Corales reclutamiento

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Coral and recruitment

Load the data set

```r
library(lme4)
library(nlme)
library(arm)
library(sjPlot)

# read data set
library(readr)
corales <- read_delim("C:/Users/diego.lizcano/Box Sync/CodigoR/Nancy2/data/corales2.csv",
                      ";", escape_double = FALSE, trim_ws = TRUE)

corales$all <- apply(corales[,35:41], 1, sum)
```
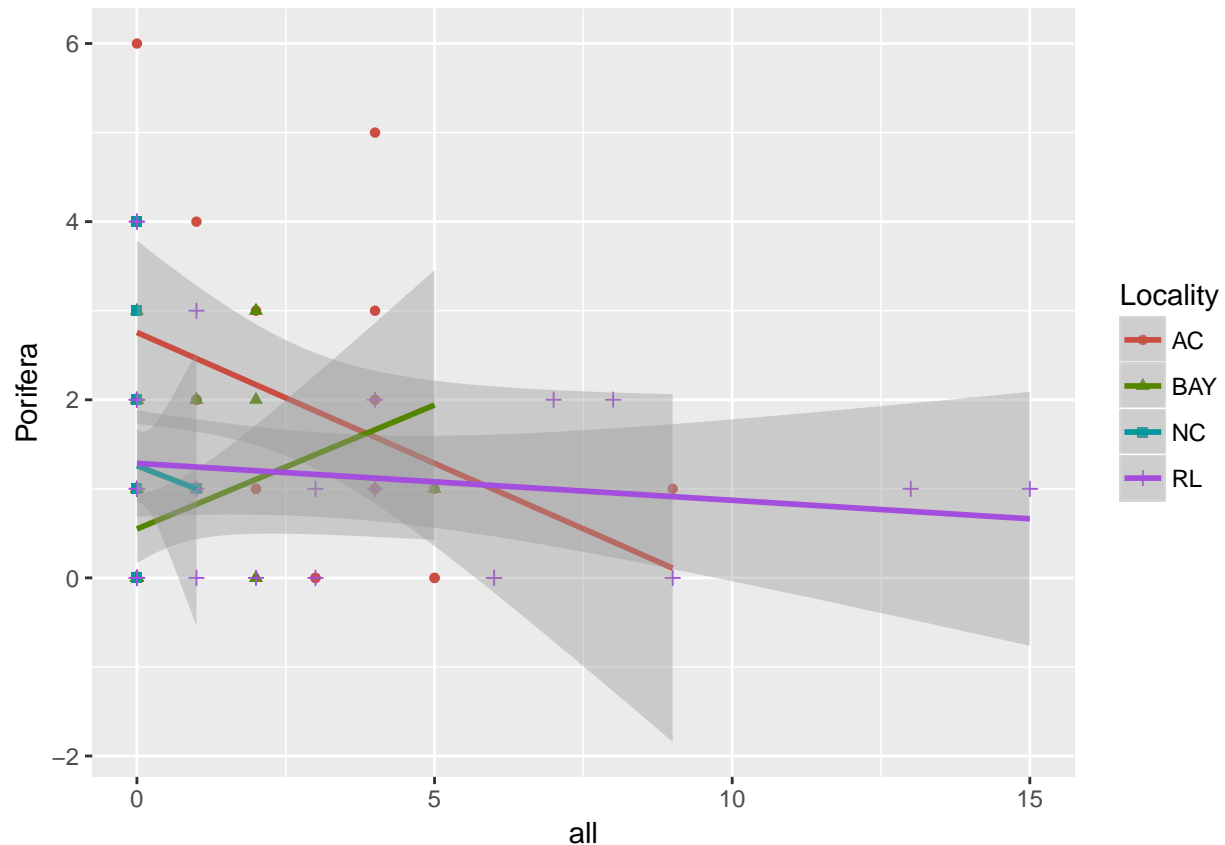
See the lineal trends by locality

```r
library(ggplot2)

# Same, but with different colors and add regression lines
ggplot(corales, aes(x=all, y=Porifera, color=Locality, shape=Locality)) +
    geom_point() +
    scale_colour_hue(l=50) + # Use a slightly darker palette than normal
    geom_smooth(method=glm,    # Add linear regression lines
                se=TRUE)# , fullrange=TRUE)    # Don't add shaded confidence region
```

Explaining Porifera recruitment as traditional GLM

as a piosson procces determined by coral recruitment and site - locality name (factor)

```
glm1 <- glm (all ~ Site_name ,family = poisson(), data = corales)
glm2 <- glm (Porifera ~ all + Site_name, family = poisson(), data = corales) # <Poisson log
glm3 <- glm (Porifera ~ all + Locality + (Locality:all) , data = corales) # <Poisson log

# summary(glm1)
summary(glm2)
```

```
##
## Call:
## glm(formula = Porifera ~ all + Site_name, family = poisson(),
##     data = corales)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.9923  -0.7746  -0.1875   0.4034   2.0466
##
## Coefficients:
##                 Estimate Std. Error z value Pr(>|z|)
## (Intercept)      1.16932    0.23908   4.891    1e-06 ***
## all             -0.07623    0.04663  -1.635 0.102095
## Site_nameACMID  -0.25516    0.33723  -0.757 0.449259
## Site_nameACRL   -1.06498    0.52070  -2.045 0.040828 *
```

```
## Site_nameBAYAC      -0.60633     0.34385  -1.763 0.077837 .
## Site_nameBAYMID     -2.37330     0.62489  -3.798 0.000146 ***
## Site_nameBAYNC     -18.47191 1226.07317  -0.015 0.987980
## Site_nameNCBAY      -1.97206     0.55389  -3.560 0.000370 ***
## Site_nameNCMID      -0.75649     0.35142  -2.153 0.031345 *
## Site_nameNCRL       -0.63869     0.34056  -1.875 0.060737 .
## Site_nameRLAC       -0.77568     0.35642  -2.176 0.029533 *
## Site_nameRLMID      -1.66927     0.55636  -3.000 0.002697 **
## Site_nameRLNC       -0.34347     0.41138  -0.835 0.403756
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 156.072  on 104  degrees of freedom
## Residual deviance:  93.333  on  92  degrees of freedom
## AIC: 282.24
##
## Number of Fisher Scoring iterations: 15
```

summary(glm3)

```
##
## Call:
## glm(formula = Porifera ~ all + Locality + (Locality:all), data = corales)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.8744  -0.9127  -0.2593   0.7407   3.4197
##
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)      2.75641    0.40969   6.728 1.20e-09 ***
## all             -0.29402    0.11695  -2.514  0.01358 *
## LocalityBAY     -2.20711    0.47886  -4.609 1.23e-05 ***
## LocalityNC      -1.49715    0.47087  -3.180  0.00198 **
## LocalityRL      -1.47002    0.50654  -2.902  0.00459 **
## all:LocalityBAY  0.57246    0.24043   2.381  0.01922 *
## all:LocalityNC   0.03476    0.89156   0.039  0.96898
## all:LocalityRL   0.25250    0.12998   1.943  0.05496 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 1.454657)
##
##     Null deviance: 173.96  on 104  degrees of freedom
## Residual deviance: 141.10  on  97  degrees of freedom
## AIC: 347.01
##
## Number of Fisher Scoring iterations: 2
```
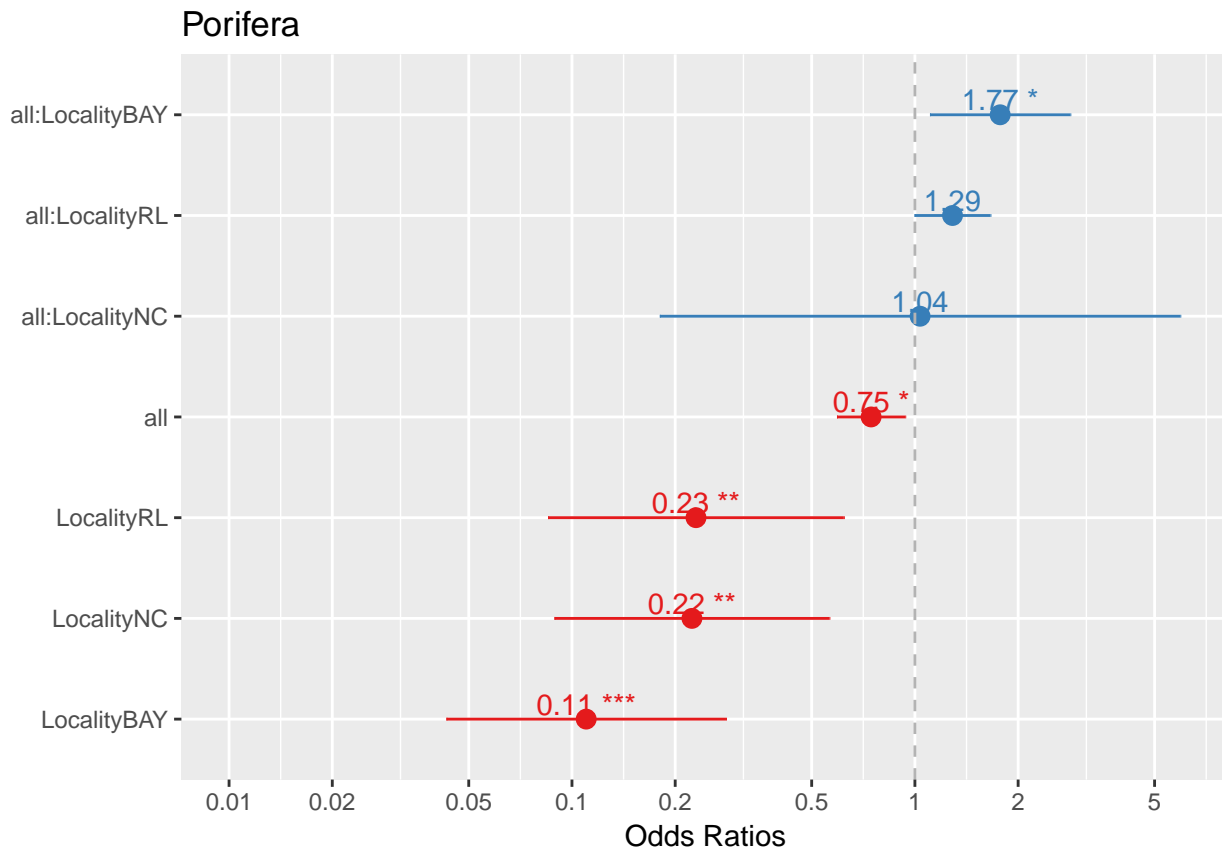
Analizing the trend

Plot odds or incident rate ratios with confidence intervalls as dot plot

```
sjp.glm(glm3,  type = "dots")
```

```
## Waiting for profiling to be done...
```

```
## Warning in sjp.glm(glm3, type = "dots"): Exp. coefficients and/or exp.
## confidence intervals may be out of printable bounds. Consider using
## `axis.lim` argument!
```



```
sjp.glm(glm3, type = "slope", show.ci = TRUE, facet.grid = FALSE, vars = "all")
```

Predicted effects for Porifera
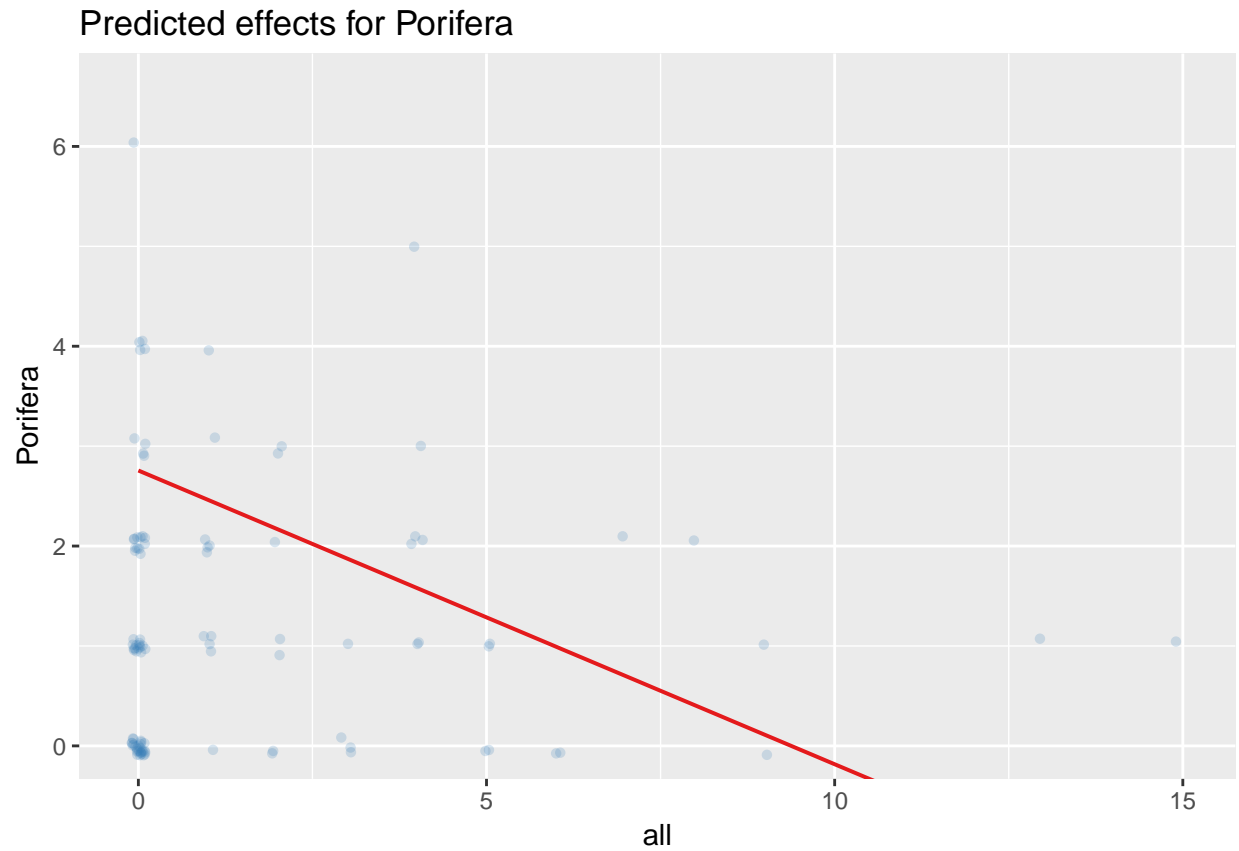

```
# sjp.glm(glm3, type = "eff")
# sjp.glm(glm3, type = "pred", vars = "all", show.ci = TRUE)

sjp.glm(glm3, type = "pred", vars = "all",
        facet.grid = FALSE, show.ci = TRUE, scatter.plot = FALSE,
        axis.lim = c(0, 4))
```

Predicted values