

The effects of urbanization and industry on cephalopod population dynamics

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1 **Introduction:**

2 In the southwestern region of Madagascar, increased urbanization and the arrival of international
3 export markets have resulted in transformation of the fishery from small-scale subsistence
4 practices to a larger scale industrial fishing economy. Since then, anecdotal reports of decreased
5 catch have been seen in the area (Laroche et al., 1997). Further, although fishing restrictions in
6 Madagascar have helped regain fish stocks and biodiversity as well as given local fisherman
7 power in establishing management strategies, their implementation combined with the specific
8 fishing practices of the Vezo people have actually further entrenched gender norms in the region
9 as community involvement is mostly made up by men and No Take Zones are typically
10 established in tidal regions where fishing by women generally occurs (Astuti, 1995; Baker-
11 Médard, 2017; Oliver et al., 2015).

12 Since 2003, when this resource first began to globalize, cephalopods have become the largest
13 class of exports (Benbow et al., 2014; Humber et al., 2006). This has since added significant
14 fishing pressure to Madagascar's cephalopod populations and yield from this fishery has
15 decreased in the southwest Andavadoaka region (Humber et al., 2006). Compared to other
16 fisheries, cephalopods have a short lifespan coupled with a fast reproduction rates and high
17 fecundity. This explains their population's ability to quickly bounce back when short term
18 MPA's are introduced into their region (Benbow et al., 2014; Humber et al., 2006; Katsanevakis
19 & Verriopoulos, 2006). Cephalopods are therefore extremely sensitive to both protection and
20 harvest levels, making them a good indicator of overfishing. Further, cephalopod growth is
21 highly variable and depends on factors such as food source and water temperature (Herwig et al.
22 2012, Van Heukelem 1973, Raberinary and Benbow 2012). This makes them difficult to model
23 as fecundity is also related to cephalopod size at maturity.

Predator-prey models are a common and useful tool in understanding population dynamics both as an ecosystem, and in predicting a population's response to different levels of harvest.

Typically, however, predator-prey dynamic models view human influence as a single parameter, such as including fishing rates incorporated into an overall death rate (Blackwood et al., 2012).

In reality, the dynamics of human practices and their interaction with the environment are a lot more complex. Socially or politically bound communities must balance the value of conservation versus the monetary gain of harvest. This tradeoff is governed by social perception, which in turn controls either the laws or injunctive norms that dictate how harvest is conducted. Previous research incorporating elements of elementary game theory and replicator dynamics has modeled how an individual's perception of conservation can influence those around them (Sigdel et al., 2017; Thampi et al., 2018). As changing the value of octopus has already been seen to alter fishing effort (Humber et al., 2006; Oliver et al., 2015), these models permit better study of socio-ecological feedback as one system, including that of the fishing practices of the Vezo community.

Our socio-ecological model will be adapted from Thampi et al. 2018. This paper replaces a fishing parameter with an equation for societal injunctive norms. Essentially, this paper utilizes concepts from evolutionary game theory to model how the proportion of "conservationists" in a community changes. Individuals are either for or against fishing based on the economic value of harvest, how likely people are to change their minds, and the current health of the ecosystem. As individuals change their stance on fishing, they then influence those around them as well, resulting in the complex replicator dynamics that alters fishing intensity.

Due to certain cultural aspects of the Vezo community, the Thampi model does not fully encapsulate the role of social influence on fishing practices. The gendered distribution of specific

fishing practices within the Vezo community of Madagascar provides an opportunity to expand current socio-ecological models; It can offer an additional level of influence: that of gender roles on fishing practices and decision-making, as Non-Governmental Organizations in the area have promoted community conservationism without considering the community's underlying gender dynamics (Baker-Médard, 2017). This will allow us to identify the social processes that need to be taken not only to better protect cephalopod communities but to show a need to open a space for women to participate in the decision-making process. Previous models have not accounted for complex gender dynamics in socio-ecological systems, which is what we are hoping to develop when revising the model. For this study, we plan on conducting statistical tests on data collected from this region to parameterize portions of this model, as well as deduce if we need to add spatial variability. Specifically, as octopus growth is highly variable based on environment, we want to see if there is any variability between octopus caught in the numerous fishing regions in the area. Further, as Vezo men and women fish differently, this study aims to see if men and women catch different numbers of octopus as this will be able to inform how we want to incorporate gender into our socio-ecological model. We hypothesize that men catch more cephalopods per landing due to this different fishing method as well as the prominence of male fishers compared to female.

Methods:

In order to parameterize our model, we will be using data collected in the southwestern region of Madagascar. From 2011 to 2020, researchers surveyed fishers selling their catch for export. They collected the date, catch type, number, weight, price of the catch, and where it was fished from. Further, they gathered information on the fisher themselves such as their name, gender, the method of fishing used, and, in some cases, the amount of time spent at sea. It is from this data

that we will assess the if different regions are more conducive to cephalopod growth and the differences in cephalopod fishing between men and women.

Models and analysis:

Model 1: Regional differences in cephalopod growth. Because there are over 50 fishing sites in this region, many with only several datapoints, we only considered the most heavily fished regions, or those with over 150 cephalopod landings. These regions are Ananose, Andamabe, Anjokozoko, Belmara, Nandoa, Nanohofa, and Tsimahofoty. In order to assess if cephalopods in different regions are different sized, we will be conducting a Bayesian ANOVA as follows:

$$\text{Mass} \sim \text{norm}(\mu, \sigma_i)$$

$$\mu = \alpha_i$$

Where the mass of cephalopod caught is assumed to come from a normal distribution with some mean μ and standard deviation σ , both of which will vary by site i .

Data was log transformed before analysis due to the model predicting multiple negative values.

This test will be conducted via the “r2jags” (Su and Yajima 2021). package in the programming

environment R version 4.1.2 (R Core Team 2021). We ran a Markov Chain Monte Carlo using

methods outlined in Kéry 2010a with 1000 iterations, discarding 100 of those as burn in values. 3

chains were run with a thinning rate of 3. We assumed normal priors for alpha-the natural log of

the average weight of cephalopods at each site. α_i used normal priors ($\text{norm}(0, 0.001)$), and the

priors for σ_i came from a uniform distribution ($\text{unif}(0,10)$). Model was assessed for convergence

using a Rhat value (Gelman and Hill, 2006) of 1 and significance was assessed if the 97.5%

credible interval of each alpha overlapped with zero.

In order to assess model accuracy, we generated artificial data from each run of our MCMC and compared those predictions with those directly from our data. Further, we supplemented this model with a frequentist Tukey test in order to assess if these regions' cephalopods are different sizes with a 95% credible interval (Appendix figure 1).

Model 2: Differences in cephalopod catch based on gender. A key component of our socio-ecological model is to understand the different relationships that men and women have with fishing. To quantify the differences in fishing output between men who fish in deeper reefs and women who fish along tidal flats, we conducted a Bayesian effects Poisson t test with a log link function:

$$\text{Cephs} \sim \text{Poisson}(\lambda)$$

$$\log(\lambda) = \beta_0 + \beta_1 * \text{SF} + \varepsilon$$

$$\varepsilon \sim \text{norm}(0, \sigma)$$

Where the number of cephalopods caught in a landing (Cephs) is assumed to come from a Poisson distribution with a mean and standard deviation of λ . The log of λ is a function of our β_0 (the number of cephalopods caught by women fishers) and β_1 (the difference between the expected catch of women and that of men fishers). SF simply refers to the sex of the fisher, with SF = 0 assigned to female fishers and SF = 1 referring to male fishers. ε was included as an overdispersion term. This term was included due to the high variability of data, especially for male fishers and is used to encapsulate variance in the data not accounted for in the Poisson distribution (Appendix figure 2).

Similar to our previous model, we used the “r2jags” (Su and Yajima 2021) package in the programming environment R version 4.1.2 (R Core Team 2021). We ran a Markov Chain Monte

Carlo with 1000 iterations, discarding 100 of those as burn in values. 3 chains were run with a thinning rate of 3. We assumed normal distributions for the priors β_0 and β_1 (norm(0, 0.001) for both) and the prior for σ was assumed to be a uniform distribution of unif(0,10). Model convergence was once again assessed by using an Rhat value (Gelman and Hill, 2006) of 1 and once again, significance was assessed if the 97.5% credible interval of each alpha overlapped with zero. Bayes P values (Kéry 2010a) and Pearson Residuals (Kéry 2010b) were also calculated. The Pearson residual was used to assess if the model recreated data with a similar sum of squared residuals as our original data.

Results:

In our ANOVA, including assuming unequal variance between sites improved our DIC value from 6669.3 to 5688.8, which is why we included it in the model. The average weight of cephalopods caught in each site is reported in table 1. Further, when we regenerated data from our model and compared that with that of our original data, a visual assessment showed that the model generally predicted similar averages and variances per site as our original dataset (figure 1).

To further assess this, we conducted the frequentist T test along with a Tukey test. The results of this test found statistical similarities between several regions, with Ananose being the only one that shared no similarity between the other sites (figure 2).

In our Poisson T-test, our model predicted an average catch size of 2.77 for women and 3.06 for men. However, our Bayes P value was 1, meaning that the model was consistently overpredicting catch sizes. The data generated by the model had a similar trend as well as the sum of squared residuals for the modeled data was higher (3,417.22) than that of the actual

measured data (2,977.9). Further, we can see a lot more variability in the posterior distribution of β_0 (average catch by women) as opposed to $\beta_0 + \beta_1$ (average catch by men) from the model (figure 3). We think this is due to the fact that there are 3078 data points collected from men as opposed to 339 data points from women.

Discussion:

As shown by our ANOVA, the heavily fished sites output a range of average cephalopod weights from 0.698 in Ananose to 0.893 in Tsimahafoty. As these sites were also considered statistically different from one another from our Tukey test, and a further literature search is needed to see if the expected reproductive output of cephalopods at these two weights is different enough to warrant adding spatial variability to our socio-ecological model. Further, knowing the average weight of cephalopods caught can better inform the “value of fishing” parameter in our model. Our T test showed that men and women are catching different numbers of cephalopods on average, therefore supporting our hypothesis that not only do men and women employ different fishing methods, but the outcome of their efforts is different as well. Depending on how we end up incorporating gender differences in our model, this could contribute to having different fishing rate parameters for men and women.

As for the accuracy of our models, we do not recommend using these for predictive purposes as we were not able to calculate an acceptable Bayesian P Value for our t test. However, as we were just using these models to understand our dataset, we can rely on these numbers to give us average counts or weights from the data we had. For the ANOVA, unequal variance greatly improved the DIC of the model, and we even attempted to include random site effects. This improved the DIC from 5688 to 5686. Even though this is an extremely small change in DIC that

157 could be attributed to different MCMC's being run each time, it's worth taking more time to
158 understand if our regions are statistically independent or not.

Figures and Tables:

Region	Average Cephalopod Weight (kg)
Ananose	0.698
Adamabe	0.813
Anjokozoko	0.866
Belmera	0.880
Nandoa	0.831
Nanohofa	0.818
Tsimahafoty	0.893

Table 1: Expected weight of cephalopods caught in each region as calculated from our Bayesian ANOVA

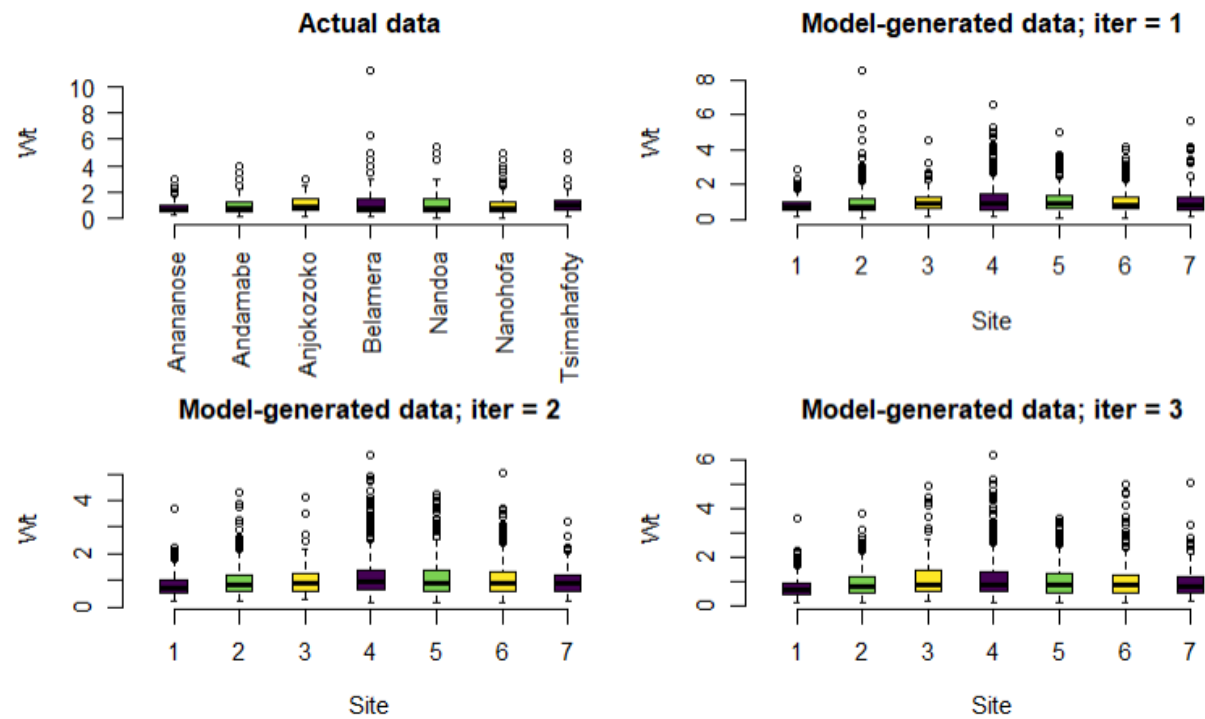


Figure 1: Model generated data compared to our actual dataset from the Bayesian ANOVA model. Each iteration of the model generated data with similar means per site.

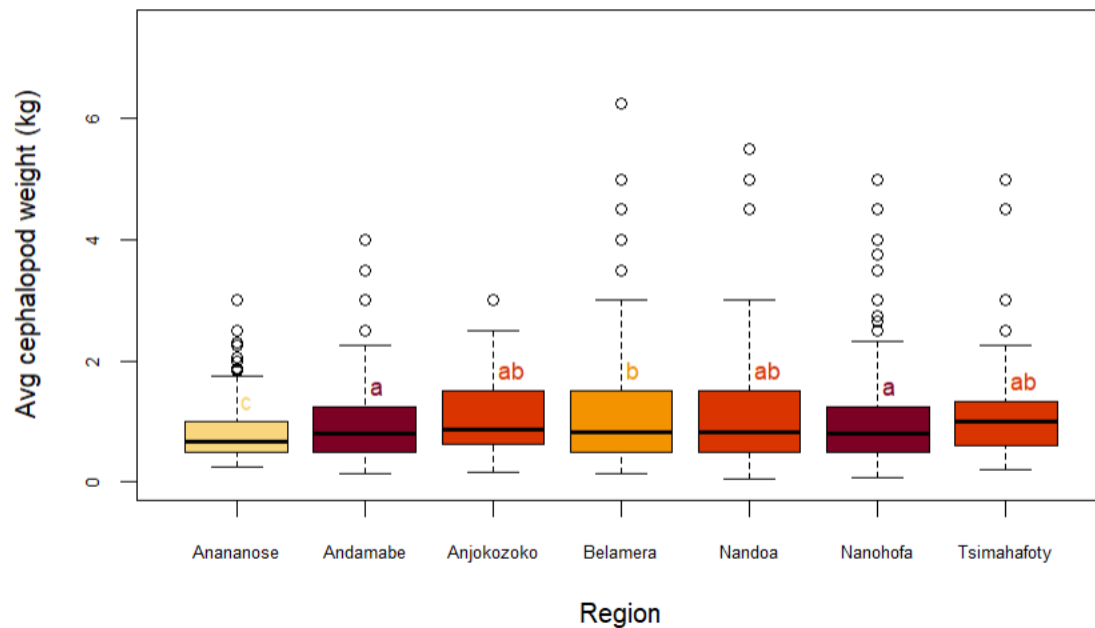


Figure 2: Results of a Tukey test comparing the different regions and the average weight of cephalopods found in each location. Same colors and letters denote statistical similarity in these weights.

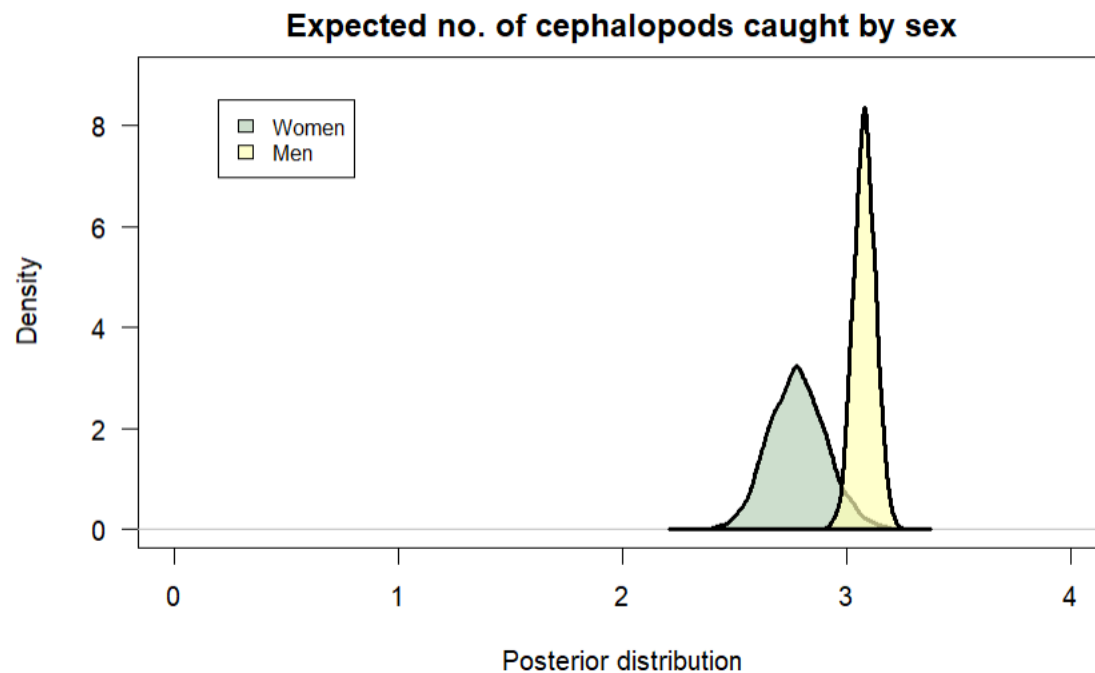


Figure 3: Distribution of posteriors calculated by our T test. We see the means of these posteriors as the predicted catch values, but the two posteriors for β_0 (predicted catch for women) and $\beta_0 + \beta_1$ (predicted catch for men) have very different spreads which we think we can attribute to the large differences in sample sizes.

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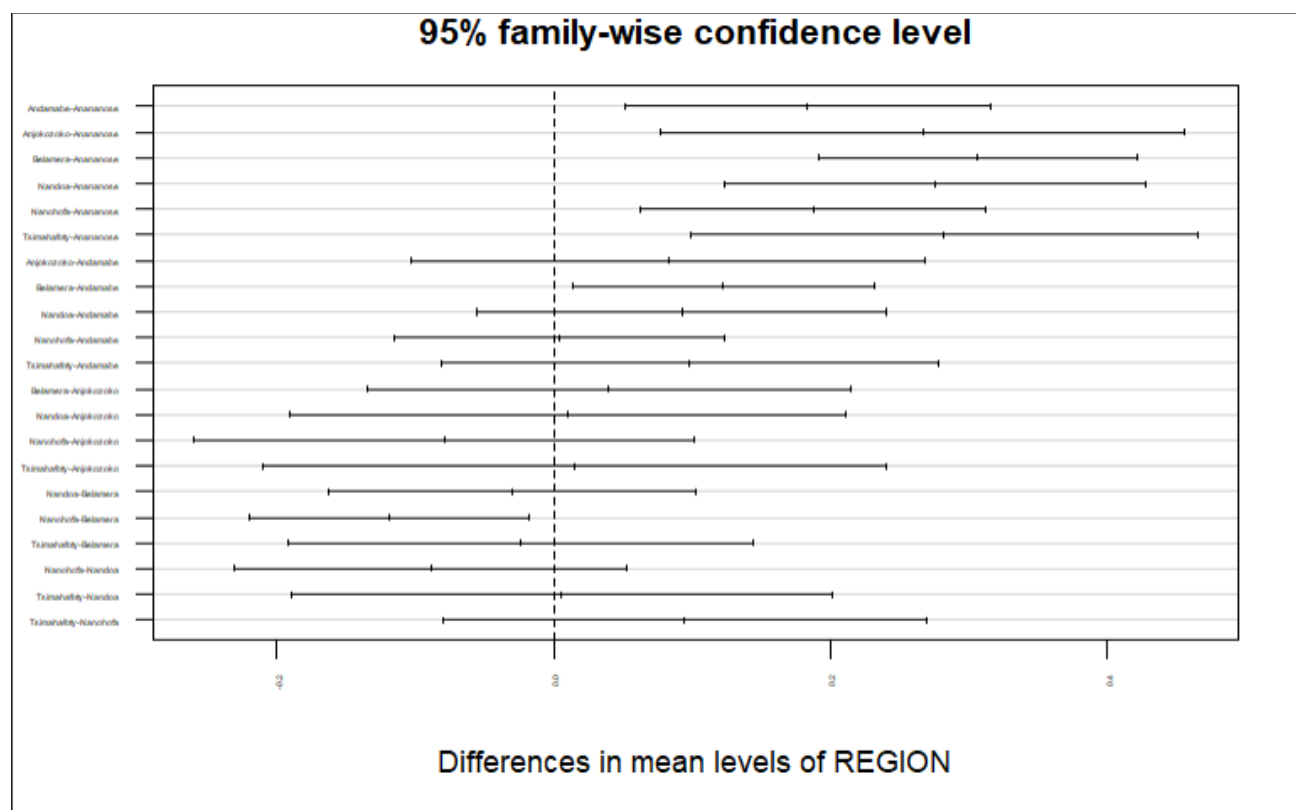
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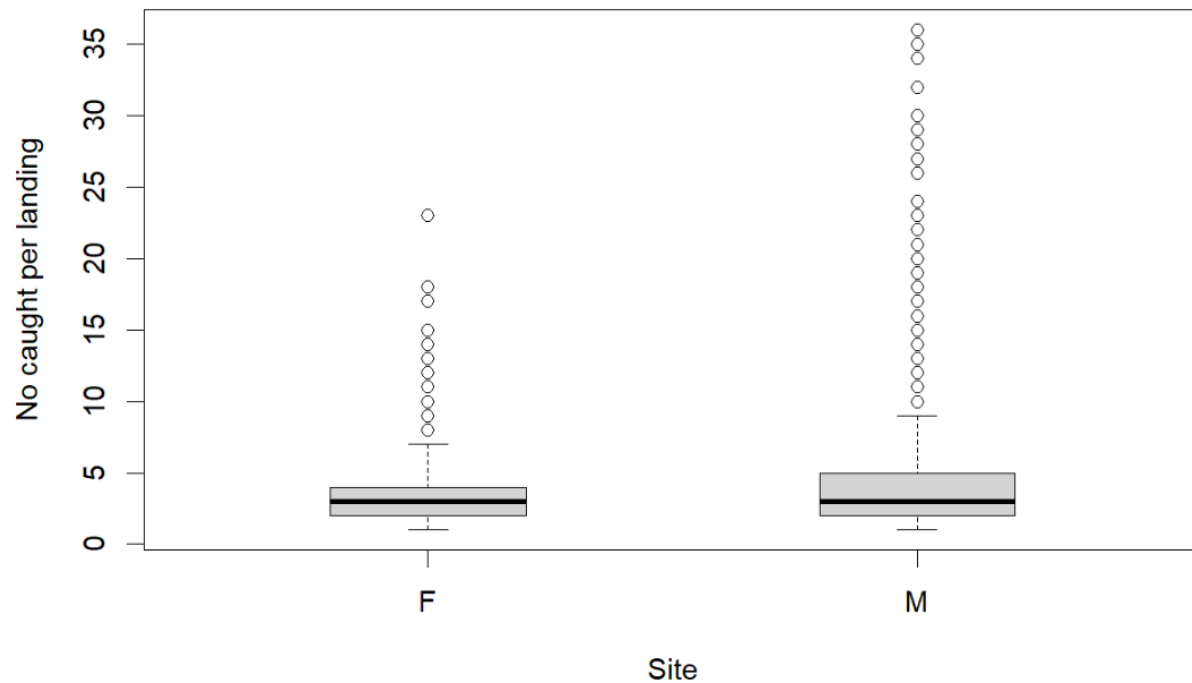
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Appendix:



Appendix Figure 1: Results of the Tukey Test



Appendix Figure 2: A bar plot of the number of catches per landing between female and male fishers. Male fishers have a wider range of catch numbers.

JAGS Code:

ANOVA:

```
sink("cephs_sitewt.txt")
cat("
  model {

    # PRIORS - Including a different variance per site
    for(i in 1:nsites){
      alpha[i] ~ dnorm(0,0.001)
      tau[i] <- 1/sigma[i]^2
      sigma[i] ~ dunif(0,10)
    }

    # LIKELIHOOD
    for(i in 1:n){
      mass[i] ~ dnorm(mu[i],tau[site[i]])
      mu[i] <- alpha[site[i]]
    } # i

    #Generating new data for each run of the MCMC
    for(i in 1:n){
```



```

    y.new[i] ~ dnorm(mu[i],tau[site[i]])
  }

  } # end of model
  ",fill = TRUE)
sink()

win.data <- list(mass    = log(as.numeric(ceph_sites2$AVG_WT)),
                site    = ceph_sites2$id,
                n        = nrow(ceph_sites2),
                nsites   = length(unique(ceph_sites2$id)),
                stdev_data = sd(as.numeric(ceph_sites2$AVG_WT), na.rm =
TRUE),
                mean_data = mean(as.numeric(ceph_sites2$AVG_WT), na.rm =
TRUE))

# Initial values
inits <- function()list(alpha = rnorm(7),
                        sigma = rlnorm(7))

# Parameters monitored
params <- c("alpha",
            "sigma",
            "y.new"
)

# MCMC settings
ni <- 1000; nt <- 3; nb <- 100; nc <- 3

#Model Output
out_stwt <- jags(win.data, inits, params, "cephas_sitewt.txt",
                n.chains = nc, n.thin = nt, n.iter = ni, n.burnin = nb,
                working.directory = getwd())

```

T-Test:

```

sink("cephas_sexno.txt")
cat("
  model {

    # PRIORS
    beta0 ~ dnorm(0,0.001) # intercept i.e. average catch of a female fisher
    beta1 ~ dnorm(0,0.001) # effect of being a male fisher
    tau <- 1/sigma^2
    sigma ~ dunif(0,10)

    # LIKELIHOOD
    for(i in 1:n){
      cephs[i] ~ dpois(lambda[i]) #Poisson distribution bc counts. error term
built in bc lambda is both mean and var
      log(lambda[i]) <- beta0 + beta1 * sex[i] +eps[i] #Remember, predictning
log of lambda not lambda
      #lambda[i] <- exp(beta0 + beta1 * sex[i] ) Alternative form
      eps[i] ~ dnorm(0,tau) #Overdispersion Param

    # CHECK MODEL FIT

```

```

    presid[i] <- (cephs[i] - lambda[i])/sqrt(lambda[i])      # Pearson
residual- corrects for larger mean => larger var
    cephs.new[i] ~ dpois(lambda[i])                          # new data
from fitted model
    presid.new[i] <- (cephs.new[i] - lambda[i])/sqrt(lambda[i]) # Pearson
residual for new data

    D[i] <- presid[i]^2          # squared Pearson residuals for observed
data
    D.new[i] <- presid.new[i]^2  # squared Pearson residuals for new data

} # i

# CHECK MODEL FIT - BAYESIAN P-VALUE
D.sum <- sum(D[])              # sum of squared residuals for raw
data
D.new.sum <- sum(D.new[])      # same, but for model-generated
data
Bayes.P <- step(D.new.sum/D.sum - 1) # step(x) tests if x >= 0

} # end of model
",fill = TRUE)
sink()

win.data <- list(cephs = as.integer(ceph_sex$NO_CAUGHT),
                 sex   = ceph_sex$sex_id,
                 n     = nrow(ceph_sex))

# Initial values
inits <- function()list(beta0 = rnorm(1),
                        betal  = rnorm(1))

# Parameters monitored
params <- c("beta0",
           "betal",
           "Bayes.P",
           "D.sum",
           "D.new.sum",
           "cephs.new")

# MCMC settings
ni <- 3000; nt <- 1; nb <- 1000; nc <- 3

#Model Output
out_sexno <- jags(win.data, inits, params, "cephs_sexno.txt",
                 n.chains = nc, n.thin = nt, n.iter = ni, n.burnin = nb,
                 working.directory = getwd())

```