

“Effect of closure to fishing on diversity, abundance and assemblage structure of NT fishes sampled by baited remote underwater video stations (BRUVS)”

Final report

September 14th, 2025

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Prepared for NT Department of Agriculture and Fisheries



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Table captions

Table 1. Summary of 420 BRUVS samples containing fish records by year, status and location.

Table 2. Summaries of Pearson correlations between covariates in the full BRUVS dataset. Significant correlations ($p < 0.005$) are shown with asterisks.

Table 3. Relative influences and partial effects in the final models of species richness and 4 categories of fish abundance on BRUVS. The “Partial effects” are the relative contribution of each predictor conditional that all other predictors were at their “average” level.

Table 4. Relative influences and partial effects in the final models of presence/absence of prized species on BRUVS. The “Partial effects” are the relative contribution of each predictor conditional that all other predictors were at their “average” level.

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Appendix 3. Summaries of the indicator species and their DLI values for all 20 nodes from the stump (“All”) to the 14 leaves defined by the mvpart in Figure 17. Prized species are highlighted in red. The higher the DLI values, the closer specificity and fidelity has to a node. The stripey snapper (*Lutjanus carponotatus*) and goldspot estuary cod (*Epinephelus coioides*) were ubiquitous with highest DLI at the stump.

Acknowledgements

I wish to acknowledge Mr Michael Usher for contracting me to conduct these analyses and Danilo Malara for supply and revision of the final dataset (NT Department of Agriculture and Fisheries).

Abstract

This report summarises analyses aimed at investigating the effects of closure to fishing, location, year of sampling, the video time interrogated for each sample (“soak”), underwater visibility in the field of view (“vis”) and depth.

The sampling design was unbalanced, with missing samples for combinations of year and location, and the count data were highly skewed and inflated with zero counts. There were significant correlations between underwater visibility and two other covariates – soak time and depth.

To cope with these features, the statistical methods used were ensembles of “machine learning” and normal linear modelling techniques. These offer the major advantages of robustness to outliers and missing data, the ability to model complex non-linear relationships, and automatic handling of interactions between predictors.

The “performance” of closures to fishing are often measured in terms of differences in the numbers of target species taken by fisheries inside and outside the closures and an increase in the numbers inside the closed areas with time.

The responses measured here were univariate summaries of richness and abundance in categories of fish according to their vulnerability to fishing (prized, target and not taken). The presence/absence of the major prized species (black jewfish *Protonibea diacanthus* and golden snapper *Lutjanus johnii*) were also examined.

Multivariate responses to the same predictors comprised the transformed abundance of 62 species occurring on at least 10 of the 408 BRUVS

The analyses presented here demonstrated that the underwater visibility in the fields of view was the prime driver of the patterns in richness, total abundance, target abundance, abundance of species not taken by fishing, and assemblage structure.

In contrast, **there were 2.8 times the abundance of prized fish species in areas closed to fishing**. Higher counts of prized fish occurred in lowest underwater visibility, but uncertainty in that effect occurred beyond the mean visibility in the dataset. Just over 31% of the BRUVS had prized fish species recorded. **The proportion of BRUVS “in” closed areas having a prized fish species in the field of view was over 3 times that of the “out” level.**

The “Lorna” location had the lowest effect of closure to fishing on prized species abundance and presence. To different multivariate techniques showed that black jewfish and golden snapper were correlated with sites closed to fishing and that “Lorna” had higher species diversity and abundance of species “not taken” by fisheries. The fauna in the assemblages identified for “Lorna” comprised genera commonly associated with tropical rocky reefs, coral reefs and “gardens” of megabenthos.

The analyses could not detect any temporal trend of increase, or decrease, in the numbers of prized fish inside or outside the sites closed to fishing with the passage of time between 2016 and 2023.

There were subtle effects of “year” including a peak in 2019 in both golden snapper numbers and the pooled abundance of all species. All the fish assemblages identified at “Lorna” were based on year of sampling.

Introduction

The “performance” of closures to fishing are often measured in terms of differences in the numbers of target species taken by fisheries inside and outside the closures and an increase in the numbers inside the closed areas with time.

Baited Remote Underwater Video Stations (BRUVS) are a popular tool to count the relative abundance of fish inside and outside closed areas through time. They are non-extractive and non-destructive of seafloor habitats. They can be used at any time of day or night (with lighting) and any depth. Unlike underwater visual counts on SCUBA, their deployment does not require field staff skilled in fish identification and field staff are not vulnerable to risks associated with saltwater crocodiles, sharks, Irukandji and box jellyfish. The video record can be as long as the batteries allow. It is permanent record that can be reviewed at any time by any observer to refine and confirm identifications and fish counts. The video records offer a direct means of communicating real results to stakeholders (see Cappo et al. 2007 for review).

For these reasons there have been many recent studies of Marine Protected Areas (MPAs) using BRUVS (eg). However, the main limitation governing their performance is the visibility and “quality” of the field of view (FOV). Recent studies have also found that effect of microhabitats visible in the FOV on the fish species sighted must be accounted for in comparisons (Switzer et al. 2023).

This introduces a fundamental need to include the effects of sampling artefacts (such as visibility and effective sampling time on the seabed) and measures of “habitat” as covariate predictors in statistical models.

The prized demersal targets in the NT demersal line fishery are the black jewfish and golden snapper, but there is also a diverse assemblage of tropical species in the families Lutjanidae, Serranidae, Lethrinidae, Labridae, Haemulidae and Carangidae that are retained as bycatch or sought after as targets. The fished species are also members of a much wider assemblage of species on the “grounds”. Some of these might be prey species and others might be competitors. Both prey and competitors might be expected to change in abundance with increase or decrease in target species abundance.

It is therefore important to look at the responses of the whole assemblage to spatial closures to fishing – not just the target species.

This report aims to investigate responses of species groups, species, and species assemblages to the effects of closure to fishing in three locations near Darwin in the macrotidal waters of the NT demersal line fishery in the period 2016 to 2023. It concludes with recommendations on how to improve the study.

Methods

The “operations” dataset provided by NT Fisheries comprised the date, location, latitude, longitude, depth, underwater visibility (vis) and sampling time (soak in minutes) for each unique BRUVS sample identified by an “opcode”. Sampling (soak) time refers to the amount of video time interrogated for each BRUVS sample. The “vis” was the estimated range in visibility beyond the camera lens

The species information provided for each opcode for each species were the maximum numbers seen together in progression of the whole video (*MaxN*) summed over adults and juveniles. Family, genus, species and a unique CAABCode with each record according to the Australian CAAB Codes

national standard (Yearsley et al. 1997). The use of common names follows Allen and Swainston (1988). The term 'fish' here refers to any marine vertebrate seen in the field of view, including sharks, rays and fish. Information on unidentifiable individuals were supplied as "Family/genus/sp", or "Family/sp" with a unique, custom CAABCode. These were treated as unique taxa in the analyses.

Counts of *maxN* made using BRUVS are often characterised by over-dispersion, with many zero counts and a very long tail with few, high counts (of schooling species, for example). The count data was therefore transformed by 4th root, to down-weight the influence of rare but highly abundant species and upgrade the influence of commonly occurring species that are not abundant.

1. Univariate models

Univariate models were constructed using aggregated boosted regression trees (abrt; De'ath 2007, Ridgeway 2007) using step-wise evaluation of all possible additions and removals of explanatory covariates. Separate models were run without interactions (main effects only) and then for 2-way, 3-way and 4-way interactions. The performance of each of these evaluations was compared on the basis of their prediction error measured by 5-fold cross validation. The most successful models were chosen by the lowest cross-validated prediction error. A "gaussian" distribution of errors was used in the abrt models of counts, and a "Bernoulli" distribution was used to model the presence/absence of the same species categories.

This approach derives from both classification and regression trees (CART) starting with a data model (De'ath and Fabricius 2000) and from 'machine learning' where no data model is specified and algorithms are used to learn the relationship between a predictor and its response (Breiman 2001). Boosted regression trees are therefore an 'ensemble' method, whereby models are improved by first fitting many simple models and then combining them for prediction (Schonlau 2005, Elith et al. 2008). The abrt offer the major advantages of robustness to outliers and missing data, the ability to model complex non-linear relationships, and automatic handling of interactions between predictors.

The model output returns a predicted error in absolute terms (ie the units of the response variable) and as a percentage of total variation (relative prediction error). An analog to "r²", as the proportion of deviance predicted, can then be represented by $(1 - \text{rel.pred.err}) \times 100$.

There are two major indices produced. The "**relative influence**" is the relative contribution of each predictor added up across all splits of all trees. The "**partial effects**" are the relative contribution of each predictor conditional that all other predictors were at their "average" level. This is equivalent to partial effects in linear regressions.

Correlation terms are produced that represent co-occurrence of effects in absolute terms. These terms are also cross-weighted by the partial effects to highlight major interactions. The results are portrayed as partial dependency plots, which show the overall effect of one particular covariate with the effects of all others held constant (Friedman 2001; Friedman & Meulman 2003).

Examples of this type of analysis applied to fish communities can be found in Leathwick et al. (2006), Elith et al. (2008) and Moore et al. (2017).

2. Multivariate models

Multivariate responses were analysed in two ways. Firstly, distance-based redundancy analysis (dbRDA; Legendre and Anderson 1999) was performed on transformed abundance (4th root) of species occurring on at least 10 BRUVS (2.4% of the total).

Extended, site standardised Manhattan distance ('xdiss' in R library mvpart), was used to produce the dissimilarity matrices for dbRDA (De'ath 1999). Function "capscale" in library vegan (Oksanen et al. 2018) was used to accomplish dbRDA of these dissimilarity matrices. At every step the Akaike Information Criteria (AIC) was evaluated for all possible additions and removals of explanatory covariates as constraints. The most parsimonious dbRDA models were selected by minimising AIC based on deviance, and variance inflation factors ($vif > 10$) were then used to drop variables that were strongly dependent on others and did not have independent information. This allowed construction of final models for eigen-analysis. The sum of the eigenvalues was the total variance in the dissimilarity matrix. Expressing individual eigenvalues as a proportion of the sum of eigenvalues gave the proportion of "squared distance variation" (Var) explained by each constrained axis.

Biplots of sites and longest species vectors were scaled by species scores from these ordinations to visualise correlations between species abundance, linear constraints and spatial separation of sites. Analysis of variance was conducted on the dbRDA models using permutation tests for significant differences in squared distance variation (Var) of the constrained eigenvalues using a "Pseudo-F" statistic. This statistic was constructed by $(\text{Model Var}/\text{Model Df})/(\text{Residual Var}/\text{Residual Df})$ where Df is the degrees of freedom.

Secondly, the abundances of a large number of species was modelled as a multivariate response to the predictor covariates using multivariate prediction and regression trees mvpart (see De'ath and Fabricius 2000, De'ath 2002). Only species occurring on at least 10 samples were included in the response. Each split in the multivariate prediction and regression tree minimises the "distance" of samples from the centroids of nodes to which they belong. This is equivalent to maximising the distance between node centroids. Each terminal node of the tree (leaf) was defined by the multivariate mean of its samples, the predictors that defined it, the number of samples that were grouped there, and by Dufrêne-Legendre species indicators (Borcard et al. 2011).

Indicator values (DLI; Dufrêne and Legendre 1997) were calculated for each species for each upper (branch) and terminal (leaf) node of the tree. For a given species and a given group of samples, the DLI was defined as the product of the mean species abundance occurring in the group divided by the sum of the mean abundances in all other groups (specificity), times the proportion of samples within the group where the species occurs (fidelity), multiplied by 100.

Each species can be associated with the tree node (assemblage) where its maximum DLI value occurred. The index distinguishes between ubiquitous species that dominate many groups in absolute abundance, and species that occur consistently within single groups but have low abundance (Dufrêne and Legendre 1997). The DLI for species at the root node were simply the prevalence of those species in the entire dataset. Species with high DLI were used as characteristic representatives of each assemblage.

Species accumulation curves for assemblages were simulated using the “specaccum” function in the R library *vegan* (Oksanen et al. 2018). These curves can be used to identify latent diversity in assemblages (Gotelli and Colwell 2001).

3. Statistical software

All analyses used the open-source “R” statistical package (R version 3.3.0) with libraries *abt* (De’ath 2017), *mvpart* (De’ath 2002, De’ath 2007, <http://www.esapubs.org/Archive/ecol/E088/015/suppl-1.htm>) and *vegan* (Oksanen et al. 2018) R version 3.6.0 was used to plot some results using *ggplot2*.

Results

1. Overview of the data structure

Data was provided for 430 BRUVS samples, but 10 of these samples had no *maxN* data (Table 1). The sampling was unbalanced in terms of spatial and temporal coverage.

Table 1. Summary of 420 BRUVS samples containing fish records by year, status and location.

	2016		2017		2018		2019		2020		2023	
	In	Out	In	Out	In	Out	In	Out	In	Out	In	Out
Bathurst	18	18	10	9	9	9	21	19	-	-	9	9
Charles	6	9	20	23	14	16	3	5	6	6	4	6
Lorna	24	22	26	27	8	9	6	8	8	6	7	8
Keats	6	6	-	-	-	-	-	-	-	-	-	-

The location of the samples is shown in Figure 1. Grounds closed to fishing were further offshore at Bathurst Island and Lorna. Samples “in” closures were also generally deeper than those “out” (Figure 2). The data for “Keats” were used only for comparisons with other macrotidal regions in the north-west, but were then dropped from the univariate and multivariate analyses due to the lack of repeated sampling there.

A total of 9829 fish from 257 species and 68 families were represented in the data (Appendix 1). They were classified into “prized” (black jewfish and golden snapper), “target” (70 species known to take a hook and be retained in tropical line fisheries, including golden snapper and black jewfish) and “non” (185 species not taken). The “non” category comprised species that are not caught (eg damselfish), and species that may be caught but are discarded (eg suckerfish *Echeneis naucrates*). The taxonomy of the categories is defined in Appendix 1.

There were significant negative correlations between underwater visibility and two other covariates (Table 2, Figure 2). Strong correlations between predictors in the *abt* models are only a challenge (to interpret) when the partial effects of those interactions on a response is large. This magnitude can be identified in later modelling using “partial interaction plots”.

Table 2. Summaries of Pearson correlations between covariates in the full BRUVS dataset. Significant correlations ($p < 0.005$) are shown with asterisks.

	depth	vis	soak
depth	1		
vis	-0.144***	1	
soak	-0.046	-0.215***	1

Like most BRUVS studies, the fish counts were highly skewed for all categories, with many low (or zero) counts and a long tail to a few high counts (Figure 3). Median, transformed, fish abundance and species richness were comparable with similar BRUVS studies at James Price Point (Cappo et al. 2011), Port Hedland and Joseph Bonaparte Gulf (unpublished) in the macrotidal north-west. In contrast, the underwater visibility for the NT samples was much poorer (Figure 4).

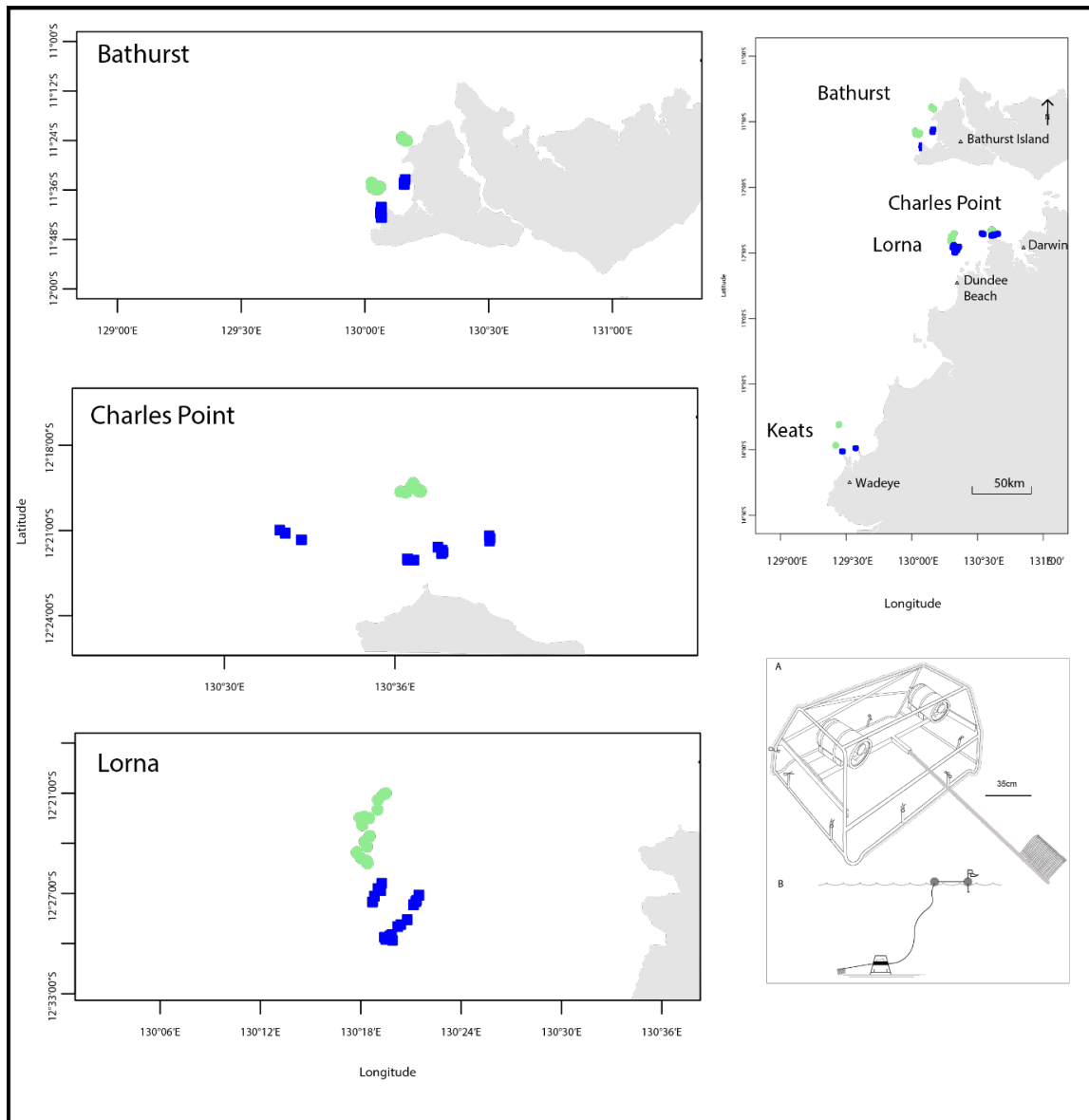


Figure 1. Maps of the locations of repeated BRUVS samples “in” grounds closed to fishing (green symbols) and “out” (blue symbols) and the Bathurst Island, Charles Point and Lorna locations. Other samples at Port Keats (inset) were not repeated. Grounds closed to fishing were further offshore at Bathurst Island and Lorna. A typical stereo-BRUVS is also illustrated.

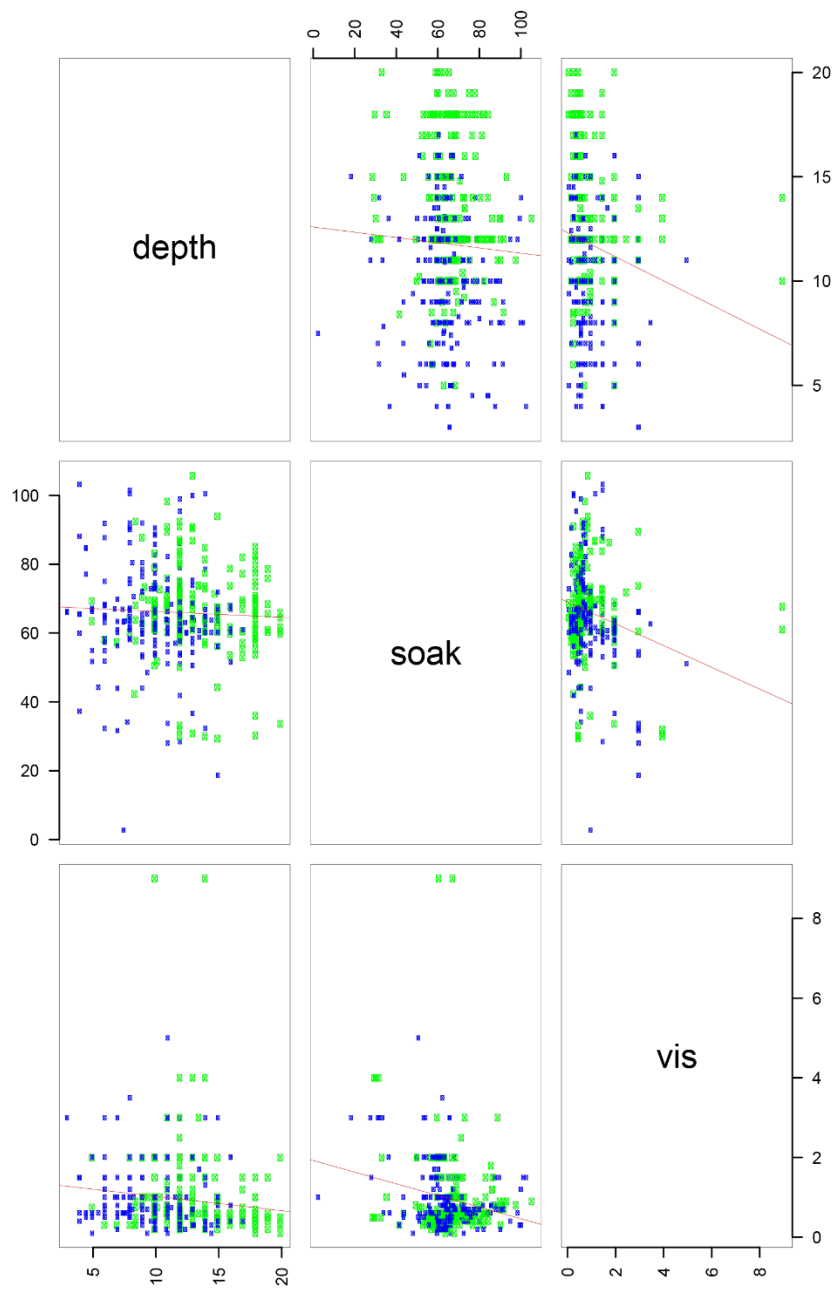


Figure 2. Pairs plots of the sampling artefacts (depth, underwater visibility and sampling time (soak)) show a wide spread in values, with some confounding with fishing status. Samples “in” (green) closures were generally deeper than those “out” (blue). Least squares trend lines are shown in red.

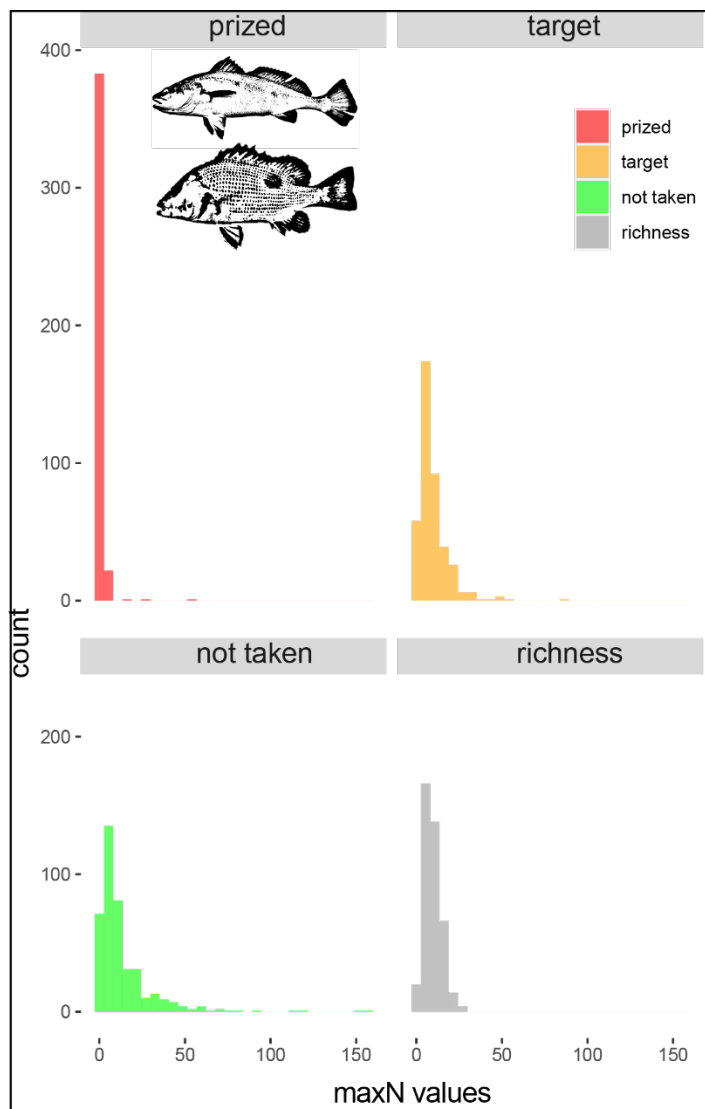


Figure 3. Histograms of the counts of *maxN* for “prized”, “all target” and “not taken” species, and total diversity (species richness) in the NT BRUVS data. The fish counts were highly skewed for all categories, with many low (or zero) counts and a long tail to a few high counts.

The median *maxN* pooled for “prized” species was 0, and the 3rd quantile was only 1, but the maximum was 54. The same statistics for the 70 “target” species pooled were 8, 12 and 85.

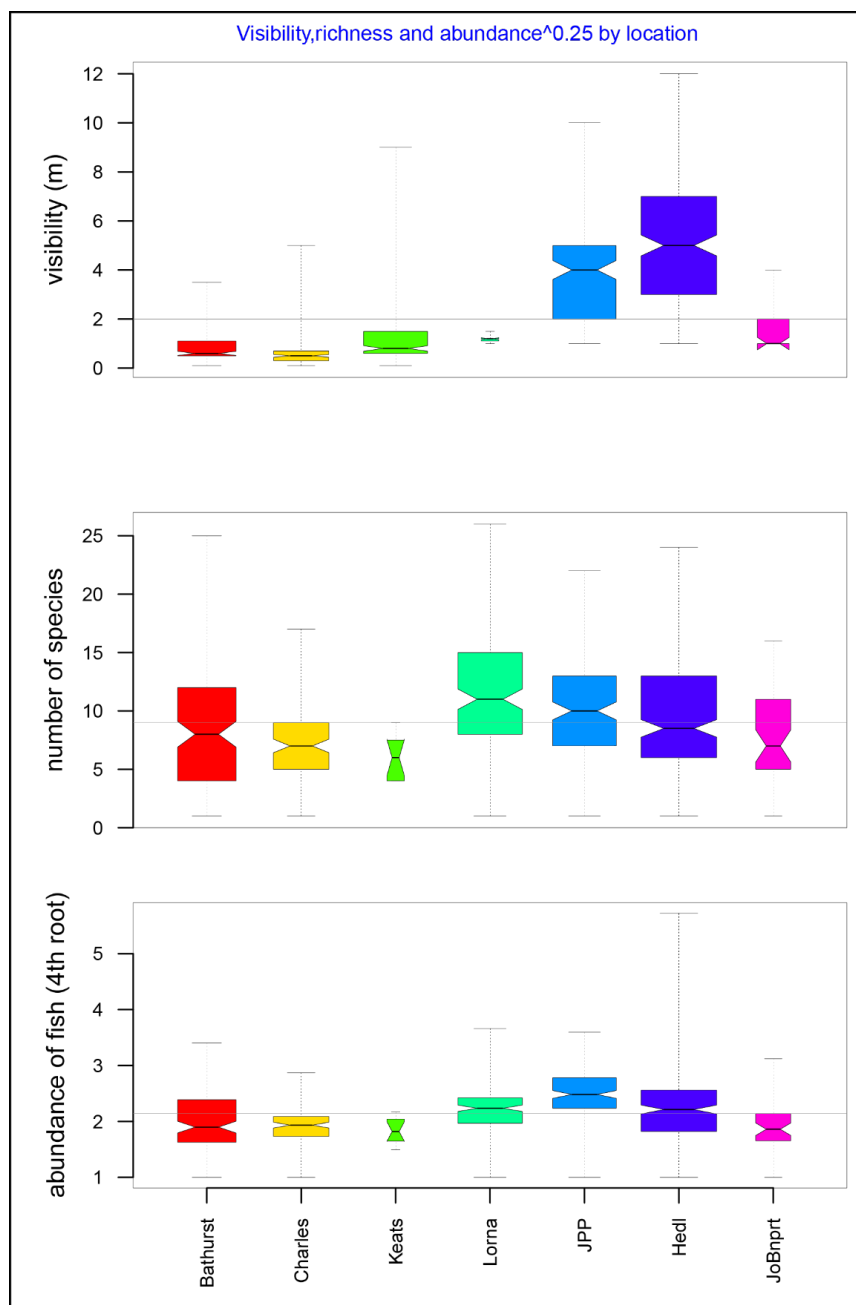


Figure 4. A regional comparison of the response data with BRUVS set in similar, macrotidal, waters. James Price Point (JPP) and Port Hedland (Hedl) are in northern WA. The Joseph Bonaparte Gulf (JoBnprt) samples were in NT waters. The width of the boxes are scaled by the square root of the number of BRUVS set in each location. Median, transformed, fish abundance and species richness were comparable with other regions, but the underwater visibility for the NT samples was poorer.

The median visibility reported was only 0.7m, with a mean of 0.96 metres and a maximum of 9 metres. Only 10% of the samples had visibility ≥ 2 metres. There were significant negative correlations between underwater visibility and two other covariates (soak time and depth; Table 2).

2. Species richness and abundance

The “Keats” data were dropped from further analyses, giving a sample size of 408 BRUVS from the 3 major locations. Species richness was transformed by square root and fish abundance ($\sum \max N$) were transformed by 4th root. Location (“loc”), “status” and “year” were all treated as factors, with continuous covariates “vis”, “soak” and “depth”. The following model was run as a base for these responses of species richness and abundance in 4 categories (total, prized, target, and not taken):

Response ~ loc + year + status + vis + soak + depth.....Equation (1)

Step-wise dropping of variables produced the optimal models of these responses in Table 3.

Underwater visibility in the field of view (vis) had the greatest partial effect on all responses except for the transformed abundance of prized fish where status was most important.

Table 3. Relative influences and partial effects in the final models of species richness and 4 categories of fish abundance on BRUVS. The “Partial effects” are the relative contribution of each predictor conditional that all other predictors were at their "average" level.

Response/interaction depth	Best model	Relative influence %	Partial effects %	Pred.err	Rsqu
Richness ^{0.5}	Vis	36.3	50.46	0.429	35.38%
2 way	Year	25.1	22.34		
	Depth	23.0	4.96		
	loc	15.6	22.24		
Total abundance ^{0.25}	Soak	33.9	19.2	0.144	30.82%
2 way	Vis	22.3	45.1		
	Year	16.7	16.7		
	Depth	15.3	4.1		
	loc	11.8	14.9		
Prized abundance ^{0.25}	Vis	43.3	34.8	0.221	22.48%
2 way	Loc	30.5	17.3		
	status	26.2	47.9		
Target abundance ^{0.25}	Vis	42.40	43.662	0.1524	18.61%
Main effects	Soak	33.64	41.244		
	Depth	8.77	4.601		
	Loc	8.65	7.616		
	Year	5.50	2.475		
	status	1.03	0.401		
Not-taken abundance ^{0.25}	Year	36.0	33.96	0.251	23.44%
2 way	Loc	28.1	9.94		
	Vis	25.9	50.68		
	status	10.0	5.42		

The partial effects plots for richness (Figure 5) show a hump-shaped relationship, rising steeply to the mean visibility and then falling. The lack of data points beyond 2 metres in the parameter space produced a very large standard error in predictions there.

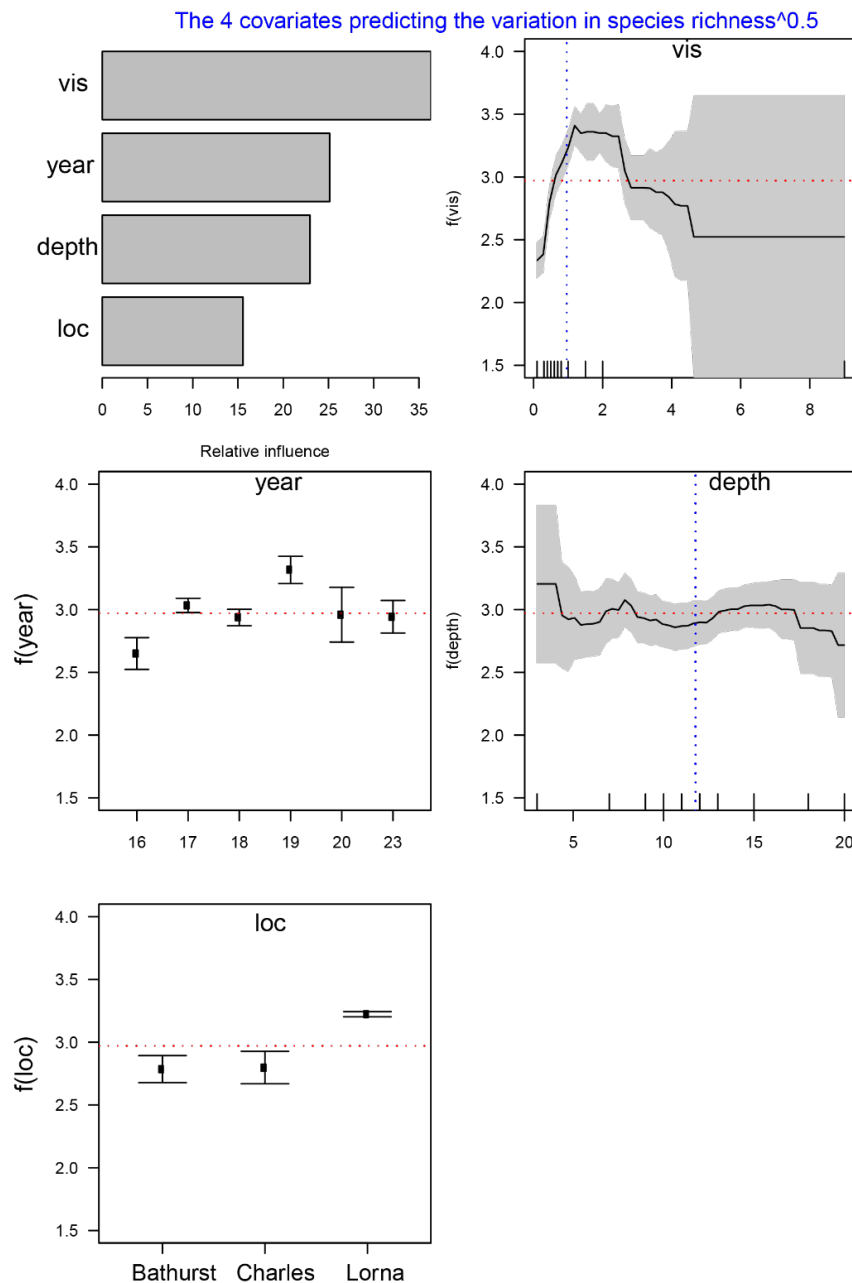


Figure 5. Relative influence and partial effects plots of the 4 covariates predicting species richness^{0.5} in the final abt models. The response curves represent the partial effect of each variable with the effects of all other covariates held to a constant. Shading and errors bars are 2 standard errors from the mean. The mean richness^{0.5} in the whole dataset is shown by the red horizontal line on the Y-Axis. Vertical blue lines represent the average value for each continuous covariate. “Rugs” on the X axes are ten-percentiles for each covariate. The rugs show only 10% of the samples had visibility ≥ 2 metres. The partial effects can be back-transformed. For example, an increase in visibility from its minimum to its mean (blue line) was accompanied by an increase of 2.3^2 to 3.25^2 ($= 5.27$) additional species.

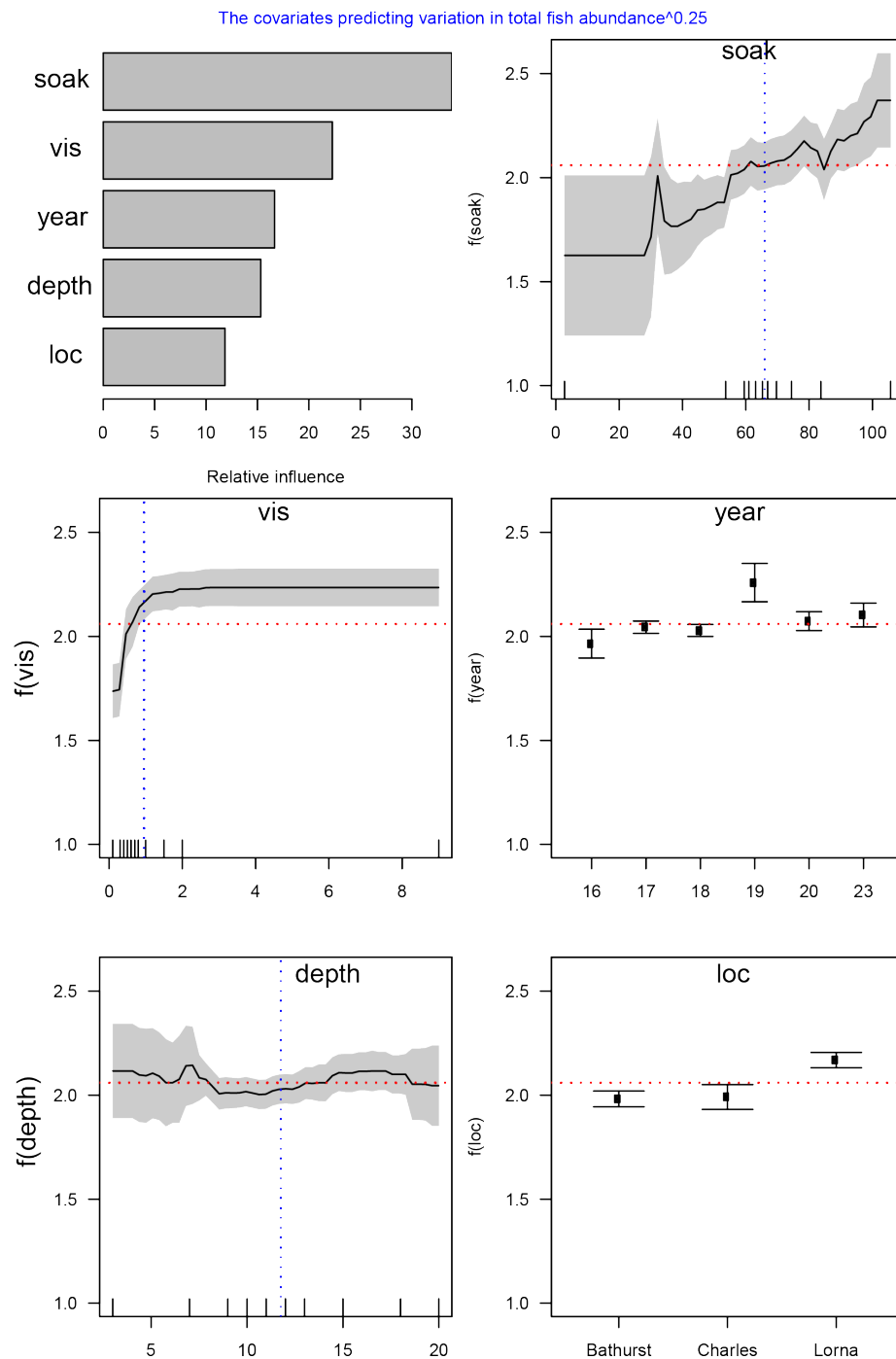


Figure 6. Relative influence and partial effects plots of the 3 covariates predicting transformed, pooled, fish abundance. Closure to fishing had no influence. All other conventions follow Figure 5.

The partial effects plots for total abundance^{0.25} (Figure 6) Soak time was the major influence, with 1.44 times the transformed abundance between the longest and shortest soak times, but vis had the greatest partial effect (Table 3). Abundance^{0.25} rose steeply to a plateau about the mean visibility. The year 2019 and location “Lorna” also had peaks in total abundance^{0.25} above the global mean.

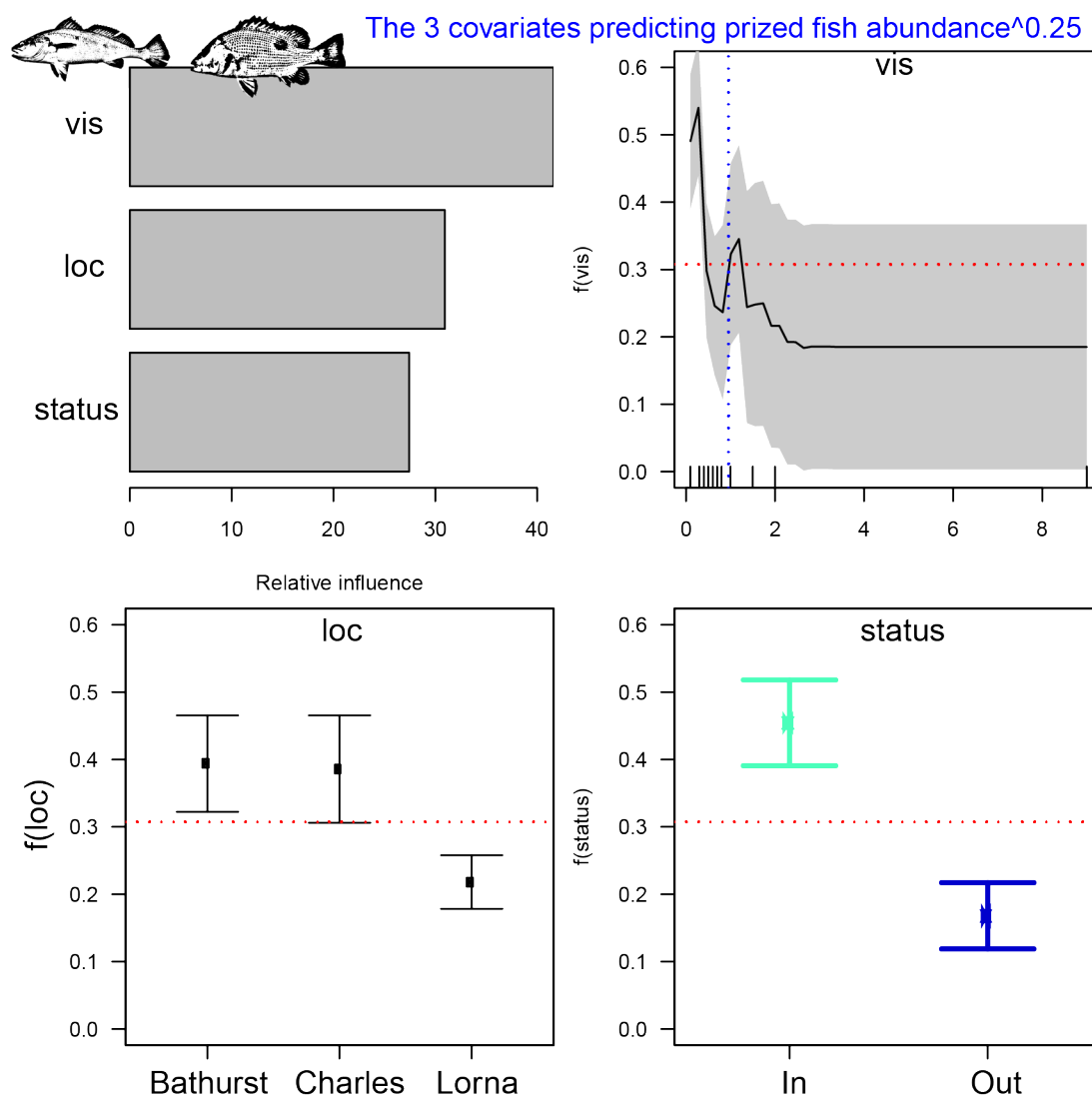


Figure 7. Relative influence and partial effects plots of the 3 covariates predicting transformed, prized, fish abundance. All other conventions follow Figure 5. Black jewfish and golden snapper comprised this category of fish.

The partial effects plots for prized abundance^{0.25} (Figure 7) showed that closure to fishing had the lowest relative influence, but highest partial effect (Table 3). There were 2.8 times more prized fish “in” than “out” on the transformed scale when all other covariates were accounted for. Higher counts of prized fish occurred in lowest underwater visibility, but uncertainty in the effect occurred beyond the mean visibility in the dataset. “Lorna” had the lowest prized abundance^{0.25} below the global mean.

partial effect of 'status' on prized fish abundance^{0.25} by location

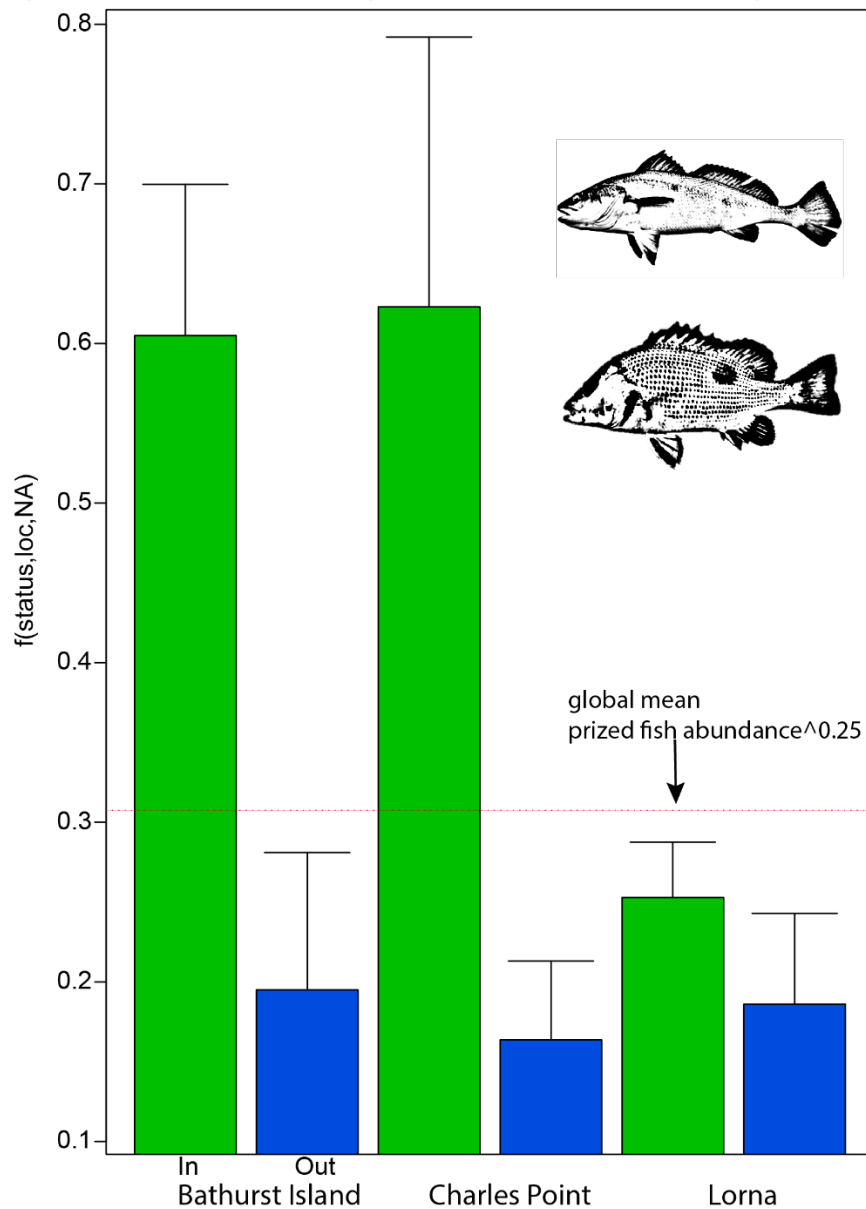


Figure 8. Partial interaction plot predicting transformed, prized, fish abundance “in” (green) and “out” (blue) given 3 levels of “location” from the model summarised in Figure 7. The effect of closure was lowest in “Lorna”, which also had below-average counts of prized fish in and outside of closed grounds.

The difference in rank of “status” in Table (3) between its relative influence and its partial effect on prized fish abundance^{0.25} may be due to the 2 way interactions captured by the model. The interaction with “loc” is shown in Figure 8. The effect of closure to fishing was lowest in “Lorna”, where counts of prized fish were below-average.

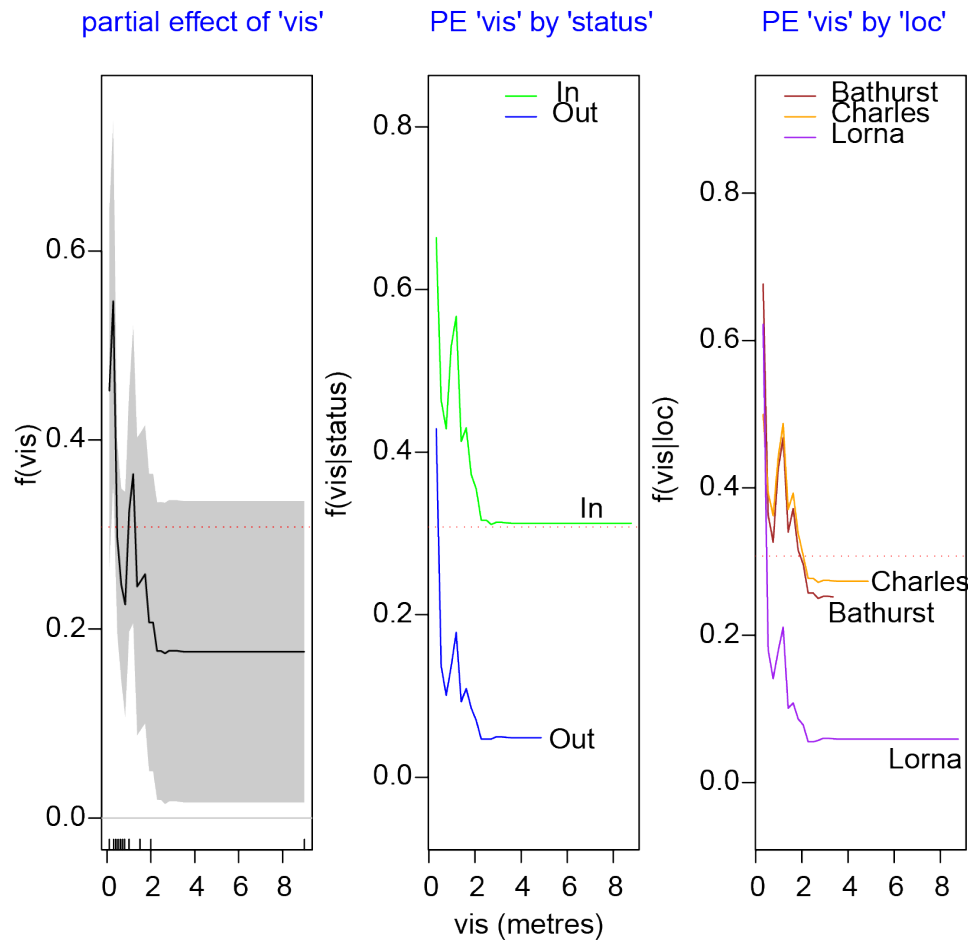


Figure 9. The partial effect of underwater visibility predicting transformed, prized, fish abundance (left), with partial interaction plots. The middle plot is the partial effect of visibility given “in” and “out” status. Points are coloured by green (“in”) and blue (“out”).

The other major interaction occurred between visibility, status and location. The partial effect of visibility given 3 levels of “location” in Figure 9 shows samples “in” had more prized fish, above the global mean, for all levels of visibility than “out”. However, “Lorna” had less prized fish for all levels of visibility than the other locations. The rugs on the x axis also show that “Lorna” had more data points in the parameter space above 6 metres visibility.

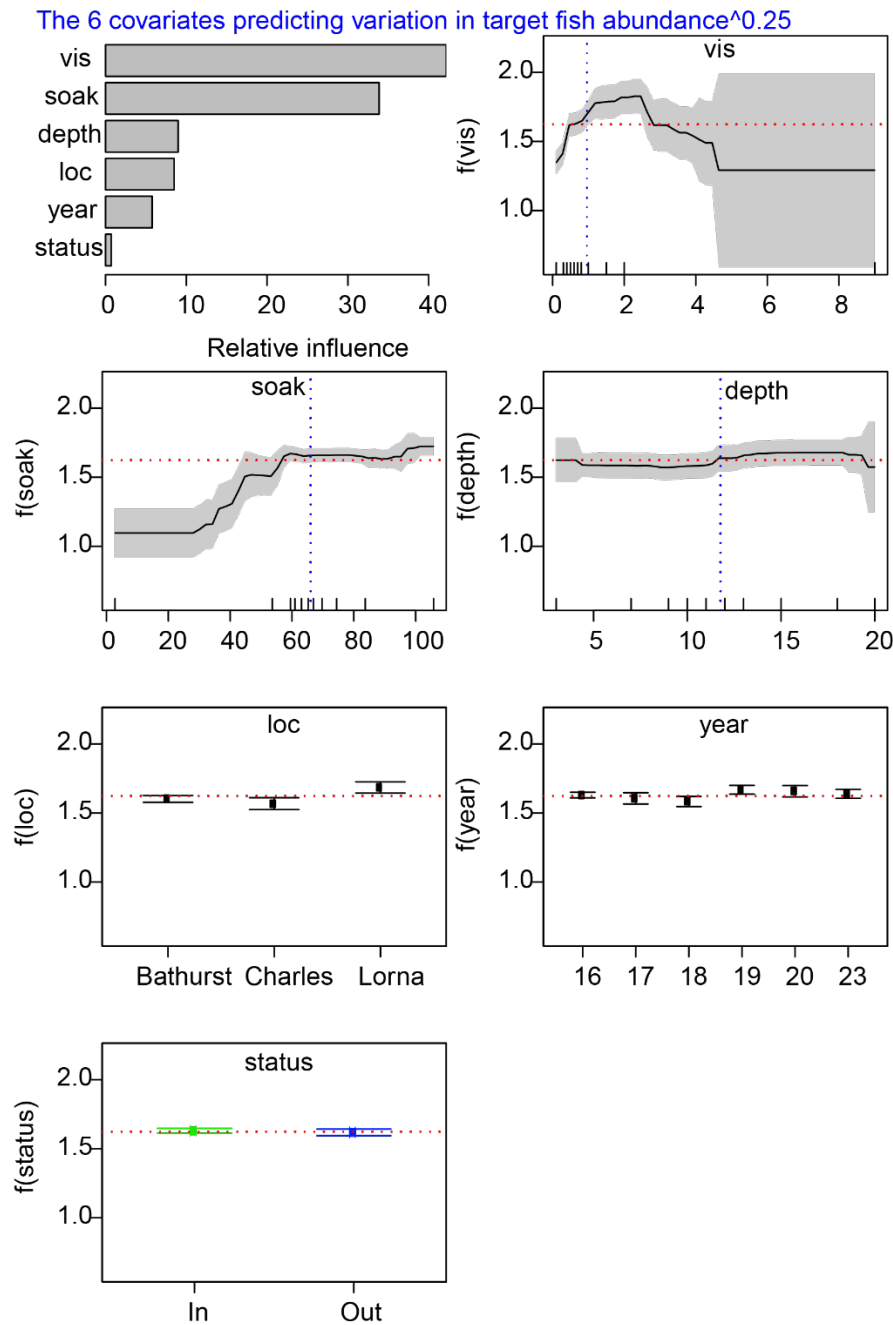


Figure 10. Relative influence and partial effects plots of the 6 covariates predicting transformed, target, fish abundance. There were 70 species classified as “targets” of line fishing, including the prized black jewfish and golden snapper. All other conventions follow Figure 5.

Target abundance^{0.25} was a main effects model with major partial effects of both visibility and soak time (Figure 10). Relationships were hump-shaped for the effect of visibility, but only 10% of the samples had visibility more than the 2 metre level where target abundance peaked and then declined.

In contrast, the response curve was somewhat sigmoidal for the effect of increasing soak time. Only 10% of the samples had a soak time less than 54 minutes. Target abundance rose steeply from 30 minutes soak time toward a plateau at a soak about 60 minutes. This parameter space comprised about 30% of the data. There was no major rise in target abundance^{0.25} beyond this soak time. The median soak time was 65.24 minutes.

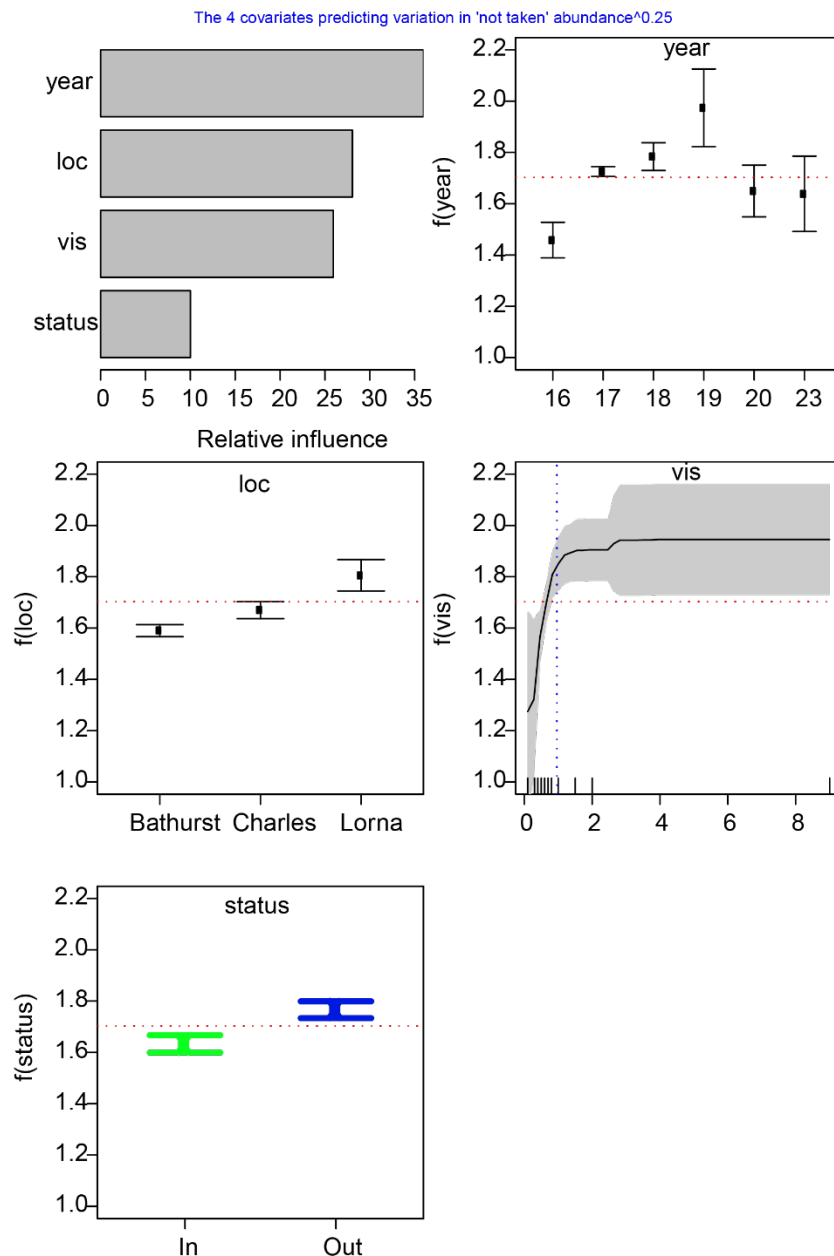


Figure 11. Relative influence and partial effects plots of the 4 covariates predicting transformed abundance of fish “not taken” by line fishing. There were 185 species in this category, which included discarded bycatch and species that do not take a hook. All other conventions follow Figure 5.

Underwater visibility and “year” both had major partial effects on the abundance^{0.25} of the “Not taken” category of fish comprising 185 species. The response rose year on year to 2019, but then fell sharply to a lower plateau in 2020 and 2023. “Lorna” had the highest abundance of this category of fish. Relationships were sigmoidal for the effect of visibility, with transformed abundance increasing sharply up to mean visibility of 0.96 metres and flattening around the 2 metre level. There were slightly less fish of this category “in” sampling sites closed to fishing.

3. Presence/absence of prized species

The poor prediction error of models for transformed abundance was no doubt due to the skew in the data, the high number of “zero” counts, and the overall variation in both counts and covariate predictors. Converting the counts to presence =1 or absence=0 overcomes most of these limitations and can be used with a “Bernoulli” distribution of errors and a log-odds link function.

Just over 31% of the BRUVS had prized fish species recorded. The black jewfish was sighted on only 9.8% of samples and golden snapper on 21.6% of samples. Only 5.14% of samples had both black jewfish and golden snapper present on the same video.

Status in or out of the closed areas had the greatest partial effect on the presence/absence of prized fish pooled and the separate, species-specific models for black jewfish and golden snapper (Table 4). The prediction error for these models was simply the number of BRUVS (out of the total 408 samples) where presence=1 or absence=0 was mis-classified. For black jewfish, this was only 36/408 (8.82%), giving a “Rsqu” analogue of 91.17%.

These error rates do not identify if the mis-classification is a false positive, or a false negative, but those metrics could be calculated by examining the residuals of the model.

Table 4. Relative influences and partial effects in the final models of presence/absence of prized species on BRUVS. The “Partial effects” are the relative contribution of each predictor conditional that all other predictors were at their “average” level.

Response/interaction depth	Best model	Relative influence %	Partial effects %	Pred.err	Rsqu
Both prized species	Vis	46.2	35.0	91	77.7%
2 way	Status	27.2	35.8		
	loc	26.6	29.2		
Black jewfish	Vis	56.2	32.9	36	91.17%
2 way	Loc	23.0	32.3		
	status	20.8	34.8		
Golden snapper	Year	37.3	32.0	86	78.92%
Main effects	Status	33.4	34.6		
	loc	29.3	33.4		

The partial effects of “visibility”, “status” and “loc” were broadly equivalent in magnitude for the presence of black jewfish and pooled prized species. The model for golden snapper presence included only main effects and lacked the predictor for visibility, but added one for “year” (Table 4).

The 3 covariates predicting 77% of the variation in prized fish presence

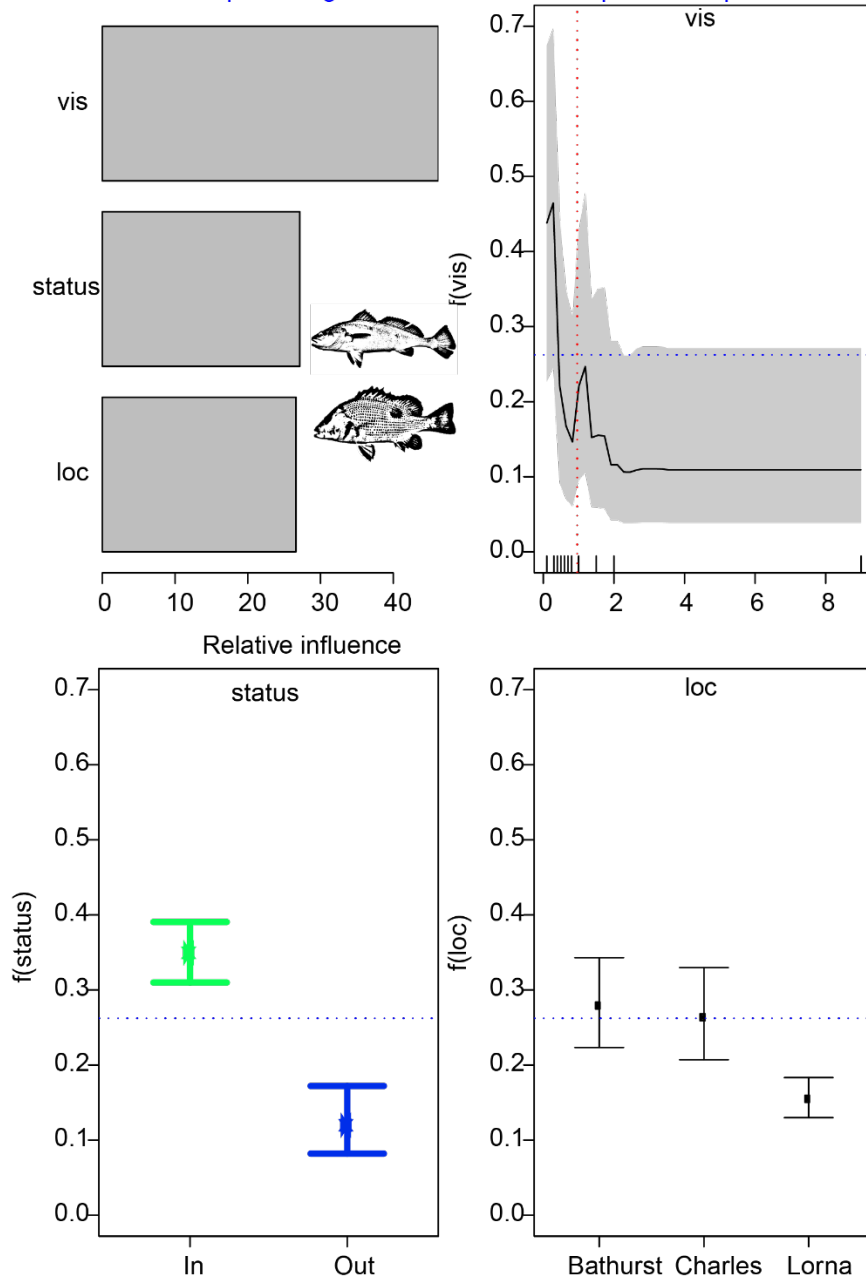


Figure 12. The counts of prized fish were transformed to presence/absence (1,0) to overcome the skew presented in Figure 3 using a “Bernoulli” distribution of errors and a log-odds link function. This model predicted 77% of the variation in presence/absence of prized fish. All other conventions follow Figure 5. The y-axes (on the scale of the response) can be read as the proportion of BRUVS having prized fish present, or the probability of encountering a prized species.

The proportion of BRUVS “in” closed areas having a prized fish species in the field of view was over 3 times that of the “out” level (Figure 12). Presence decreased with increasing visibility from the minimum of 0.1 metres to just below the mean of 0.96 metres. However, the response rose again through the mean visibility to a second peak before declining again. “Lorna” had the lowest probability of encountering a prized fish.

The 3 covariates predicting 91% of the variation in black jewfish presence

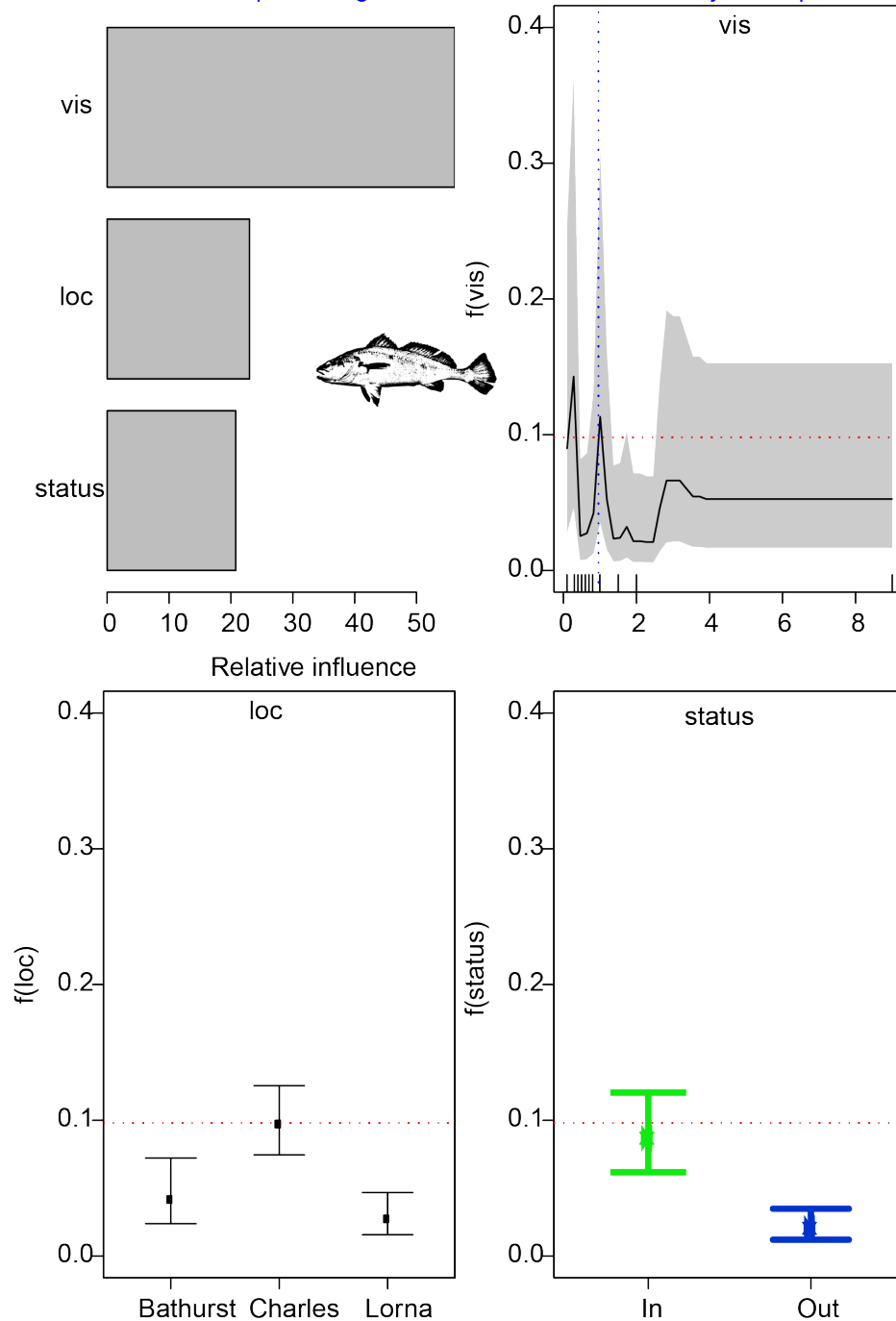


Figure 13. A species-specific abt model predicted 91% of the variation in presence/absence of black jewfish. All other conventions follow Figure 12.

The global average was only 0.1, or a black jewfish sighted for 1 out of every 10 BRUVS. Presence had peaks in lower visibility, but “status” had the highest partial effect with sightings of black jewfish about 3 times more likely in areas closed to fishing (Figure 13). Charles Point had highest probability of black jewfish sightings.

The 3 covariates predicting 79% of the variation in golden snapper presence

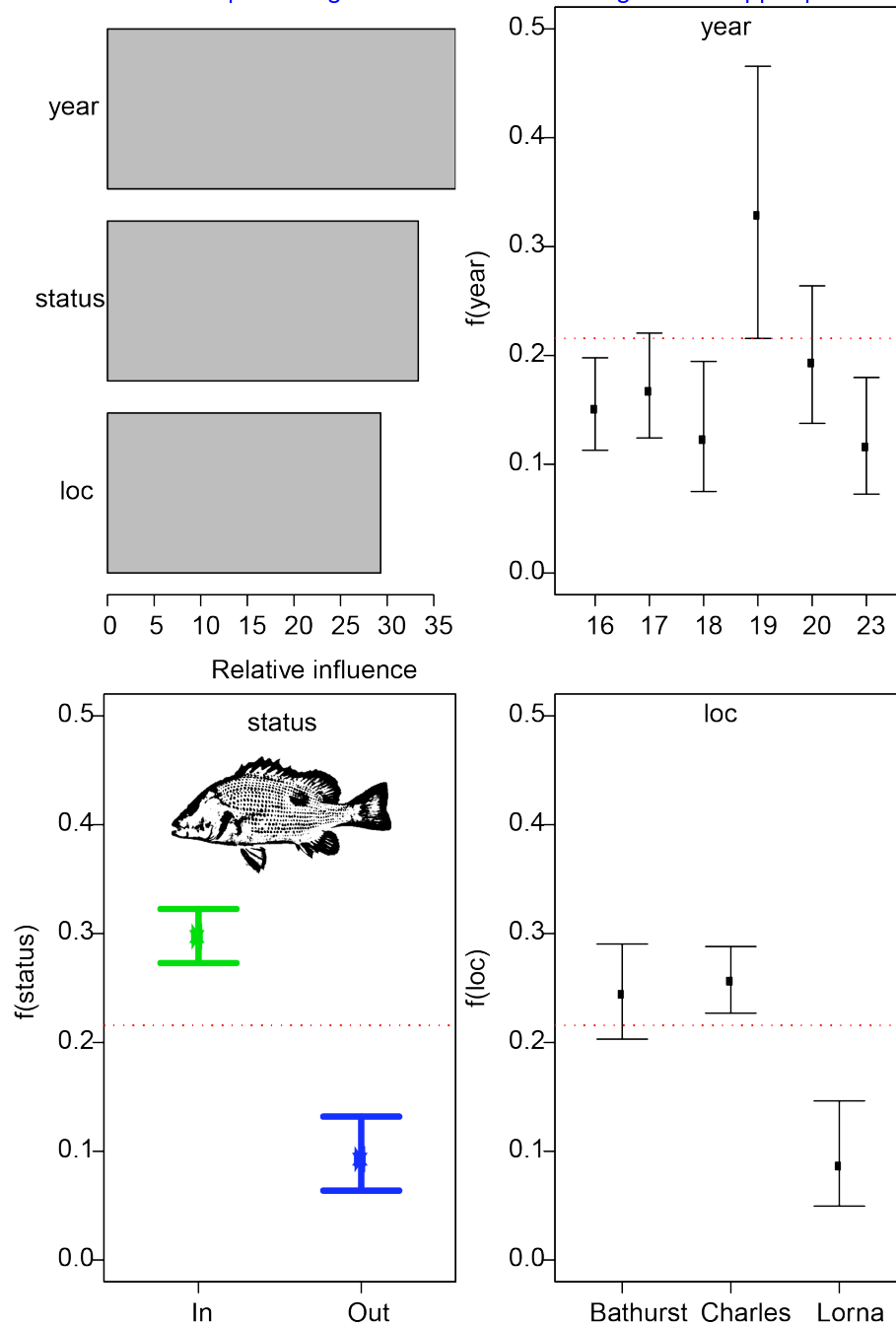


Figure 14. A species-specific abt model predicted 79% of the variation in presence/absence of golden snapper. All other conventions follow Figure 12.

The global average was about 0.21, or a golden snapper sighted on 2 out of every 10 BRUVS. “Year” had the highest influence without a clear temporal trend up or down, but “status” had the highest partial effect of a three-fold difference in presence of golden snapper (Figure 14). Year 2019 had the highest presence of golden snapper, with wide variability, and “Lorna” the lowest.

4. distance-based redundancy analysis of the multivariate response

“Year” was not treated as a factor in both the multivariate analyses. Instead it was treated as a continuous numeric variable to investigate if there were any temporal trends visible in community assemblages.

Distance-based redundancy analysis (db-RDA) makes a dissimilarity matrix, creates a PCoA using metric scaling, then runs an RDA of the principal coordinates created in the PCoA constrained by the explanatory variables. The dbRDA modelled the transformed abundance (4th root) of 62 fish species with at least 10 occurrences in the BRUVS dataset (2.46% of the samples) in response to all of the covariates in Table (2) and Equation (1).

The response was the dissimilarity matrix “abun.diss”, constructed using site-standardised (by mean) Manhattan distance (“xdiss” in library (mvpart); see De’ath (1999)).

Function “capscale” in R library “vegan” (Oksanen et al. 2018) was used to identify the most parsimonious model by analysing in comparison to the null model (abun.diss=1). This function builds a model so that it maximizes adjusted R² at every addition of covariates, and stops when the adjusted R² starts to decrease, or the adjusted R² of the scope is exceeded, or the selected permutation P-value is exceeded (Blanchet et al. 2008).

The best model dropped “depth” and was:

abun.diss = loc + status + vis + soak + year

This model explained 24.88% of the squared distance variation (“inertia”) in the species composition (Table 5). The first two constrained axes (CAP1 and CAP2) explained 23.24 units of the 24.88 units (93.4%). CAP1 explained 20.88% and CAP2 a further 2.35% of this total, explainable variation. The explained “inertia” can be used as a measure of how well species composition is explained by the variables, when compared to total inertia.

Table 5. Partitioning of squared distance variation (“inertia”) in the db-RDA of the transformed abundance (4th root *MaxN*) of 62 species in 408 BRUVS samples. This model explained 24.88% of the squared distance variation in the dissimilarity matrix.

Source	Inertia	Proportion (%)
Total	85.84	100
Constrained	21.35	24.88
Unconstrained	64.48	75.12

Analysis of variance of the "marginal" effect of each variable, as if it were the only predictor in the distance-based redundancy analysis, is shown in Table (6). The "conditional" (or "partial") effect of each variable conditioned by the presence of all other terms (as covariates) are shown in Table (7).

Table 6. Analysis of variance of the "marginal" effect of each variable, as if it were the only predictor in the distance-based redundancy analysis (dbRDA). The squared distance variation, or inertia, is represented by "Var". This model explained 24.88% of the squared distance variation in the dissimilarity matrix.

Term	Df	Var	Pseudo-F value	N.Perm	Pr(>F)
loc	2	12.379	38.2981	199	0.005 **
status	1	3.536	21.8804	199	0.015 *
vis	1	0.919	5.6840	199	0.005 **
soak	1	2.331	14.4221	199	0.01 **
year	1	0.564	3.4923	199	0.01 **
Residuals	399	64.482			
Signif. codes: '***' 0.001 '**' 0.01 '*' 0.05					

Table 7. Analysis of variance of the "conditional" (or "partial") effect of each variable conditioned by the presence of all other terms (as covariates) in the dbRDA model. The partial effects are also shown as percentages of the total squared distance constrained. All other conventions follow Table 6.

Term	Df	Var	Var as%	Pseudo-F value	N.Perm	Pr(>F)
loc	2	14.472	67.8%	44.7740	99	0.01 **
status	1	3.310	15.5%	20.4804	99	0.01 *
vis	1	0.776	3.6%	4.8043	99	0.03 *
soak	1	2.232	10.5%	13.8141	99	0.01 **
year	1	0.564	2.6%	3.4923	99	0.03 *
Residuals	399	64.482				
Signif. codes: '***' 0.001 '**' 0.01 '*' 0.05						

The partial effect of "status" in the dbRDA accounted for 15.5% of the squared distance variation accounted for by the model, but location had the major partial effect (Table 7).

The arrow-head positions in the ordination biplot of "site scores" (Figure 15) show the directions of vectors and centroids representing the 5 covariates in the db-RDA scaled by their correlations, so that "weak" predictors have shorter arrows than "strong" predictors. The greatest influence was separation of "Lorna" from the other locations, and sites closed and open to fishing, along the first axis. "Year" was a weak predictor and not significantly correlated with both axes (Table 8). The r^2 represents the proportion of variance in the vector explained by the two axes.

Table 8. Factor centroids and vector arrowhead coordinates on the first two axes accounting for 93.5% for the squared distance variation (24.88%) constrained by the dbRDA model in Figure 15.

	CAP1	CAP2	r2	Pr(>r)
vis	0.91619	-0.40075	0.1238	0.001 ***
soak	0.23660	0.97161	0.0775	0.001 ***
year	-0.37164	0.92838	0.0008	0.874
loc			0.1436	0.001 ***
locBathurst	-0.0832	-0.6021		
locCharles	-0.7821	0.5388		
locLorna	0.6435	0.0958		
status			0.0188	0.004 **
statusIn	-0.2615	-0.0746		
statusOut	0.2514	0.0717		

The very short vector for “year” shows lack of correlation of this vector with the first two dimensions separating “in” and “out” samples (Figure 15).

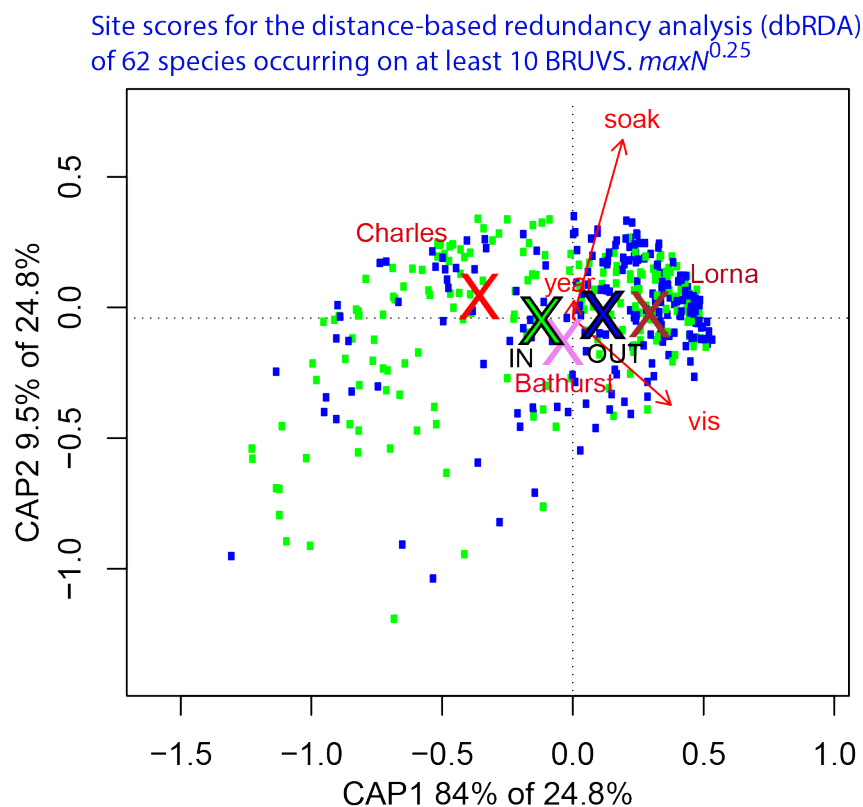


Figure 15. Ordination biplots of site scores in the distance-based redundancy analysis (dbRDA) for the transformed abundance (4th root $MaxN$) of 62 species of fish occurring on at least 10 (2.46%) of the BRUVS samples. The site scores are shaded for status=“in” (green) and “out” (blue). The centroids for the significant factors “location” and “status” are also shown with significant vectors for the continuous variables “year”, “visibility” (vis) and “soak”.

Significant species vectors ($p \leq 0.005$) correlated with the significant ($p < 0.005$) constraints of the distance-based redundancy analysis (dbRDA) of 62 species occurring on at least 10 BRUVs. $\max N^{0.25}$

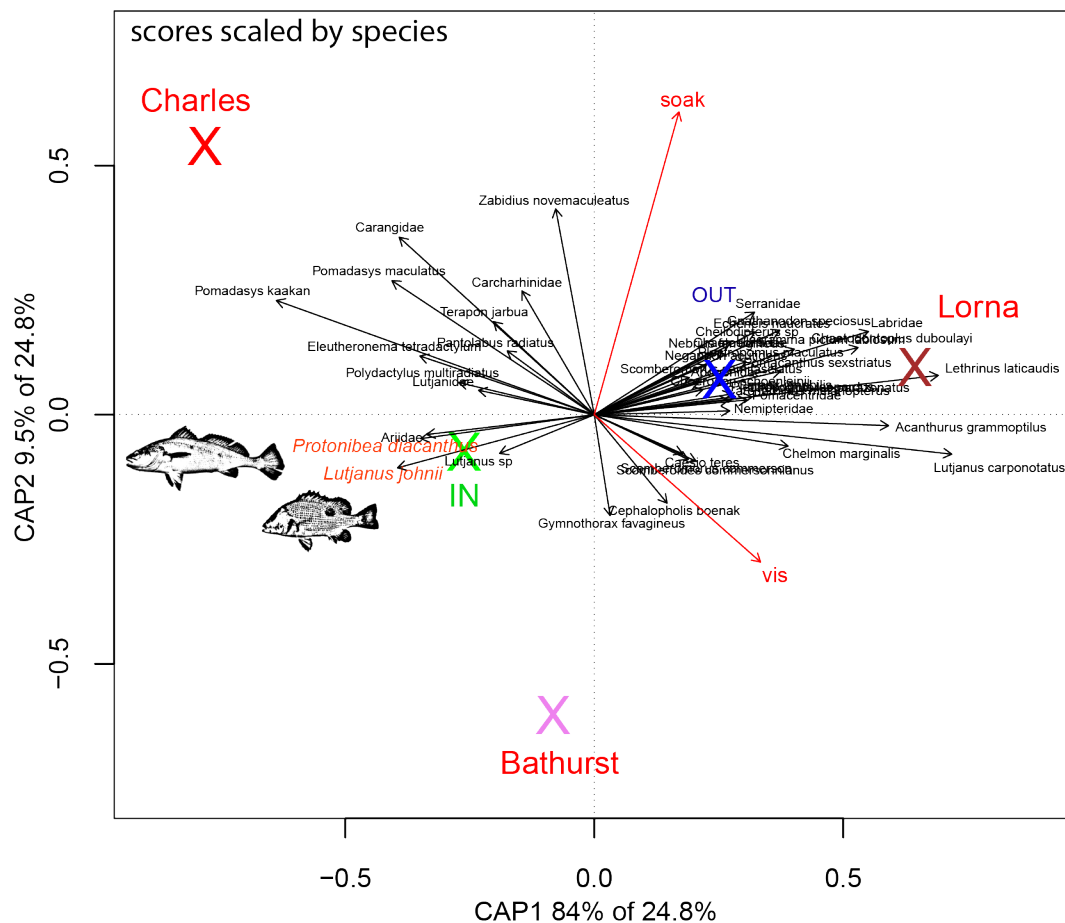


Figure 16. Ordination biplots of species scores in the dbRDA for the transformed abundance (4th root $\max N$) of 62 species of fish. Only the 41 species for which the significance of correlation was $p \leq 0.005$ are shown. These are scaled by their correlation so that “weaker” predictors have shorter arrows than “stronger” predictors. The longer arrows for the prized black jewfish (*Protonibea diacanthus*) and golden snapper (*Lutjanus johnii*) indicates the variance in these species was accounted for well by the fit of the dbRDA model to the linear constraint of status=“in”. Many other species were correlated with the first axis separating “out” and “Lorna” centroids along the first axis.

A “species” biplot projects species scores onto the ordination (Figure 16). The length and orientation of the species arrows in relation to the 2 significant vectors show the correlations with underwater visibility and soak time. “Year” does not appear, as it was not a significant constraint with these two axes. The factor centroids show the averages of the levels of “location” and “status”. The vectors shown in Figure (16) are restricted to the subset of 41 species for which the probability of correlation by chance alone with the axes is $p \leq 0.005$, to prevent clutter in the overlays.

For example, both the prized species are closely correlated with status=“in” away from “Lorna” on the first axis. In contrast, the variance in abundance of the grassy sweetlip *Lethrinus laticaudis* was aligned with the status “out” toward “Lorna”. A relatively large number of species vectors followed this alignment.

5. Definition of assemblages and key predictors of the multivariate response (mvpart)

The best tree structure from mvpart of transformed fish abundance had high error predicting the fauna of sites (13.4% success rate) and explained 21.9% of the multivariate variation (Figure 17). The best fit identified 14 fish assemblages.

The first split separated the Lorna samples and contributed 6.2% of the multivariate variation. The following 11 splits contributed the other 15.7%. Surrogates for this first split on “loc” (6.2%), and their contributions to improvement, were “vis” (4.27%), depth (3.56%), status (1.42%) and year(1.39%). None of the splits or terminal leaves in the tree was based on “depth”.

On the Lorna side of the tree, the terminal “leaves” were all based on individual sampling years and the length of soak either side of the mean soak time. The clear separation of years was in stark contrast to the lack of significance and correlation of “year” with species scores in the dbRDA (Figure 16).

The other side of the tree split the Charles Point samples on underwater visibility and status “in” the area closed to fishing. The Bathurst Island samples also split into leaves on the basis of varying degrees of low visibility in both “in” and “out” branches. The “out” branches split further on soak time.

The size, diversity and abundance in each of the 14 terminal fish assemblages is summarised in Appendix 2. The Dufrene-Legendre species indicators (DLI) are shown in Figure 17 and listed for all branches and leaves in Appendix 3.

Prized target species had highest DLI on the nodes splitting “in” samples at Bathurst Island. Species with highest DLI at the tree stump were ubiquitous and not characteristic of any particular node or leaf. It was notable that these included known “target” species (eg stripey snapper *Lutjanus carponotatus* and goldspot cod *Epinephelus coioides*). Others had high DLI on the terminal leaves (eg *Caesio teres* on “Bathurst.Out.longSoak”).

The Lorna side of the tree had more species with high DLI and a large number of these were from genera often associated with more with tropical coral or rocky reefs than soft unconsolidated substrata (eg *Chaetodon*, *Chaetodontoplus*, *Choerodon*, *Siganus*, *Acanthurus*). In contrast the Bathurst/Charles side had fewer species with highest DLI and these included genera often associated with muddy or sandy seabeds (eg *Pomadasys*, *Terapon*, *Polydactylus*, *Eleutheronema*).

The species accumulation curves were generally still ascending toward an asymptote in Figure (19), indicating that there remained latent fish diversity in the assemblages remaining to be recorded. The flattest curve with few species was the one with the worst visibility (*Bathurst.In.noVis*). It was furthest from the steepest one with highest diversity and highest visibility (*Bathurst.Out.avSoak.hiVis*). The assemblages represented by the first 2 years of sampling at Lorna also had high diversity and a large number of member samples.

Top 10 DLI per group; 62 species, 4th root abundance

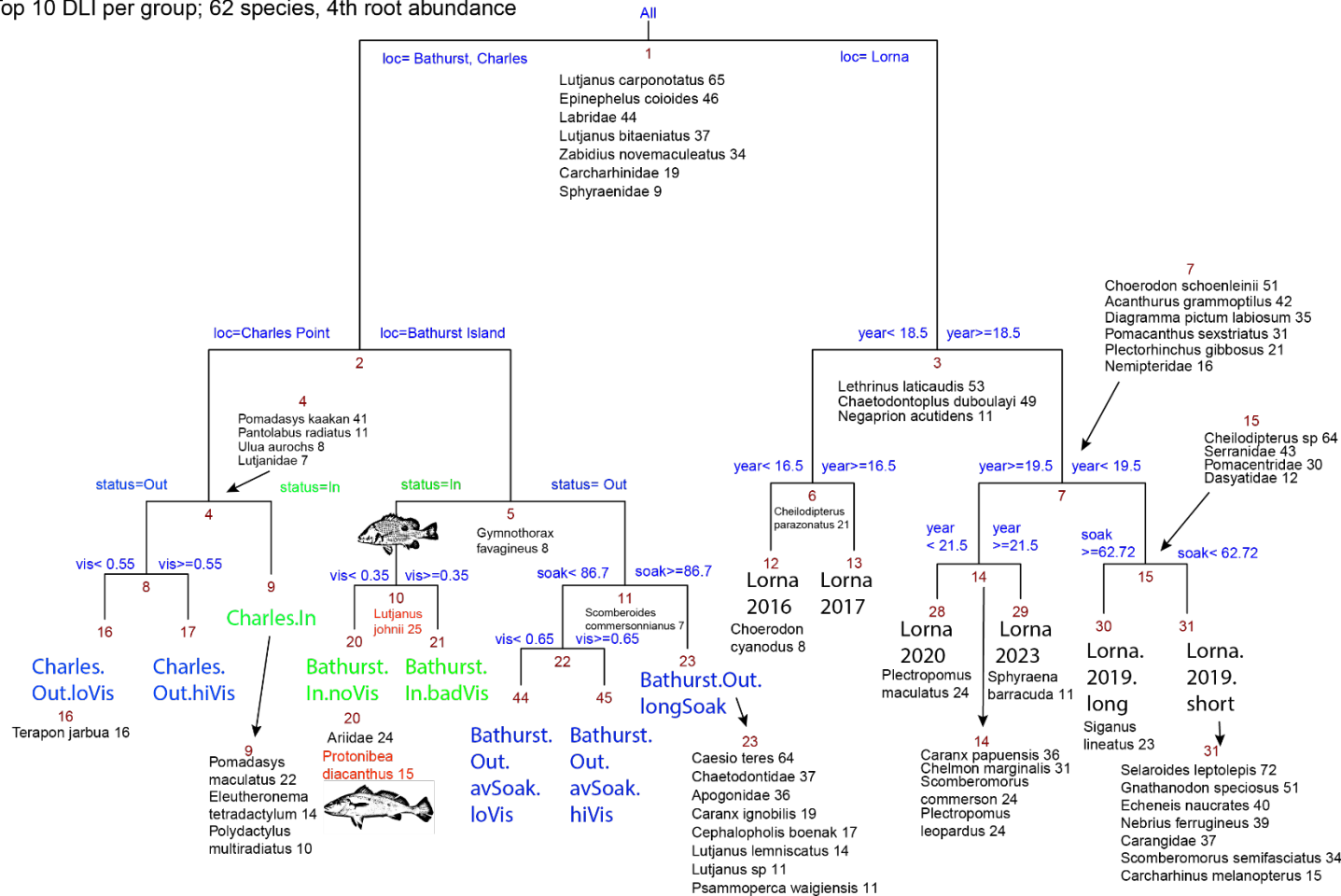


Figure 17. The best tree structure from a multivariate analysis of the transformed abundance (4th root $\max N$) of 62 species present on at least 10 BRUVS (~2.6% of samples). The model had high error predicting the fauna of sites (only 13.4% success rate) and explained 21.9% of the multivariate variation. The best fit recognised 14 fish assemblages. The Dufrene-Legendre species indicators (DLI) are shown for all branches and leaves. Prized targets are highlighted in red.

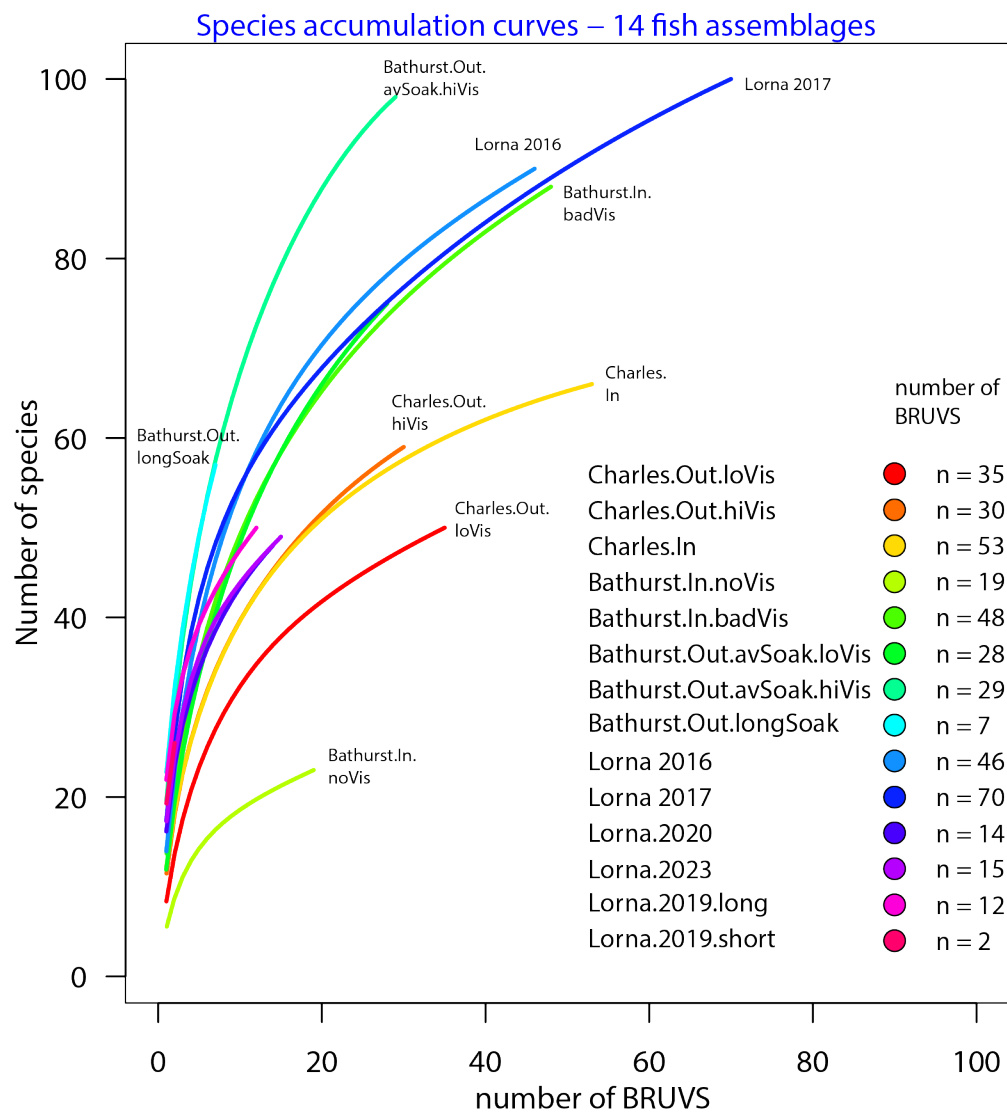


Figure 18. Species accumulation curves derived for the 14 assemblages identified in Figure (17). The numbers and node names are shown with the number of BRUVS sites in each node. In general the curves were still ascending toward an asymptote, indicating that there remained latent fish diversity in the assemblages.

Discussion

The models presented here detect higher numbers of prized fish in sites closed to fishing and some major interactions with location, but not any temporal trends in their abundance. There was high variability, skewed counts and many zeroes resulting in high prediction errors for models of abundance. There may also have been some confounding of covariate predictors.

Grounds closed to fishing were further offshore at Bathurst Island and Lorna than the inshore sites they were being compared with. Distance offshore can change the turbidity and wave action at the seabed which, in turn, defines the types and abundance of marine plants and sessile invertebrates that can attach there. Samples “in” closures were also generally deeper than those “out” but the effect of “depth” in almost all models was insignificant. It may be that this reflects less on the effect of depth and more on a confounding of the effect of depth with the effect of closure to fishing. Further sampling would be needed offshore in deeper grounds closed to fishing to help balance the sampling design with adjacent, open sites.

Status

Closure to fishing had the highest partial effect on prized fish abundance. There were 2.8 times more prized fish “in” than “out” on the transformed scale when all other covariates were accounted for. Higher counts of prized fish occurred in lowest underwater visibility, but high uncertainty in the effect occurred beyond the mean visibility in the dataset due to lack of data points

There were important 2-way interactions in this effect. It was lowest in “Lorna”, where counts of prized fish were below-average. Samples “in” had more prized fish, above the global mean, for all levels of visibility than “out”.

The partial effect of “status” was broadly equivalent in magnitude to that of “visibility” and “loc” for the presence of black jewfish and pooled prized species. The model for golden snapper presence included partial effects of similar size for “year”, “status” and location.

The proportion of BRUVS “in” closed areas having a prized fish species present in the FOV was over 3 times that of the “out” level. Black jewfish were relatively rare, with the global average only 1 black jewfish sighted every 10 BRUVS. Presence had peaks in lower visibility, but “status” had the highest partial effect with sightings of black jewfish about 3 times more likely in areas closed to fishing.

There was a three-fold difference in presence of golden snapper in site closed to fishing. “Year” had the highest influence with, a peak in records in 2019, but there was no clear temporal trend up or down.

Both black jewfish and golden snapper were indicator species for nodes on the Bathurst Island branches in the mvpart tree closed to fishing. It was notable that the ubiquitous species at the mvpart tree stump included well-known “target” species (eg stripey snapper/Spanish flag and goldspot cod). These species take a hook eagerly and are often retained in tropical fisheries yet there was no “signal” of an effect of fishing on them in the study.

Visibility

Fish abundance and species richness were comparable with other macrotidal regions in northern Australia, but the underwater visibility for the NT samples was much poorer. The median visibility reported was only 0.7m and only 10% of the samples had visibility ≥ 2 metres.

BRUVS surveys by the Australian Institute of Marine Science (AIMS) classify as “unreadable” any videos in which the bait canister is invisible. That represents a range of about 1 metre visibility from the camera lens, yet the mean visibility of the NT BRUVS as 0.96 metres. Such a visibility would be deemed “unreadable” in the AIMS protocol and the sample would be invalid.

Underwater visibility in the field of view (“vis”) had the greatest partial effect on all responses except for the transformed abundance of prized fish in the NT dataset. However, the results were counter-intuitive. Higher visibility did not produce higher counts. Instead, there were hump-shaped or sigmoidal relationships.

Prized fish were more likely to be sighted, and more abundant, in the poorest visibility when all other covariates were accounted for. “Lorna” had the most samples with higher visibility, but the least prized species. Visibility also separated fish assemblages at Bathurst Island and Charles Point in the mvpart tree. The indicators species for those assemblages included *Pomadasys* spp and threadfin salmon in the family Polynemidae known to inhabit turbid waters.

It may be that golden snapper and black jewfish prefer such turbid waters or that they will come closer in range of the BRUVS in turbid waters, or a combination of both. It also may be that the turbidity itself is not the preferred habitat but the turbidity results from preferred sediment types or microhabitats such as “pressure points” where tidal currents strike seafloor features.

BRUVS sampling by AIMS (Meekan and Cappel, unpublished data) in Darwin Harbour in 2004 found that visibility was best at the wrecks in the few days *after* the neaps – not on the day of lowest tidal range. This may be because the sediments in the macrotidal NT have been scoured so much by the tides that they are large particles and settle very quickly. This would give them some “inertia” requiring a large, building, tide to resuspend them.

It would be fundamentally advantageous to improve visibility in the FOV by pilot studies of the timing of least turbidity at the seabed in the sampling locations. Perhaps there have already been relevant studies done by local authorities concerned with dredging, land reclamation and port expansion in Darwin harbour?

Soak time

Effective sampling time at the seabed, represented as “soak time”, was not standardised in the NT dataset. This had a major relative influence on total abundance of all fish sighted, with 1.44 times the transformed abundance between the longest and shortest soak times. Target abundance also rose steeply from 30 minutes soak time toward a plateau at a soak about 60 minutes. As a consequence, soak time was an important splitting predictor in the mvpart tree producing leaves for samples in the fished sites at Bathurst Island and amongst the 2019 samples at Lorna.

There was a significant negative correlation between underwater visibility and soak time. This might be expected if video readers truncated the reading time of “poor” samples in turbid waters, but such an effect could not be demonstrated. Some samples in high visibility had short soaks. Only 10% of the samples had a soak time less than 54 minutes.

Effective sampling time can be easily standardised even if the BRUVS are left recording on the seabed for a long time. This is because an entire video can be interrogated by accumulating the time and counts as *maxN* increases for a species. EventMeasure stores these events as “*cumulativeMaxN*”. Exported data can then be filtered to select only the records where “time of *maxN*” minus “time start reading” is greater than or equal to 60 minutes. This duration has become standard for tropical studies (Birt et al. 2021, Currey-Randall et al. 2020).

Year

The only clear temporal trend in abundance was a steady rise year on year from 2016 to 2019 in the abundance of species “not taken” followed by a sharp fall to a lower plateau in 2020 and 2023.

“Lorna” had the highest abundance of this category of fish. The year 2019 also had peaks in species richness, total abundance and the presence of golden snapper.

The conditions for BRUVS sampling in 2019 may have been exceptional or fish abundance may have changed due to un-measured environmental influences. There may also have been effects of experience and training on observers interrogating the videos, staff turn-over, or other “readr effects” known to affect BRUVS data (see).

“Year” was treated as a continuous variable in the multivariate analysis. It was a weak predictor in the dbRDA but the major determinant of terminal assemblages at “Lorna” in one whole side of the mvpart tree.

Location

Much of the contrast amongst the three sampling locations came from the separation of “Lorna” from the other two locations. “Lorna” also had the highest peaks in species richness, total abundance and the abundance of the “not taken” category -- but the lowest prized abundance below the global mean.

The greatest influence in the dbRDA biplots was separation of “Lorna” from the other locations, and sites closed to fishing along the first axis. The variance in abundance of a relatively large number of species vectors followed this alignment

The mvpart recognised 14 fish assemblages. None of the splits or terminal leaves in the tree was based on “depth”, but “location” was a primary splitting variable. On the “Lorna” side of the tree, the terminal “leaves” were all based on individual sampling years and the length of soak.

The Lorna side of the tree had more indicator species and a large number of these were from genera often associated with more with tropical coral or rocky reefs than soft unconsolidated substrata (eg *Chaetodon*, *Chaetodontoplus*, *Choerodon*, *Siganus*, *Acanthurus*).

It may be that “Lorna” habitats are very different from those at Bathurst Island and Charles Point. Only classification and estimated cover of the topography, substratum, sediment type and epibenthic cover in the FOV of samples can account for that. There are national approaches to classifying epibenthos in still photos and video imagery being used now by other BRUVS programs (eg CATAMI see Althaus et al. 2015). Multibeam derivatives can also be measured from seafloor mapping of BRUVS sites chosen for repeated sampling (see Moore et al. 2017 for example).

There is a range of readily available image annotation software and platforms available such as TransectMeasure (seagis.com.au/transect.html), Squidle+ (squidle.org), CoralNet (coralnet.ucsd.edu), Benthobox (benthobox.com), and ReefCloud (reefcloud.ai), all of which are suitable for mono-video annotation (see Langlois et al. 2025).

The “quality” of the FOV can be counted for in statistical models by roughly measuring %water column, %seabed and %blocked in images to use as covariates in statistical models. These are not routinely measured yet by other institutions (except AIMS pers comm Stacy Bierwagen) but they were demonstrated to explain much of the variation in fish abundance and diversity in a recent unpublished study.

This is because BRUVS settle on seabeds in an uncontrolled manner and can topple in current. If no “horizon” with the water column is visible, then no pelagic and semi-pelagic species will be recorded. Likewise, if the BRUVS perches atop a rock or bommie and has a skyward aspect to any degree the seafloor will not be visible and there will be less or no demersal, site-attached species recorded.

Even if the BRUVS settles well with a horizontal aspect, the FOV can be largely blocked by obstacles in front of the bait canister such as rocks, coral colonies, sponges, gorgonians and macroalgae. Simple metrics of the “quality” in Plates 1 and 2 below can suffice and could be measured with “AI” (pers comm. Brooke Gibbons).

Recommendations

1. Collaborate with the national push for BRUVS data collection and standardisation (see Langlois et al. 2020) and the other groups working with BRUVS in the NT (Northern Australian Marine Monitoring Alliance Namma/ AIMS).
The best over-arching contact for national collaboration would be through the “Fish Collective” and “Global Archive” of BRUVS data and methodology. Contact:
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2. Seek the best possible visibility for sampling.
3. Standardise effective sampling time (minutes of video interrogated) to 60 minutes
4. Measure characteristics of seafloor rugosity, topography, substratum and epibenthos as far as possible in every image consistently following national approaches to classifying epibenthos in still photos and video imagery used by other BRUVS programs.
5. Estimate the “quality” of the field of view by roughly measuring %water column, %seabed and %blocked in images to use as covariates in statistical models (see plates 1 and 2 below)
6. Develop and implement a quality assurance protocol to:
 - maintain and check a relational database linked by unique fields (such as an opcode and a “reader” name)
 - collect reference images of all fish species identified with standardised, custom CAABcodes

- identify “reader effects” introduced by experience gained versus staff turnover

Plate 1. Example of an excellent field of view (FOV) with an estimated “vis” of 30 metres where the proportion of the still image comprised of “water column” (A) is 60% and the pc.seabed is 40% (B). There is no” blockage” of the FOV by rough topographic features or epibenthos.

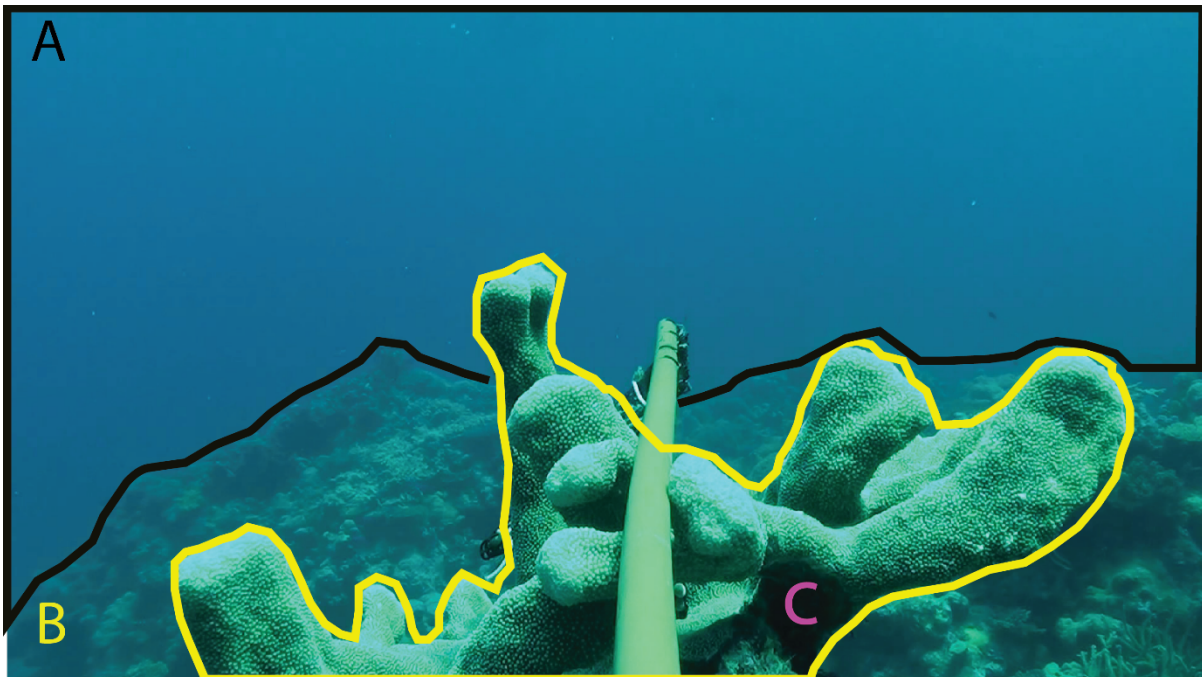
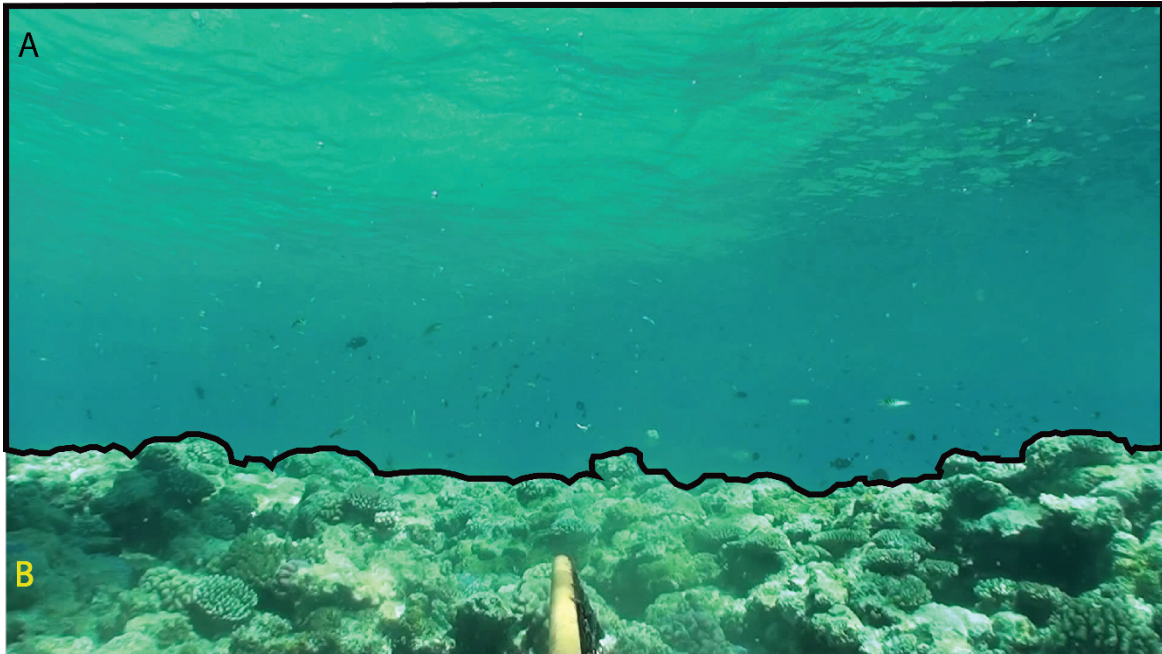


Plate 2. Example of a poor field of view (FOV) with an estimated “vis” of 30 metres where the proportion of the still image comprised of “water column” (A) is 50% and the pc.seabed is 50% (B), but there is pc.blockage of 30% (C).

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Appendix 1. Taxonomy of 257 species from 68 Families recorded on the NT BRUVS set at Bathurst Island, Charles Point and Lorna. Categorisation by target status (“prized”, “target” and “non”) is also shown.

Family	Genus	Species	CAABcode	target status
Acanthuridae	<i>Acanthurus</i>	<i>auranticavus</i>	37437005	non
	<i>Acanthurus</i>	<i>blochii</i>	37437007	non
	<i>Acanthurus</i>	<i>fowleri</i>	37437044	non
	<i>Acanthurus</i>	<i>grammoptilus</i>	37437002	non
	<i>Acanthurus</i>	<i>sp</i>	37437001	non
	NA	NA	37437000	non
Ambassidae	<i>Ambassis</i>	<i>spp</i>	37310901	non
Apogonidae	<i>Apogon</i>	<i>cavitiensis</i>	37327028	non
	<i>Apogon</i>	<i>neotes</i>	37327150	non
	<i>Apogon</i>	<i>spp</i>	37327901	non
	<i>Cheilodipterus</i>	<i>nigrotaeniatus</i>	99999999	non
	<i>Cheilodipterus</i>	<i>parazonatus</i>	37327092	non
	<i>Cheilodipterus</i>	<i>sp</i>	37327906	non
	NA	NA	37327926	non
Ariidae	<i>Arius</i>	<i>sp</i>	99379052	non
	<i>Arius</i>	<i>thalassinus</i>	37188001	non
	NA	NA	37188000	non
	<i>Neoarius</i>	<i>graeffei</i>	37188005	non
	<i>Neoarius</i>	<i>sp</i>	37188907	non
Atherinidae	NA	NA	37246000	non
Balistidae	NA	NA	37465900	non
Blenniidae	NA	NA	37408000	non
Brachaeluridae	<i>Brachaelurus</i>	<i>waddi</i>	37013007	non
Caesionidae	<i>Caesio</i>	<i>cuning</i>	37346018	non
	<i>Caesio</i>	<i>teres</i>	37346037	non
	NA	NA	37346931	non
	<i>Pterocaesio</i>	<i>digramma</i>	37346050	non
Caracanthidae	NA	NA	37289000	non
Carangidae	<i>Alepes</i>	<i>apercna</i>	37337010	non
	<i>Atule</i>	<i>mate</i>	37337024	non
	<i>Carangoides</i>	<i>equula</i>	37337013	non
	<i>Carangoides</i>	<i>malabaricus</i>	37337005	non
	<i>Carangoides</i>	<i>sp</i>	37337001	non
	<i>Caranx</i>	<i>ignobilis</i>	37337027	target
	<i>Caranx</i>	<i>lugubris</i>	37337053	target
	<i>Caranx</i>	<i>papuensis</i>	37337064	target
	<i>Caranx</i>	<i>sexfasciatus</i>	37337039	target
	<i>Caranx</i>	<i>sp</i>	99379125	target
	<i>Decapterus</i>	<i>sp</i>	99379222	non
	<i>Gnathanodon</i>	<i>speciosus</i>	37337012	target
	NA	NA	37337000	non
	<i>Pantolabus</i>	<i>radiatus</i>	37337047	non
	<i>Pseudocaranx</i>	<i>dentex</i>	37337062	non
	<i>Scomberoides</i>	<i>commersonnianus</i>	37337032	target
	<i>Scomberoides</i>	<i>lysan</i>	37337046	non
	<i>Scomberoides</i>	<i>sp</i>	37337905	non
	<i>Selaroides</i>	<i>leptolepis</i>	37337015	non
	<i>Ulua</i>	<i>aurochs</i>	37337041	non
	<i>Ulua</i>	<i>mentalis</i>	37337048	non
	<i>Ulua</i>	<i>sp</i>	37337929	non
Carcharhinidae	<i>Carcharhinus</i>	<i>limbatus</i>	37018039	non
	<i>Carcharhinus</i>	<i>melanopterus</i>	37018036	non
	<i>Carcharhinus</i>	<i>sp</i>	99379138	non
	<i>Carcharhinus</i>	<i>tilstoni</i>	37018014	non
	<i>Galeocerdo</i>	<i>cuvier</i>	37018022	non
	NA	NA	37018900	non
	<i>Negaprion</i>	<i>acutidens</i>	37018029	non
	<i>Rhizoprionodon</i>	<i>acutus</i>	37018006	non
Chaetodontidae	<i>Chaetodon</i>	<i>adiergastos</i>	37365033	non
	<i>Chaetodon</i>	<i>aureofasciatus</i>	37365013	non
	<i>Chaetodon</i>	<i>guentheri</i>	37365039	non
	<i>Chaetodon</i>	<i>sp</i>	37365905	non
	<i>Chelmon</i>	<i>marginalis</i>	37365007	non
	<i>Chelmon</i>	<i>muelleri</i>	37365015	non
	<i>Chelmon</i>	<i>sp</i>	99379164	non

Family	Genus	Species	CAABcode	target status
	<i>Coradion</i>	<i>chrysozonus</i>	37365004	non
	<i>Heniochus</i>	<i>acuminatus</i>	37365011	non
	<i>Heniochus</i>	<i>diphreutes</i>	37365005	non
	NA	NA	37365900	non
Chirocentridae	<i>Chirocentrus</i>	<i>dorab</i>	37087001	non
Clupeidae	NA	NA	37085922	non
Clupeidae	<i>Sardinella</i>	<i>gibbosa</i>	37085013	non
Dasyatidae	<i>Dasyatis</i>	<i>kuhlui</i>	37035004	non
	<i>Dasyatis</i>	<i>leylandi</i>	37035013	non
	<i>Dasyatis</i>	<i>thetidis</i>	37035002	non
	<i>Himantura</i>	<i>sp</i>	99379321	non
	<i>Himantura</i>	<i>toshi</i>	37035020	non
	<i>Himantura</i>	<i>uarnak</i>	37035003	non
	<i>Himantura</i>	<i>undulata</i>	37035026	non
	NA	NA	37035000	non
	<i>Taeniura</i>	<i>lymma</i>	37035009	non
Echeneidae	<i>Echeneis</i>	<i>naucratus</i>	37336001	non
	NA	NA	37336000	non
	<i>Remora</i>	<i>remora</i>	37336002	non
Elopidae	<i>Elops</i>	<i>hawaiensis</i>	37053001	non
	<i>Elops</i>	<i>sp</i>	37053000	non
Engraulidae	NA	NA	37086000	non
Ephippidae	NA	NA	37362904	non
	<i>Platax</i>	<i>batavianus</i>	37362002	non
	<i>Platax</i>	<i>orbicularis</i>	37362007	non
	<i>Platax</i>	<i>pinnatus</i>	37362006	non
	<i>Platax</i>	<i>teira</i>	37362004	non
	<i>Zabidius</i>	<i>novemaculeatus</i>	37362003	non
Gerreidae	<i>Gerres</i>	<i>oyena</i>	37349004	non
	<i>Gerres</i>	<i>sp</i>	37349901	non
	<i>Gerres</i>	<i>subfasciatus</i>	37349005	non
	NA	NA	37349000	non
	<i>Pentaprion</i>	<i>longimanus</i>	37349002	non
Ginglymostomatidae	<i>Nebrius</i>	<i>ferrugineus</i>	37013010	non
Glaucosomatidae	<i>Glaucosoma</i>	<i>magnificum</i>	37320002	non
Glaucostegidae	<i>Glaucostegus</i>	<i>typus</i>	37027010	non
Gobiidae	NA	NA	37428000	non
Gymnuridae	<i>Gymnura</i>	<i>sp</i>	37037901	non
Haemulidae	<i>Diagramma</i>	<i>pictum labiosum</i>	37350003	target
	NA	NA	37350000	target
	<i>Plectorhinchus</i>	<i>flavomaculatus</i>	37350007	target
	<i>Plectorhinchus</i>	<i>gibbosus</i>	37350012	target
	<i>Plectorhinchus</i>	<i>multivittatus</i>	37350018	target
	<i>Plectorhinchus</i>	<i>sp</i>	99379524	target
	<i>Pomadasys</i>	<i>kaakan</i>	37350011	target
	<i>Pomadasys</i>	<i>maculatus</i>	37350002	target
Hemigaleidae	<i>Hemigaleus</i>	<i>australiensis</i>	37018020	non
	<i>Hemipristis</i>	<i>elongata</i>	37018011	non
Hemiramphidae	NA	NA	37234000	non
Hemiscylliidae	<i>Chiloscyllium</i>	<i>punctatum</i>	37013008	non
	<i>Hemiscyllium</i>	<i>ocellatum</i>	37013014	non
Labridae	<i>Choerodon</i>	<i>cauteroma</i>	37384005	target
	<i>Choerodon</i>	<i>cyanodus</i>	37384072	target
	<i>Choerodon</i>	<i>rubescens</i>	37384039	target
	<i>Choerodon</i>	<i>schoenleinii</i>	37384010	target
	<i>Choerodon</i>	<i>sp</i>	99379173	target
	<i>Choerodon</i>	<i>vitta</i>	37384006	non
	<i>Coris</i>	<i>caudimacula</i>	37384092	non
	<i>Coris</i>	<i>pictoides</i>	37384096	non
	<i>Coris</i>	<i>sp</i>	37384912	non
	<i>Halichoeres</i>	<i>sp</i>	37384920	non
	<i>Labroides</i>	<i>dimidiatus</i>	37384028	non
	NA	NA	37384000	non
	<i>Scarus</i>	<i>ghobban</i>	37386001	non
	<i>Scarus</i>	<i>scaber</i>	99379999	non
	<i>Scarus</i>	<i>sp</i>	99379609	non
Latidae	<i>Psammoperca</i>	<i>waigiensis</i>	37310001	target
Leiognathidae	<i>Leiognathus</i>	<i>sp</i>	37341901	non
	NA	NA	37341000	non
Lethrinidae	<i>Lethrinus</i>	<i>atkinsoni</i>	37351013	target

Family	Genus	Species	CAABcode	target status
	<i>Lethrinus</i>	<i>harak</i>	37351017	target
	<i>Lethrinus</i>	<i>laticaudis</i>	37351006	target
	<i>Lethrinus</i>	<i>lentjan</i>	37351007	target
	<i>Lethrinus</i>	<i>nebulosus</i>	37351008	target
	<i>Lethrinus</i>	<i>sp</i>	37351902	target
	NA	NA	37351000	target
Lutjanidae	<i>Lutjanus</i>	<i>biguttatus</i>	37346039	target
	<i>Lutjanus</i>	<i>bitaeniatus</i>	37346025	target
	<i>Lutjanus</i>	<i>carponotatus</i>	37346011	target
	<i>Lutjanus</i>	<i>erythropterus</i>	37346005	target
	<i>Lutjanus</i>	<i>fulviflamma</i>	37346034	target
	<i>Lutjanus</i>	<i>johnii</i>	37346030	prized
	<i>Lutjanus</i>	<i>kasmira</i>	37346044	target
	<i>Lutjanus</i>	<i>lemniscatus</i>	37346010	target
	<i>Lutjanus</i>	<i>lutjanus</i>	37346008	target
	<i>Lutjanus</i>	<i>rivulatus</i>	37346016	target
	<i>Lutjanus</i>	<i>russellii</i>	37346065	target
	<i>Lutjanus</i>	<i>sp</i>	37346905	target
	<i>Lutjanus</i>	<i>vitta</i>	37346003	target
	NA	NA	37346932	target
Mobulidae	<i>Manta</i>	<i>birostris</i>	37041004	non
Monacanthidae	NA	NA	37465903	non
Mullidae	NA	NA	37355000	non
	<i>Parupeneus</i>	<i>barberinus</i>	37355022	non
	<i>Parupeneus</i>	<i>chrysopleuron</i>	37355016	non
	<i>Parupeneus</i>	<i>indicus</i>	37355005	non
	<i>Upeneus</i>	<i>tragula</i>	37355014	non
	<i>Upeneus</i>	<i>vittatus</i>	37355031	non
Muraenidae	<i>Gymnomuraena</i>	<i>sp</i>	37060905	non
	<i>Gymnothorax</i>	<i>favagineus</i>	37060016	non
	<i>Gymnothorax</i>	<i>thysoideus</i>	37060010	non
	NA	NA	37060000	non
Myliobatidae	<i>Aetobatus</i>	<i>narinari</i>	37039003	non
Nemipteridae	NA	NA	37347000	non
	<i>Nemipterus</i>	<i>sp</i>	37347901	non
	<i>Pentapodus</i>	<i>paradiseus</i>	37347028	non
	<i>Pentapodus</i>	<i>sp</i>	37347904	non
	<i>Scaevius</i>	<i>mili</i>	37347020	non
	<i>Scolopsis</i>	<i>affinis</i>	37347030	non
	<i>Scolopsis</i>	<i>sp</i>	99379616	non
Ophichthidae	NA	NA	37068000	non
Orectolobidae	<i>Eucrossorhinus</i>	<i>dasypogon</i>	37013011	non
Ostraciidae	<i>Rhynchostracion</i>	<i>rhinorhynchos</i>	37466009	non
Paralichthyidae	NA	NA	37460924	non
Pempheridae	<i>Parapriacanthus</i>	<i>ransonneti</i>	37357004	non
Platycephalidae	NA	NA	37296000	non
Plotosidae	NA	NA	37192000	non
	<i>Plotosus</i>	<i>lineatus</i>	37192002	non
Polynemidae	<i>Eleutheronema</i>	<i>tetradactylum</i>	37383004	non
	NA	NA	37383000	non
	<i>Polydactylus</i>	<i>multiradiatus</i>	37383002	non
Pomacanthidae	<i>Chaetodontoplus</i>	<i>duboulayi</i>	37365009	non
	<i>Chaetodontoplus</i>	<i>mesoleucus</i>	37365083	non
	NA	NA	37365901	non
	<i>Pomacanthus</i>	<i>sexstriatus</i>	37365010	non
Pomacentridae	<i>Abudefduf</i>	<i>bengalensis</i>	37372003	non
	<i>Abudefduf</i>	<i>septemfasciatus</i>	37372010	non
	<i>Abudefduf</i>	<i>sp</i>	37372901	non
	<i>Abudefduf</i>	<i>whitleyi</i>	37372014	non
	<i>Chromis</i>	<i>sp</i>	37372907	non
	<i>Chrysiptera</i>	<i>sp</i>	37372908	non
	<i>Dischistodus</i>	<i>sp</i>	37372910	non
	<i>Hemiglyphidodon</i>	<i>plagiometopon</i>	37372081	non
	NA	NA	37372000	non
	<i>Neopomacentrus</i>	<i>filamentosus</i>	37372090	non
Rachycentridae	<i>Rachycentron</i>	<i>canadum</i>	37335001	target
Rhinidae	<i>Rhynchobatus</i>	<i>australiae</i>	37026005	non
	<i>Rhynchobatus</i>	<i>palpebratus</i>	37026004	non
	<i>Rhynchobatus</i>	<i>sp</i>	37026900	non
Rhinobatidae	NA	NA	37027000	non

Family	Genus	Species	CAABcode	target status
Sciaenidae	<i>Protonibea</i>	<i>diacanthus</i>	37354003	prized
Scombridae	NA	NA	37441000	target
	<i>Scomberomorus</i>	<i>commerson</i>	37441007	target
	<i>Scomberomorus</i>	<i>queenslandicus</i>	37441014	target
	<i>Scomberomorus</i>	<i>semifasciatus</i>	37441018	target
	<i>Scomberomorus</i>	<i>sp</i>	99379624	target
Scorpaenidae	NA	NA	37287900	non
Scyliorhinidae	<i>Atelomycterus</i>	<i>macleayi</i>	37015028	non
Serranidae	<i>Anyperodon</i>	<i>leucogrammicus</i>	37311085	target
	<i>Cephalopholis</i>	<i>boenak</i>	37311008	target
	<i>Cephalopholis</i>	<i>sp</i>	37311904	non
	<i>Diplopriion</i>	<i>bifasciatum</i>	37312002	non
	<i>Epinephelus</i>	<i>areolatus</i>	37311009	target
	<i>Epinephelus</i>	<i>coioides</i>	37311007	target
	<i>Epinephelus</i>	<i>hexagonatus</i>	37311064	target
	<i>Epinephelus</i>	<i>lanceolatus</i>	37311061	target
	<i>Epinephelus</i>	<i>maculatus</i>	37311011	target
	<i>Epinephelus</i>	<i>malabaricus</i>	37311150	target
	<i>Epinephelus</i>	<i>merra</i>	37311063	target
	<i>Epinephelus</i>	<i>quoyanus</i>	37311040	target
	<i>Epinephelus</i>	<i>rivulatus</i>	37311022	target
	<i>Epinephelus</i>	<i>sp</i>	37311911	target
	NA	NA	37311954	target
	<i>Plectropomus</i>	<i>areolatus</i>	37311081	target
	<i>Plectropomus</i>	<i>leopardus</i>	37311078	target
	<i>Plectropomus</i>	<i>maculatus</i>	37311012	target
	<i>Plectropomus</i>	<i>oligacanthus</i>	37311162	target
	<i>Plectropomus</i>	<i>sp</i>	37311940	target
Siganidae	NA	NA	37438000	non
	<i>Siganus</i>	<i>corallinus</i>	37438008	non
	<i>Siganus</i>	<i>javus</i>	37438005	non
	<i>Siganus</i>	<i>lineatus</i>	37438010	non
	<i>Siganus</i>	<i>punctatus</i>	37438003	non
	<i>Siganus</i>	<i>sp</i>	99379643	non
Sillaginidae	NA	NA	37330000	non
Sphyraenidae	NA	NA	37382000	target
	<i>Sphyraena</i>	<i>barracuda</i>	37382008	target
	<i>Sphyraena</i>	<i>jello</i>	37382004	target
	<i>Sphyraena</i>	<i>obtusata</i>	37382001	target
	<i>Sphyraena</i>	<i>sp</i>	37382901	target
Sphyrnidae	NA	NA	37019000	non
	<i>Sphyrna</i>	<i>mokarran</i>	37019002	non
Stegostomatidae	<i>Stegostoma</i>	<i>fasciatum</i>	37013006	non
Terapontidae	NA	NA	37321000	non
	<i>Terapon</i>	<i>jarbua</i>	37321002	non
	<i>Terapon</i>	<i>puta</i>	37321006	non
	<i>Terapon</i>	<i>theraps</i>	37321003	non
Tetraodontidae	<i>Arothron</i>	<i>stellatus</i>	37467014	non
	<i>Lagocephalus</i>	<i>sp</i>	37467900	non
	NA	NA	37467000	non
Trichiuridae	<i>Trichiurus</i>	<i>lepturus</i>	37440004	non

Appendix 2. Summaries of the 14 terminal nodes (assemblages) defined by the mvpart in Figure 17. Number of BRUVS samples in each leaf node (n), total species richness (S), total number of fish ($\sum \max N$), the number of DLI indicator species (nDLI), and the ranges and means in species richness (S) and abundance (N). The abundance (N) is the $\sum \max N$ for the samples in each leaf node.

node	n	long.name	S	sum (maxN)	nDLI	Srange	Smean	Nrange	Nmean
16	35	Charles.Out.loVis	50	385	1	(2 - 12)	(6.4 ± 2.8)	(2 - 23)	(11 ± 5.2)
17	30	Charles.Out.hiVis	59	474	0	(2 - 15)	(8.6 ± 3.3)	(2 - 47)	(15.8 ± 9.1)
9	53	Charles.In	66	1054	4	(1 - 17)	(7.7 ± 3.1)	(1 - 68)	(19.9 ± 14.4)
20	19	Bathurst.In.noVis	23	127	2	(2 - 9)	(4.4 ± 1.8)	(2 - 24)	(6.7 ± 5)
21	48	Bathurst.In.badVis	88	938	0	(2 - 17)	(8.2 ± 3.8)	(2 - 134)	(19.5 ± 22.8)
44	28	Bathurst.Out.avSoak .loVis	75	518	0	(2 - 17)	(7.3 ± 4.1)	(2 - 96)	(18.5 ± 21.6)
45	29	Bathurst.Out.avSoak .hiVis	98	923	0	(1 - 23)	(12 ± 5.4)	(1 - 64)	(31.8 ± 17.7)
23	7	Bathurst.Out.longSoak	57	463	9	(13 - 25)	(18.6 ± 4.1)	(31 - 108)	(66.1 ± 27.8)
12	46	Lorna 2016	90	932	1	(1 - 18)	(8.3 ± 4.6)	(1 - 154)	(20.3 ± 23.4)
13	70	Lorna 2017	100	1910	0	(2 - 24)	(11.4 ± 4.1)	(2 - 97)	(27.3 ± 17.8)
28	14	Lorna.2020	48	412	1	(8 - 17)	(12.6 ± 2.8)	(14 - 48)	(29.4 ± 9.3)
29	15	Lorna.2023	49	596	1	(7 - 26)	(14 ± 4.7)	(13 - 134)	(39.7 ± 31.2)
30	12	Lorna.pre19.long	50	605	1	(11 - 26)	(18.2 ± 4.6)	(19 - 93)	(50.4 ± 20)
31	2	Lorna.pre19.short	26	342	7	(18 - 19)	(18.5 ± 0.7)	(162 - 180)	(171 ± 12.7)

Appendix 3. Summaries of the indicator species and their DLI values for all 20 nodes from the stump (“All”) to the 14 leaves defined by the mvpart in Figure 17. Prized species are highlighted in red. The higher the DLI values, the closer specificity and fidelity has to a node. The stripey snapper (*Lutjanus carponotatus*) and goldspot estuary cod (*Epinephelus coioides*) were ubiquitous with highest DLI at the stump.

nodename	Tree node	dli_list
All	1	<i>Lutjanus carponotatus</i> (65), <i>Epinephelus coioides</i> (46), <i>Labridae</i> (44), <i>Lutjanus bitaeniatus</i> (37), <i>Zabidius novemaculeatus</i> (34), <i>Carcharhinidae</i> (19), <i>Sphyaenidae</i> (9), <i>Scombridae</i> (5)
Bathurst_Charles	2	<i>Lutjanus russellii</i> (5)
Lorna	3	<i>Lethrinus laticaudis</i> (53), <i>Chaetodontoplus duboulayi</i> (49), <i>Negaprion acutidens</i> (11)
Charles	4	<i>Pomadasys kaakan</i> (41), <i>Pantolabus radiatus</i> (11), <i>Ulua aurochs</i> (8), <i>Lutjanidae</i> (7), <i>Caracanthidae</i> (4)
Bathurst	5	<i>Gymnothorax favagineus</i> (8)
Lorna_pre19	6	<i>Cheilodipterus parazonatus</i> (21)
Lorna_post18	7	<i>Choerodon schoenleinii</i> (51), <i>Acanthurus grammoptilus</i> (42), <i>Diagramma pictum labiosum</i> (35), <i>Pomacanthus sexstriatus</i> (31), <i>Plectorhinchus gibbosus</i> (21), <i>Nemipteridae</i> (16)
Charles_In	9	<i>Pomadasys maculatus</i> (22), <i>Eleutheronema tetradactylum</i> (14), <i>Polydactylus multiradiatus</i> (10), <i>Rhizoprionodon acutus</i> (4)
Bathurst_In	10	<i>Lutjanus johnii</i> (25)
Bathurst_Out	11	<i>Scomberoides commersonnianus</i> (7)
Lorna_2016	12	<i>Choerodon cyanodus</i> (8)
Lorna_post19	14	<i>Caranx papuensis</i> (36), <i>Chelmon marginalis</i> (31), <i>Scomberomorus commerson</i> (24), <i>Plectropomus leopardus</i> (24)
Lorna_pre19	15	<i>Cheilodipterus</i> sp (64), <i>Serranidae</i> (43), <i>Pomacentridae</i> (30), <i>Dasyatidae</i> (12)
Charles_Out_loVis	16	<i>Terapon jarbua</i> (16)
Bathurst_In_noVis	20	<i>Ariidae</i> (24), <i>Protonibea diacanthus</i> (15)
Bathurst_Out_longSoak	23	<i>Caesio teres</i> (64), <i>Chaetodontidae</i> (37), <i>Apogonidae</i> (36), <i>Caranx ignobilis</i> (19), <i>Cephalopholis boenak</i> (17), <i>Lutjanus lemniscatus</i> (14), <i>Lutjanus</i> sp (11), <i>Psammoperca waigiensis</i> (11), <i>Gerreidae</i> (5)
Lorna_2020	28	<i>Plectropomus maculatus</i> (24)
Lorna_2023	29	<i>Sphyaena barracuda</i> (11)
Lorna_2019_long	30	<i>Siganus lineatus</i> (23)
Lorna_2019_short	31	<i>Selaroides leptolepis</i> (72), <i>Gnathanodon speciosus</i> (51), <i>Echeneis naucrates</i> (40), <i>Nebrius ferrugineus</i> (39), <i>Carangidae</i> (37), <i>Scomberomorus semifasciatus</i> (34), <i>Carcharhinus melanopterus</i> (15)