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Estimating regional patterns of benthic invertebrates along the Namibian coast to comply with the post-2020 Global Biodiversity Framework

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Declaration of authorship of work

I declare I am the author of this work, which is original and unpublished. The sources consulted have been duly cited in the text and included in the list of references.

(signature)

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AUC: Area Under the receiver operating characteristic Curve

BCLME: Benguela Current Large Marine Ecosystem

CBD: Convention on Biological Diversity

DNN: Deep Neural Network

EBSA: Ecologically or Biologically Significant Marine Areas

EEZ: Exclusive Economic Zone

IUCN: International Union for Conservation of Nature

MFMR: Ministry of Fisheries and Marine Resources

MPA: Marine Protected Area

MRA: Marine Resources Act

MSP: Marine Spatial Planning

NIMPA: Namibian Islands Marine Protected Area

Rv: Research vessel

SDM: Species Distribution Modelling

sjSDM: scalable joint Species Distribution Modelling

TAC: Total Allowable Catch

TSS: True Skills Statistics

UNEP-WCMC: United Nations Environment Programme - World Conservation Monitoring Centre

Estimating regional patterns of benthic invertebrates along the Namibian coast to comply with the post-2020 Global Biodiversity Framework

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ABSTRACT

Assessing benthic biodiversity patterns is crucial to ensure the conservation of marine biodiversity and essential ecosystem services, especially in the context of climate change. Importantly, benthic biodiversity estimates are still lacking along the Benguela Current Large Marine Ecosystem (BCLME), which encompasses the broad coastlines of Angola, Namibia, and South Africa. Moreover, anthropogenic pressures have led to biodiversity threats and declines in benthic invertebrate populations, potentially shifting biodiversity baselines. To address this knowledge gaps, we provide the first biodiversity estimate of marine invertebrates in the Namibian coastline by means of deep neural network modelling fitting high-resolution predictor variables and field surveys data collected over a period of four years. Our models matched the known distribution of benthic invertebrate species with high estimates throughout the entire study extent and hotspots located in the Central regions of the Marine Spatial planning (MSP) area. Our findings also show that achieving the post-2020 biodiversity targets of protecting 30% of the Namibian Exclusive Economic Zone (EEZ) leads to 12 out of 143 taxa being preserved, particularly the mantis shrimp *Squilla acuelata calmani*; the crabs *Mursia cristiata*, Mixed Hermit crabs, *Macropipus australis*, *Bathynectes piperitus*, *Chaceon maritae* and *Lithodes ferox;* the lobsters *Stereomastis sp.* and *Jasus lalandii*; the gastropods *Amalda bullioides* and Gastropods mixed; and the *Sea anemone pink*. This new assessment can guide and enhance decision-making in the management and conservation of different areas like Ecologically or Biologically Significant Marine Areas.

Keywords: BCLME, invertebrates, Biodiversity, Conservation, Marine Protected Areas, Marine Spatial Planning, Namibia.

1. INTRODUCTION

Assessing and understating biodiversity patterns is crucial for safeguarding marine biodiversity and preserving essential ecological ecosystem services, particularly in the face of climate change (Harris et al., 2022). The climate-driven marine species reshuffling may comprise the expansion of ranges towards the poles and losses in regions located at lower, warmer latitudes (Assis et al., 2022; Gorman et al., 2016; Hodapp et al., 2023). These trans boundary movements and migration into new areas have been a growing concern regarding the management of the species based on their ecological and economic value (Scheffers and Pecl, 2019). In this context, the Post-2020 Global Biodiversity Framework (CBD, 2021) was implemented to mitigate biodiversity loss by 2030, and the International Union for Conservation of Nature (IUCN) set a target to protect at least 30% oceans for effective marine biodiversity conservation (Zhao et al., 2020). However, although the number and extension of Marine Protected Areas (MPAs) has increased in the past decade, most are ineffective, and the fully protected areas only cover 2% of the ocean (Costello and Ballantine, 2015). In the global ocean, benthic invertebrates provide essential marine ecosystem services, and their significance extends beyond habitat construction and food provision; they also contribute to erosion control in shorelines, as well as carbon storage in sediments by sinking their shells and tissues when they die on the ocean floor (Prather et al., 2013).

Africa is known for its significant high levels of biodiversity, sheltering approximately one-quarter of the world's mammal and bird species and several ecological groups of marine species (Chapman et al., 2022). Biodiversity estimates have been addressed for terrestrial organisms in some African countries, mainly in the Sub-Saharan African ones like Uganda, Kenya, Ghana, Seychelles, Congo, Nigeria, and Cameroon (Midgley and Bond, 2015; Rouget et al., 2003; Schipper et al., 2020). Nevertheless, marine biodiversity estimates remain underrepresented, particularly for the Benguela Current Large Marine Ecosystem (BCLME; Fig.1). The BCLME encompasses the coastlines of three developing countries (Angola, Namibia, and South Africa) widely recognized for high productivity (Kainge et al., 2020). Previous reports of Africa´s biodiversity have predominantly centered around a limited range of species, focusing on fish, seabirds, and

marine mammals (Finke et al., 2020a; Kirkman et al., 2019). Additionally, compared to charismatic species, marine invertebrates are often overlooked in IUCN reports and national conservation efforts (Chen, 2021). High-priority invertebrate groups like mollusks attract more attention and research funding for economic interest, neglecting other exploited invertebrates at higher risk and being overlooked in conservation efforts (Chen, 2021; Collier et al., 2016).

Despite being considered a "relatively pristine" marine environment, Namibia faces biodiversity threats and losses of benthic invertebrate populations due to anthropogenic pressures and natural phenomena (Sakko, 1998)(e.g., agriculture, land and water use, and urbanization) (King, 2023). Therefore, delineating Ecologically or Biologically Significant Marine Areas (EBSAs) (Harris et al., 2022; King, 2023) to implementing policies to safeguard African marine biodiversity and maintaining essential ecological processes, in line with the post-2020 framework, are crucial. The BCLME is the only Southeast Atlantic region where efforts have been made to safeguard biodiversity within the context of EBSAs (Harris et al., 2022). The Namibian government has committed to strengthening its protection levels in line with international targets and has updated its EBSAs to provide a solid basis to inform such processes (Harris et al., 2022). In this way, Namibia declared its entire coastline as protected, which resulted in the establishment of the Namibian Islands Marine Protected Area (NIMPA) in 2009 (Finke et al., 2020b). However, proper management plans and policies are still lacking. In this context, Namibia, together with Angola and South Africa, have adopted Marine Spatial Planning (MSP) as a strategy to improve sustainable ocean development and enhance well-informed conservation actions (Finke et al., 2020b). This initiative makes it one of the first countries in Africa and among the first developing countries worldwide to seek to manage human activities in the ocean strategically (Finke et al., 2020b; Harris et al., 2022). Strong upwelling, frontal movements, oxygen-less bottoms, and various biological indicators (e.g., mussels, oysters, top predators) characterize Namibia's coastal ecosystem (Bartholomae and Van der Plas, 2007), which result in a wealth of biomass and unique biodiversity (Finke et al., 2020a; Kirkman et al., 2019). Therefore, for the successful management of this African country, it is essential to consider overlooked marine groups of benthic invertebrates that play a crucial role in Namibian ecosystems. For instance, trophic cascade changes have been observed in this region, particularly by the proliferation of jellyfish where small pelagic fish abundance has been severely depleted

(Rogers et al., 2020; Roux et al., 2013). Only the two most economically critical benthic invertebrate species for the Namibian fishing industry, *Chaceon maritae* (Manning & Holthuis, 1981) and *Jasus lalandii* (H. Milne Edwards, 1837) are currently commercially harvested and managed through an annual Total Allowable Catch (TAC), which limit the quantity of harvesting in a given period, according to scientific information available and agents of ministry as documented in the Namibian Marine Resources Act (MRA) 27 of 2000.

Even though 94% (32 out 34) coastal ecosystems have been classified and protected in Namibia, benthic and pelagic areas still lack information and protection (Kirkman et al., 2019) (UNEP-WCMC and IUCN, 2022). To address this research gap, the present study provides estimates of marine invertebrate diversity patterns in the Namibian coastline by using deep neural network modelling fitting high-resolution predictor variables and field expedition data on the distribution of species of marine benthic invertebrates. This approach, in the scope of Species distribution modelling (SDM), is crucial for mapping taxa spatially and are essential to provide biodiversity patterns (Franklin, 2023). However, common SDMs often encounter limitations to deal with presence-only data, resulting in a bias in actual species distribution due to the absence of real absence data. To overcome these challenges, Scalable Joint Species Distribution Models (sjSDM; Pichler and Hartig, 2021), have been applied enhancing the precision of estimates for species association assemblages. As a result of implementing this novel methodology, more accurate species richness maps can be achieved. Our results allowed to explore the present-day biodiversity hotspots along the Namibian coastline and serve as a baseline to guide actions for conservation and management of marine biodiversity, particularly in the scope of the post-2020 Biodiversity Framework which considers the designation of new MPAs at the global scale.

2. METHODS

2.1 Study area and field survey

This study focuses on the Namibian coastal region, which comprises a coastline of ~1572 km from the northern border with Angola (17°16'S) to the southern border with South Africa (30°52'S) (Fig. 1). Field sampling surveys onboard the Ministry of Fisheries and Marine Resources (MFMR) research vessel (RV Mirabilis*;* Fig. 2) collected presence and

absences records (Fig. 3a) of benthic species during a period of four years (2018, 2020-2022). Each sampling survey lasted for 2 months (January-February). A total of 828 trawls were sampled from 214 stations, covering bottom depths between 84.5 m and 682 m, using a Gisund Super two-panel bottom trawl with a head length of 31 m, a footrope of 47 m and a vertical net opening of 4.5 to 5.5 m. The survey followed a systematic transect design. They ran perpendicular to the Namibian coastline, and were 20-25 nautical miles (NM) apart, each 100-m bottom depth had at least one station per transect. Random sampling was carried out on the deck at each trawled station by filling up 1 to 3 sampling bins (depending on the catch) with a randomized sample. All benthic species were removed from the random sample and further sorted for identification onboard the vessel with the aid of identification guides (Atkinson and Sink, 2018; Bianchi et al., 1999). The sorted benthic species were subsequently counted individually and grouped into smaller containers per species. Species that were not able to be identified onboard were preserved in formalin (96%) and ethanol (96%) and live images were captured for further identification with the assistance of expert taxonomists. These species were then identified up to the family level and recorded on the survey sampling forms.

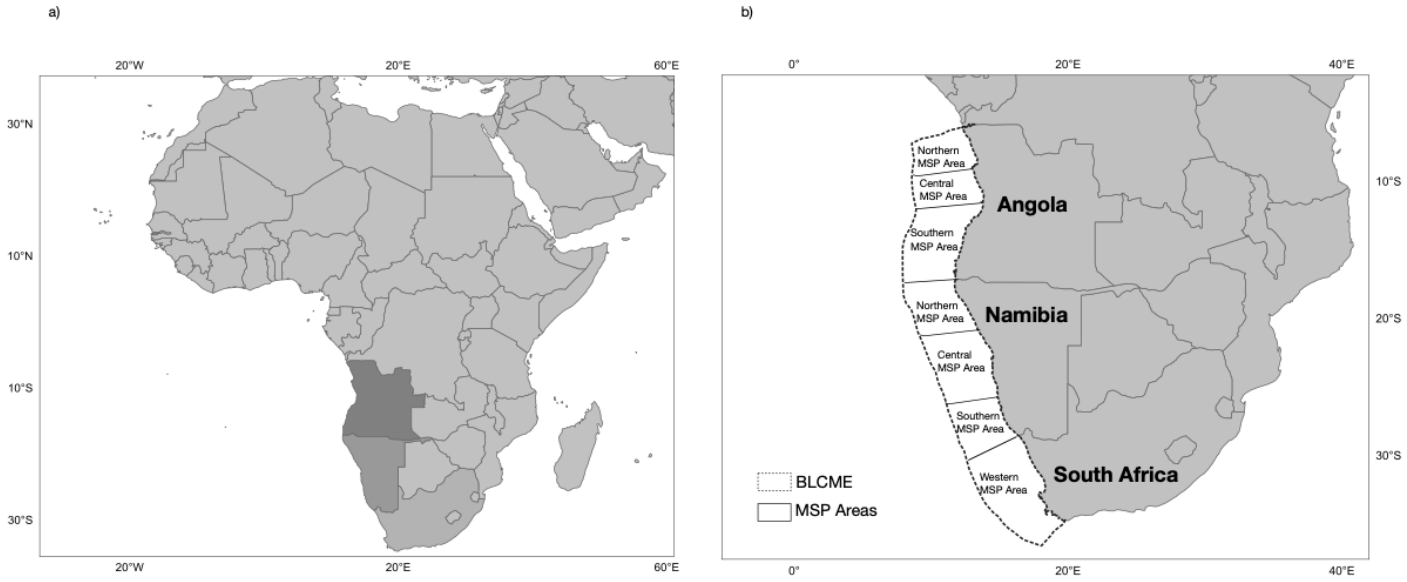

Figure 1: (a) Africa map and (b) Benguela Current Large Marine Ecosystem (BCLME) and the Marine Spatial Planning (MSP) areas of Angola, Namibia and South Africa (Finke et al., 2020a, 2020b).

Figure 2: Deep-sea and Pelagic fisheries research vessel (Rv Mirabilis) used for scientific surveys along the Namibian coast. The vessel is under the ownership of the Ministry of Fisheries and Marine Resources of Namibia.

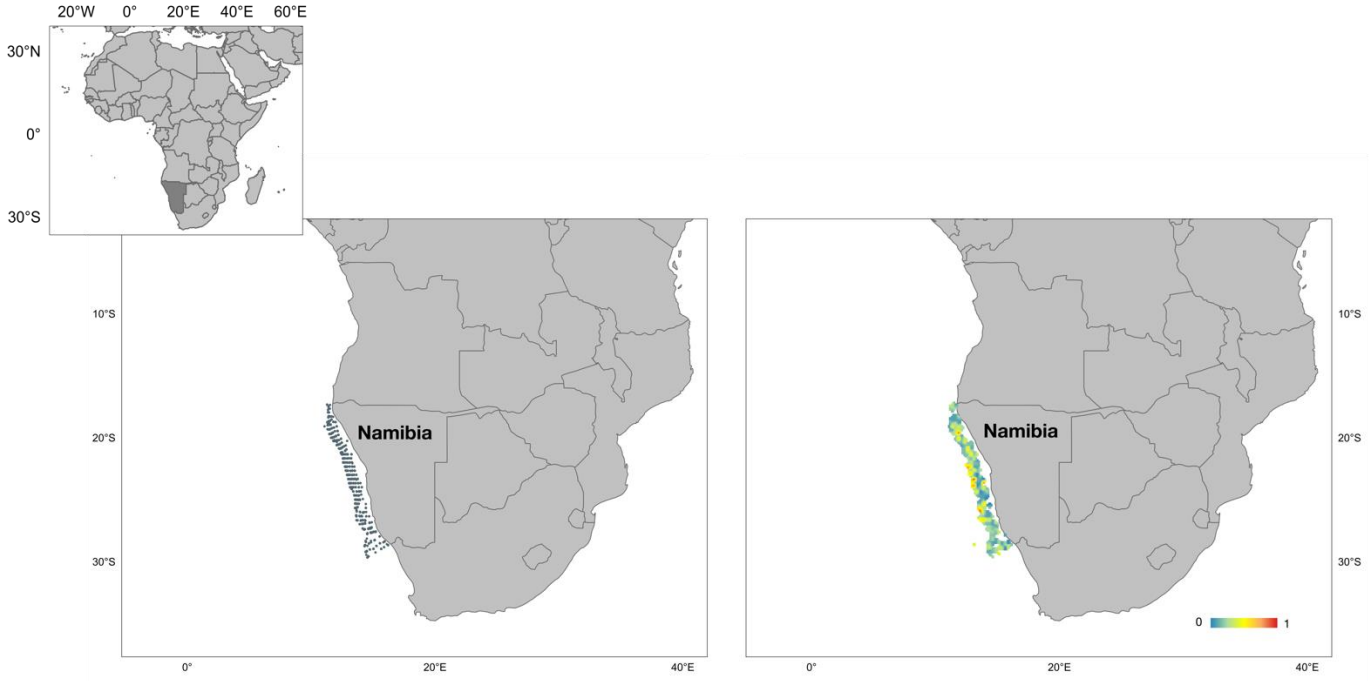

Fig. 3: (a) Sampling locations derived from field transect, where occurrence records were collected, and (b) observed species richness of marine invertebrate species (scaled between 0-1).

2.2 Data preparation

Namibian waters are divided into three sub-national planning units (North, Central and South) based on administrative considerations, types of ecosystem distribution and significant biodiversity areas (Finke et al., 2020b). This was taken into consideration in the analyses by dividing the presences and absences records into the sub-national

planning units according to latitude coordinates (the North open space coordinates range from 17°S - 21.9°S; Central open space coordinates range from 22°S - 25.9°S and the South open space coordinates range from 26°S - 30°S).

The tidy-verse R package (Wickham et al., 2019) was used to prepare the data for the species distribution modelling analyses (See the Data Tidying R-script in the Supplementary Material). All analyses were performed in RStudio v.3.6.6 (R Core Team, 2018).

2.3 Species distribution modelling

Estimates of benthic marine community diversity were explored using scalable joint Species Distribution Modelling (sjSDM; Pichler and Hartig, 2021) to inform conservation and management decisions. This approach supports a comprehensive understanding of spatial variations in community composition with significant potential as a flexible tool for community ecology and macro-ecology studies (Pichler and Hartig, 2021). The models considered the effect of environmental factors, biotic associations, and the potential presence of spatially structured residual covariance. One high-performance machine learning algorithm was chosen, namely, Deep Neural Network (DNN), which has the ability to capture complex interactions between predictor and response variables. This statistical tool allows improved performance of models and allows tuning specific hyper-parameters for reducing over-fitting and improving model transferability (Deneu et al., 2021).

Seven environmental data layers were downloaded from Bio-ORACLE v2.0 (Assis et al., 2018; Tyberghein et al., 2012) for present-day conditions (from 2010 to 2020), namely, benthic temperature (long-term average of monthly maximum and minimum), dissolved molecular oxygen, nitrate, phytoplankton, salinity and seawater speed. The benthic biodiversity data compiled from field surveys comprised 3,021 records of 14 ecological groups.

Model performance and predictive error were assessed with a 10-fold cross-validation framework algorithm hyper parameters by training competitive models in nine random folds of data, while one-fold was held at each run to test performance. The process was performed using the grid search method, which involved testing a span of hidden (0, 2, 3, 4), alpha (0.25, 0.5, 0.1), lambda (0.01, 0.1) and number of iterations (50 to 200). After this step, the performance of sjSDMs was determined with the area under the receiver

operating characteristic curve (AUC) and true skills statistic (TSS) (Hirzel et al., 2006), that varies between 0 and 1. AUC and TSS above 0.5, indicate model predictions better than random, while values close to 1 suggest that predictions agree with the observed patterns. The final model was built using the combination of hyper parameters retrieving higher performance in cross-validation.

3. RESULTS

During the surveys, a total of 143 taxa were sampled of which 79 were identified until species level (see Table S1). Subsequently, these species were then grouped into 14 ecological groups, namely Bivalves, Corals, Crabs, Gastropods, Lobsters, Mantis shrimps, Polychaetes, Sea anemones, Sea urchins, Sea pens, Sponges, Starfishes and Tunicates (Table 1). The main groups that occurred in high numbers (> 60 occurrences records) across all three regions were Crabs, Gastropods, Mantis shrimps and Sponges (Table 1). The Northern and Central regions showed a high number of Lobster occurrences, and their presence declined significantly in the Southern region, with only 44 recorded presences. Conversely, the Anemones, Starfish and Sea urchins' groups were the least recorded in the Northern region (38, 13, and 3 recorded occurrences, respectively), but were more commonly found in the Central and Southern regions (Table 1). Overall, the Central region comprised the highest group occurrences (1,375 records) followed by Southern and Northern regions with 789 and 823 records, respectively.

Table 1: Table summarizing the groups that were observed and the number of records per group.

Crude Types	Northern Region records	Central Region records	Southern Region records
Bivalve	25	47	9
Coral	9	12	8
Crab	272	314	197
Gastropod	80	198	92
Lobster	143	209	44
Mantis shrimp	69	78	75
Polychaetes	25	32	31
Sea anemone	38	72	62
Sea cucumber	7	26	12
Sea urchins	3	58	58
Sea pens	39	20	10
Sponges	67	110	79
Starfish	13	146	110
Tunicate	58	53	11

3.1 Species distribution modelling

The distribution model retrieved high predictive performance (AUC= 0.85; TSS=0.90). Optimal DNN hyper parameters of models with lower standard deviation were achieved with such combination (hidden=10L, lambda= 0.01, alfa = 0.5 and iterations= 100). The observed species richness matched with predicted models, with all Namibian coastline supporting high diversity of marine species with hotspots located in the Central regions of the MSP area (Fig. 4, Fig. 5). Considering the Post-2020 targets, if 10% of the Namibia coastline (Fig. 5a) is to be protected, the following species would be preserved: the mantis shrimp *Squilla aculeata calmani* Holthuis, 1959; the crabs *Mursia cristiata* H. Milne Edwards, 1837, Mixed Hermit crabs, *Macropipus australis* Guinot, 1961, *Bathynectes piperitus* Manning & Holthuis, 1981, *Chaceon maritae,* and *Lithodes ferox* Filhol, 1885*; the lobster Stereomastis sp.* Spence Bate, 1888*;* the gastropods *Amalda bullioides* (Reeve, 1864) and Gastropods mixed; and the Sea anemone pink. Moreover, if the target protection increases to 30% (Fig. 5b), in addition to all the species mentioned above, the lobster *Jasus lalandii* would also be included in the list of species to be protected (Table S1).

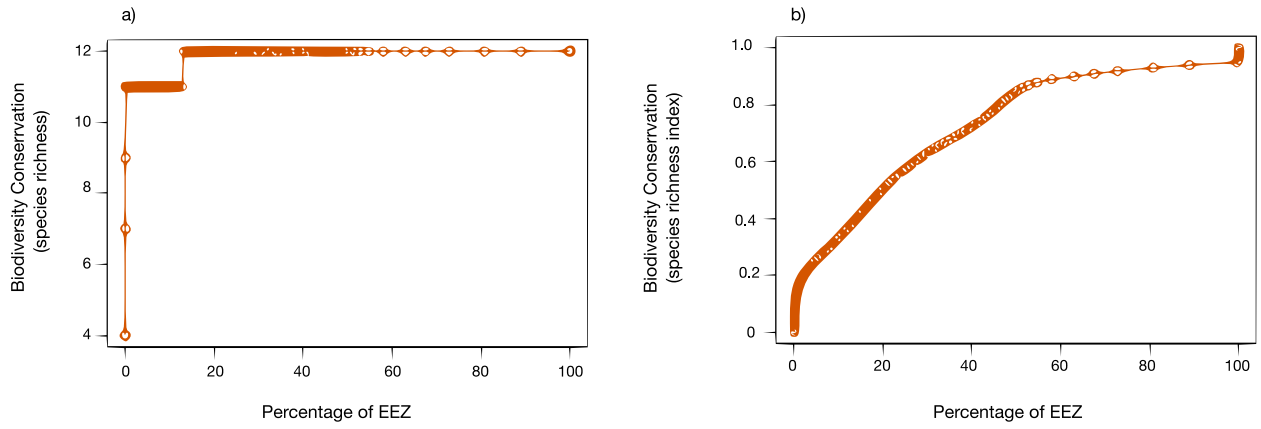

Fig.4: Biodiversity conservation based on the percentage of the Exclusive Economic Zone (EEZ) considered by (a) species richness and (b) species richness index (scaled between 0-1).

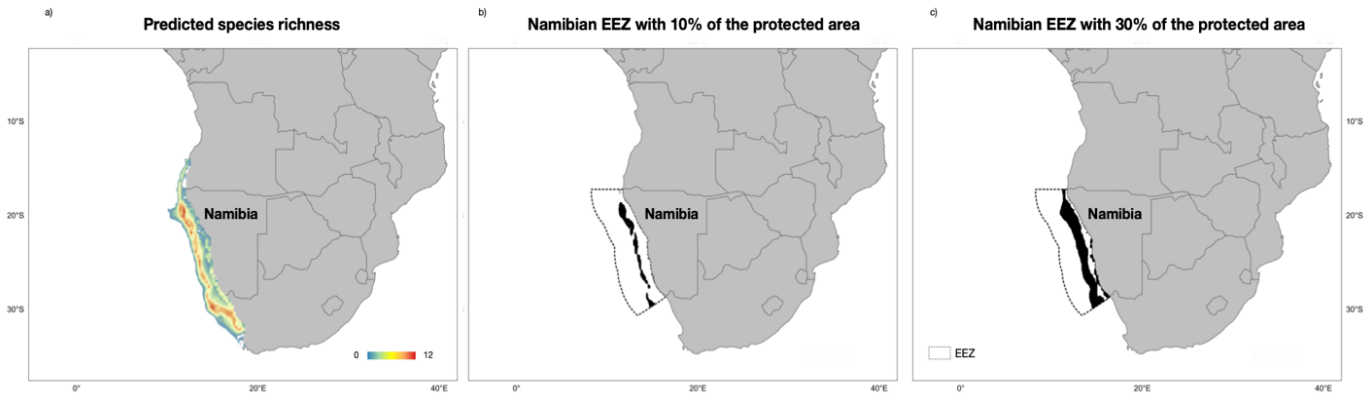

Fig. 5: (a) Species richness patterns of benthic invertebrates predicted along the Namibia coastline, (b) Namibian Exclusive Economic Zone (EEZ) encompassing 10% of designated protected regions considering higher species richness, represented in black, and (c) Namibian Exclusive Economic Zone (EEZ) encompassing 30% of the designated protected regions considering higher species richness, represented in black.

4. DISCUSSION

Predictive modelling of diversity patterns of marine invertebrate species in the Namibian coastline estimated high diversity throughout entire extent, with hotspots located in the center of the MSP area. The protection of 30% of EEZ means 12 out of 143 taxa might be preserved, particularly the mantis shrimp *Squilla acuelata calmani*; the crabs *Mursia cristiata*, Mixed Hermit crabs, *Macropipus australis*, *Bathynectes piperitus, Chaceon maritae* and *Lithodes ferox*; the lobsters *Stereomastis sp.* and *Jasus lalandii*; the gastropods *Amalda bullioides* and Gastropods mixed; and the Sea anemone pink. These estimates can now support and inform management and conservation decisions under directives like Ecologically or Biologically Significant Marine Areas, since these key species provide crucial ecosystems ecological services, such as nutrient cycling, dynamic of food webs, carbon sequestration, water quality improvement and food source.

The model's prediction matched the known distribution of benthic invertebrate species (Fig. 3b). Our approach allowed mapping the diversity hotspots driven by environmental predictors, that can influence the metabolic rates, reproduction, survival, and food sources of benthic invertebrates (Hoppit and Schmidt, 2022). The upwelling in this region promotes changes in the environmental conditions, such as irregular anomalies in temperature, oxygen concentration, and salinity that tend to favor the persistence of few,

generalist species, with high productivity and large abundances (Amorim and Zettler, 2023; Sakko, 1998). This trend is evident in all major marine habitats of Namibia, where diversity is often lower than in comparable habitats in the southern Benguela system of the west coast of South Africa. The findings of a prior study, which considered both fauna and flora diversity, pointed to a pattern of declining species richness from the southern to the northern stretches of Namibia's marine system (Sakko, 1998). In contrast, our results for benthic invertebrate species diversity indicate a different pattern.

The BCLME is an extremely intricate and inconstant ecosystem and this is a huge challenge when it comes to monitoring, assessing, forecasting and predicting the altering environment and its resources (Kainge et al., 2020). In fact, climate change has over the years resulted in the decline of the upwelling winds in central Luderitz (a Namibian region), which has subsequently compromised the food security due to the movement of species and changing of primary productivity and biodiversity (Kainge et al., 2020). Additional observed changes have included warming temperatures, changes in salinity, such as nutrient depleted water with low dissolved oxygen, which result in a frequent mass dieback of marine organisms (e.g., commercially important species like the *Merluccius spp.* (Kainge et al., 2020). The 1993-1994 Benguela Niño event had also severe consequences, including a 30% reduction in the cape fur seal population and a southward migration of the *Sardinops sagax* (Jenyns, 1842) population, the primary food source in this place. Additionally, this event led to algal blooms that released toxins, posing a significant threat to both the entire marine ecosystem and human health, as highlighted by Kainge et al. (2020).

Our findings underscore the potential of Marine Protected Areas (MPAs) encompassing 10% and 30% of EEZ to safeguard key ecological groups. If 10% of the Namibian coastline will be protected, important species like *Squilla acuelata cadmani*, Gastropods mixed, *Mursia cristemanu*, Mixed Hermit crabs, *Macropipus australis*, Sea anemone pink, *Bathynectes piperitus, Stereomastis sp, Chaceon maritae, Lithodes ferox, and Amalda bullioides* could be protected. Additionally, if the target protection area is magnified to 30% (Fig. 4), in addition to all the species mentioned above, *Jassus lalandii* (crustacea) and *Amalda bullioides* (mollusca) would also be included in the list of species to be protected.

Although our models have achieved high performance, it is important to recognize certain limitations inherent of the approach. For instance, the limited number of presences observed in field do not allow the models to get species-species association matrix. Additionally, data limitations can preclude the use of thresholds reclassifying probabilistic predictions of species occurrence. Mapping biodiversity patterns and how they are linked to environmental drivers are crucial for a small country like Namibia, which has an extremely high productive ecosystem. The lack of benthic data has been challenging in terms of safeguarding the benthic biodiversity and maintaining essential ecological processes (Kirkman et al., 2019).

In recent years much focus has been given to benthic studies through the International Networks. In 2020, the MFMR in collaboration with One Ocean Hub have established a Namibian Deep-Sea Benthos Collection Project as baseline for data collection (Baker et al., 2022). The information derived from the Benthos monitoring project will play a pivotal role in supporting decision-makers in their efforts to establish new MPAs in Namibia. Currently, there is only one MPA in Namibia called the Namibia Island Marine Protected Area (NIMPA), and the MFMR is actively working on revising its regulations, with the formalization and implementation still pending (Rippe, 2021). In addition, Namibia is using the MSP tool to get two more Ecologically or Biologically Significant Marine Areas (EBSAs) (Cape Fria and Namibe) declared as MPAs (Rippe, 2021). Therefore, our results are of utmost importance as they can serve as a reference point for improved planning and prioritizing areas for conservation, management and climate change mitigation strategies to protect the marine environment especially the poorly studied benthic environment (Harris et al., 2022; Simmons et al., 1998). The maps produced through this study and our findings will be an added fundamental tool for supporting the ministry and policy makers in the decision-making process of demarcating key sites for conserving marine biodiversity and maintaining essential ecological processes (e.g., EBSAs) through the MSP process in the BCLME (Angola, Namibia, and South Africa) in order to guide the establishment of MPAs. Our study can serve as a foundation for other African countries aiming to achieve their Sustainable Development Goals (SDGs), including SDG13 (Climate action), and SDG14 (Life below water), by using the MSP tool to establish MPAs for the conservation of biodiversity and the well-being of present and future generations.

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Conflict of Interest: The authors declare that they have no conflict of interest.

Data availability: All data and code are openly available in Figshare at xxxxxx.

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Supplementary material

Table S1: Ecological groups, species names and occurrences across the trawled stations during the 2018-2022 survey time series.

Ecological groups	Scientific Name	Northern region pressences	Central region pressences	South region pressences
Bivalve	*Bivalvia*	x	x	x
Bivalve	*Bivalvia*	x	x	x
Bivalve	*Lucinoma capensis*	x	x	
Bivalve	*Mytilus*		x	
Bivalve	*Ostreidae*		x	
Bivalve	*Pecten sulcicostatus*		x	
Bivalve	*Pseudamussium gilchristi*		x	x
Crab	*Chirostylidae*	x		
Crab	*Eumunida squamifera*	x	x	
Crab	*Diogenidae*		x	x
Lobster	*Galatheidae*	x		
Lobster	*Munida*	x	x	
Lobster	*Munidopsis*	x	x	x
Lobster	*Munida benguela*	x	x	x
Crab	*Parapaguridae*	x	x	x
Sea anemone	*Actinaraea*	x	x	x
Sea anemone	*Actinaraea*		x	x
Sea anemone	*Anthosactis capensis*	x	x	x
Sea anemone	*Actinostola capensis*	x	x	x
Sea anemone	*Isophellia algoaensis*		x	
Sea anemone	*Halcurias capensis*		x	
Sea anemone	*Actinaraea*	x		
Sea anemone	*Actinaraea*	x	x	x
Sea anemone	*Anthozoa*	x	x	x
Sea anemone	*Actinaraea*	x	x	x
Sea anemone	*Actinaraea*	x		
Sea anemone	*Actinaraea*	x	x	x
Sea anemone	*Actinaraea*	x		
Bryozoan	*Bryozoa*		x	
Coral	*Caryophylliidae*		x	x
Coral	*Desmophyllum pertusum*	x		
Coral	*Anthozoa*		x	
Seapen	*Anthoptilum grandiflorum*	x	x	
Coral	*Anthozoa*	x		
Coral	*Flabellum (Ulocyathus) messum*		x	
Coral	*Alcyonacea*		x	x
Coral	*Anthozoa*			x
Coral	*Isididae*	x		
Coral	*Anthozoa*		x	
Coral	*Anthozoa*	x		x
coral	*Acanella arbuscula*		x	x
Coral	*Anthozoa*	x		
Coral	*Anthozoa*			x

Seapen	*Pennatulacea*	x	x	x
Coral	*Anthozoa*			x
Sea cucumber	*Hemiocnus insolens*		x	x
Sea cucumber	*Holothuroidea*		x	
Sea cucumber	*Holothuroidea*	x	x	x
Coral	*Antipatharia*	x		
Crab	*Crustacea*	x	x	x
Crab	*Brachyura*			x
Crab	*Calappidae*	x	x	x
Crab	*Calappa*			x
Crab	*Calappa pelii*	x		
Crab	*Mursia*			x
Crab	*Mursia cristiata*		x	x
Crab	*Acanthocarpus brevispinis*	x		
Crab	*Calappidae*			x
Crab	*Corystidae*	x		x
Crab	*Diogenidae*			x
Crab	*Dromiidae*		x	x
Crab	*Exodromidia*		x	x
Crab	*Dromidia*			x
Crab	*Pseudodromia latens*			x
Crab	*Chaceon maritae*	x	x	x
Crab	*Chaceon chuni*		x	
Crab	*Goneplacidae*	x		x
Crab	*Goneplax*	x		x
Crab	*Goneplax rhomboides*	x		
Crab	*Goneplax rhomboides*	x		x
Crab	*Grapsidae*			x
Crab	*Decapoda*		x	x
Crab	*Homolidae*		x	x
Crab	*Inachidae*			x
Crab	*Leucosiidae*			x
Crab	*Philyra*			x
Crab	*Lithodidae*	x	x	
Crab	*Neolithodes asperrimus*	x	x	x
Crab	*Lithodes*	x		
Crab	*Lithodes ferox*	x	x	x
Crab	*Paralomis africana*	x		
Crab	*Majidae*	x	x	x
Crab	*Majidae*			x
Crab	*Maja squinado*		x	x
Crab	*Rochinia*			x
Crab	*Ocypodidae*	x		x
Crab	*Portunidae*	x	x	x
Crab	*Charybdis (Archias) smithii*			x
Crab	*Callinectes*		x	x
Crab	*Bathynectes piperitus*		x	x
Crab	*Macropipus*	x		

Crab	*Macropipus australis*	x	x	x
Crab	*Parapaguridae*	x	x	x
Crab	*Parapagurus*		x	x
Crab	*Parapaguridae*		x	x
Crab	*Parapagurus pilosimanus*		x	x
Crab	*Parapagurus andreui*		x	
Crab	*Parapagurus bouvieri*		x	x
Crab	*Sympagurus dimorphus*		x	
Crab	*Parapagurus pilosimanus*			x
Crab	*Xanthidae*		x	x
Crab	*Calappa*	x		
Mantis shrimp	*Squilla*	x	x	x
Mantis shrimp	*Squilla mantis*	x	x	x
Mantis shrimp	*Squilla aculeata calmani*	x		x
Mantis shrimp	*Squilla biformis*		x	x
Mantis shrimp	*Oratosquilla oratoria*	x	x	
Mantis shrimp	*Squilla cadenati*	x		
Mantis shrimp	*Oratosquillina*			x
Mantis shrimp	*Pterygosquilla capensis*		x	x
Sea urchins	*Echinoidea*		x	x
Sea cucumber	*Holothuroidea*	x	x	x
Sea urchins	*Echinoidea*		x	x
Starfish	*Ophiuroglypha costata*		x	
Starfish	*Ophiactis abyssicola*		x	
Starfish	*Asteroidea*		x	x
Starfish	*Asteroidea*		x	
Starfish	*Lophaster quadrispinus*			x
Sea cucumber	*Holothuroidea*	x	x	x
Sea cucumber	*Holothuroidea*		x	
Starfish	*Ophiuroidea*		x	x
Starfish	*Crossaster penicillatus*			x
Starfish	*Dipsacaster sladeni capensis*		x	
Starfish	*Astropecten irregularis pontoporeus*		x	
Starfish	*Asteroidea*			x
Starfish	*Asteroidea*		x	
Starfish	*Asteroidea*	x		
Starfish	*Asteroidea*	x	x	x
Starfish	*Asteroidea*		x	
Starfish	*Diplopteraster multipes*		x	
Starfish	*Cladaster macrobrachius*		x	

Starfish	*Pseudarchaster tessellatus*	x	x	
Starfish	*Toraster tuberculatus*		x	
Sea urchins	*Echinoidea*		x	x
Sea urchins	*Brissopsis lyrifera capensis*		x	x
Sea urchins	*Echinoidea*	x	x	x
Sea urchins	*Echinoidea*	x	x	x
Gastropod	*Gastropoda*	x	x	x
Gastropod	*Gastropoda*		x	x
Gastropod	*Chryseofusus bonaespei*	x		x
Gastropod	*Comitas saldanhae*	x		x
Gastropod	*Nassarius speciosus*		x	x
Gastropod	*Euspira napus*		x	x
Gastropod	*Afrocominella capensis simoniana*		x	
Gastropod	*Nassarius vinctus*	x	x	
Gastropod	*Nassarius niveus*	x		
Gastropod	*Bullia*		x	
Gastropod	*Cypraeidae*		x	x
Gastropod	*Conidae*			x
Gastropod	*Kilburnia scholvieni*		x	
Gastropod	*Africolaria rutila*		x	
Gastropod	*Haliotidae*			x
Gastropod	*Pteropurpura*		x	
Gastropod	*Muricidae*		x	
Gastropod	*Nassariidae*		x	
Gastropod	*Nassarius vinctus*		x	
Gastropod	*Nudibranchia*		x	
Gastropod	*Amalda bullioides*		x	
Gastropod	*Patellidae*			x
Gastropod	*Ranellidae*		x	
Gastropod	*Fusitriton magellanicus*		x	
Gastropod	*Gastropoda*		x	x
Gastropod	*Coluzea radialis*		x	
Gastropod	*Turritella declivis*		x	
Gastropod	*Velutinidae*		x	
Gastropod	*Lamellidea*		x	
Gastropod	*Athleta abyssicola*	x	x	
Gastropod	*Athleta lutosa*	x	x	x
Gastropod	*Fusivoluta pyrrhostoma*		x	
Lobster	*Decapoda*		x	
Lobster	*Axiidae*	x	x	x
Lobster	*Axius*			x
Lobster	*Calocaris barnardi*	x	x	x
Lobster	*Axiidae*	x		
Lobster	*Galatheidae*	x	x	x
Lobster	*Munida*	x	x	x
Lobster	*Munidopsis chuni*	x	x	x
Lobster	*Munidopsis*	x		
Lobster	*Nephropidae*	x	x	
Lobster	*Nephropsis aculeata*	x		
Lobster	*Nephropsis atlantica*	x	x	x

Lobster	*Palinuridae*	x	x	
Lobster	*Panulirus*	x		
Lobster	*Panulirus regius*	x		
Lobster	*Jasus lalandii*		x	x
Lobster	*Polychelidae*	x	x	x
Lobster	*Polycheles*	x		
Lobster	*Stereomastis*	x	x	x
Lobster	*Stereomastis sculpta*	x	x	x
Lobster	*Scyllarides herklotsii*	x		
Sponges	*Porifera*	x	x	x
Polychetes	*Aphrodita alta*		x	
Polychetes	*Polychaeta*		x	x
Polychetes	*Polychaeta*	x	x	x
Polychetes	*Hyalinoecia tubicola*	x	x	
Polychetes	*Polychaeta*	x	x	x
Polychetes	*Polychaeta*	x		
Polychetes	*Polychaeta*	x		
Sponges	*Porifera*	x	x	x
Sponges	*Porifera*		x	
Sponges	*Porifera*	x	x	x
Sponges	*Porifera*		x	x
Sponges	*Porifera*	x	x	
Sponges	*Porifera*		x	
Sponges	*Suberites*	x	x	x
Sea urchins	*Echinoidea*	x	x	x
Starfish	*Astropecten*	x		
Starfish	*Asteroidea*	x	x	x
Tunicate	*Molgula scutata*	x	x	x
Tunicate	*Ascidiacea*	x		x
Tunicate	*Ascidiacea*	x	x	
Tunicate	*Pyrosoma*		x	
Tunicate	*Ascidiacea*		x	x
Tunicate	*Salpa*	x	x	
Tunicate	*Salpa*	x	x	x

Supplementary Material: R-scripts 1-5

1. Data Tidying

```
#first load all the libraries you are going to use at the beginning of the script
library(readxl)  # to load excel files into R
library(tidyverse) # to organize your data
library(dplyr) # to organize your data
library (ggplot2)
 #source("https://bioconductor.org/biocLite.R")
#biocLite("phyloseq")
setwd("D:/MSc Thesis/Data")
#how to check for the data path
getwd()
#How to see if the dataset is in the selected folder
list.files()
#To load file into R, specify file name, if multiple sheets indicate the sheet you are working on,
# and specify if sheets have column names (set colnames to true/False)
data <- read_xlsx("species codes Taxa(2).xlsx", sheet = "Benthos only", col_names = TRUE)
#To remove zeros from columns and replace them with the desired character or value, use the mutate
#function but make sure you load the dplyr library first (eg dplyr::mutate, in brackets specify the)
```

```
#column you wish to mutate followed by %in% to indicate that the values you are replacing are in
#that column, insert the value you wish to replace (0), specify the new character in this case it
#is NA_character_, and then the column name again. At the end of the line add %>% if you are
changing
#more than 1 column for the same dataset,
data_no0 <- data %>%
  #use the mutate function to replace the zeros with N/A
  dplyr::mutate(Order = if_else(Order %in% 0, NA_character_, Order)) %>%
  dplyr::mutate(Family = if_else(Family %in% 0, NA_character_, Family)) %>%
  dplyr::mutate(Genus = if_else(Genus %in% 0, NA_character_, Genus)) %>%
  dplyr::mutate(Subgenus = if_else(Subgenus %in% 0, NA_character_, Subgenus)) %>%
  dplyr::mutate(Species = if_else(Species %in% 0, NA_character_, Species)) %>%
  dplyr::mutate(Subspecies = if_else(Subspecies %in% 0, NA_character_, Subspecies)) %>%
  dplyr::mutate(Class = if_else(Class %in% 0, NA_character_, Class))
#To remove the blanks follow the same procedure as above but make sure the word Blank is written
#as "Blanks" for R to recognise it as it is not a value but a character
data_noBlanks <- data_no0 %>%
  dplyr::mutate(Order = if_else(Order %in% "Blank", NA_character_, Order)) %>%
  dplyr::mutate(Family = if_else(Family %in% "Blank", NA_character_, Family)) %>%
  dplyr::mutate(Genus = if_else(Genus %in% "Blank", NA_character_, Genus)) %>%
  dplyr::mutate(Subgenus = if_else(Subgenus %in% "Blank", NA_character_, Subgenus)) %>%
  dplyr::mutate(Species = if_else(Species %in% "Blank", NA_character_, Species)) %>%
  dplyr::mutate(Subspecies = if_else(Subspecies %in% "Blank", NA_character_, Subspecies)) %>%
  dplyr::mutate(Class = if_else(Class %in% "Blank", NA_character_, Class))
#Standardizing the regions to the same region value (region codes in the past to what we use now
# to indicate if it is N,C,S. Region1=5030(S), Region2=5020I, Region3=5010(N))
data_regions <- data_noBlanks %>%
  dplyr::mutate(region = if_else(region %in% 3, 5010, region)) %>%
  dplyr::mutate(region = if_else(region %in% 2, 5020, region)) %>%
  dplyr::mutate(region = if_else(region %in% 1, 5030, region)) %>%
  dplyr::mutate(region = if_else(lat >= -21.99 & lat <= -17, 5010, region)) %>%
  dplyr::mutate(region = if_else(lat >= -25.99 & lat <= -22, 5020, region)) %>%
  dplyr::mutate(region = if_else(lat >= -32 & lat <= -26, 5030, region))
#To create a new column with the region names
data_NCS_regions <- data_regions %>%
  dplyr::mutate(region_name = case_when((region == 5010) ~ "North",
                                (region == 5020) ~ "Central",
                                (region == 5030) ~ "South")) %>%
  #reordering the columns 25amibian25 to preffered order, in this case I want the new column
  #region_name (N,C,S) to be moved after the region codes (5010,5020,5030)
  dplyr::relocate(region_name, .after = region)
  survey_station_sample_species <- data_NCS_regions %>%
  unite(survey,station,sample,species,col="individual_species",sep="_",remove=FALSE)
#creating dataset for the years of interest (1018-2022)
Benthos_2018_2022 <-  survey_station_sample_species %>%
    filter(survey > 2017901)
#numbers1,4 indicates the number positions you wish to keep(eg 2018901)we only want 2018
Benthos_2018_2022$survey <- substr(Benthos_2018_2022$survey, 1,4)
write.csv(Benthos_2018_2022,file="Cleaned_benthos18_22.csv", row.names = FALSE)
saveRDS(Benthos_2018_2022,file="Cleaned_benthos18_22.rds")
write.csv(survey_station_sample_species,file="Cleaned_benthos.csv", row.names = FALSE)
saveRDS(survey_station_sample_species,file="Cleaned_benthos.rds")
```

2. Presence Absence Matrix

```
library(readxl)  # to load excel files into R
library(tidyverse) # to organize your data
library(dplyr) # to organize your data
library (ggplot2)
setwd("D:/MSc Thesis/Data")
```

```
#how to check for the data path
getwd()
#How to see if the dataset is in the selected folder
list.files()
data <-read.csv("Cleaned_benthos18_22.csv")
#selecting the columns of interest
PAM_data <- select(data,station,lon, lat, species, number)
#Group lon, lat and species by station;Summarise the total number of each species
PAM_data %>%
  group_by(station,lon,lat,species)%>%
  #summarise(species)
  summarise(species,mean(number))
PAM <- ungroup(PAM_data)
#Putting each species as columns and value as total number
PAM2<-PAM %>%
dplyr::group_by(station,species)%>%
dplyr::summarise(n=dplyr::n(), .groups = "drop")
Pres_Abs <- pivot_wider(PAM2,names_from = "species",values_from = "n")
#Replacing the NA with 0
#Pres_Abs %>%
  #dplyr::mutate_if(is.numeric),funs(if_else(is.na(.), 0, replace=TRUE))
#replace_na(Pres_Abs,list("CNIANTW"=0))
#Pres_Abs %>%
#replace(is.na("n"),0)
Pres_Abs <- Pres_Abs%>%
    mutate_at(c(2:144), ~replace_na(.,0))
#Pres_Abs %>%
  #replace_na(list("column2:column144"= 0, replace=TRUE))
Pres_Abs %>%
  mutate_all(c(2:144), ~replace(>0=1))
#replacing all values greater than 0 with 1
PAM_richness <-Pres_Abs%>%
  mutate_if(is.numeric, ~1 * (. > 0))
write.csv(PAM_richness,file="Presence_Absence_Matrix.csv", row.names = FALSE)
```

3. Extracting Environmental Data

```
library(readxl)  # to load excel files into R
library(raster)
library(sp)
library(rnaturalearth)
library(rnaturalearthdata)

setwd("D:/MSc Thesis/Data")
#opening raster layers
O2 <- raster("DissolvedMolecularOxygen_BenthicMean_Mean_2010.2020.tif")
Nitrate <-raster("Nitrate_BenthicMean_Mean_2010.2020.tif")
MaxTemp <-raster("OceanTemperature_BenthicMean_LtMax_2010.2020.tif")
MinTemp <-raster("OceanTemperature_BenthicMean_LtMin_2010.2020.tif")
Phyto <- raster("Phytoplankton_BenthicMean_Mean_2010.2020.tif")
Sal <-raster("Salinity_BenthicMean_Mean_2010.2020.tif")
SWS <-raster("SeaWaterSpeed_BenthicMean_Mean_2010.2020.tif")
#Stacking the raster layers
rasters<-stack(O2,Nitrate,MaxTemp,MinTemp,Phyto,Sal,SWS)
#Ploting raster data
plot(O2,main="DissolvedMolecularOxygen_Mean",xlab="Lon",ylab="Lat",cex.axis=1.3,cex.la
b=1.4,cex.main=1.5,col=rev(heat.colors(10)))
```

```
plot(Nitrate,main="Nitrate_BenthicMean_Mean",xlab="Lon",ylab="Lat",cex.axis=1.3,cex.lab=
1.4,cex.main=1.5,col=rev(heat.colors(10)))
plot(MaxTemp,main="OceanTemperature_BenthicMean_LtMax",xlab="Lon",ylab="Lat",cex.a
xis=1.3,cex.lab=1.4,cex.main=1.5,col=rev(heat.colors(10)))
plot(MinTemp,main="OceanTemperature_BenthicMean_LtMin",xlab="Lon",ylab="Lat",cex.ax
is=1.3,cex.lab=1.4,cex.main=1.5,col=rev(heat.colors(10)))
plot(Phyto,main="Phytoplankton_BenthicMean",xlab="Lon",ylab="Lat",cex.axis=1.3,cex.lab=
1.4,cex.main=1.5,col=rev(heat.colors(10)))
plot(Sal,main="Salinity_BenthicMean",xlab="Lon",ylab="Lat",cex.axis=1.3,cex.lab=1.4,cex.m
ain=1.5,col=rev(heat.colors(10)))
plot(SWS,main="SeaWaterSpeed_BenthicMean",xlab="Lon",ylab="Lat",cex.axis=1.3,cex.lab=
1.4,cex.main=1.5,col=rev(heat.colors(10)))
#loading Lat and Lon into R
data<-read.csv("Lon_Lat.csv",header=TRUE,sep=",")
head(data)
#visualizing the distribution on a map
world <- ne_countries(scale = 'medium')
class(world)
#Ploting the records on map
plot(world, col="Gray", border="Gray", axes=TRUE, main="Distribution records" ,
ylab="latitude", xlab="longitude")
points(data[,2:3], pch=20, col="Black")
#Selecting the Lon and Lat columns
variables <- extract(rasters,data[,2:3])
head(variables)
##Add the values extracted from environmental variables in the final data
full <- data.frame(data, variables)
head(full)
write.csv(full,file="NamBenthos_EnviroData.csv",row.names=FALSE)
```

4. Namibian Benthos Merged

```
library(dplyr)
setwd("D:/MSc Thesis/Data")
df1 <- read.csv("NamBenthos_EnviroData.csv", header=TRUE, sep=",")
df2 <- read.csv("Presence_Absence_Matrix.csv", header=TRUE, sep=",")
r <- merge(df1,df2,by=c("station","station"),all.x=T)
write.csv(r,file="NamBenthos_Merged.csv", row.names = FALSE)
```

5. SJ-SDM model

```
#Install packages
devtools::install_version("ggplot2", version = "3.4.0")
devtools::install_git('https://bitbucket.org/nicholasehamilton/ggtern')
devtools::install_github("https://github.com/TheoreticalEcology/s-jSDM", subdir = "sjSDM",
ref = "master")
#Load libraries
library(sjSDM)
library(raster)
library(PresenceAbsence)
library(pROC)
## Open data of presence and absences (Occ), geographical coordinates (SP) and environmental
predictors (Env)
#The data must be converted into a  matrix format to be applied on the model after
#Presence and absences
Occ <- read.csv("../Mapping Namibian benthic biodiversity for
conservation/Data/NamBenthos_Merged – 1.csv",header=TRUE,sep=";")[,11:153]
Occ1 <- as.matrix(Occ)
Occ1 <- Occ1[,which(apply(Occ1,2,var) != 0)]
```

```
head(Occ1)
## Geographical coordinates (x and y)
SP <- read.csv("../Mapping Namibian benthic biodiversity for
conservation/Data/NamBenthos_Merged – 1.csv",header=TRUE,sep=";")[,2:3]
SP1 <- as.matrix(SP)
head(SP1)
## Environmental predictors extracted from raster layers
Env <- read.csv("../Mapping Namibian benthic biodiversity for
conservation/Data/NamBenthos_Merged – 1.csv",header=TRUE,sep=";")[,4:10]
Env1 <- as.matrix(Env)
head(Env1)
####Model#########
#The optimal set of hyper-parameter values for the model were determined based on achieving
the highest Area Under the Curve (AUC) score,
#indicating the best performance.
Model = sjSDM(Y = Occ1, env = DNN(Env1,hidden = c(10L, 10L), lambda = 0.01, alpha =
0.5), iter = 100, family = binomial("logit"), seed=1)
##Predict the output for a new dataset considering environmental predictors of model above
pred = predict(model, newdata = Env1)
#Convert predict and observed data in numeric and vector to plot the ROC curve
predicted <- as.numeric(pred)
observed <- as.vector(Occ1)
#The ROC curve visualizes how well a binary classification model performs by comparing the
true positive rate (sensitivity) to the false positive rate (1-specificity).
pROC::plot.roc(observed, predicted)
auc <- pROC::auc(observed,predicted)
auc
##Correlation between observed and predicted data
cor(observed,predicted)
#### Predict the model to all rasters
#Location of rasters
rasterDirectory <- "../Mapping Namibian benthic biodiversity for conservation/Data/Climate/"
##Environmental predictors (Rasterlayers) for modelling
rasterFiles <-
c("DissolvedMolecularOxygen_BenthicMean_Mean_2010.2020.tif","Nitrate_BenthicMean_Me
an_2010.2020.tif","OceanTemperature_BenthicMean_LtMax_2010.2020.tif","OceanTemperatur
e_BenthicMean_LtMin_2010.2020.tif","Phytoplankton_BenthicMean_Mean_2010.2020.tif","S
alinity_BenthicMean_Mean_2010.2020.tif","SeaWaterSpeed_BenthicMean_Mean_2010.2020.ti
f")
rasters <- stack(list.files(rasterDirectory,full.names = TRUE)[sapply(rasterFiles,function(x) {
which( grepl(x,list.files(rasterDirectory,full.names = TRUE))) } )])
# Consider only the extent of Namibia (xmin, xmax, ymin, ymax)
extent_Nam <- extent(6,20, -34, -14)
# Crop rasters for Namibia region
curr_climate <- (crop(rasters, extent_Nam))
curr_climate.loc <- as.data.frame(subset(curr_climate,1), xy=TRUE, na.rm=T)[,1:2]
curr_climate.mat <- as.data.frame(curr_climate, xy=FALSE, na.rm=T)
pred.rasters <- predict(model, newdata = curr_climate.mat)
names(pred.rasters) <- names(Occ1)
mainResults <- data.frame(curr_climate.loc,pred.rasters)
####Prediction on map
##Observed species richness of species
shapeObs <- subset(curr_climate,1)
shapeObs[] <- NA
shapeObs[cellFromXY(shapeObs,SP1)] <- apply(Occ1,1,sum)
shapeObs <- (shapeObs – cellStats(shapeObs,min)) / cellStats( shapeObs –
cellStats(shapeObs,min) , max)
plot(shapeObs)
writeRaster(shapeObs,filename="speciesRichnessPresentObserved.tif",format="Gtiff",overwrite
=T)
```

```
##Predicted species richness of species
shapePred <- subset(curr_climate,1)
shapePred[] <- NA
shapePred[cellFromXY(shapePred,curr_climate.loc)] <- apply(pred.rasters,1,sum)
shapePred <- (shapePred – cellStats(shapePred,min)) / cellStats( shapePred –
cellStats(shapePred,min) , max)
plot(shapePred)
writeRaster(shapePred,filename=”speciesRichnessPresentPredicted.tif”,format=”Gtiff”,overwrit
e=T)
#Disaggregate raster to create a new RasterLayer with a higher resolution (smaller cells) to
better visualization
shapePredHR <- disaggregate(shapePred, 5, method=’bilinear’)
plot(shapePredHR)
writeRaster(shapePredHR,filename=”speciesRichnessPresentPredictedHR.tif”,format=”Gtiff”,o
verwrite=T)
### Open the shapefile for Namibian Exclusive Economic Zone
EEZ_Namibia <- shapefile(“Data/EEZ_Namibia.shp”)
##Add the shapefile on map
plot(shapePredHR)
plot(EEZ, border = “grey20”, lwd = 0.8, add=T)
#### Get the top biodiversity regions that allows covering 10% and 30%
shapePredHR.namibian <- mask(shapePredHR,EEZ)
shapePredHR.namibian.area <- area(shapePredHR.namibian)
shapePredHR.namibian.area <- mask(shapePredHR.namibian.area,shapePredHR.namibian)
result <- data.frame()
for( I in seq(0,1, length.out=100) ) {
  shapePredHR.namibian.i <- shapePredHR.namibian
  shapePredHR.namibian.i[shapePredHR.namibian.i < i] <- NA
  shapePredHR.namibian.i[!is.na(shapePredHR.namibian.i)] <- 1
  locationsWithinRaster <- which(extract(shapePredHR.namibian.i,curr_climate.loc) == 1)
  richness <- length(which( sapply(1:ncol(pred.rasters) , function(x) {
max(pred.rasters[locationsWithinRaster,x]) }) >= 0.05))
  res <- data.frame(index=1-I,nSpecies=richness,percentageEEZ = 100 * cellStats(
calc(stack(shapePredHR.namibian.i , shapePredHR.namibian.area),prod), sum,na.rm=T) /
cellStats(shapePredHR.namibian.area, sum,na.rm=T), reclass=i)
  result <- rbind(result,res)}
#Plot the species richness predicted from 0 to 100% of EEZ
plot(result[,c(3,2)], ylab=”Biodiversity conservation (species richness)”, xlab=”Percentage of
EEZ”)
lines(result[,c(3,2)])
#Plot the species richness index (from 0 to 1) predicted in percentage of EEZ
plot(result[,c(3,1)], ylab=”Biodiversity conservation (species richness index)”, xlab=”Percentage
of EEZ”)
lines(result[,c(3,1)])
result
##Plot the area covered by 30% of EEZ
shapePredHR.namibian.30 <- shapePredHR.namibian
shapePredHR.namibian.30[shapePredHR.namibian.30 < 0.38383838] <- NA
shapePredHR.namibian.30[!is.na(shapePredHR.namibian.30)] <- 1
plot(shapePredHR.namibian.30)
writeRaster(shapePredHR.namibian.30,filename=”conservationArea30.tif”,format=”Gtiff”,over
write=T)
##Plot the area covered by 10% of EEZ
shapePredHR.namibian.10 <- shapePredHR.namibian
shapePredHR.namibian.10[shapePredHR.namibian.10 < 0.67676768] <- NA
shapePredHR.namibian.10[!is.na(shapePredHR.namibian.10)] <- 1
plot(shapePredHR.namibian.10, add=T, col=”black”)
plot(EEZ, add=T)
writeRaster(shapePredHR.namibian.10,filename=”conservationArea10ofEEZ.tif”,format=”Gtiff
”,overwrite=T)
```

```
plot(shapePredHR)
plot(shapePredHR.namibian.10, add=T, col="black")
plot(EEZ, add=T)
plot(shapePredHR)
plot(shapePredHR.namibian.30, add=T, col="black")
plot(EEZ, add=T)
##Plot the observed data in EEZ
plot(shapeObs)
plot(EEZ, add=T)
# Which Species are present in  30% of EEZs
locationsWithinRaster <- which(extract(shapePredHR.namibian.30,curr_climate.loc) == 1)
which( sapply(1:ncol(pred.rasters) , function(x) { max(pred.rasters[locationsWithinRaster,x]) })
>= 0.05)
#  1  2  7  8 17 18 22 23 32 33 34 82
# Which Species are present in  10% of EEZs
locationsWithinRaster <- which(extract(shapePredHR.namibian.10,curr_climate.loc) == 1)
which( sapply(1:ncol(pred.rasters) , function(x) { max(pred.rasters[locationsWithinRaster,x]) })
>= 0.05)
#1  7  8 17 18 22 23 32 33 34 82
```