

Investigating influential ecosystem characteristics on commercially important reef fish assemblages within Dauin, Philippines

A dissertation submitted in part fulfilment of the MSc in Marine Environmental
Management

Department of Environment and Geography,
University of York

Yasmine Watkins
Supervised by Jennifer Brand

October 2020

ABSTRACT

Coral reef ecosystems are vital to the food security and livelihood of people in the Philippines, however, many reefs have now been destroyed by anthropogenic induced stressors such as destructive fishing methods and overexploitation of commercially important reef fish. Understanding the drivers of variability in the composition of fish assemblages across the local reefs of Dauin is vital for conservation development and effective reef fisheries management. In this study highly influential factors driving fish assemblage characteristics of commercially important fish families (Labridae: Wrasse, Lutjanidae: Snapper, and Serranidae: Seabass and Groupers) were identified. Four key biological and physical variables (Abiotic [+], Coral cover [-], Octocoral [-] and Depth) were found to highly influence Labridae assemblage characteristics, with coral and abiotic cover (%) to be significant. Fish species abundance, biomass and total length of the commercially important snapper family (Lutjanidae) were correlated positively with increasing cover of sponges. Individuals of the Serranidae family significantly correlated with a variety of benthic substratum (Live coral [-], Dead coral [+] and Algae [+]) with significant abundance at shallower depths of 5 m. Ultimately, this study, will help guide marine conservation management decisions to sustain commercially important fish assemblages within the Municipality of Dauin, Philippines.

TABLE OF ABBREVIATIONS

Abbreviation	Description
MPA	Marine Protected Area
IMR	Institute for Marine Research
SCUBA	Self-contained underwater breathing apparatus
DO-SVS	Diver-Operated Stereo Video System
UVC	Underwater Visual Census
AIMS	Australian Institute of Marine Science
CPCe	Coral Point Count with Excel extensions
3D	3- Dimensional
VIF	Variation Inflation Factors
AIC _c	Akaike Information Criteria (corrected)
SfM	Structure from Motion
MAM	Minimum Adequate Model
GLM	Generalised Linear Model
ANOVA	Analysis of Variance
FAC(s)	Fish Assemblage Characteristic(s)

1.0 INTRODUCTION

1.1 The Philippines

Located in the apex of the coral triangle, the Philippines has long been considered the global hotspot of marine biodiversity and multi-taxa marine endemism, supporting the highest concentration of marine fish and coral diversity (DeVantier & Turak, 2017; Cabral et al., 2014; Roberts et al., 2012; Carpenter & Springer, 2005). The Philippines is made up of over 7,100 islands, of which 18,000 km of the country's coastline is lined by fringing coral reefs, submerged offshore reefs or coral atolls (Licuanan et al., 2019; White et al., 2000). An estimated total reef area of 27,000 km² is the third largest in the world and is home to over 1,700 reef fish species (Rohrer, 2017; White et al., 2000; Gomez et al., 1994) and therefore is widely recognized as a priority for marine conservation and research.

Coral reef ecosystems are critical for providing the most substantial and sustainable supply of food to people in the Philippines (White et al., 2000). Over 50% of the country's source protein is derived from marine fisheries and aquaculture, with more than one million small-scale fishers directly dependent on reef fisheries for their livelihoods (White et al., 2000; White & Cruz, 1998). Reef fish are estimated to contribute 8 to 20 % (143,200 to 58,000 t) of total fisheries catch in the Philippines in the early 1980s, however, despite their economic importance to local communities, many reefs have now been destroyed by anthropogenic induced stressors (e.g., Primavera, 1995; Nañola Jr. et al., 2011; Honda et al., 2016). A major finding from a study conducted by Nañola et al., (2011) was the apparent local extinction of fishes in densely populated areas in central Philippines that used to be the country's center of diversity. Further studies have documented complete disappearance and, in some cases, severe declines in biomass of some large-bodies and commercially important fish across the country (Maypa et al., 2002; Lavides et al., 2009; Mamauag et al., 2009; Muallil et al., 2015), with drastic reductions in fisheries catches at major fishing grounds (Green et al., 2003; Muallil et al., 2014). The key causes of fishery decline are attributed to anthropogenic pressures, in particular overfishing from a rapidly expanding fishing population and unregulated destructive fishing practices (White and Yim, 2010; Muallil et al., 2015). Of the total fish market in the Philippines, 45% comes from small-scale and near-shore fisheries, which means that the decrease in Philippine marine resources, both in terms of income and food security, has and will continue to have a significant effect on the poorer sectors of the population (Green et al., 2003; Bianchessi, 2012). Rising pressure from near-shore overfishing is a leading threat to marine resources and raises concerns over the sustainability of local fisheries (Horigue et al., 2012; White et al., 2000; Bianchessi, 2012).

Marine protected areas (MPA) are among the most commonly implemented conservation tools across the Philippines to reverse habitat degradation and the declining productivity of coral reef fisheries (Rohrer, 2017; Muallil et al., 2015). Studies have shown evidence of an increased abundance and biomass of commercially important species of reef fish through successful management within marine reserves and thus protecting fisheries (Honda et al., 2016; Muallil et al., 2015; Halpern, 2003). In the Philippines, there are over 1, 600

community-based or locally managed MPAs, consisting of mainly no-take zones surrounded by managed fishing grounds (White et al., 2014; Cabral et al., 2014). When properly managed, MPAs established in the Philippines have demonstrated the ability to sustain small-scale fisheries, however, only 30% of all existing MPAs maintain adequate levels of management and thus only 1% of coral reef areas with the MPAs are effectively protected (Indab, 2004; Alcala & Russ, 2006; White et al., 2014).

1.2 Coral reef assemblages

Coral reefs are a highly complex and biodiverse ecosystem, subject to a wide variety of natural and anthropogenic factors that function at both local and global scales. Studies suggest levels of fishing and reef benthic structure to be the drivers affecting population abundance and assembly structure of reef fish species multiple scales in the Indo-Pacific (Friedlander et al., 2003; Pinca et al., 2012; Jouffray et al., 2014; Graham et al., 2015; McClanahan et al., 2016; Samoily et al., 2018). Reef fish assemblages can therefore be strong indicators and explanatory factors of such external stressors, as various species of fish play important ecological and functional roles within a coral reef ecosystem (Bellwood et al., 2004; Pratchett et al., 2011). For example, herbivorous fish have shown to be essential for algal abundance control, reducing the potential for reef state shifts and promoting ecosystem resilience (Hughes, 1994; Hughes et al., 2007; Graham et al., 2015). Therefore, regulation of the reef ecosystem can include both bottom-up and top-down mechanisms through resource and predation respectively (Samoily et al., 2018). Changes in coral cover reflect bottom-up control, while herbivore depletion through fishing reflects top-down control, and thus undermining their functional role (Mumby, 2006; Bonaldo et al., 2007). Understanding the relationship between these drivers and their relative effect on reef fish assemblages is also vital for conservation development and effective reef fisheries management (Samoily et al., 2018).

1.3 Aims and objectives

In the present study, I examined the relationships between abundance, biomass and length of commercially important fish species, and habitat characteristics within the local coral reefs of Dauin, Philippines. Small-scale fishing in the Philippines is becoming increasingly less selective in its target species and it is therefore difficult to classify species as commercially important or not for a given area (Muallil et al., 2015). Therefore, this study considered three fish families (Labridae: Wrasse, Lutjanidae: Snapper and Serranidae: Seabass and Groupers) of commercial importance for the status of reef health and importance to local fishermen according to FishBase (Froese and Pauly, 2016). The objective was to determine the relative influence of particular habitat characteristics in explaining commercially important fish assemblage and populations, with the hope to aid in vital marine conservation management decisions and sustain fisheries within the Municipality of Dauin.

2.0 METHODOLOGY

2.1 Study site

This study was conducted off the coastline of Dauin, a fourth-class Municipality in the province Negros Oriental, central Philippines (Abesamis & Russ, 2010; Bianhessi, 2012; Waters et al., 2019). The Dauin coastline stretches nine kilometers along the Eastern shores of Negros island and is bordered by Bacong in the north and Zamboanguita in the south (Waters et al., 2019). A patchy reef ecosystem separated by sand or seagrass is situated between the depths of <1-30 meters and is located less than 300 meters from the shore (Absamis & Russ, 2010). A total of 19 sites varying in coral reef composition, benthic and fish communities were selected for monitoring and data collection (Figure 1.). Selected study sites account for the zoning history of its associated no-take marine protected areas (MPA's) and non-MPA locations across the Municipality. Benthic, fish and reef structure surveys were conducted along 50m transects that run parallel to the reef crest, between the depths of 1-6m and 7-12m at each core site. Data collection occurred during the months February – July and August – January for both ‘wet’ and ‘dry’ seasons respectively, to account for seasonal variability.

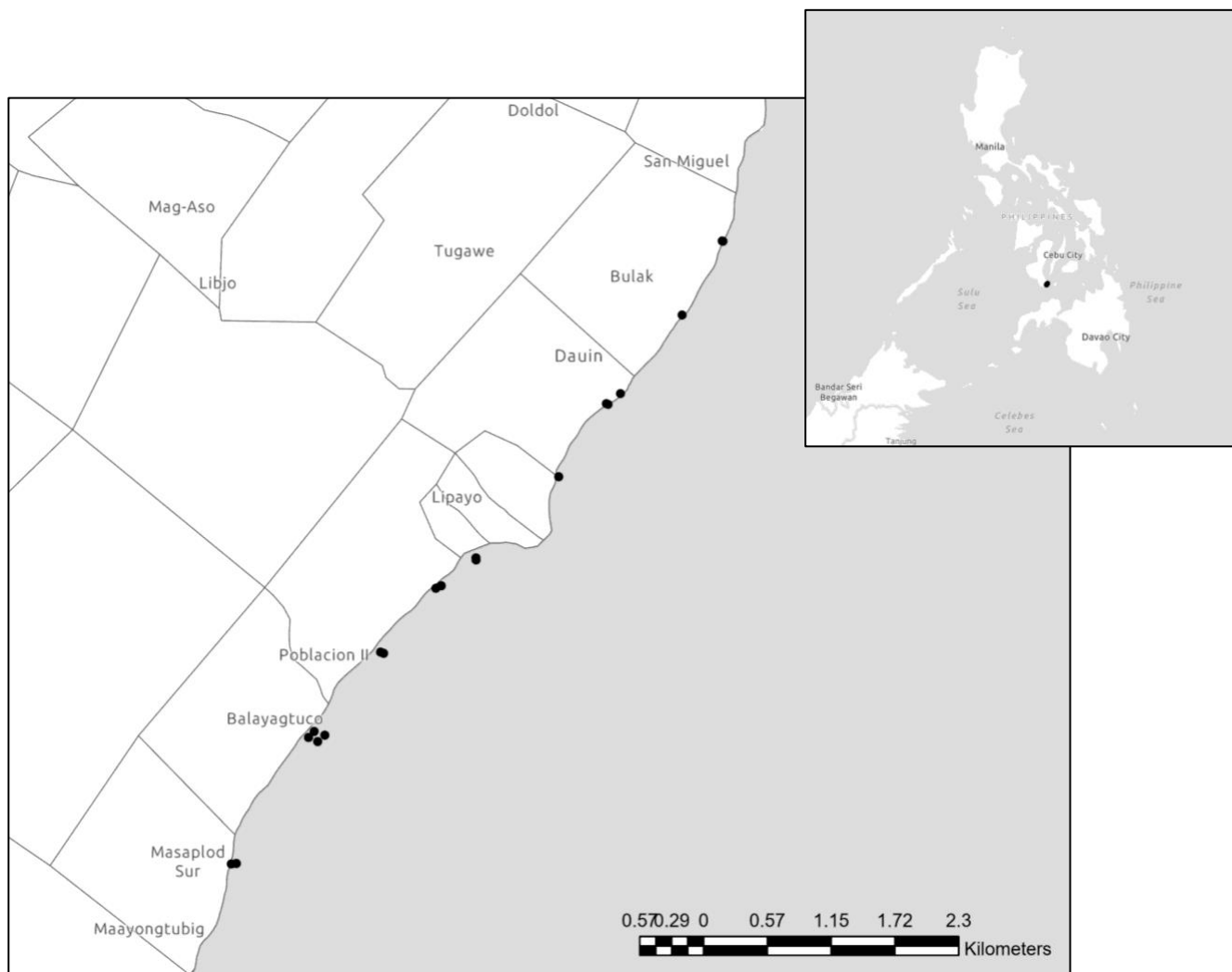


Figure 1. Map of the Municipality of Dauin and location of 19 survey sites on Negros Oriental, the Philippines. Maps generated using ArcGIS Pro. Version 2.3.3.

All data was collected by research associates under the 'Institute for Marine Research' (IMR) as part of a long-term, fine scale monitoring program of the inshore reef ecosystem within the Municipality of Dauin, Philippines. Methodology follows that of IMR's 2019 outlook report (Waters, Brand & Manrique, 2020).

2.3 Data collection

2.3.1 Benthic composition

Benthic assays were conducted following the Australian Institute of Marine Science (AIMS) LTMP to assess benthic habitat composition at each survey site (Miller et al., 2018; Jonker et al., 2008). Images along a transect were captured using a *GoPro*, held approximately 0.5m above the substratum capturing one image per 1m interval. Identification of benthos and its percentage cover was estimated from overlaid images and 30 randomly distributed points using Coral Point Count with Excel extensions (CPCe) visual software (Kohler & Gill, 2006). Points were classified according to a predetermined codec containing all Indo-Pacific organisms and substrate. Major benthos categories identified are displayed in appendix 1. Mean percentage cover per site for each major benthic category was calculated for further statistical analysis.

2.3.2 Fish survey

Transect surveys at each study site were conducted using a diver-operated stereo video system (DO-SVS, SeaGIS, Melbourne, Australia) comprising of two *GoPro Hero 5 Black* cameras. DO-SVS allows for more efficient and precise fish community monitoring in water than conventional underwater visual census (UVC) techniques, and to estimate fish biomass more accurately (Holmes *et al*, 2013; Waters, Brand & Manrique, 2020). Cameras are pre-set to record and synchronized to reduce potential disturbance to the fish community. Cameras were angled approximately 20 degrees downward and orientated parallel to the substrate. DO-SVS operator films the reef scape along the transect swimming at a steady pace, correcting for currents. All surveys were carried out using SCUBA and took approximately 5-6 minutes.

All footage was calibrated and synchronized using EventMeasure software v5.25 (seaGIS, Melbourne, Australia). Center points for each individual fish encountered along the transect were resolved into distances on a three-dimensional coordinate system, allowing for those beyond 2.5m on either side and 5m in front of the camera system to be excluded from analysis. Each individual fish encountered within the belt transect was measured and identified down to species level where possible. Finally, fish species were classified for their commercial value (Commercial, Minor, Subsistence fisheries and None) according to FishBase (Froese and Pauly, 2016).

2.3.3 3-Dimensional Reef Modelling

To obtain video footage of each 50m survey transect, a 3D camera rig comprising of two *GoPro Hero 5 Black* cameras mounted 0.9 m apart on a one-meter-long aluminum pole was used. Cameras were programmed to a capture rate of 60 frames per second at a resolution of 1080 pixels and set to a wide-angle facing directly

down toward the substratum. Operator moves the camera rig in a lawnmower motion approximately 2m above the substrate, ensuring 1m either side of the 50m transect is captured. To ensure image alignment, the operator aims to cover at least 60% overlap of each motion. 3-Dimensional (3D) reef models per site were developed using Structure from Motion (SfM) software and photogrammetry principles by extracting stills from both cameras at a rate of one per 30 frames, aligning images with high accuracy. Surface line length (reef length) and rugosity (Rq) were then calculated ready for statistical analysis.

2.4 Statistical analysis

2.4.1 Data analysis and model assumptions

Fish length measurements obtained were converted into biomass (Eqs 1.), where W is weight (g), L is fish length (cm) and a and b represent species-specific allometric constants derived from FishBase (Froese and Pauly, 2016).

$$W = aL^b \quad \text{[Eq 1.]}$$

Where fish length measurements or species-specific allometric constants were unobtainable, the mean species length recorded across all depths and survey sites or genus mean was used respectively. Fish abundance, biomass and length were calculated as mean per dive site.

A total of 11 biological and environmental variables were determined to predict the abundance, biomass and length of three families of fish 'Labridae', 'Lutjanidae' and 'Serranidae' across 19 different reef sites (n=19). Appendix 1. includes full variable descriptions. Rstudio software (Version 1.2.5033) was used for all data exploration, statistical analysis and visual presentation of results. Statistical test of normality (Shapiro-wilk) was used to assess all variables and the skew, linearity and heteroscedasticity of residuals were evaluated through visual diagnostic plots (histogram, kernel density and Quantiles-Quantiles), standard error (2SE) values (0 = normal) and calculation of variance ratios, looking for equal variances either side of the mean (Little et al., 2016; Zuur et al., 2010). Tukey's ladder of powers transformation of response variables was required to eliminate heteroscedasticity or lack of residual normality and to reduce outliers. The remaining outliers were not removed from the modelling process due to the relatively small sample size and must be taken into consideration during analysis (Zuur et al., 2010). Calculation of Pearson correlation coefficients ($|r|$) and Variance Inflation Factors (VIFs) were carried out to detect potential problems in multi-collinearity between independent variables and to identify those that highly correlate with each dependent variable (abundance, biomass, length) (Zuur et al., 2010). Intercorrelation was based on a critical correlation value ($|r| > 0.7$) from Pearson (Dormann et al., 2012) and a VIF threshold of < 2 as seen in Little et al., (2016). Multiple groups of variables were selected, separating those that highly correlated with each other to avoid the exclusion of potentially influential variables (Little et al., 2016; Crawley, 2005). Variables that related significantly (p -value < 0.05) with fish assemblages of all families were included in all models.

2.4.2 Statistical testing and model selection

Generalised Linear Models were generated for each group using Gaussian, Poisson or Negative binomial error distribution depending on data type and overdispersion (Crawley, 2005). For each model, a VIF reduction process eliminated variables with high VIFs (> 2) that were least associated first with the response variables and further reduced for parsimony to create a Minimum Adequate Model (MAM) using forward-backward stepwise with Akaike Information Criterion (AIC) (Marshall et al., 2012). AIC presents the model and maximum likelihood estimation of the parameters and thus gives the minimum AIC (Akaike, 1974). Leverage, linearity and residuals were checked against diagnostic plots for a robust regression analysis, where outliers were considered above 1.0 Cook 's Distance (Little et al., 2016; Maindonald & Braun, 2006). Model analytics included Analysis of Variance (ANOVA) to determine statistically significant differences between each full model and its corresponding MAM. The percentage deviance (% D), a measure of the 'goodness of fit' of the GLM, was computed for each model (Eq 2.) and models were classed equivalent within 2 AIC corrected values (AICc) based upon weight and %D (Burnham & Anderson, 2002).

$$\left(1 - \frac{\text{residual deviance}}{\text{null deviance}}\right) 100 \quad [\text{Eq 2.}]$$

Fish characteristics (abundance, biomass and length) between shallow and deep depth strata and between wet and dry season were further compared using a Kruskal Wallace test and one-way ANOVAs. These techniques allowed for the selection of regression models with the best performing explanatory variables for the abundance, biomass and length of the three commercially important fish families across sample sites.

3.0 RESULTS

3.1 Correlation analysis

Strong intercorrelation was found between variables reef length and rugosity ($|r|$ 0.789) and were therefore separated during the modeling process (Zurr et al., 2010). Variables abiotic and coral cover were also treated separately despite a slightly lower Pearson's value ($|r|$ 0.679). Of the 11 variables (Appendix 1.) derived from data surveys, no predictor variables showed a strong covariate relationship with any response variables based on the critical values for Pearson's correlation ($|r| > 0.7$). However, four key variables (Abiotic, Coral cover, Octocoral and Depth) were identified to have a statistically significant correlations ($p < 0.05$) with Labridae assemblage characteristics, one key variable (Sponge) significantly correlated with all response variables of Lutjanidae and three key variables (Coral cover, Algae and Dead coral) had significant relationships with Serranidae response variables (Table 1). No significant differences were found in FACs between sites at 5 m depth and 10 m depth for Lutjanidae, however, Labridae and Serranidae average abundance was significantly greater at shallower depths of 5 m (Table 2). No significant differences were found in FACs between wet and dry season for all three commercially important fish families (Table 2).

Table 1. Influence of various environmental variables on fish assemblage characteristics (FACs) for Labridae, Lutjanidae and Serranidae, across reef study sites in Dauin, Philippines. Results of Pearson correlation coefficient ($|r|$) with direction of trend (+/-). Statistically significant values are displayed in bold.

Variable	Abundance		Biomass		Length		
	$ r $	P	$ r $	P	$ r $	P	
Labridae	Physical						
	Depth	0.276	0.093	0.096	0.564	0.091	0.588
	Season	0.075	0.656	0.058	0.732	0.143	0.392
	Rugosity	0.186	0.263	0.168	0.314	0.082	0.623
	Reef length	0.117	0.484	0.079	0.639	0.061	0.716
	Abiotic	(+) 0.423	0.008	(+) 0.576	<0.001	(+) 0.483	0.002
	Biotic						
	Coral cover	(-) 0.390	0.016	(-) 0.396	0.014	0.145	0.385
	Hexacoral	0.022	0.897	0.070	0.678	0.128	0.446
	Octocoral	0.011	0.950	0.288	0.079	(-) 0.418	0.009
	Sponge	0.090	0.592	0.156	0.349	0.223	0.178
	Algae	0.201	0.227	0.141	0.399	0.241	0.144
	Dead coral	0.088	0.598	0.063	0.706	0.176	0.290
Lutjanidae	Physical						
	Depth	0.214	0.198	0.077	0.645	0.082	0.625
	Season	0.188	0.260	0.041	0.808	0.010	0.954
	Rugosity	0.159	0.339	0.094	0.574	0.103	0.538
	Reef length	0.167	0.316	0.037	0.824	0.022	0.894
	Abiotic	0.014	0.934	0.072	0.667	0.079	0.637
	Biotic						
	Coral cover	0.017	0.919	0.056	0.737	0.052	0.756
	Hexacoral	0.113	0.498	0.012	0.943	0.003	0.987
	Octocoral	0.077	0.647	0.094	0.574	0.103	0.537
	Sponge	(+) 0.456	0.004	(+) 0.415	0.010	(+) 0.403	0.012
	Algae	0.082	0.623	0.072	0.771	0.065	0.698
	Dead coral	0.023	0.893	0.038	0.819	0.046	0.786
Serranidae	Physical						
	Depth	0.296	0.071	0.181	0.277	0.178	0.286
	Season	0.079	0.636	0.142	0.396	0.147	0.378
	Rugosity	0.090	0.591	0.022	0.896	0.020	0.904
	Reef length	0.180	0.279	0.016	0.922	0.016	0.924
	Abiotic	0.008	0.963	0.142	0.396	0.137	0.412
	Biotic						
	Coral cover	(-) 0.395	0.014	(-) 0.408	0.011	(-) 0.398	0.013
	Hexacoral	0.117	0.483	0.128	0.444	0.132	0.430
	Octocoral	0.166	0.321	0.000	0.998	0.014	0.935
	Sponge	0.059	0.727	0.217	0.192	0.224	0.177
	Algae	(+) 0.334	0.040	0.088	0.600	0.080	0.631
	Dead coral	(+) 0.438	0.006	0.172	0.301	0.164	0.326

Table 2. Statistical differences between 'physical' factorial variables on fish assemblage characteristics (FACs) for Labridae, Lutjanidae and Serranidae, across reef study sites in Dauin, Philippines. Results of parametric and non-parametric statistical tests and statistically significant values are displayed in bold.

		Season, Pr(>F)	Depth, Pr(>F)	Statistical Test
Labridae	Abundance	0.248	0.021	Kruskal wallis
	Biomass	0.737	0.086	Kruskal wallis
	Length	0.392	0.588	ANOVA
Lutjanidae	Abundance	0.940	0.298	Kruskal wallis
	Biomass	0.610	0.903	Kruskal wallis
	Length	0.697	0.808	Kruskal wallis
Serranidae	Abundance	0.547	0.047	Kruskal wallis
	Biomass	0.333	0.124	Kruskal wallis
	Length	0.277	0.147	Kruskal wallis

3.2 Multivariate regression analysis using stepAIC

Backward-forward stepwise reduction, based on Akaike Information Criteria (AIC), produced Minimum Adequate Models (MAMs), by dismissing less influential predictors (Little et al, 2016). Results from multivariate GLMs are shown in Table 3.

Table 3. Akaike Information Criteria corrected (AIC_c) values in multi-model inference ranking for full models and reduced model (Minimum Adequate Model (MAM)), percentage deviance (%D) of reduced model and their weighted probability of being the best model (Akaike weight).

Response Variable	Full model	Reduced model variables	Reduced model (MAM)	%D (MAM)	Akaike weight (MAM)
Labridae					
Abundance	272.20	(abiotic, depth)	261.30	45.595	0.39
Biomass	-143.90	(abiotic, dead coral, algae, hexacoral)	-160.10	47.114	0.31
Length	149.30	(abiotic, hexacoral, octocoral)	136.10	34.173	0.27
Lutjanidae					
Abundance	175.30	(dead coral, octocoral, sponge)	151.10	45.391	0.20
Biomass	2.90	(reef length, octocoral, sponge)	-14.50	31.028	0.23
Length	524.90	(octocoral, sponge)	501.70	24.562	0.20
Serranidae					
Abundance	137.20	(coral cover, dead coral, algae, octocoral)	123.80	45.524	0.49
Biomass	60.90	(coral cover, depth, season, sponge)	36.80	30.781	0.30
Length	209.30	(coral cover, depth, season, sponge)	185.0	30.656	0.29

3.2.1 Labridae

The multi-model inference used, ranked all reduced and full abundance models according to their AIC corrected (AIC_c) values (Symonds & Moussalli, 2011), indicating that the reduced model containing physical variables 'abiotic' and 'depth' were the most influential predictors of Labridae abundance across study reefs (Table 3). Abundance of individuals increased with average percentage abiotic cover (sand, rubble, rock) and decreased at deeper depths of 10 m. The reduced model explained $\sim 45\%$ of deviance and supported early correlation analysis. Labridae biomass was best modelled by a combination of physical and biological variables, average percentage 'abiotic', 'dead coral', 'algae' and 'hexacoral' cover and explained $\sim 47\%$ of deviance (Table 3). Labridae average biomass increased with average percentage abiotic cover and had a slight negative correlation with average percentage algal and dead coral cover (Figure 2). Finally, stepwise modelling indicated variables, 'abiotic', 'hexacoral' and 'octocoral' to be the best at describing the total average length of the Labridae family according to the MAM AIC_c values and explained $\sim 34\%$ of deviance. Average total length of individuals had a positive relationship with abiotic and hexacoral cover (%) and a strong negative correlation with octocoral cover (%).

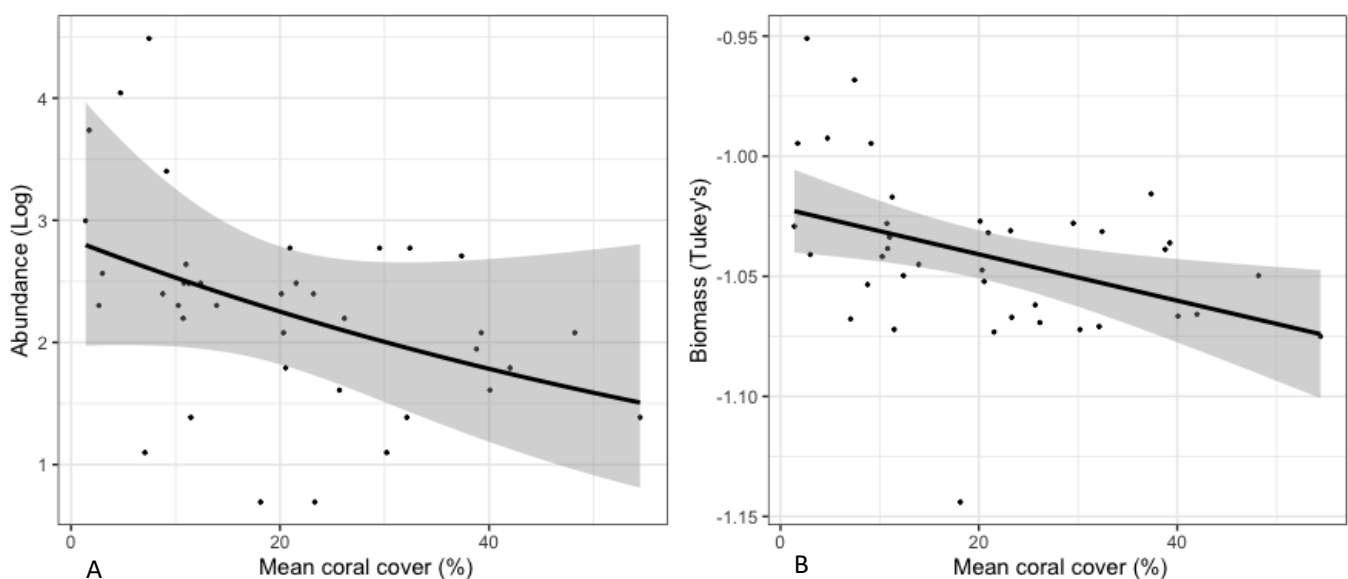


Figure 2. Correlations of mean coral cover (%) sampled across reef survey sites and mean abundance (log) (a), biomass (Tukey's) (b) of commercially and ecologically important Labridae species. Univariate logistic regression line of variables derived from stepAIC regression analysis and corresponding 95% confidence intervals shaded in grey.

Abiotic cover was the strongest predictor across all final reduced models, explaining 28.6%, 33.23% and 23.29% variation individually of Labridae abundance, biomass and total length respectively. Biological variable 'coral cover' was not included in any models containing 'abiotic cover' due to high intercorrelation, despite

its significant negative correlation with Labridae abundance and biomass. Therefore, coral cover (%) should be considered as a strong influential predictor variable that explains 27.2% and 15.7% variation individually of abundance and biomass respectively.

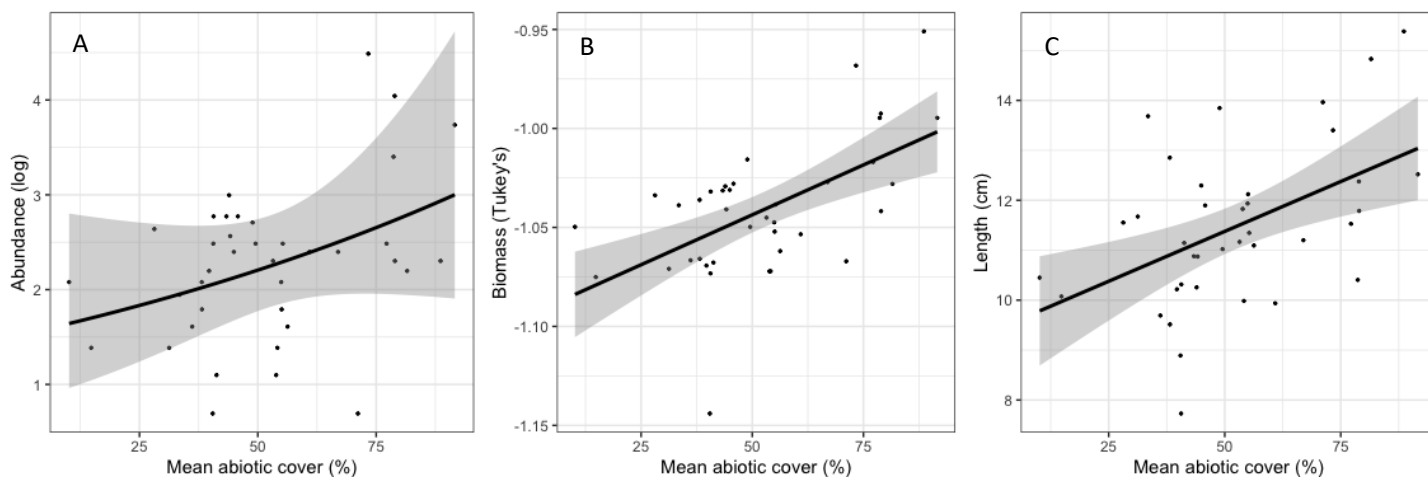


Figure 3. Significant correlations of mean abiotic cover (%) sampled across reef survey sites and mean abundance (log) (a), biomass (Tukey's) (b) and length (c) of commercially and ecologically important Labridae species. Univariate logistic regression line of 'abiotic' variable derived from stepAIC regression analysis and corresponding 95% confidence intervals shaded in grey.

3.2.2 Lutjanidae

All reduced models for Lutjanidae abundance, biomass and length suggested that biotic variables 'octocoral' and 'sponge' were highly influential factors that help explain their assemblage characteristics (Table 3). FACs showed statistically significant positive correlations with sponge cover (%) and a slight negative correlation with octocoral cover (%) (Figure 4). Model determination of variable 'sponge' supported early Pearson's correlation analysis and explained 20.78%, 17.19% and 16.24% variation individually for Lutjanidae abundance, biomass and length respectively. Additional influential variables included dead coral cover (%) and reef length to explain abundance and biomass respectively, as both showed slight negative relationships to corresponding FACs (Table 1 & Figure 4). Based on all the reduced model information criteria, abundance MAM explained ~45% variation, biomass MAM explained ~31% variation and length MAM explained ~24% variation of Lutjanidae fish assemblages.

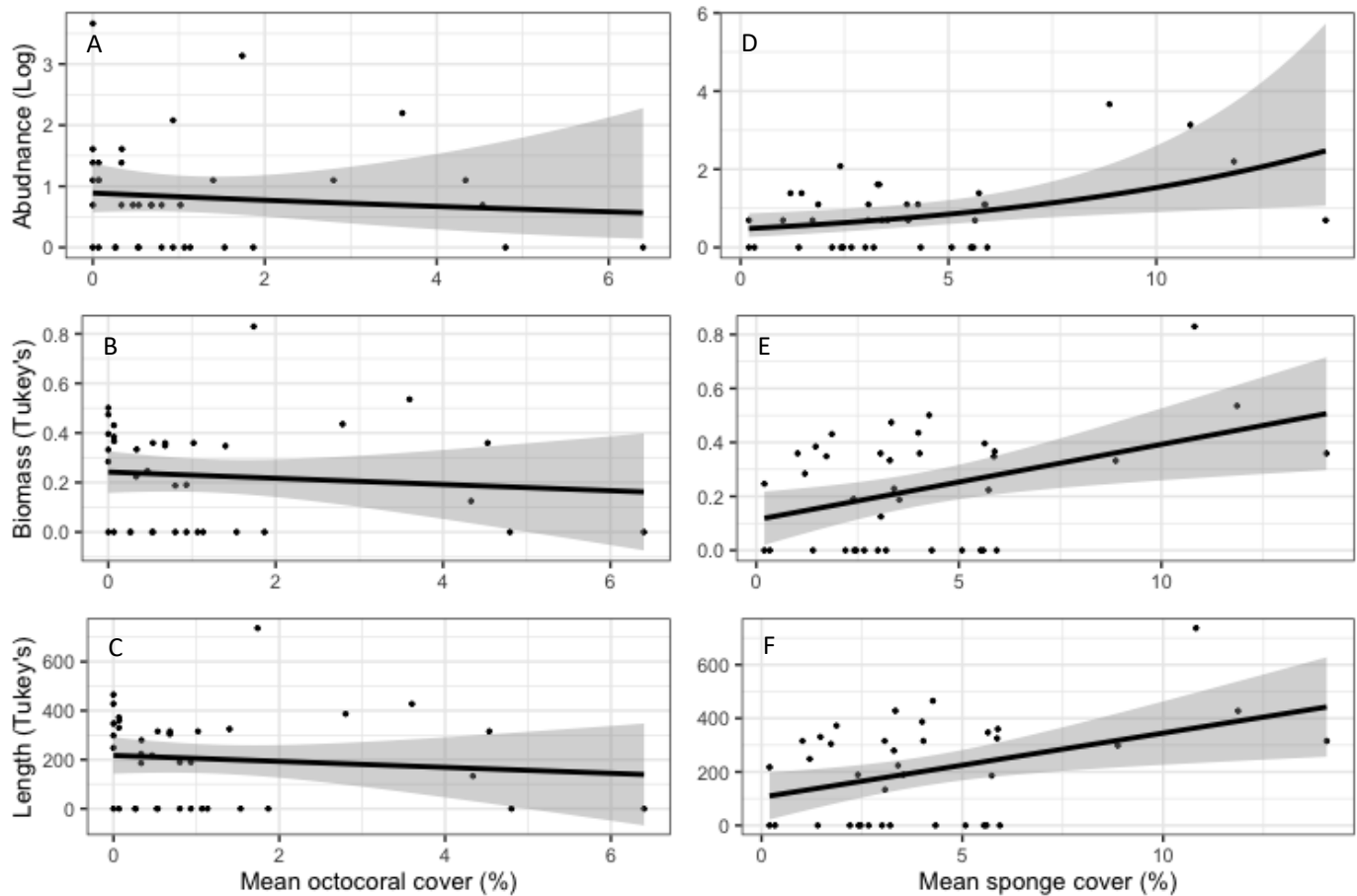


Figure 4. AIC stepwise model proposed variables ‘octocoral’ and ‘sponge’ and their relationship with Lutjanidae fish assemblages across study reefs in Dauin, Philippines. A-C: Correlation between percentage octocoral cover correlation and Lutjanidae abundance, biomass and total length. D-F: Significant correlations between percentage sponge cover and Lutjanidae abundance, biomass and total length. Abundance (Log transformed), biomass (Tukey’s ladder of power transformed) and length (Tukey’s ladder of power transformed). Univariate logistic regression line of variable (black) and corresponding 95% confidence intervals (shaded in grey).

3.2.3 Serranidae

Predictor variable ‘coral cover’ was shown to influence Serranidae abundance, biomass and total length, as it appeared in all final MAMs and supported early univariate Pearson’s correlation analysis (Table 1 & 3). As coral cover increased Serranidae assemblage characteristics decreased (Figure 6). The final reduced abundance model further suggested physical and biological variables ‘dead coral’, ‘algae’ and ‘octocoral’ best described Serranidae abundance and explained 45.5% deviance (Table 3). Both biomass and length MAMs determined from stepAIC and AIC corrected (AIC_c) values identified the same three additional variables that helped elucidate these assemblage characteristics. Variables ranged in physical and biological factors, consisting of ‘depth’, ‘season’ and ‘sponge’, with both models explaining ~30% deviance (Table 3). Serranidae average biomass (kg) and length (cm) were both greater at study sites during the wet season and at shallower depths of 5 m and both assemblage characteristics increased with mean percentage sponge cover (Figure 5).

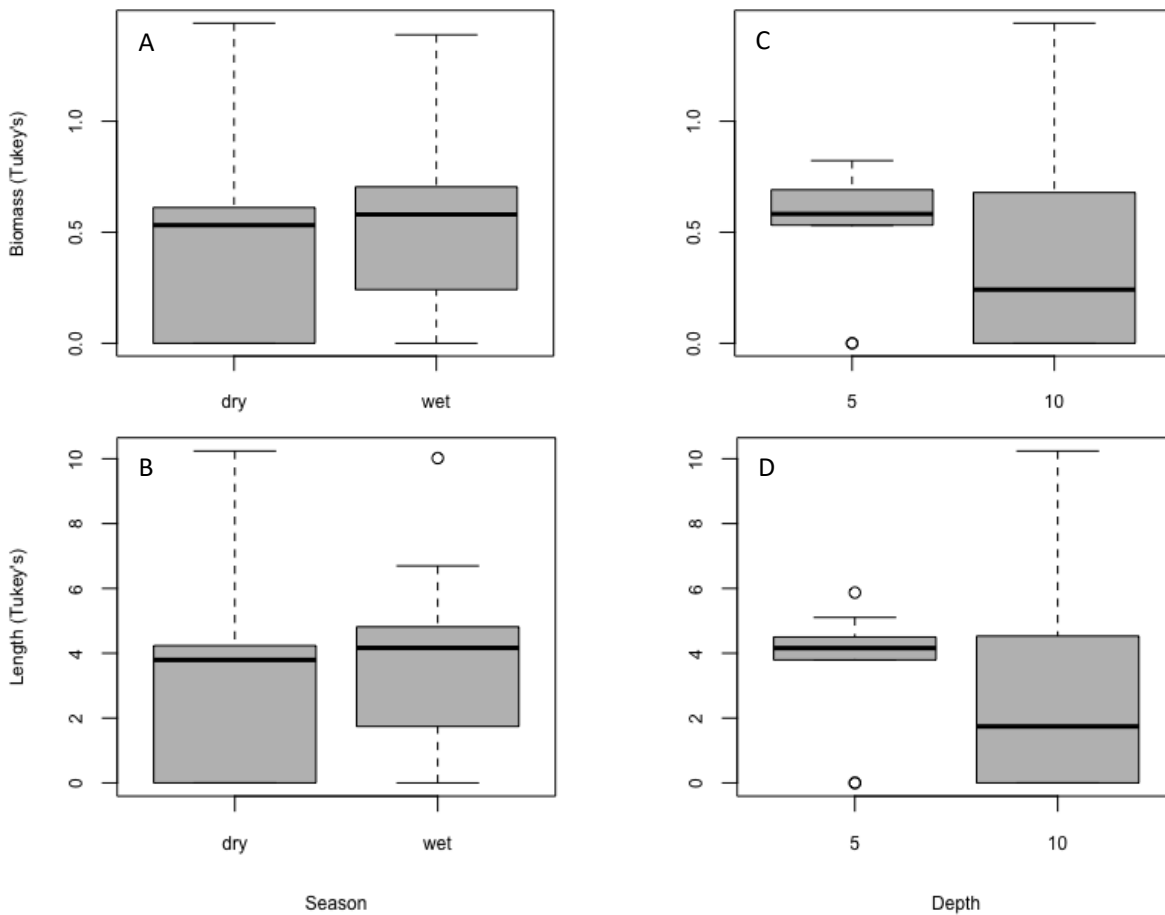


Figure 5. Effect of season (wet/dry) and depth (5/10 m) on the biomass and length of *Serranidae*. Bars represent univariate logistic regression and the 95% confidence interval (CI).

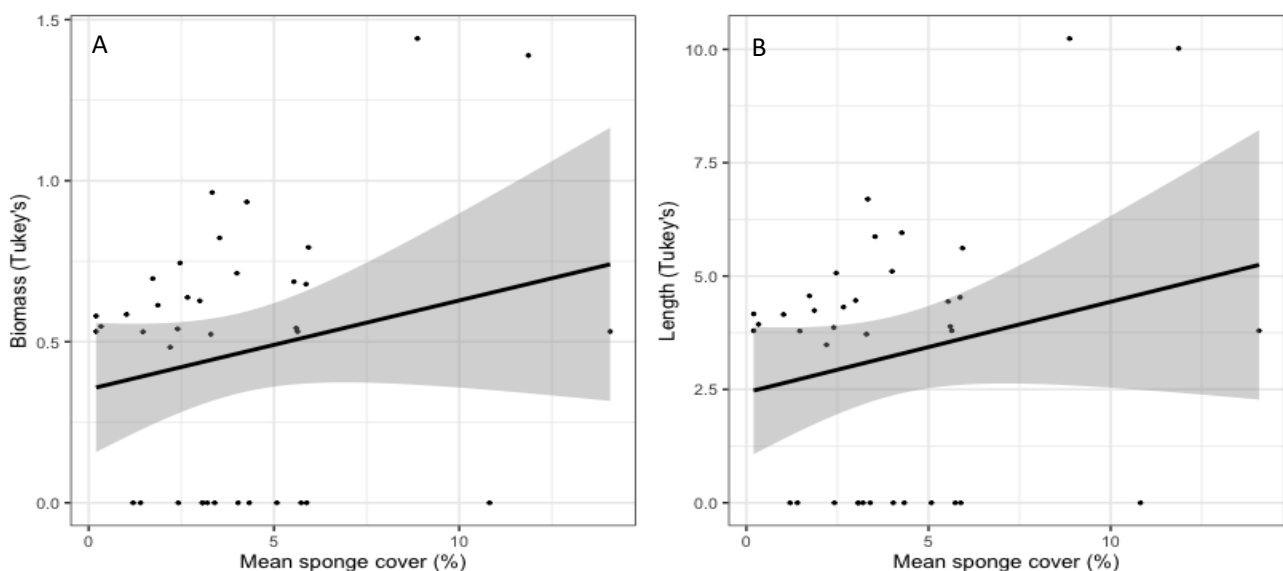


Figure 6. Significant correlations of mean sponge cover (%) sampled across reef survey sites and mean biomass (Tukey's) (a), length (Tukey's) (b) of commercially and ecologically important *Serranidae* species. Univariate logistic regression line of 'sponge' variable derived from stepAIC regression analysis and corresponding 95% confidence intervals shaded in grey.

4.0 DISCUSSION

4.1 Labridae assemblage

A combination of biological and physical habitat characteristics was found to influence FACs of Labridae (Wrasse) species across study reefs. Live coral cover and abiotic cover showed significant intercorrelation and therefore inverse relationships with Labridae abundance and biomass. Previous studies have continuously failed to detect clear relationships between labrid density and biological characteristics of habitat zones, including percentage live coral cover (Nanami et al., 2002; Green, 1996). Green (1996) suggests families such as Labrids exhibit broad home ranges, encompassing a variety of habitat characteristics and thus is unlikely to demonstrate strong relationships with specific habitat features. Labridae abundance across sites of this study was highly dominated by the *Thalassoma* genus (~70% of all recorded Labridae individuals), particularly *T. Lunare*, commonly known as the moonwrasse. According to Wilson et al. (2010) these species along with *T. Hardwicke* and *Anampses caeruleopunctatus* are not known to feed or closely associate with live corals after maturity. Fulton et al., (2002) found four broad discernible groups of substratum preferences across Labridae species: live coral, dead coral heads, aggregate substrates and species that exhibited neutral selection for most substratum types, however the only significant trend for all species (except two coral foragers) was neutral to negative selection towards live coral and is consistent with the findings of this study. Additional findings of Fulton et al. (2002) reports species such as *Hemigymnus melapterus* and *Gomphosus varius* to be predominately found foraging on dead coral substratum. It is possible that these foraging behaviors may explain model selection of dead coral cover as an influential factor of Labridae biomass, as both species were consistently observed across reef study sites.

Fishes of the Labridae family show great diversity of body shapes, numerous morphological adaptations for feeding and variations in behavioral characteristics, and subsequently have trophic versatility, which is important in structuring reef communities (José de Anchieta et al., 2013; DeLoach & Humann, 1999). With one exception, Labrids are exclusively carnivores and represent a dominant group of coral reef benthic carnivores (Williams & Hatcer, 1983). Most Labridae species recorded during this study such as the *Halichoeres* and *Thalassoma* genus exhibit opportunistic behavioral traits, feeding on juvenile fish and invertebrates (Sazima et al., 2005; José de Anchieta et al., 2013). Tsounis, Steele and Edmunds (2020) suggest carnivorous Labrids to be ecotone specialists, finding 1.3-2.3 times more individuals at the edge of octocoral patches that within the reefs in St. John, US Virgin Islands. Ecotone specialists are highly abundant in areas of transition between sandy bottom and hard bottom substrate (Tsounis et al., 2020). This habitat association allows for shelter and nesting within reef rubble but increases the availability of invertebrates that burrow in sand for foraging (e.g. Forrester & Steele, 2004). Significant correlations between abiotic and octocoral cover and Labridae FACs are potential indicator of this foraging characteristic. Such patterns have been linked to predation as the underlying cause for some species and is likely driven by differential distribution of their prey (Smith et al., 2011; Tsounis & Edmunds, 2020). Furthermore, in determining the relative abundance of Labridae, depth seemed to be of overriding importance, with most species occurring in shallower 5 m habitat zones. These findings are consistent with those of Green (1996) and Nanami et al., (2002) reporting significant correlations between abundance of most Labridae species and changes in depth of inhabitants.

4.2 Lutjanidae assemblage

The Lutjanidae family (Snappers) comprises of approximately 125 species and are significant constituents of artisanal, sport and commercial catches in tropical marine environments such as the Philippines and throughout the world (Quéré & Leis, 2010). The local reefs of Dauin surveyed in this study were heavily dominated by species within the *Lutjanus* and *Macolor* genus. Mean percentage octocoral and sponge cover were the most influential factors identified during model reduction and appeared in all three FAC models. The importance of habitat complexity in structuring fish assemblages has been recognised by a number of authors, mainly regarding that of stony coral cover (e.g. Jones and Syms 1998, Floeter et al. 2007, Krajewski et al. 2010). Sponges, however, are known to provide a range of commercially targeted fish species such as those of the Lutjanidae family with important shelter and foraging habitats (Newman et al., 2000; Farmer & Wilson, 2011). McLean et al. (2019) observed greater abundances of Lutjanidae species in areas of greater sponge complexity and density which both species are known to associate with (Newman et al., 2000) and thus further supports the significant positive relationships highlighted in this study. The variable 'reef length' is a form of habitat complexity measure and highly correlated with Lutjanidae biomass. Young juvenile snappers utilize cavities found within greater complex habitats for refuge from predators and fishing pressures (Díaz-Pulido et al., 2004; Sierra-Rozo et al., 2012; Huijbers et al., 2015). This behavioral characteristic increases the chances of individuals recruitment into mature adults and therefore increases stock availability of commercially important species for local fisheries.

Loss of snapper presence can have a negative effect on the biological control of prey herbivorous and coral-eating fish (González-Gamboa et al., 2019). Coral communities are at greater risk of damage and over grazing under dominance of such individuals within the ecosystem, allowing the establishment of habitat shifts to one that is algal dominated (Wilkinson, 2000; Weil, 2006; Sierra-Rozo et al., 2012; González-Gamboa et al., 2019). While most Lutjanidae species feed on benthic invertebrates and small fish (Rooker, 1995; Nagelkerken et al., 2000; Grober-Dunsmore et al., 2007), other species observed across study sites (*Macolor* genus) are classified as planktivorous, feeding on phytoplankton suspended within shallow water columns (Froese and Pauly, 2016). Factors such as phytoplankton availability were not included in this analysis but should be considered as a potential influencer of *Macolor* species assemblages. Benthic species found to practice similar feeding strategies are those comprised under the benthic substratum octocoral, found within this study such as sea pens and Gorgonians (Seafans) (Tsounis et al., 2020). Gorgonians were found to have a negative correlation with Lutjanidae abundance, biomass and length. Habitats dominated by gorgonians are generally low in rugosity and are relatively structureless compared to areas dominated by hard coral (Wolff et al., 1999). Highly mobile species such as Lutjanidae, are subject to higher pressures of fishing in gorgonian dominated habitats potentially due to lack of shelter and refuge and has been demonstrated through many studies (e.g., Furevik, 1994; Wolff et al., 1999). These studies are consistent with the negative correlation between Lutjanidae FACs and octocoral cover (%) found within this study, particularly that of biomass.

4.3 Serranidae

Serranidae (Seabass and Groupers) are among the top predators of coral reef ecosystems and are often considered fundamental to maintaining reef community structures (Dulvy et al., 2004; Boaden & Kingsford, 2015; Hackradt et al., 2020). This study observed nine different species of Serranidae belonging to four various genera, *Cephalopholis*, *Epinephelus*, *Plectropomus* and *Pseudanthias*. Species within the *Cephalopholis* genus are known to occur in the shallower waters of coral reef habitats and demonstrate overlap in their distribution, utilizing different food sources within a habitat (Hackradt et al., 2020). These complex dynamics commonly found within reef ecosystems are highly influenced by coral health and coral cover (Shpigel & Fishelson, 1989). Previous studies have reported significant responses of groupers to the cover of live coral and topographic complexity of reefs (Connell et al. 1998; Sale, 2002; Nagelkerken, 1979) and while model reduction indicates coral influence to be strong, these results of negative correlations contradict those of others. Strong intercorrelations were identified between coral cover and abiotic cover during early analysis and have consistently shown inverse effects to fish assemblages. Light and Jones (1997) found that habitat associations of newly settled and growing juvenile *Plectropomus spp.* are potentially important to the demography of adult populations. Densities of recruits within this study were found to be highly related to the amount of available rubble-sand substrata and may support the negative relationship of coral cover found in this study. Additionally, some studies have even found little or no effect of hard coral cover on fish abundance (Khalaf and Crosby, 2005; Stockwell et al., 2009).

During model reduction the variable 'depth' was discarded as an influencer of Serranidae assemblage however, significant differences were observed between 5 and 10 m during early analysis. Greater abundance of individuals found at shallower depths of 5 m are likely to vary by species due to predator-prey behavior characteristics. For example, larger individuals such as *Plectropomus laevis* species observed in this study, may be less susceptible to predation and thus allows movement to habitats of greater depths, where exposure is typically higher due to reduced structural complexity (Andradi-Brown et al., 2016). Fish generally occupy habitats that better promote growth rate, however in the presence of predator's, fish occupy more structurally complex habitats (Werner et al., 1983; Andradi-Brown et al., 2016).

Due to the high economic value of this family to fisheries (Sadovy de Mitcheson et al., 2013), populations of groupers are under some degree of threat worldwide (Craig et al., 2011), with some species such as *Epinephelus fuscoguttatus* listed as Vulnerable on IUCN red list (IUCN, 2020). It is possible that populations of these species identified across Dauin's reefs may only remain stable and of high abundance through locally managed marine reserves (Garcia-Charton et al., 2008; Hackradt et al., 2014).

4.4 Limitations and recommendations

Although AIC-based stepwise reduction has previously been criticised for potentially overlooking key variables (Burnham et al, 2011; Mundry & Nunn, 2009), others find its predictive capability comparable to other methodologies (Murtaugh, 2009). Manually deciding on further reduced models, in addition to the stepwise

reduction, meant that AIC (or AICc) was not solely used and tradeoffs between high deviance and low AIC scores were considered. Furthermore, a sample size of less than 30 could be considered too small and may have affected the conclusions by overemphasizing the influence of the outlying points and thus reducing the statistical power of some analyses (Crawley, 2005; Seavy et al., 2005). Sampling of a greater number of reef sites within the area, focusing on the variables shown here to be key influencers of commercially important fish assemblages, is recommended to increase the analytical power and allow for more significant conclusions to be drawn (Little et al., 2016). Moreover, additional information pertaining the reef site conditions would be valuable in order to give more context to the findings, as factors such as nutrient availability and anthropogenic pressure levels influence reef fish populations (Hixon, 1991; Mora et al., 2003). MPA system management can be better focused from the findings of this study, prioritizing significant influential factors to maximize the conservation of commercially important fish and sustain local fisheries within the area.

5.0 CONCLUSION

This study determined the most influential factors driving fish assemblage characteristics of three commercially important fish families (Labridae, Lutjanidae and Serranidae) across reefs in the municipality of Dauin, Philippines. Benthic substratum dominated by live coral or abiotic cover such as rubble and sand were found to be highly influential of Labridae and Serranidae abundance, whereas Lutjanidae was only significantly correlated to percentage sponge cover. Species association to specific biological and physical variables show evidence of sensitivity to bottom-up control, however the influence of top-down processes such as fishing should not be dismissed as this factor was not included in analysis. There is hope that influential factors highlighted and discussed throughout this paper can help guide marine management strategies to increase the assemblages of commercially important reef fish.

ACKNOWLEDGEMENTS

I would like to express my deepest and sincere gratitude to my project supervisor, Jennifer Brand (Head of Science) and the Directors Chelsea Waters and Rafael Manrique from the Institute for Marine Research for their support, guidance and expert advice. I would also like to thank Dr Bryce Beukers-Stewart at the University of York.

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APPENDIX

Appendix 1. Full variable descriptions used in stepAIC modelling to identify factors influencing fish assemblage characteristics.

Variable	Variable description
Physical	
Depth	5/10 m
Season	Wet/dry
Rugosity	Rugosity measurement of the surface roughness
Reef length	Length of surface (length of draped chain)
Abiotic	Mean abiotic cover (%) – sand, rubble, rock
Biotic	
Coral cover	Mean live coral cover (%)
Hexacoral	Mean hexacoral cover (%) – Anemone, Corallimorph, Zoanthid
Octocoral	Mean octocoral cover (%) – Gorgonian, Sea pen, Soft coral
Sponge	Mean sponge cover (%)
Algae	Mean algae cover (%)
Dead coral	Mean dead coral cover (%)

Appendix 2. Rscript for stepAIC and regression modelling.

```
## WHAT FACTORS AFFECT THE PRESENCE, BIOMASS AND LENGTH OF LABRIDAE ON CORAL REEFS OF DAUIN, PHILLIPINES
#####

## installing packages
install.packages("MASS")
install.packages("car")
```

```
install.packages("carData")
install.packages("ggplot2")
install.packages("pastecs")
install.packages("psych")
install.packages("bbmle")
install.packages("stats4")
install.packages("visreg")
install.packages("rcompanion")

library(MASS)
library(carData)
library(car)
library(ggplot2)
library(pastecs)
library(psych)
library(stats4)
library(bbmle)
library(visreg)
library(rcompanion)
# Set the working directory using the setwd() function

setwd("~/Desktop/IMR/DATA")

# Import the data using function read.table()
# Make sure the data is saved as a csv file and not a xlx.
# Save dataframe under object "fish_dry"

fish_dry <- read.csv(file.choose(), header=TRUE, row.names = 1)

# check that the data has imported correctly by recalling it

fish_dry

# Have a look at the variable names

names(fish_dry)

# We need to find and define data into factors. This will tell R to use the data in the correct way, when plotting and running
models. The str() function will show the structure of the data

str(fish_dry)

# From the output we can now change the integers into 'ordered factors'

fish_dry[, 4] <- factor(fish_dry[, 4], ordered=TRUE)

# attach data to access the variables

attach(fish_dry)

#Plot all riable to check for obvious errors

plot(abundance)
plot(biomass)
plot(length)
plot(depth)
plot(coral_cover)
plot(hexacoral)
plot(octocoral)
```

```

plot(bivalve)
plot(hydroid)
plot(sponge)
plot(algae)
plot(seagrass)
plot(other_live)
plot(abiotic)
plot(dead_coral)
plot(worms)
plot(rugosity)
plot(reeflength)

```

```

#####
# ----- CHECKING FOR OUTLIERS / ASSESSING NORMALITY OF DATA / UNEVEN SAMPLING ----- #
#####
# Most parametric test require data to be normally distributed and homoscedastic
# When residuals fail to meet these conditions, variables need to be transformed to better follow a normal distribution
# Here i am going to now assess the normality of each variable

```

```
#### Data exploration #####
```

```
# Looking at normality
```

```
# ----- ABUNDANCE ----- #
# NOTE: abundance - dependent variable
```

```
# Firstly i am going to use graphical displays to visually view the data and look at the distribution
```

```
# GRAPHICAL DISPLAYS
```

```
# To do this i am going to plot a histogram, Q-Q plot (diagnostic plot), kernel density plot and a box plot
```

```

oldpar <- par(mfrow = c(2,2), oma = c(0,0,2,0) + 0.1)
truehist(fish_dry$abundance, nbins = "FD", col = "white", main = "Histogram", xlab = "Abundance", ylab = "Frequency", prob =
FALSE) + box()
plot(density(fish_dry$abundance), xlab = "Aundance (No. of individuals", main = "Kernel Density")
rug(fish_dry$abundance)
qqnorm(fish_dry$abundance) + qqline(fish_dry$abundance)
boxplot(fish_dry$abundance, ylab = "Abundance (No. of individuals)", main = "Boxplot")
mtext("Data Exploration Plots for Abundance", font = 2, outer = TRUE)

```

```
# I am then going to look at the frequency distribution in more detail by displaying the relationship in a histogram with line of fit
(from the mean and standard deviation) using the ggplot() function
```

```

fish_dry.hist <- ggplot(fish_dry, aes(fish_dry$abundance)) + labs(legend.position = "none") + geom_histogram(aes(y=..density..),
colour="black", fill="white") + labs(x="Abundance", y = "Density") + stat_function(fun = dnorm, args = list(mean =
mean(fish_dry$abundance, na.rm = TRUE), sd = sd(fish_dry$abundance, na.rm = TRUE)), colour = "red", size = 1)
fish_dry.hist

```

```
# GENERATING SKEW AND KURTOSIS (SE) VALUES
```

```
# The stat.desc() fucntion can be used to generate these values and from the output we can veiw just the skewness, skew.2SE,
kurtosis, and kurt.2SE
```

```

skkur.abundancedry <- stat.desc(fish_dry$abundance, basic = FALSE, norm = TRUE)
skkur.abundancedry[8:11]

```

```
#TESTING FOR NORMALITY
```

```
# To test for normality i am going to perform a Sharpiro-wilk test using the shapiro.test() function
```

```
# Shapiro-wilk test:
```

```
shapiro.test(fish_dry$abundance)
```

```
# ----- BIOMASS ----- #
```

```
# NOTE: biomass - dependent variable
```

```
# GRAPHICAL DISPLAYS
```

```
# To do this i am going to plot a histogram, Q-Q plot (diagnostic plot), kernel density plot and a box plot
```

```
oldpar <- par(mfrow = c(2,2), oma = c(0,0,2,0) + 0.1)
```

```
truehist(fish_dry$biomass, nbins = "FD", col = "white", main = "Histogram", xlab = "Biomass", ylab = "Frequency", prob = FALSE) + box()
```

```
plot(density(fish_dry$biomass), xlab = "Biomass (kg)", main = "Kernel Density")
```

```
rug(fish_dry$biomass)
```

```
qqnorm(fish_dry$biomass) + qqline(fish_dry$biomass)
```

```
boxplot(fish_dry$biomass, ylab = "Biomass (kg)", main = "Boxplot")
```

```
mtext("Data Exploration Plots for Biomass", font = 2, outer = TRUE)
```

```
# I am then going to look at the frequency distribution in more detail by displaying the relationship in a histogram with line of fit (from the mean and standard deviation) using the ggplot() function
```

```
Bfish_dry.hist <- ggplot(fish_dry, aes(biomass)) + labs(legend.position = "none") + geom_histogram(aes(y=..density..), colour="black", fill="white") + labs(x="Biomass", y = "Density") + stat_function(fun = dnorm, args = list(mean = mean(biomass), na.rm = TRUE), sd = sd(fish_dry$biomass, na.rm = TRUE)), colour = "red", size = 1)
```

```
Bfish_dry.hist
```

```
# GENERATING SKEW AND KURTOSIS (SE) VALUES
```

```
# The stat.desc() function can be used to generate these values and from the output we can view just the skewness, skew.2SE, kurtosis, and kurt.2SE
```

```
skkur.biomassdry <- stat.desc(fish_dry$biomass, basic = FALSE, norm = TRUE)
```

```
skkur.biomassdry[8:11]
```

```
# TESTING FOR NORMALITY
```

```
# To test for normality i am going to perform a Shapiro-wilk test using the shapiro.test() function
```

```
# Shapiro-wilk test:
```

```
shapiro.test(fish_dry$biomass)
```

```
# ----- LENGTH ----- #
```

```
# NOTE: length - dependent variable
```

```
# GRAPHICAL DISPLAYS
```

```
# To do this i am going to plot a histogram, Q-Q plot (diagnostic plot), kernel density plot and a box plot
```

```
oldpar <- par(mfrow = c(2,2), oma = c(0,0,2,0) + 0.1)
```

```
truehist(fish_dry$length, nbins = "FD", col = "white", main = "Histogram", xlab = "Length", ylab = "Frequency", prob = FALSE) + box()
```

```
plot(density(fish_dry$length), xlab = "length (cm)", main = "Kernel Density")
```

```
rug(fish_dry$length)
```

```
qqnorm(fish_dry$length) + qqline(fish_dry$length)
```

```
boxplot(fish_dry$length, ylab = "length (cm)", main = "Boxplot")
```

```
mtext("Data Exploration Plots for Length", font = 2, outer = TRUE)
```

I am then going to look at the frequency distribution in more detail by displaying the relationship in a histogram with line of fit (from the mean and standard deviation) using the ggplot() function

```
Lfish_dry.hist <- ggplot(fish_dry, aes(fish_dry$length)) + labs(legend.position = "none") + geom_histogram(aes(y=..density..),
colour="black", fill="white") + labs(x="Length", y = "Density") + stat_function(fun = dnorm, args = list(mean =
mean(fish_dry$length, na.rm = TRUE), sd = sd(fish_dry$length, na.rm = TRUE)), colour = "red", size = 1)
Lfish_dry.hist
```

GENERATING SKEW AND KURTOSIS (SE) VALUES

The stat.desc() function can be used to generate these values and from the output we can view just the skewness, skew.2SE, kurtosis, and kurt.2SE

```
skkur.lengthdry <- stat.desc(fish_dry$length, basic = FALSE, norm = TRUE)
skkur.lengthdry[8:11]
```

TESTING FOR NORMALITY

To test for normality i am going to perform a Shapiro-wilk test using the shapiro.test() function

Shapiro-wilk test:

```
shapiro.test(fish_dry$length)
```

```
#----- #
```

PREDICTOR VARIABLES

```
# ----- CORAL COVER ----- #
```

GRAPHICAL DISPLAYS

To do this i am going to plot a histogram, Q-Q plot (diagnostic plot), kernel density plot and a box plot

```
oldpar <- par(mfrow = c(2,2), oma = c(0,0,2,0) + 0.1)
truehist(fish_dry$coral_cover, nbins = "FD", col = "white", main = "Histogram", xlab = "% average coral cover", ylab =
"Frequency", prob = FALSE) + box()
plot(density(fish_dry$coral_cover), xlab = "% average coral cover", main = "Kernel Density")
rug(fish_dry$coral_cover)
qqnorm(fish_dry$coral_cover) + qqline(fish_dry$coral_cover)
boxplot(fish_dry$coral_cover, ylab = "% average coral cover", main = "Boxplot")
mtext("Data Exploration Plots for average % coral cover", font = 2, outer = TRUE)
```

```
##### ABUNDANCE #####
```

CHECKING FOR HETEROSCEDASTICITY:

Firstly, i am going to view the predictor variable (coral cover) against the dependent variable (abundance)

```
par(mfrow = c(1,1))
plot(fish_dry$coral_cover, abundance) + abline(v=mean(fish_dry$coral_cover), col="red")
```

Next i am going to calculate the ratio of variance either side of the mean and we expect a value of 1 to confirm the data is not heteroscedastic

```
var.coral_cover1 <- var(abundance[fish_dry$coral_cover < mean(fish_dry$coral_cover)])
var.coral_cover2 <- var(abundance[fish_dry$coral_cover > mean(fish_dry$coral_cover)])
var.coral_cover2/var.coral_cover1
```

```
##### BIOMASS #####
```

CHECKING FOR HETEROSCEDASTICITY:

Firstly, i am going to view the predictor variable (coral cover) against the dependent variable (biomass)

```
par(mfrow =c(1,1))
plot(fish_dry$coral_cover, fish_dry$biomass_cub) + abline(v=mean(fish_dry$coral_cover), col="red")
```

Next i am going to calculate the ratio of variance eitherside of the mean and we expect a value of 1 to confirm the data is not heteroscedastic

```
var.coral_cover3<-var(fish_dry$biomass_cub[fish_dry$coral_cover<mean(fish_dry$coral_cover)])
var.coral_cover4<-var(fish_dry$biomass_cub[fish_dry$coral_cover>mean(fish_dry$coral_cover)])
var.coral_cover4/var.coral_cover3
```

LENGTH

CHECKING FOR HETEROSCEDASTICITY:

Firstly, i am going to view the predictor variable (coral cover) against the dependent variable (length)

```
par(mfrow =c(1,1))
plot(fish_dry$coral_cover, fish_dry$length) + abline(v=mean(fish_dry$coral_cover), col="red")
```

Next i am going to calculate the ratio of variance eitherside of the mean and we expect a value of 1 to confirm the data is not heteroscedastic

```
var.coral_cover5<-var(fish_dry$length[fish_dry$coral_cover<mean(fish_dry$coral_cover)])
var.coral_cover6<-var(fish_dry$length[fish_dry$coral_cover>mean(fish_dry$coral_cover)])
var.coral_cover6/var.coral_cover5
```

REPEAT FOR ALL VARIABLES

```
#####
# ----- TESTING FOR NORMALITY COMPLETE ----- #
#####
```

```
#####
# ----- CHECKING FOR CO-LINEARITY ----- #
#####
```

```
#
*****
*****
```

NEED TO TEST WHICH PREDICTOR VARIABLES CORRELATE HIGHLY WITH LENGTH

I am now going to run a pearsons correlation coefficient test to see which predictor vaiables highly correlate with the response variables

ABUNDANCE

```
cor.test(fish$abundance, fish$coral_cover, method=c("pearson")) # |r| 0.3899913
cor.test(fish$abundance, fish$hexacoral, method=c("pearson")) # |r| 0.02169444
cor.test(fish$abundance, fish$octocoral, method=c("pearson")) # |r| 0.01050759
cor.test(fish$abundance, fish$sponge, method=c("pearson")) # |r| 0.08985529
cor.test(fish$abundance, fish$algae, method=c("pearson")) # |r| 0.2007275
cor.test(fish$abundance, fish$abiotic, method=c("pearson")) # |r| 0.4231957
cor.test(fish$abundance, fish$dead_coral, method=c("pearson")) # |r| 0.08830504
cor.test(fish$abundance, fish$rugosity, method=c("pearson")) # |r| 0.1862311
cor.test(fish$abundance, fish$reeflength, method=c("pearson")) # |r| 0.1171948
cor.test(fish$abundance, fish$depth, method=c("pearson")) # |r| 0.2762428
cor.test(fish$abundance, fish$season, method=c("pearson")) # N |r| 0.0746891
```

BIOMASS


```

cor.test(fish$biomass_tuk, fish$coral_cover, method=c("pearson")) # |r| 0.3962394
cor.test(fish$biomass_tuk, fish$hexacoral, method=c("pearson")) # |r| 0.06969759
cor.test(fish$biomass_tuk, fish$octocoral, method=c("pearson")) # |r| 0.2881465
cor.test(fish$biomass_tuk, fish$sponge, method=c("pearson")) # |r| 0.1562374
cor.test(fish$biomass_tuk, fish$algae, method=c("pearson")) # |r| 0.1408211
cor.test(fish$biomass_tuk, fish$abiotic, method=c("pearson")) # |r| 0.5764128
cor.test(fish$biomass_tuk, fish$dead_coral, method=c("pearson")) # |r| 0.06329094
cor.test(fish$biomass_tuk, fish$rugosity, method=c("pearson")) # |r| 0.1678186
cor.test(fish$biomass_tuk, fish$reeflength, method=c("pearson")) # |r| 0.07858328
cor.test(fish$biomass_tuk, fish$depth, method=c("pearson")) # |r| 0.0964928
cor.test(fish$biomass_tuk, fish$season, method=c("pearson")) # |r| 0.0575462
##### LENGTH #####
cor.test(fish$length, fish$coral_cover, method=c("pearson")) # |r| 0.1451583
cor.test(fish$length, fish$hexacoral, method=c("pearson")) # |r| 0.1275132
cor.test(fish$length, fish$octocoral, method=c("pearson")) # |r| 0.4181479
cor.test(fish$length, fish$sponge, method=c("pearson")) # |r| 0.223353
cor.test(fish$length, fish$algae, method=c("pearson")) # |r| 0.2414349
cor.test(fish$length, fish$abiotic, method=c("pearson")) # |r| 0.482642
cor.test(fish$length, fish$dead_coral, method=c("pearson")) # |r| 0.1762083
cor.test(fish$length, fish$rugosity, method=c("pearson")) # |r| 0.08241389
cor.test(fish$length, fish$reeflength, method=c("pearson")) # |r| 0.0610067
cor.test(fish$length, fish$depth, method=c("pearson")) # |r| 0.09078758
cor.test(fish$length, fish$season, method=c("pearson")) # |r| 0.1429388

cor(fish, use = "complete.obs", method = "pearson")

# VARIABLES THAT HIGHLY CORRELATE WITH WACH OTHER

# abiotic and coral cover **
# rugosity and reeplength ***

# *****
# *****

#####
# ----- CREATING MODELS ----- #
#####
#
#
#
#
##### ABUNDANCE #####

# GROUP 1 - Abiotic + reeplength + everything
# GROUP 2 - Coral cover + reeplength + everything
# GROUP 3 - Abiotic + rugosity + everything
# GROUP 4 - Coral cover + rugosity + everything
# GROUP 5 - everything

### GROUP 1 ### -----

g1.glm<- glm.nb(abundance ~ abiotic + reeplength + dead_coral + depth + algae + season + hexacoral + octocoral + sponge, data
= fish)

summary(g1.glm)
g1.aic<-extractAIC(g1.glm)

vif(g1.glm)

```

```

g1.glm1 <- update(g1.glm, ~. -octocoral, data = fish)
vif(g1.glm1)

stepAIC(g1.glm1, direction = "both")

g1.glmR <- glm.nb(formula = abundance ~ abiotic + depth, data = fish, init.theta = 3.122954324, link = log)

summary(g1.glmR)
g1R.aic<- extractAIC(g1.glmR)

RD_g1.glm <- summary(g1.glm)$deviance
ND_g1.glm<- summary(g1.glm)$null
D_g1.glm <- 1 - (RD_g1.glm/ND_g1.glm)
full<- D_g1.glm*100
full
RD_g1.glmR <- summary(g1.glmR)$deviance
ND_g1.glmR<- summary(g1.glmR)$null
D_g1.glmR <- 1 - (RD_g1.glmR/ND_g1.glmR)
red<- D_g1.glmR*100
red

full-red

g1.aic-g1R.aic

par(mfrow=c(1,1))
plot(g1.glmR)
visreg(g1.glmR)

anova(g1.glm, g1.glmR, test="Chisq") # p>0.05 (p = 0.5765), not significantly different. stepwise reduction hasnt significantly
reduced deviance explained.

### GROUP 2 ### -----

g2.glm<- glm.nb(abundance ~ coral_cover + dead_coral + depth + algae + reeflength + season + hexacoral + octocoral + sponge,
data = fish)

summary(g2.glm)
g2.aic<-extractAIC(g2.glm)

vif(g2.glm)

stepAIC(g2.glm, direction = "both")

g2.glmR <- glm.nb(formula = abundance ~ coral_cover + dead_coral + depth,
data = fish, init.theta = 3.081254631, link = log)

summary(g2.glmR)

g2R.aic<- extractAIC(g2.glmR)

RD_g2.glm <- summary(g2.glm)$deviance
ND_g2.glm<- summary(g2.glm)$null
D_g2.glm <- 1 - (RD_g2.glm/ND_g2.glm)
full2<- D_g2.glm*100
full2

RD_g2.glmR <- summary(g2.glmR)$deviance
ND_g2.glmR<- summary(g2.glmR)$null

```

```

D_g2.glmR <- 1 - (RD_g2.glmR/ND_g2.glmR)
red2<- D_g2.glmR*100
red2

full2-red2

g2.aic-g2R.aic

par(mfrow=c(2,2))
plot(g2.glmR) # over dispersion cooks >1
visreg(g2.glmR)

anova(g2.glm, g2.glmR, test="Chisq") # p>0.05 (p = 0.2631), not significantly different. stepwise reduction hasnt significantly
reduced deviance explained.

### GROUP 3 ### -----
g3.glm<- glm.nb(abundance ~ abiotic + rugosity + dead_coral + depth + algae + season + hexacoral + octocoral + sponge, data =
fish)

summary(g3.glm)
g3.aic<-extractAIC(g3.glm)

vif(g3.glm)

g3.glm1 <- update(g3.glm, ~. -octocoral, data = fish)
vif(g3.glm1)

stepAIC(g3.glm1, direction = "both")

g3.glmR <- glm.nb(formula = abundance ~ abiotic + depth, data = fish, init.theta = 3.122954322,
link = log)

summary(g3.glmR)
g3R.aic<- extractAIC(g3.glmR)

RD_g3.glm <- summary(g3.glm)$deviance
ND_g3.glm<- summary(g3.glm)$null
D_g3.glm <- 1 - (RD_g3.glm/ND_g3.glm)
full3<- D_g3.glm*100
full3

RD_g3.glmR <- summary(g3.glmR)$deviance
ND_g3.glmR<- summary(g3.glmR)$null
D_g3.glmR <- 1 - (RD_g3.glmR/ND_g3.glmR)
red3<- D_g3.glmR*100
red3

full3-red3

g3.aic-g3R.aic

par(mfrow=c(2,2))
plot(g3.glmR)
visreg(g3.glmR)

```

```
anova(g3.glm, g3.glmR, test="Chisq") # p>0.05 (p = 0.821), not significantly different. stepwise reduction hasnt significantly reduced deviance explained.
```

```
### GROUP 4 ### -----
```

```
g4.glm<- glm.nb(abundance ~ coral_cover + dead_coral + depth + algae + rugosity + season + hexacoral + octocoral + sponge, data = fish)
```

```
summary(g4.glm)
```

```
g4.aic<-extractAIC(g4.glm)
```

```
vif(g4.glm)
```

```
stepAIC(g4.glm, direction = "both")
```

```
g4.glmR <-glm.nb(formula = abundance ~ coral_cover + dead_coral + depth, data = fish, init.theta = 3.081254628, link = log)
```

```
summary(g4.glmR)
```

```
g4R.aic<- extractAIC(g4.glmR)
```

```
RD_g4.glm <- summary(g4.glm)$deviance
```

```
ND_g4.glm<- summary(g4.glm)$null
```

```
D_g4.glm <- 1 - (RD_g4.glm/ND_g4.glm)
```

```
full4<- D_g4.glm*100
```

```
full4
```

```
RD_g4.glmR <- summary(g4.glmR)$deviance
```

```
ND_g4.glmR<- summary(g4.glmR)$null
```

```
D_g4.glmR <- 1 - (RD_g4.glmR/ND_g4.glmR)
```

```
red4<- D_g4.glmR*100
```

```
red4
```

```
full4-red4
```

```
g4.aic-g4R.aic
```

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

```
plot(g4.glmR)
```

```
visreg(g4.glmR)
```

```
anova(g4.glm, g4.glmR, test="Chisq") # p>0.05 (p = 0.1815), not significantly different. stepwise reduction hasnt significantly reduced deviance explained.
```

```
### GROUP 5 ### -----
```

```
g5.glm<- glm.nb(abundance ~ coral_cover + abiotic + dead_coral + depth + algae + rugosity + reeflength + season + hexacoral + octocoral + sponge, data = fish)
```

```
summary(g5.glm)
```

```
g5.aic<-extractAIC(g5.glm)
```

```
vif(g5.glm)
```

```
g5.glm1 <- update(g5.glm, ~. -dead_coral, data = fish)
```

```
vif(g5.glm1)
```

```
g5.glm2 <- update(g5.glm1, ~. -reeflength, data = fish)
```

```
vif(g5.glm2)
```

```

stepAIC(g5.glm2, direction = "both")

g5.glmR <- glm.nb(formula = abundance ~ abiotic + depth + octocoral, data = fish,
  init.theta = 3.822480603, link = log)

summary(g5.glmR)

g5R.aic<- extractAIC(g5.glmR)

RD_g5.glm <- summary(g5.glm)$deviance
ND_g5.glm<- summary(g5.glm)$null
D_g5.glm <- 1 - (RD_g5.glm/ND_g5.glm)
full5<- D_g5.glm*100
full5

RD_g5.glmR <- summary(g5.glmR)$deviance
ND_g5.glmR<- summary(g5.glmR)$null
D_g5.glmR <- 1 - (RD_g5.glmR/ND_g5.glmR)
red5<- D_g5.glmR*100
red5

full5-red5

g5.aic-g5R.aic

par(mfrow=c(2,2))
plot(g5.glmR)
visreg(g5.glmR)

anova(g5.glm, g5.glmR, test="Chisq") # p>0.05 (p = 2.203e-06), SIGNIFICANT different. stepwise reduction HAS significantly
reduced deviance explained.AND increased the AIC value.

#####
# ----- COMPARING MODELS ----- #
#####
# Final reduced models:
# g1.glmR
# g2.glmR
# g3.glmR
# g4.glmR
# g5.glmR

AICctab(g1.glmR, g2.glmR, g3.glmR, g4.glmR,g1.glm, g2.glm, g3.glm, g4.glm, base = T, weights = T, nobs =
length(fish$abundance))

##### REPEAT FOR BIOMASS AND LENGTH

#####
# REPEAT FOR ALL FAMILIES

#####

### END

```