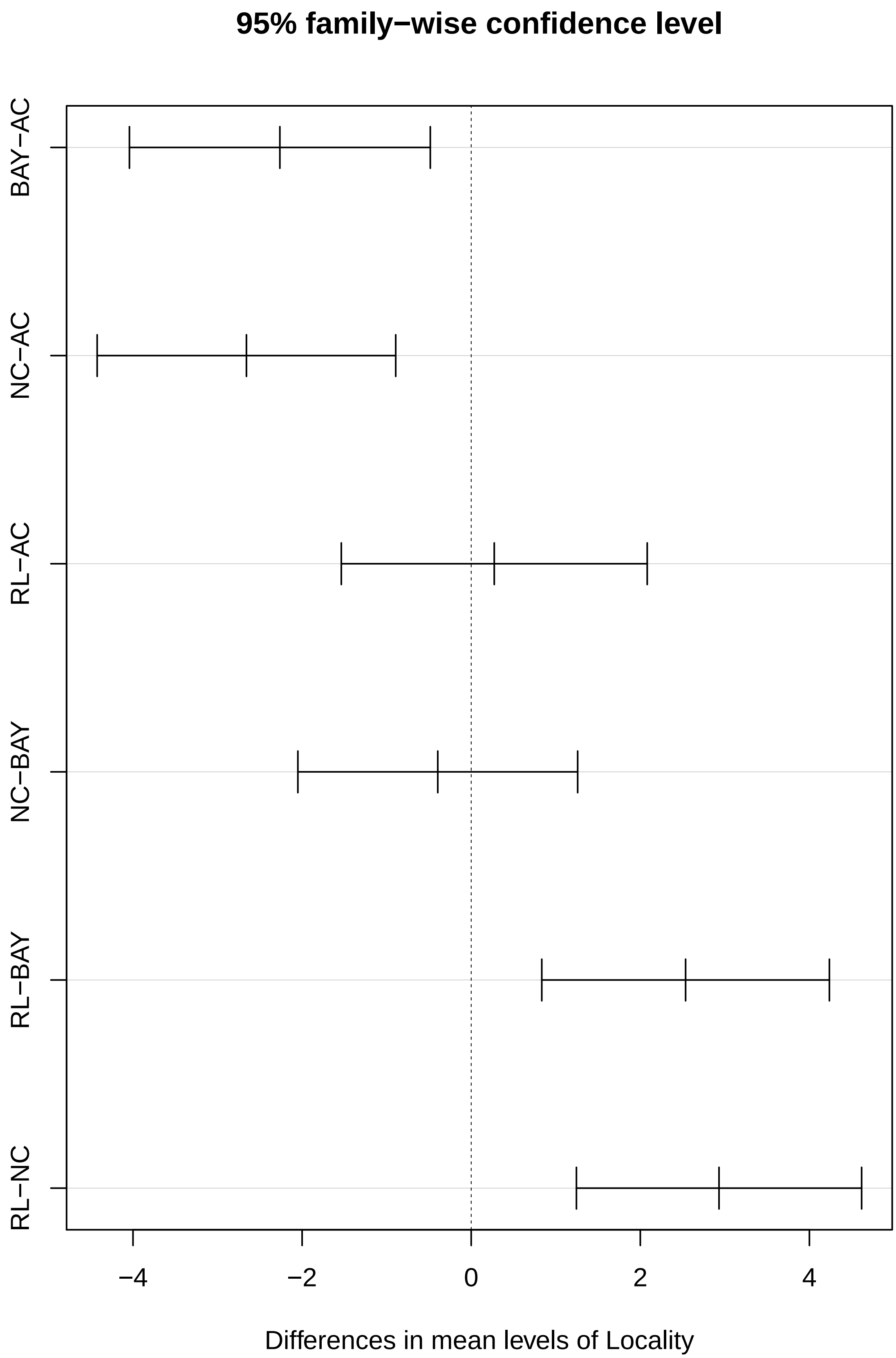


Figure 3: The graph shows the multiple comparison (Tukey test) between Localities. The pairs RL-AC and NC-BAY are not differents.

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

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = glm5)
##
## $site
##                    diff          lwr        upr     p adj
## II-I      -2.166667e-01 -0.788239582  0.35490625 0.9851738
## III-I     -2.166667e-01 -0.822911293  0.38957796 0.9908152
## IV-I      -1.981481e-01 -0.785383496  0.38908720 0.9943386
## IX-I      -1.000000e-01 -0.671572916  0.47157292 0.9999896
## V-I       -2.000000e-01 -0.771572916  0.37157292 0.9922992
## VI-I      -2.166667e-01 -0.788239582  0.35490625 0.9851738
## VII-I      8.250000e-01  0.218755373  1.43124463 0.0005848
## VIII-I     2.208333e-01 -0.385411293  0.82707796 0.9892558
## X-I        4.500000e-01 -0.209995553  1.10999555 0.5233297
## XI-I       2.833333e-01 -0.288239582  0.85490625 0.8989902
## XII-I     -5.000000e-02 -0.709995553  0.60999555 1.0000000
## III-II     1.360023e-15 -0.606244627  0.60624463 1.0000000
## IV-II      1.851852e-02 -0.568716829  0.60575387 1.0000000
## IX-II      1.166667e-01 -0.454906249  0.68823958 0.9999501
## V-II       1.666667e-02 -0.554906249  0.58823958 1.0000000
## VI-II     -5.828671e-15 -0.571572916  0.57157292 1.0000000
## VII-II     1.041667e+00  0.435422040  1.64791129 0.0000017
## VIII-II    4.375000e-01 -0.168744627  1.04374463 0.4298946
## X-II       6.666667e-01  0.006671113  1.32666222 0.0451776
## XI-II      5.000000e-01 -0.071572916  1.07157292 0.1544409
## XII-II     1.666667e-01 -0.493328887  0.82666222 0.9995955
## IV-III     1.851852e-02 -0.602514736  0.63955177 1.0000000
## IX-III     1.166667e-01 -0.489577960  0.72291129 0.9999725
## V-III      1.666667e-02 -0.589577960  0.62291129 1.0000000
## VI-III    -7.188694e-15 -0.606244627  0.60624463 1.0000000
## VII-III    1.041667e+00  0.402628720  1.68070461 0.0000082
## VIII-III   4.375000e-01 -0.201537947  1.07653795 0.5166432
## X-III      6.666667e-01 -0.023573205  1.35690654 0.0696563
## XI-III     5.000000e-01 -0.106244627  1.10624463 0.2257865
## XII-III    1.666667e-01 -0.523573205  0.85690654 0.9997373
## IX-IV      9.814815e-02 -0.489087199  0.68538350 0.9999935
## V-IV      -1.851852e-03 -0.589087199  0.58538350 1.0000000
## VI-IV     -1.851852e-02 -0.605753866  0.56871683 1.0000000
## VII-IV     1.023148e+00  0.402114894  1.64418140 0.0000060
## VIII-IV    4.189815e-01 -0.202051773  1.04001474 0.5404893
## X-IV       6.481481e-01 -0.025456993  1.32175329 0.0720875
## XI-IV      4.814815e-01 -0.105753866  1.06871683 0.2337005
## XII-IV     1.481481e-01 -0.525456993  0.82175329 0.9998948
## V-IX      -1.000000e-01 -0.671572916  0.47157292 0.9999896
## VI-IX     -1.166667e-01 -0.688239582  0.45490625 0.9999501
## VII-IX     9.250000e-01  0.318755373  1.53124463 0.0000465
## VIII-IX    3.208333e-01 -0.285411293  0.92707796 0.8507927
## X-IX       5.500000e-01 -0.109995553  1.20999555 0.2121765
## XI-IX      3.833333e-01 -0.188239582  0.95490625 0.5500477
```

```
## XII-IX    5.000000e-02 -0.609995553  0.70999555 1.0000000
## VI-V     -1.666667e-02 -0.588239582  0.55490625 1.0000000
## VII-V     1.025000e+00  0.418755373  1.63124463 0.0000028
## VIII-V    4.208333e-01 -0.185411293  1.02707796 0.4939513
## X-V       6.500000e-01 -0.009995553  1.30999555 0.0580431
## XI-V      4.833333e-01 -0.088239582  1.05490625 0.1937030
## XII-V     1.500000e-01 -0.509995553  0.80999555 0.9998546
## VII-VI    1.041667e+00  0.435422040  1.64791129 0.0000017
## VIII-VI   4.375000e-01 -0.168744627  1.04374463 0.4298946
## X-VI      6.666667e-01  0.006671113  1.32666222 0.0451776
## XI-VI     5.000000e-01 -0.071572916  1.07157292 0.1544409
## XII-VI    1.666667e-01 -0.493328887  0.82666222 0.9995955
## VIII-VII -6.041667e-01 -1.243204613  0.03487128 0.0842168
## X-VII    -3.750000e-01 -1.065239871  0.31523987 0.8272076
## XI-VII   -5.416667e-01 -1.147911293  0.06457796 0.1325710
## XII-VII  -8.750000e-01 -1.565239871 -0.18476013 0.0021465
## X-VIII    2.291667e-01 -0.461073205  0.91940654 0.9950729
## XI-VIII   6.250000e-02 -0.543744627  0.66874463 1.0000000
## XII-VIII -2.708333e-01 -0.961073205  0.41940654 0.9805407
## XI-X     -1.666667e-01 -0.826662220  0.49332889 0.9995955
## XII-X    -5.000000e-01 -1.237897461  0.23789746 0.5334277
## XII-XI   -3.333333e-01 -0.993328887  0.32666222 0.8866938
```

```
# plot(posthoc2)
```

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

Predicting recruitmentof all corals as a function of taxa and algae richness (several algae). No mater stepwise procedure

```
library(sjPlot)
```

```
## Warning: package 'sjPlot' was built under R version 3.4.1
## Install package "strengejacke" from GitHub (`devtools::install_github("strengejacke/strengejacke")`)
```

```
library(glmulti)
```

```
## Warning: package 'glmulti' was built under R version 3.4.1
## Loading required package: rJava
```

```
library(bbmle)
```

```
## Loading required package: stats4
```

```
# 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)
```

```r
glm7 <- glm(corales_algunos_sum ~  Porifera * algae_richnes, family = poisson(), data = corales)


glm8 <- glm(corales_algunos_sum ~  Polychaeta * algae_richnes, family = poisson(), data = corales)

glm9 <- glm(corales_algunos_sum ~  algae_richnes, family = poisson(), data = corales)

glm10 <- glm(corales_algunos_sum ~  Polychaeta, family = poisson(), data = corales)

glm11 <- glm(corales_algunos_sum ~  Porifera, family = poisson(), data = corales)




AICctab(glm7, glm8, glm9, glm10, glm11,
        base=T, weights=T, delta=T, sort=T,
    nobs = length(corales))
```

```
##       AICc  dAICc df weight
## glm8  441.2   0.0 4  1
## glm9  468.7  27.6 2  <0.001
## glm7  469.0  27.8 4  <0.001
## glm10 475.4  34.2 2  <0.001
## glm11 505.6  64.4 2  <0.001
```

```r
### Best Model of all!!!!!
summary(glm8)
```

```
##
## Call:
## glm(formula = corales_algunos_sum ~ Polychaeta * algae_richnes,
##     family = poisson(), data = corales)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -2.8826  -1.3873  -1.0737   0.5046   4.8439
##
## Coefficients:
##                          Estimate Std. Error z value Pr(>|z|)
## (Intercept)               0.55022    0.31770   1.732  0.08330 .
## Polychaeta               -2.12613    0.44875  -4.738 2.16e-06 ***
## algae_richnes             0.14567    0.08575   1.699  0.08935 .
## Polychaeta:algae_richnes  0.36682    0.11885   3.086  0.00203 **
## ---
## 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: 314.1  on 101  degrees of freedom
## AIC: 440.14
##
## Number of Fisher Scoring iterations: 6
```

```r
newdato <- as.data.frame(cbind(Polychaeta=rep(0:1, each = 10), algae_richnes=rep(1:8, 10)) )
predichos <- predict(glm8, newdata = newdato, type = "response")

require(geoR)
```

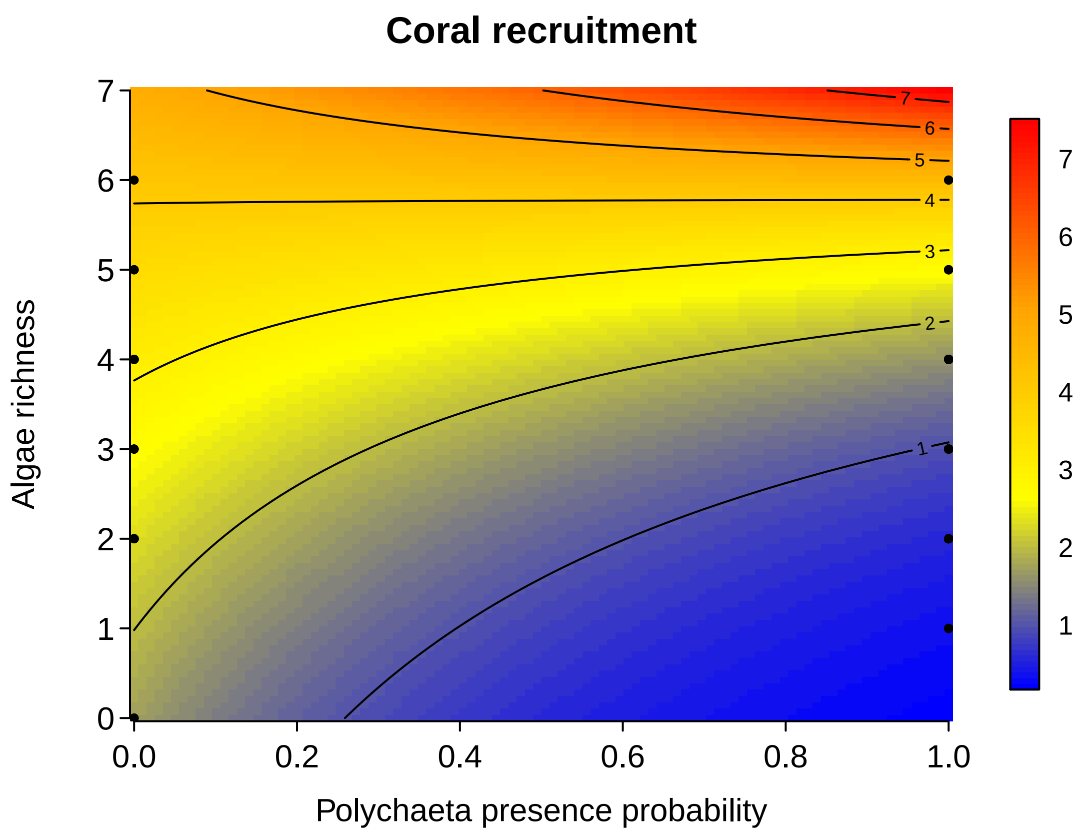
```
## Loading required package: geoR

## --------------------------------------------------------------
##  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
## --------------------------------------------------------------
```

```r
data(elevation)
library(fields)
```

```
## Warning: package 'fields' was built under R version 3.4.1

## Loading required package: spam

## Warning: package 'spam' was built under R version 3.4.1

## Loading required package: dotCall64

## Warning: package 'dotCall64' was built under R version 3.4.1

## Loading required package: grid

## Spam version 2.1-1 (2017-07-02) 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:stats4':
##
##     mle

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

## Loading required package: maps

## Warning: package 'maps' was built under R version 3.4.1
```

```r
grid = expand.grid(list(Polychaeta = seq(0, 1, 0.1), algae_richnes = seq(0, 6, 1)))

z = predict(glm8, newdata = grid)
grid$Height = as.numeric(z)

#### 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(Polychaeta=seq(0,
                                1,
                                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(glm8, newdata=data.frame(
          Polychaeta=pr.mat$Polychaeta[i],
         # mean=pr.mat$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$Polychaeta, y = pr.mat$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$Polychaeta, y = pr.mat$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, "Polychaeta presence probability", line = 1.8)
mtext(side = 2, "Algae richness", line = 2.3)

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



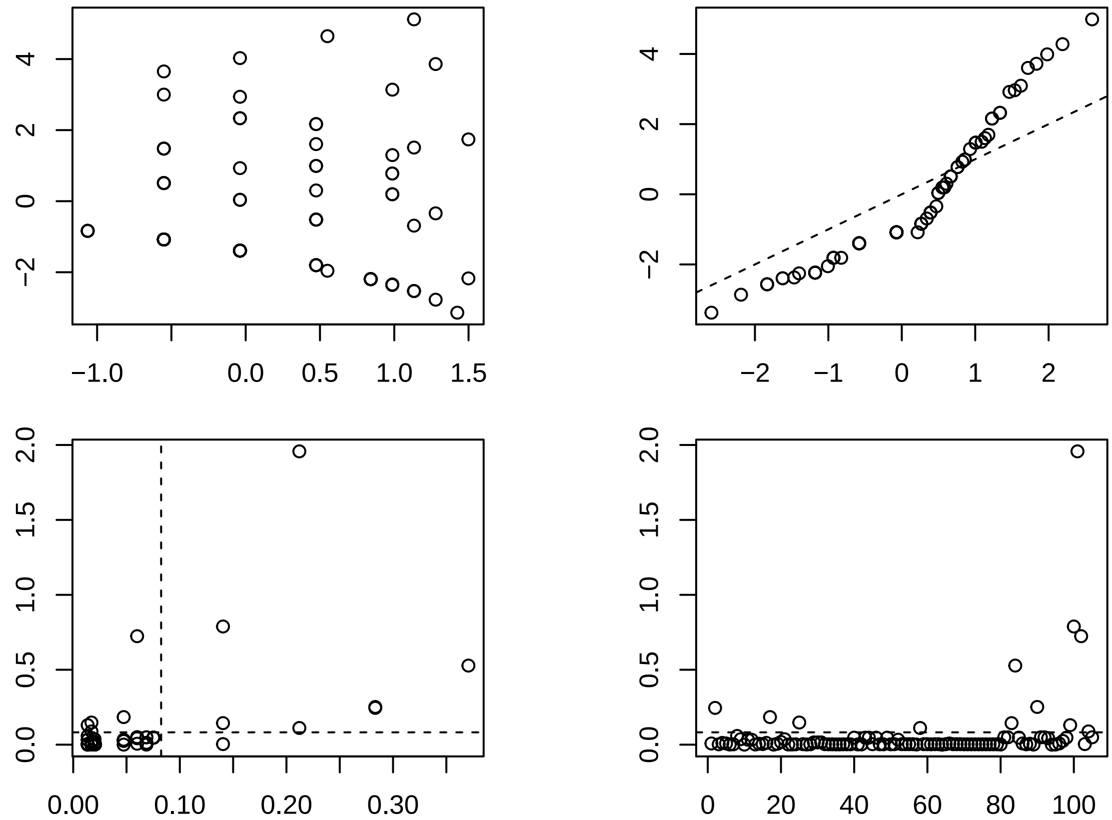

```
# dev.off()



###########################################################
###### Cross-validation for Generalized Linear Models
############################################################
library("boot")
cost <- function(r, pi = 0) mean(abs(r - pi) > 0.5)  ## cost function necessary for binomial data
m11.cv <- cv.glm(data = corales, glm8, cost, K = 10)  # use leave-one-out cross validation (can use K-f
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

# Now lets see what our error rate was:

m11.cv$delta
```

```
## [1] 0.8761905 0.8969615
```

```
## [1] 0.2381 0.2438
# That's not too bad.

muhat <- fitted(glm8)
glm8.diag <- glm.diag(glm8)
(cv.err <- mean((glm8$y - muhat)^2/(1 - glm8.diag$h)^2))
```

```
## [1] 7.37773
```

```r
glm.diag.plots(glm8, glm8.diag)
```




```r
#########################################################
## Make your reciever-operater curve
#########################################################

# library(pROC)
#
#
# m.roc <- multiclass.roc(corales$corales_algunos_sum, predict(glm8, backtransform = TRUE))
# auc(m.roc)
# ci(m.roc)
# plot(m.roc[[1]], m.roc[[2]])
# m.roc[[7]]
```

Looking the functional groups

```r
library(bootStepAIC)
```

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

```r
library(lattice)
```

```
##
## Attaching package: 'lattice'
```

```
## The following object is masked from 'package:boot':
##
##     melanoma
```

```
library(fields)
glm12 <- glm (corales_algunos_sum ~  Polychaeta +
                          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)
summary(glm12)
```

```
##
## Call:
## glm(formula = corales_algunos_sum ~ Polychaeta + 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
## -3.1999  -1.0405  -0.9955   0.2884   5.0844
##
## Coefficients:
##                           Estimate Std. Error z value Pr(>|z|)
## (Intercept)                0.20231    0.37679   0.537  0.59132
## Polychaeta                -0.61925    0.18897  -3.277  0.00105 **
## Branching.coralline.algae  0.08836    0.20624   0.428  0.66833
## Branching.erect.algae     -0.05977    0.18399  -0.325  0.74530
## Sheet.like.algae           0.28931    0.21971   1.317  0.18792
## Coarsely.branched.algae    0.22327    0.21561   1.036  0.30043
## Filamentous.algae         -0.50840    0.36830  -1.380  0.16746
## Jointed.calcareus.algae   -0.66662    1.03154  -0.646  0.51812
## Crustose.algae             1.34011    0.22838   5.868 4.41e-09 ***
## Thick.leathery.algae      -1.30084    1.09711  -1.186  0.23574
## turf.algae                 0.61372    1.03328   0.594  0.55254
## unbranched.erect.algae     0.51069    0.26958   1.894  0.05817 .
## ---
## 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: 283.24  on  93  degrees of freedom
## AIC: 425.28
##
## Number of Fisher Scoring iterations: 6
```

```
fit.boot <- boot.stepAIC(glm12, data = corales, B = 100) # That's it !
fit.boot
```

```
##
```

```
## Summary of Bootstrapping the 'stepAIC()' procedure for
##
## Call:
## glm(formula = corales_algunos_sum ~ Polychaeta + 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
## Polychaeta                 91
## Filamentous.algae          75
## unbranched.erect.algae     66
## Branching.erect.algae      55
## Sheet.like.algae           53
## Branching.coralline.algae  44
## Coarsely.branched.algae    41
## Thick.leathery.algae       37
## Jointed.calcareus.algae    17
## turf.algae                  5
##
## Coefficients Sign
##                            + (%) - (%)
## Crustose.algae            100.00  0.00
## turf.algae                100.00  0.00
## unbranched.erect.algae     90.91  9.09
## Sheet.like.algae           79.25 20.75
## Coarsely.branched.algae    78.05 21.95
## Branching.coralline.algae  63.64 36.36
## Branching.erect.algae      47.27 52.73
## Filamentous.algae          34.67 65.33
## Thick.leathery.algae       18.92 81.08
## Jointed.calcareus.algae     5.88 94.12
## Polychaeta                  5.49 94.51
##
## Stat Significance
##                             (%)
## Crustose.algae            99.00
## Polychaeta                94.51
## Sheet.like.algae          90.57
## Coarsely.branched.algae   85.37
## Branching.erect.algae     81.82
## unbranched.erect.algae    80.30
## Filamentous.algae         72.00
## turf.algae                60.00
## Branching.coralline.algae 59.09
## Thick.leathery.algae      43.24
## Jointed.calcareus.algae   17.65
```

```
##
##
## The stepAIC() for the original data-set gave
##
## Call:  glm(formula = corales_algunos_sum ~ Polychaeta + Crustose.algae +
##     unbranched.erect.algae, family = poisson(), data = corales)
##
## Coefficients:
##            (Intercept)              Polychaeta          Crustose.algae
##              -0.006194               -0.684486                1.348262
## unbranched.erect.algae
##               0.446796
##
## Degrees of Freedom: 104 Total (i.e. Null);  101 Residual
## Null Deviance:       383.4
## Residual Deviance: 288.1     AIC: 414.1
##
## Stepwise Model Path
## Analysis of Deviance Table
##
## Initial Model:
## corales_algunos_sum ~ Polychaeta + 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 ~ Polychaeta + Crustose.algae + unbranched.erect.algae
##
##
##                          Step Df  Deviance Resid. Df Resid. Dev      AIC
## 1                                                93   283.2358 425.2789
## 2     - Branching.erect.algae  1 0.1059986        94   283.3418 423.3849
## 3 - Branching.coralline.algae  1 0.1694701        95   283.5113 421.5543
## 4                - turf.algae  1 0.3897017        96   283.9010 419.9440
## 5   - Jointed.calcareus.algae  1 0.5019514        97   284.4029 418.4460
## 6   - Coarsely.branched.algae  1 0.7938597        98   285.1968 417.2398
## 7         - Filamentous.algae  1 1.2159133        99   286.4127 416.4558
## 8      - Thick.leathery.algae  1 0.8027077       100   287.2154 415.2585
## 9          - Sheet.like.algae  1 0.8462370       101   288.0617 414.1047
```

Los Polychaeta y las algas de tipo: - Branching.erect.algae
- Branching.coralline.algae
- turf.algae
- Jointed.calcareus.algae
- Coarsely.branched.algae
- Filamentous.algae
- Thick.leathery.algae
- Sheet.like.algae

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

Crustose.algae + unbranched.erect.algae SI son buenas predictoras

```
glm13 <- glm(corales_algunos_sum ~  Polychaeta + Crustose.algae + unbranched.erect.algae, family = pois
```

```r
glm14 <- glm(corales_algunos_sum ~  Polychaeta + Crustose.algae, family = poisson(), data = corales)

glm15 <- glm(corales_algunos_sum ~  Crustose.algae + unbranched.erect.algae, family = poisson(), data =

glm16 <- glm(corales_algunos_sum ~  Polychaeta + unbranched.erect.algae, family = poisson(), data = cora

AICctab(glm13, glm14, glm15, glm16,
        base=T, weights=T, delta=T, sort=T,
    nobs = length(corales))
```

```
##       AICc  dAICc df  weight
## glm13 415.1   0.0 4  0.53
## glm14 415.4   0.3 3  0.47
## glm15 428.5  13.4 3  <0.001
## glm16 466.8  51.6 3  <0.001
```

```r
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      stats4    stats     graphics  grDevices utils     datasets
## [8] methods   base
##
## other attached packages:
##  [1] lattice_0.20-35   bootStepAIC_1.2-0 MASS_7.3-47
##  [4] boot_1.3-19       fields_9.0        maps_3.2.0
##  [7] spam_2.1-1        dotCall64_0.9-04  geoR_1.7-5.2
## [10] bbmle_1.0.19      glmulti_1.0.7     rJava_0.9-8
## [13] sjPlot_2.3.3      ggplot2_2.2.1
##
## loaded via a namespace (and not attached):
##  [1] RandomFieldsUtils_0.3.25 nlme_3.1-131
##  [3] rprojroot_1.2            numDeriv_2016.8-1
##  [5] tools_3.4.0              TMB_1.7.11
##  [7] backports_1.1.0          R6_2.2.2
##  [9] DT_0.2                   sjlabelled_1.0.1
## [11] lazyeval_0.2.0           colorspace_1.3-2
## [13] nnet_7.3-12              sp_1.2-5
## [15] splancs_2.01-40          mnormt_1.5-5
## [17] compiler_3.4.0           RandomFields_3.1.50
## [19] sandwich_2.4-0           labeling_0.3
## [21] effects_3.1-2            scales_0.4.1
## [23] lmtest_0.9-35            mvtnorm_1.0-6
## [25] psych_1.7.5              blme_1.0-4
```

```
## [27] stringr_1.2.0           digest_0.6.12
## [29] foreign_0.8-67          minqa_1.2.4
## [31] rmarkdown_1.6           stringdist_0.9.4.6
## [33] pkgconfig_2.0.1         htmltools_0.3.6
## [35] lme4_1.1-13             highr_0.6
## [37] pwr_1.2-1               htmlwidgets_0.9
## [39] rlang_0.1.2             shiny_1.0.5
## [41] bindr_0.1               zoo_1.8-0
## [43] dplyr_0.7.2             magrittr_1.5
## [45] modeltools_0.2-21       Matrix_1.2-11
## [47] Rcpp_0.12.12            munsell_0.4.3
## [49] abind_1.4-5             stringi_1.1.5
## [51] multcomp_1.4-6          yaml_2.1.14
## [53] merTools_0.3.0          plyr_1.8.4
## [55] parallel_3.4.0          sjmisc_2.6.1
## [57] forcats_0.2.0           haven_1.1.0
## [59] splines_3.4.0           sjstats_0.11.0
## [61] knitr_1.17              tcltk_3.4.0
## [63] reshape2_1.4.2          codetools_0.2-15
## [65] glue_1.1.1              evaluate_0.10.1
## [67] modelr_0.1.1            nloptr_1.0.4
## [69] httpuv_1.3.5            gtable_0.2.0
## [71] purrr_0.2.3             tidyr_0.7.0
## [73] assertthat_0.2.0        mime_0.5
## [75] coin_1.2-1              xtable_1.8-2
## [77] broom_0.4.2             coda_0.19-1
## [79] survival_2.41-3         tibble_1.3.4
## [81] arm_1.9-3               glmmTMB_0.1.1
## [83] bindrcpp_0.2            TH.data_1.0-8
```