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# Vulnerable Marine Ecosystems (VMEs) in the Northeast Part of the North Pacific Fisheries Commission Convention Area

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### ABSTRACT

This working paper is an update to Canada's proposed quantitative approach to identifying Vulnerable Marine Ecosystems (VMEs) described in NPFC-2021-SSC BFME-WP05 (Warawa et al. 2021). In this approach we use predictive habitat models to identify areas likely to be VMEs and visual data to identify VMEs, as outlined by the North Pacific Fisheries Commission (NPFC) framework for identifying data that can be used to identify VMEs in the NW and NE parts of the NPFC's Convention Area (NPFC 2021). Our quantitative approach is based on work by Rowden et al. (2020) who identify thresholds related to the amount of VME indicator taxa in an area and how it contributes to an increase in associated species richness as a result of providing structural complexity. Canada's proposed approach to identifying VMEs shows an example of an extension of the Rowden et al. (2020) approach to presence absence data and models. Our preliminary results from the Cobb-Eickelberg seamount chain study area detect a VME density threshold of 0.57 VME indicators taxa/m<sup>2</sup> and a VME occurrence threshold of 0.78. Applying these thresholds to visual data and predictive habitat models result in a total area of 750m<sup>2</sup> identified as VMEs on Cobb seamount and a total area of 1,542 km<sup>2</sup> identified as likely to be VMEs along the Cobb-Eickelberg seamount chain, respectively.

#### INTRODUCTION

The United Nations General Assembly (UNGA) Resolution 61/105 calls on states to protect VMEs from destructive fishing practices. The Food and Agriculture Organization (FAO) published guidelines for the management of deep-sea fisheries in international waters, which outline five criteria of areas, habitats, or ecosystems that could be used to identify VMEs: (1) uniqueness or rarity, (2) functional significance of the habitat, (3) fragility, (4) life-history traits of component species that make recovery difficult, and (5) structural complexity (FAO 2009).

Regional Fisheries Management Organizations (RFMOs) are encouraged to implement the FAO guidelines. In response, the North Pacific Fisheries Commission (NPFC) has developed a list of taxonomic groups accepted as VME indicator taxa, which include: (*Alcyonacea* (excluding Gorgonians), *Antipatharia*, *Gorgonacea* (now within the *Alcyonacea*), and *Scleractinia*) as VME indicator taxa (NPFC 2019, 2021a). Further, the NPFC has outlined a framework on data that can be used to use to identify VMEs and areas likely to be VMEs (NPFC 2021b). Despite the FAO guidelines, and frameworks for identifying VMEs, there are few case-specific quantitative and repeatable definitions that have been used to identify VMEs both within the NPFC Convention Area (CA) or around the world.

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Of the few case-specific examples of methods used to identifying VMEs, the methods and data are not generally applicable to the Northeastern part of the NPFC CA, in part because they rely on analysis of VME indicator incidental catch data. Many approaches to identifying VMEs rely on using qualitative information and expert judgement, which can be inconsistent and lack transparency (Morato et al. 2018). Morato et al. (2018) emphasize that it would be advantageous for analysts to develop robust and repeatable quantitative methods to identify VMEs. For example, Kenchington et al. (2014) used a kernel density estimation approach to analyze research trawl survey data and identified significant concentrations of VME indicator biomass as VMEs. This approach could not be applied to the Northeastern part of the NPFC CA because research surveys have not been undertaken there. There is also limited incidental catch of VME indicator taxa with the longline gears used by Canada to fish for Sablefish in the CA (no VME indicator taxa were found in the fisheries database as incidental catch for the Sablefish fisheries in the years 2006-2021).

The steps outlined in Canada's proposed approach describe a potential method to quantitatively identify VMEs and areas likely to be VMEs using the above guidance, criteria, and framework. This working paper is an update to Canada's proposed approach to identifying Vulnerable Marine Ecosystems (VMEs) described in NPFC-2021-SSC BFME-WP05 (Warawa et al. 2021). The main updates in this revision include:

- Ensemble modelling vs Maxent modelling for suitable habitat predictions of VME indicator taxa
- Improved VME threshold modelling
- Identification of VMEs using a density-based threshold in addition to identifying areas likely to be VMEs using an occurrence threshold

Our objective is to outline Canada's refined approach to identifying VMEs and areas likely to be VMEs and have this methodology endorsed as one approach that could be used to identify VMEs in the NPFC's CA by the Scientific Committee.

# MATERIALS AND METHODS

### **Study Area**

Our study area is the Cobb-Eickelberg seamount chain located in the eastern NPFC CA approximately 450 km offshore Vancouver Island, Canada (Figure 1). The chain is composed of eight named seamounts ranging in pinnacle depth of approximately 24 m (Cobb seamount) (Parker & Tunnicliffe 1994) to 1200 m (Hoh seamount) (Harris et al. 2014). The Canadian commercial Sablefish fishery has been active in the study area since the 1980s using mainly longline trap and some longline hook and line gear. Historically there are records of Japan using stern trawlers, bottom longline, and gillnet gear as early as the 1970's, as well as the USA using bottom longline, pot traps and mid-water trawl gear from the 1980s until 2003 (Douglas, 2011).



Figure 1. Study area map of the Cobb-Eickelberg seamount chain in the NPFC CA. The inset shows the location of autonomous underwater vehicle (AUV) transects completed on Cobb Seamount in 2012 (see Curtis et al. 2012).

# General approach to identifying VMEs and areas likely to be VMEs

The main steps in our refined general approach are: 1) develop quantitative VME thresholds, 2) gather data on VME indicator taxa distribution, 3) apply the threshold to the data, 4) identify VMEs or areas likely to be VMEs. The data and criteria differ for identifying VMEs and areas likely to be VMEs (Figure 2). Identifying VMEs is based on applying a density VME threshold to visual data and any areas with visual data showing VME indicator taxa equal to or greater than the threshold are considered VMEs. Identifying areas that are likely to be VMEs is based on applying an occurrence VME threshold to predictive habitat models. Areas where at least one VME indicator taxon has habitat suitability predictions equal to or above the threshold is considered likely to be a VME.

	Step 1. Develop quantitative VME threshold	•	Step 2. Gather data on VME indicator taxa distribution	•	Step 3. Apply the threshold to the data	•	Step 4. Identify VMEs or areas likely to be VMEs
Identifying VMEs	VME indicator taxa <b>density threshold</b>	•	Calculate VME indicator taxa <b>density from</b> <b>visual data</b>	•	Apply the VME visual density threshold to the visual data to identify areas as VMEs		Areas where VME indicator are taxa in densities equal to or greater than the VME visual density threshold are considered VMEs
Identifying areas likely to be VMEs	VME indicator taxa occurrence threshold	•	Develop predictive habitat models	•	Apply the VME visual occurrence threshold to PHMs		Areas where at least one VME indicator taxa has PHM predictions above the VME occurrence threshold are considered areas likely to be VMEs

Figures 2. Steps used to identify VMEs and areas likely to be VMEs.

We use the four groups of corals recognized by NPFC as VME indicator taxa for identifying areas that are VMEs and likely to be VMEs in the NE part of the NPFC CA; the orders are *Antipatharia* (black corals), *Scleractinia* (stony corals), and *Alcyonacea* (soft corals and gorgonian corals). The NPFC recognizes gorgonian and soft corals as separate groups and they can be split into taxonomically valid groups using a family level of identification (see Miyamoto et al. 2017).

# Visual Data

Visual data were collected from Cobb Seamount in 2012 (Curtis et al. 2015). Photos were taken using a SeaBED-class autonomous underwater vehicle (AUV) deployed by the National Oceanic and Atmospheric Administration (NOAA), capable of diving to 1,400 m. Curtis et al. (2015) describe the survey, including specifics of the submersible setups, cameras, deployments, and sampling design, and Du Preez et al. (2015) provide a photo-documented checklist of species observed at Cobb Seamount in 2012. We used the fully annotated dataset by NOAA which consisted of 2506 AUV photos taken from 4 transects with an average length of 1805 m ranging from 435 – 1154 m in depth. Transects were divided into area-standardized segments of 50 m<sup>2</sup> for analysis.

# Predictive habitat models for VME indicator taxa

In this update, we used a performance-weighted ensemble modeling approach instead of the Maxent approached used by Warawa et al. 2021). Ensemble modelling has been shown to improve model performance and interpretability (Araújo and New 2007). Three modeling techniques were used that have successfully predicted the distribution of cold-water corals in other studies (e.g. Rooper et al. 2017; Morato et al. 2020; Georgian et al. 2021): Boosted Regression Tree (BRT), Generalized Additive Models (GAM), and Random Forest (RF). Each model outputs a habitat suitability score between 0-1, with 1 indicating more suitable predicted habitat. The outputs of individual model approaches (BRT, GAM, and RF) were combined using the AUC weighted-average into a single ensemble model for each taxon. As each modeling approach

relies on differing underlying structures and distinct statistical assumptions, they are therefore likely to produce dissimilar outputs and predictions (see Robert et al. 2016). Ensemble modeling can produce more robust predictions that are less reliant on model selection and parameterization (Araújo and New 2007). BRT, GAM, and RF models were built and tested using a combination of 'biomod2' (Thuiller et al. 2016), 'gbm' (Ridgeway 2004), 'dismo' (Hijmans et al. 2015), 'mgcv' (Wood 2006), and 'randomForest' (Liaw and Wierner 2002) in R (v3.6.1; R Core Team 2019). BRT models were built using a minimum of 3,000 trees, an assumed Bernoulli distribution, and an interaction depth of 7 to prevent limiting interactions between terms. After testing a variety of model parameters during preliminary construction, GAMs were created using a binomial distribution and four degrees of freedom. RF models were constructed as classification models using 1001 trees and a node size of five.

<u>Dependent data</u> – The original dataset of georeferenced observations of NPFC's VME indicator taxa in the NE Pacific Ocean from four data sources (see Warawa et al. 2021) was used in this update (Figure 3). Observations of presence from scientific data and museum collections were obtained from the NOAA deep-sea coral data portal (https://deepseacoraldata.noaa.gov/). Presence or absence of VME indicator taxa were also obtained from (1) standardized bottom trawl catch data from research surveys in the Gulf of Alaska, Aleutian Islands and eastern Bering Sea, (2) standardized bottom trawl catch data from research surveys on the U.S. West Coast of Washington, Oregon and California (Stauffer 2004, Nottingham et al. 2018)

Records were identified to various levels of taxonomy and updated to reflect current taxonomic relationships with the World Register of Marine Species (WoRMS, Horton et al. 2021). Records with at least an order (black corals, stony corals) or family (gorgonian corals, non-gorgonian soft corals) level of identification were pooled for use as the presence data for each of their respective predictive habitat models (PHMs). Final sets of presence records used for PHM model development were also spatially restricted to those occurring within the four marine ecoregions of the world (MEOW) that characterize the oceanographic conditions from the Gulf of Alaska to the West Coast of North America (Spalding et al. 2007). No commercial bycatch records were included in the data used for PHMs. Because the trawl surveys occurred only on the continental shelf and slope, most of the data are not from NPFC seamounts. All the absence records came from the continental shelf and a total of 42 presence records among the four NPFC indicator taxa groups were from offshore seamounts (4 black corals, 22 gorgonian, 16 non-gorgonian soft, zero stony). We prioritized keeping as many of these rare seamount observations in our models as possible and addressed this sampling bias by restricting the inclusion of offshore presence records to those occurring within the sampling depth range of the absence records, which sampled a maximum depth of 1600 m.



Figure 3. Species presence and absence data used in PHM models. (a) Distribution of VME indicator taxa presence records and (b) Distribution of trawl absence data. Records were geographically limited to those occurring within four marine ecoregions and the adjacent international waters (Spalding et al. 2007). Seamount areas are from Harris et al. (2014). Note that the four groups of VME indicator taxa are plotted in panel (a) but are not visible because of the overlapping points.

Independent data – We used a set of 30 environmental layers gridded at a 1 km<sup>2</sup> resolution including bathymetry-derived terrain metrics, physiochemical variables, and oceanographic properties that are known to be strong predictors of benthic species distributions (see Table 1 in Annex 1 for a summary of details, native resolutions, and units associated with the environmental data layers). Terrain metrics included aspect (as eastness and northness), general curvature, cross-sectional curvature, longitudinal curvature, roughness, slope, Topographic Position Index (TPI), and Vector Ruggedness Measure (VRM). Water chemistry data were obtained as depth-binned variables from a variety of sources and interpolated to seafloor conditions using the approach in Davies and Guinotte (2011). Depth-binned carbon data were obtained from Steinacher et al. (2009), including total alkalinity, dissolved inorganic carbon, and the saturation states of aragonite and calcite. Seafloor salinity, dissolved oxygen, temperature, and nutrients (phosphate, nitrate, and silicate) were obtained from the World Ocean Atlas (Boyer et al. 2018). Particulate organic flux to the seafloor was obtained from Lutz et al. (2007), and regional and vertical current velocities were obtained from Carton et al. (2005). A suite of surface variables was obtained at a 4 km resolution and regridded to a 1 km resolution with no additional interpolation, including chlorophyll *a*, photosynthetically available radiation (PAR), sea surface temperature, particulate organic carbon, and particulate inorganic carbon.

Variable Selection and Model Performance – As the inclusion of highly correlated variables can reduce model performance and interpretably (Huang et al. 2011), collinearity among predictors was addressed by examining variance inflation factors (VIF) and iteratively reducing the set of environmental data layers used for each model until the final subset of variables all had VIF < 10 (see Nephin et al. 2020 for using VIF < 10) (Table 1). A ten-fold cross validation procedure was used to assess model performance by randomly partitioning the presence and absence data into 30% testing data and 70% training data over ten model runs. Model performance was assessed via three standard metrics: Area Under the Curve (AUC), kappa, and the true skill statistic (TSS). AUC is the most commonly reported metric, with a score of 0.5 indicating model performance no better than random and scores closer to 1 indicating better model performance. Kappa compares the calculated model accuracy with the result expected by chance, with lower values indicating more random performance and higher values indicating better-than-expected performance. TSS is similar to kappa, but is independent of species prevalence (which is generally unknowable; Allouche et al. 2006). Final models used the entire set of species presences and absences from each taxon to generate maps of predicted suitable habitat.

Table 1. Input occurrence and environmental data used in model construction: Number of 1 km<sup>2</sup> gridded presence and absence records, and the subset of environmental data layers used as predictors. TPI is the Topographic Position Index at the corresponding scale in meters, PAR is the Photosynthetically Active Radiation, and SST is Sea Surface Temperature. Table 1 in Annex 1 provides details on the full set of environmental variables considered for use in PHM development.

VME taxa	Presence records	Absence records	Environmental variables included in final model
Black corals	497	22,145	Chlorophyl-a, cross-sectional curvature, current angle, current aspect, current direction, east-facing aspect, north-facing aspect, oxygen,

			PAR, particulate organic carbon, regional current velocity, slope, SST, TPI20000, vertical flow velocity, roughness
Stony corals	291	22,145	Omega Aragonite, Chlorophyl-a, cross-sectional curvature, current aspect, current direction, east-facing aspect, north-facing aspect, oxygen, PAR, particulate organic carbon, regional current velocity, slope, SST, TPI20000, roughness
Gorgonian corals	1,378	22,145	Omega calcite, Chlorophyl-a, current direction, east-facing aspect, north-facing aspect, oxygen, PAR, particulate organic carbon, regional current velocity, slope, SST, TPI5000, TPI20000, roughness
Non- gorgonian soft corals	611	22,145	Omega calcite, Chlorophyl-a, cross-sectional curvature, current direction, current angle, east-facing aspect, north-facing aspect, oxygen, PAR, regional current velocity, slope, SST, TPI20000, roughness

# **Quantitative VME threshold**

Our quantitative definition of a VME is based on the FAO VME criterion of structural complexity, where increasing structurally complex habitat has been shown to increase the richness of associated species. As associated richness increases, the number of species that can be supported is hypothesized to reach a threshold as niches become occupied, after which it plateaus (see discussion in Rowden et al. 2020). We use the density or occurrence of VME indicator taxa to quantify structural complexity and aim to identify how much structurally complex habitat corresponds to maximum associated species richness. Areas with VME indicator taxa at or above that threshold value will be considered a VME. Due to limited visual data available we combine the VME indicator taxa into a single threshold, but we recognize there may be taxa-specific thresholds.

The VME threshold values based on density or occurence are calculated from the 2012 visual survey data from Cobb Seamount (see Curtis et al. 2015). For each transect segment, the associated species richness is calculated along with metrics representing the density or presence of VME taxa. We use two VME threshold metrics: 1) VME indicator taxa density measured as the number of individuals per meter, hereafter referred to as the "VME density threshold", which is applied to visual data annotated with density values and used to identify VMEs, and 2) the proportion of transect segment with VME indicator taxa PHMs and used to identify areas likely to be VMEs. The metrics are calculated as follows:

 $VME \text{ density threshold} = \frac{\# \text{ of VME indicator taxa individuals per transect segment}}{\text{Segment area } (m^2)}$  $VME \text{ occurrence threshold} = \frac{\# \text{ of images with VME indicator taxa per transect segment}}{\# \text{ of images per transect segment}}$ 

To identify the breakpoint, or threshold, for each VME threshold metric we used piecewise linear regression models built using the segmented() R package (Muggeo 2008). The model variables were selected using a backward stepwise selection method and the final model was identified based on AIC value.

#### **RESULTS AND DISCUSSION**

#### Predictive habitat models for VME indicator taxa

BRT, GAM, and RF models developed using presence-absence data performed well with test AUC scores ranging from 0.795–0.898, kappa of 0.138–0.501, and TSS of 0.489–0.656 among all taxa (Table 2). The most important predictors varied among taxa and modeling approaches, with dissolved oxygen, chlorophyll *a*, roughness, aspect, slope, TPI-20000, PAR, and the saturation state of calcite generally contributing significantly to models (Table 3). Model predictions varied both among taxa and modeling approach (Figure 4). However, shared areas of high habitat suitability in the final ensemble models were generally concentrated along the continental shelf in domestic waters and mostly at seamount areas within the international waters of the NPFC CA (Figure 4). These results mirror those of Chu et al. (2019) who used a similar PHM approach on a subset of the same presence and absence data. The complimentary findings reinforce the importance of the expansive oxygen minimum zone in the Northeast Pacific Ocean and its influence on the distribution of VME indicator taxa in this region.

Таха	Model	TSS	ROC	Карра
Black	RF	0.489±0.038	0.807±0.020	0.138±0.018
	BRT	0.592±0.027	0.858±0.020	0.227±0.021
	GAM	0.596±0.037	0.863±0.015	0.231±0.023
Stony	RF	0.537±0.056	0.797±0.031	0.439±0.053
	BRT	0.541±0.048	0.869±0.019	0.452±0.056
	GAM	0.530±0.034	0.842±0.019	0.408±0.057
Gorgonian	RF	0.550±0.018	0.852±0.006	0.413±0.017
	BRT	0.558±0.021	0.861±0.008	0.429±0.018
	GAM	0.521±0.016	0.834±0.008	0.353±0.015
Soft	RF	0.544±0.036	0.795±0.021	0.494±0.040
	BRT	0.656±0.030	0.898±0.015	0.501±0.035
	GAM	0.596±0.026	0.886±0.012	0.474±0.029

Table 2. Model evaluation of testing data as assessed via a ten-fold cross validation procedure.

Table 3. Summary of final model parameters. AUC of the ensemble model and the top three most important predictor variables based on their relative importance in each model are presented (given as the average importance across BRT, GAM, and RF models). Variable acronyms: PAR – photosynthetically active radiation, POC – particulate organic carbon, TPI-20000 – topographic position index at a 20,000 m scale, SST – Sea Surface Temperature. The full ranked list of variable importance is provided in Table 2 of Annex 1.

VME group	Ensemble AUC	1 <sup>st</sup> ranked	2 <sup>nd</sup> ranked	3 <sup>rd</sup> ranked
Black corals	0.898	Dissolved Oxygen (28.9%)	PAR (21.4%)	POC (9.5%)
Stony corals	0.917	SST (28.0%)	Regional current flow (19.7%)	Roughness (14.8%)

Gorgonian corals	0.880	Eastness (26.4)	Slope (22.2)	Chlorophyll <i>a</i> (9.2%)
Non-gorgonian soft corals	0.918	Roughness (26.0%)	Chlorophyll a (19.1%)	TPI-20000 (13.6%)



Figure 4. Ensemble model predictions of habitat suitability index (HSI) for the four NPFC VME indicator taxa in the NE Pacific Ocean. The high habitat suitability areas in the northeast part of the NPFC's CA (Canada's EEZ boundary indicated by a line) occur at seamounts. Model predictions have been restricted to the maximum depth of 1,600 m.

Identifying areas that are likely to be VMEs using PHMs will be strongly influenced by the taxa being modelled. Although our PHM models performed well, the NPFC's VME indicator taxa groups (black corals, stony corals, gorgonians and non-gorgonian soft corals) are taxonomically broad and capture a wider range of habitat conditions than what species-specific PHMs would resolve. Ideally, we would develop PHMs for taxa at lower taxonomic levels (e.g., species or family) which could reduce the amount of species-specific habitat requirements being pooled into a single model. This could improve how well our PHMs predict the occurrence of VME indicator taxa.

### VME visual thresholds

Visual threshold metrics of occurrence and density of VME indicator taxa was calculated for  $n = 221 50 m^2$  divisions of the AUV transects on Cobb Seamount. All four VME indicator taxa were represented in the AUV data, with black and gorgonian coral being the most abundant (see Table 1 in Annex 2 for a list of observed taxa).

Associated species richness ranged from 1 to 16 per segment of the AUV transects with a mean of 7.5. A general comparison of model fit showed the piecewise regression fit the data better than a linear regression which indicates a threshold relationship occurring in our data. In addition, Davies' test from the segmented() R package detected a non-zero difference in the slope of the response variables, further indicating a break point in the data.

The VME density ranged from 0 to 1.14 individuals/m<sup>2</sup> per 50 m<sup>2</sup> segments of AUV transect. The best model to predict species richness based on VME density was a segmented linear model using VME density, depth, and transect as predictor variables. This model resulted in a threshold of 0.57 individuals/m<sup>2</sup> (95% CI = 0.17,  $adjR^2 = 0.35$ ) (Figure 5a). In comparison, Rowden et al. (2020) identified an average threshold of 0.11 for the number of coral heads per m<sup>2</sup> at the same spatial scale.

The proportion of 50 m<sup>2</sup> AUV transects where VME taxa occurred ranged from 0 to 1, where 1 indicated that all images for that transect segment contained at least one VME indicator taxon (Figure 5b). The best model to predict species richness using visual occurrence values was a segmented linear model using occurrence of VME and transect as predictors. This model resulted in a threshold where the proportion of transect with one or more VME indicator taxa occurring is 0.78 (95% CI = 0.13, adjR<sup>2</sup> = 0.35) (Figure 5b).



Figure 5. Associated species richness plotted as a function of the density (a) or occurrence (b) of VME indicator taxa. Piecewise regressions indicate the location of the a) visual density threshold and b) visual occurrence threshold. The black square along bottom indicates the threshold breakpoint and the accompanying line represents the 95% CI of the breakpoint. Shading indicates 95%CI for the piecewise models.

# Areas that are VMEs and likely to be VMEs

VMEs were identified on three out of the four AUV transects on Cobb seamount. 6.7% of transect segments had density values above the VME density threshold of 0.56 individuals/m<sup>2</sup>. This resulted in 15 out of the 221 50 m<sup>2</sup> areas identified as VMEs ranging in depth from approximately 500 m to 1150 m (Figure 6). Only a total of 0.01 km<sup>2</sup> of Cobb Seamount has been assessed for VMEs using visual data, of which 0.00075 km<sup>2</sup> was identified as such in this study.



Figure 6. Areas that are identified as VMEs (15 50 m<sup>2</sup> transect segments) based on visual data that meets or exceeds the density threshold of 0.57 individuals/m<sup>2</sup>. Black lines are four AUV visual surveys from 2012 Cobb Seamount expedition.

Areas identified as likely to be VMEs in our study area resulted in a total area of 1,542 km<sup>2</sup> ranging in depths from 30 m to 1600 m (Figure 7). Gorgonian coral and black coral had the highest frequency of predictions above the VME occurrence threshold of 0.78, which had maximum predictions of 0.95 and 0.93 respectively. Stony corals had the lowest overall predictions with a maximum of 0.79. Therefore, the resulting spatial distribution of areas likely to be VMEs is largely driven by the prediction of suitable habitat for gorgonian corals (Figure 8).



Figure 7. Areas identified as likely to be VMEs (blue) where at least one VME indicator taxon predicted model value meets or exceeds the VME occurrence threshold of 0.78. Seamount boundaries are from Harris et al. (2014).



Figure 8. Frequency distribution of Habitat Suitability Index (HSI) values for each VME indicator taxon in relation to the VME occurrence threshold of 0.78 (blue line). Areas with at least one VME indicator taxon HSI above the threshold were identified as likely to be VMEs.

VME indicator taxa density and occurrence values are significantly and positively correlated (Spearman's rank correlation rho ( $r_s$ ) = 0.97, p < 0.05) (Figure 9). For comparison purposes, if we apply the VME occurrence threshold of 0.78 to the transect segments where VMEs were identified with the VME density threshold, 87% of the same segments are identified. Nevertheless, the VME occurrence threshold identified more segments than the VME density threshold (24 vs 15 segments identified, respectfully) (Figure 10). The correlation between VMEs and areas likely to be VMEs on the AUV transects show that high habitat suitability predictions represented by a VME visual occurrence threshold can be a good proxy for VME density.



*Figure 9. Spearman's correlation between VME indicator taxa density and VME occurrence per transect segment at the 50 m<sup>2</sup> segment scale.* 



Figure 10. Comparison of the VME occurrence threshold (right y axis, green dashed line) vs the VME density threshold (left y axis, blue dashed line) when applied to the visual data from Cobb Seamount AUV transect 4. The blue solid line represents the VME density and the green solid line represents the VME occurrence proportion for each 50 m<sup>2</sup> transect segment.

Our general application of PHMs can be used to assess all seamounts in the NPFC's CA to preliminarily identify areas that are likely to be VMEs. Targeted visual surveys can then be used to ground truth high priority areas identified in the PHMs to confirm VME areas.

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#### ANNEX 1 – PHM ENSEMBLE MODELLING

Table 1. Overview of environmental data used or considered for use in model construction.

Variable name	Abbreviation	Units	Native Resolution	Reference
Bathymetry	bathy	meters	0.0083°	Becker et al. 2009
				Sandwell et al. 2014
Terrain Variables				
Aspect – Eastness	eastness		0.0083°	Jenness 2013a
Aspect – Northness	northness		0.0083°	Jenness 2013a
Curvature – General	gencurve		0.0083°	Jenness 2013a
Curvature – Cross-Sectional	crosscurve		0.0083°	Jenness 2013a
Curvature – Longitudinal	longcurve		0.0083°	Jenness 2013a
Roughness	roughness		0.0083°	Jenness 2013a
Slope	slope	Degrees	0.0083°	Jenness 2013a
Topographic Position Index	TPI		0.0083°	Jenness 2013b
Vector Ruggedness Measure	VRM		0.0083°	Walbridge et al. 2018
Benthic Variables				
Alkalinity	alk_stein	µmol l <sup>-1</sup>	3.6x0.8-1.8°	Steinacher et al. (2009)
Dissolved inorganic carbon	dic_stein	µmol l⁻¹	3.6x0.8-1.8°	Steinacher et al. (2009)
Omega aragonite ( $\Omega_{ARAG}$ )	arag_stein		3.6x0.8-1.8°	Steinacher et al. (2009)
Omega calcite ( $\Omega_{CALC}$ )	calc_stein		3.6x0.8-1.8°	Steinacher et al. (2009)
Dissolved oxygen	dissox	µmol l⁻¹	1°	Garcia et al. 2018a
Salinity	salinity		0.25°	Zweng et al. 2018
Temperature	temp	°C	0.25°	Locarnini et al. 2018
Phosphate	phosphate	µmol l <sup>-1</sup>	1°	Garcia et al. 2018b
Silicate	silicate	µmol l <sup>-1</sup>	1°	Garcia et al. 2018b
Nitrate	nitrate	µmol l <sup>-1</sup>	1°	Garcia et al. 2018b
Particulate organic carbon	POC	g C m <sup>-2</sup> yr <sup>-1</sup>	0.05°	Lutz et al. (2007)
Regional current velocity	regfl	m s⁻¹	0.5°	Carton et al. (2005)
Vertical current velocity	vertfl	m s⁻¹	0.5°	Carton et al. (2005)
Regional Currents and Aspect	curaspect		0.5°	Derived
Surface Variables				
Chlorophyll a	chla	mg m⁻³	4 km	NASA (2021)
Photosynthetically Available	PAR	Einstein m <sup>-2</sup>	4 km	NASA (2021)
Radiation		day⁻¹		
Sea Surface Temperature	SST	°C	4 km	NASA (2021)
Particulate organic carbon	POC_S	mg m⁻³	4 km	NASA (2021)
Particulate inorganic carbon	PIC_S	mg m⁻³	4 km	NASA (2021)

**Table 2**. Percent variable importance for Boosted Regression Tree (BRT), Random Forest (RF), and Generalized Additive Models (GAM). Aragonite saturation state ( $\Omega_{ARAG}$ ) was used for stony coral models, and calcite saturation state ( $\Omega_{CALC}$ ) was used for soft coral, gorgonian, and black coral models.

Таха	Model	$\mathbf{\Omega}_{ARAG/CALC}$	Cur-	Diss.	Slope	Bottom	TPI-	TPI-
			Aspect	Oxygen		Temp.	1000	20000

Stony corals	BRT	3.3	1.0	2.7	30.7	20.6	8.7	33.0
	GAM	1.4	2.7	11.8	38.3	3.7	9.2	32.9
	RF	10.3	3.9	21.1	17.4	21.7	6.1	19.4
Soft corals	BRT	1.1	0.0	1.1	65.7	3.1	7.5	21.4
	GAM	12.0	1.3	17.9	27.4	18.4	5.6	17.3
	RF	23.8	0.0	0.8	17.4	4.0	5.6	48.3
Gorgonians	BRT	25.1	0.0	7.1	6.6	2.6	1.6	57.0
	GAM	20.2	0.4	14.1	5.2	41.4	0.8	17.9
	RF	5.2	0.0	1.2	14.8	2.0	3.3	73.4
Black corals	BRT	5.5	0.1	14.8	1.0	60.6	4.0	13.9
	GAM	10.3	0.4	22.5	0.4	46.4	2.7	17.3
	RF	23.0	3.1	16.1	9.7	35.6	6.2	6.4



Figure 1. Pearson's correlations among all environmental variables considered for inclusion in models.



**Figure 2.** Cluster diagram demonstrating the relationships among all environmental variables considered for inclusion in models. Preliminary Random Forest models were constructed, and a combination of 1) initial model performance, 2) known biological relevance, and 3) relationships among variables were used to select a smaller group of high performing, less-correlated variables for the final models.



Figure 3. ROC-weighted ensemble model for stony corals in the vicinity of Cobb Seamount.



Figure 4. ROC-weighted ensemble model for black corals in the vicinity of Cobb Seamount.



Figure 5. ROC-weighted ensemble model for soft corals in the vicinity of Cobb Seamount.



Figure 6. ROC-weighted ensemble model for gorgonians in the vicinity of Cobb Seamount.

# ANNEX 2 – TAXA OBSERVED ON COBB SEAMOUNT AUV TRANSECTS IN 2012

Table 1. Species list and counts from AUV photo data from Cobb seamount (2012) grouped by VME indicator taxa

VME indicator taxa group	Morphotype name	Count	VME indicator taxa group count
Black Coral	Bathypathes sp	373	715
	Lillipathes sp	281	
	Stichopathes sp	61	
Gorgonian	Isididae	570	787
	Primnoidae	188	
	Swiftia simplex	29	
Soft Coral Non Gorgonian	Gersemia sp	40	285
	Heteropolypus ritteri	245	
Stony Coral	Desmophyllum dianthus	8	8
Associated non VME	Actinostola faeculenta	302	5695
indicator taxa	Ampheraster marianus	29	
	Anoplopoma fimbria	2	
	Anthoptilum sp	91	
	Antimora microlepis	4	
	Brisingidae sp	57	
	Chionoecetes tanneri	179	
	Chirostylidae	1532	
	Chorilia longipes	11	
	Coryphaenoides acrolepis	69	
	Embassichthys bathybius	17	
	Euretidae	27	
	Farrea omniclavata	39	
	Florometra serratissima	24	
	Glyptocephalus zachirus	2	
	Halipteris willemoesi	2	
	Hippasteria phrygiana	14	
	Hormathiidae	34	
	Liponema brevicornis	4	
	Lithodes couesi	17	
	Microstomus pacificus	1	
	Molpadia intermedia	1	
	Octopus sp	2	
	Pannychia mosleyi	1013	
	Pseudarchaster	38	
	Psolus squamatus	240	
	Pteraster sp	7	
	Rathbunaster californicus	7	

Rossellidae - Sp 1	66	
Rossellidae - Sp 2	62	
Scyliorhinidae	5	
Sebastes sp	9	
Sebastolobus alascanus	6	
Sebastolobus sp	544	
Staurocalyptus sp	8	
Stylaster sp	14	
Thrissacanthias sp	4	
Tritoniidae	6	
Umbellula lindahli	1	
Unidentified anemone	291	
Unidentified coral	298	
Unidentified Crab	4	
Unidentified fish	34	
Unidentified invertebrate	26	
Unidentified sea cucumber	3	
Unidentified sea pen	35	
Unidentified sea star	340	
Unidentified sponge	174	