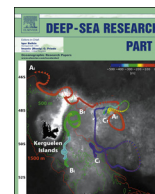




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# Habitat suitability models for predicting the occurrence of vulnerable marine ecosystems in the seas around New Zealand



Owen F. Anderson<sup>a,\*</sup>, John M. Guinotte<sup>b</sup>, Ashley A. Rowden<sup>a</sup>, Dianne M. Tracey<sup>a</sup>, Kevin A. Mackay<sup>a</sup>, Malcolm R. Clark<sup>a</sup>

<sup>a</sup> National Institute of Water and Atmospheric Research, Wellington, New Zealand

<sup>b</sup> Marine Conservation Institute, Seattle, USA

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## ABSTRACT

Spatial management planning for vulnerable marine ecosystems (VME) across broad areas of un-sampled seafloor requires detailed predictions of species distribution. We utilised two habitat suitability modelling techniques, boosted regression trees (BRT) and maximum entropy (MaxEnt), to create potential distribution maps for 11 VME indicator taxa in the New Zealand area and adjacent seas. New bathymetry data were combined with existing environmental, chemical and physical data to produce a set of 45 predictor variables describing conditions at the seafloor. Nine of these variables were selected for use in the models based on low covariance and high explanatory power. Historical biological survey data were used to provide models with absence data (BRT) or target-group background data (MaxEnt). Model agreement was high, with each model predicting similar areas of suitable habitat both in the vicinity of known VME indicator taxa presence locations as well as across broad regions of un-sampled seafloor. Model performance measures, including cross-validation testing against sets of spatially independent data, did not clearly indicate a preferred modelling method across all taxa. Previous habitat suitability modelling efforts have rarely accounted for model precision, and in this study we used a bootstrap re-sampling technique to produce model uncertainty maps to accompany each habitat suitability map. Because of the similar performance of BRT and MaxEnt methods in this study, we conclude that the best approach to incorporating the results into decision-support tools for spatial conservation planning is to average predictions and uncertainty from both.

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## 1. Introduction

Vulnerable marine ecosystems (VMEs) are ecosystems which are at significant risk from the effects of fishing activity or other kinds of disturbance, as determined by the vulnerability of their components (e.g. habitats, communities or species) (FAO, 2009). The United Nations General Assembly has passed a number of resolutions that require nation states and fishery management organisations to identify VMEs within their jurisdiction as one of the steps towards their protection (see Ardron et al. (2014) for details). Species or taxonomic groups that can be used as indicators of the presence of VMEs have been identified for particular ocean regions in order to assist agencies responsible for their protection (e.g., the South Pacific Regional Fisheries Management Organisation (SPRFMO) in the South Pacific region - Parker et al., 2009, Commission for the Conservation of Antarctic Marine Living

Resources (CCAMLR) in the Antarctic region - Parker and Bowden, 2010). These taxa possess characteristics such as slow growth rates, longevity, late maturity, fragility, and include species that form structurally complex features like coral reefs and sponge gardens, which provide three dimensional structure for diverse communities.

Habitat suitability modelling (or species distribution modelling) is a tool for predicting the suitability of a location for a given species or group of species based on observed affinities with environmental conditions. Habitat suitability modelling techniques are increasingly being used to predict patterns of VME indicator taxa distribution in the deep sea where data are sparse (Vierod et al., 2014), and are seen as useful for marine ecosystem management (Ross and Howell, 2013; Reiss et al., 2014). Among the many habitat suitability models, examples for deep-sea corals alone include; Bryan and Metaxas (2006), Bryan and Metaxas (2007), Davies et al. (2008), Tittensor et al. (2009), Woodby et al. (2009), Tittensor et al. (2010), Davies and Guinotte (2011), Tracey et al. (2011), Yesson et al. (2012), and Guinotte and Davies (2014). However, the ability to predict species distributions accurately is

\* Corresponding author.

E-mail address: [owen.anderson@niwa.co.nz](mailto:owen.anderson@niwa.co.nz) (O.F. Anderson).

strongly dependent on how the models are constructed; the quantity, quality, and distribution of species presence records; the availability of true absence records; and the environmental predictor variables used to model the potential distribution of the species (Araújo and Guisan, 2006; Guisan et al., 2006).

A recent effort using Boosted Regression Tree (BRT) and Maximum Entropy (MaxEnt) methods to model habitat suitability for deep-sea VME indicator species in the SPRFMO convention area, and a subsequent field survey to validate model results for six seamounts on the Louisville Seamount Chain, revealed model predictions were inaccurate for reef-forming deep-sea corals at fine scales ( $\sim 1 \text{ km} \times 1 \text{ km}$ ) (Anderson et al., 2016). The primary reasons for the poor performance of these models included lack of information on substrate type (critical for coral settlement and growth), depth errors in the global bathymetry (SRTM30) used and hence error introduced into the seafloor environmental variables by inaccurate bathymetry, and the complex geomorphology of the Louisville seamounts. The authors concluded that better model performance would be unlikely without significant improvement in the accuracy of basin-scale bathymetric and sediment data, and future modelling attempts should focus on smaller regions where more precise data are available. The research described here attempts to incorporate these and other recommendations of Anderson et al. (2016) by: using higher resolution ( $250 \text{ m} \times 250 \text{ m}$ ) bathymetry derived from an expanded set of more accurate echosoundings data to produce new terrain and seafloor environmental variables; producing regional habitat suitability models, again using BRT and MaxEnt but also combining the output from

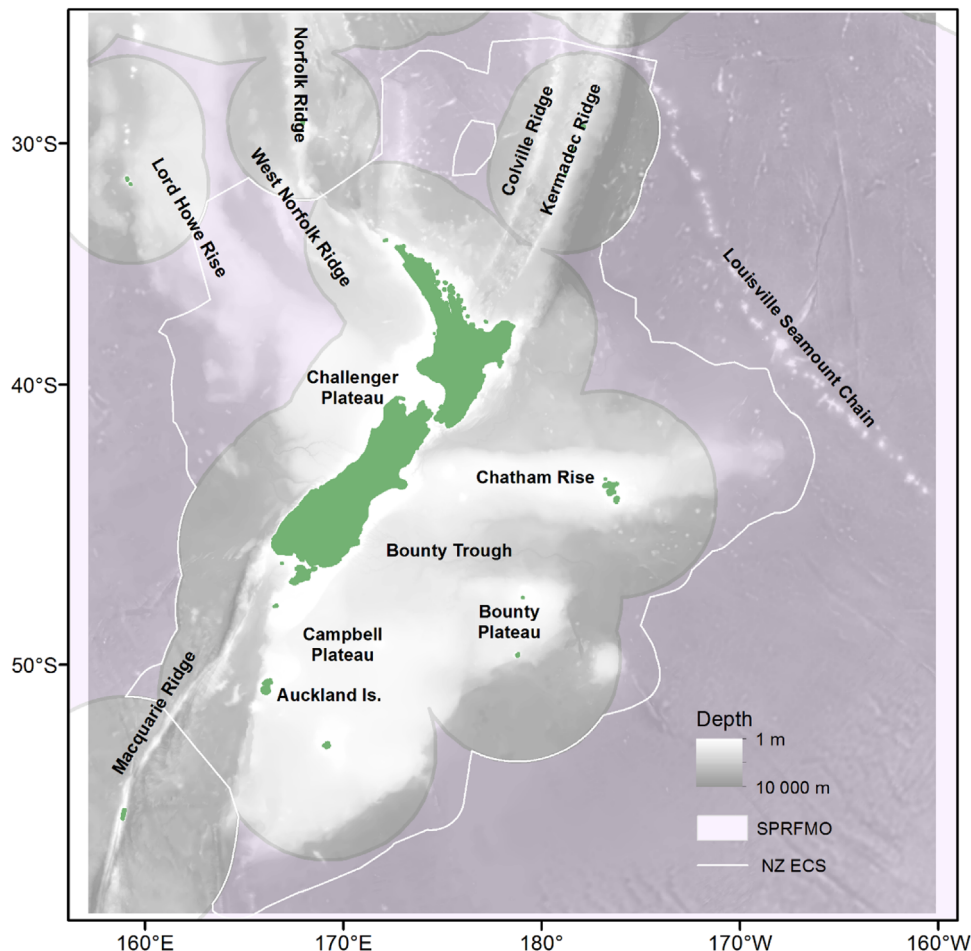
both into ensemble models; incorporating sediment data into the models; constructing true absence data sets for BRT models and target group background data (based on real sampling locations rather than randomly generated points) for MaxEnt models; and by using bootstrap techniques to produce spatially explicit measures of uncertainty for predicted results.

We describe the process of predictor variable selection and habitat suitability model construction for 11 VME indicator taxa, and present habitat suitability maps that can be used to inform spatial management planning for protecting VMEs in the seas around New Zealand, including key bottom trawling regions within the SPRFMO convention area.

## 2. Materials and methods

### 2.1. Model extent

The model was constrained to the wider New Zealand region, a rectangle bounded by the following coordinates ( $157^\circ\text{E}$ ,  $160^\circ\text{W}$ ,  $24^\circ\text{S}$ ,  $57.5^\circ\text{S}$ ) (Fig. 1). This region includes all of the New Zealand Exclusive Economic Zone (EEZ) and extended continental shelf; and parts of the SPRFMO convention area including the Louisville Seamount Chain, Lord Howe Rise, and Norfolk Ridge – sites of particular importance to the New Zealand deep-sea fishery (Clark, 2008). Although bathymetry data were available at  $250 \text{ m} \times 250 \text{ m}$  the spatial resolution of the models was set to  $1 \text{ km}^2$  because the source of the majority of presence-absence records for VME



**Fig. 1.** Study region showing bathymetry, feature names used in the text, and the boundaries of the SPRFMO convention area. NZ ECS=boundary of the New Zealand Extended Continental Shelf.

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