Corales reclutamiento

Diego L. Lizcano

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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

1. 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)

1. 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).

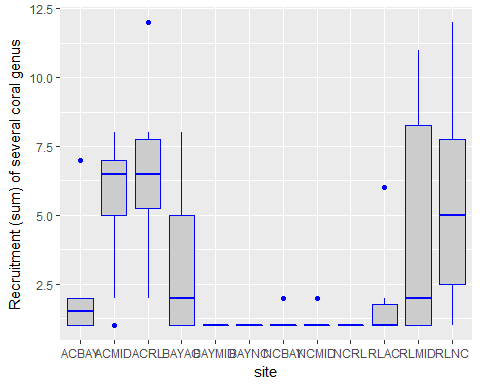
## Load the data set and put together tables

## 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")



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

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)),  
 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

tabla\_Locality <- corales %>%   
 group\_by(Locality) %>%   
 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)),  
 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.)))

## Testing diferences by ANOVA

### diferences in coral recruitment by a piosson procces determined by genus

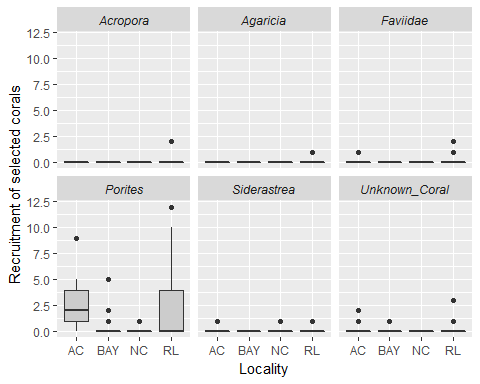
glm2 <- glm(formula = recruitment ~ genus, family = poisson(),data = corales\_algunos3)  
model2 <- aov(glm2)  
summary(model2)

## Df Sum Sq Mean Sq F value Pr(>F)   
## genus 5 115.9 23.18 23.4 <2e-16 \*\*\*  
## Residuals 624 618.0 0.99   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

# glm3 <- glm (corales\_algunos\_sum ~ Site\_name, family = poisson(), data = corales)  
  
# summary(glm1)  
# summary(glm2)  
# summary(glm3)  
# anova(glm3, test = "Chisq")  
# anova1 <- aov(glm3)  
# (posthoc1 <- TukeyHSD(x=anova1, "Site\_name", conf.level=0.95))  
# 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") +  
 theme(strip.text.x = element\_text(face = "italic"))



The second boxplot shows recruitment by locality wraped by genus

## Testing diferences 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)  
summary(glm4)

##   
## Call:  
## glm(formula = corales\_algunos\_sum ~ Locality, family = poisson(),   
## data = corales)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -2.4495 -0.9636 -0.3714 0.1625 4.9278   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) 1.00330 0.12910 7.772 7.75e-15 \*\*\*  
## LocalityBAY -1.77056 0.30592 -5.788 7.14e-09 \*\*\*  
## LocalityNC -3.67745 0.71880 -5.116 3.12e-07 \*\*\*  
## LocalityRL 0.09531 0.17172 0.555 0.579   
## ---  
## 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: 237.47 on 101 degrees of freedom  
## AIC: 363.51  
##   
## Number of Fisher Scoring iterations: 6

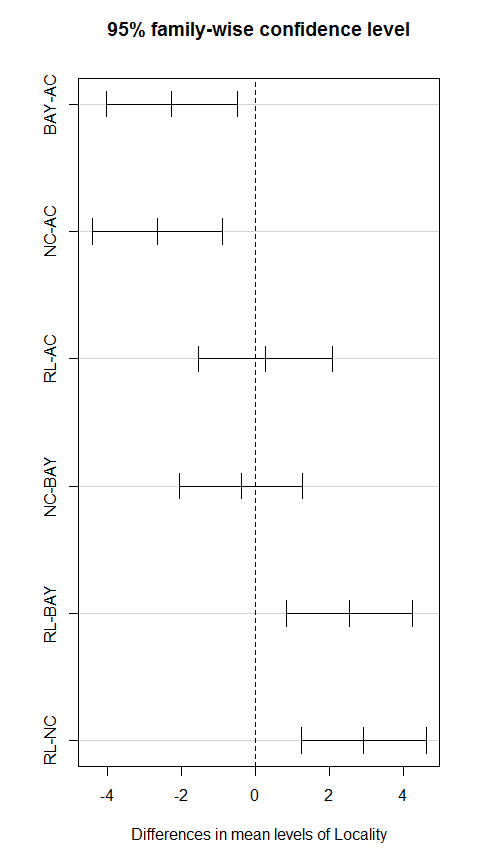
anova(glm4, test = "Chisq")

## 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   
## 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)



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

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, "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

# 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)  
  
glm9 <- glm(corales\_algunos\_sum ~ algae\_richnes, family = poisson(), data = corales)  
  
glm11 <- glm(corales\_algunos\_sum ~ Porifera, family = poisson(), data = corales)  
  
glm13 <- glm(corales\_algunos\_sum ~ Porifera \* Filamentous.algae, family = poisson(), data = corales)  
  
glm14 <- glm(corales\_algunos\_sum ~ Porifera \* Crustose.algae, family = poisson(), data = corales)   
  
glm15 <- glm(corales\_algunos\_sum ~ Porifera \* Thick.leathery.algae, family = poisson(), data = corales)  
  
glm16 <- glm(corales\_algunos\_sum ~ Porifera \* unbranched.erect.algae, family = poisson(), data = corales)  
  
glm17 <- glm(corales\_algunos\_sum ~ Porifera \* Sheet.like.algae, family = poisson(), data = corales)  
  
  
  
  
AICctab(glm7, glm9, glm11, glm13, glm14, glm15, glm16, glm17,   
 base=T, weights=T, delta=T, sort=T,  
 nobs = length(corales))

## AICc dAICc df weight  
## glm14 431.2 0.0 4 1   
## glm9 468.2 37.0 2 <0.001  
## glm7 468.4 37.2 4 <0.001  
## glm17 473.2 42.0 4 <0.001  
## glm16 492.6 61.4 4 <0.001  
## glm11 505.6 74.4 2 <0.001  
## glm13 506.3 75.1 4 <0.001  
## glm15 507.7 76.5 3 <0.001

### Best Model of all!!!!!  
summary(glm14)

##   
## Call:  
## glm(formula = corales\_algunos\_sum ~ Porifera \* Crustose.algae,   
## family = poisson(), data = corales)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -2.5316 -1.0801 -1.0801 0.1385 5.6937   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -5.390e-01 2.304e-01 -2.340 0.0193 \*   
## Porifera -3.923e-14 1.565e-01 0.000 1.0000   
## Crustose.algae 1.704e+00 2.628e-01 6.481 9.09e-11 \*\*\*  
## Porifera:Crustose.algae -1.470e-01 1.717e-01 -0.856 0.3920   
## ---  
## 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: 304.12 on 101 degrees of freedom  
## AIC: 430.17  
##   
## Number of Fisher Scoring iterations: 7

newdato <- as.data.frame(cbind(Porifera=rep(0:6, each = 10), Crustose.algae=rep(0:1, 10)) )

## Warning in cbind(Porifera = rep(0:6, each = 10), Crustose.algae =  
## rep(0:1, : number of rows of result is not a multiple of vector length (arg  
## 2)

predichos <- predict(glm14, 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  
## --------------------------------------------------------------

data(elevation)  
library(fields)

## Loading required package: spam

## Loading required package: dotCall64

## 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'

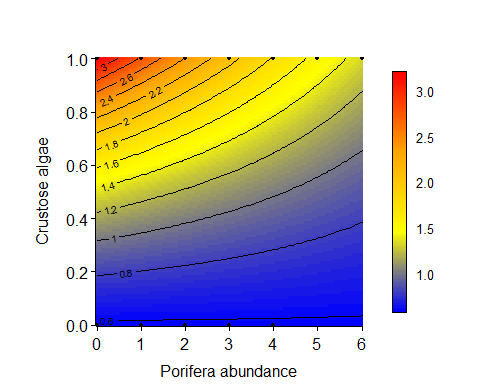
## The following object is masked from 'package:stats4':  
##   
## mle

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

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

## Loading required package: maps

grid = expand.grid(list(Porifera = seq(0, 6, 1), Crustose.algae = seq(0, 1, 0.1)))  
  
z = predict(glm14, 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(Porifera=seq(0,   
 6,   
 length.out=100),  
 Crustose.algae=seq(0, 1,   
 length.out=100))  
  
for(i in 1:100){  
 for(j in 1:100){  
 psi.matrix[i, j]<-predict(glm14, newdata=data.frame(  
 Porifera=pr.mat$Porifera[i],  
 # mean=pr.mat$mean[j]),   
 # range=pr.mat$range[j]),   
 Crustose.algae=pr.mat$Crustose.algae[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$Porifera, y = pr.mat$Crustose.algae , 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$Porifera, y = pr.mat$Crustose.algae, 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, "Crustose algae", line = 2.3)  
  
points(corales$Porifera, corales$Crustose.algae, pch=19, cex=0.5,   
 col="black")



# dev.off()  
  
  
  
########################################################  
###### Cross-validation for Generalized Linear Models  
#########################################################  
library("boot")

##   
## Attaching package: 'boot'

## The following object is masked from 'package:lattice':  
##   
## melanoma

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

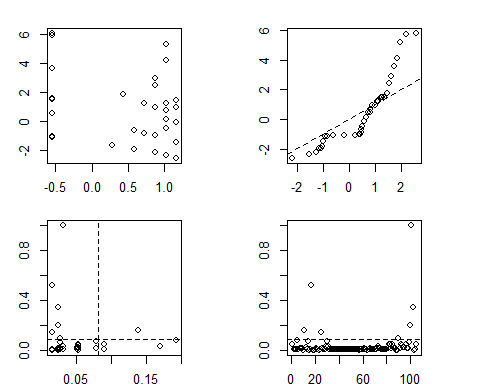
cost <- function(r, pi = 0) mean(abs(r - pi) > 0.5) ## cost function necessary for binomial data  
m11.cv <- cv.glm(data = corales, glm14, cost, K = 10) # use leave-one-out cross validation (can use K-fold cross validation for larger data sets)  
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred  
  
# Now lets see what our error rate was:  
  
m11.cv$delta

## [1] 0.8190476 0.9009524

## [1] 0.2381 0.2438  
# That’s not too bad.  
  
muhat <- fitted(glm14)  
glm14.diag <- glm.diag(glm14)  
(cv.err <- mean((glm14$y - muhat)^2/(1 - glm14.diag$h)^2))

## [1] 6.509953

glm.diag.plots(glm14, glm14.diag)



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

library(bootStepAIC)  
library(lattice)  
library(fields)  
glm12 <- glm (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)  
summary(glm12)

##   
## 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 + unbranched.erect.algae,   
## family = poisson(), data = corales)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -2.9424 -1.1191 -1.0393 0.1091 5.7792   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) 0.23048 0.37855 0.609 0.5426   
## Porifera -0.12900 0.06960 -1.853 0.0638 .   
## Branching.coralline.algae 0.16533 0.20074 0.824 0.4102   
## Branching.erect.algae 0.01898 0.18890 0.101 0.9199   
## Sheet.like.algae 0.33464 0.21815 1.534 0.1250   
## Coarsely.branched.algae 0.08891 0.20467 0.434 0.6640   
## Filamentous.algae -0.80654 0.36187 -2.229 0.0258 \*   
## Jointed.calcareus.algae -0.78402 1.03065 -0.761 0.4468   
## Crustose.algae 1.34484 0.22834 5.890 3.87e-09 \*\*\*  
## Thick.leathery.algae -2.07530 1.08126 -1.919 0.0549 .   
## unbranched.erect.algae 0.60255 0.26474 2.276 0.0228 \*   
## ---  
## 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: 290.28 on 94 degrees of freedom  
## AIC: 430.33  
##   
## 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 ~ 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 + 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 69  
## Branching.erect.algae 55  
## Porifera 55  
## Sheet.like.algae 52  
## Branching.coralline.algae 45  
## Coarsely.branched.algae 41  
## Thick.leathery.algae 39  
## Jointed.calcareus.algae 23  
##   
## Coefficients Sign  
## + (%) - (%)  
## Crustose.algae 100.00 0.00  
## unbranched.erect.algae 89.86 10.14  
## Branching.coralline.algae 88.89 11.11  
## Sheet.like.algae 88.46 11.54  
## Coarsely.branched.algae 82.93 17.07  
## Branching.erect.algae 56.36 43.64  
## Filamentous.algae 41.46 58.54  
## Porifera 10.91 89.09  
## Thick.leathery.algae 2.56 97.44  
## Jointed.calcareus.algae 0.00 100.00  
##   
## Stat Significance  
## (%)  
## Crustose.algae 98.00  
## unbranched.erect.algae 85.51  
## Sheet.like.algae 84.62  
## Branching.erect.algae 80.00  
## Thick.leathery.algae 79.49  
## Coarsely.branched.algae 75.61  
## Porifera 72.73  
## Filamentous.algae 69.51  
## Branching.coralline.algae 55.56  
## Jointed.calcareus.algae 13.04  
##   
##   
## 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 + 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 94 290.2823 430.3253  
## 2 - Branching.erect.algae 1 0.01008517 95 290.2924 428.3354  
## 3 - Coarsely.branched.algae 1 0.18968388 96 290.4821 426.5251  
## 4 - Branching.coralline.algae 1 0.53745281 97 291.0195 425.0626  
## 5 - Jointed.calcareus.algae 1 0.49083957 98 291.5104 423.5534

Los Porifera y las algas de tipo: 2 - Branching.erect.algae  
3 - Coarsely.branched.algae  
4 - turf.algae  
5 - Branching.coralline.algae  
6 - Jointed.calcareus.algae

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

Sheet.like.algae + Filamentous.algae + Crustose.algae + Thick.leathery.algae + unbranched.erect.algae SI son buenas predictoras

sessionInfo()

## R version 3.3.3 (2017-03-06)  
## Platform: x86\_64-w64-mingw32/x64 (64-bit)  
## Running under: Windows 10 x64 (build 14393)  
##   
## 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] bootStepAIC\_1.2-0 boot\_1.3-18 fields\_9.0   
## [4] maps\_3.2.0 spam\_2.1-1 dotCall64\_0.9-04   
## [7] geoR\_1.7-5.2 bbmle\_1.0.20 glmulti\_1.0.7   
## [10] rJava\_0.9-9 bindrcpp\_0.2 readr\_1.1.1   
## [13] vegan\_2.4-4 lattice\_0.20-34 permute\_0.9-4   
## [16] ggplot2\_2.2.1 dplyr\_0.7.4 sjPlot\_2.4.0.9000  
## [19] arm\_1.9-3 MASS\_7.3-45 nlme\_3.1-131   
## [22] lme4\_1.1-14 Matrix\_1.2-8   
##   
## loaded via a namespace (and not attached):  
## [1] RandomFieldsUtils\_0.3.25 rprojroot\_1.2   
## [3] numDeriv\_2016.8-1 tools\_3.3.3   
## [5] TMB\_1.7.11 backports\_1.1.1   
## [7] R6\_2.2.2 sjlabelled\_1.0.5   
## [9] DT\_0.2 lazyeval\_0.2.1   
## [11] mgcv\_1.8-17 colorspace\_1.3-2   
## [13] nnet\_7.3-12 sp\_1.2-5   
## [15] splancs\_2.01-40 tidyselect\_0.2.3   
## [17] mnormt\_1.5-5 RandomFields\_3.1.50   
## [19] sandwich\_2.4-0 labeling\_0.3   
## [21] effects\_4.0-0 scales\_0.5.0   
## [23] lmtest\_0.9-35 mvtnorm\_1.0-6   
## [25] psych\_1.7.8 blme\_1.0-4   
## [27] stringr\_1.2.0 digest\_0.6.12   
## [29] foreign\_0.8-67 minqa\_1.2.4   
## [31] rmarkdown\_1.7 stringdist\_0.9.4.6   
## [33] pkgconfig\_2.0.1 htmltools\_0.3.6   
## [35] highr\_0.6 pwr\_1.2-1   
## [37] htmlwidgets\_0.9 rlang\_0.1.4   
## [39] shiny\_1.0.5 bindr\_0.1   
## [41] zoo\_1.8-0 magrittr\_1.5   
## [43] modeltools\_0.2-21 bayesplot\_1.4.0   
## [45] Rcpp\_0.12.13 munsell\_0.4.3   
## [47] abind\_1.4-5 prediction\_0.2.0   
## [49] stringi\_1.1.5 multcomp\_1.4-8   
## [51] yaml\_2.1.14 merTools\_0.3.0   
## [53] snakecase\_0.5.1 carData\_3.0-0   
## [55] plyr\_1.8.4 parallel\_3.3.3   
## [57] sjmisc\_2.6.2 forcats\_0.2.0   
## [59] ggeffects\_0.2.2 haven\_1.1.0   
## [61] splines\_3.3.3 hms\_0.3   
## [63] sjstats\_0.12.0 knitr\_1.17   
## [65] tcltk\_3.3.3 reshape2\_1.4.2   
## [67] codetools\_0.2-15 glue\_1.2.0   
## [69] evaluate\_0.10.1 modelr\_0.1.1   
## [71] nloptr\_1.0.4 httpuv\_1.3.5   
## [73] gtable\_0.2.0 purrr\_0.2.4   
## [75] tidyr\_0.7.2 assertthat\_0.2.0   
## [77] mime\_0.5 coin\_1.2-1   
## [79] xtable\_1.8-2 broom\_0.4.2   
## [81] survey\_3.32-1 coda\_0.19-1   
## [83] survival\_2.40-1 tibble\_1.3.4   
## [85] glmmTMB\_0.1.4 cluster\_2.0.5   
## [87] TH.data\_1.0-8