

Fueling a predator death-trap: data analysis

T. Micheletti

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Introduction

This analysis examines Mabuya (*Trachylepis atlantica*; skink) populations across three distinct sites (i.e., Secondary Islands, PARNAMAR and APA) on Fernando de Noronha archipelago, investigating how invasive species presence and food supplementation affect population density, body size, and injury rates.

Study Area Context

The study encompasses the following areas:

- **Main Island: 16.89 km²**
 - PARNAMAR: 11.424 km²
 - APA: 5.466 km²
- **Secondary Islands: 1.33 km²**
- **TOTAL PARNA: 12.754 km²**
- **TOTAL TERRESTRIAL AREA (PARNA + APA): 18.22 km²**

Package Setup

We'll use the `Require` package for better dependency management across all analyses.

```
if(!require("Require")){
  install.packages("Require")
}
library("Require")

Require::Require("data.table")
Require::Require("emmeans")
Require::Require("DHARMa")
Require::Require("glmmTMB")
Require::Require("performance")
Require::Require("RMark")
Require::Require("xlsx")
Require::Require("ggplot2")
Require::Require("multcompView")
Require::Require("dplyr")
```

Survey Effort Analysis

Before analyzing the biological data, we assessed whether our sampling effort was balanced across the study area.

Loading Density Data

```
mabuia_dd <- fread("data/Density_Data.csv")
```

Calculating Sampling Effort Distribution

```
pointsCounts <- mabuia_dd[, .N, by = "Site"]
pointsCounts[Site == "APA", pointsArea := 5.466]
pointsCounts[Site == "PARNA", pointsArea := 11.424]
pointsCounts[Site == "Secundaria", pointsArea := 1.33]
pointsCounts[, pointsDensity := N/pointsArea]
pointsCounts[, propPoints := N/(sum(pointsCounts[, N]))]
pointsCounts[, propSize := pointsArea/(sum(pointsCounts[, pointsArea]))]

print("Survey effort distribution:")

## [1] "Survey effort distribution:"
print(pointsCounts)
```

```
## Index: <Site>
##      Site      N pointsArea pointsDensity propPoints  propSize
##      <char> <int>      <num>      <num>      <num>      <num>
## 1:      APA     58      5.466      10.611050  0.3866667  0.30000000
## 2:      PARNA    55     11.424       4.814426  0.3666667  0.62700329
## 3: Secundaria   37      1.330     27.819549  0.2466667  0.07299671
```

Survey Effort Assessment

There is indeed a bit of unbalance but it is not as critical as it seems:

- **APA:** 39% points over 30% area
- **PARNA:** 37% points over 62% area
- **Secondary:** 25% points over 7% area

The sampling is reasonably proportional to area, with only modest over-sampling of Secondary Islands and slight under-sampling of PARNAMAR relative to area.

Population Density Analysis

Step 1: Survey Area Calculation

Each survey point was a circle with 2m radius, giving us a standardized survey area.

```
mabuia_dd[, survey_area := pi * (2^2)]
print(paste("Survey area per point:", round(mabuia_dd$survey_area[1], 3), "m^2"))
```

```
## [1] "Survey area per point: 12.566 m^2"
```

The survey area is approximately 12.566 m² per point, which we'll use as an offset in our density models.

Step 2: Creating Predictor Variables

We need to convert site identity into ecologically meaningful predictor variables based on site characteristics.

```
siteLevels <- factor(c("APA", "PARNA", "Secundaria"),
                    levels = c("APA", "PARNA", "Secundaria"))

# Invasive Species Presence (assuming key invasives like Cats and Tejus are largely absent from Secundaria)
mabuia_dd[Site == "APA", InvasiveSpeciesPresence := 1]
mabuia_dd[Site == "PARNA", InvasiveSpeciesPresence := 1]
mabuia_dd[Site == "Secundaria", InvasiveSpeciesPresence := 0]

# Food Supplementation
mabuia_dd[Site == "APA", FoodSupplementation := 1]
mabuia_dd[Site == "PARNA", FoodSupplementation := 0]
mabuia_dd[Site == "Secundaria", FoodSupplementation := 0]

# Convert to factors for modeling
mabuia_dd[, InvasiveSpeciesPresence := as.factor(InvasiveSpeciesPresence)]
mabuia_dd[, FoodSupplementation := as.factor(FoodSupplementation)]
head(mabuia_dd)
```

##	LocationID	Date	Time	Location	Site	Island	Habitat	Temp_oC
##	<char>	<char>	<char>	<char>	<char>	<char>	<char>	<int>
## 1:	IPA56	2/11/2016	16:25	3 Paus	APA	Main	Urbana	29
## 2:	IPA106	11/8/2016	8:16	Abreus	PARNA	Main	Arbustiva Alta	30
## 3:	IPA107	11/8/2016	8:30	Abreus	PARNA	Main	Arborea Baixa	30
## 4:	IPA108	11/8/2016	8:45	Abreus	PARNA	Main	Gram\xednea	30
## 5:	IPA109	11/8/2016	9:07	Abreus	PARNA	Main	Pedreira (costa)	30
## 6:	IPA110	11/8/2016	9:30	Abreus	PARNA	Main	Pedreira (costa)	31

##	UTM	NOR	EAS	Counts	ObsMin	survey_area	InvasiveSpeciesPresence
##	<int>	<int>	<int>	<int>	<int>	<num>	<fctr>
## 1:	25	564037	9574144	3	7	12.56637	1
## 2:	25	564199	9573143	1	7	12.56637	1
## 3:	25	564452	9572968	1	7	12.56637	1
## 4:	25	564676	9572953	1	7	12.56637	1
## 5:	25	565228	9573056	0	7	12.56637	1
## 6:	25	565055	9573102	0	7	12.56637	1

##	FoodSupplementation
##	<fctr>
## 1:	1
## 2:	0
## 3:	0
## 4:	0
## 5:	0
## 6:	0

This creates a 2x2 factorial design where we can test the independent and interactive effects of invasive species presence and food supplementation.

Step 3: Fitting the Main Density Model

We use a negative binomial GLM because count data often shows overdispersion (variance > mean).

```
model_hierarchical_main <- MASS::glm.nb(
  Counts ~ InvasiveSpeciesPresence + FoodSupplementation + offset(log(survey_area)),
```

```

data = mabuia_dd,
na.action = na.omit
)
summary(model_hierarchical_main)

##
## Call:
## MASS::glm.nb(formula = Counts ~ InvasiveSpeciesPresence + FoodSupplementation +
##   offset(log(survey_area)), data = mabuia_dd, na.action = na.omit,
##   init.theta = 1.151932299, link = log)
##
## Coefficients:
##               Estimate Std. Error z value Pr(>|z|)
## (Intercept)      -0.8897     0.1694  -5.252 1.51e-07 ***
## InvasiveSpeciesPresence1 -0.9666     0.2318  -4.169 3.05e-05 ***
## FoodSupplementation1    0.2687     0.2162   1.243  0.214
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Negative Binomial(1.1519) family taken to be 1)
##
## Null deviance: 184.46 on 149 degrees of freedom
## Residual deviance: 165.06 on 147 degrees of freedom
## AIC: 663.54
##
## Number of Fisher Scoring iterations: 1
##
##
##           Theta: 1.152
##        Std. Err.: 0.206
##
## 2 x log-likelihood: -655.544

```

The offset term `log(survey_area)` allows us to model density (individuals per unit area) rather than raw counts.

Step 4: Model Validation

Good model validation is critical for reliable inference.

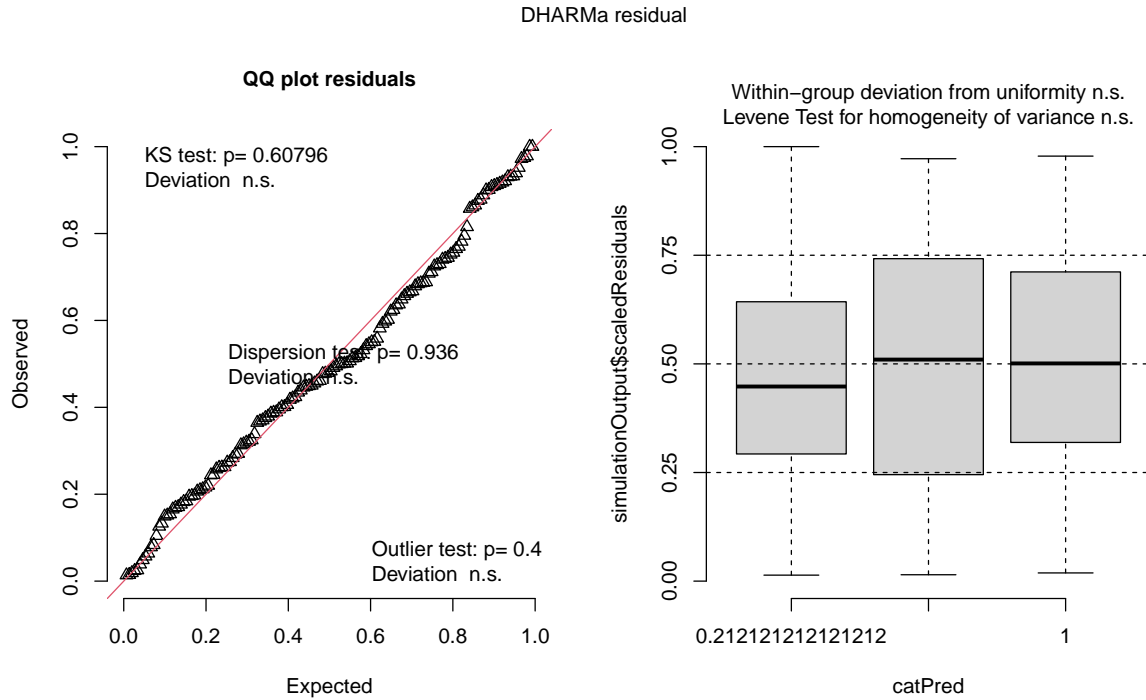
```

r2(model_hierarchical_main)

## # R2 for Generalized Linear Regression
## Nagelkerke's R2: 0.172

sim_res <- simulateResiduals(model_hierarchical_main)
plot(sim_res)

```



DHARMA provides robust residual diagnostics by simulating from the fitted model. Good residuals should show uniform distribution in QQ plots and no patterns in residual vs. fitted plots.

Step 5: Alternative Model Formulations

We test several alternative model structures to ensure we've chosen the best approach.

Interaction Model

```
model_interaction <- MASS::glm.nb(
  Counts ~ InvasiveSpeciesPresence * FoodSupplementation + offset(log(survey_area)),
  data = mabuia_dd
)
summary(model_interaction)
```

```
##
## Call:
## MASS::glm.nb(formula = Counts ~ InvasiveSpeciesPresence * FoodSupplementation +
##   offset(log(survey_area)), data = mabuia_dd, init.theta = 1.151932299,
##   link = log)
##
## Coefficients: (1 not defined because of singularities)
##
##              Estimate Std. Error z value
## (Intercept)    -0.8897    0.1694  -5.252
## InvasiveSpeciesPresence1    -0.9666    0.2318  -4.169
## FoodSupplementation1     0.2687    0.2162   1.243
## InvasiveSpeciesPresence1:FoodSupplementation1      NA         NA      NA
##
##              Pr(>|z|)
## (Intercept)    1.51e-07 ***
## InvasiveSpeciesPresence1    3.05e-05 ***
```

```
## FoodSupplementation1 0.214
## InvasiveSpeciesPresence1:FoodSupplementation1 NA
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Negative Binomial(1.1519) family taken to be 1)
##
## Null deviance: 184.46 on 149 degrees of freedom
## Residual deviance: 165.06 on 147 degrees of freedom
## AIC: 663.54
##
## Number of Fisher Scoring iterations: 1
##
##
## Theta: 1.152
## Std. Err.: 0.206
##
## 2 x log-likelihood: -655.544
```

Mixed Effects Models

```
model_random <- glmmTMB::glmmTMB(
  Counts ~ InvasiveSpeciesPresence + FoodSupplementation + offset(log(survey_area)) + (1 | Site),
  family = nbinom2,
  data = mabuia_dd
)
summary(model_random)
```

```
## Family: nbinom2 ( log )
## Formula:
## Counts ~ InvasiveSpeciesPresence + FoodSupplementation + offset(log(survey_area)) +
## (1 | Site)
## Data: mabuia_dd
##
## AIC BIC logLik deviance df.resid
## 665.5 680.6 -327.8 655.5 145
##
## Random effects:
##
## Conditional model:
## Groups Name Variance Std.Dev.
## Site (Intercept) 7.525e-10 2.743e-05
## Number of obs: 150, groups: Site, 3
##
## Dispersion parameter for nbinom2 family (): 1.15
##
## Conditional model:
## Estimate Std. Error z value Pr(>|z|)
## (Intercept) -0.8897 0.1694 -5.252 1.51e-07 ***
## InvasiveSpeciesPresence1 -0.9666 0.2318 -4.169 3.05e-05 ***
## FoodSupplementation1 0.2687 0.2162 1.243 0.214
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```

model_random_interaction <- glmmTMB::glmmTMB(
  Counts ~ InvasiveSpeciesPresence * FoodSupplementation + offset(log(survey_area)) + (1 | Site),
  family = nbinom2,
  data = mabuia_dd
)
summary(model_random_interaction)

## Family: nbinom2 ( log )
## Formula:
## Counts ~ InvasiveSpeciesPresence * FoodSupplementation + offset(log(survey_area)) +
## (1 | Site)
## Data: mabuia_dd
##
##      AIC      BIC   logLik deviance df.resid
##    665.5    680.6   -327.8    655.5     145
##
## Random effects:
##
## Conditional model:
## Groups Name      Variance Std.Dev.
## Site (Intercept) 7.525e-10 2.743e-05
## Number of obs: 150, groups: Site, 3
##
## Dispersion parameter for nbinom2 family (): 1.15
##
## Conditional model:
##
##              Estimate Std. Error z value
## (Intercept)      -0.8897    0.1694  -5.252
## InvasiveSpeciesPresence1      -0.9666    0.2318  -4.169
## FoodSupplementation1         0.2687    0.2162   1.243
## InvasiveSpeciesPresence1:FoodSupplementation1      NA         NA      NA
##              Pr(>|z|)
## (Intercept)      1.51e-07 ***
## InvasiveSpeciesPresence1      3.05e-05 ***
## FoodSupplementation1         0.214
## InvasiveSpeciesPresence1:FoodSupplementation1      NA
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Model Selection

```

model_comparison <- AIC(
  model_hierarchical_main,      # Original glm.nb model
  model_interaction,           # GLM with interaction
  model_random,                # GLMM with random effect
  model_random_interaction     # GLMM with both interaction + random
)
print("Model AIC Comparison:")

## [1] "Model AIC Comparison:"
print(model_comparison)

```

```
##              df      AIC
```



```
## model_hierarchical_main    4 663.5444
## model_interaction          4 663.5444
## model_random               5 665.5444
## model_random_interaction    5 665.5444
```

Conclusion: The original model has the best AIC, is interpretable, answers the ecological question clearly, and passes all residual diagnostics.

Step 6: Estimated Marginal Means

```
emm_density_hierarchical <- emmeans(model_hierarchical_main,
                                     specs = ~ InvasiveSpeciesPresence + FoodSupplementation,
                                     type = "response",
                                     offset = 0)

summary(emm_density_hierarchical, infer = TRUE)
```

```
## InvasiveSpeciesPresence FoodSupplementation response      SE df asymp.LCL
## 0                        0                    0.411 0.0696 Inf      0.295
## 1                        0                    0.156 0.0247 Inf      0.115
## 0                        1                    0.537 0.1476 Inf      0.314
## 1                        1                    0.204 0.0301 Inf      0.153
## asymp.UCL null z.ratio p.value
##    0.573    1  -5.252 <.0001
##    0.213    1 -11.730 <.0001
##    0.921    1  -2.261 0.0238
##    0.273    1 -10.782 <.0001
##
## Confidence level used: 0.95
## Intervals are back-transformed from the log scale
## Tests are performed on the log scale
```

Setting offset = 0 gives us density per unit area rather than total abundance.

Step 7: Creating the Density Visualization

Data Preparation for Plotting

```
density_df <- as.data.frame(summary(emm_density_hierarchical, infer = TRUE))

# Map factor combinations to meaningful site names
density_df$Site <- ifelse(
  density_df$InvasiveSpeciesPresence == 0 & density_df$FoodSupplementation == 1, "Hypothetical Site",
  ifelse(
    density_df$InvasiveSpeciesPresence == 0 & density_df$FoodSupplementation == 0, "Secondary Islands",
    ifelse(
      density_df$InvasiveSpeciesPresence == 1 & density_df$FoodSupplementation == 1, "APA",
      "PARNAMAR"
    )
  )
)

density_df$Site <- factor(density_df$Site, levels = c("Hypothetical Site", "Secondary Islands", "APA", "PARNAMAR"))

# Rename columns for clarity
```

```

names(density_df)[names(density_df) == 'response'] <- 'mean_density'
names(density_df)[names(density_df) == 'asympt.LCL'] <- 'lower_ci'
names(density_df)[names(density_df) == 'asympt.UCL'] <- 'upper_ci'
print(density_df)

```

```

## InvasiveSpeciesPresence FoodSupplementation mean_density SE df
## 0 0 0.4107918 0.06959005 Inf
## 1 0 0.1562612 0.02472831 Inf
## 0 1 0.5374264 0.14759153 Inf
## 1 1 0.2044318 0.03009994 Inf
## lower_ci upper_ci null z.ratio p.value Site
## 0.2947300 0.5725577 1 -5.252 <.0001 Secondary Islands
## 0.1145905 0.2130854 1 -11.730 <.0001 PARNAMAR
## 0.3137303 0.9206223 1 -2.261 0.0238 Hypothetical Site
## 0.1531863 0.2728204 1 -10.782 <.0001 APA
##
## Confidence level used: 0.95
## Intervals are back-transformed from the log scale
## Tests are performed on the log scale

```

Statistical Significance Testing

```

pairs_emm <- contrast(emm_density_hierarchical, method = "pairwise", adjust = "tukey")
summary_pw <- summary(pairs_emm)
p_values <- summary_pw$p.value
print(p_values)

```

```

## [1] 0.0001790051 0.5993115525 0.0101326414 0.0079318154 0.5993115525
## [6] 0.0001790051

```

Processing Significance Letters

```

# Helper function to clean emmeans factor level names
clean_level_name <- function(level_string) {
  cleaned <- gsub("InvasiveSpeciesPresence", "", level_string)
  cleaned <- gsub("FoodSupplementation", "", cleaned)
  cleaned <- gsub(" ", "", cleaned)
  return(cleaned)
}

contrast_names_raw <- as.character(summary_pw$contrast)
p_value_names <- sapply(contrast_names_raw, function(contrast) {
  parts <- strsplit(contrast, " / ")[[1]]
  key1 <- clean_level_name(trimws(parts[1]))
  key2 <- clean_level_name(trimws(parts[2]))
  return(paste(key1, key2, sep = "-"))
})
names(p_values) <- p_value_names

# Generate significance letters
letters_result <- multcompLetters(p_values)
significance_letters <- letters_result$Letters

# Add letters to plotting data

```

```

density_df$key <- paste0(density_df$InvasiveSpeciesPresence, density_df$FoodSupplementation)
density_df$significance_group <- significance_letters[density_df$key]
density_df$y_position_for_text <- density_df$upper_ci + 0.05

```

Creating the Final Density Plot

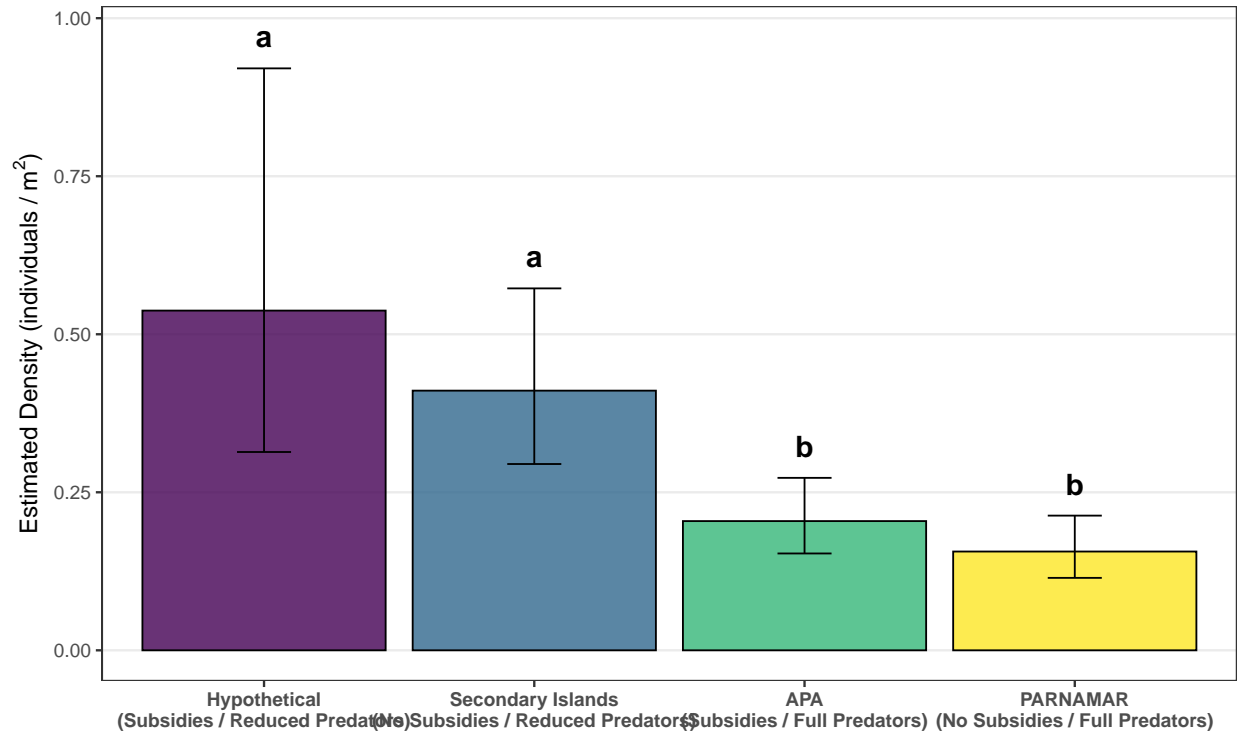
```

two_line_labels <- c(
  "Hypothetical\n(Subsidies / Reduced Predators)",
  "Secondary Islands\n(No Subsidies / Reduced Predators)",
  "APA\n(Subsidies / Full Predators)",
  "PARNAMAR\n(No Subsidies / Full Predators)"
)

density_plot <- ggplot(density_df, aes(x = Site, y = mean_density, fill = Site)) +
  geom_bar(stat = "identity", color = "black", alpha = 0.8) +
  geom_errorbar(aes(ymin = lower_ci, ymax = upper_ci),
    width = 0.2, color = "black", linewidth = 0.5) +
  geom_text(aes(y = y_position_for_text, label = significance_group),
    size = 6, fontface = "bold", color = "black") +
  scale_x_discrete(labels = two_line_labels) +
  scale_fill_viridis_d(option = "D") +
  labs(y = expression("Estimated Density (individuals / m"2*)")) +
  theme_bw(base_size = 14) +
  theme(
    axis.title = element_text(face = "bold"),
    axis.text.x = element_text(face = "bold"),
    axis.title.x = element_blank(),
    panel.grid.major.x = element_blank(),
    panel.grid.minor = element_blank(),
    legend.position = "none"
  )

print(density_plot)

```



Mark-Recapture Analysis

Analysis was performed using the Poisson-log normal mark-resight model to separate detection probability from true abundance.

Step 1: Loading CMR Data

```
ch <- read.xlsx(file = file.path(getwd(), "data/CRM_Data.xlsx"),
               header = TRUE,
               sheetName = "ch",
               as.data.frame = TRUE)
ch$ch <- as.character(ch$ch)
ch$colonies <- as.factor(ch$colonies)

covars <- read.xlsx(file = file.path(getwd(), "data/CRM_Data.xlsx"),
                   header = TRUE,
                   sheetName = "covars",
                   as.data.frame = TRUE)
```

Step 2: Creating Model Variables

```
nocc <- 6 # Number of occasions
groupsNames <- unique(covars$colonies)
nGroups <- length(groupsNames)

# Create matrices for different count types
unmarkedSeen <- matrix(covars[, "unmarkedSeen"],
                      nrow = nGroups,
```

```

        ncol = nocc,
        byrow = TRUE)

markedUnidentified <- matrix(covars[, "markedUnidentified"],
                             nrow = nGroups,
                             ncol = nocc,
                             byrow = TRUE)

knownMarks <- matrix(covars[, "knownMarks"],
                     nrow = nGroups,
                     ncol = nocc,
                     byrow = TRUE)

effort <- matrix(covars[, "effort"],
                 nrow = nGroups,
                 ncol = nocc,
                 byrow = TRUE)

site <- matrix(covars[, "site"],
               nrow = nGroups,
               ncol = nocc,
               byrow = TRUE)

```

Step 3: Data Processing

```

mabuya.process <- process.data(ch,
                              model = "PoissonMR",
                              time.intervals = rep(1, times = (nocc-1)),
                              groups = "colonies",
                              counts = list("Unmarked Seen" = unmarkedSeen,
                                             "Marked Unidentified" = markedUnidentified,
                                             "Known Marks" = knownMarks))

mabuya.ddl <- make.design.data(mabuya.process)

```

Step 4: Adding Covariates

Now we include covariates such as effort and site type where they should be placed.

For Alpha (Detection Probability)

```

mabuya.ddl$alpha$effort <- as.numeric(apply(X = mabuya.ddl$alpha, 1, function(x){
  col <- x[["group"]]
  occ <- as.numeric(x[["time"]])
  eff <- covars[covars$colonies==col&covars$occasion==occ, "effort"]
}))

mabuya.ddl$alpha$site <- as.character(apply(X = mabuya.ddl$alpha, 1, function(x){
  col <- x[["group"]]
  occ <- as.numeric(x[["time"]])
  site <- covars[covars$colonies==col&covars$occasion==occ, "site"]
}))

```

For U (Abundance)

```
mabuya.ddl$U$site <- as.character(apply(X = mabuya.ddl$U, 1, function(x){
  col <- x[["group"]]
  occ <- as.numeric(x[["time"]])
  site <- covars[covars$colonies==col&covars$occasion==occ, "site"]
})))
```

Step 5: Defining Model Formulas

```
# Parameter formulas for alpha (detection probability)
alpha.dot <- list(formula = ~ 1)
alpha.effort <- list(formula = ~ effort)
alpha.site <- list(formula = ~ site)
alpha.additive <- list(formula = ~ effort + site)
alpha.interaction <- list(formula = ~ effort * site)

# Parameters that will be the same in all models
U.site <- list(formula = ~ site)
Phi.fixed1 <- list(formula = ~ 1, fixed = 1)
zero <- list(formula = ~ 1, fixed = 0) # For sigma and Gammas
```

Step 6: Building Model List

```
model.list <- list(
  "alpha(.) U(site)" = list(
    alpha = alpha.dot,
    U = U.site,
    Phi = Phi.fixed1,
    sigma = zero,
    GammaDoublePrime = zero,
    GammaPrime = zero
  ),
  "alpha(effort) U(site)" = list(
    alpha = alpha.effort,
    U = U.site,
    Phi = Phi.fixed1,
    sigma = zero,
    GammaDoublePrime = zero,
    GammaPrime = zero
  ),
  "alpha(site) U(site)" = list(
    alpha = alpha.site,
    U = U.site,
    Phi = Phi.fixed1,
    sigma = zero,
    GammaDoublePrime = zero,
    GammaPrime = zero
  ),
  "alpha(effort+site) U(site)" = list(
    alpha = alpha.additive,
    U = U.site,
    Phi = Phi.fixed1,
```

```

    sigma = zero,
    GammaDoublePrime = zero,
    GammaPrime = zero
  ),
  "alpha(effort*site) U(site)" = list(
    alpha = alpha.interaction,
    U = U.site,
    Phi = Phi.fixed1,
    sigma = zero,
    GammaDoublePrime = zero,
    GammaPrime = zero
  )
)

```

Step 7: Fitting All Models

```

mabuya_model_1 <- mark(
  data = mabuya.process,
  ddl = mabuya.ddl,
  model.parameters = model.list[["alpha(.) U(site)"]],
  delete = TRUE
)

```

```

##
## Output summary for PoissonMR model
## Name : alpha(~1)sigma(~1)U(~site)Phi(~1)Gamma' (~1)Gamma' (~1)
##
## Npar : 3
## -2lnL: 872.2775
## AICc : 878.3273
##
## Beta
##
## estimate se lcl ucl
## alpha:(Intercept) -1.354831 0.0940721 -1.539212 -1.170450
## U:(Intercept) 4.158624 0.1063001 3.950276 4.366973
## U:sitePARNA -1.760433 0.1292842 -2.013830 -1.507036
##
##
## Real Parameter alpha
##
## 1 2 3 4 5
## Group:coloniesAmericano 0.2579909 0.2579909 0.2579909 0.2579909 0.2579909
## Group:coloniesCapimAcu 0.2579909 0.2579909 0.2579909 0.2579909 0.2579909
## Group:coloniesForteBoldro 0.2579909 0.2579909 0.2579909 0.2579909 0.2579909
## Group:coloniesLeao 0.2579909 0.2579909 0.2579909 0.2579909 0.2579909
## Group:coloniesPedreiraSueste 0.2579909 0.2579909 0.2579909 0.2579909 0.2579909
## Group:coloniesPiquinho 0.2579909 0.2579909 0.2579909 0.2579909 0.2579909
## Group:coloniesPraiaBoldro 0.2579909 0.2579909 0.2579909 0.2579909 0.2579909
## Group:coloniesTejuAcu 0.2579909 0.2579909 0.2579909 0.2579909 0.2579909
##
## 6
## Group:coloniesAmericano 0.2579909
## Group:coloniesCapimAcu 0.2579909
## Group:coloniesForteBoldro 0.2579909
## Group:coloniesLeao 0.2579909

```

```

## Group:coloniesPedreiraSueste 0.2579909
## Group:coloniesPiquinho      0.2579909
## Group:coloniesPraiaBoldro   0.2579909
## Group:coloniesTejuAcu       0.2579909
##
##
## Real Parameter sigma
##
##      1  2  3  4  5  6
## Group:coloniesAmericano      NA NA NA NA NA NA
## Group:coloniesCapimAcu       NA NA NA NA NA NA
## Group:coloniesForteBoldro    NA NA NA NA NA NA
## Group:coloniesLeao           NA NA NA NA NA NA
## Group:coloniesPedreiraSueste NA NA NA NA NA NA
## Group:coloniesPiquinho       NA NA NA NA NA NA
## Group:coloniesPraiaBoldro    NA NA NA NA NA NA
## Group:coloniesTejuAcu        NA NA NA NA NA NA
##
##
## Real Parameter U
##
##      1      2      3      4      5
## Group:coloniesAmericano      63.98345 63.98345 63.98345 63.98345 63.98345
## Group:coloniesCapimAcu       11.00326 11.00326 11.00326 11.00326 11.00326
## Group:coloniesForteBoldro    63.98345 63.98345 63.98345 63.98345 63.98345
## Group:coloniesLeao           11.00326 11.00326 11.00326 11.00326 11.00326
## Group:coloniesPedreiraSueste 11.00326 11.00326 11.00326 11.00326 11.00326
## Group:coloniesPiquinho       11.00326 11.00326 11.00326 11.00326 11.00326
## Group:coloniesPraiaBoldro    63.98345 63.98345 63.98345 63.98345 63.98345
## Group:coloniesTejuAcu        63.98345 63.98345 63.98345 63.98345 63.98345
##
##      6
## Group:coloniesAmericano      63.98345
## Group:coloniesCapimAcu       11.00326
## Group:coloniesForteBoldro    63.98345
## Group:coloniesLeao           11.00326
## Group:coloniesPedreiraSueste 11.00326
## Group:coloniesPiquinho       11.00326
## Group:coloniesPraiaBoldro    63.98345
## Group:coloniesTejuAcu        63.98345
##
##
## Real Parameter Phi
## Group:coloniesAmericano
##      1  2  3  4  5
##      1
##      2
##      3
##      4
##      5
##
## Group:coloniesCapimAcu
##      1  2  3  4  5
##      1
##      2
##      3
##      4

```



```

## 5
##
## Group:coloniesForteBoldro
## 1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
## Group:coloniesLeao
## 1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
## Group:coloniesPedreiraSueste
## 1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
## Group:coloniesPiquinho
## 1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
## Group:coloniesPraiaBoldro
## 1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
## Group:coloniesTejuAcu
## 1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
##
## Real Parameter GammaDoublePrime
## Group:coloniesAmericano
## 1 2 3 4 5

```

```

## 1
## 2
## 3
## 4
## 5
##
## Group:coloniesCapimAcu
## 1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
## Group:coloniesForteBoldro
## 1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
## Group:coloniesLeao
## 1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
## Group:coloniesPedreiraSueste
## 1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
## Group:coloniesPiquinho
## 1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
## Group:coloniesPraiaBoldro
## 1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##

```

```

## Group:coloniesTejuAcu
## 1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
##
## Real Parameter GammaPrime
## Group:coloniesAmericano
## 2 3 4 5
## 1
## 2
## 3
## 4
##
## Group:coloniesCapimAcu
## 2 3 4 5
## 1
## 2
## 3
## 4
##
## Group:coloniesForteBoldro
## 2 3 4 5
## 1
## 2
## 3
## 4
##
## Group:coloniesLeao
## 2 3 4 5
## 1
## 2
## 3
## 4
##
## Group:coloniesPedreiraSueste
## 2 3 4 5
## 1
## 2
## 3
## 4
##
## Group:coloniesPiquinho
## 2 3 4 5
## 1
## 2
## 3
## 4
##
## Group:coloniesPraiaBoldro
## 2 3 4 5

```

```

## 1
## 2
## 3
## 4
##
## Group:coloniesTejuAcu
##   2 3 4 5
## 1
## 2
## 3
## 4

mabuya_model_2 <- mark(
  data = mabuya.process,
  ddl = mabuya.ddl,
  model.parameters = model.list[["alpha(effort) U(site)"]],
  delete = TRUE
)

##
## Output summary for PoissonMR model
## Name : alpha(~effort)sigma(~1)U(~site)Phi(~1)Gamma'(~1)Gamma'(~1)
##
## Npar : 4
## -2lnL: 849.1093
## AICc : 857.1925
##
## Beta
##           estimate      se      lcl      ucl
## alpha:(Intercept) -1.8070139 0.1359359 -2.0734483 -1.5405795
## alpha:effort      0.0189359 0.0039292  0.0112346  0.0266371
## U:(Intercept)     4.1289170 0.1067975  3.9195938  4.3382401
## U:sitePARNA       -1.5993993 0.1343945 -1.8628125 -1.3359862
##
##
## Real Parameter alpha
##           1           2           3           4           5
## Group:coloniesAmericano 0.4230688 0.2180620 0.2635223 0.2397169 0.2180620
## Group:coloniesCapimAcu  0.2442994 0.2021552 0.2180620 0.2180620 0.2180620
## Group:coloniesForteBoldro 0.3184600 0.2180620 0.2635223 0.2635223 0.3008733
## Group:coloniesLeao      0.2308082 0.2397169 0.2099580 0.2264788 0.2099580
## Group:coloniesPedreiraSueste 0.2397169 0.2264788 0.2442994 0.2308082 0.2222305
## Group:coloniesPiquinho  0.2308082 0.2060197 0.2736938 0.2180620 0.2180620
## Group:coloniesPraiaBoldro 0.2308082 0.3008733 0.3500851 0.2789258 0.2060197
## Group:coloniesTejuAcu   0.2180620 0.1909914 0.1909914 0.1983633 0.1983633
##           6
## Group:coloniesAmericano 0.2180620
## Group:coloniesCapimAcu  0.2352204
## Group:coloniesForteBoldro 0.2635223
## Group:coloniesLeao      0.2180620
## Group:coloniesPedreiraSueste 0.2139716
## Group:coloniesPiquinho  0.1983633
## Group:coloniesPraiaBoldro 0.3500851
## Group:coloniesTejuAcu   0.1983633
##

```

```

##
## Real Parameter sigma
##          1  2  3  4  5  6
## Group:coloniesAmericano      NA NA NA NA NA NA
## Group:coloniesCapimAcu       NA NA NA NA NA NA
## Group:coloniesForteBoldro    NA NA NA NA NA NA
## Group:coloniesLeao           NA NA NA NA NA NA
## Group:coloniesPedreiraSueste NA NA NA NA NA NA
## Group:coloniesPiquinho       NA NA NA NA NA NA
## Group:coloniesPraiaBoldro    NA NA NA NA NA NA
## Group:coloniesTejuAcu        NA NA NA NA NA NA
##
##
## Real Parameter U
##          1          2          3          4          5
## Group:coloniesAmericano      62.11062 62.11062 62.11062 62.11062 62.11062
## Group:coloniesCapimAcu       12.54745 12.54745 12.54745 12.54745 12.54745
## Group:coloniesForteBoldro    62.11062 62.11062 62.11062 62.11062 62.11062
## Group:coloniesLeao           12.54745 12.54745 12.54745 12.54745 12.54745
## Group:coloniesPedreiraSueste 12.54745 12.54745 12.54745 12.54745 12.54745
## Group:coloniesPiquinho       12.54745 12.54745 12.54745 12.54745 12.54745
## Group:coloniesPraiaBoldro    62.11062 62.11062 62.11062 62.11062 62.11062
## Group:coloniesTejuAcu        62.11062 62.11062 62.11062 62.11062 62.11062
##          6
## Group:coloniesAmericano      62.11062
## Group:coloniesCapimAcu       12.54745
## Group:coloniesForteBoldro    62.11062
## Group:coloniesLeao           12.54745
## Group:coloniesPedreiraSueste 12.54745
## Group:coloniesPiquinho       12.54745
## Group:coloniesPraiaBoldro    62.11062
## Group:coloniesTejuAcu        62.11062
##
##
## Real Parameter Phi
## Group:coloniesAmericano
##   1  2  3  4  5
## 1
## 2
## 3
## 4
## 5
##
## Group:coloniesCapimAcu
##   1  2  3  4  5
## 1
## 2
## 3
## 4
## 5
##
## Group:coloniesForteBoldro
##   1  2  3  4  5
## 1

```

```

## 2
## 3
## 4
## 5
##
## Group:coloniesLeao
## 1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
## Group:coloniesPedreiraSueste
## 1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
## Group:coloniesPiquinho
## 1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
## Group:coloniesPraiaBoldro
## 1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
## Group:coloniesTejuAcu
## 1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
##
## Real Parameter GammaDoublePrime
## Group:coloniesAmericano
## 1 2 3 4 5
## 1
## 2
## 3
## 4
## 5

```

```

##
## Group:coloniesCapimAcu
## 1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
## Group:coloniesForteBoldro
## 1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
## Group:coloniesLeao
## 1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
## Group:coloniesPedreiraSueste
## 1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
## Group:coloniesPiquinho
## 1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
## Group:coloniesPraiaBoldro
## 1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
## Group:coloniesTejuAcu
## 1 2 3 4 5
## 1
## 2
## 3

```

```

## 4
## 5
##
##
## Real Parameter GammaPrime
## Group:coloniesAmericano
## 2 3 4 5
## 1
## 2
## 3
## 4
##
## Group:coloniesCapimAcu
## 2 3 4 5
## 1
## 2
## 3
## 4
##
## Group:coloniesForteBoldro
## 2 3 4 5
## 1
## 2
## 3
## 4
##
## Group:coloniesLeao
## 2 3 4 5
## 1
## 2
## 3
## 4
##
## Group:coloniesPedreiraSueste
## 2 3 4 5
## 1
## 2
## 3
## 4
##
## Group:coloniesPiquinho
## 2 3 4 5
## 1
## 2
## 3
## 4
##
## Group:coloniesPraiaBoldro
## 2 3 4 5
## 1
## 2
## 3
## 4
##

```



```
## Group:coloniesTejuAcu
## 2 3 4 5
## 1
## 2
## 3
## 4
```

```
mabuya_model_3 <- mark(
  data = mabuya.process,
  ddl = mabuya.ddl,
  model.parameters = model.list[["alpha(site) U(site)"]],
  delete = TRUE
)
```

```
##
## Output summary for PoissonMR model
## Name : alpha(~site)sigma(~1)U(~site)Phi(~1)Gamma'(~1)Gamma'(~1)
##
## Npar : 4
## -2lnL: 871.1816
## AICc : 879.2648
##
```

```
## Beta
##           estimate      se      lcl      ucl
## alpha:(Intercept) -1.4182458 0.1139607 -1.6416087 -1.1948830
## alpha:sitePARNA    0.2142728 0.2019031 -0.1814573  0.6100029
## U:(Intercept)      4.2220392 0.1242465  3.9785161  4.4655623
## U:sitePARNA        -1.9747053 0.2397484 -2.4446121 -1.5047985
##
```

```
## Real Parameter alpha
```

	1	2	3	4	5
## Group:coloniesAmericano	0.2421384	0.2421384	0.2421384	0.2421384	0.2421384
## Group:coloniesCapimAcu	0.2999999	0.2999999	0.2999999	0.2999999	0.2999999
## Group:coloniesForteBoldro	0.2421384	0.2421384	0.2421384	0.2421384	0.2421384
## Group:coloniesLeao	0.2999999	0.2999999	0.2999999	0.2999999	0.2999999
## Group:coloniesPedreiraSueste	0.2999999	0.2999999	0.2999999	0.2999999	0.2999999
## Group:coloniesPiquinho	0.2999999	0.2999999	0.2999999	0.2999999	0.2999999
## Group:coloniesPraiaBoldro	0.2421384	0.2421384	0.2421384	0.2421384	0.2421384
## Group:coloniesTejuAcu	0.2421384	0.2421384	0.2421384	0.2421384	0.2421384

	6
## Group:coloniesAmericano	0.2421384
## Group:coloniesCapimAcu	0.2999999
## Group:coloniesForteBoldro	0.2421384
## Group:coloniesLeao	0.2999999
## Group:coloniesPedreiraSueste	0.2999999
## Group:coloniesPiquinho	0.2999999
## Group:coloniesPraiaBoldro	0.2421384
## Group:coloniesTejuAcu	0.2421384

```
## Real Parameter sigma
```

	1	2	3	4	5	6
## Group:coloniesAmericano	NA	NA	NA	NA	NA	NA
## Group:coloniesCapimAcu	NA	NA	NA	NA	NA	NA

```

## Group:coloniesForteBoldro    NA NA NA NA NA NA
## Group:coloniesLeao           NA NA NA NA NA NA
## Group:coloniesPedreiraSueste NA NA NA NA NA NA
## Group:coloniesPiquinho       NA NA NA NA NA NA
## Group:coloniesPraiaBoldro    NA NA NA NA NA NA
## Group:coloniesTejuAcu        NA NA NA NA NA NA
##
##
## Real Parameter U
##           1           2           3           4           5
## Group:coloniesAmericano      68.172360 68.172360 68.172360 68.172360 68.172360
## Group:coloniesCapimAcu       9.462474 9.462474 9.462474 9.462474 9.462474
## Group:coloniesForteBoldro    68.172360 68.172360 68.172360 68.172360 68.172360
## Group:coloniesLeao           9.462474 9.462474 9.462474 9.462474 9.462474
## Group:coloniesPedreiraSueste 9.462474 9.462474 9.462474 9.462474 9.462474
## Group:coloniesPiquinho       9.462474 9.462474 9.462474 9.462474 9.462474
## Group:coloniesPraiaBoldro    68.172360 68.172360 68.172360 68.172360 68.172360
## Group:coloniesTejuAcu        68.172360 68.172360 68.172360 68.172360 68.172360
##           6
## Group:coloniesAmericano      68.172360
## Group:coloniesCapimAcu       9.462474
## Group:coloniesForteBoldro    68.172360
## Group:coloniesLeao           9.462474
## Group:coloniesPedreiraSueste 9.462474
## Group:coloniesPiquinho       9.462474
## Group:coloniesPraiaBoldro    68.172360
## Group:coloniesTejuAcu        68.172360
##
##
## Real Parameter Phi
## Group:coloniesAmericano
##   1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
## Group:coloniesCapimAcu
##   1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
## Group:coloniesForteBoldro
##   1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##

```

```

## Group:coloniesLeao
## 1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
## Group:coloniesPedreiraSueste
## 1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
## Group:coloniesPiquinho
## 1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
## Group:coloniesPraiaBoldro
## 1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
## Group:coloniesTejuAcu
## 1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
##
## Real Parameter GammaDoublePrime
## Group:coloniesAmericano
## 1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
## Group:coloniesCapimAcu
## 1 2 3 4 5
## 1
## 2

```

```

## 3
## 4
## 5
##
## Group:coloniesForteBoldro
## 1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
## Group:coloniesLeao
## 1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
## Group:coloniesPedreiraSueste
## 1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
## Group:coloniesPiquinho
## 1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
## Group:coloniesPraiaBoldro
## 1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
## Group:coloniesTejuAcu
## 1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
##
## Real Parameter GammaPrime

```

```

## Group:coloniesAmericano
## 2 3 4 5
## 1
## 2
## 3
## 4
##
## Group:coloniesCapimAcu
## 2 3 4 5
## 1
## 2
## 3
## 4
##
## Group:coloniesForteBoldro
## 2 3 4 5
## 1
## 2
## 3
## 4
##
## Group:coloniesLeao
## 2 3 4 5
## 1
## 2
## 3
## 4
##
## Group:coloniesPedreiraSueste
## 2 3 4 5
## 1
## 2
## 3
## 4
##
## Group:coloniesPiquinho
## 2 3 4 5
## 1
## 2
## 3
## 4
##
## Group:coloniesPraiaBoldro
## 2 3 4 5
## 1
## 2
## 3
## 4
##
## Group:coloniesTejuAcu
## 2 3 4 5
## 1
## 2
## 3

```

```
## 4
mabuya_model_4 <- mark(
  data = mabuya.process,
  ddl = mabuya.ddl,
  model.parameters = model.list[["alpha(effort+site) U(site)"]],
  delete = TRUE
)

##
## Output summary for PoissonMR model
## Name : alpha(~effort + site)sigma(~1)U(~site)Phi(~1)Gamma'(~1)Gamma'(~1)
##
## Npar : 5
## -2lnL: 845.2658
## AICc : 855.3908
##
## Beta
##
## estimate se lc1 uc1
## alpha:(Intercept) -1.9612543 0.1597802 -2.2744234 -1.6480852
## alpha:effort 0.0205160 0.0040357 0.0126060 0.0284260
## alpha:sitePARNA 0.4154279 0.2066882 0.0103191 0.8205367
## U:(Intercept) 4.2427291 0.1249664 3.9977950 4.4876632
## U:sitePARNA -2.0009952 0.2402727 -2.4719298 -1.5300606
##
##
## Real Parameter alpha
##
## 1 2 3 4 5
## Group:coloniesAmericano 0.3924079 0.1913762 0.2349567 0.2120498 0.1913762
## Group:coloniesCapimAcu 0.3279186 0.2670952 0.2899386 0.2899386 0.2899386
## Group:coloniesForteBoldro 0.2884615 0.1913762 0.2349567 0.2349567 0.2712426
## Group:coloniesLeao 0.3083444 0.3212595 0.2782826 0.3020828 0.2782826
## Group:coloniesPedreiraSueste 0.3212595 0.3020828 0.3279186 0.3083444 0.2959484
## Group:coloniesPiquinho 0.3083444 0.2726315 0.3708736 0.2899386 0.2899386
## Group:coloniesPraiaBoldro 0.2035251 0.2712426 0.3196229 0.2498722 0.1799525
## Group:coloniesTejuAcu 0.1913762 0.1657746 0.1657746 0.1727182 0.1727182
##
## 6
## Group:coloniesAmericano 0.1913762
## Group:coloniesCapimAcu 0.3147357
## Group:coloniesForteBoldro 0.2349567
## Group:coloniesLeao 0.2899386
## Group:coloniesPedreiraSueste 0.2840508
## Group:coloniesPiquinho 0.2616713
## Group:coloniesPraiaBoldro 0.3196229
## Group:coloniesTejuAcu 0.1727182
##
##
## Real Parameter sigma
##
## 1 2 3 4 5 6
## Group:coloniesAmericano NA NA NA NA NA NA
## Group:coloniesCapimAcu NA NA NA NA NA NA
## Group:coloniesForteBoldro NA NA NA NA NA NA
## Group:coloniesLeao NA NA NA NA NA NA
## Group:coloniesPedreiraSueste NA NA NA NA NA NA
## Group:coloniesPiquinho NA NA NA NA NA NA
```

```

## Group:coloniesPraiaBoldro    NA NA NA NA NA NA
## Group:coloniesTejuAcu        NA NA NA NA NA NA
##
##
## Real Parameter U
##           1           2           3           4           5
## Group:coloniesAmericano      69.597532 69.597532 69.597532 69.597532 69.597532
## Group:coloniesCapimAcu        9.409632  9.409632  9.409632  9.409632  9.409632
## Group:coloniesForteBoldro     69.597532 69.597532 69.597532 69.597532 69.597532
## Group:coloniesLeao            9.409632  9.409632  9.409632  9.409632  9.409632
## Group:coloniesPedreiraSueste  9.409632  9.409632  9.409632  9.409632  9.409632
## Group:coloniesPiquinho        9.409632  9.409632  9.409632  9.409632  9.409632
## Group:coloniesPraiaBoldro     69.597532 69.597532 69.597532 69.597532 69.597532
## Group:coloniesTejuAcu         69.597532 69.597532 69.597532 69.597532 69.597532
##           6
## Group:coloniesAmericano      69.597532
## Group:coloniesCapimAcu        9.409632
## Group:coloniesForteBoldro     69.597532
## Group:coloniesLeao            9.409632
## Group:coloniesPedreiraSueste  9.409632
## Group:coloniesPiquinho        9.409632
## Group:coloniesPraiaBoldro     69.597532
## Group:coloniesTejuAcu         69.597532
##
##
## Real Parameter Phi
## Group:coloniesAmericano
##   1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
## Group:coloniesCapimAcu
##   1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
## Group:coloniesForteBoldro
##   1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
## Group:coloniesLeao
##   1 2 3 4 5
## 1
## 2

```

```

## 3
## 4
## 5
##
## Group:coloniesPedreiraSueste
## 1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
## Group:coloniesPiquinho
## 1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
## Group:coloniesPraiaBoldro
## 1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
## Group:coloniesTejuAcu
## 1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
##
## Real Parameter GammaDoublePrime
## Group:coloniesAmericano
## 1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
## Group:coloniesCapimAcu
## 1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##

```



```

## Group:coloniesForteBoldro
## 1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
## Group:coloniesLeao
## 1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
## Group:coloniesPedreiraSueste
## 1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
## Group:coloniesPiquinho
## 1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
## Group:coloniesPraiaBoldro
## 1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
## Group:coloniesTejuAcu
## 1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
##
## Real Parameter GammaPrime
## Group:coloniesAmericano
## 2 3 4 5
## 1
## 2

```

```

## 3
## 4
##
## Group:coloniesCapimAcu
## 2 3 4 5
## 1
## 2
## 3
## 4
##
## Group:coloniesForteBoldro
## 2 3 4 5
## 1
## 2
## 3
## 4
##
## Group:coloniesLeao
## 2 3 4 5
## 1
## 2
## 3
## 4
##
## Group:coloniesPedreiraSueste
## 2 3 4 5
## 1
## 2
## 3
## 4
##
## Group:coloniesPiquinho
## 2 3 4 5
## 1
## 2
## 3
## 4
##
## Group:coloniesPraiaBoldro
## 2 3 4 5
## 1
## 2
## 3
## 4
##
## Group:coloniesTejuAcu
## 2 3 4 5
## 1
## 2
## 3
## 4
mabuya_model_5 <- mark(
  data = mabuya.process,

```

```

ddl = mabuya.ddl,
model.parameters = model.list[["alpha(effort*site) U(site)"]],
delete = TRUE
)

##
## Output summary for PoissonMR model
## Name : alpha(~effort * site)sigma(~1)U(~site)Phi(~1)Gamma'(~1)Gamma'(~1)
##
## Npar : 6
## -2lnL: 845.0471
## AICc : 857.2225
##
## Beta
##
## estimate se lcl ucl
## alpha:(Intercept) -1.9710750 0.1612669 -2.2871581 -1.6549919
## alpha:effort 0.0208696 0.0041051 0.0128237 0.0289156
## alpha:sitePARNA 0.5931867 0.4306514 -0.2508901 1.4372636
## alpha:effort:sitePARNA -0.0103921 0.0221580 -0.0538218 0.0330375
## U:(Intercept) 4.2434972 0.1249911 3.9985146 4.4884797
## U:sitePARNA -2.0002849 0.2403150 -2.4713023 -1.5292675
##
##
## Real Parameter alpha
##
## 1 2 3 4 5
## Group:coloniesAmericano 0.3955042 0.1905138 0.2347265 0.2114678 0.1905138
## Group:coloniesCapimAcu 0.3141575 0.2829074 0.2950160 0.2950160 0.2950160
## Group:coloniesForteBoldro 0.2891996 0.1905138 0.2347265 0.2347265 0.2716483
## Group:coloniesLeao 0.3044364 0.3108831 0.2888983 0.3012633 0.2888983
## Group:coloniesPedreiraSueste 0.3108831 0.3012633 0.3141575 0.3044364 0.2981233
## Group:coloniesPiquinho 0.3044364 0.2858871 0.3345411 0.2950160 0.2950160
## Group:coloniesPraiaBoldro 0.2028230 0.2716483 0.3210077 0.2498922 0.1789517
## Group:coloniesTejuAcu 0.1905138 0.1646196 0.1646196 0.1716361 0.1716361
##
## 6
## Group:coloniesAmericano 0.1905138
## Group:coloniesCapimAcu 0.3076429
## Group:coloniesForteBoldro 0.2347265
## Group:coloniesLeao 0.2950160
## Group:coloniesPedreiraSueste 0.2919411
## Group:coloniesPiquinho 0.2799587
## Group:coloniesPraiaBoldro 0.3210077
## Group:coloniesTejuAcu 0.1716361
##
##
## Real Parameter sigma
##
## 1 2 3 4 5 6
## Group:coloniesAmericano NA NA NA NA NA NA
## Group:coloniesCapimAcu NA NA NA NA NA NA
## Group:coloniesForteBoldro NA NA NA NA NA NA
## Group:coloniesLeao NA NA NA NA NA NA
## Group:coloniesPedreiraSueste NA NA NA NA NA NA
## Group:coloniesPiquinho NA NA NA NA NA NA
## Group:coloniesPraiaBoldro NA NA NA NA NA NA
## Group:coloniesTejuAcu NA NA NA NA NA NA

```

```

##
##
## Real Parameter U
##          1          2          3          4          5
## Group:coloniesAmericano 69.651008 69.651008 69.651008 69.651008 69.651008
## Group:coloniesCapimAcu  9.423554 9.423554 9.423554 9.423554 9.423554
## Group:coloniesForteBoldro 69.651008 69.651008 69.651008 69.651008 69.651008
## Group:coloniesLeao      9.423554 9.423554 9.423554 9.423554 9.423554
## Group:coloniesPedreiraSueste 9.423554 9.423554 9.423554 9.423554 9.423554
## Group:coloniesPiquinho  9.423554 9.423554 9.423554 9.423554 9.423554
## Group:coloniesPraiaBoldro 69.651008 69.651008 69.651008 69.651008 69.651008
## Group:coloniesTejuAcu   69.651008 69.651008 69.651008 69.651008 69.651008
##          6
## Group:coloniesAmericano 69.651008
## Group:coloniesCapimAcu  9.423554
## Group:coloniesForteBoldro 69.651008
## Group:coloniesLeao      9.423554
## Group:coloniesPedreiraSueste 9.423554
## Group:coloniesPiquinho  9.423554
## Group:coloniesPraiaBoldro 69.651008
## Group:coloniesTejuAcu   69.651008
##
##
## Real Parameter Phi
## Group:coloniesAmericano
##   1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
## Group:coloniesCapimAcu
##   1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
## Group:coloniesForteBoldro
##   1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
## Group:coloniesLeao
##   1 2 3 4 5
## 1
## 2
## 3
## 4

```

```

## 5
##
## Group:coloniesPedreiraSueste
## 1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
## Group:coloniesPiquinho
## 1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
## Group:coloniesPraiaBoldro
## 1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
## Group:coloniesTejuAcu
## 1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
##
## Real Parameter GammaDoublePrime
## Group:coloniesAmericano
## 1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
## Group:coloniesCapimAcu
## 1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
## Group:coloniesForteBoldro
## 1 2 3 4 5

```

```

## 1
## 2
## 3
## 4
## 5
##
## Group:coloniesLeao
## 1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
## Group:coloniesPedreiraSueste
## 1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
## Group:coloniesPiquinho
## 1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
## Group:coloniesPraiaBoldro
## 1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
## Group:coloniesTejuAcu
## 1 2 3 4 5
## 1
## 2
## 3
## 4
## 5
##
##
## Real Parameter GammaPrime
## Group:coloniesAmericano
## 2 3 4 5
## 1
## 2
## 3
## 4

```

```

##
## Group:coloniesCapimAcu
## 2 3 4 5
## 1
## 2
## 3
## 4
##
## Group:coloniesForteBoldro
## 2 3 4 5
## 1
## 2
## 3
## 4
##
## Group:coloniesLeao
## 2 3 4 5
## 1
## 2
## 3
## 4
##
## Group:coloniesPedreiraSueste
## 2 3 4 5
## 1
## 2
## 3
## 4
##
## Group:coloniesPiquinho
## 2 3 4 5
## 1
## 2
## 3
## 4
##
## Group:coloniesPraiaBoldro
## 2 3 4 5
## 1
## 2
## 3
## 4
##
## Group:coloniesTejuAcu
## 2 3 4 5
## 1
## 2
## 3
## 4

```

Step 8: Model Selection and Best Model Results

```
tb <- collect.models(lx = c("mabuya_model_1", "mabuya_model_2",
                           "mabuya_model_3", "mabuya_model_4",
                           "mabuya_model_5"))

tbDT <- data.table(print(tb))

##                                model npar
## 4 alpha(~effort + site)sigma(~1)U(~site)Phi(~1)Gamma' (~1)Gamma' (~1)    5
## 2      alpha(~effort)sigma(~1)U(~site)Phi(~1)Gamma' (~1)Gamma' (~1)    4
## 5 alpha(~effort * site)sigma(~1)U(~site)Phi(~1)Gamma' (~1)Gamma' (~1)    6
## 1      alpha(~1)sigma(~1)U(~site)Phi(~1)Gamma' (~1)Gamma' (~1)    3
## 3      alpha(~site)sigma(~1)U(~site)Phi(~1)Gamma' (~1)Gamma' (~1)    4
##      AICc DeltaAICc      weight Deviance
## 4 855.3908  0.000000 5.535834e-01 845.2658
## 2 857.1925  1.801710 2.248779e-01 849.1093
## 5 857.2225  1.831715 2.215293e-01 845.0471
## 1 878.3273 22.936543 5.788635e-06 872.2775
## 3 879.2648 23.874000 3.622512e-06 871.1816

print("Model selection table:")

## [1] "Model selection table:"

tbDT[, modelPosition := rownames(print(tb))]

##                                model npar
## 4 alpha(~effort + site)sigma(~1)U(~site)Phi(~1)Gamma' (~1)Gamma' (~1)    5
## 2      alpha(~effort)sigma(~1)U(~site)Phi(~1)Gamma' (~1)Gamma' (~1)    4
## 5 alpha(~effort * site)sigma(~1)U(~site)Phi(~1)Gamma' (~1)Gamma' (~1)    6
## 1      alpha(~1)sigma(~1)U(~site)Phi(~1)Gamma' (~1)Gamma' (~1)    3
## 3      alpha(~site)sigma(~1)U(~site)Phi(~1)Gamma' (~1)Gamma' (~1)    4
##      AICc DeltaAICc      weight Deviance
## 4 855.3908  0.000000 5.535834e-01 845.2658
## 2 857.1925  1.801710 2.248779e-01 849.1093
## 5 857.2225  1.831715 2.215293e-01 845.0471
## 1 878.3273 22.936543 5.788635e-06 872.2775
## 3 879.2648 23.874000 3.622512e-06 871.1816

best_model <- get(paste0("mabuya_model_", which(tbDT[,modelPosition == 1])))
```

Step 9: Interpreting Best Model Results

```
betaTable <- data.table(best_model$results$beta, keep.rownames = TRUE)
names(betaTable)[names(betaTable) == "rn"] <- "parameter"
betaTable[, Z.value := estimate / se]
betaTable[, p.value := 2 * (1 - pnorm(abs(Z.value)))]

print("Parameter estimates from best CMR model:")

## [1] "Parameter estimates from best CMR model:"

print(betaTable)

##      parameter      estimate      se      lcl      ucl      Z.value
##      <char>      <num>      <num>      <num>      <num>      <num>
## 1: alpha:(Intercept) -1.9612543 0.1597802 -2.2744234 -1.6480852 -12.274702
```



```
## 2:      alpha:effort  0.0205160 0.0040357 0.0126060 0.0284260 5.083629
## 3:   alpha:sitePARNA 0.4154279 0.2066882 0.0103191 0.8205367 2.009926
## 4:      U:(Intercept) 4.2427291 0.1249664 3.9977950 4.4876632 33.950959
## 5:      U:sitePARNA -2.0009952 0.2402727 -2.4719298 -1.5300606 -8.328017
##      p.value
##      <num>
## 1: 0.000000e+00
## 2: 3.702916e-07
## 3: 4.443907e-02
## 4: 0.000000e+00
## 5: 0.000000e+00
```

This table shows us that alpha (resighting rate/detection probability) is significantly **HIGHER** in PARNA while U (population size) is significantly **LOWER** in PARNA. So, this means that we DO see/capture more in PARNA, and yet, the population size is considerably smaller. This is due to a clear pressure of invasive species and the potential effects of food supplementation.

Note: We did not manage capture-recapture on Secondary islands due to impossible logistics.

Body Size Analysis

Using head length as the most stable morphometric variable.

Step 1: Loading Size Data

```
mabuia_ds <- fread("data/Size_Data.csv")
```

Step 2: Assessing Size Analysis Sampling Balance

```
pointsCounts_size <- mabuia_ds[, .N, by = "site"]
pointsCounts_size[site == "APA", pointsArea := 5.466]
pointsCounts_size[site == "PARNA", pointsArea := 11.424]
pointsCounts_size[site == "Secondary", pointsArea := 1.33]
pointsCounts_size[, pointsDensity := N/pointsArea]
pointsCounts_size[, propPoints := N/(sum(pointsCounts_size[, N]))]
pointsCounts_size[, propSize := pointsArea/(sum(pointsCounts_size[, pointsArea]))]
```

```
print("Size analysis sampling distribution:")
```

```
## [1] "Size analysis sampling distribution:"
```

```
print(pointsCounts_size)
```

```
## Index: <site>
##      site      N pointsArea pointsDensity propPoints  propSize
##      <char> <int>      <num>      <num>      <num>      <num>
## 1:    APA     58      5.466      10.611050  0.4754098 0.30000000
## 2:   PARNA    44     11.424       3.851541  0.3606557 0.62700329
## 3: Secondary   20      1.330      15.037594  0.1639344 0.07299671
```

There is indeed a bit of unbalance but it is not as critical as it seems:

- **APA:** 47% points over 30% area
- **PARNA:** 36% points over 62% area
- **Secondary:** 16% points over 7% area

Step 3: Factor Level Setup

```
mabuia_ds[, site := factor(site, levels = c("Secondary", "APA", "PARNA"))] # "Secondary" as reference
mabuia_ds[, sex := factor(sex)] # R will pick a reference, usually "F" alphabetically
```

Step 4: Outlier Detection

```
detect_outlier <- function(x) {
  Quantile1 <- quantile(x, probs=.25)
  Quantile3 <- quantile(x, probs=.75)
  IQR = Quantile3-Quantile1
  x > Quantile3 + (IQR*1.5) | x < Quantile1 - (IQR*1.5)
}

outliers <- detect_outlier(mabuia_ds$headLength[!is.na(mabuia_ds$headLength)])
print(paste("Number of outliers detected:", sum(outliers)))
```

```
## [1] "Number of outliers detected: 0"
```

No outliers detected, indicating good data quality.

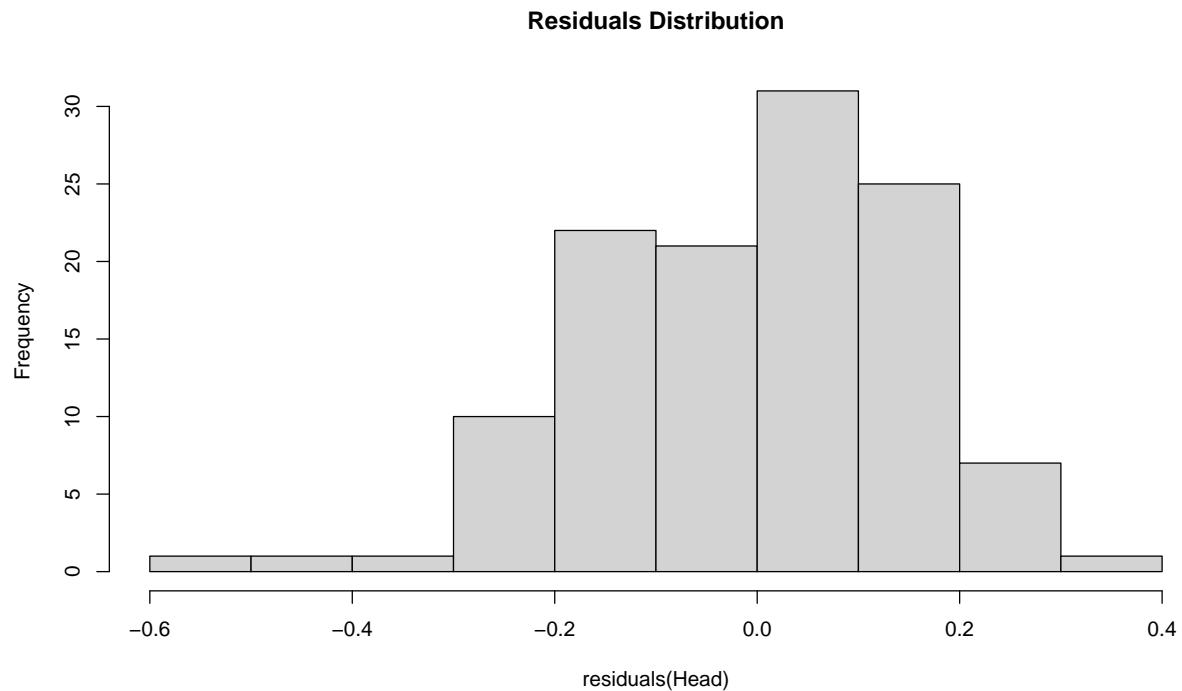
Step 5: Head Length Model

```
Head <- glm(headLength ~ sex + site,
            family = Gamma(link = "log"),
            data = mabuia_ds)
summary(Head)

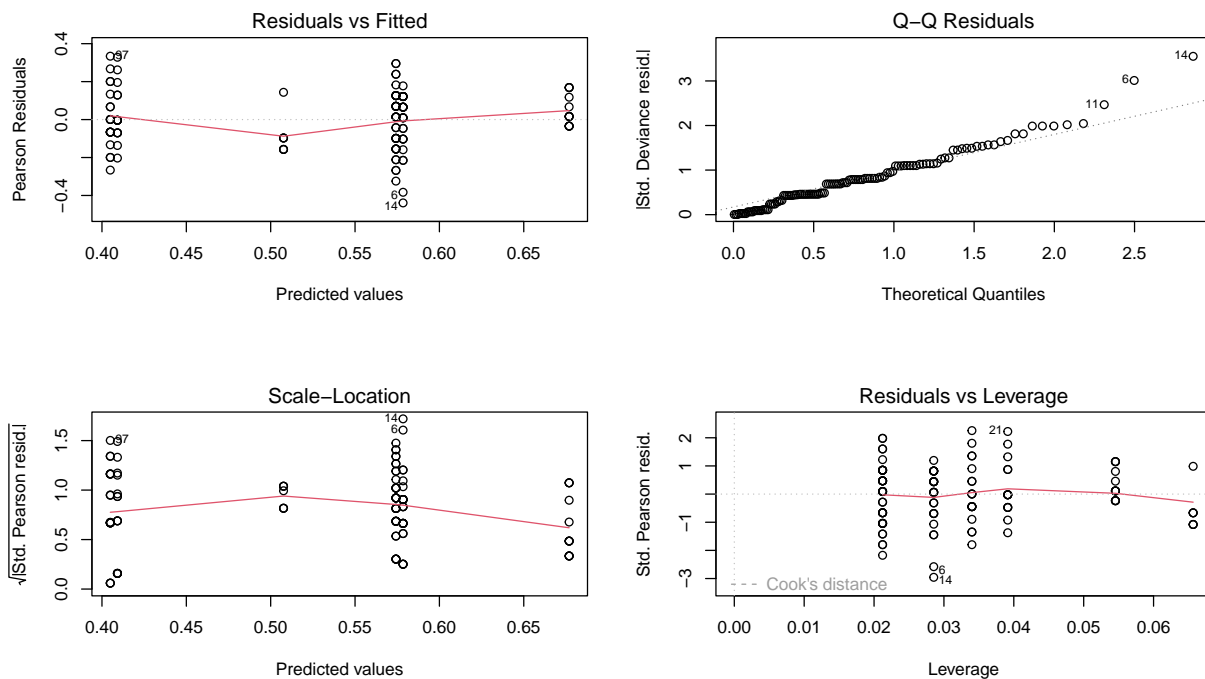
##
## Call:
## glm(formula = headLength ~ sex + site, family = Gamma(link = "log"),
##      data = mabuia_ds)
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.50760    0.03862  13.143 < 2e-16 ***
## sexM         0.16930    0.02902   5.833 5.01e-08 ***
## siteAPA     -0.10267    0.03909  -2.627 0.00979 **
## sitePARNA   -0.09844    0.04095  -2.404 0.01780 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.02271701)
##
## Null deviance: 3.7328  on 119  degrees of freedom
## Residual deviance: 2.7855  on 116  degrees of freedom
## (2 observations deleted due to missingness)
## AIC: 25.051
##
## Number of Fisher Scoring iterations: 4
```

Step 6: Model Diagnostics

```
hist(residuals(Head), main = "Residuals Distribution")
```



```
par(mfrow=c(2,2))  
plot(Head)
```



```
par(mfrow=c(1,1))
```

Step 7: Estimated Marginal Means for Head Length

```
emm_hF <- emmeans(Head, specs = ~ site + sex)
pairwise_head <- pairs(emm_hF, adjust = "tukey")
emm_hDT <- data.table(summary(emm_hF, type = "response"))

print("Head length estimated marginal means:")
```

```
## [1] "Head length estimated marginal means:"
```

```
print(emm_hDT)
```

##	site	sex	response	SE	df	lower.CL	upper.CL
##	<fctr>	<fctr>	<num>	<num>	<num>	<num>	<num>
## 1:	Secondary	F	1.661307	0.06416478	116	1.538960	1.793380
## 2:	APA	F	1.499204	0.04166956	116	1.418903	1.584050
## 3:	PARNA	F	1.505558	0.04488972	116	1.419223	1.597146
## 4:	Secondary	M	1.967770	0.06926544	116	1.835254	2.109854
## 5:	APA	M	1.775764	0.03898873	116	1.700197	1.854690
## 6:	PARNA	M	1.783290	0.04540648	116	1.695587	1.875529

```
print("Pairwise comparisons:")
```

```
## [1] "Pairwise comparisons:"
```

```
print(pairwise_head)
```

##	contrast	estimate	SE	df	t.ratio	p.value
##	Secondary F - APA F	0.10267	0.0391	116	2.627	0.0991
##	Secondary F - PARNA F	0.09844	0.0409	116	2.404	0.1634
##	Secondary F - Secondary M	-0.16930	0.0290	116	-5.833	<.0001
##	Secondary F - APA M	-0.06663	0.0483	116	-1.380	0.7392
##	Secondary F - PARNA M	-0.07086	0.0503	116	-1.408	0.7219
##	APA F - PARNA F	-0.00423	0.0305	116	-0.138	1.0000
##	APA F - Secondary M	-0.27197	0.0491	116	-5.542	<.0001
##	APA F - APA M	-0.16930	0.0290	116	-5.833	<.0001
##	APA F - PARNA M	-0.17353	0.0427	116	-4.061	0.0012
##	PARNA F - Secondary M	-0.26774	0.0501	116	-5.347	<.0001
##	PARNA F - APA M	-0.16507	0.0415	116	-3.973	0.0017
##	PARNA F - PARNA M	-0.16930	0.0290	116	-5.833	<.0001
##	Secondary M - APA M	0.10267	0.0391	116	2.627	0.0991
##	Secondary M - PARNA M	0.09844	0.0409	116	2.404	0.1634
##	APA M - PARNA M	-0.00423	0.0305	116	-0.138	1.0000
##						

Results are given on the log (not the response) scale.
P value adjustment: tukey method for comparing a family of 6 estimates

Step 8: Testing for Interaction Effects

```
Head_Interaction <- glm(headLength ~ sex * site,
                        family = Gamma(link = "log"),
                        data = mabuia_ds)
summary(Head_Interaction)
```

```
##
## Call:
## glm(formula = headLength ~ sex * site, family = Gamma(link = "log"),
##      data = mabuia_ds)
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    0.414944   0.056381   7.360 3.07e-11 ***
## sexM           0.308509   0.069931   4.412 2.34e-05 ***
## siteAPA       -0.002486   0.065954  -0.038  0.9700
## sitePARNA      0.025459   0.068280   0.373  0.7099
## sexM:siteAPA   -0.150422   0.081438  -1.847  0.0673 .
## sexM:sitePARNA -0.188238   0.084841  -2.219  0.0285 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.02225138)
##
## Null deviance: 3.7328  on 119  degrees of freedom
## Residual deviance: 2.6737  on 114  degrees of freedom
## (2 observations deleted due to missingness)
## AIC: 24.116
##
## Number of Fisher Scoring iterations: 4
emm_interaction <- emmeans(Head_Interaction, specs = ~ sex * site)
pairs_interaction_head <- pairs(emm_interaction, adjust = "tukey")
print("Interaction model pairwise comparisons:")

## [1] "Interaction model pairwise comparisons:"
print(pairs_interaction_head)

## contrast estimate SE df t.ratio p.value
## F Secondary - M Secondary -0.30851 0.0699 114 -4.412 0.0003
## F Secondary - F APA 0.00249 0.0660 114 0.038 1.0000
## F Secondary - M APA -0.15560 0.0612 114 -2.541 0.1210
## F Secondary - F PARNA -0.02546 0.0683 114 -0.373 0.9990
## F Secondary - M PARNA -0.14573 0.0633 114 -2.303 0.2013
## M Secondary - F APA 0.31099 0.0537 114 5.792 <.0001
## M Secondary - M APA 0.15291 0.0478 114 3.201 0.0214
## M Secondary - F PARNA 0.28305 0.0565 114 5.008 <.0001
## M Secondary - M PARNA 0.16278 0.0504 114 3.233 0.0195
## F APA - M APA -0.15809 0.0417 114 -3.788 0.0033
## F APA - F PARNA -0.02795 0.0515 114 -0.542 0.9943
## F APA - M PARNA -0.14822 0.0447 114 -3.318 0.0151
## M APA - F PARNA 0.13014 0.0453 114 2.872 0.0537
## M APA - M PARNA 0.00987 0.0373 114 0.264 0.9998
## F PARNA - M PARNA -0.12027 0.0480 114 -2.504 0.1317
##
## Results are given on the log (not the response) scale.
## P value adjustment: tukey method for comparing a family of 6 estimates
```

Step 9: Ecological Interpretation of Size Patterns

```
dt <- as.data.table(emm_interaction)

# Compare sex ratios across sites
male_props <- table(mabuia_ds[sex == "M", site])/NROW(mabuia_ds[sex == "M",])
female_props <- table(mabuia_ds[sex == "F", site])/NROW(mabuia_ds[sex == "F",])

print("Proportion of males by site:")

## [1] "Proportion of males by site:"
print(male_props)

##
## Secondary      APA      PARNA
## 0.1645570 0.4936709 0.3417722
print("Proportion of females by site:")

## [1] "Proportion of females by site:"
print(female_props)

##
## Secondary      APA      PARNA
## 0.1627907 0.4418605 0.3953488
```

Injury Analysis (Autotomy)

Step 1: Creating Autotomy Variable

```
mabuia_ds[, has_autotomy := ifelse(autotomy == "", "No", "Yes")]
```

Step 2: Autotomy Proportions and Statistical Test

```
autotomy_table_3way <- table(mabuia_ds$site, mabuia_ds$has_autotomy)
propTable <- prop.table(autotomy_table_3way, margin = 1)
chi_test_autotomy_3way <- chisq.test(autotomy_table_3way)
correctedProportion <- round(propTable*100, 2)
colnames(correctedProportion) <- c("No autotomy signs", "Autotomy signs")

print("Autotomy proportions by site (%):")

## [1] "Autotomy proportions by site (%):"
print(correctedProportion)

##
##           No autotomy signs Autotomy signs
## Secondary           85.00           15.00
## APA                 70.69           29.31
## PARNA               75.00           25.00
print("Chi-square test results:")

## [1] "Chi-square test results:"
```

```
print(chi_test_autotomy_3way)
```

```
##  
## Pearson's Chi-squared test  
##  
## data: autotomy_table_3way  
## X-squared = 1.613, df = 2, p-value = 0.4464
```

Proportionally, we also have more autotomized individuals in the APA than in PARNA and half in secondary islands, which is also an indication of higher predation pressure on the main island. But, this is not significant. It would be interesting to increase our samples to be able to infer better.

Combined Size and Injury Visualization

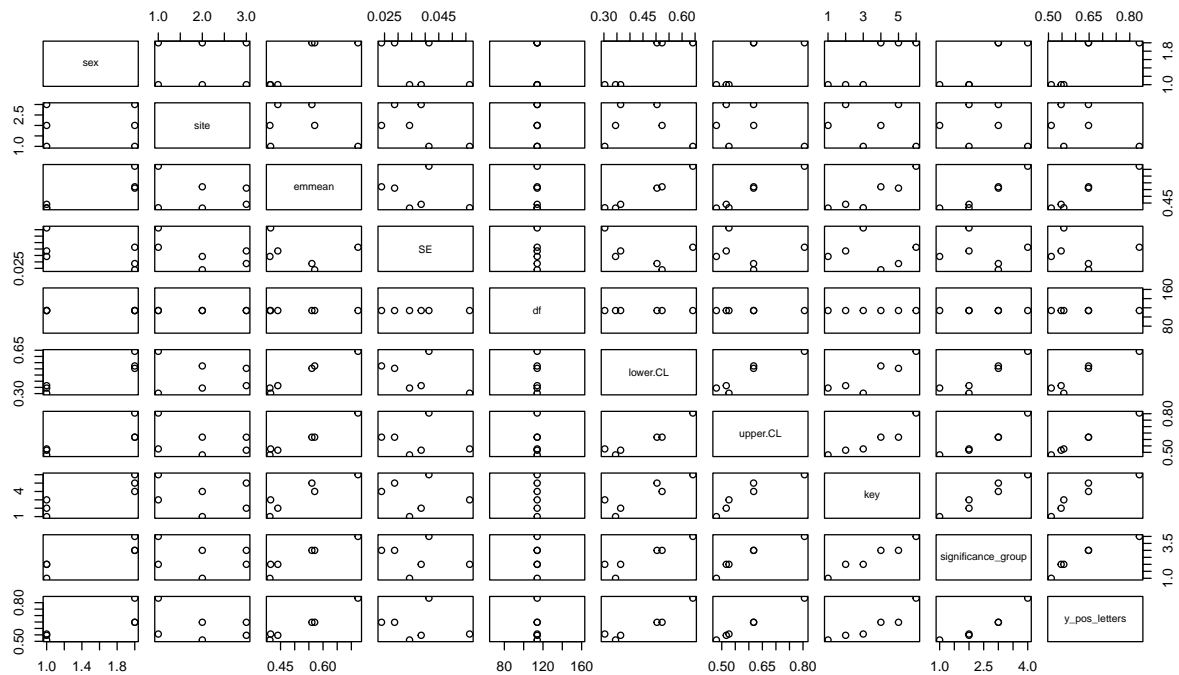
Step 1: Preparing Interaction Data for Plotting

```
dt_df <- as.data.frame(dt)  
dt_df$site <- factor(dt_df$site, levels = c("Secondary", "APA", "PARNA"))  
  
# Get significance testing for interaction model  
pairs_interaction <- contrast(emm_interaction, method = "pairwise", adjust = "tukey")  
summary_pw_int <- summary(pairs_interaction)  
p_values_int <- summary_pw_int$p.value  
print(p_values_int)
```

```
## [1] 3.312743e-04 1.000000e+00 1.210025e-01 9.990378e-01 2.012888e-01  
## [6] 9.272989e-07 2.142024e-02 2.956024e-05 1.949409e-02 3.262026e-03  
## [11] 9.942631e-01 1.505577e-02 5.373153e-02 9.998207e-01 1.316787e-01
```

Step 2: Processing Significance Letters for Interaction

```
contrast_names_raw_int <- as.character(summary_pw_int$contrast)  
p_value_names <- sapply(contrast_names_raw_int, function(contrast) {  
  parts <- strsplit(contrast, " - ")[[1]]  
  key1 <- gsub(" ", "", parts[1])  
  key2 <- gsub(" ", "", parts[2])  
  return(paste(key1, key2, sep = "-"))  
})  
names(p_values_int) <- p_value_names  
  
letters_result_int <- multcompLetters(p_values_int)  
significance_letters_int <- letters_result_int$Letters  
  
dt_df$key <- paste0(dt_df$sex, dt_df$site)  
dt_df$significance_group <- significance_letters_int[dt_df$key]  
dt_df$y_pos_letters <- dt_df$upper.CL + 0.03  
plot(dt_df)
```

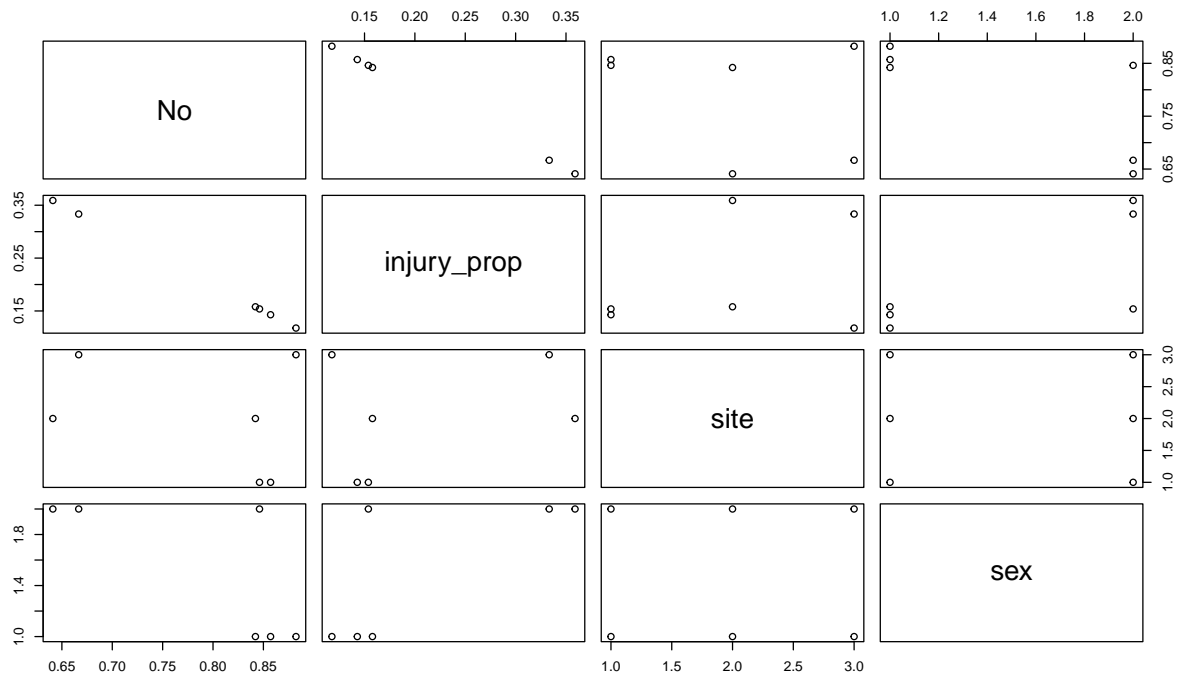


Step 3: Preparing Autotomy Data by Sex

```
# For males
males_data <- mabuia_ds[mabuia_ds$sex == 'M', ]
prop_table_males <- prop.table(table(males_data$site, males_data$has_autotomy), margin = 1)
males_autotomy_df <- as.data.frame.matrix(prop_table_males)
names(males_autotomy_df)[names(males_autotomy_df) == "Yes"] <- "injury_prop"
males_autotomy_df$site <- rownames(males_autotomy_df)
males_autotomy_df$sex <- "Males"

# For females
females_data <- mabuia_ds[mabuia_ds$sex == 'F', ]
prop_table_females <- prop.table(table(females_data$site, females_data$has_autotomy), margin = 1)
females_autotomy_df <- as.data.frame.matrix(prop_table_females)
names(females_autotomy_df)[names(females_autotomy_df) == "Yes"] <- "injury_prop"
females_autotomy_df$site <- rownames(females_autotomy_df)
females_autotomy_df$sex <- "Females"

# Combine
autotomy_df_final <- rbind(males_autotomy_df, females_autotomy_df)
autotomy_df_final$site <- factor(autotomy_df_final$site, levels = c("Secondary", "APA", "PARNA"))
autotomy_df_final$sex <- factor(autotomy_df_final$sex, levels = c("Females", "Males"))
plot(autotomy_df_final)
```

Step 4: Formatting for Unified Plot

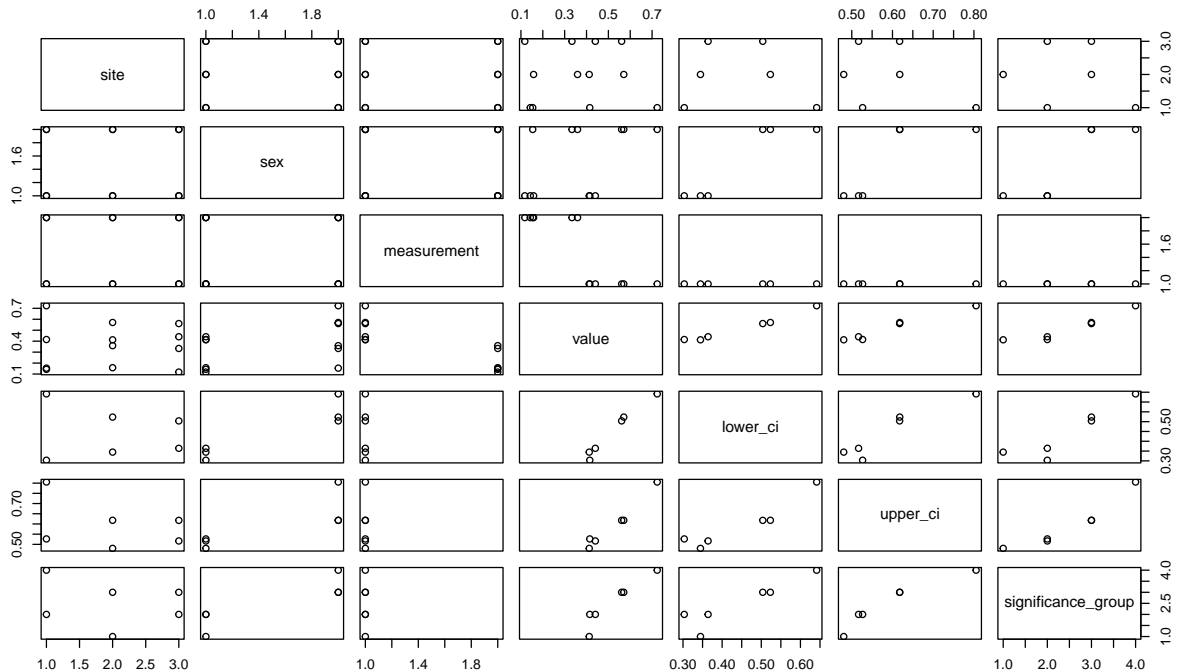
```
dt_df$sex <- ifelse(dt_df$sex == "F", "Females", "Males")
dt_df$sex <- factor(dt_df$sex, levels = c("Females", "Males"))

# Create unified plotting dataset
# Select and rename columns from head length data
plot_data_head <- data.frame(
  site = dt_df$site,
  sex = dt_df$sex,
  measurement = "Head Length (cm)",
  value = dt_df$emmean,
  lower_ci = dt_df$lower.CL,
  upper_ci = dt_df$upper.CL,
  significance_group = dt_df$significance_group
)

# Select and rename columns from injury data
plot_data_injury <- data.frame(
  site = autotomy_df_final$site,
  sex = autotomy_df_final$sex,
  measurement = "Proportion Injury",
  value = autotomy_df_final$injury_prop,
  lower_ci = NA, # No error bars for injury rate
  upper_ci = NA,
  significance_group = NA # No significance letters for injury rate
)

plot_data_unified <- rbind(plot_data_head, plot_data_injury)
```

```
plot(plot_data_unified)
```



Creating the Final Size and Injury Plot

```
body_size_plot <- ggplot(
  plot_data_unified,
  aes(x = site, y = value, fill = site, color = site)
) +
  # --- Geoms that use SUBSETS of the data ---
  # Add bars ONLY for the injury rate data
  geom_bar(
    data = plot_data_unified[plot_data_unified$measurement == "Proportion Injury", ],
    stat = "identity", color = "black", alpha = 0.8
  ) +
  # Add error bars ONLY for the head length data
  geom_errorbar(
    data = plot_data_unified[plot_data_unified$measurement == "Head Length (cm)", ],
    aes(ymin = lower_ci, ymax = upper_ci), width = 0.25, linewidth = 1
  ) +
  # Add points ONLY for the head length data
  geom_point(
    data = plot_data_unified[plot_data_unified$measurement == "Head Length (cm)", ],
    size = 4, stroke = 1.5
  ) +
  # Add text ONLY for the head length data
  geom_text(
    data = plot_data_unified[plot_data_unified$measurement == "Head Length (cm)", ],
    aes(y = upper_ci + 0.1, label = significance_group), # Increase offset for % scale
    color = "black", size = 6, fontface = "bold"
```

```

) +

# --- Faceting ---
# Facet by both sex and measurement, and allow y-axes to be independent
facet_grid(
  measurement ~ sex,
  scales = "free_y"
) +

# --- Scales and Labels ---
scale_color_viridis_d(option = "D") +
scale_fill_viridis_d(option = "D") +

# --- Theming ---
theme_bw(base_size = 14) +
theme(
  legend.position = "none",
  plot.title = element_text(face = "bold", size = 16),
  strip.text = element_text(size = 12, face = "bold"),
  strip.placement = "outside", # Ensures strips are next to the axis
  axis.title = element_text(face = "bold"),
  panel.grid.major.x = element_blank(),
  panel.grid.minor = element_blank(),
  # Add a bit more space between facets
  panel.spacing = unit(1.0, "lines"),
  axis.title.x = element_blank(),
  axis.title.y = element_blank(),
)

```

Summarizing the findings:

Results from point counts:

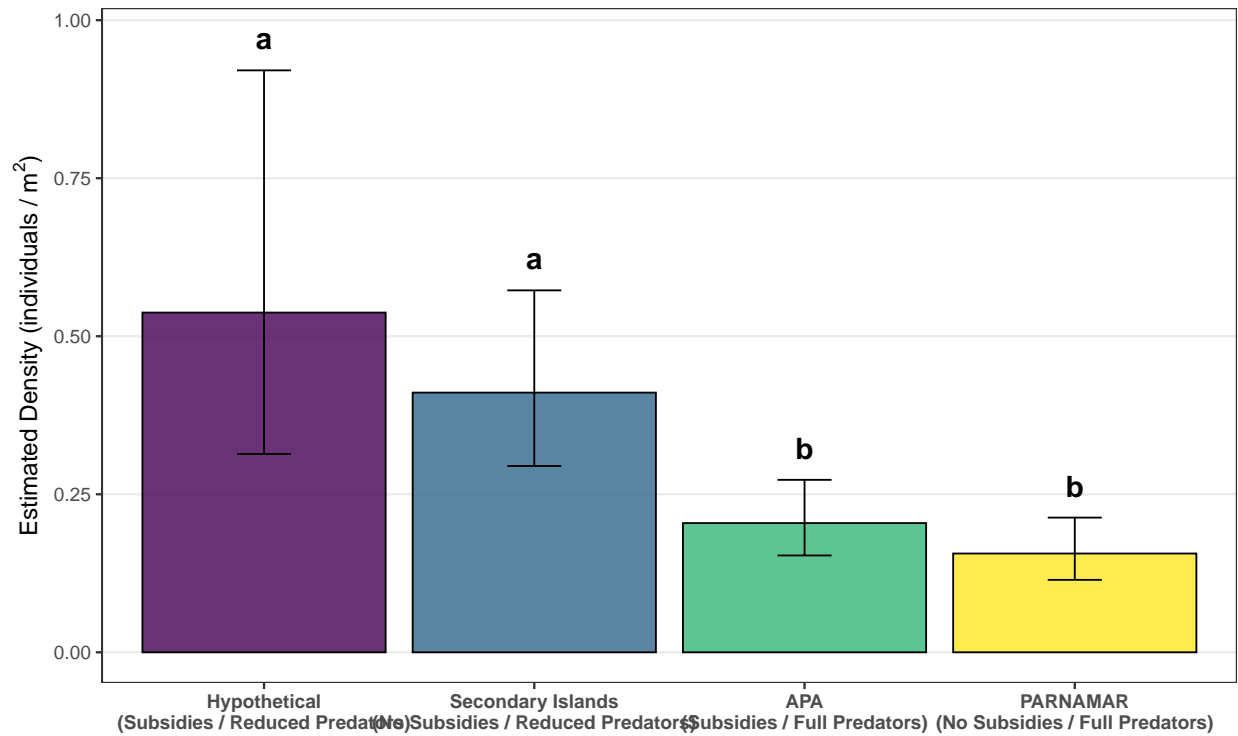
```
summary(emm_density_hierarchical, infer = TRUE)
```

```

## InvasiveSpeciesPresence FoodSupplementation response      SE df asymp.LCL
## 0                        0          0.411 0.0696 Inf      0.295
## 1                        0          0.156 0.0247 Inf      0.115
## 0                        1          0.537 0.1476 Inf      0.314
## 1                        1          0.204 0.0301 Inf      0.153
## asymp.UCL null z.ratio p.value
##   0.573    1  -5.252  <.0001
##   0.213    1 -11.730  <.0001
##   0.921    1  -2.261  0.0238
##   0.273    1 -10.782  <.0001
##
## Confidence level used: 0.95
## Intervals are back-transformed from the log scale
## Tests are performed on the log scale

```

```
density_plot
```



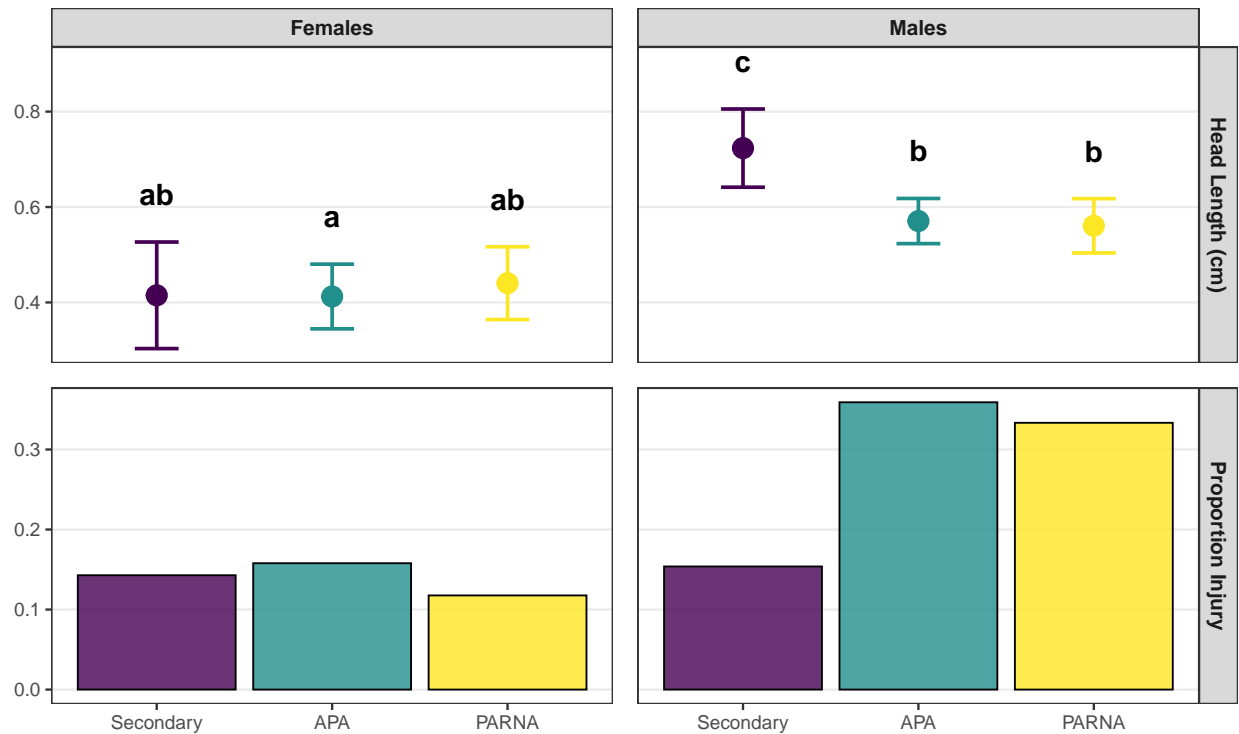
Results from CMR:

```
print(betaTable)
```

```
##           parameter    estimate        se      lcl      ucl    Z.value
##           <char>      <num>      <num>    <num>    <num>    <num>
## 1: alpha:(Intercept) -1.9612543 0.1597802 -2.2744234 -1.6480852 -12.274702
## 2:   alpha:effort    0.0205160 0.0040357  0.0126060  0.0284260   5.083629
## 3:   alpha:sitePARNA 0.4154279 0.2066882  0.0103191  0.8205367   2.009926
## 4:      U:(Intercept) 4.2427291 0.1249664  3.9977950  4.4876632  33.950959
## 5:      U:sitePARNA  -2.0009952 0.2402727 -2.4719298 -1.5300606  -8.328017
##           p.value
##           <num>
## 1: 0.000000e+00
## 2: 3.702916e-07
## 3: 4.443907e-02
## 4: 0.000000e+00
## 5: 0.000000e+00
```

Results from size analysis:

```
body_size_plot
```



Results from sublethal injuries:

```
print(correctedProportion)
```

```
##
##           No autotomy signs Autotomy signs
## Secondary           85.00           15.00
## APA                 70.69           29.31
## PARNA                75.00           25.00
```

```
print(chi_test_autotomy_3way)
```

```
##
## Pearson's Chi-squared test
##
## data: autotomy_table_3way
## X-squared = 1.613, df = 2, p-value = 0.4464
```

Saving the plots for manuscript

```
ggsave(
  filename = "outputs/Density_Plot.png", # The name of the output file
  plot = density_plot,                  # The plot object to save
  width = 12,                           # Width of the image in inches
  height = 6,                           # Height of the image in inches
  dpi = 300,                            # Dots per inch (standard for publication)
  bg = "white"                          # Set a white background
)
```

```

# Save as a high-resolution TIFF file
ggsave(
  filename = "outputs/Density_Plot.tiff",
  plot = density_plot,
  width = 12,
  height = 6,
  dpi = 300
)

ggsave(
  filename = "outputs/Size_Injury.png",
  plot = body_size_plot,
  width = 8,    # Keep it reasonably wide for the two columns
  height = 7,  # A bit taller to accommodate the stacked facets
  dpi = 300,
  bg = "white"
)

ggsave(
  filename = "outputs/Size_Injury.tiff",
  plot = body_size_plot,
  width = 8,    # Keep it reasonably wide for the two columns
  height = 7,  # A bit taller to accommodate the stacked facets
  dpi = 300,
  bg = "white"
)

```