Modelos lineales y aditivos en ecología

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Modelos lineales generalizados

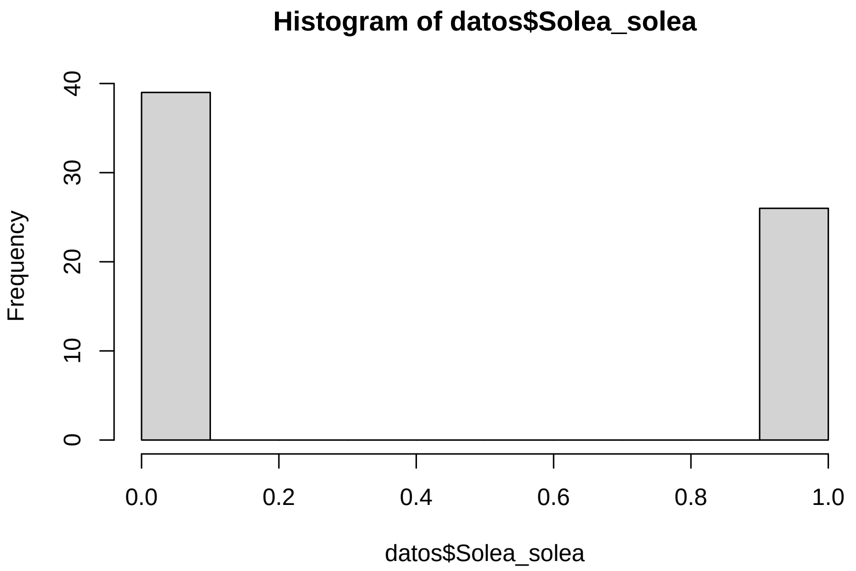
Datos de presencia-ausencia

Cabral et al. (2007) estudiaron la distribución de platijas (*Solea solea*) en el estuario Tagus, Portugal (`Solea.txt`). Se desea saber qué factores (temperatura, transparencia, salinidad) están relacionados con la presencia esta especie.

```
# Analisis exploratorio
datos <- read.table("Solea.txt", header = TRUE)
str(datos)
```

```
## ’data.frame':    65 obs. of  13 variables:
##  $ Sample       : int  1 2 3 4 5 6 7 8 9 10 ...
##  $ season       : int  1 1 1 1 1 1 1 1 1 1 ...
##  $ month        : int  5 5 5 5 5 5 5 5 5 5 ...
##  $ Area         : int  2 2 2 4 4 4 3 3 3 1 ...
##  $ depth        : num  3 2.6 2.6 2.1 3.2 3.5 1.6 1.7 1.8 4.5 ...
##  $ temperature  : int  20 18 19 20 20 20 19 17 19 21 ...
##  $ salinity     : int  30 29 30 29 30 32 29 28 29 12 ...
##  $ transparency : int  15 15 15 15 15 7 15 10 10 35 ...
##  $ gravel       : num  3.74 1.94 2.88 11.06 9.87 ...
##  $ large_sand   : num  13.15 4.99 8.98 11.96 28.6 ...
##  $ med_fine_sand: num  11.93 5.43 16.85 21.95 19.49 ...
##  $ mud          : num  71.2 87.6 71.3 55 42 ...
##  $ Solea_solea  : int  0 0 1 0 0 0 1 1 0 1 ...
```

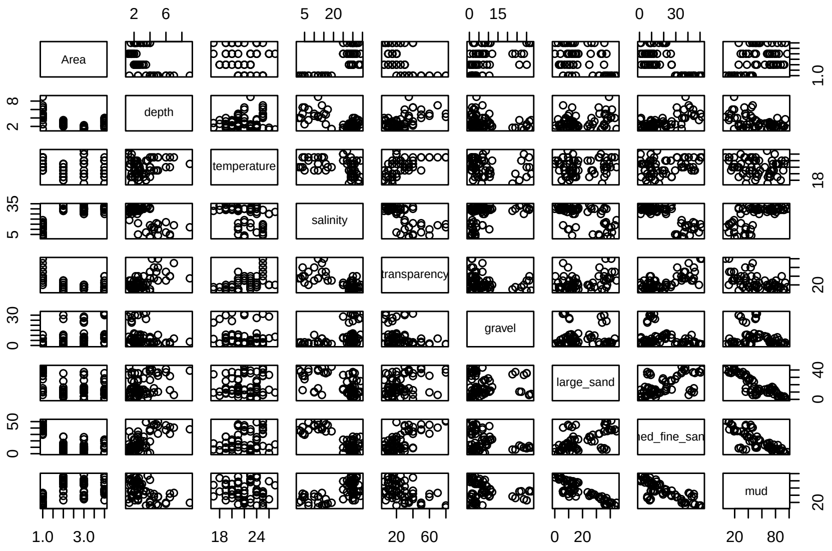
```
hist(datos$Solea_solea)
```



```
table(datos$Solea_solea)
```

```
##
##  0  1
## 39 26
```

```
pairs(datos[, 4:12])
```



```
round(cor(datos[, 4:12]), 2)
```

```
##                Area depth temperature salinity transparency gravel large_sand
## Area           1.00 -0.55       -0.18     0.76        -0.56   0.44      -0.44
## depth         -0.55  1.00        0.14    -0.66         0.57  -0.24       0.31
## temperature   -0.18  0.14        1.00    -0.35         0.54  -0.16       0.12
## salinity       0.76 -0.66       -0.35     1.00        -0.66   0.38      -0.54
## transparency  -0.56  0.57        0.54    -0.66         1.00  -0.25       0.37
## gravel         0.44 -0.24       -0.16     0.38        -0.25   1.00       0.01
## large_sand    -0.44  0.31        0.12    -0.54         0.37   0.01       1.00
## med_fine_sand -0.69  0.67        0.25    -0.80         0.69  -0.32       0.56
## mud            0.49 -0.47       -0.16     0.63        -0.52  -0.19      -0.87
##               med_fine_sand   mud
## Area                  -0.69  0.49
## depth                  0.67 -0.47
## temperature            0.25 -0.16
## salinity              -0.80  0.63
## transparency           0.69 -0.52
## gravel                -0.32 -0.19
## large_sand             0.56 -0.87
## med_fine_sand          1.00 -0.78
## mud                   -0.78  1.00
```

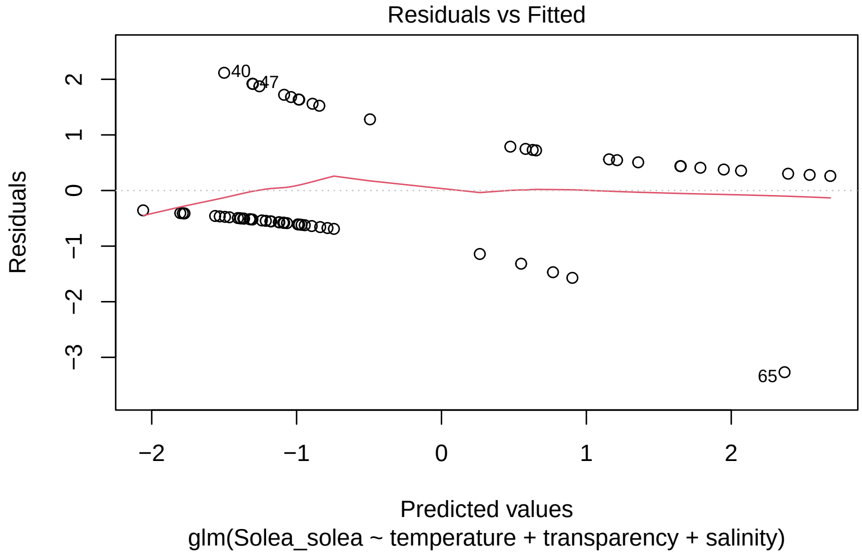
GLM binomial

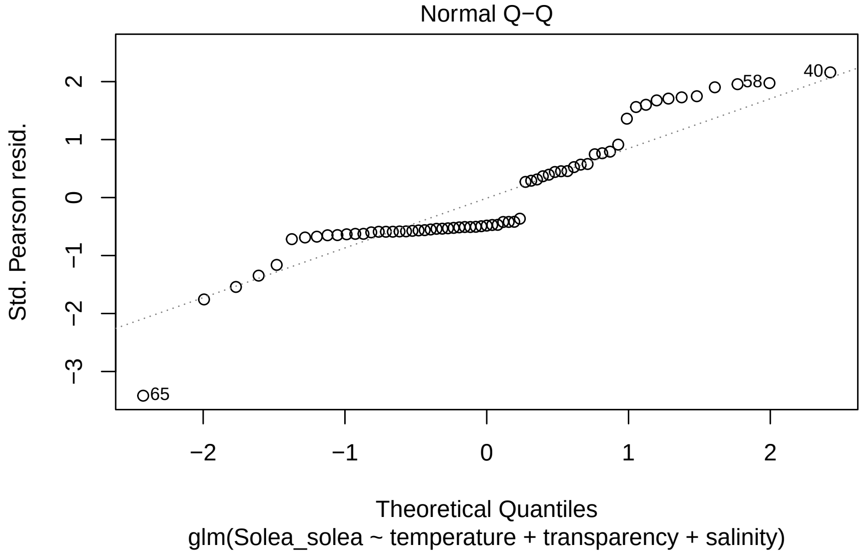
```
m.bin <- glm(Solea_solea ~ temperature + transparency + salinity, family = binomial, da
summary(m.bin)
```

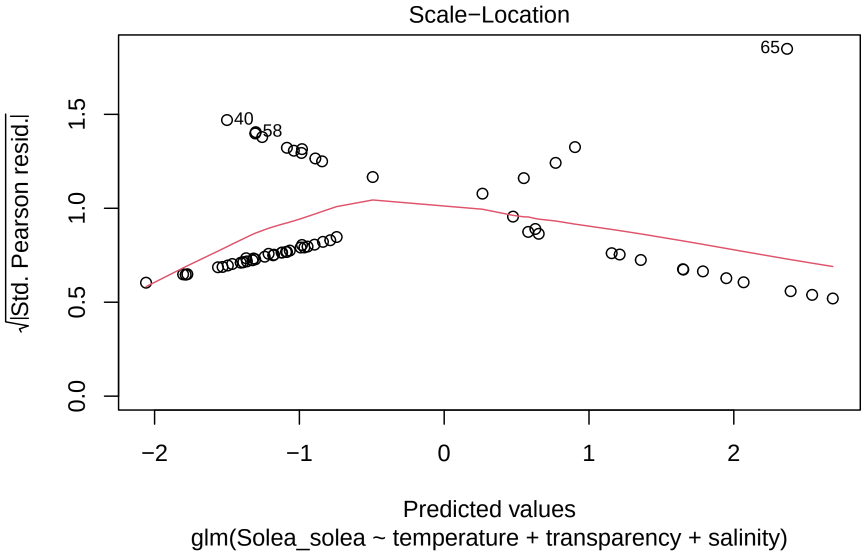
```
##
## Call:
## glm(formula = Solea_solea ~ temperature + transparency + salinity,
##     family = binomial, data = datos)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -2.2170  -0.7607  -0.6364   0.7219   1.8447
##
## Coefficients:
##               Estimate Std. Error z value Pr(>|z|)
## (Intercept)   5.221629   3.524358   1.482  0.13845
## temperature  -0.100542   0.148829  -0.676  0.49932
## transparency -0.001162   0.025347  -0.046  0.96343
## salinity     -0.142652   0.049986  -2.854  0.00432 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 87.492  on 64  degrees of freedom
## Residual deviance: 67.973  on 61  degrees of freedom
## AIC: 75.973
##
## Number of Fisher Scoring iterations: 4
```

Diagnósticos

```
plot(m.bin)
```

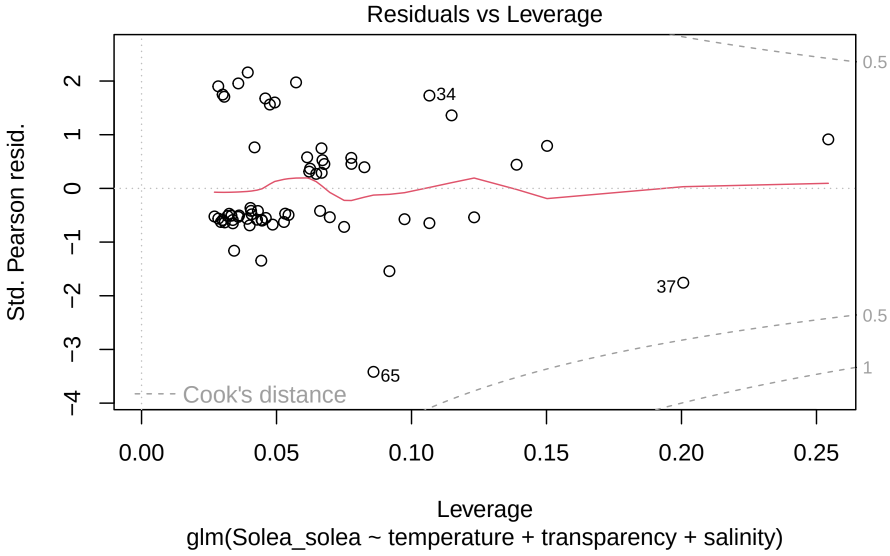

Residuals vs Fitted
Residuals
2
1
0
−1
−2
−3
40
47
65
−2
−1
0
1
2
Predicted values
glm(Solea_solea ~ temperature + transparency + salinity)


Normal Q−Q
Std. Pearson resid.
2
1
0
−1
−2
−3
40
58
65
−2
−1
0
1
2
Theoretical Quantiles
glm(Solea_solea ~ temperature + transparency + salinity)

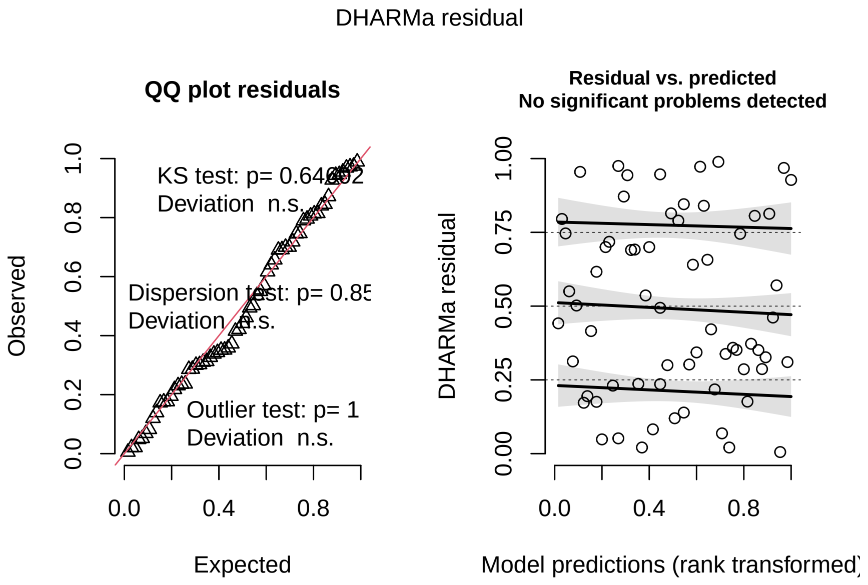


```
library(DHARMa)
```

```
## This is DHARMa 0.4.5. For overview type ’?DHARMa’. For recent changes, type news(pac
```



```
plot(simulateResiduals(fittedModel = m.bin))
```



Bondad del ajuste

```
summary(m.bin)
```

```
##
## Call:
## glm(formula = Solea_solea ~ temperature + transparency + salinity,
##     family = binomial, data = datos)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -2.2170  -0.7607  -0.6364   0.7219   1.8447
##
## Coefficients:
##               Estimate Std. Error z value Pr(>|z|)
## (Intercept)   5.221629   3.524358   1.482  0.13845
## temperature  -0.100542   0.148829  -0.676  0.49932
## transparency -0.001162   0.025347  -0.046  0.96343
## salinity     -0.142652   0.049986  -2.854  0.00432 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 87.492  on 64  degrees of freedom
## Residual deviance: 67.973  on 61  degrees of freedom
## AIC: 75.973
##
## Number of Fisher Scoring iterations: 4
```

```
# Pseudo-R2
1 - (m.bin$dev/m.bin$null)
```

```
## [1] 0.2230856
```

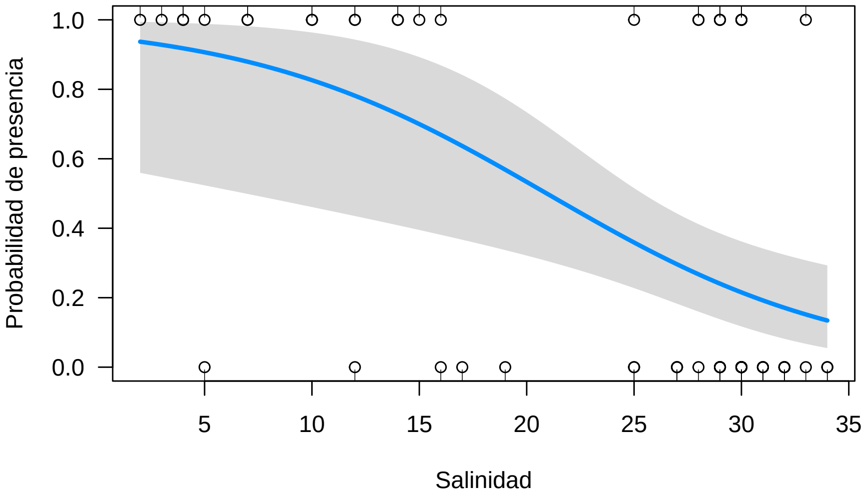
```
library(performance)

# Coeficiente de determinación de Tjur
r2_tjur(m.bin)
```

```
## Tjur's R2
## 0.2840808
```

Gráfico del modelo

```
library(visreg)
visreg(fit = m.bin, xvar = "salinity", scale = "response", ylim = c(0, 1),
       xlab = "Salinidad", ylab = "Probabilidad de presencia")
points(datos$salinity, datos$Solea_solea)
```



Interpretación de los coeficientes

```
exp(m.bin$coeff[2]) # Razon de odds
```

```
## temperature
##   0.9043472
```

Esto quiere decir que, por unidad de salinidad, la relacion $\frac{P(presencia)}{P(ausencia)}$ (odd) disminuye en 0.90 unidades

Ecuación

```
library(equatiomatic)
extract_eq(m.bin, use_coefs = TRUE, fix_signs = TRUE)
```

$$\log\left[\frac{P(\widehat{\text{Solea\_solea}} = 1)}{1 - P(\widehat{\text{Solea\_solea}} = 1)}\right] = 5.22 - 0.1(\text{temperature}) + 0(\text{transparency}) - 0.14(\text{salinity}) \tag{1}$$

Capacidad predictiva

```
# Matriz de confusión
obs <- datos$Solea_solea
pred <- ifelse(predict(m.bin, type = "response")>0.5, 1, 0)
matriz.conf <- table(obs, pred)
matriz.conf
```

```
##    pred
## obs  0  1
##   0 34  5
##   1 11 15
```

```
# Porcentajes de clasificación
matriz.conf/rowSums(matriz.conf)
```

```
##    pred
## obs         0         1
##   0 0.8717949 0.1282051
##   1 0.4230769 0.5769231
```

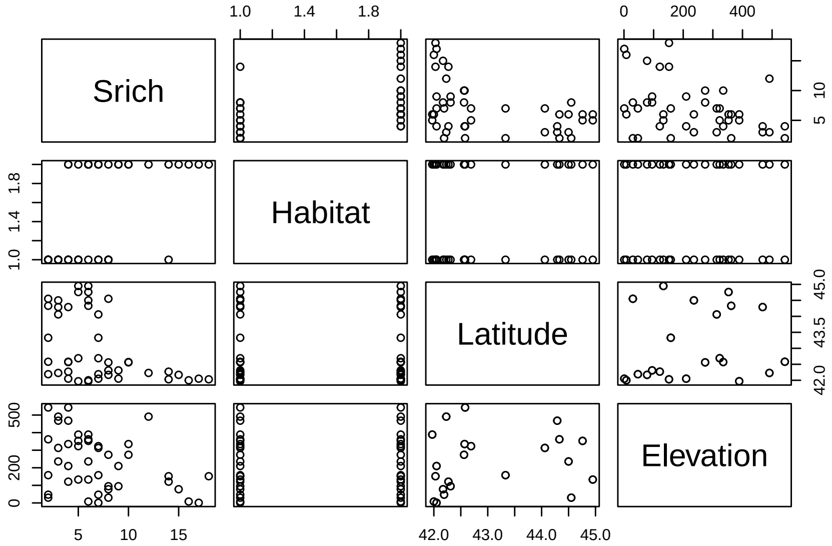
Conteos I

Gotelli & Ellison (2002) analizaron los determinantes biogeográficos de la riqueza de hormigas (`Srich`) a escala regional (`hormigas.txt`). Para esto se describieron el tipo de hábitat (`Habitat`), la latitud (`Latitude`) y la altitud (`Elevation`).

```
# Análisis exploratorio
h <- read.table("hormigas.txt", header = T)
str(h)
```

```
## ’data.frame’:    44 obs. of  5 variables:
##  $ Site     : chr  "TPB" "HBC" "CKB" "SKP" ...
##  $ Srich    : int  6 16 18 17 9 15 7 12 14 9 ...
##  $ Habitat  : chr  "Forest" "Forest" "Forest" "Forest" ...
##  $ Latitude : num  42 42 42 42 42 ...
##  $ Elevation: int  389 8 152 1 210 78 47 491 121 95 ...
```

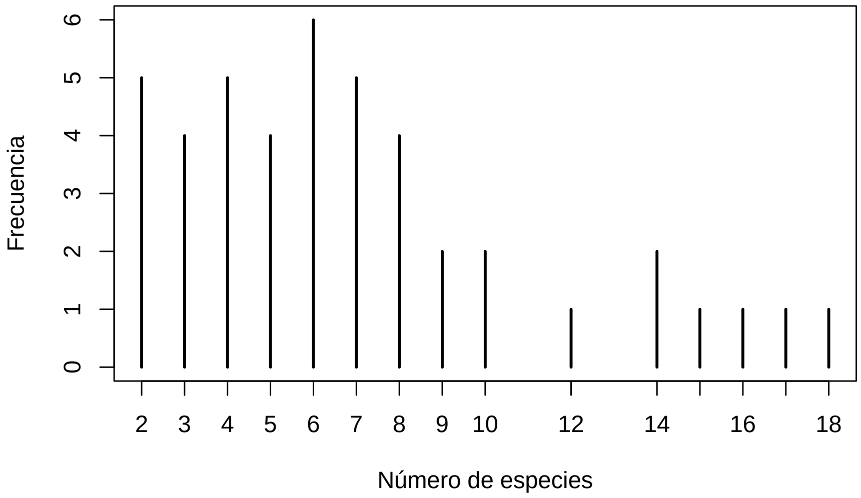
```
h$Habitat <- as.factor(h$Habitat)
pairs(h[, 2:5])
```



```r
round(cor(h[, c(2, 4:5)]), 2)
```

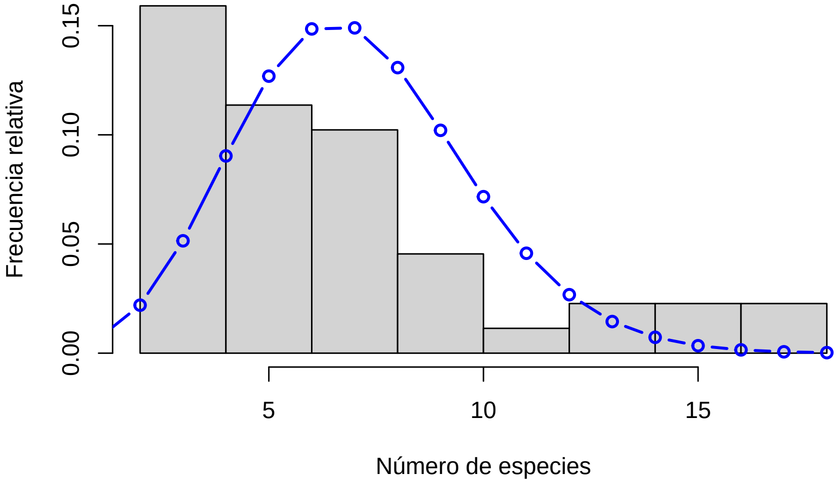
```
##           Srich Latitude Elevation
## Srich      1.00    -0.44     -0.38
## Latitude  -0.44     1.00      0.18
## Elevation -0.38     0.18      1.00
```

```r
plot(table(h$Srich), xlab = "Número de especies", ylab = "Frecuencia")
```



```
hist(h$Srich, xlab = "Número de especies", ylab = "Frecuencia relativa", main = "", fre

# Ajuste de distribución a los datos
sim.pois <- dpois(x = 0:max(h$Srich), lambda = mean(h$Srich))
lines(x = 0:max(h$Srich), y = sim.pois, col = "blue", lwd = 2, type = "b")
```



```
var(h$Srich)/mean(h$Srich)
```

```
## [1] 2.566343
```

GLMs Poisson y quasi-Poisson

GLM Poisson

```
m.pois <- glm(Srich ~ Latitude + Elevation + Habitat, family = poisson, data = h)
summary(m.pois)
```

```
##
## Call:
## glm(formula = Srich ~ Latitude + Elevation + Habitat, family = poisson,
##     data = h)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -2.20939  -0.72643  -0.05933   0.51571   2.60147
##
## Coefficients:
##                  Estimate Std. Error z value Pr(>|z|)
## (Intercept)   11.9368121  2.6214970   4.553 5.28e-06 ***
## Latitude      -0.2357930  0.0616638  -3.824 0.000131 ***
## Elevation     -0.0011411  0.0003749  -3.044 0.002337 **
## HabitatForest  0.6354389  0.1195664   5.315 1.07e-07 ***
## ---
## Signif. codes:  0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1 ’ ’ 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 102.76  on 43  degrees of freedom
## Residual deviance:  40.69  on 40  degrees of freedom
## AIC: 209.04
##
## Number of Fisher Scoring iterations: 4
```

GLM quasi-Poisson

```
m.qpois <- glm(Srich ~ Latitude + Elevation + Habitat, family = quasipoisson, data = h)
summary(m.qpois)
```

```
##
## Call:
## glm(formula = Srich ~ Latitude + Elevation + Habitat, family = quasipoisson,
##     data = h)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -2.20939  -0.72643  -0.05933   0.51571   2.60147
##
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)   11.9368121  2.6594025   4.489 5.94e-05 ***
## Latitude      -0.2357930  0.0625554  -3.769 0.000529 ***
## Elevation     -0.0011411  0.0003803  -3.000 0.004626 **
## HabitatForest  0.6354389  0.1212952   5.239 5.52e-06 ***
## ---
## Signif. codes:  0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1 ’ ’ 1
##
## (Dispersion parameter for quasipoisson family taken to be 1.029128)
##
##     Null deviance: 102.76  on 43  degrees of freedom
## Residual deviance:  40.69  on 40  degrees of freedom
## AIC: NA
```

```
##
## Number of Fisher Scoring iterations: 4
```

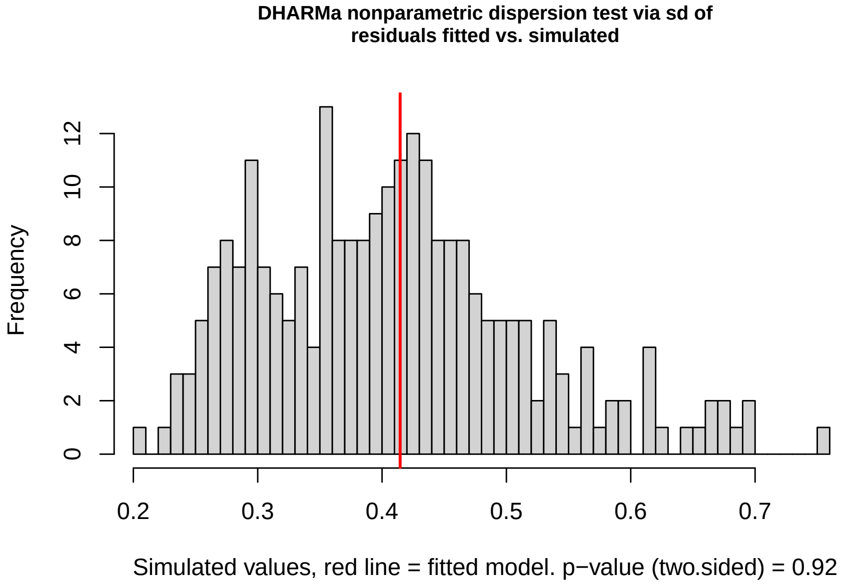
```
# Parámetro de sobredispersión
resid <- residuals(m.qpois, type = "pearson")
nparam <- length(m.qpois$coeff)
ndatos <- nrow(h)
disp.param <- sum(resid^2)/(ndatos - nparam)
disp.param
```

```
## [1] 1.029116
```

```
m.qpois.null <- glm(Srich ~ 1, family = quasipoisson, data = h)
summary(m.qpois.null)
```

```
##
## Call:
## glm(formula = Srich ~ 1, family = quasipoisson, data = h)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -2.2409  -1.2420  -0.3959   0.4492   3.4539
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.94915    0.09113   21.39   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for quasipoisson family taken to be 2.566343)
##
##     Null deviance: 102.76  on 43  degrees of freedom
## Residual deviance: 102.76  on 43  degrees of freedom
## AIC: NA
##
## Number of Fisher Scoring iterations: 5
```

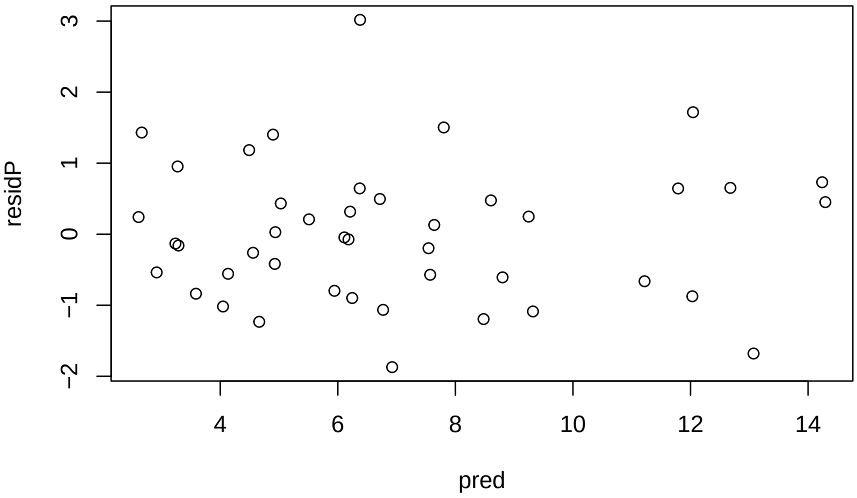
```
library(DHARMa)
testDispersion(m.pois)
```



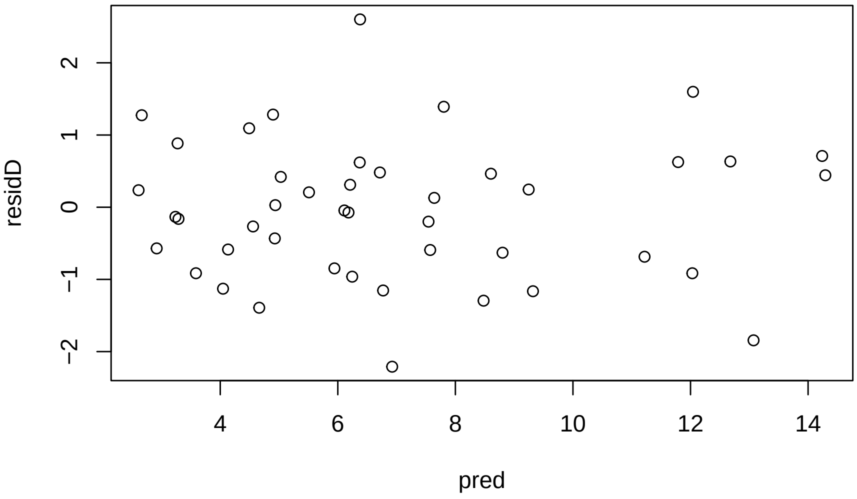
```
##
##  DHARMa nonparametric dispersion test via sd of residuals fitted vs.
##  simulated
##
## data:  simulationOutput
## dispersion = 1.0136, p-value = 0.92
## alternative hypothesis: two.sided
```

Diagnósticos

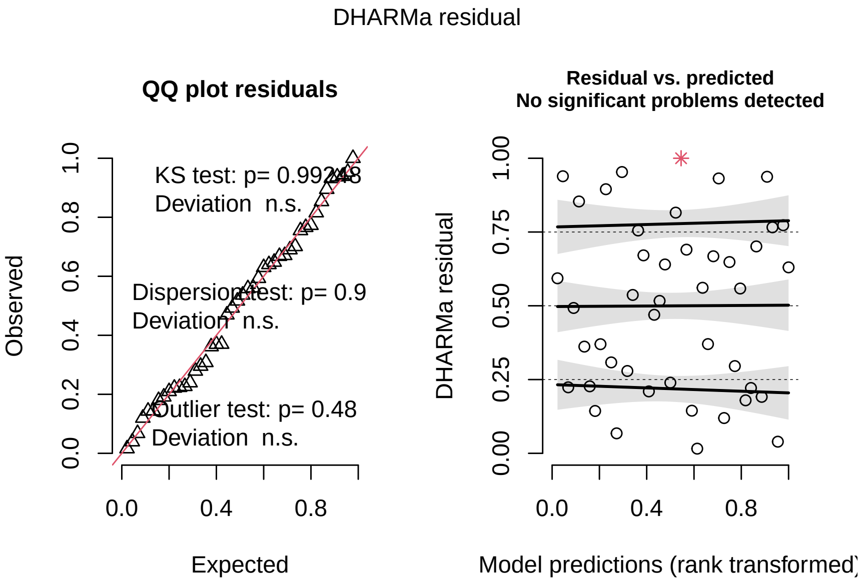
```
residP <- resid(m.qpois, type = "pearson")  # residuos de Pearson
residD <- resid(m.qpois, type = "deviance") # residuos de devianza
pred <- predict(m.qpois, type = "response") # valores predichos
plot(pred, residP)
```



```
plot(pred, residD)
```



```
plot(simulateResiduals(fittedModel = m.pois))
```



Bondad del ajuste

```
1 - (m.qpois$dev/m.qpois$null) # Pseudo-R2
```

```
## [1] 0.6040372
```

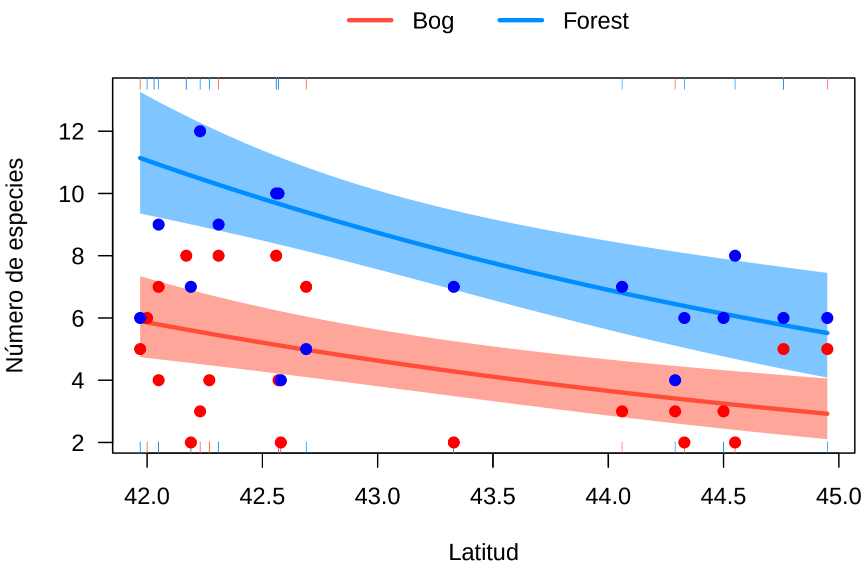
Ecuación

```
library(equatiomatic)
extract_eq(m.qpois, use_coefs = TRUE, fix_signs = TRUE)
```

$$\log(\widehat{E(\text{Srich})}) = 11.94 - 0.24(\text{Latitude}) + 0(\text{Elevation}) + 0.64(\text{Habitat}_{\text{Forest}}) \quad (2)$$

Gráfico del modelo

```
library(visreg)
visreg(fit = m.qpois, xvar = "Latitude", by = "Habitat", overlay = TRUE,
       scale = "response", xlab = "Latitud", ylab = "Número de especies",
       type = "conditional", cond = list(Latitude = mean(h$Latitude), Elevation = mean(h$Elevatio
bg <- h[h$Habitat == "Bog", ]
ft <- h[h$Habitat == "Forest", ]
points(bg$Latitude, bg$Srich, pch=19, col = "red")
points(ft$Latitude, ft$Srich, pch=19, col = "blue")
```



GLM binomial negativo

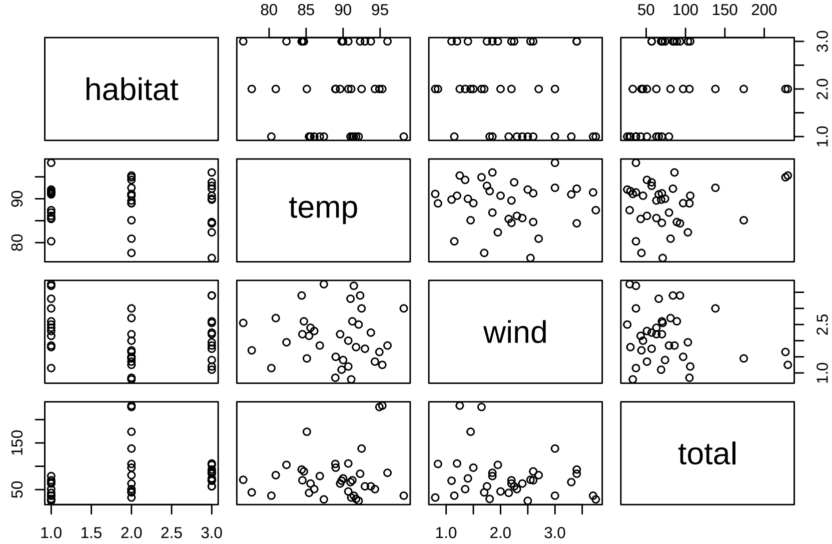
Leong et al. (2014) estudiaron el efecto del paisaje (urbano, agrícola y natural) sobre el número de interacciones de polinizadores nativos en *Centaureasolstitialis* (Asteraceae). Se quiere evaluar si existen diferencias en el número de interacciones (`total`) entre los 3 tipos de ambientes (`type`) teniendo en cuenta la temperatura (`temp`) y la velocidad del viento (`wind`).

```
# Análisis exploratorio
pol <- read.table("bees_data.txt", header = T)
str(pol)
```

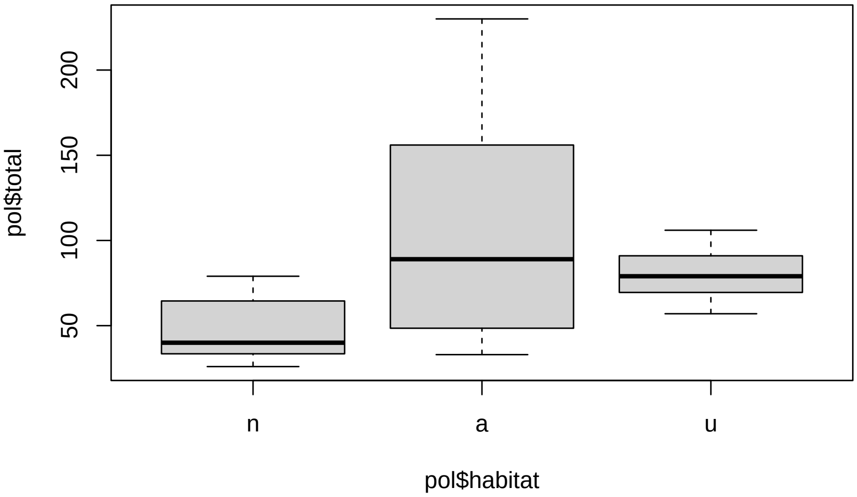
```
## 'data.frame':    36 obs. of  34 variables:
```

```
##  $ locality    : chr  "arabian" "arabian" "arabian" "bdm_f" ...
##  $ type        : chr  "a" "a" "a" "n" ...
##  $ lat         : num  37.9 37.9 37.9 38 38 ...
##  $ long        : num  -122 -122 -122 -122 -122 ...
##  $ water       : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ urban       : int  18900 18900 18900 37800 37800 37800 4500 4500 4500 198000 ...
##  $ agr         : int  252000 252000 252000 0 0 0 16200 16200 16200 558000 ...
##  $ natural     : int  513900 513900 513900 747900 747900 747900 765000 765000 765000
##  $ bare        : int  1800 1800 1800 0 0 0 0 0 0 0 ...
##  $ bloom.cat   : int  3 3 3 3 3 3 4 4 4 4 ...
##  $ time        : chr  "am" "mid" "pm" "am" ...
##  $ wind        : num  2.7 1.35 0.8 2.3 3.75 3.7 2.4 2.15 2.5 0.85 ...
##  $ temp        : num  80.9 94.3 91.1 86.1 87.4 ...
##  $ hb          : int  70 44 24 34 24 27 40 29 14 88 ...
##  $ bumble      : int  0 0 0 1 0 4 0 0 0 0 ...
##  $ carpenter   : int  0 0 0 0 0 1 0 0 0 0 ...
##  $ hlb         : int  2 0 0 7 2 0 9 2 0 1 ...
##  $ svastra     : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ agtex       : int  4 1 0 0 0 0 0 0 0 0 ...
##  $ ssb.med     : int  0 0 0 0 0 0 1 0 0 1 ...
##  $ ssb.small   : int  0 0 1 4 0 4 1 3 2 9 ...
##  $ sdb.round   : int  1 0 6 1 1 1 2 3 4 2 ...
##  $ sdb.shield  : int  3 2 2 0 2 0 0 0 0 0 ...
##  $ shbb.large  : int  0 0 0 0 0 0 0 0 0 2 ...
##  $ shbb.med    : int  0 1 0 4 0 0 8 5 5 2 ...
##  $ shbb.small  : int  1 3 0 0 0 0 1 1 1 0 ...
##  $ anthidium   : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ cuckoo      : int  0 0 0 0 0 0 1 0 0 0 ...
##  $ total.native: int  11 7 9 17 5 10 23 14 12 17 ...
##  $ total       : int  81 51 33 51 29 37 63 43 26 105 ...
##  $ min         : int  90 90 90 90 90 90 90 90 90 90 ...
##  $ num.group   : int  6 5 4 6 4 5 8 6 5 7 ...
##  $ shannon     : num  0.597 0.575 0.817 1.096 0.642 ...
##  $ even        : num  0.333 0.357 0.59 0.612 0.463 ...
```

```
pol$habitat <- factor(pol$type, levels = c("n", "a", "u"))
pairs(pol[, c("habitat", "temp", "wind", "total")])
```



```
boxplot(pol$total ~ pol$habitat)
```

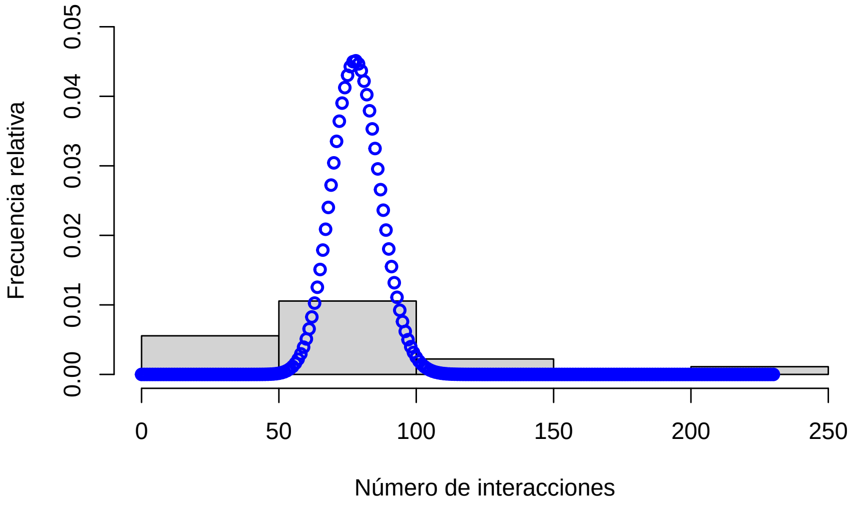


```
cor(pol$temp, pol$wind)
```

```
## [1] -0.02087349
```

```
hist(pol$total, xlab = "Número de interacciones", ylab = "Frecuencia relativa", main =

# Ajuste de distribución a los datos
sim.pois <- dpois(x = 0:max(pol$total), lambda = mean(pol$total))
lines(x = 0:max(pol$total), y = sim.pois, col = "blue", lwd = 2, type = "b")
```



```
var(pol$total)/mean(pol$total)
```

```
## [1] 30.01128
```

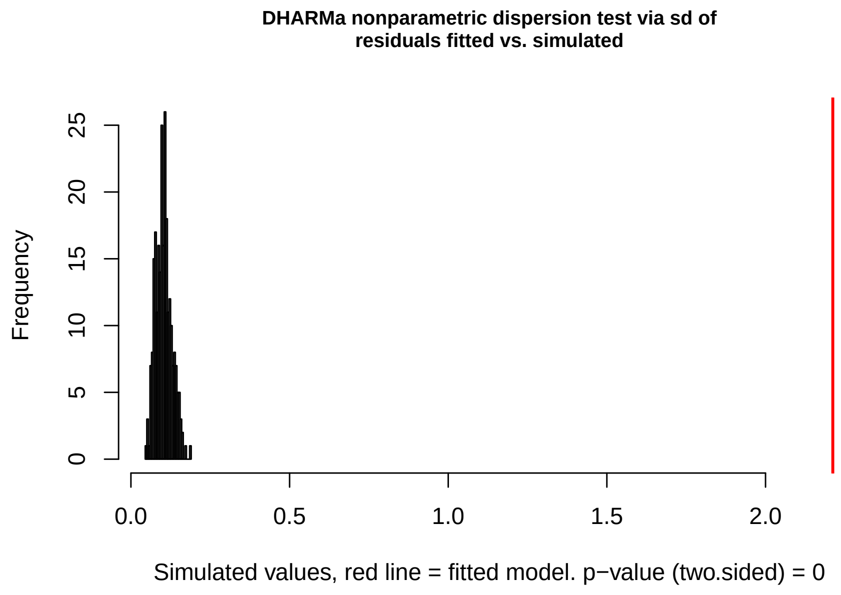
Chequear sobredispersión

```
mqpoi.pol <- glm(total ~ habitat + temp + wind, family = quasipoisson, data = pol)
summary(mqpoi.pol)
```

```
##
```

```
## Call:
## glm(formula = total ~ habitat + temp + wind, family = quasipoisson,
##     data = pol)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -8.7048  -2.7630  -0.5307   2.2527   8.9461
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  2.244844   1.518268   1.479  0.14935
## habitata     0.813256   0.238963   3.403  0.00186 **
## habitatu     0.535908   0.233539   2.295  0.02868 *
## temp         0.018127   0.016226   1.117  0.27252
## wind        -0.001247   0.116820  -0.011  0.99155
## ---
## Signif. codes:  0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1 ’ ’ 1
##
## (Dispersion parameter for quasipoisson family taken to be 18.37662)
##
##     Null deviance: 876.87  on 35  degrees of freedom
## Residual deviance: 565.09  on 31  degrees of freedom
## AIC: NA
##
## Number of Fisher Scoring iterations: 5
```

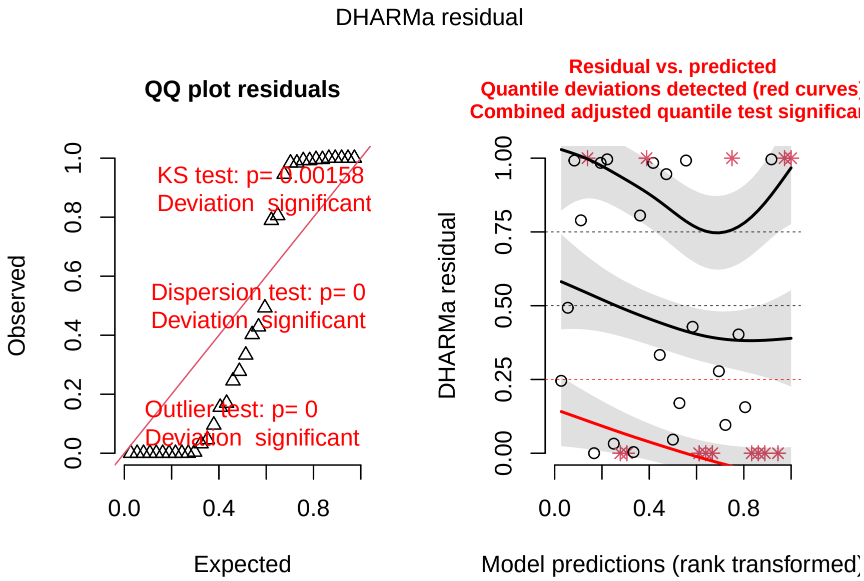
```
library(DHARMa)
mpoi.pol <- glm(total ~ habitat + temp + wind, family = poisson, data = pol)
testDispersion(mpoi.pol)
```



```
##
##  DHARMa nonparametric dispersion test via sd of residuals fitted vs.
##  simulated
##
## data:  simulationOutput
## dispersion = 21.413, p-value < 2.2e-16
## alternative hypothesis: two.sided
```

Validación del modelo quasi-Poisson

```
plot(simulateResiduals(fittedModel = mpoi.pol))
```



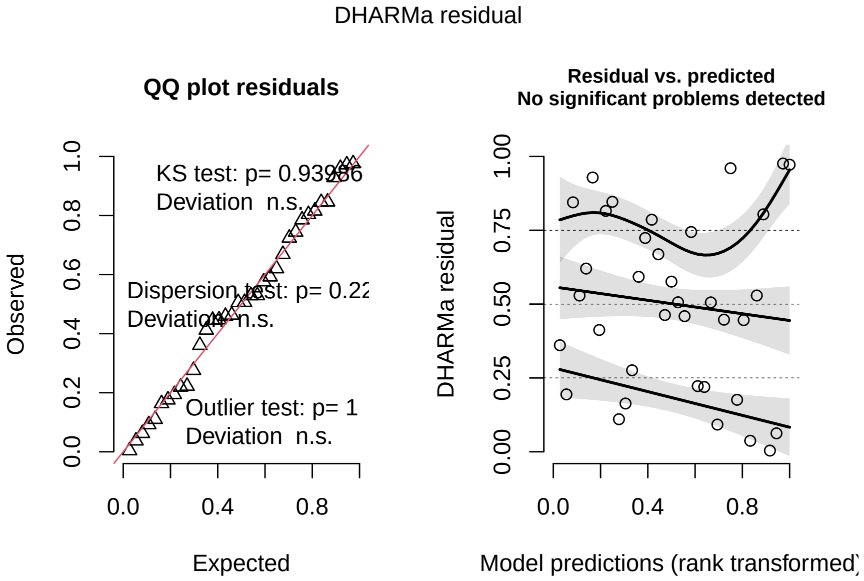
Modelo binomial negativo

```
library(MASS)
mbn.pol <- glm.nb(total ~ habitat + temp + wind, data = pol)
summary(mbn.pol)
```

```
##
## Call:
## glm.nb(formula = total ~ habitat + temp + wind, data = pol, init.theta = 5.957692263,
##     link = log)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -2.3561  -0.8982  -0.1773   0.5760   1.8680
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  2.82455    1.28889   2.191  0.02842 *
## habitata     0.78487    0.19397   4.046  5.2e-05 ***
## habitatu     0.52773    0.18051   2.924  0.00346 **
## temp         0.01218    0.01406   0.866  0.38652
## wind        -0.01878    0.10041  -0.187  0.85161
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Negative Binomial(5.9577) family taken to be 1)
##
##     Null deviance: 58.860  on 35  degrees of freedom
## Residual deviance: 36.513  on 31  degrees of freedom
## AIC: 358.06
##
## Number of Fisher Scoring iterations: 1
##
##
##               Theta:  5.96
##           Std. Err.:  1.47
##
##  2 x log-likelihood:  -346.062
```

Validación del modelo binomial negativo

```
plot(simulateResiduals(fittedModel = mbn.pol))
```



Bondad del ajuste

```
1 - (mbn.pol$dev/mbn.pol$null) # Pseudo-R2
```

```
## [1] 0.3796712
```

Ecuación

```
extract_eq(mbn.pol, use_coefs = TRUE, fix_signs = TRUE)
```

$$\log(\widehat{E(\text{total})}) = 2.82 + 0.78(\text{habitat}_{\text{a}}) + 0.53(\text{habitat}_{\text{u}}) + 0.01(\text{temp}) - 0.02(\text{wind}) \tag{3}$$

Comparaciones múltiples

```
library(multcomp)
```

```
## Loading required package: mvtnorm
```

```
## Loading required package: survival
```

```
## Loading required package: TH.data
```

```
##
## Attaching package: 'TH.data'
```

```
## The following object is masked from 'package:MASS':
##
##     geyser
```

```
comp <- glht(mbn.pol, mcp(habitat = "Tukey"))
summary(comp)
```

```
##
##   Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: glm.nb(formula = total ~ habitat + temp + wind, data = pol, init.theta = 5.957
##     link = log)
##
## Linear Hypotheses:
##            Estimate Std. Error z value Pr(>|z|)
## a - n == 0   0.7849     0.1940   4.046 0.000146 ***
## u - n == 0   0.5277     0.1805   2.924 0.009585 **
## u - a == 0  -0.2571     0.1785  -1.441 0.319562
## ---
## Signif. codes:  0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1 ’ ’ 1
## (Adjusted p values reported -- single-step method)
```

Incluyendo un offset

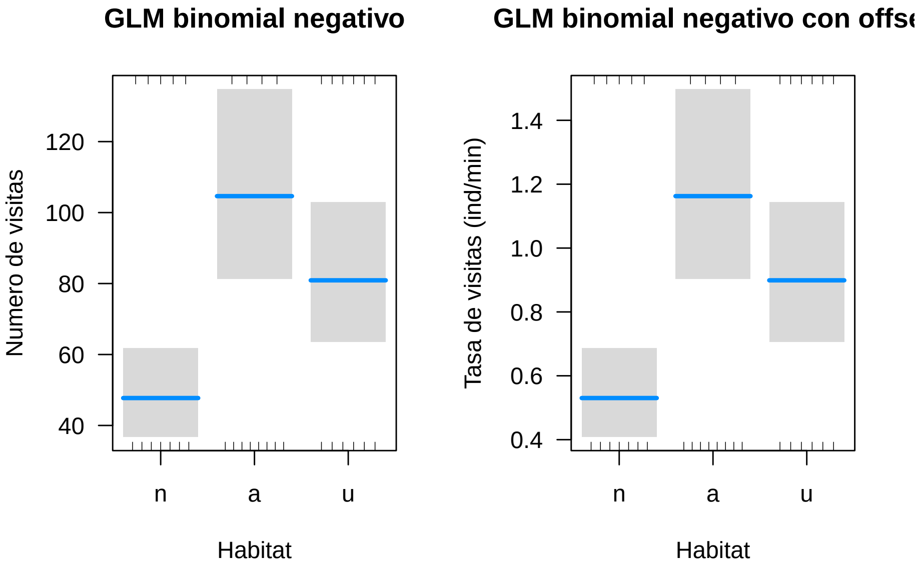
```
mbn.pol.off <- glm.nb(total ~ habitat + temp + wind + offset(log(min)), data = pol)
summary(mbn.pol.off)
```

```
##
## Call:
## glm.nb(formula = total ~ habitat + temp + wind + offset(log(min)),
##     data = pol, init.theta = 5.957692263, link = log)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -2.3561  -0.8982  -0.1773   0.5760   1.8680
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -1.67526    1.28889  -1.300  0.19368
## habitata     0.78487    0.19397   4.046  5.2e-05 ***
## habitatu     0.52773    0.18051   2.924  0.00346 **
## temp         0.01218    0.01406   0.866  0.38652
## wind        -0.01878    0.10041  -0.187  0.85161
## ---
## Signif. codes:  0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1 ’ ’ 1
##
## (Dispersion parameter for Negative Binomial(5.9577) family taken to be 1)
```

```
##
##     Null deviance: 58.860  on 35  degrees of freedom
## Residual deviance: 36.513  on 31  degrees of freedom
## AIC: 358.06
##
## Number of Fisher Scoring iterations: 1
##
##
##                 Theta:  5.96
##             Std. Err.:  1.47
##
##  2 x log-likelihood:  -346.062
```

Gráficos de los modelos

```
layout(matrix(1:2, 1, 2))
visreg(fit = mbn.pol, xvar = "habitat", scale = "response", cond = list(temp = mean(pol$temp), wi
visreg(fit = mbn.pol.off, xvar = "habitat", scale = "response", cond = list(temp = mean(pol$temp)
```



```
layout(1)
```

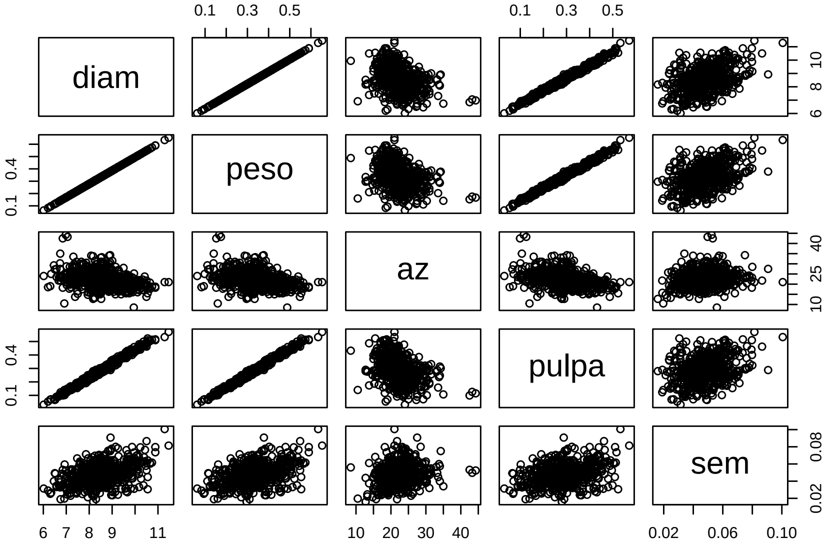
Modelo lineal general

Palacio et al. (2014) estudiaron la selección natural mediada por aves frugívoras sobre rasgos de los frutos de *Celtis tala* (`frutos Celtis 2013.txt`), incluyendo el diámetro (`diam`), peso (`peso`), concentración de azúcares (`az`), peso de pulpa (`pulpa`), peso de semilla (`sem`) y relación peso de pulpa/peso de semilla (`pulpa.sem`). Analizar qué factores explican el tamaño del fruto.

```
celtis <- read.delim("frutos Celtis 2013.csv", sep = ";")
str(celtis)
```

```
## 'data.frame':    617 obs. of  8 variables:
##  $ planta   : chr  "P1-10" "P1-10" "P1-10" "P1-10" ...
##  $ parche   : chr  "P1" "P1" "P1" "P1" ...
##  $ diam     : num  9.26 8.12 9.01 8.57 7.48 ...
##  $ peso     : num  0.414 0.291 0.387 0.339 0.222 0.307 0.318 0.35 0.259 0.294 ...
##  $ az       : num  18.5 21.5 18.5 23.5 16.5 ...
##  $ pulpa    : num  0.361 0.252 0.331 0.287 0.177 0.252 0.272 0.292 0.217 0.253 ...
##  $ sem      : num  0.0523 0.0393 0.0556 0.0519 0.0443 0.0555 0.0453 0.0581 0.0419 0
##  $ pulpa.sem: num  6.91 6.41 5.96 5.53 4 ...
```

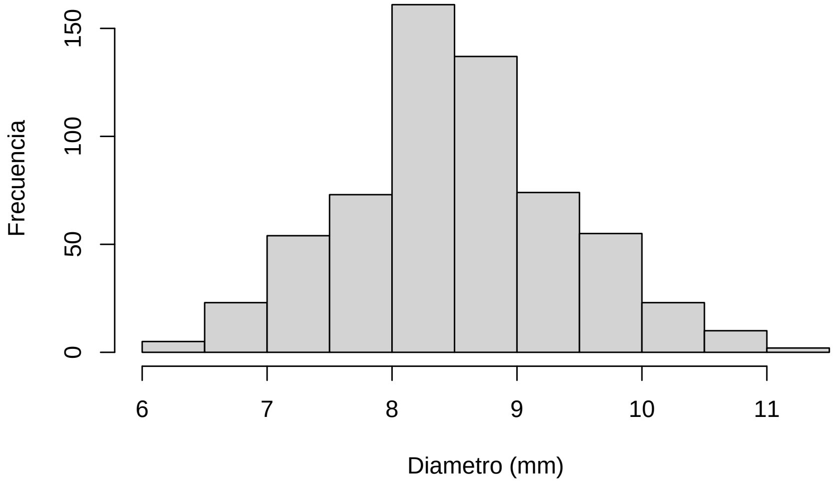
```
pairs(celtis[, 3:7])
```



```
round(cor(celtis[, 4:7], use = "complete.obs"), 2)
```

```
##        peso    az pulpa  sem
## peso   1.00 -0.33  0.99 0.45
## az    -0.33  1.00 -0.37 0.20
## pulpa  0.99 -0.37  1.00 0.34
## sem    0.45  0.20  0.34 1.00
```

```
hist(celtis$diam, xlab = "Diametro (mm)", ylab = "Frecuencia", main = "")
```



```
mlg <- glm(diam ~ az + sem, family = gaussian, data = celtis)
summary(mlg)
```

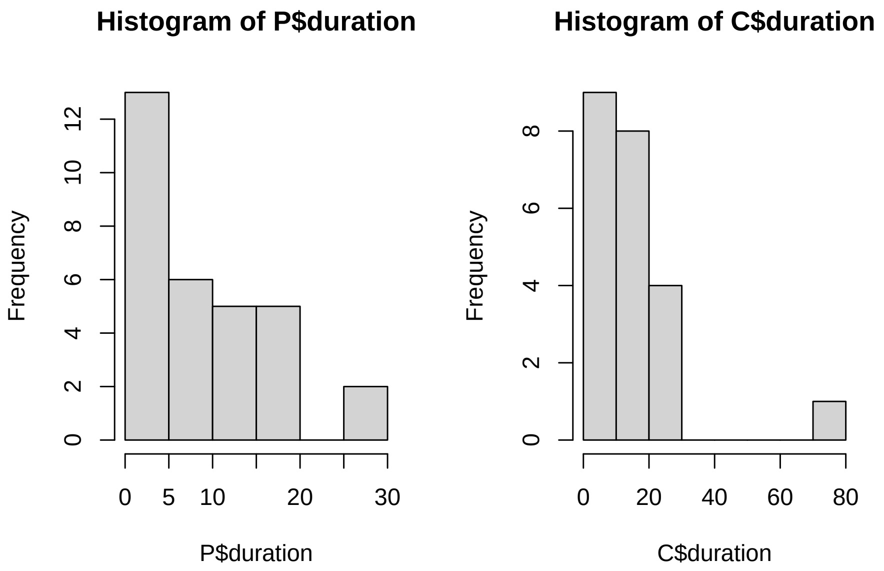
```
##
## Call:
## glm(formula = diam ~ az + sem, family = gaussian, data = celtis)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -1.96247  -0.49375  -0.01025   0.46537   2.04017
##
## Coefficients:
```

```
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  8.750071   0.176681   49.52   <2e-16 ***
## az          -0.094204   0.006975  -13.51   <2e-16 ***
## sem         39.834317   2.400758   16.59   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 0.4902039)
##
##     Null deviance: 487.54  on 613  degrees of freedom
## Residual deviance: 299.51  on 611  degrees of freedom
##   (3 observations deleted due to missingness)
## AIC: 1309.7
##
## Number of Fisher Scoring iterations: 2
```

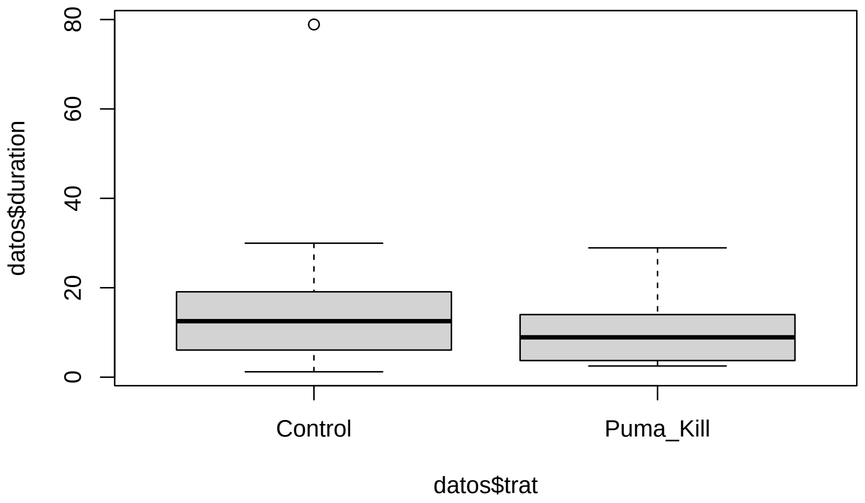
GLM Gamma

Allen et al. (2015) analizaron el efecto de grandes carnívoros (*Ursusamericanus* y *Pumaconcolor*) sobre la actividad de carroñeros. Registraron la duración media del evento de alimentación (`duration`) por carroñeros en sitios con cadáveres producto de pumas y sitios control donde se colocaron cadáveres colectados en la ruta (`trat`).

```
# Gráficos exploratorios
datos <- read.table("puma.txt", header = TRUE)
datos$trat <- as.factor(datos$trat)
P <- subset(datos, trat == "Puma_Kill")
C <- subset(datos, trat == "Control")
layout(matrix(1:2, 1, 2))
hist(P$duration)
hist(C$duration)
```



```
layout(1)
boxplot(datos$duration ~ datos$trat)
```



```r
# GLM Gamma
m.Gamma <- glm(duration ~ trat, family = Gamma, data = datos)
summary(m.Gamma)
```

```
## 
## Call:
## glm(formula = duration ~ trat, family = Gamma, data = datos)
## 
## Deviance Residuals: 
##     Min       1Q   Median       3Q      Max  
## -1.7942  -0.8165  -0.1525   0.3143   2.2724  
## 
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)    
## (Intercept)    0.06639    0.01251   5.308 2.43e-06 ***
## tratPuma_Kill  0.03731    0.02067   1.805    0.077 .  
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## (Dispersion parameter for Gamma family taken to be 0.7808647)
## 
##     Null deviance: 35.695  on 52  degrees of freedom
## Residual deviance: 33.092  on 51  degrees of freedom
## AIC: 363.65
## 
## Number of Fisher Scoring iterations: 6
```

```r
# Comparaciones múltiples
library(multcomp)
comp <- glht(m.Gamma, mcp(trat = "Tukey"))
summary(comp)
```

```
## 
##   Simultaneous Tests for General Linear Hypotheses
## 
## Multiple Comparisons of Means: Tukey Contrasts
## 
## 
## Fit: glm(formula = duration ~ trat, family = Gamma, data = datos)
## 
## Linear Hypotheses:
##                          Estimate Std. Error z value Pr(>|z|)  
## Puma_Kill - Control == 0  0.03731    0.02067   1.805   0.0711 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)
```

Actividades

Ejercicio 2.1

Identifique qué tipo de distribuciones de probabilidad utilizaría para las siguientes variables de respuesta. Justifique en cada caso.

a. Densidad de especies de plantas en parcelas de un bosque.

b. Probabilidad de detección de una especie de anfibio en charcas temporarias.

c. La tasa de crecimiento en pichones de una especie de ave.

d. El sexo en una especie de lagarto.

Ejercicio 2.2

Se estimó la prevalencia del parásito *Elaphostrongylus cervi* en ciervos colorados de granjas de España (`Tbdeer`). En cada granja (`Farm`) se muestreó un grupo de animales (`DeerSampledCervi`) y se registró si eran positivos para la enfermedad (`DeerPosCervi`). Además, se registraron variables de hábitat, como porcentaje de áreas abiertas (`OpenLand`), arbustos (`ScrubLand`) y plantaciones de pino (`PinePlantation`), densidad de plantas y árboles de *Quercus* sp. (`QuercusPlants`, `QuercusTrees`). También se estimaron abundancias relativas de jabalí (`WildBoarIndex`) y ciervo colorado (`RedDeerIndex`), área del campo (`EstateSize`) y si el campo estaba cercado (1 = cercado, 0 = no cercado).

- Determine, cuáles de estas variables están involucradas en la prevalencia de la enfermedad.
- Valide y grafique el modelo resultante.

Ejercicio 2.3

Simule un modelo lineal general (utilice la función `rnorm`) con dos variables (una con un efecto positivo y otra con un efecto negativo sobre la respuesta) y ajuste un modelo con las funciones `lm` y `glm`. Compare ambos modelos ¿Qué conclusión obtiene?

Ejercicio 2.4

Desarrolle un script para calcular el R^2 de Tjur utilizando el GLM binomial de Solea.txt, donde:

$$R^2_{Tjur} = \frac{\sum \hat{p}(y=1)}{n_1} + \frac{\sum \hat{p}(y=0)}{n_0}$$

Corrobore el resultado con la función `r2_tjur` del paquete `performance` ¿En qué situación hipotética el R^2 vale 0?

Conteos II

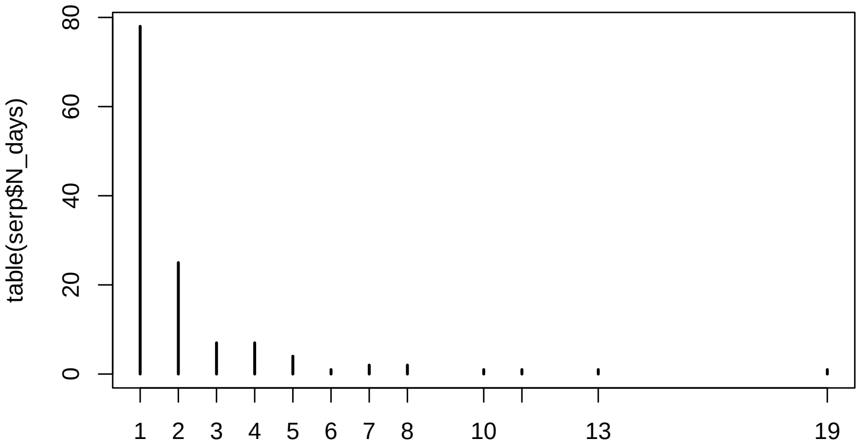
Modelos truncados en cero

Santos et al. (2011) estudiaron la probabilidad de persistencia de las carcasas de animales muertos en ruta (`Snakes.txt`). La variable respuesta es la cantidad de días que perduraban las carcasas sin ser removidas (`N_days`). Las variables explicatorias son la longitud de cada especie (`Size_cm`), la proporción de días con lluvia (`PDayRain`), las precipitaciones totales (`Tot_Rain`), la temperatura diaria promedio (`Temp_avg`), la identidad de la ruta que representa la intesidad del tráfico (`Road`; EN114 tiene alto tránsito, EN4 tiene tráfico medio, y EN370_EN114_4 tiene bajo tráfico), la ubicación en la ruta (`Road_Loc`; L = asfalto, V = borde), la estación (`Season`), y la especie (`Species`).

```r
# Analisis exploratorio
serp <- read.table("Snakes.txt", header = T)
str(serp)
```

```
## ’data.frame’:    130 obs. of  11 variables:
##  $ ID      : int  2176 2448 2917 2927 2845 2849 2860 2760 2758 2764 ...
##  $ Road    : chr  "EN114" "EN114" "EN114" "EN114" ...
##  $ Month   : chr  "Jul" "Aug" "Oct" "Oct" ...
##  $ Season  : chr  "Summer" "Summer" "Autumn" "Autumn" ...
##  $ N_days  : int  4 1 4 2 1 1 2 1 2 2 ...
##  $ Species : chr  "Coluberhippocrepis" "Elaphescalaris" "Elaphescalaris" "Elaphescal
##  $ Road_Loc: chr  "L" "L" "L" "L" ...
##  $ Size_cm : int  115 150 150 150 150 150 150 150 150 150 ...
##  $ PDayRain: num  0.75 0 1 1 0 0 0 0 0 0 ...
##  $ Tot_Rain: num  15 0 40.2 35.6 0 0 0 0 0 0 ...
##  $ Temp_avg: num  24.6 27.4 19.1 17.8 22.3 22.3 19.7 19.9 19.4 19.4 ...
```

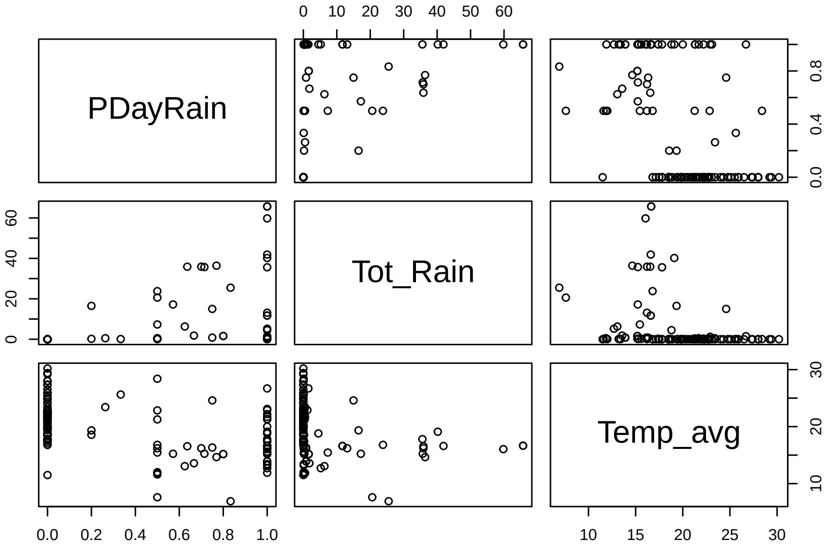
```
plot(table(serp$N_days))
```



```
mean(serp$N_days)
```

```
## [1] 2.2
```

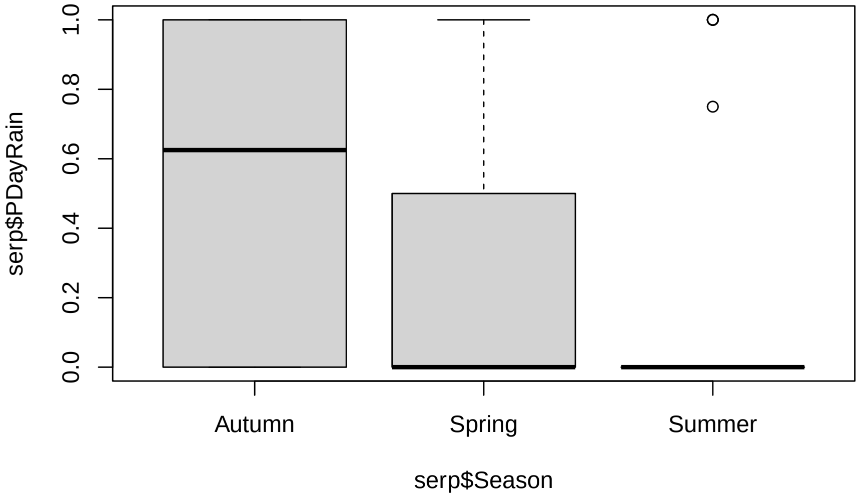
```
pairs(serp[, c("PDayRain", "Tot_Rain", "Temp_avg")])
```



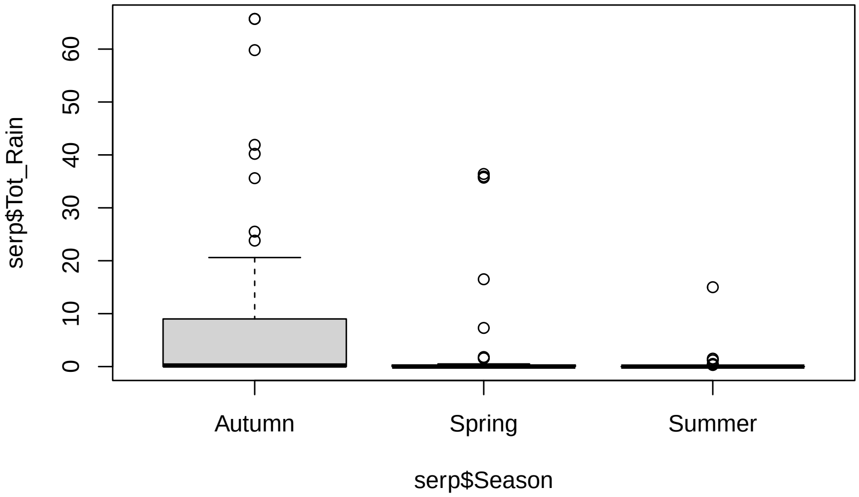
```
round(cor(serp[, c("PDayRain", "Tot_Rain", "Temp_avg")]), 2)
```

```
##           PDayRain Tot_Rain Temp_avg
## PDayRain      1.00     0.42     -0.5
## Tot_Rain      0.42     1.00     -0.3
## Temp_avg     -0.50    -0.30      1.0
```

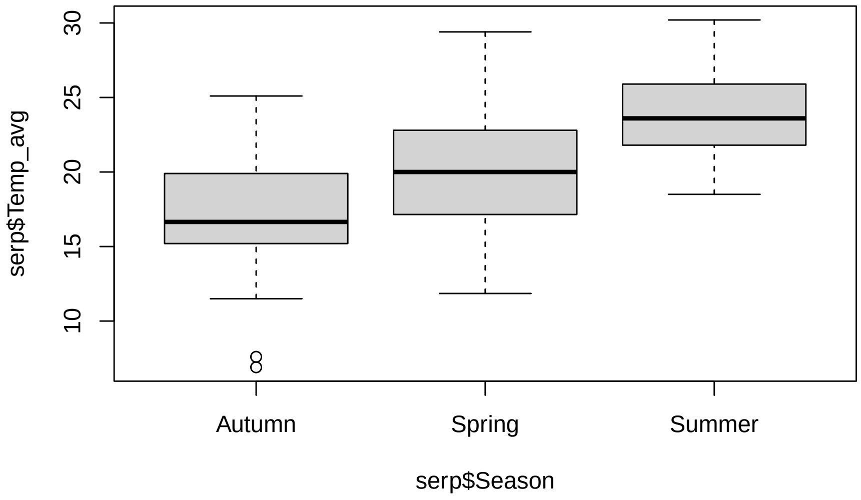
```
boxplot(serp$PDayRain ~ serp$Season)
```



```
boxplot(serp$Tot_Rain ~ serp$Season)
```



```
boxplot(serp$Temp_avg ~ serp$Season)
```



Comparación con el GLM Poisson

```
m.pois <- glm(N_days ~ Size_cm + PDayRain + Tot_Rain + Road + Size_cm + Road_Loc + Siz
summary(m.pois)
```

```
##
## Call:
## glm(formula = N_days ~ Size_cm + PDayRain + Tot_Rain + Road +
##     Size_cm + Road_Loc + Size_cm:PDayRain, family = poisson,
##     data = serp)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -2.0869  -0.7901  -0.4193   0.2448   5.9495
##
## Coefficients:
##                   Estimate Std. Error z value Pr(>|z|)
## (Intercept)      -0.114527   0.463263  -0.247 0.804739
## Size_cm           0.004782   0.002965   1.613 0.106848
## PDayRain          0.957714   0.768545   1.246 0.212713
## Tot_Rain           0.022763   0.003797   5.994 2.04e-09 ***
## RoadEN370_EN114_4 -0.146154   0.172785  -0.846 0.397626
## RoadEN4           -0.352271   0.147973  -2.381 0.017282 *
## Road_LocV          0.530610   0.158214   3.354 0.000797 ***
## Size_cm:PDayRain  -0.006869   0.005161  -1.331 0.183215
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 226.38  on 129  degrees of freedom
## Residual deviance: 166.85  on 122  degrees of freedom
## AIC: 498.68
##
## Number of Fisher Scoring iterations: 5
```

GLM Poisson truncado en cero

```
library(VGAM)
```

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

```
## Loading required package: splines
```

```
m.pois.trun <- vglm(N_days ~ Size_cm + PDayRain + Tot_Rain + Road + Size_cm + Road_Loc + Size_cm:
summary(m.pois.trun)
```

```
##
## Call:
## vglm(formula = N_days ~ Size_cm + PDayRain + Tot_Rain + Road +
##     Size_cm + Road_Loc + Size_cm:PDayRain, family = pospoisson,
##     data = serp, control = vglm.control(maxit = 100))
##
## Coefficients:
##                    Estimate Std. Error z value Pr(>|z|)
## (Intercept)       -1.214880   0.764099  -1.590  0.11185
## Size_cm            0.009725   0.004830   2.014  0.04406 *
## PDayRain           1.782494   1.097674   1.624  0.10440
## Tot_Rain           0.028863   0.004270   6.760 1.38e-11 ***
## RoadEN370_EN114_4 -0.217333   0.225081  -0.966  0.33425
## RoadEN4           -0.558705   0.181936  -3.071  0.00213 **
## Road_LocV          0.811896   0.200842   4.042 5.29e-05 ***
## Size_cm:PDayRain  -0.012131   0.007245  -1.674  0.09404 .
## ---
## Signif. codes:  0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1 ’ ’ 1
##
## Name of linear predictor: loglink(lambda)
##
## Log-likelihood: -211.1832 on 122 degrees of freedom
##
## Number of Fisher scoring iterations: 5
##
## No Hauck-Donner effect found in any of the estimates
```

GLM binomial negativo truncado en cero

```
m.nb.trun <- vglm(N_days ~ Size_cm + PDayRain + Tot_Rain + Road + Size_cm + Road_Loc +
```

```
## Warning in slot(family, "linkinv")(eta, extra = extra): estimates of ’size’ are
## very small. Taking evasive action.
```

```
## Warning in slot(family, "validparams")(eta, y = y, extra = extra): parameter
## ’size’ has very large values relative to ’munb’; try fitting a positive-Poisson
## model instead.
```

```
## Warning in eval(slot(family, "deriv")): solution near the boundary; either there
## is no need to fit a positive NBD or the distribution is centred on the value 1
```

```
## Warning in slot(family, "validparams")(eta, y, extra = extra): parameter ’size’
## has very large values relative to ’munb’; try fitting a positive-Poisson model
## instead.
```

```
## Warning in vglm.fitter(x = x, y = y, w = w, offset = offset, Xm2 = Xm2, :
## iterations terminated because half-step sizes are very small
```

```
## Warning in vglm.fitter(x = x, y = y, w = w, offset = offset, Xm2 = Xm2, : some
## quantities such as z, residuals, SEs may be inaccurate due to convergence at a
## half-step
```

```
summary(m.nb.trun)
```

```
## Warning in eval(expr): solution near the boundary; either there is no need to
## fit a positive NBD or the distribution is centred on the value 1
## Warning in eval(expr): solution near the boundary; either there is no need to
## fit a positive NBD or the distribution is centred on the value 1

## Warning in eval(expr): solution near the boundary; either there is no need to
## fit a positive NBD or the distribution is centred on the value 1

## Warning in eval(expr): solution near the boundary; either there is no need to
## fit a positive NBD or the distribution is centred on the value 1

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## fit a positive NBD or the distribution is centred on the value 1

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## fit a positive NBD or the distribution is centred on the value 1

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## fit a positive NBD or the distribution is centred on the value 1

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## fit a positive NBD or the distribution is centred on the value 1

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## fit a positive NBD or the distribution is centred on the value 1

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## fit a positive NBD or the distribution is centred on the value 1

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## fit a positive NBD or the distribution is centred on the value 1

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## fit a positive NBD or the distribution is centred on the value 1

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## fit a positive NBD or the distribution is centred on the value 1

## Warning in eval(expr): solution near the boundary; either there is no need to
## fit a positive NBD or the distribution is centred on the value 1

## Warning in eval(expr): solution near the boundary; either there is no need to
## fit a positive NBD or the distribution is centred on the value 1

## Warning in eval(expr): solution near the boundary; either there is no need to
## fit a positive NBD or the distribution is centred on the value 1

## Warning in eval(expr): solution near the boundary; either there is no need to
## fit a positive NBD or the distribution is centred on the value 1

## Warning in eval(expr): solution near the boundary; either there is no need to
## fit a positive NBD or the distribution is centred on the value 1

## Warning in eval(expr): solution near the boundary; either there is no need to
## fit a positive NBD or the distribution is centred on the value 1


##
## Call:
## vglm(formula = N_days ~ Size_cm + PDayRain + Tot_Rain + Road +
##     Size_cm + Road_Loc + Size_cm:PDayRain, family = posnegbinomial,
##     data = serp, control = vglm.control(maxit = 100))
##
## Coefficients:
##                     Estimate Std. Error  z value Pr(>|z|)
## (Intercept):1     -18.650956   9.622924       NA       NA
## (Intercept):2     -19.201942   0.087878 -218.508   <2e-16 ***
## Size_cm             0.006975   0.062006    0.112    0.910
## PDayRain            1.196235  18.692101    0.064    0.949
## Tot_Rain            0.067164   0.117128    0.573    0.566
## RoadEN370_EN114_4  -0.276550   4.059935   -0.068    0.946
## RoadEN4            -0.558499   3.643634   -0.153    0.878
## Road_LocV           1.072722   3.817984    0.281    0.779
## Size_cm:PDayRain   -0.009605   0.126436   -0.076    0.939
## ---
## Signif. codes:  0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1 ’ ’ 1
##
## Names of linear predictors: loglink(munb), loglink(size)
##
## Log-likelihood: -186.7285 on 251 degrees of freedom
##
## Number of Fisher scoring iterations: 3
##
## Warning: Hauck-Donner effect detected in the following estimate(s):
## ’(Intercept):1’
```

Comparación de coeficientes entre modelos

```
data.frame(coef.Poisson = summary(m.pois)$coeff[, 1],
           coef.Poisson.truncado = summary(m.pois.trun)@coef3[, 1])
```

```
##                    coef.Poisson coef.Poisson.truncado
## (Intercept)       -0.114527460         -1.214879652
## Size_cm            0.004781715          0.009724801
## PDayRain           0.957714141          1.782494406
## Tot_Rain           0.022763117          0.028863331
## RoadEN370_EN114_4 -0.146153654         -0.217333044
## RoadEN4           -0.352270790         -0.558704924
## Road_LocV          0.530609962          0.811896312
## Size_cm:PDayRain  -0.006868709         -0.012131485
```

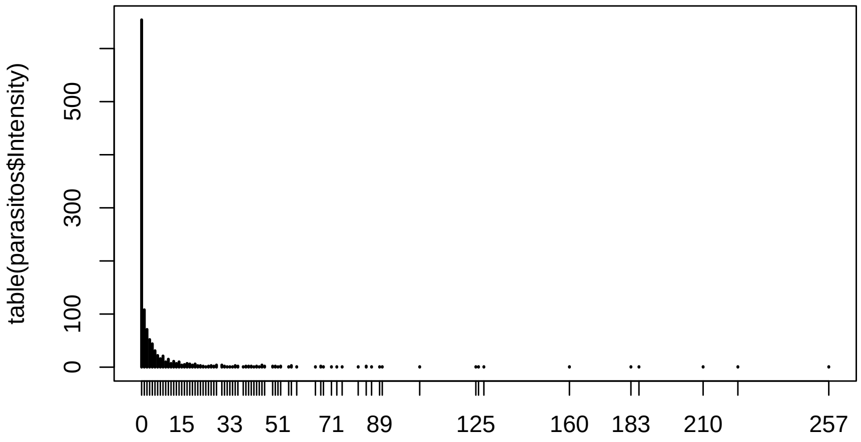
Modelos inflados en ceros

Hemmingsen et al. (2005) analizaron las infecciones por *Trypanosoma* en bacalaos (*Gadus morhua*) durante cruceros anuales en la costa norte de Noruega (`ParasiteCod.txt`). La variable respuesta es la prevalencia de parásitos (`Prevalence`). Posibles variables explicatorias son el año (`Year`), el área (`Area`) y la profundidad de captura (`Depth`).

```
# Análisis exploratorio
parasitos <- read.table("ParasiteCod.txt", header = T)
str(parasitos)
```

```
## 'data.frame':    1254 obs. of  11 variables:
##  $ Sample    : int  1 2 3 4 5 6 7 8 9 10 ...
##  $ Intensity : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ Prevalence: int  0 0 0 0 0 0 0 0 0 0 ...
##  $ Year      : int  1999 1999 1999 1999 1999 1999 1999 1999 1999 1999 ...
##  $ Depth     : int  220 220 220 220 220 220 220 194 194 194 ...
##  $ Weight    : int  148 144 146 138 40 68 52 3848 2576 1972 ...
##  $ Length    : int  26 26 27 26 17 20 19 77 67 60 ...
##  $ Sex       : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ Stage     : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ Age       : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ Area      : int  2 2 2 2 2 2 2 3 3 3 ...
```

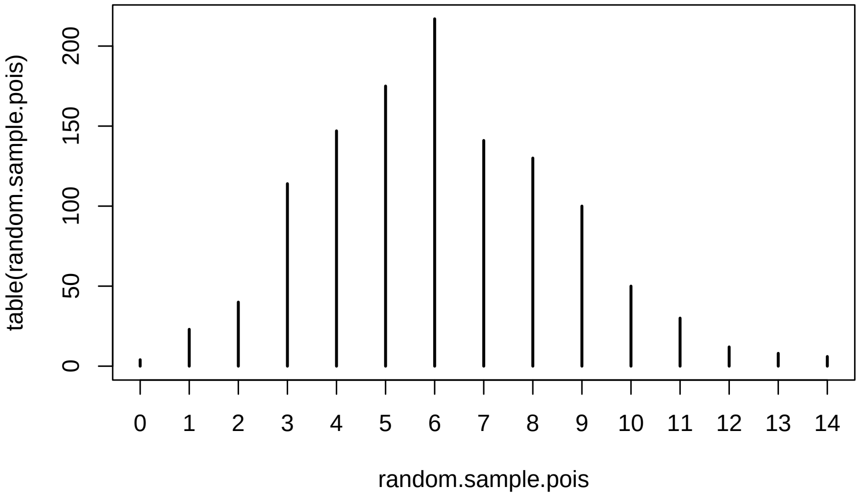
```
plot(table(parasitos$Intensity))
```



```
table(parasitos$Intensity)[1] # Número de ceros observados
```

```
##   0
## 654
```

```
# Ajuste de distribución a los datos
xIntensity <- mean(parasitos$Intensity, na.rm = TRUE)
sim.pois <- dpois(x = 0:max(parasitos$Intensity, na.rm = TRUE), lambda = xIntensity)
ndatos <- length(na.omit(parasitos$Intensity))
random.sample.pois <- rpois(n = ndatos, lambda = xIntensity)
plot(table(random.sample.pois))
```



```
dpois(x = 0, lambda = xIntensity) # Probabilidad de observar un cero
```

```
## [1] 0.002064314
```

```
table(random.sample.pois) # Numero de ceros esperados
```

```
## random.sample.pois
##   0   1   2   3   4   5   6   7   8   9  10  11  12  13  14
##   4  23  40 114 147 175 217 141 130 100  50  30  12   8   6
```

Modelos de dos partes o “valla” (ZAP y ZANB)

```
# La primera parte de la formula contiene las covariables para el proceso de conteo, la segunda p
library(pscl)
```

```
## Classes and Methods for R developed in the
## Political Science Computational Laboratory
## Department of Political Science
## Stanford University
## Simon Jackman
## hurdle and zeroinfl functions by Achim Zeileis
```

```
ZAP <- hurdle(Intensity ~ Depth | Length + Depth, dist = "poisson",
link = "logit", data = parasitos)
summary(ZAP)
```

```
##
## Call:
## hurdle(formula = Intensity ~ Depth | Length + Depth, data = parasitos,
##     dist = "poisson", link = "logit")
##
## Pearson residuals:
##     Min      1Q  Median      3Q     Max
## -1.3420 -0.8995 -0.6450 -0.2622 32.6701
##
## Count model coefficients (truncated poisson with log link):
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) 1.7740079  0.0412390   43.02   <2e-16 ***
## Depth       0.0041351  0.0001857   22.27   <2e-16 ***
## Zero hurdle model coefficients (binomial with logit link):
##               Estimate Std. Error z value Pr(>|z|)
## (Intercept) -1.6523797  0.2870146  -5.757 8.56e-09 ***
## Length       0.0039426  0.0042165   0.935     0.35
## Depth        0.0070509  0.0008584   8.214  < 2e-16 ***
## ---
## Signif. codes:  0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1 ’ ’ 1
##
## Number of iterations in BFGS optimization: 10
## Log-likelihood: -8542 on 5 Df
```

```
ZANB <- hurdle(Intensity ~ Depth | Length + Depth, dist = "negbin",
link = "logit", data = parasitos)
summary(ZANB)
```

```
##
## Call:
## hurdle(formula = Intensity ~ Depth | Length + Depth, data = parasitos,
##     dist = "negbin", link = "logit")
##
## Pearson residuals:
##     Min      1Q  Median      3Q     Max
## -0.4350 -0.3729 -0.3281 -0.1126 16.3175
##
## Count model coefficients (truncated negbin with log link):
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -0.415345   0.844211  -0.492 0.622725
## Depth        0.006271   0.001537   4.080 4.51e-05 ***
## Log(theta)  -3.019216   0.867902  -3.479 0.000504 ***
## Zero hurdle model coefficients (binomial with logit link):
##               Estimate Std. Error z value Pr(>|z|)
## (Intercept) -1.6523797  0.2870146  -5.757 8.56e-09 ***
## Length       0.0039426  0.0042165   0.935     0.35
## Depth        0.0070509  0.0008584   8.214  < 2e-16 ***
## ---
## Signif. codes:  0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1 ’ ’ 1
##
## Theta: count = 0.0488
## Number of iterations in BFGS optimization: 16
## Log-likelihood: -2559 on 6 Df
```

Comparación de ZAP y ZANB

```
library(lmtest)
```

```
## Loading required package: zoo
```

```
##
## Attaching package: ’zoo’
```

```
## The following objects are masked from ’package:base’:
##
##     as.Date, as.Date.numeric
```

```
##
## Attaching package: ’lmtest’
```

```
## The following object is masked from ’package:VGAM’:
##
##     lrtest
```

```
lrtest(ZAP, ZANB) # Test de razón de verosimilitud
```

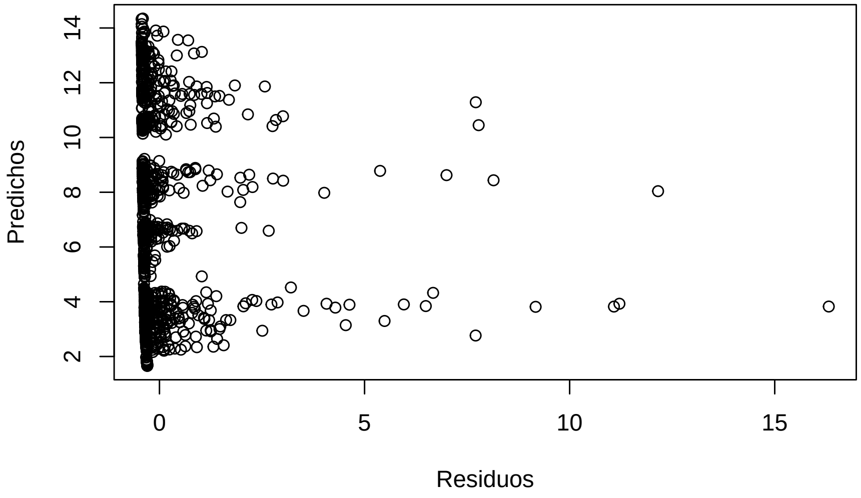
```
## Likelihood ratio test
##
## Model 1: Intensity ~ Depth | Length + Depth
## Model 2: Intensity ~ Depth | Length + Depth
##   #Df  LogLik Df Chisq Pr(>Chisq)
## 1   5 -8542.3
## 2   6 -2559.4  1 11966  < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
AIC(ZAP, ZANB)
```

```
##      df      AIC
## ZAP   5 17094.58
## ZANB  6  5130.85
```

Validación

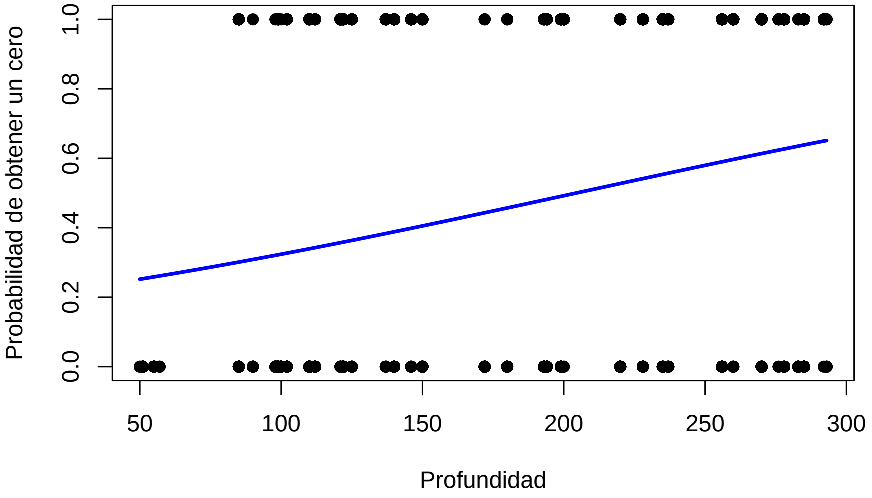
```
resid <- residuals(ZANB, type = "pearson")
plot(resid, predict(ZANB), xlab = "Residuos", ylab = "Predichos")
```



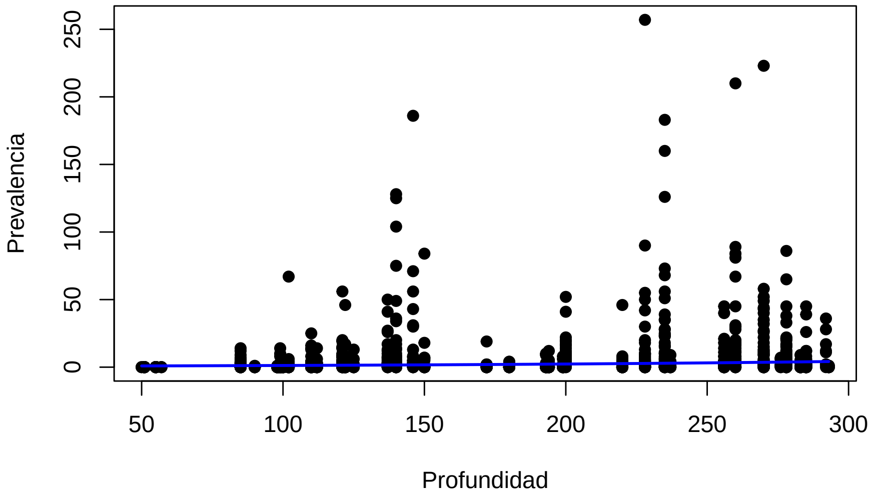
Interpretación y gráficos del modelo

```
# Proceso de falsos ceros
Depth <- seq(min(parasitos$Depth), max(parasitos$Depth), length = 500)
Length <- mean(parasitos$Length, na.rm = TRUE)
```

```
zero.model.coef <- ZANB$coefficients$zero # Coeficientes
u <- zero.model.coef[1] + Length*zero.model.coef[2] + Depth*zero.model.coef[3]
zero.model.pred <- exp(u)/(1 + exp(u)) # Predicciones
parasitos$ceros <- ifelse(parasitos$Intensity == 0, 0, 1) # Ceros vs no ceros
plot(parasitos$Depth, parasitos$ceros, pch = 19, xlab = "Profundidad", ylab = "Probabilidad de ob
lines(Depth, zero.model.pred, col = "blue", lwd = 2.5, main = "ZANB")
```



```
# Proceso de conteo
count.model.coef <- ZANB$coefficients$count # Coeficientes
u <- count.model.coef[1] + Depth*count.model.coef[2]
count.model.pred <- exp(u) # Predicciones
plot(parasitos$Depth, parasitos$Intensity, pch = 19, xlab = "Profundidad", ylab = "Prevalencia")
lines(Depth, count.model.pred, col = "blue", lwd = 2)
```



GLMs de mezcla (ZIP y ZINB)

```
library(pscl)
# La primera parte de la fórmula contiene las covariables para el proceso de conteo, l
ZIP <- zeroinfl(Intensity ~ Depth | Length + Depth, dist = "poisson",
link = "logit", data = parasitos)
summary(ZIP)
```

```
##
## Call:
## zeroinfl(formula = Intensity ~ Depth | Length + Depth, data = parasitos,
##     dist = "poisson", link = "logit")
##
## Pearson residuals:
##     Min      1Q  Median      3Q     Max
## -1.3420 -0.8995 -0.6450 -0.2622 32.6703
##
## Count model coefficients (poisson with log link):
##                Estimate Std. Error z value Pr(>|z|)
## (Intercept) 1.7740079  0.0412533   43.00   <2e-16 ***
## Depth       0.0041351  0.0001857   22.27   <2e-16 ***
##
```

```
## Zero-inflation model coefficients (binomial with logit link):
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  1.6523797  0.2870373   5.757 8.58e-09 ***
## Length      -0.0039426  0.0042167  -0.935     0.35
## Depth       -0.0070509  0.0008585  -8.213  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Number of iterations in BFGS optimization: 1
## Log-likelihood: -8542 on 5 Df
```

```
ZINB <- zeroinfl(Intensity ~ Depth | Length + Depth, dist = "negbin",
link = "logit", data = parasitos)
summary(ZINB)
```

```
##
## Call:
## zeroinfl(formula = Intensity ~ Depth | Length + Depth, data = parasitos,
##     dist = "negbin", link = "logit")
##
## Pearson residuals:
##      Min       1Q   Median       3Q      Max
## -0.45165 -0.44692 -0.33559 -0.07448 15.18154
##
## Count model coefficients (negbin with log link):
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  0.868040   0.252504   3.438 0.000587 ***
## Depth        0.005512   0.001216   4.534  5.8e-06 ***
## Log(theta)  -1.572514   0.058398 -26.927  < 2e-16 ***
##
## Zero-inflation model coefficients (binomial with logit link):
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  6.25506    1.36666   4.577 4.72e-06 ***
## Length       0.03373    0.02168   1.556     0.12
## Depth       -0.08659    0.01519  -5.699 1.21e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Theta = 0.2075
## Number of iterations in BFGS optimization: 26
## Log-likelihood: -2537 on 6 Df
```

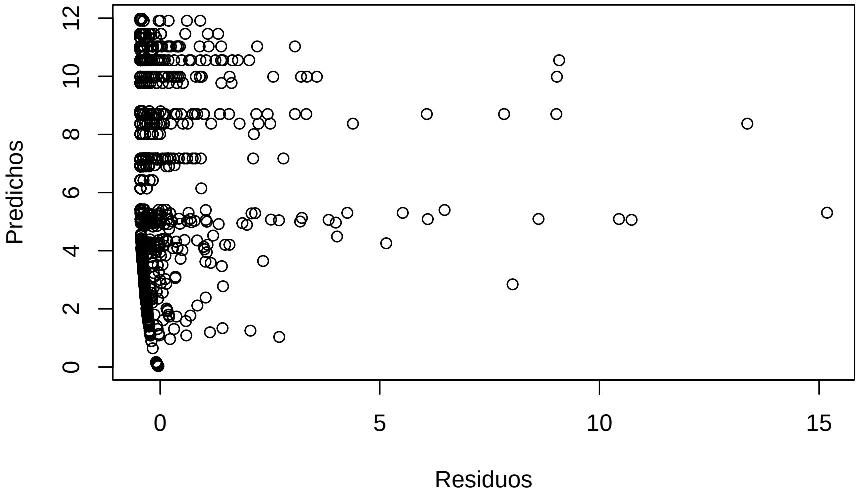
Comparacion de ZIP y ZINB

```
library(lmtest)
lrtest(ZIP, ZINB) # Test de razón de verosimilitud
```

```
## Likelihood ratio test
##
## Model 1: Intensity ~ Depth | Length + Depth
## Model 2: Intensity ~ Depth | Length + Depth
##   #Df  LogLik Df Chisq Pr(>Chisq)
## 1   5 -8542.3
## 2   6 -2537.5  1 12010  < 2.2e-16 ***
## ---
## Signif. codes:  0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1 ’ ’ 1
```

Validación

```
resid <- residuals(ZINB, type = "pearson")
plot(resid, predict(ZINB), xlab = "Residuos", ylab = "Predichos")
```

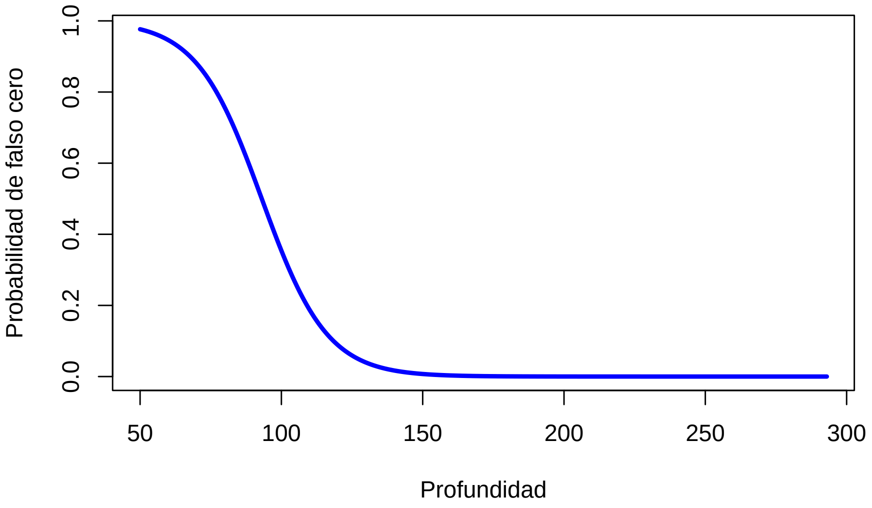


```
AIC(ZIP, ZINB)
```

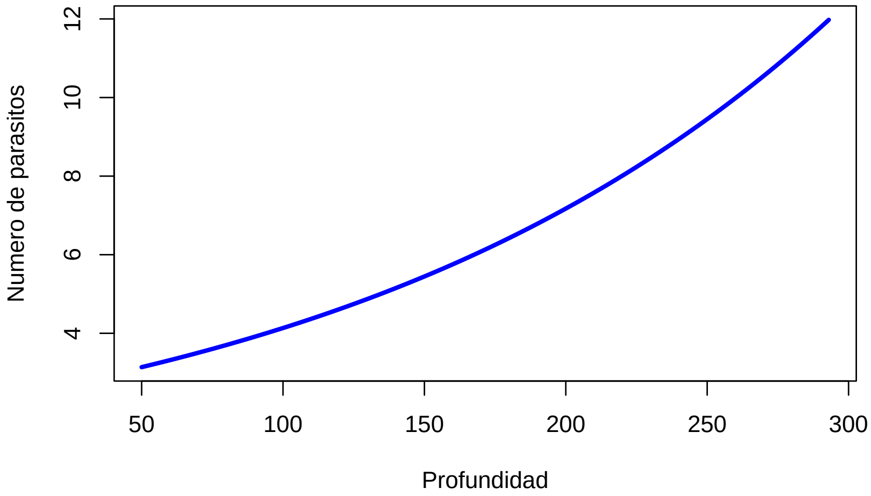
```
##      df       AIC
## ZIP   5 17094.549
## ZINB  6  5086.954
```

Interpretación y gráficos del modelo

```
# Proceso de falsos ceros
Depth <- seq(min(parasitos$Depth), max(parasitos$Depth), length = 500)
Length <- mean(parasitos$Length, na.rm = TRUE)
zero.model.coef <- ZINB$coefficients$zero # Coeficientes
u <- zero.model.coef[1] + Length*zero.model.coef[2] + Depth*zero.model.coef[3]
zero.model.pred <- exp(u)/(1 + exp(u)) # Predicciones
plot(Depth, zero.model.pred, col = "blue", type = "l", lwd = 3, xlab = "Profundidad", ylab = "Pro
```



```
# Proceso de conteo
count.model.coef <- ZINB$coefficients$count # Coeficientes
u <- count.model.coef[1] + Depth*count.model.coef[2]
count.model.pred <- exp(u) # Predicciones
plot(Depth, count.model.pred, col = "blue", type = "l", lwd = 3, xlab = "Profundidad", ylab = "Nu
```



Inferencia multimodelo

Cabral et al. (2007) estudiaron la distribución de platijas (*Solea solea*) en el estuario Tagus, Portugal (`Solea.txt`). Se desea saber qué factores del agua y sustrato están relacionados con la presencia esta especie.

```
# Análisis exploratorio
datos <- read.table("Solea.txt", header = TRUE)
str(datos)
```

```
## 'data.frame':    65 obs. of  13 variables:
##  $ Sample       : int  1 2 3 4 5 6 7 8 9 10 ...
##  $ season       : int  1 1 1 1 1 1 1 1 1 1 ...
##  $ month        : int  5 5 5 5 5 5 5 5 5 5 ...
##  $ Area         : int  2 2 2 4 4 4 3 3 3 1 ...
##  $ depth        : num  3 2.6 2.6 2.1 3.2 3.5 1.6 1.7 1.8 4.5 ...
##  $ temperature  : int  20 18 19 20 20 20 19 17 19 21 ...
##  $ salinity     : int  30 29 30 29 30 32 29 28 29 12 ...
##  $ transparency : int  15 15 15 15 15 7 15 10 10 35 ...
##  $ gravel       : num  3.74 1.94 2.88 11.06 9.87 ...
##  $ large_sand   : num  13.15 4.99 8.98 11.96 28.6 ...
##  $ med_fine_sand: num  11.93 5.43 16.85 21.95 19.49 ...
##  $ mud          : num  71.2 87.6 71.3 55 42 ...
##  $ Solea_solea  : int  0 0 1 0 0 0 1 1 0 1 ...
```

```
round(cor(datos[, 4:12]), 2)
```

```
##                Area depth temperature salinity transparency gravel large_sand
## Area           1.00 -0.55       -0.18     0.76        -0.56   0.44      -0.44
## depth         -0.55  1.00        0.14    -0.66         0.57  -0.24       0.31
## temperature   -0.18  0.14        1.00    -0.35         0.54  -0.16       0.12
## salinity       0.76 -0.66       -0.35     1.00        -0.66   0.38      -0.54
## transparency  -0.56  0.57        0.54    -0.66         1.00  -0.25       0.37
## gravel         0.44 -0.24       -0.16     0.38        -0.25   1.00       0.01
## large_sand    -0.44  0.31        0.12    -0.54         0.37   0.01       1.00
## med_fine_sand -0.69  0.67        0.25    -0.80         0.69  -0.32       0.56
## mud            0.49 -0.47       -0.16     0.63        -0.52  -0.19      -0.87
##               med_fine_sand   mud
## Area                  -0.69  0.49
## depth                  0.67 -0.47
## temperature            0.25 -0.16
## salinity              -0.80  0.63
## transparency           0.69 -0.52
## gravel                -0.32 -0.19
## large_sand             0.56 -0.87
## med_fine_sand          1.00 -0.78
## mud                   -0.78  1.00
```

Modelos candidatos

```
# modelo nulo
m1 <- glm(Solea_solea ~ 1, family = binomial, data = datos)
# modelo de temperatura
m2 <- glm(Solea_solea ~ temperature, family = binomial, data = datos)
# modelo de salinidad
m3 <- glm(Solea_solea ~ salinity, family = binomial, data = datos)
# modelo de transparencia
m4 <- glm(Solea_solea ~ transparency, family = binomial, data = datos)
# modelo de profundidad
m5 <- glm(Solea_solea ~ depth, family = binomial, data = datos)
# modelo caracteristicas del agua
m6 <- glm(Solea_solea ~ temperature + salinity + transparency, family = binomial, data = datos)
# Modelo ubicacion en el espacio
m7 <- glm(Solea_solea ~ Area + depth + Area:depth, family = binomial, data = datos)
# Modelo de caracteristicas del sutrato
m8 <- glm(Solea_solea ~ gravel + large_sand + med_fine_sand, family = binomial, data = datos)
```

```
# Modelo de caracteristicas del sustrato grueso
m9 <- glm(Solea_solea ~ gravel + large_sand, family = binomial, data = datos)
# Modelo de caracteristicas del sustrato fino
m10 <- glm(Solea_solea ~ med_fine_sand, family = binomial, data = datos)
# Modelo de profundidad y sustrato
m11 <- glm(Solea_solea ~ depth + gravel + large_sand + med_fine_sand, family = binomial
```

Selección de modelos

```
library(MuMIn)
```

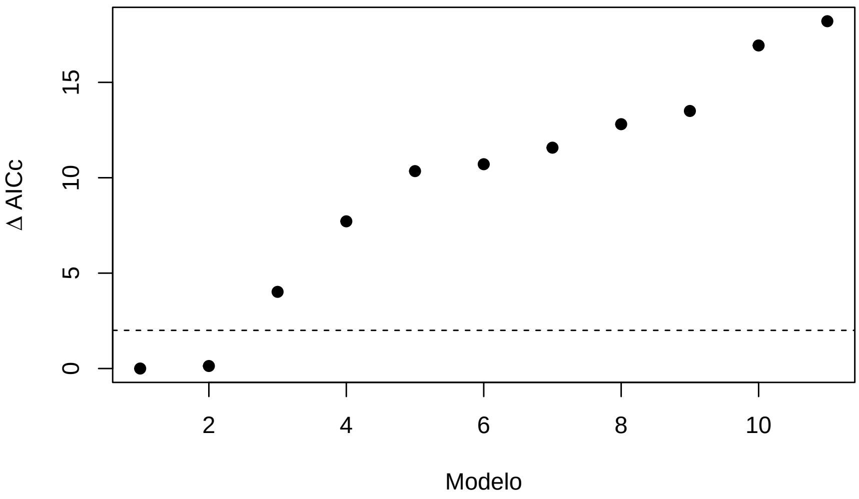
```
##
## Attaching package: 'MuMIn'

## The following object is masked from 'package:VGAM':
##
##     AICc
```

```
modelos <- list(m1, m2, m3, m4, m5, m6, m7, m8, m9, m10, m11)
ranking.modelos <- model.sel(modelos, rank = "AICc")
ranking.modelos
```

```
## Model selection table
##      (Int)     tmp     sln       trn    dpt    Are Are:dpt       grv lrg_snd
## 7  -1.4470                           1.0730 0.5759 -0.6021
## 3   2.6610         -0.1299
## 6   5.2220 -0.1005 -0.1427 -0.001162
## 5  -2.3250                           0.6152
## 10 -1.5180
## 11 -3.0370                           0.5575                 0.008671 0.04312
## 4  -1.5410                  0.043430
## 8  -1.9980                                                  0.011060 0.03151
## 9  -1.3880                                                 -0.014340 0.05502
## 1  -0.4055
## 2  -2.6330  0.1006
##    med_fin_snd df  logLik AICc delta weight
## 7                4 -31.977 72.6  0.00  0.474
## 3                2 -34.280 72.8  0.13  0.444
## 6                4 -33.987 76.6  4.02  0.064
## 5                2 -38.071 80.3  7.72  0.010
## 10    0.052640  2 -39.388 83.0 10.35  0.003
## 11   -0.001628  5 -36.156 83.3 10.71  0.002
## 4                2 -40.002 84.2 11.58  0.001
## 8     0.041010  4 -38.381 85.4 12.81  0.001
## 9                3 -39.864 86.1 13.50  0.001
## 1                1 -43.746 89.6 16.93  0.000
## 2                2 -43.316 90.8 18.20  0.000
## Models ranked by AICc(x)
```

```
plot(1:length(modelos), ranking.modelos$delta, pch = 19, xlab = "Modelo", ylab = expression(Delta
abline(a = 2, b = 0, lty = 2)
```



Promediado de modelos

```
modelo.promedio <- model.avg(ranking.modelos, subset = delta < 2)
summary(modelo.promedio)
```

```
##
## Call:
## model.avg(object = ranking.modelos, subset = delta < 2)
##
## Component model call:
## glm(formula = <2 unique values>, family = binomial, data = datos)
##
```

```
## Component models:
##     df logLik  AICc delta weight
## 234  4 -31.98 72.62  0.00   0.52
## 1    2 -34.28 72.75  0.13   0.48
##
## Term codes:
##   salinity      depth       Area Area:depth
##          1          2          3          4
##
## Model-averaged coefficients:
## (full average)
##             Estimate Std. Error Adjusted SE z value Pr(>|z|)
## (Intercept)  0.53879    2.60505     2.62506   0.205    0.837
## Area         0.29744    0.75111     0.76410   0.389    0.697
## depth        0.55409    0.68398     0.68935   0.804    0.422
## Area:depth  -0.31101    0.41353     0.41749   0.745    0.456
## salinity    -0.06278    0.06929     0.06946   0.904    0.366
##
## (conditional average)
##             Estimate Std. Error Adjusted SE z value Pr(>|z|)
## (Intercept)  0.53879    2.60505     2.62506   0.205 0.837378
## Area         0.57586    0.96536     0.98489   0.585 0.558752
## depth        1.07273    0.59108     0.60304   1.779 0.075260 .
## Area:depth  -0.60213    0.39469     0.40268   1.495 0.134837
## salinity    -0.12985    0.03494     0.03562   3.645 0.000267 ***
## ---
## Signif. codes:  0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1 ’ ’ 1
```

```
sw(modelo.promedio)
```

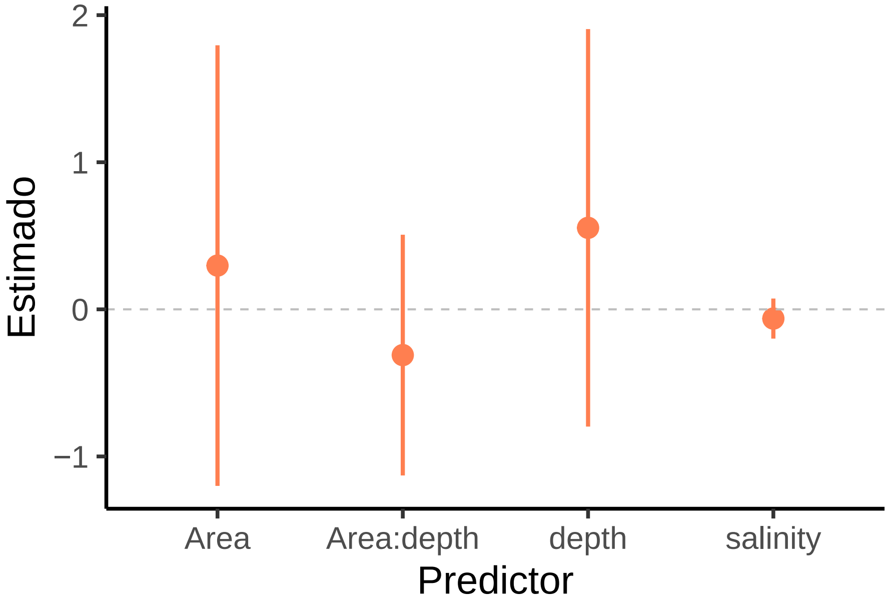
```
##                      depth Area Area:depth salinity
## Sum of weights:      0.52  0.52 0.52       0.48
## N containing models:    1     1    1          1
```

Gráfico del modelo promedio

```
model.coeff <- data.frame(estimate = modelo.promedio$coefficients[1,])
CI <- as.data.frame(confint(modelo.promedio, full = TRUE))
model.coeff$CI.min <- CI$`2.5 %`
model.coeff$CI.max <- CI$`97.5 %`
model.coeff$coef <- rownames(model.coeff)

library(ggplot2)
```

```
ggplot(data = model.coeff[2:5, ], aes(x = coef, y = estimate)) +
  theme_classic(base_size = 20) +
  geom_pointrange(aes(ymin = CI.min, ymax = CI.max), size = 1, color = "coral") +
  xlab("Predictor") + ylab("Estimado") +
        geom_hline(yintercept = 0, linetype = "dashed", color = "gray")
```



Actividades

Ejercicio 3.1

Los datos del archivo `gala.xls` corresponden a un estudio donde se relevó la diversidad de especies de tortugas de las Islas Galápagos. De cada isla se obtuvo la riqueza de especies (`Species`), el área (`Area`), la altitud (`Elevation`), la distancia a la isla más cercana (`Nearest`), la distancia a la isla Santa Cruz (`Scruz`) y el área de la isla más cercana (`Adjacent`).

- Construya un modelo adecuado que relacione el número de especies endémicas (`Endemics`) con las variables medidas y analice su poder explicativo.
- Realice uno o más gráficos que representen el modelo ajustado.

- Debido a disponibilidad presupuestaria, sólo se podrán concentrar esfuerzos de conservación en islas con un alto número de especies endémicas (>80). ¿A partir de qué valor de elevación el modelo predice más de 25 especies endémicas? Para esto considere valores constantes en el resto de las covariables incluidas en su modelo.

Ejercicio 3.2

Radim et al. (2015) analizaron la ocurrencia de muérdagos (*Loranthus europaeus*) en robles de República Checa, teniendo en cuenta el área basal (`basal_area`), el número de tallos (`Number_of_stems`), el área basal promedio de los tallos (`mean_stem_basal_area`), la competencia con árboles infectados basada en el índice de Hegyi (`CI_stem`) y el rango de los multicaules en ciertas direcciones (`Xrange`, `Yrange` y `RangeAvg`) (https://doi.org/10.1371/journal.pone.0127055). El conjunto de datos corresponde al archivo `Matula_mistletoes_csv`.

- Encontrar un modelo que mejor explique la probabilidad de infección por muérdagos (`infected`) en robles.
- Construya una o más tablas que muestren los resultados principales.
- Realice uno o más gráficos que represente el modelo ajustado.

Ejercicio 3.3

Tomando como base el conjunto de datos `parasitos.txt` y el modelo ZAP (de dos partes o "valla") ajustado, ajuste un modelo ZAP con los mismos predictores pero de forma manual. Para esto, considere utilizar dos GLMs por separado: uno para la probabilidad de obtener un cero, y otro para la distribución de los conteos. Compare los resultados con el modelo obtenido con la función `hurdle` (paquete `pscl`).

Ejercicio 3.4

Raventos et al. (2019) evaluaron la respuesta de rasgos de historia de vida a diferentes variables ambientales (mediante técnicas reconstructivas de otolitos) en varias especies de peces (https://doi.org/10.1111/1365-2656.13435). Para esto, se estimaron caracteres de historia de vida, incluyendo la duración larval pelágica (`PLD`), la tasa de crecimiento (`Pre-settlement_growth`), el tamaño de asentamiento (`Size_of_settlement`) y la fecha de puesta (`Hatching_day_date`). El conjunto de datos se encuentra en el archivo `Raventos_etal_2021_JAE_data.txt`.

- Analice qué factores determinan la respuesta de las tasas de crecimiento de dos especies considerando la temperatura de la superficie del agua (`SST`), la clorofila A mensual promedio en mg/m (`ChLA`) y la estación (`Season`).

- Compare los predictores de los modelos de cada especie ¿Cuál es más importante para cada una y en qué magnitud?

Modelos no lineales

Placeholder

Regresión no paramétrica

Regresión polinómica

Funciones a trozos

Splines de regresión

Polinomios a trozos

Splines de suavizado

Modelos aditivos generalizados

GAM con otras distribuciones e interacciones

Comparación de modelos

Validación

Modelo con variables continuas (efectos principales + interacciones)

Actividades

Ejercicio 4.1

Ejercicio 4.2

Ejercicio 4.3

Modelos mixtos

Placeholder

Dependencia temporal

Dependencia espacial

Introducción a los modelos mixtos

Un caso especial

Modelos lineales generalizados mixtos

Diseño anidado

Diseño cruzado

Modelos mixtos con estructura espacial

Modelos mixtos con filogenia

Modelos aditivos generalizados mixtos

Ajuste de modelos

Gráficos

Autocorrelación temporal

Actividades

Ejercicio 5.1

Ejercicio 5.2

Ejercicio 5.3

Ejercicio 5.4

Ejercicio 5.5