*Helgoland Marine Research*

**SUPPORTING INFORMATION**

***Neohelice granulata* burrow fidelity behaviour related to landscape heterogeneity**

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S1. **An example of the evaluation the body size using hierarchical bayesian model for the number of “faithful” crabs at MCH site.**

Analyses of model performance following a Binomial distribution:

eqn 1

*mt~*Binomial (*nt*, *pt*)

Including a lower-level [beta regression](https://stats.stackexchange.com/questions/29038/regression-for-an-outcome-ratio-or-fraction-between-0-and-1) mode to hierarchical especification:

*p[t] ~ dbeta(alpha[t], beta[t]) describes the variability among days of observation*

*alpha[t] = phi[day[t]] \* mu[day[t]]*

*beta[t] = phi[day[t]] \* (1 – mu[day[t]])*

where *alpha[t]* and *beta[t]* are the shape and scale parameters of the Beta distribution for day i, calculated using the value of mu.

The linear equation is:

 eqn 2

*logit*(*mu*)*t*= *b0t*+ *b1t*\*(size)

where, *mui,t* denotes the number of “faithful” individuals for sex *t* (male or female), *nt* is the number of crabs measured (“faithful” + “unfaithful” individuals) at each sex, *logit(p)t* is the linear relation between size(carapace width) crabs and indicates the mean of success probability at sex *t.* The term *b0t* indicates the intercept at size *t* for sex *t* and *b1t*.

 MCH is a dataset that describe the presence (1) and absence (0).

R specification

md <- mydata

N <- rowSums(!is.na(md)) # Count the number of to each surveyed burrow

x <- nrow(md) # Total number of surveyed burrow

y <- rowSums(md, na.rm = TRUE) # number of times that the crab was register at each surveyed burrow.siz: size as covariate variable

sex: factor variable (*male or female)*

nsex: definition the sex variable levels

#Full model considering all variables of this study

bugs<- file.path(".../full\_jags.bug")

bugs

data <- list("y", "N", "x", "siz", "nsex", "sex")

inits <- function() {

 list(b0 = rnorm(nsex,1,0.01), b1 = rnorm(nsex,1,0.01))

}

parameters <- c("b0", "b1", "psi0")

Cand.models <- list( )

Cand.models[[1]]<- jags(data, inits, parameters, bugs, n.chains = xx, n.thin = xx,

 n.iter = xx, n.burnin = xx )

#without sex

bugs<- file.path(".../withoutsex\_jags.bug")

bugs

data <- list("y", "N", "x", "siz") #data as list

inits <- function() {

 list(b0 = rnorm(1,1,0.01), b1 = rnorm(1,1,0.01))

}

parameters <- c("b0", "b1","psi0")

Cand.models[[2]] <- jags(data, inits, parameters, bugs, n.chains = 3, n.thin = 1,

 n.iter = 100.000, n.burnin = 10.000)

##create a vector of names to trace back models in set

Modnames <- paste("mod", 1:length(Cand.models), sep = " ")

DIC(cand.set = Cand.models, modnames = Modnames)

##generate DIC table

dictab(cand.set = Cand.models, modnames = Modnames, sort = TRUE)

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An example of JAGS specification code of a complete model of the effect of the studied variables in the site fidelity by crabs for MCH dataset.

*model{*

*# The number of “faithful” crabs with a Binomial distribution*

 *#model*

*for(i in 1:N){*

 *y[i] ~ dbinom(p[i], x[i])*

 *p[i] ~ dbeta(alpha[i], beta[i])*

 *alpha[i] = phi[day[i]] \* mu[day[i]]*

 *beta[i] = phi[day[i]] \* (1 - mu[day[i]])*

 *logit(mu[i])<- b0[sex[i]]+b1[sex[i]]\*size+b2[sex[i]]\*den }*

*#Specification of no-informative priors to linear regression*

*for(j in 1:nsex){*

 *b0[j] ~ dnorm(0,0.01)*

 *b1[j] ~ dnorm(0,0.01)*

 *b2[j] ~ dnorm(0,0.01)*

 *}*

*#Specification of no-informative priors to random variable*

 *for(l in 1:nday){*

 *phi[l] ~ dnorm(0,0.01)*

 *}*

*# mean of probability to faithful crabs*

*logit(psi0) <- b0*

*}*

Model without incorporating body size

*# The number of “faithful” crabs with a Binomial distribution*

 *#model*

*for(i in 1:N){*

 *y[i] ~ dbinom(p[i], x[i])*

 *p[i] ~ dbeta(alpha[i], beta[i])*

 *alpha[i] = phi[day[i]] \* mu[day[i]]*

 *beta[i] = phi[day[i]] \* (1 - mu[day[i]])*

 *logit(mu[i])<- b0[sex[i]]+b2[sex[i]]\*den }*

*#Specification of no-informative priors to linear regression*

*for(j in 1:nsex){*

 *b0[j] ~ dnorm(0,0.01)*

 *b2[j] ~ dnorm(0,0.01)*

 *}*

*#Specification of no-informative priors to random variable*

 *for(l in 1:nday){*

 *phi[l] ~ dnorm(0,0.01)*

 *}*

*# mean of probability to faithful crabs*

*logit(psi0) <- b0*

*}*

S2. **Fidelity of females crab related to reproductive status**

During the study, we found a little number of gravid females in all the sites, whereby the analysis for those females at different reproductive status was not very informative (due to the high number of zeros). Thus, we calculated a descriptive Posterior Probability of the females crab, pooling the data of all the sites related to reproductive status. Probabilities estimated showed a potential evident differentiation between females of different reproductive status with a higher proportion of “faithful” gravid compare to non-gravid females.

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**Figure 3**: Bar-plot of the Posterior Probability (PP) of the number of “faithful” female crab related to reproductive status. The y-axis shows the mean of the posterior probability and credibility interval estimated and the x-axis the reproductive status.

S3. **Evaluation of the differences in the population densities among sites and zones**

**Aim**

We evaluate whether differences in degree of cannibalism of *Neohelice granulata* among populations could be related with population densities. To achieve this goal, we compared crabs density of *N. granulata* of different sites with different degree of cannibalism reported in the literature.

**Method**

Crabs density of *N. granulata* was measured in both zones (mudflat and saltmarsh) of each sites (MCH: Mar chiquita, SAO: San Antonio Oeste and RSJ: Riacho San José), as the number of individuals higher than 20 mm of carapace width within ten 50 × 50 cm haphazardly placed square frames.

**Data analysis**

A General Linear Model (GLM) with a gaussian distribution and a link “log” [1] was performed to determine whether densities of crabs (dependent variable) vary according to the independent variables (i.e. sites and zones). Considering our data did not meet the assumptions of homoscedasticity, we used the generalized least squares (GLS) statistical modelling approach structuring the variance with the VarIdent function [1]. These models were compared to the equivalent model without the GLS extension using Akaike’s information criterion (AIC), and then plots of residuals versus fitted values were examined to check the homoscedasticity. The model with the zone as variance structured was the most appropriate model, and therefore we used this as a starting point for determining the most appropriate fixed structure. GLS were fitted using maximum likelihood with “nlme” package [2]. Then, where necessary, we conducted mean comparisons using an interaction means test in the “phia” package for mixed or multivariate linear models for repeated measures experiments [3]. All statistical analyses were conducted in R 3.3.1 [4].

**Results**

Crabs density was different among all zones and sites and it showed a significant interaction between factors (χ2=79.586, df=2, P-value<0.05). Subsequent pairwise analysis detected differences among all shore heights (P-value <0.05). To saltmarsh zone the pairwise analysis showed a higher density at RSJ (P-value <0.05) than at MCH (P-value <0.05) and at SAO (P-value <0.05) while between MCH and SAO was not significant (P-value >0.05).

**Conclusion**

Due to we find the lowest density of individuals where high degrees of cannibalism are reported (see Fig S2), these results do not support the hypothesis that the population with higher densities may increase the degree of cannibalism. Therefore, the degree of cannibalism in *N. granulata* may depends on the proportion of organic matter content of the sediment, as previously reported [5,6].



**Figure S3**: Bar-plot of the crabs density to both zones (mudflat and saltmarsh) of each sites (MCH: Mar Chiquita, SAO: San Antonio Oeste and RSJ: Riacho San José). Letters over the bar indicate differences showed by posterior pairwise test. Words under box code indicate the degree of cannibalism on smaller crabs extracted to Mendez Casariego et al. [5] and Bas et al. [6] for SAO and MCH and from Bas et al. submitted for RSJ.

**References**

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