

# SIOFA BIOREGIONALISATION AND VMEs PROJECT

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*Progress Report*

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Boris Leroy, Berta Ramiro Sánchez  
Muséum National d'Histoire Naturelle

*This consultancy builds upon work carried out in a parallel consultancy aimed at developing a series of bioregionalisation schemes for VME indicators in the Southern Indian Ocean using state-of-the-art modelling techniques. This progress report aims at describing the methods and preliminary results which will be used to develop the conservation planning aspect of the present consultancy.*



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## 1. Introduction

Effective management in ABNJs requires conservation objectives based on the identification of areas of importance for deep-sea benthic biodiversity (Clark et al., 2014; Pereira et al., 2013; Tittensor et al., 2014), which in turn rely on biogeographical maps of deep-sea biodiversity. The objective of this consultancy is to provide biogeographical maps of Vulnerable Marine Ecosystem (VME) indicator taxa in the Southern Indian Ocean Fisheries Agreement (SIOFA) area.

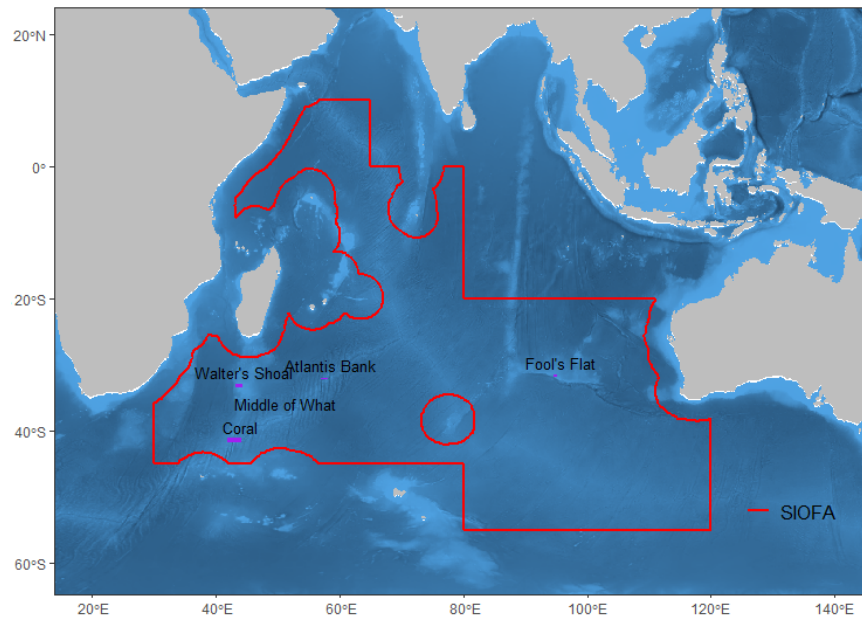
The SIOFA area is a very large area with a rich biodiversity, especially in terms of VME indicator taxa, with an observed species richness of 1921 species and an estimated total richness of 2906 species (updated from Ramiro-Sánchez et al., 2021). It is typically complex to interpret at once the distributions of hundreds of species over such a large spatial scale – which, in turn, makes it difficult to derive management recommendations. Consequently, to be able to understand the distribution of biodiversity in such contexts, biogeographers engage in biogeographical classifications, also known as bioregionalisation (Ebach and Parenti, 2015). Bioregionalisations partition the geographical space into biological and physical units based on the distribution of multiple species, communities, ecosystems or other biological characteristics – these homogeneous units are called biogeographical regions or bioregions. Bioregions are therefore a simplification (a model) of the true biogeographical distribution of biodiversity, generally on the basis of taxa that share similar distributions. These organisms share similar distributions because of similar ecological and physical preferences and of a shared history (Lomolino et al., 2016; Leroy et al., 2019; Woolley et al., 2020).

Managers need to know first the extent of bioregions of VME indicator taxa to apply adequate spatial management. However, the extreme scarcity of data available in the SIOFA area make it impossible to map the entire study area on the basis of observed samplings only (Ramiro-Sánchez et al., 2021). Therefore, to fulfil the objective of this consultancy, we have to rely on predictive modelling approaches. There are many predictive approaches to map bioregions, which can be generally classified into three categories (Woolley et al. 2020). The first one consists in grouping biological features into bioregions first, and then spatially predict these bioregions (“group first, then predict”). The second one consists in spatially predicting all biological features first, and then group them with a clustering approach (“predict first, then group”). The last one consists in grouping and predicting bioregions in a single modelling approach (“analyze simultaneously”). Each method has its set of advantages and disadvantages that make them complementary in the information they provide; although, ultimately, the kind of data available will often limit the choice of method (Woolley et al., 2020). In addition, it is important for the implementation of management tools based on bioregionalisation approaches that the method used is reproducible.

In this draft report, we synthesise results for the first term of reference (classification of key biological, geological, and oceanographic data) on the basis of previous consultancies. To achieve this aim, we report on the results obtained in our previous consultancy “VME mapping” where we implemented all three predictive approaches. Note, however, that

we modified some of the methods to follow state-of-the-art recommendations. For example, a “group, then predict” modelling approach known as Generalized Dissimilarity Models was initially planned; however, it has been recently criticized for their inadequacy in identifying relevant predictors of turnover in species composition between regions (Woolley et al., 2017). Consequently, to provide the most accurate results, we have decided to change the methods in the VME mapping consultancy (Generalized Dissimilarity Models or other appropriate techniques) to Regions of Common Profile (Foster et al., 2013; Woolley et al., 2020), which corresponds to category 3 approach “analyze simultaneously”. Likewise, we have changed the modelling techniques initially proposed to model each indicator taxa in the “predict, then group” approach of the VME mapping consultancy. Indeed, the modelling of indicator taxa requires to apply presence-only modelling techniques in a data-poor situation, and these techniques have very recently been significantly improved (Valavi et al., 2021a, b). Therefore, we implemented these new methods in order to improve the predictions of individual taxa, which in turn has significant positive impacts on the prediction of bioregions in this “predict first, then group” approach.

We provide preliminary results from the first consultancy here. We note that improvements of the models will continue until the end of the consultancy and thus, results shown here should be interpreted with caution.



*Figure 1. The Southern Indian Ocean Fisheries Agreement (SIOFA) area of competence and designated Benthic Protected Areas. Background map shows the bathymetry of the Indian Ocean seafloor.*