Filipe Tobana Nhanquê
N^0 70089

First checklist, mapping and review of the marine biodiversity data for the Bijagós Archipelago (Guinea-Bissau, Africa) - implications for conservation

UNIVERSIDADE DO ALGARVE

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Mestrado em Biodiversidade, Pescas e Conservação Marinha

Supervisors:

M. Pilar Cabezas

Ester A. Serrão

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Declaro ter a autoria deste trabalho, que é original e inédito. Autores e trabalhos consultados estão devidamente citados no texto e constam da listagem de referências incluída.

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I declare I am the author of this work, which is original and unpublished.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.

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Abstract

The Bijagós Archipelago, rich in marine life, serves as a vital nursery and supports local fisheries. International marine research programs have been developed for the Bijagós, especially targeting macrofauna, but the information on marine biodiversity of the Bijagós is scattered and insufficiently available and integrated for a comprehensive assessment. The main goal of this study was to compile, using different sources (scientific fishing campaigns, technical reports, scientific papers, bioportals, etc.), the existing marine biodiversity data in the Bijagós Archipelago, to identify hotspots, knowledge gaps, and conservation priorities in this important region. For this, records were compared inside and outside national parks, or marine protected areas, and species with conservation status according to the IUCN and those with commercial value were identified. A total of 7,222 marine biodiversity records, belonging to 420 species, were found, most of them corresponding to birds and fish taxa. However, most of records are concentrate on specific islands. Of the 420 species, 136 of them were identified as having commercial interest, and most of them were found inside protected areas. Nevertheless, most species identified as critically endangered by the IUCN were found outside protected areas. The results of this study allowed the creation of a platform to make biodiversity information available on an easy-to-use portal, https://www.marafrica.net/Bijagós/. This is free for everyone, and it is dedicated to provide valuable information to managers, stakeholders, scientists, students and the general public for education, management and conservation activities. The present study is the first one that compiles and map all available marine biodiversity data reported to date in the Bijagós Archipelago, and could serve as a baseline to inform conservation measures for preserving the marine biodiversity and ecosystem services of this archipelago and other important African regions.

Resumo

O Arquipélago dos Bijagós, rico em vida marinha, atua como um berçário vital e apoia as pescarias locais. Programas internacionais de pesquisa marinha foram desenvolvidos para os Bijagós, especialmente direcionados à macrofauna, mas as informações sobre a biodiversidade marinha dos Bijagós estão dispersas e insuficientemente disponíveis e integradas para uma avaliação abrangente. O principal objetivo deste estudo foi compilar, a partir de diversas fontes (campanhas científicas de pesca, relatórios técnicos, artigos científicos, bioportais, etc.), os dados existentes sobre biodiversidade marinha no Arquipélago dos Bijagós, identificando pontos de destaque, lacunas de conhecimento e prioridades de conservação nessa importante região. Para isso, foram comparados registros dentro e fora de parques nacionais ou áreas marinhas protegidas, e foram identificadas espécies com status de conservação de acordo com a IUCN, bem como aquelas de valor comercial. Um total de 7.222 registros de biodiversidade marinha, pertencentes a 420 espécies, foi encontrado, a maioria correspondendo a aves e peixes. No entanto, a maioria dos registros está concentrada em ilhas específicas. Das 420 espécies, 136 delas foram identificadas como tendo interesse comercial, e a maioria delas foi encontrada dentro de áreas protegidas. No entanto, a maioria das espécies identificadas como criticamente ameaçadas pela IUCN foi encontrada fora de áreas protegidas. Os resultados deste estudo permitiram a criação de uma plataforma para disponibilizar informações sobre biodiversidade em um portal de fácil utilização, https://www.marafrica.net/Bijagós/. Este é gratuito para todos e é dedicado a fornecer informações valiosas para gestores, partes interessadas, cientistas, estudantes e o público em geral para atividades de educação, gestão e conservação. O presente estudo é o primeiro a compilar e mapear todos os dados de biodiversidade marinha disponíveis até a data no Arquipélago dos Bijagós e pode servir como uma linha de base para informar medidas de conservação para preservar a biodiversidade marinha e os serviços ecossistêmicos deste arquipélago e outras regiões importantes da África.

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List of Abbreviations:

AGA KHAN - The Aga Khan Development Network (AKDN)
AMPCI Urok - Urok Islands Community Marine Protected Area
CAOPA - Confédération Africaine des Organisations de Pêche Artisanale
CIPA - Centre for Applied Fisheries Research
CR - Critically Endangered
DD - Data Deficient
GBIF - Global Biodiversity Information Facility
GPC - Coastal Planning Office
GPS - Global Positioning System
IBAP - Institute of Biodiversity and Protected Areas
iNaturalist - scientific and citizen project and a connected social network of naturalists, scientists and biologists with the aim of building and mapping biodiversity across the globe by sharing observations.
INEP - National Institute of Statistics and Research
INIPO - National Institute for Fisheries and Oceanographic Research Bissau, Guiné-Bissau
IUCN - International Union for Conservation of Nature
LC - Least Concern
MPAs - Marine Protect Areas
NT - Near Threatened
OBIS - Ocean Biodiversity Information System
ODZH - Organization for the Defense of Wetlands, Wetlands International
ONG - Palmeirinha
ONG - Tininguena
PNMJVP - João Vieira and Poilão Marine National Park
PNO - Orango National Park
RAMSAR - Convention on Wetlands is the intergovernmental treaty that provides the framework for the conservation and wise use of wetlands and their resources.
SIAP - Fishery Information and Analysis System Project
UNESCO - United Nations Educational, Scientific and Cultural Organization
VU - Vulnerable
WGS84 Datum - World Geodetic System
WoRMS- WoRMS - World Register of Marine Species
WWF - World Wide Fund for Nature

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Filipe Tobana Nhanquê[1,2*], M. Pilar Cabezas[2*], Jorge Assis[2], Ester A. Serrão[2,3]

[1]*INIPO – National Institute for Fisheries and Oceanographic Research Bissau, Guiné-Bissau*
[2]*CCMAR – Centre of Marine Sciences, Universidade do Algarve, Faro, Portugal*
[3]*CIBIO-InBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, Porto, Portugal*

*The first two authors share equal responsibility in the paper. Corresponding author: lavinhanque@gmail.com and pilarcabezas84@gmail.com

Abstract

The Bijagós Archipelago, rich in marine life, serves as a vital nursery and supports local fisheries. International marine research programs have been developed for the Bijagós, especially targeting macrofauna, but the information on marine biodiversity of the Bijagós is scattered and insufficiently available and integrated for a comprehensive assessment. The main goal of this study was to compile, using different sources (scientific fishing campaigns, technical reports, scientific papers, bioportals, etc.), the existing marine biodiversity data in the Bijagós Archipelago, to identify hotspots, knowledge gaps, and conservation priorities in this important region. For this, records were compared inside and outside national parks, or marine protected areas, and species with conservation status according to the IUCN and those with commercial value were identified. A total of 7,222 marine biodiversity records, belonging to 420 species, were found, most of them corresponding to birds and fish taxa. However, most of records are concentrate on specific islands. Of the 420 species, 136 of them were identified as having commercial interest, and most of them were found inside protected areas. Nevertheless, most species identified as critically endangered by the IUCN were found outside protected areas. The results of this study allowed the creation of a platform to make biodiversity information available on an easy-to-use portal, https://www.marafrica.net/Bijagós/. This is free for everyone, and it is dedicated to provide valuable information to managers, stakeholders, scientists, students and the general public for education, management and conservation activities. The present study is the first one that compiles and map all available marine biodiversity data reported to date in the Bijagós Archipelago, and could serve as a baseline to inform conservation measures for preserving the marine biodiversity and ecosystem services of this archipelago and other important African regions.

Keywords: Bijagós Archipelago Marine Biodiversity, temporal, spatial records, taxonomy and distribution

1- Introduction

Information about species numbers and distributions are essential to understand biodiversity patterns and ecological and evolutionary processes, and to preserve the great variety of life on Earth, which has been reported to be declining dramatically in the past 50 years (WWF, 2022). The gap in data on distribution of biodiversity on Earth is particularly strong for the oceans. Presently, a total of 242,929 marine species are known and validated (WoRMS, 2023); however, this number could be 10-fold higher than currently estimated (Lotze, 2021). The "Census of Marine Life" initiative, between 2000 and 2010, highlighted that many habitats have been poorly sampled worldwide, especially those from deep waters, and that several species-rich taxonomic groups, mostly small-sized taxa, remain poorly studied (Miloslavich, 2008; Costello et al., 2010; Alexander et al., 2011).

The marine biodiversity knowledge gap is particularly striking for Africa. Africa is one of the richest regions in the world in terms of marine biodiversity, hosting eight of the world's biodiversity hotspots (Von der Heyden, 2022; Myers et al., 2000) and supporting critical ecosystem services that benefit approximately 16% of the global population (Von der Heyden, 2022). The West African region in particular, is considered a natural sanctuary for marine biodiversity and one of the major fishing zones worldwide (Benchimol, et al., 2009), thanks to upwelling phenomena and marine current that characterize this area (Sidibe, 2010; Griffiths et al., 2010). The last census of marine fish species, carried out within the framework of the Fishery Information and Analysis System project (SIAP), reported nearly 700 species of marine fish in all seven countries (Mauritania, Senegal, Gambia, Guinea-Bissau, Guiné Conacri, Cape Verde, and Sierra Leone) of the Sub-Regional Fisheries Commission (Sidibe, 2010). These fishery resources have vital importance for people living in this area and around the world, as they constitute a good source of protein, fatty acids, vitamins, minerals, and are available at low prices (CAOPA & Fröcklin, 2016). Nevertheless, the effects of climate change and overexploitation in this region are seriously threatening Africa's marine biodiversity and the ecosystems services they provide (Dejene, 2018; Archer et al., 2021). Thus, much loss is happening before African marine biodiversity is well known. Critically, marine biodiversity of Africa remains poorly studied (Boufahja et al., 2015; Friedlander et al., 2014), mainly due to the lack of research infrastructures and financial support (Von der Heyden, 2022), which render difficult the proper assessment, knowledge and monitoring of African marine ecosystems (Friedlander et al., 2014; Von der Heyden, 2022).

Among African countries, Guinea-Bissau is considered the richest place in natural resources and coastal and marine biodiversity (Catry et al., 2010; Junior et al., 2019). Located between Cape Roxo (Senegal) to the north, Ponta Gardete (Republic of Guinea-Conakry) to the south and east, and the Atlantic Ocean to its west (Silva, 2000; Biai, 2009; Catry et al., 2010; Secretaria De Estado Do Ambiente da Guiné-Bissau, 2015; Moreira, 2021; Cafete, 2021) (Figure 1), Guinea-Bissau has an extensive coastline over 280 km long, and a large continental shelf of approximately 45,000 km^2 (Edmundson, 2014;

Insambé, 2021). The platform has a depth of up to 20 m, extends for 180 km from the coast inland (Insambé, 2021). It has major rivers and estuaries such as Cacheu, Mansoa, Geba, Buba Cacine, which allow connectivity to the sea (Auliya et al., 2012). All coastal river systems add fresh, cold, nutrient-rich water to the warm, shallow waters of the continental shelf (Edmundson, 2014), contributing to the great biodiversity richness of the Bijagós Archipelago as a major coastal extension of the country.

The Bijagós Archipelago occupies a preponderant place among the great natural monuments of the West African coast (Saraiva, 2015), and comprehends most of the Marine Protected Areas (MPAs) of Guinea-Bissau (Benzinho & Rosa, 2015). Covering nearly 10,000 km^2 off the coast of Guinea-Bissau (Ferreira, 2012; Auliya et al., 2012), this archipelago has a rich macrozoobenthic biodiversity (Lourenço, et al. 2018), hosts one of the largest intertidal areas in the region, represents one of the major nursing areas worldwide to both coastal and pelagic fish species, including commercial ones captured in the industrial fisheries, and supports local (artisanal) fisheries (Leurs et al., 2023). The Bijagós comprises 88 islands and islets (Figure 1), twenty-one of them are permanently inhabited (Ferreira, 2012; Auliya et al., 2012). It constitutes a particular natural and cultural space that is still well preserved and maintained thanks to the strong integration of cultural and natural values of the region (Saraiva, 2015). The great abundance of fish, crustaceans and mollusks has been described by numerous oceanographic expeditions throughout the region, testifying its fundamental role as a reproduction area of many species with a commercial value (Madeira, 2009, 2010, 2016). One of the expeditions, conducted three decades ago, detected 175 fish species (Lafrance, 1994). Sharks and rays are particularly well represented (Janeiro et al., 2008; Dulvy et al., 2016; Campredon & Catry, 2016). Cetaceans (Benzinho & Rosa, 2015), five of the seven world species of sea turtles (Rebelo & Catry, 2011; Ferreira, 2016), and several marine bird species (Dodmand et al., 2004) have also been recorded. This archipelago is even considered the second most important wintering area for shorebirds in Africa (Catry et al., 2010; Campredon & Catry, 2016; Lourenço et al., 2018). Moreover, it is home to several species of international conservation concern such as sea turtles, marine mammals, fish, and seabirds (Coelho et al., 2022).

Despite the known richness of marine biodiversity at the Bijagós, the scientific studies conducted at this archipelago are sparse and usually directed to the same taxonomic groups (mostly fish, turtles, and seabirds) or have been conducted on a small spatial scale, as in the same groups of islands (this study). Moreover, other groups like marine invertebrates and algae seem practically not known from the archipelago. That means several biodiversity information still lacks for this important region, which could have a serious negative effect on the knowledge and processes of ecosystem services on marine environments (Boufahja et al., 2015; Leurs et al., 2023), and thus on marine biodiversity conservation.

The main purpose of this study was to compile and map all available data with marine biodiversity records reported to date in the Bijagós Archipelago. Specifically, biodiversity records per taxonomic group and island through time were compiled; and the hotspots of biodiversity, and major gaps of knowledge regarding taxonomic groups and locations within the archipelago were identified. Moreover, marine biodiversity was compared inside and outside national parks, or marine protected areas, and species with conservation status according to the IUCN and those with commercial value were identified. This study represents an important baseline for more effective conservation measures to protect the marine biodiversity of the Bijagós Archipelago, crucial to ensure future ecosystem health and the preservation of ecosystem services in this important region.

2- Methods

2.1. Study area

The Bijagós Archipelago is located in the insular area of Guinea-Bissau (Cardoso, 2013), at 11°14'00.0"N 16°02'00.0"W” not far from the mainland coast (Figure 1), and was defined in this study according to Campredon & Catry (2016). This region covers an area of around 2,624 km^2 (Carvalho et al., 2018). The land area is around 90,000 ha, while another 100,000 ha are uncovered during low tide, of which around 76,000 ha correspond to mudflats and 35,000 ha to mangroves (Dodman & Sá, 2005; Rebelo & Catry, 2011). The Bijagós is the only active deltaic archipelago on the Atlantic coast of Africa (Campredon & Catry, 2016). According to several studies, Bijagós seems to have a continental origin, formed due to the flood of the old delta of the Geba River on the West African coast. The rocks of this archipelago have a Miocene genesis, and that would have been the results of continuous flows to the African continent on several occasions when sea levels fell in cold phases of glacial cycles (Rebelo & Catry, 2011; Cardoso, 2013).

In April 1996, the Bijagós Archipelago was classified as a Biosphere Reserve by UNESCO, and in 2014 was recognized as a wetland of international importance by the Convention on Wetlands of International Interest for Waterfowl (RAMSAR). In 2015, its classification as a World Heritage Site was requested (Madeira, 2016, 2019). This Biosphere Reserve consists of three protected areas: the “João Vieira and Poilão Marine National Park” (PNMJVP), the “Orango Islands National Park” (PNO), and the “Community Protected Marine Area of the Urok Islands” (AMPCI Urok) (Figure 1). A network of channels, which rarely reach 15 m depth (Diouf et al., 1994; Campredon & Catry, 2016), separates all these islands. In general, mangroves, sand flats and extensive mud surround the Bijagós Archipelago, which together represent the most extensive intertidal area in Africa (Binet, 2015; Campredon & Catry, 2016). The climate of the region is tropical and bi-seasonal, with a wet season from May to October, and a dry season from November to April (Coelho et al., 2022). The archipelago is influenced by the Canary Current during the dry season and by the Guinean Current during the rainy season. The sea temperature usually ranges between 26 to 30 °C, and the salinity from 30 to 36 ppt. Despite seasonal differences, the marine biodiversity of this region seems to remain largely unchanged through the year (Correia et al., 2017).

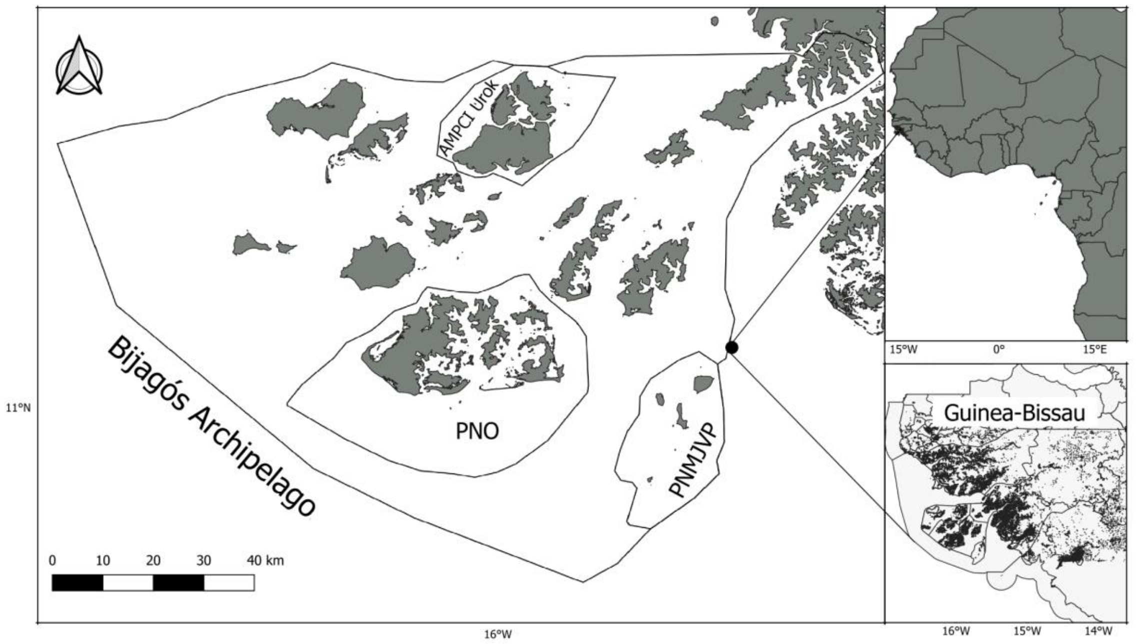


Figure 1. Study area of the Bijagós Archipelago including the limits of the three protected areas: João Vieira and Poilão Marine National Park (PNMJVP), the Orango Islands National Park (PNO), and the Community Protected Marine Area of the Urok Islands (AMPCI Urok).

2.2. Data Collection

From January to August 2023, biodiversity-associated data for all marine taxa recorded at the Bijagós Archipelago were collected from all available sources, namely scientific fishing campaigns, literature (books, reports, scientific papers, etc.), institutions and bioportals (GBIF and iNaturalist). Data were complemented with additional information from WORMS-World Register of Marine Species, to obtain the most updated taxonomic name, the taxonomic categories. Data collected included the original scientific name of the species (or taxon if it was not identified until species level), the present valid name for each taxon, the taxonomic rank, the localities and National Parks or Marine Protected Area where they were found, the geographical coordinates and accuracy of coordinates, the date in which they were recorded, and the bibliographic references from which the information was extracted. The geographical coordinates were all converted to decimal (WGS84 Datum). When only the location was described without coordinates reported, approximate coordinates were selected, with corresponding degree of accuracy relative to the detail in the site description.

All data compiled for this study are in the Supplementary Table S1.

The complete database has been made publicly available online at the specific MARAFRICA webportal designed by biodiversityDataScience for the compilation of all marine biodiversity information of the Bijagós: https://www.marafrica.net/ Bijagós/. This Bijagós Biodiversity portal provides access not only to the information here compiled, which is exclusively marine and only up to August 2023, but also to all the terrestrial species biodiversity of the Bijagós Archipelago available in GBIF and iNaturalist. Furthermore, it is automatically updated monthly with the new records added from these two bioportals, and links to iNaturalist for citizens to add new photographic records of biodiversity: https://www.inaturalist.org/projects/biodiversity-of-the- Bijagós-archipelago.

2.2.1. Scientific Fishing Campaigns carried out by INIPO

INIPO - National Institute of Fisheries and Oceanographic Research (previously CIPA, Centre for Applied Fisheries Research) is the governmental institution responsible for research in the field of fisheries resources and the production of scientific data necessary for the implementation of a sustainable management system for marine resources in Guinea-Bissau.

Scientific fishing campaigns were conducted in April and May 2022, and July 2023 in João Vieira, one of the main islands of the João Vieira and Poilão Marine National Park, and in other locations in the archipelago such as around the islands of Canhabaque, Caravela, Carache, Imbone, and Orango. In each campaign, a canoe of 13 meters in length and 2.5 meters in width was used, with two nets, one at the surface and the other in the water column to catch the organisms. Nets were placed taking into account the amplitude of the tides (high and low), between 5 and 6 pm local time, and were removed the next morning (around 10 am) on low tide. Samples were separated according to the mesh size of the nets and identified one by one until species level, when possible, with the help of taxonomic experts or using taxonomic keys (Bianchi, 1986; Sanches, 1991). A GPS, two 200 cm ichthyometers, a scale with a precision of 0.5 g, tweezers and a field notebook, were used to record the data (e.g., weight, length, maturation state, sex, etc.).

2.2.2. Bibliographic Review

The bibliographic revision was carried out by researching and reading different sources of literature such as scientific articles, theses, dissertations, monographs, reports and working documents of the Guinea-Bissau institutions focused on conservation of marine biodiversity. In the online research for literature we used keywords such as “Bijagós”, “Bijagós Biodiversity”, “Bijagós Archipelago”, “Bijagós Guinea-Bissau”, “West Africa Bijagós”, “Bijagós Conservation”, “João Vieira Poilão Marine National Park”, “Orango National Park”, “Marine Community Area of the Islands of Urok” and “the Bijagós Archipelago Biosphere Reserve”, either in Portuguese, English or French, on Google and Google Scholar.

2.2.3. Contact with Guinea-Bissau institutions dedicated to marine research

Between April and July 2023, we contacted and received reports and strategic documents, with biodiversity data from several institutions in Guinea-Bissau: INIPO - National Institute for Fisheries and Oceanographic Research; IBAP - Institute of Biodiversity and Protected Areas; INEP - National Institute of Statistics and Research; GPC - Coastal

Planning Office; ODZH - Organization for the Defense of Wetlands, Wetlands International; ONG - Palmeirinha, and ONG - Tininguena.

2.2.4. Data from GBIF and iNaturalist

In August 2023, we extracted data from the portal of the Global Biodiversity Information Facility - GBIF (2023a, b) and the citizen science portal iNaturalist (www.iNaturalist.org), for the Bijagós Archipelago. On both platforms, data were obtained through a polygon drawn around the area corresponding to the Biosphere Reserve. OBIS (Ocean Biodiversity Information System) was not used due to replicated information at GBIF.

All these data were filtered to keep only marine species using R v.4.2.1. (R Core Team, 2022) and Perl (Wall et al., 2000) scripts (see scripts 1-3 in the Supplementary Material). In R, the tidy-verse (Wickham et al., 2019) and worrms (Chamberlain & Vanhoorne, 2023) packages were used.

2.2.5. Data Analysis

For each record, the complete taxonomic information, was obtained using the R script "Get_Taxonomy.R" (see script 4 in the Supplementary Material). Moreover, those records identified till species level were classified into one of the nine categories of the IUCN Red List of Threatened Species (IUCN, 2022) using the R script "Get_IUCN_category.R" (see script 5 in the Supplementary Material). In addition, species of commercial interest were identified.

All this information was organized and gathered in a single table (see Table S2 in the Supplementary Material) using two custom R scripts (see scripts 6.1 and 6.2 in the Supplementary Material). These data were analyzed for temporal, spatial and taxonomic distribution of records, and considering their conservation status and commercial interest. The tidy-verse (Wickham et al., 2019) and ggplot2 (Wickham, 2016) packages were used for these analyses.

All analyses were performed in RStudio v.4.2.1 (Posit Team, 2023).

3- Results

3.1. Temporal Distribution and Sources of Records

A total of 7,222 records of marine biodiversity were found for the study area the Bijagós archipelago in the period between 1847 and August 2023. Over all these years, the highest number of records was in 2019, with 1,217 registrations.

Other years with high number of records were 2015, 2008 and 2014, when 771, 690 and 546 records were observed, respectively.

The first record that we found of marine biodiversity in the Bijagós archipelago, with just one record, was in January 1847 for a coral species then called *Eunicella papillifera* (Milne Edwards & Haime, 1857) of the class Anthozoa and the family of Eunicellidae. This species was recorded outside of conserved areas by the authors mentioned above.

After the record in 1847, 66 years later, fourteen new species were record such as *Fontitrygon margarita* (Günther, 1870), *Sardinella maderensis* (Lowe, 1838), *Fodiator acutus* (Valenciennes, 1847), *Hemiramphus brasiliensis* (Linnaeus, 1758), *Parachelon grandisquamis* (Valenciennes, 1836), *Neochelon falcipinnis* (Valenciennes, 1836), *Pomadasys suillus* (Valenciennes, 1833), *Sarotherodon melanotheron* (Rüppell, 1852), *Psettodes bennettii* (Steindachner, 1870), *Cynoglossus senegalensis* (Kaup, 1858), *Ephippus goreensis* (Cuvier, 1831), *Fontitrygon margaritella* (Compagno & Roberts, 1984), *Plectorhinchus mediterraneus* (Guichenot, 1850) and *Sheldonella minutalis* (P. G. Oliver & Cosel, 1993) in 1913.

Species records began to increase successively in the region since 1945 with 26 records, but the rate of increase in observations of marine biodiversity recorded was not constant, sometimes decreasing drastically in some years (as shown in Figure 2).

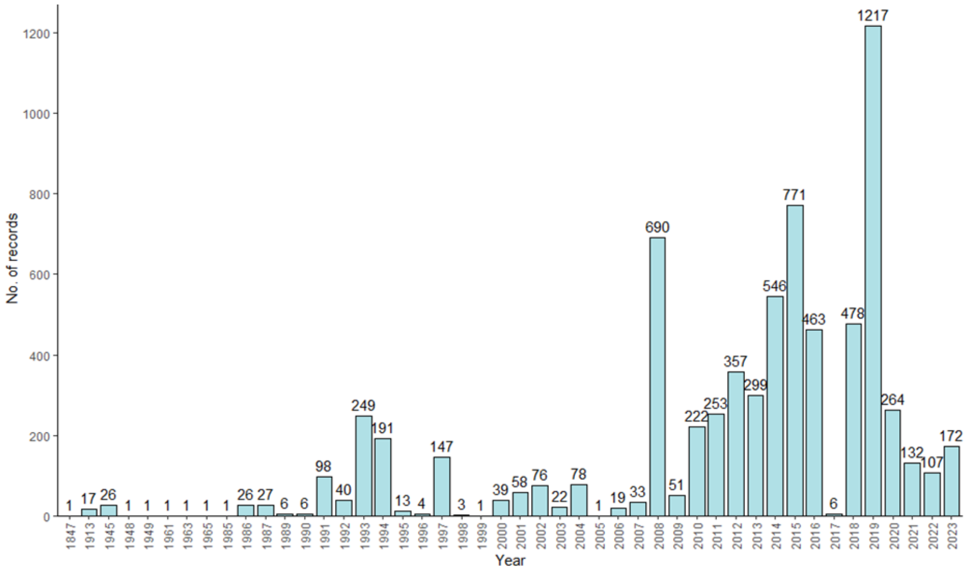


Figure 2. Number of records over time

The main source of biodiversity records was the Bioportal platform GBIF with 2,305. Scientific papers follow in second position with 1,702 records and Technical reports with 1,351 records. The remaining sources have approximately equal values in terms of proportions, but different in total numbers. Of these it is noteworthy that 378 records are derived from unpublished sources (Figure 3).

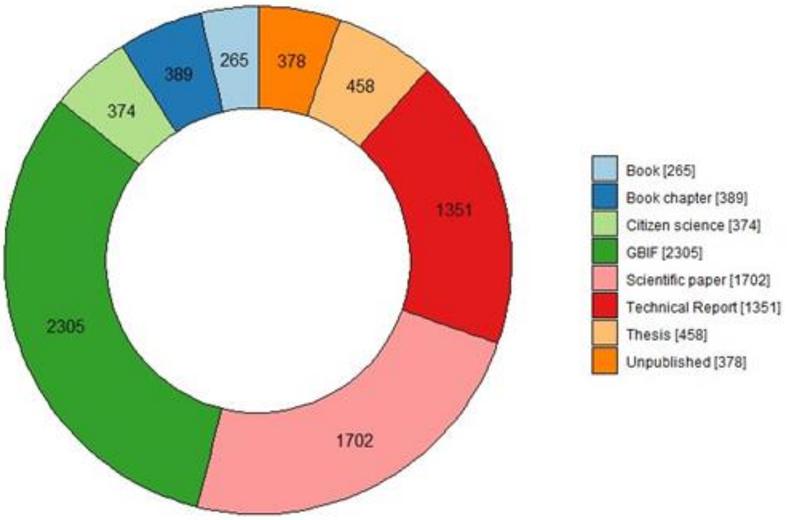


Figure 3. Number of records per source studied

There are eight sources of information compiled; in all of them, GBIF is the only one with a historical timeline of storing records of marine biodiversity starting in 1847 until the present. This is followed by book chapters starting in 1950, and subsequently books and Citizen Science, both starting recording between 1960 and 1970 (Figure 4). However, in general, all compiled sources present had a greater concentration of records from the late 1990s to the present year.

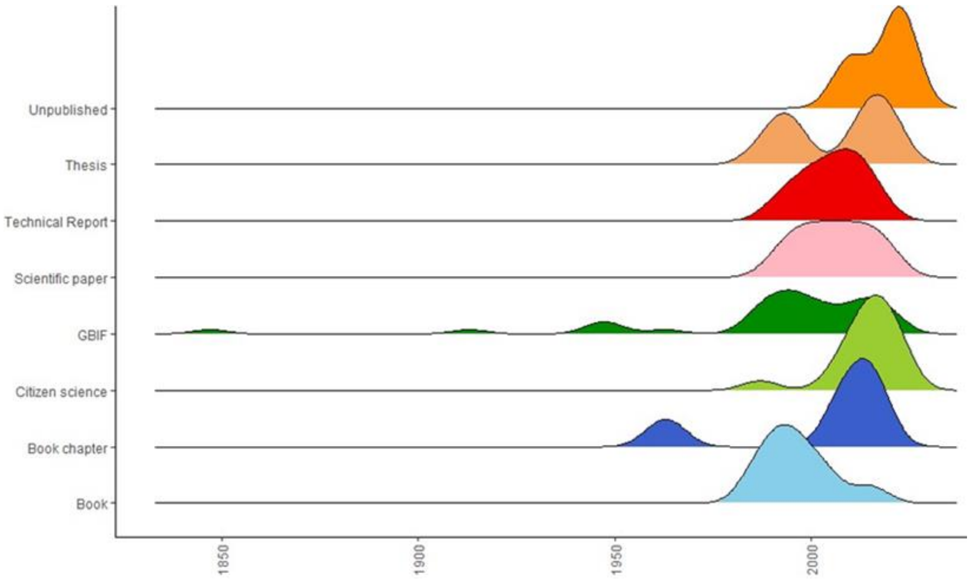


Figure 4. Number of records over time per source

The temporal analysis of taxonomic classifications of the records obtained in this study revealed that in 1993 there was an increase in the taxonomic levels of the family, genus and species. Likewise, in 2007 and 2008, the three taxonomic levels increased again to an increasing and significant level, but with the situation different from that of 1993. In these years it is seen that new species were registered that belong to a family and genus that had not existed before (Figure 5).

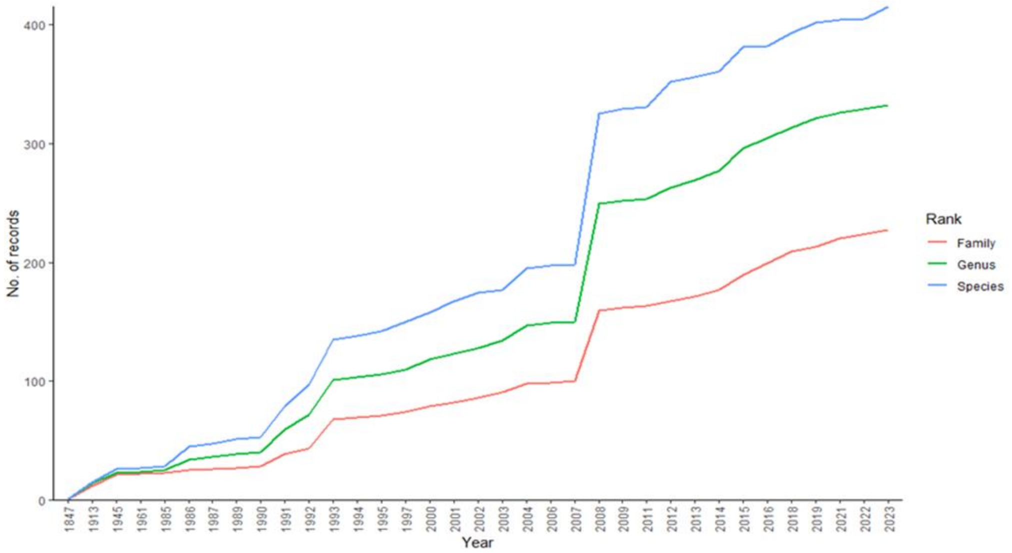


Figure 5. Cumulative number of new records over time

For the entire study area, the results of this study reveal that since the first records in 1847 until 2023, it was possible to identify the records down to the species level. A small proportion of records have not been identified to species level, only to a higher taxonomic category (Figure 6), mostly in the more recent years since 2007, when there was a large increase in the number of new families observed (Figure 5). In 2023, some records have only been identified to Phylum, corresponding mostly to recent citizen science photographic records (iNaturalist) not yet identified to species.

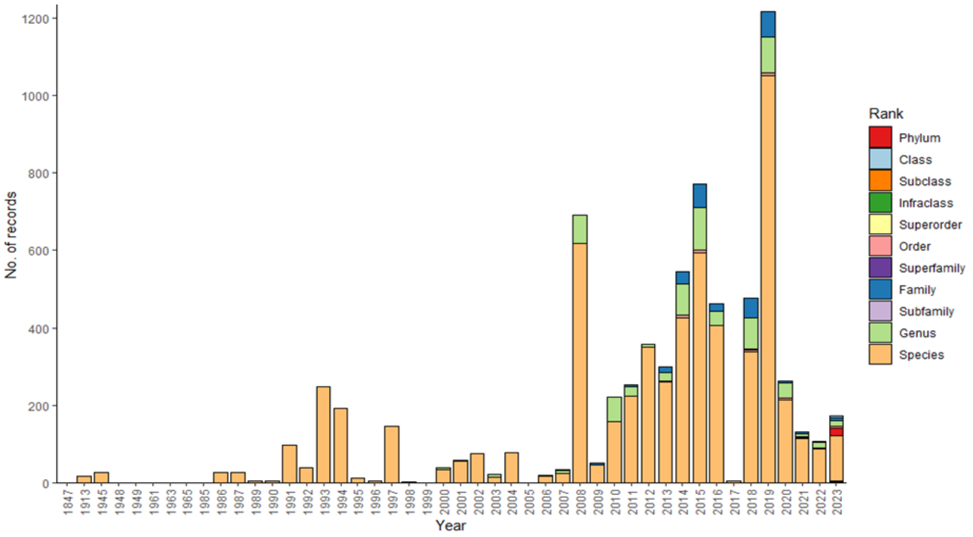


Figure 6. Number of records per taxonomic group over time

3.2. Taxonomic Distribution of Marine Biodiversity Records

There were in total twelve different Phyla found in this study; the most represented group was Phylum Chordata with 5695 records (Figure 7), representing vertebrates like fish, birds and turtles, all disproportionally more represented than all other groups. In much smaller proportions were other animal Phyla: the Phylum Mollusca was the second representative with 569 records, mostly gastropods and bivalves, and Arthropoda with 324 records of Crustaceans. Phylum Bryozoa was found just with one record (Figure 7). There were a few hundred records of plants (Tracheophyta), and algae (Rhodophyta, Ochrohyta, Chlorophyta) (Figure 7).

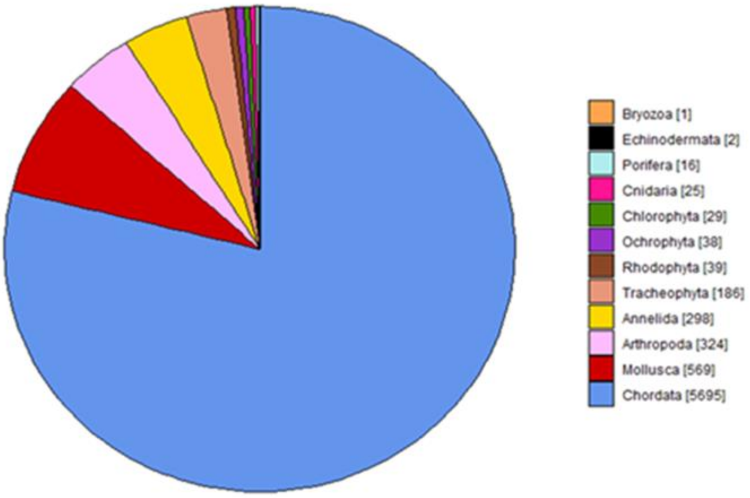


Figure 7. Proportion of records per Phylum

In numbers of species observed per Phylum, the Chordata were still the largest by far with 302 species, followed by the Phylum Mollusca with 51 species and the Arthropoda with 23 species. The remaining Phyla had 10 or fewer species observed (Figure 8).

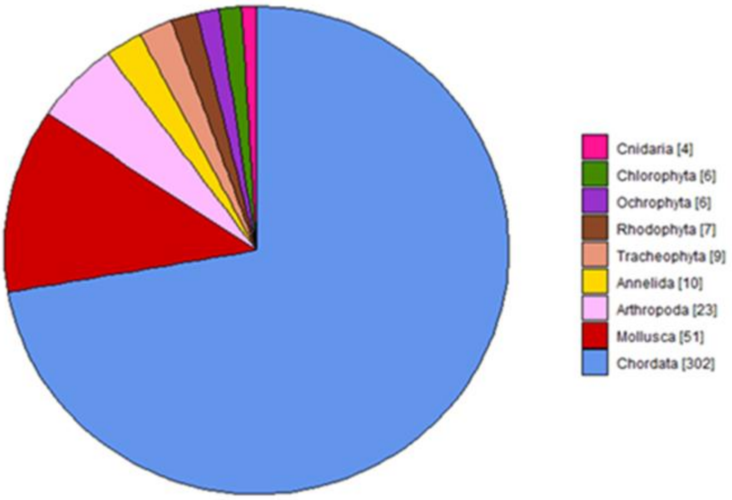


Figure 8. Number of Species recorded per Phylum

Among the four classes of the Phylum Chordata most recorded (Teleost, Reptile, Elasmobranch and Mammalia), Teleost and Reptiles represent the most studied classes with more than 2000 records each one. Reptiles were represented separately for Birds (Aves) because this group comprised the majority of the records, ca. 2500 just for Aves. Elasmobranch and Mammalia were the lowest studied classes, both more than 200 records (Figure 9).

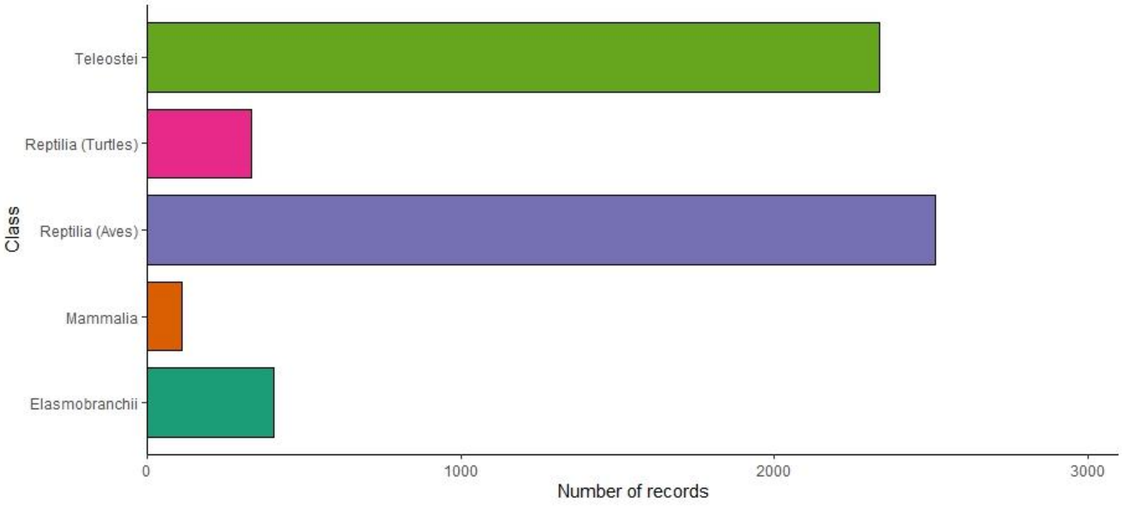


Figure 9. Most recorded Classes (Phylum=Chordata)

Considering the non-Chordata, the Mollusca is the phylum with much more observations, mostly of bivalves and gastropodes (and only few Scaphopoda). The Arthropoda and Annelida are then the other most observed phyla (with most observations of classes Malacostraca and Polychaeta, respectively per phyla). The Tracheophyta then has almost 200 observations, mostly of Magnoliopsida (and few records of Polypodiopsida). The other phyla of macroinvertebrates and algae, such as the Porifera, Cnidaria, Echinodermata, Bryozoa, and Rhodophyta and Ochrophyta, present only a few number of observations (Figure 10).

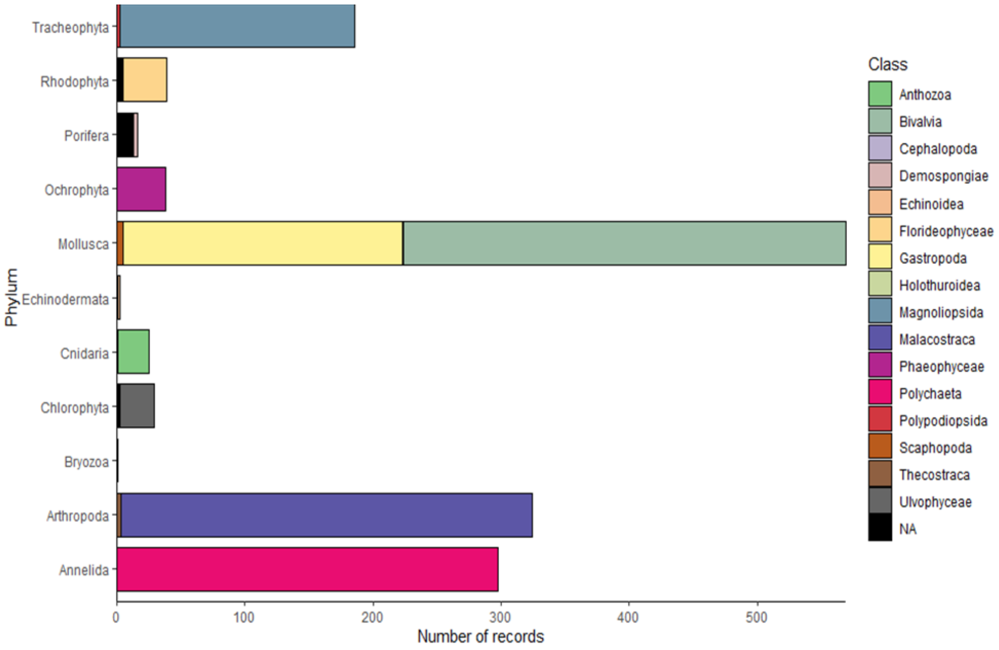


Figure 10. Number of records per Phylum discriminated by Class (excluding Chordate)

The greatest proportion of chordates species considered in this study belong to the class Teleostei (more than 150 species) (Figure 11).

Bird reptiles (Aves) and Elasmobranchs with similar approximately values came in second most representative groups, and for Mammalia there were not many records.

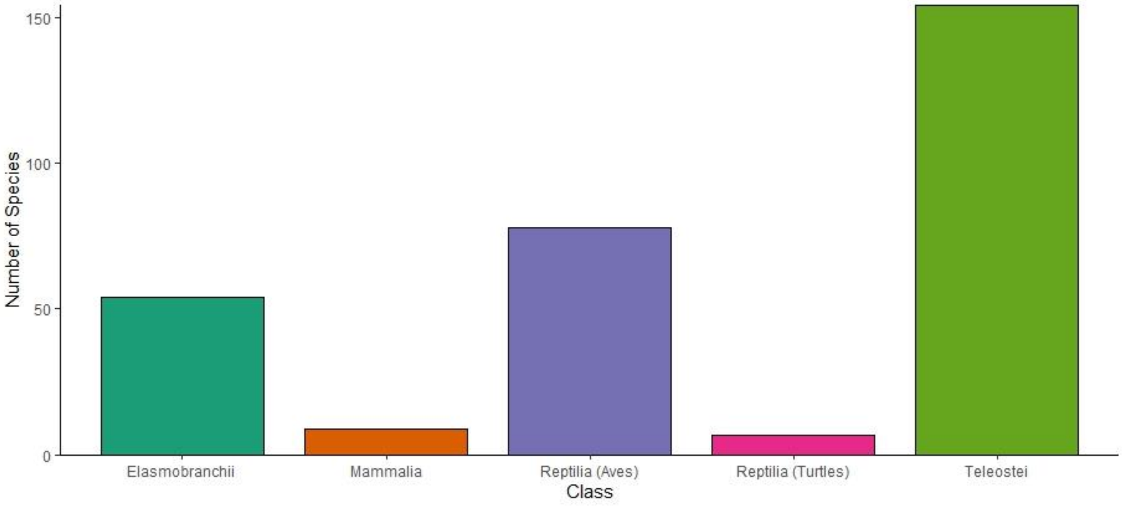


Figure 11. Number of Species per Class (Phylum=Chordate)

3.3. Spatial Distribution of Records

We found many records in places identified only as Bijagós Archipelago, that do not have the name of the island or exact sites. Thus, the category Bijagós had the most studies and consequently also with the greatest number of records of the species.

The island of Bubaque was the second most studied site, but it has a smaller number of species compared to the island of Orango, with a greater number of species and fewer studies.

The sites known as Canhabaque, Cavalos, Imbone, João Vieira, Kéré, Maio, Meio, Orangozinho, Poilão, Rubane, Soga, Unhocomo, Unhocomozinho and Uracane were all identified as sites with a higher number of species in relation to the number of studies carried out in these localities (Figure 12).

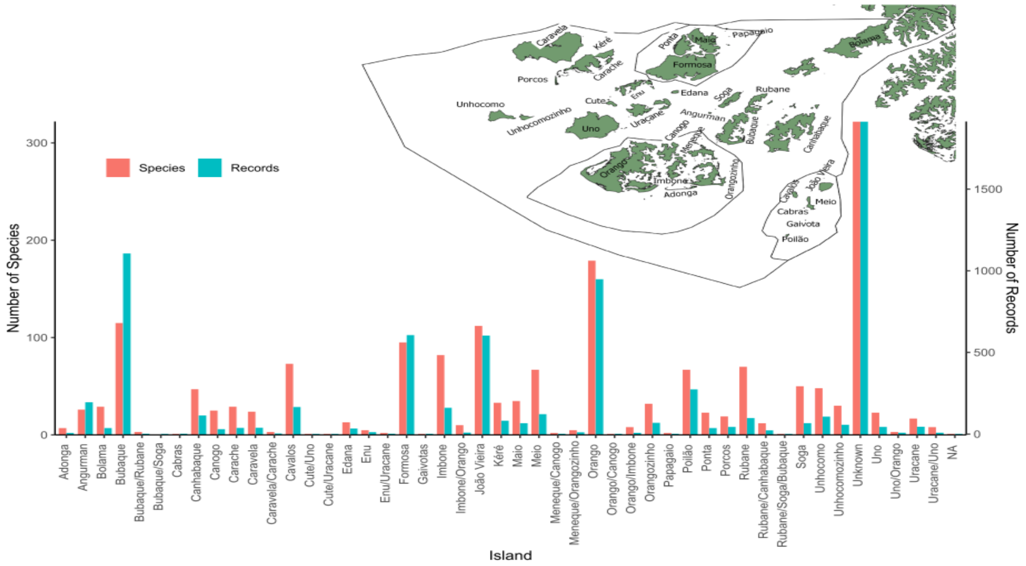


Figure 12. Most studied Island and Number of Species recorded in each island

3.4. Distribution of Records per Spatial Level Conservation

In a total 7,222 records found within the limit of the Bolama Bijagós Archipelago Biosphere Reserve, we compared them into four zones, 3 protected areas (Community Marine Protected Area of Urok, National Park of the Group of Islands of Orango, National Marine Park João Vieira and Poilão) and a 4th zone representing all limits outside of protected areas.

The observations in non-protected zones totaled 3,022 records. Observations were also significant in the National Marine Park João Vieira and Poilão with 1667 records and National Park of the Group of Islands of Orango with 1612 records.

Considering taxonomic groups, it is clear that the records are well distributed inside and outside parks or marine protected areas, allowing comparisons to be made (Figure 13).

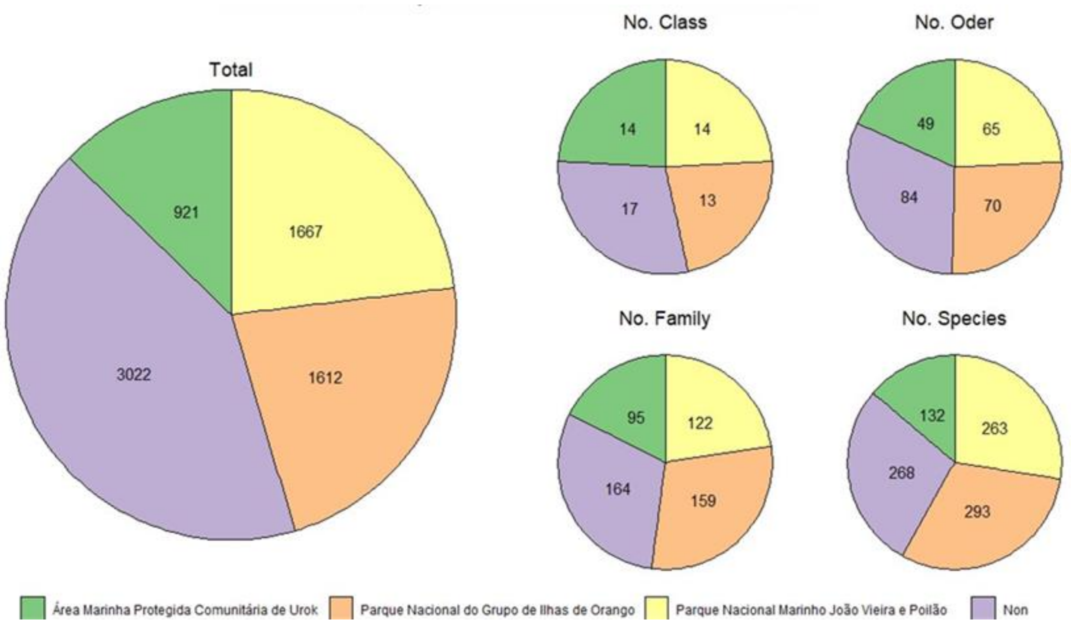


Figure 13. Number of records per National Park/Marine Protected Area

The marine biodiversity records over time within each protected area or non protected other regions, show trends and peaks of marine biodiversity observations in distinct years, that vary among sites and dates, indicating high unevenness of sampling effort and dependence on particular events of sampling (Figure 14). For example, for the AMPCI Urok, marine biodiversity records began in 1945 and continued until 2008 in almost equal proportions. From 2011 to 2013, declining in 2014 - 2016, followed by a peak of new observations in 2018-2019, and a subsequent decrease during the pandemic years.

In the Orango Group of Islands National Park, the first records were dated in 1945, growing slightly until 2007. After the last year with normal records in 2008 and 2019 were the two years with the highest records of marine biodiversity on this area. The remaining years 2009 to 2018 and 2020 to 2022 were the years with records in almost equal proportions. In National Marine Park João Vieira and Poilão, the first record was observed in 1913, which also grew slightly until 2007. In 2008, 2014, 2015 and 2016 were the years with the highest records. Outside protected areas/marine parks, the first records were dated in 1847, these gradually accumulated throughout the years until 2013. In addition, the years 1993, 1997, 2012, 2014, 2015, 2018 and 2019 had more important significant new records.

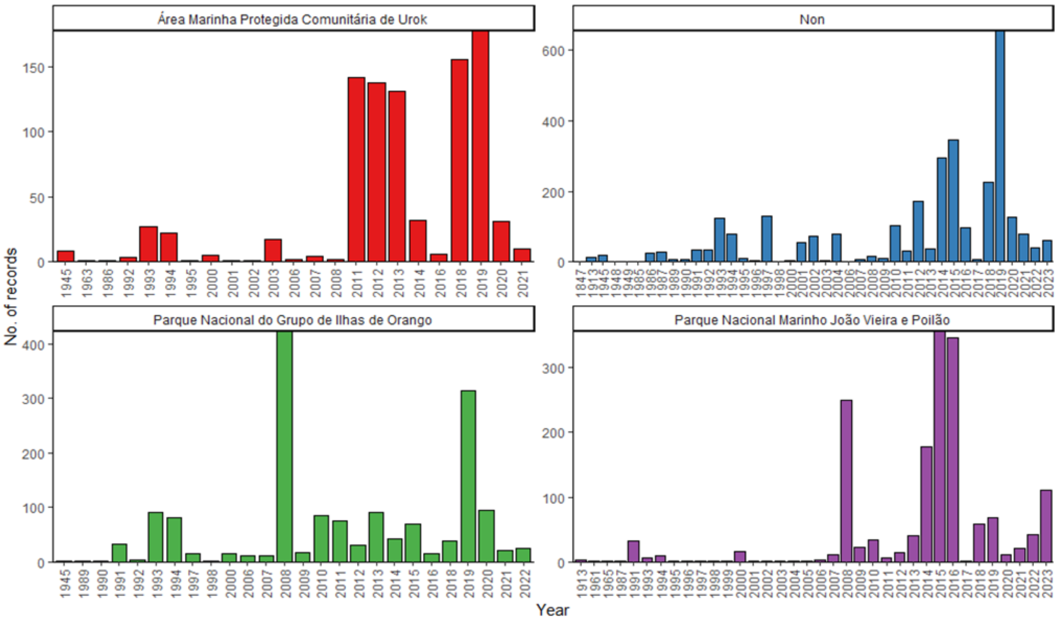


Figure 14. Number of records over time per Protected Area and Non-Protected

Comparing the Chordata among the 4 classified / non-classified areas, shows that the class Reptilia-birds were more often recorded outside the marine protected areas/parks. The largest record of the Teleostei was observed in the National Marine Park João Vieira and Poilão, followed by Orango Group of Islands National Park. The classes of Elasmobranchii and Mammalia had low and proportionally similar numbers in each area of distribution (Figure 15).

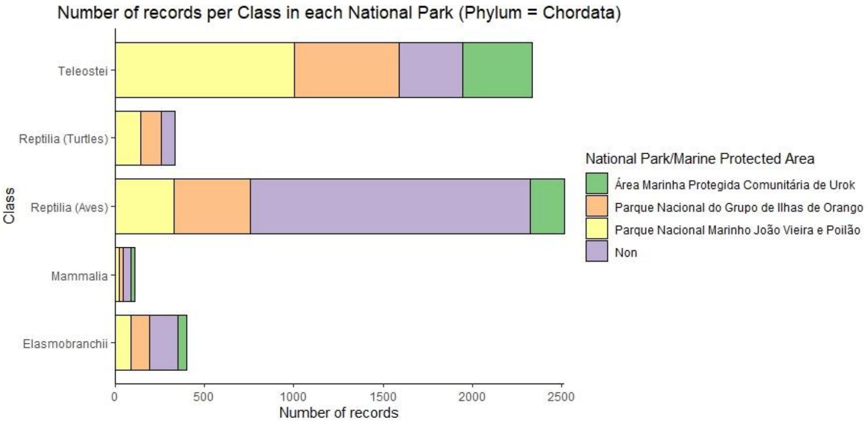


Figure 15. Number of records per Class per Protected Area and Non-Protected (Phylum=Chordata)

The remaining Phyla found in this study were analyzed in each area of the Biosphere Reserve, excluding the Chordata (Figure 16).

The Mollusca had high number of records everywhere except National Marine Park João Vieira and Poilão, especially two classes (Bivalve and Gastropods) and in Orango also Scaphoda. Likewise for the Arthropods, the two largest records were observed, one outside protected areas with only one class (Malacostraca) and the other in National Marine Park João Vieira and Poilão with two classes (Malacostraca and Thecostraca).

The Phylum Annelida with the class Polychaeta remains in third place with the most records and distributed across three areas of the Biosphere Reserve except for the João Vieira and Poilão National Marine Park. Likewise, it was observed that the phylum Cnidaria with the class Anthozoa was also distributed in three areas of the Biosphere Reserve, except for the Orango Group of Islands National Park.

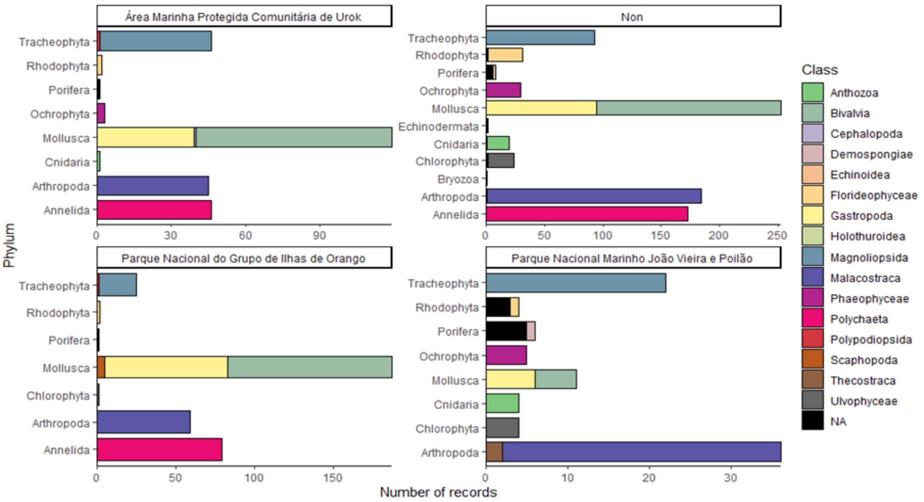


Figure 16. Number of records per Phylum discriminated by Class per Protected Area and Non-Protected (excluding Chordata)

The number of species per class per region, without the Chordata, shows a diversity of groups everywhere but especially diverse outside the three main protected areas, with most groups present there (Figure 17). The phylum Mollusca, represented in three classes (Gastropoda, Bivalve and Scaphopoda) is mainly in the National Park of the Group of Islands of Orango.

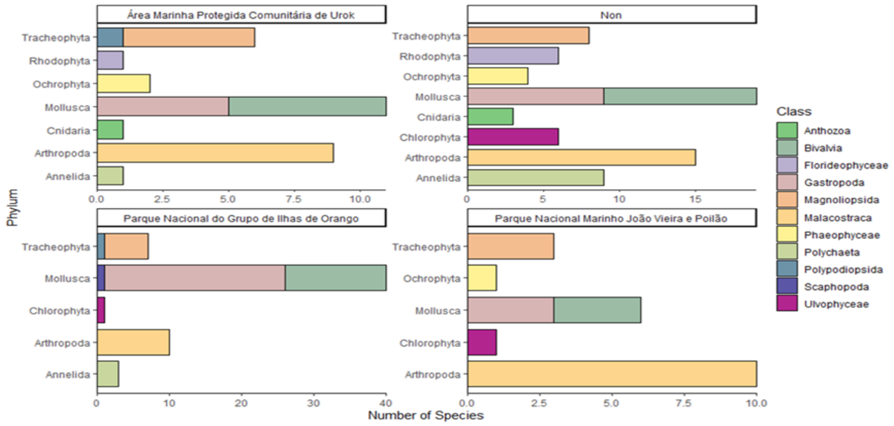


Figure 17. Number of Species per Class per Protected Area and Non-Protected (excluding Chordata)

3.5. Distribution of Records of Commercial Interest

As Bijagós are an area that supports artisanal fishing activity for local communities and sub regions, it was possible through this study to determine the occurrences of species of commercial interest. In a total of 420 species recorded throughout the study area, 136 were species of commercial interest. Considering the three conservation areas that exist in the Bijagós archipelago, the large records of commercial species have been resisted in all of them and some records outside the conserved areas (Figure 18).

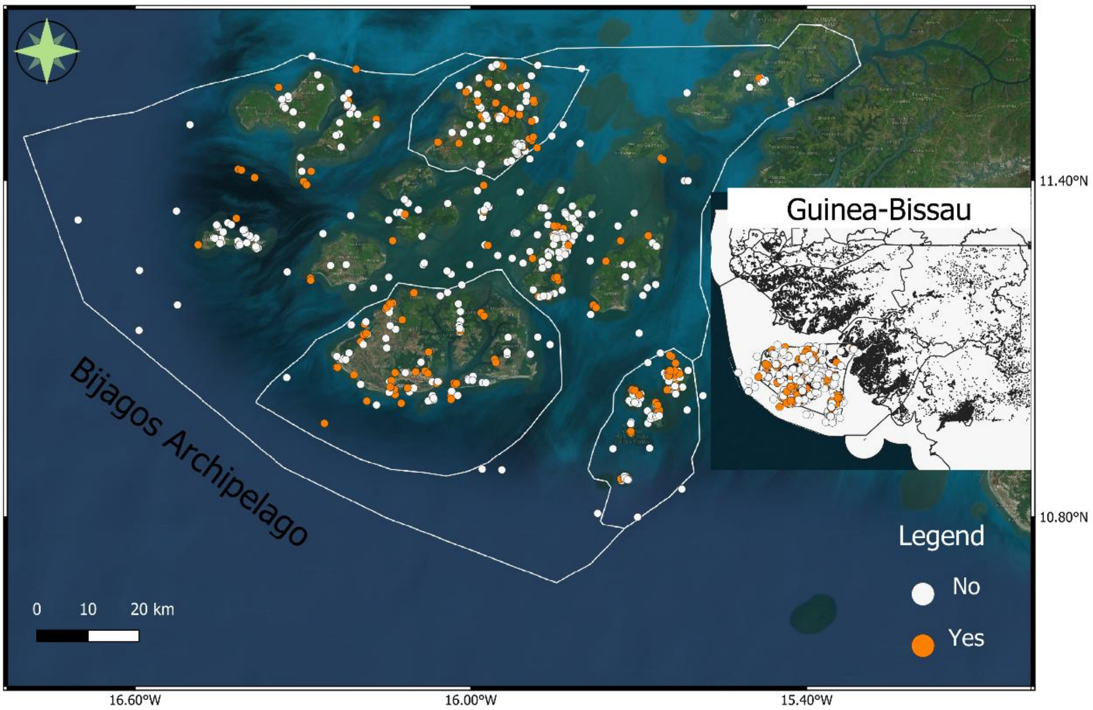


Figure 18. Map of Commercial Species of Bijagós - 2023

3.6. Distribution of Records per IUCN Status

The IUCN red list was applied for 420 species registered in this study, throughout the area of the Bolama Bijagós Biosphere Reserve.

Species with the least concern (LC) category and Data Deficient (DD) were observed throughout the entire area of the Biosphere reserve. Species with conservation status, Vulnerable (VU), Near Threatened (NT), Critically Endangered (CR) were also recorded on the entire area and with the greatest number of species in National Park of the Group of Islands of Orango and National Marine Park João Vieira and Poilão. The area without protection had the highest record of species in the Critically Endangered (CR) and Endangered (EN) category, in relation to other areas whose values are proportionally equal (Figure 19).

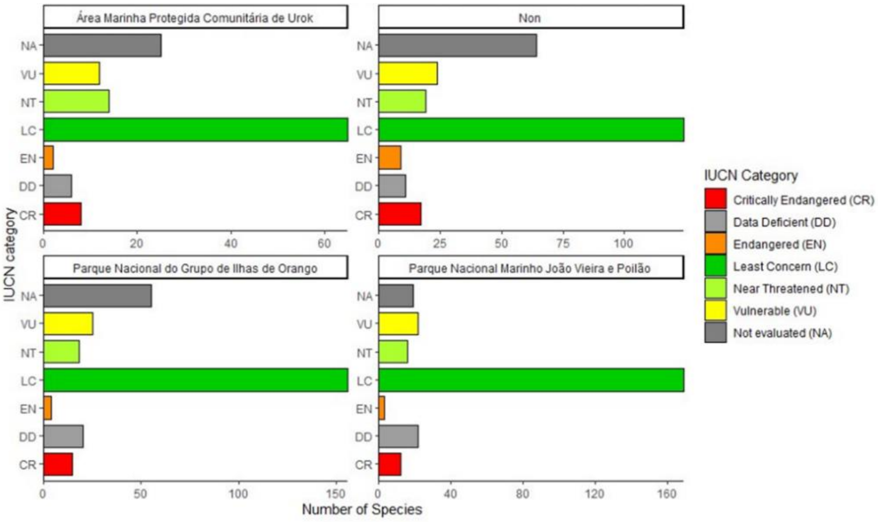


Figure 19. Number of Species IUCN category per Protected and Non-Protected Area

Regarding just the four most vulnerable categories on the IUCN red list (Figure 20), many species in the Critically Endangered (CR) and Near Threatened (NT) category occur in spaces outside of the conserved areas. On the other hand, there is a strong occurrence of species classified as Endangered (EN) in the National Marine Park João Vieira and Poilão, but also in non-conserved areas. The islands of Unhocomo and Unhocomozinho have a dense recording of endangered species despite their lack of protection.

The Community Marine Protected Area of Urok and National Park of the Group of Islands of Orango, based on the results of this study, were considered as the areas with the largest records of species with the Vulnerable (VU) category and with some important records in the limits outside of park/marine protected area.

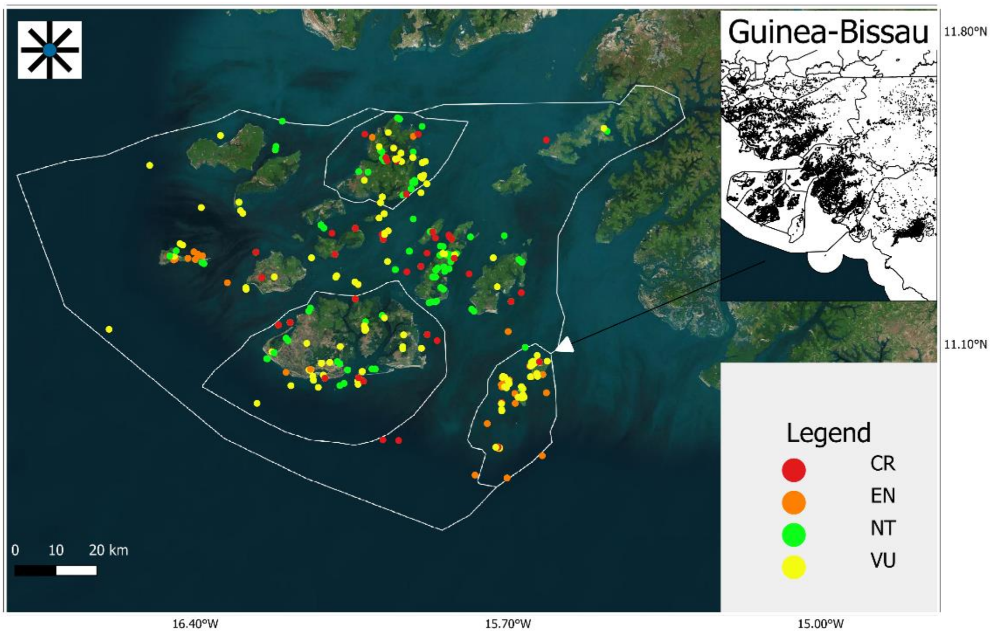


Figure 20. Most Vulnerable IUCN category in each National Park/Marine Protected Area

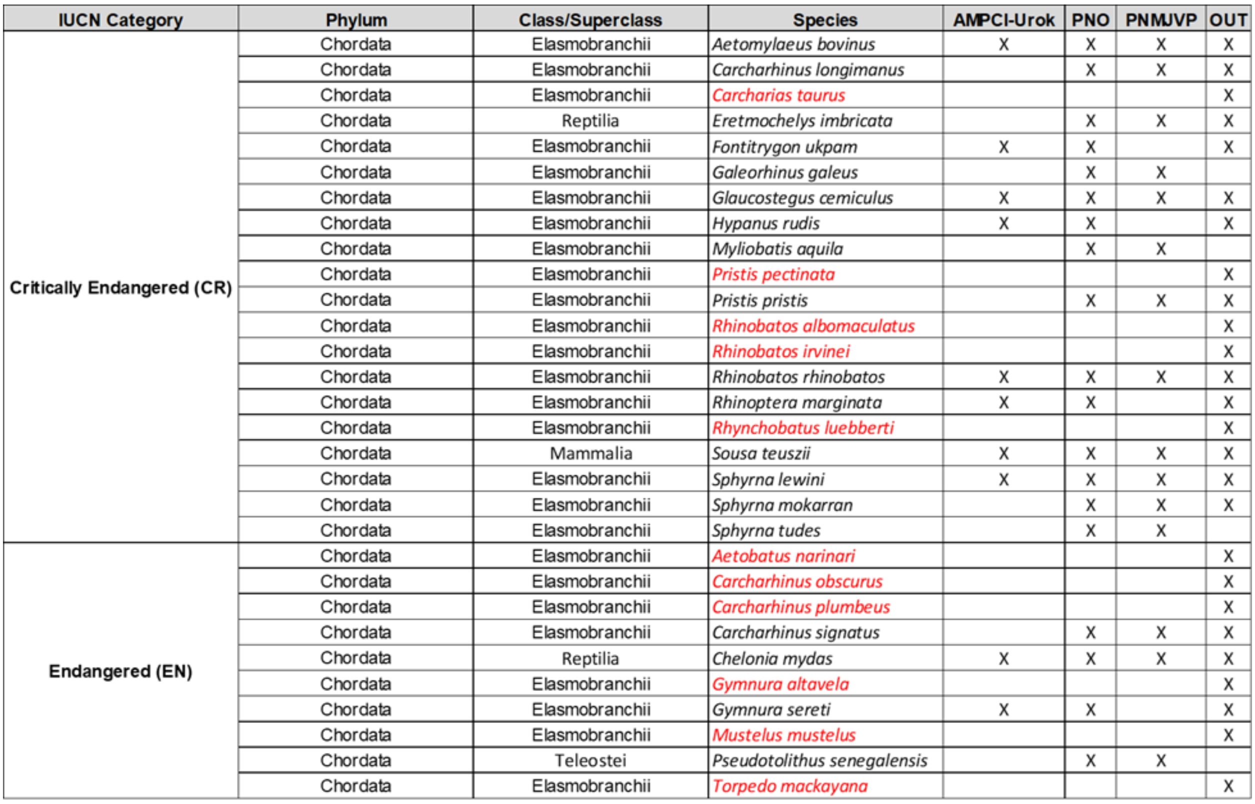
The species in any if the four concerning conservation categories according to the IUCN red list are indicated in table 1 according to their areas of occurrence.

A total of 17 species are recorded that occur only in the limits outside of park/marine protected area, thus with no protection. Five of these species have IUCN categories (Critically Endangered (CR), six with Endangered (EN), four with Vulnerable (VU) and two with Near Threatened (NT).

Species with Vulnerable (VU) categories are the most recorded in National Park of the Group of Islands of Orango and then in the limits outside of park/marine protected area. For the Critically Endangered (CR), the records for both the National Park of the Group of Islands of Orango as well as for limits outside of park/marine protected area are similar, unlike the National Marine Park João Vieira and Poilão and Community Marine Protected Area of Urok with the lowest number of species.

In addition, in the category of Endangered (EN), in the limits outside of park/marine protected area there were records of nine of these species, followed by National Park of the Group of Islands of Orango with four records and three for National Marine Park João Vieira and Poilão, and two for Community Marine Protected Area of Urok.

Table 1: Species table by National Park/ Marine Protected Are with IUCN category



IUCN Category	Phylum	Class/Superclass	Species	AMPCI-Urok	PNO	PNMJVP	OUT
Critically Endangered (CR)	Chordata	Elasmobranchii	*Aetomylaeus bovinus*	X	X	X	X
	Chordata	Elasmobranchii	*Carcharhinus longimanus*		X	X	X
	Chordata	Elasmobranchii	*Carcharias taurus*				X
	Chordata	Reptilia	*Eretmochelys imbricata*		X	X	X
	Chordata	Elasmobranchii	*Fontitrygon ukpam*	X	X		X
	Chordata	Elasmobranchii	*Galeorhinus galeus*		X	X	
	Chordata	Elasmobranchii	*Glaucostegus cemiculus*	X	X	X	X
	Chordata	Elasmobranchii	*Hypanus rudis*	X	X		X
	Chordata	Elasmobranchii	*Myliobatis aquila*		X	X	
	Chordata	Elasmobranchii	*Pristis pectinata*				X
	Chordata	Elasmobranchii	*Pristis pristis*		X	X	X
	Chordata	Elasmobranchii	*Rhinobatos albomaculatus*				X
	Chordata	Elasmobranchii	*Rhinobatos irvinei*				X
	Chordata	Elasmobranchii	*Rhinobatos rhinobatos*	X	X	X	X
	Chordata	Elasmobranchii	*Rhinoptera marginata*	X	X		X
	Chordata	Elasmobranchii	*Rhynchobatus luebberti*				X
	Chordata	Mammalia	*Sousa teuszii*	X	X	X	X
	Chordata	Elasmobranchii	*Sphyrna lewini*	X	X	X	X
	Chordata	Elasmobranchii	*Sphyrna mokarran*		X	X	X
	Chordata	Elasmobranchii	*Sphyrna tudes*		X	X	
Endangered (EN)	Chordata	Elasmobranchii	*Aetobatus narinari*				X
	Chordata	Elasmobranchii	*Carcharhinus obscurus*				X
	Chordata	Elasmobranchii	*Carcharhinus plumbeus*				X
	Chordata	Elasmobranchii	*Carcharhinus signatus*		X	X	X
	Chordata	Reptilia	*Chelonia mydas*	X	X	X	X
	Chordata	Elasmobranchii	*Gymnura altavela*				X
	Chordata	Elasmobranchii	*Gymnura sereti*	X	X		X
	Chordata	Elasmobranchii	*Mustelus mustelus*				X
	Chordata	Teleostei	*Pseudotolithus senegalensis*		X	X	
	Chordata	Elasmobranchii	*Torpedo mackayana*				X

IUCN Category	Phylum	Class/Superclass	Species	AMPCI-Urok	PNO	PNMJVP	OUT
Vulnerable (VU)	Chordata	Elasmobranchii	*Bathytoshia centroura*		X	X	X
	Chordata	Elasmobranchii	*Bathytoshia lata*	X	X		X
	Chordata	Elasmobranchii	*Carcharhinus amboinensis*				X
	Chordata	Elasmobranchii	*Carcharhinus brevipinna*		X	X	X
	Chordata	Elasmobranchii	*Carcharhinus falciformis*		X	X	X
	Chordata	Elasmobranchii	*Carcharhinus leucas*	X	X	X	X
	Chordata	Elasmobranchii	*Carcharhinus limbatus*	X	X	X	X
	Chordata	Reptilia	*Caretta caretta*		X	X	X
	Chordata	Elasmobranchii	*Dasyatis pastinaca*				X
	Chordata	Reptilia	*Dermochelys coriacea*		X	X	X
	Chordata	Elasmobranchii	*Fontitrygon margarita*	X	X	X	X
	Chordata	Elasmobranchii	*Ginglymostoma cirratum*	X	X	X	X
	Chordata	Teleostei	*Hippocampus algiricus*		X		
	Chordata	Teleostei	*Hippocampus erectus*		X		
	Chordata	Elasmobranchii	*Hypanus berthalutzae*	X	X		X
	Chordata	Reptilia	*Lepidochelys olivacea*		X	X	X
	Chordata	Elasmobranchii	*Leptocharias smithii*	X	X	X	X
	Chordata	Elasmobranchii	*Negaprion brevirostris*				X
	Chordata	Teleostei	*Pentanemus quinquarius*		X	X	
	Chordata	Mammalia	*Physeter macrocephalus*			X	
	Chordata	Teleostei	*Pomatomus saltatrix*		X	X	
	Chordata	Teleostei	*Pseudotolithus senegallus*	X	X	X	X
	Chordata	Teleostei	*Pseudupeneus prayensis*			X	
	Chordata	Elasmobranchii	*Rhinoptera bonasus*	X	X	X	X
	Chordata	Elasmobranchii	*Rhizoprionodon acutus*	X	X	X	X
	Chordata	Teleostei	*Sardinella maderensis*	X	X	X	X
	Chordata	Elasmobranchii	*Sphyrna zygaena*		X	X	X
	Chordata	Elasmobranchii	*Torpedo marmorata*		X		X
	Chordata	Mammalia	*Trichechus senegalensis*	X	X	X	X
	Chordata	Reptilia	*Trionyx triunguis*		X	X	
	Chordata	Elasmobranchii	*Zanobatus schoenleinii*				X

IUCN Category	Phylum	Class/Superclass	Species	AMPCI-Urok	PNO	PNMJVP	OUT
Near Threatened (NT)	Chordata	Teleostei	*Albula vulpes*	X	X	X	X
	Chordata	Mammalia	*Aonyx capensis*	X	X		X
	Chordata	Teleostei	*Brachydeuterus auritus*		X	X	
	Chordata	Aves	*Calidris canutus*	X	X	X	X
	Chordata	Aves	*Calidris ferruginea*	X	X	X	X
	Chordata	Elasmobranchii	*Carcharhinus altimus*				X
	Chordata	Teleostei	*Cynoglossus monodi*		X	X	X
	Chordata	Teleostei	*Cynoglossus senegalensis*	X	X	X	X
	Chordata	Elasmobranchii	*Dasyatis marmorata*	X	X		X
	Chordata	Teleostei	*Epinephelus aeneus*	X	X	X	X
	Chordata	Elasmobranchii	*Fontitrygon margaritella*	X	X	X	X
	Chordata	Elasmobranchii	*Galeocerdo cuvier*	X	X	X	X
	Chordata	Teleostei	*Galeoides decadactylus*	X	X	X	X
	Chordata	Elasmobranchii	*Gymnura micrura*		X	X	X
	Chordata	Aves	*Haematopus ostralegus*	X	X	X	X
	Chordata	Aves	*Limosa lapponica*	X	X	X	X
	Chordata	Aves	*Numenius arquata*	X	X	X	X
	Chordata	Aves	*Phoeniconaias minor*			X	X
	Chordata	Elasmobranchii	*Prionace glauca*		X	X	
	Chordata	Elasmobranchii	*Rhinoptera steindachneri*	X	X		X
	Chordata	Elasmobranchii	*Taeniurops grabatus*				X

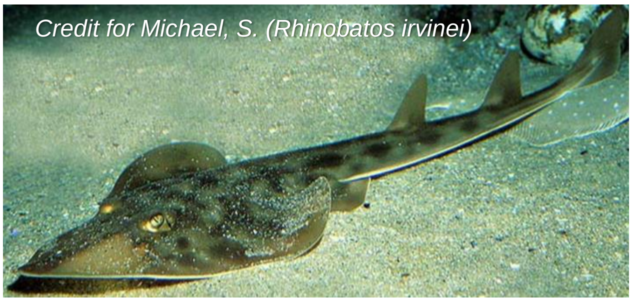
3.6.1. Vulnerable species according to the IUCN category found only outside the marine protected areas

Table 2: Vulnerable species according to the IUCN category


Credit for Choromanski, J.M. (Carcharias Taurus**)**


Credit for iNaturalist (Rhinobatos


Credit for Hernandez, S. (2016) (Pristis pectinata)


Credit for Michael, S. (Rhinobatos irvinei)


Credit for India Biodiversity Portal (Rhynchobatus luebberti)


Credit for Randall, J.E. (1997). Carcharhinus obscurus


Credit for McAuley, R. (Carcharhinus plumbeus)


Credit for Flescher, D. (Gymnura altavela)

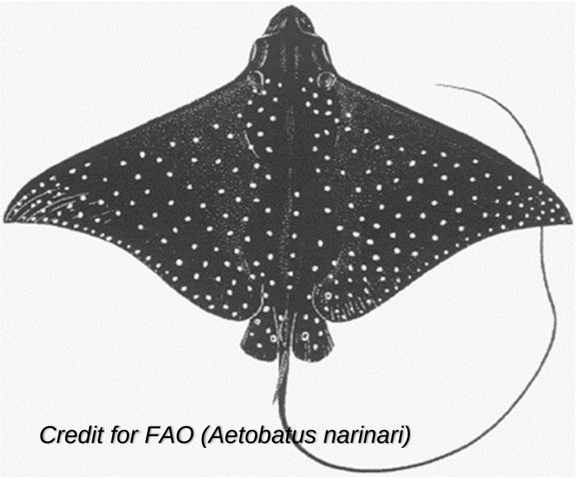

Credit for Duarte, P. N. (Mustelus mustelus)

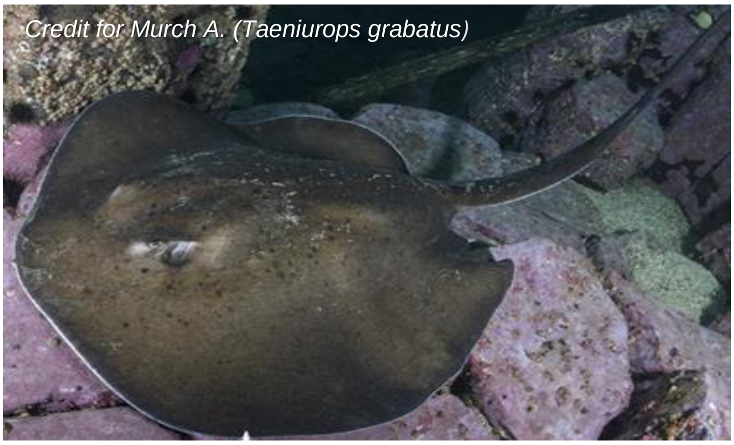

Credit for Randall, J.E. (1997). (Carcharhinus amboinensis)


Credeit for Cambraia Duarte, P.M.N. (Carcharhinus altimus)


Credit for Cada, L.A. (Negaprion brevirostris)


Credit for Wikipédia, a enciclopédia livre (Dasyatis pastinaca)


Credit for FAO (Aetobatus narinari)


Credit for Murch A. (Taeniurops grabatus)


Credit for Murch A. (Zanobatus schoenleinii)


Credit for Shark-References (Torpedo mackayana)

4- Discussion

This study of the present information on marine biodiversity of the Bijagós Archipelago has important results that allow for a broad and serious debate about the marine life of this region and the state of conservation. These results existed already from studies previously carried out in the Bijagós Archipelago, but thanks to their reintegration into a single study it was possible to draw emerging conclusions that could not be inferred before the data integration. This shows the importance of compiling the information and analyzing it in an integrated way. The present study initiated a baseline database of marine biodiversity of the Bijagós, which will continue to be updated in the future as more information is produced, allowing for temporal and spatial comparisons of biodiversity trends in the future. This study has also for the first time made all this information publicly and freely available in a user-friendly portal, https://www.marafrica.net/ Bijagós/ , free for everyone, dedicated to provide information for education, management and conservation, of high value for managers, stakeholders, scientists, students and the general public.

The temporal distribution of records of marine biodiversity in the Bijagós Islands, recorded at least since 1847, shows that studies date back to this region since the 19th century or even earlier (if in the future more ancient records can be found). There were already some studies at the end of the 20th century**.** It was only at the end of the 1980s that records of marine biodiversity in the Bijagós started increasing. It is still notable that it was in the year 2000 or in the last decade and a half that there were most records of marine biodiversity for the Bijagós. The lack of results at the beginning and middle of the last century might have been due to global political instability and consequently in Guinea-Bissau, and on the other hand, the increasing number of records observed in the last century was mainly due to investments from third countries but also of local government entities. It can also be considered that the interests of creating the Biosphere Reserve in 1996, the protected marine areas in 2000 and the sustainable management measures of marine resources did probably greatly influence the increase in biodiversity records (IBAP, 2008) (Figure 1).

Most of the marine biodiversity records were obtained from GBIF sources, scientific papers and technical reports (Figure 2). Of these records, all were taxonomically identified at the species level and with some records at the genus, family and phylum level (Figure 5), particularly those recorded during the last century (Figure 3).

Throughout this century, the number of families, genus and species has gradually increased over the years, with the largest number of these groups being recorded in 2008. Moreover, the inventories might have benefited from specific studies of marine biodiversity carried out in the Bijagós Archipelago for management purposes, such as the elaboration of management plans for both park, the Orango Island Groups National Park and the João Vieira and Poilão Marine National Parks, both valid for ten years" (IBAP, 2008). "Inventory of the biodiversity of mangroves and coastal mudflats in the Orango National Park, Bijagós Archipelago" (Larénie, & Thiberge, 2008) and "Ecological Study of Exploited Molluscs in the Bijagós Archipelago (Limnologue, 2008). Interestingly, the trend clearly explains that the number of the three taxonomic groups observed in this study has grown in a similar way over the last 15 years, suggesting that a large part of the marine biodiversity in Bijagós is still to be revealed (Figure 4).

Some marine phyla dominate the records of marine biodiversity in the Bijagós. The proportion represented by Chordata was (78%) followed by Molluscs with (7%), Arthropoda with (4%), Annelida with (4%) and Tracheophyta with (2%). This represents 95% of these groups and the remaining seven groups found are only 5% of the total observed. With this, it´s possible to admit that the other taxonomic groups that belong to the tree of life are only weakly represented. Including Cnidaria, which corresponded to the first record observed by Milne Edwards & Haime in 1847, even so, there are still few observations compared to other groups (Figure 6, 7).

Within the Chordata group, birds have the largest number of records followed by fish (Figure 8), although fish have practically double the number of species compared to birds, it can still be seen that there are around 52 species of Elasmobranchii more seven that were only identified to the genus level (Figure 9). Sea turtles for the Bijagós archipelago were over time recorded for five species, as observed by Barbosa, et al., (2018); Bamba, (2020) and Patrício, et al., (2021). Despite being considered to date, that only five turtle species occur among the seven worldwide, nevertheless, in this study the species "*Trionyx triunguis*" Forsskål, 1775, was found recorded, a considerably marine species, but which can be found in the environments that are brackish, fresh (WoRMs, www.marinespecies.org/). There are also records of 11 species of Mammalia; differently from what was found by Barbosa & Regalla (2018), with only seven observations and IBAP (2008) with two observations (Figure 9). In relation to the other phyla, Mollusca are mainly represented by two classes, with other more represented phyla (Arthropoda, Annelida and Tracheophyta) having mainly one class (Figure 10).

Comparing observations across islands, in the Bijagós archipelago, the islands of Orango, João Vieira, Formosa and Bubaque have been the most studied and with the largest records of species. Among them, the island of Bubaque has the highest records. It is the capital of the archipelago, has the largest populations and receives numerous tourist visitors compared to the other islands (Figure 11). In general terms, the largest number of records and species were observed in non-conserved areas, but with similar proportions in terms of taxonomic groups recorded between the marine protected areas and outside of them (Figure 12).

Comparisons by year and zone revealed that the Community Marine Protected Area of Urok has had a greater number of species observations since 2011, through the development of the BioCos project with the management of West African Coastal Marine Biodiversity to reinforce Conservation initiatives (De Barros, et al., 2013 unpublished). In 2008, Orango Group of Islands National Park and National Marine Park João Vieira and Poilão, both received a greater number of species records respectively, due to the management plans drawn up containing all records of existing biodiversity in parks (IBAP, 2008). On the other hand, in 2019 Orango Group of Islands National Park, National Marine Park João Vieira, Poilão, and the limit outside of the conserved areas, also received the largest number of records, based on the impulse of scientific research registered in the same year in the archipelago. A strong effort was particularly focused on sea turtles in the specific case of National Marine Park João Vieira and Poilão (Bamba, 2020; Patricio, et al. 2021). Moreover, other diversified studies, with the representation of birds and fish for Orango Group of Islands National Park, and for the limit outside of the park mostly registered birds, fish, Elasmobranchs and Reptiles. Most of these records were published on peer-reviewed scientific papers (Figure 13).

The largest proportion of records of birds, Elasmobranchs, Molluscs, Arthropoda, Annelida and Tracheophyta (mainly seagrasses) were curiously found in areas outside of the park (Figure 14, 15). In terms of species, these taxonomic groups also present greater diversity in areas outside of the park, with the exception of Molluscs, which are more recorded in the Orango Group of Islands National Park, and the largest proportion of fish were mainly in the National Marine Park João Vieira and Poilão and Orango Group of Islands National Park (Figure 14, 16). The high fish records on those two areas are explained by the numerous scientific fishing campaigns carried out by local institutions (CIPA, 2010; CIPA, 2022; INIPO, 2023), and with the development of the “Noe Conservation – Guinea-Bissau” project, focusing on resources fisheries (Dias, 2013).

The number of commercial species observed was significant in the conserved areas, which indicates conservation strategies well drawn for marine fishing resources with economic interest in the country (Figure 17). In addition to appearing effective in terms of protecting marine fishing resources given the commercial species records in protected areas, we find also that observations of some emblematic species continue to occur in the marine protected areas for which they were important at their creation. This is the case of sea turtles, gray timneh parrot in the João Vieira and Poilão National Marine Park, hippopotamus, hamphibians, gray timneh parrot, mangrove, manatee, and sea birds in the Orango Group of Islands National Park and sea birds, mangrove, gray timneh parrot, among others to the Urok Community Marine Area.

Given the IUCN conservation status of the species, that we verified in this compilation, it is worth highlighting that the largest number of species with Critical Endangered (CR) status are observed outside any Marine Protected Areas (Figure 18, 19). Five and six species with Critical Endangered (CR) and Endangered (EN) status, respectively, were only found in unprotected areas outside of all the marine parks. All these species belong to the Elasmobranch group, whose conservation value is mandatory to be considered in the areas where they are found (Table 2). This result is important and has implications for the future management of marine protected areas, particularly within a Biosphere Reserve.

5- Conclusion

In general, the conclusion of this study shows the lack of knowledge of marine biodiversity in the Bijagós Archipelago, and even the knowledge that exists was not easily available for managers, scientists and the general public. However, the results obtained so far demonstrate also an enormous effort on the part of the institutions responsible for research in this sector and by independent researchers that have developed strong research lines in the Bijagós. Despite all this, it is clear that the studies have been focused on vertebrates and most of the marine biodiversity, which comprises a much wider diversity of taxonomic groups in the tree of life, are underrepresented or unknown.

It is recommended that planning about biodiversity and conservation should consider principles and objectives of maintaining the great biodiversity of life. This does not appear to be the case for the Bijagós due to insufficient information, as shown by the existing biodiversity records that are mostly concentrated only in the Chordata phylum, in the birds (reptiles) and fish classes.

Some remarkable taxa from the Bijagós are noticeably absent, namely the widespread and diverse corals and sponges, that we have just started to record (unpublished data). In this study it was possible to identify as first ever marine species record identified and published as the coral species *"Eunicella papillifera"* recorded in the 19th century, as the first and last record to date. For detailed knowledge of biodiversity in the archipelago, we propose additional and exhaustive studies, which can contribute not only to the identification of organisms, but also to understand present and predict future distributions and threats.

The Bijagós have a decade gap in marine biodiversity records, as no document was found locally with a record of marine biodiversity between the 80s and the beginning of the 90s. Only in 1961 and 1965 was the first record observed in the Gaivota bank between Meio and Poilão, the bank that currently disappeared. On the other hand, the historical record of species over the years allowed us to understand the period with the highest records, with the majority of species concentrated in the last 15 years. Including a significant number of unpublished documents.

Among all the study areas classified in the Bijagós Archipelago, the area outside any Marine Protected Areas has a significant difference in records, both qualitatively in species and quantitatively in the numbers of observations. The cause for this is unclear but the quantity and wide range of studies in this category may be biased by studies that simply mention “Bijagós archipelago” and do not report if the observations were actually inside a protected area. The ones that are inside protected areas were assigned there with confidence, the ones outside include some less certain studies and others with high confidence, namely for the unprotected region of region of Unhocomo / Unhocomozinho, a hotspot of endangered species records.

The marine protected areas in the Bijagós Archipelago have been effective in terms of fisheries management considering that important records of species of commercial value were found in these areas. Moreover, at the same time, they could be considered to have failed in terms of protecting vulnerable species with Critically Endangered (CR) and Endangered (EN) status; that are recorded outside the conserved areas almost exclusively. This is the case of the Elasmobranchs registered in the Bijagós with a considerable number of species, so there need even more studies, greater protection, as they are very vulnerable groups.

It is expected that the information collected in this study will contribute positively to inform education initiatives, conservation strategies, fishing management, and future research studies to be developed in the Bijagós. The results obtained in the present study are a baseline synthesizing all the previous knowledge of species occurrence and distribution, and making this information available integrated in a free easy to use portal, that will continue to be updated regularly as new information is produced. This public availability of information that is collected by public research is crucial for future assessments, and for that it is important that the data are easy to find and to use and to compare. Our data portal provides the result of a large effort in compiling all existing information and standardizing it in a common format, to make it available following the FAIR data principles: Findability, Accessibility, Interoperability, and Reusability. It is advisable that future research programs deliberately take the initiative of adding their data to public databases (like https://www.marafrica.net/ Bijagós/ or GBIF or iNaturalist) rather than submitting a pdf in a report or research paper appendix, that contrary to the FAIR principles becomes very hard to find, to access, to integrate with other data and it reuse. This information should be useful for evaluating the current situation of Bijagós marine biodiversity and identifying priority areas for conservation. These are a responsibility of the two state institutions for research, conservation and monitoring of biodiversity in Guinea-Bissau, the “National Institute of Research, Fisheries and Oceanography (INIPO), the Institute of Biodiversity and Protected Areas (IBAP) aided by research organizations and local NGOs.

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6- Supplementary Material

1. Get_marine_SpList_GBIF

```
library(dplyr)
library(tidyr)
library(worrms)
library(tidyverse)
# Read the excel file
data <- read.csv(file = "GBIF_data.csv", header = TRUE)
# Extract the columns containing the species name:
data_filtered <- data %>%
  dplyr::select(species) %>%
  dplyr::distinct(.keep_all = TRUE) %>% # Remove duplicate rows
  filter(species != '') # Remove empty rows
# Export the complete list of species
write.table(data_filtered, file ="SpList_Bijagos_GBIF.txt", row.names = FALSE, col.names = FALSE,
quote = FALSE)
# Get the WoRMS records for each species (to see which sp is marine and which one is a freshwater
sp), specifying exact match only (fuzzy = FALSE) and restricting to marine species (marine_only =
TRUE)
my_sp_mar1_100 <- wm_records_names(name = data_filtered$species[1:100], fuzzy = FALSE,
marine_only = TRUE)
my_sp_mar101_200 <- wm_records_names(name = data_filtered$species[101:200], fuzzy = FALSE,
marine_only = TRUE)
my_sp_mar201_300 <- wm_records_names(name = data_filtered$species[201:300], fuzzy = FALSE,
marine_only = TRUE)
my_sp_mar301_400 <- wm_records_names(name = data_filtered$species[301:400], fuzzy = FALSE,
marine_only = TRUE)
my_sp_mar401_500 <- wm_records_names(name = data_filtered$species[401:500], fuzzy = FALSE,
marine_only = TRUE)
my_sp_mar501_600 <- wm_records_names(name = data_filtered$species[501:600], fuzzy = FALSE,
marine_only = TRUE)
my_sp_mar601_692 <- wm_records_names(name = data_filtered$species[601:692], fuzzy = FALSE,
marine_only = TRUE)
# Convert the returned data into a neat dataframe
my_sp_mar1_100 <- bind_rows(my_sp_mar1_100)
my_sp_mar101_200 <- bind_rows(my_sp_mar101_200)
my_sp_mar201_300 <- bind_rows(my_sp_mar201_300)
my_sp_mar301_400 <- bind_rows(my_sp_mar301_400)
my_sp_mar401_500 <- bind_rows(my_sp_mar401_500)
my_sp_mar501_600 <- bind_rows(my_sp_mar501_600)
# Join all dataframe together
df_list <- list(my_sp_mar1_100, my_sp_mar101_200, my_sp_mar201_300, my_sp_mar301_400,
                my_sp_mar401_500, my_sp_mar501_600)
my_sp_mar <- df_list %>% reduce(full_join, by='scientificname')
```

```
# If we want to obtain the list of marine species, we can use the following command
sp_list_mar <- my_sp_mar %>%
  dplyr::select(scientificname) %>%
  dplyr::distinct(.keep_all = TRUE) %>% # Remove duplicate rows
  dplyr::rename(Species = "scientificname")
# Export list of marine species
write.table(sp_list_mar, file ="Marine_SpList_Bijagos_GBIF.txt", row.names = FALSE, col.names = FALSE, quote = FALSE)
```

1.1.Get_marine_SpList_iNat

```
library(dplyr)
library(tidyr)
library(worrms)
library(tidyverse)
# Read the excel file
data <- read.csv(file = "iNaturalist_data.csv", header = TRUE)
# Extract the columns containing the species name:
data_filtered <- data %>%
  dplyr::select(scientific_name) %>%
  dplyr::distinct(.keep_all = TRUE) %>% # Remove duplicate rows
  filter(scientific_name != '') # Remove empty rows
# Export the complete list of species
write.table(data_filtered, file ="SpList_Bijagos_iNat.txt", row.names = FALSE, col.names = FALSE, quote = FALSE)
# Get the WoRMS records for each species (to see which sp is marine and which one is a freshwater sp), specifying exact match only (fuzzy = FALSE) and restricting to marine species (marine_only = TRUE)
my_sp_mar1_100 <- wm_records_names(name = data_filtered$scientific_name[1:100], fuzzy = FALSE, marine_only = TRUE)
my_sp_mar101_200 <- wm_records_names(name = data_filtered$scientific_name[101:200], fuzzy = FALSE, marine_only = TRUE)
my_sp_mar201_300 <- wm_records_names(name = data_filtered$scientific_name[201:300], fuzzy = FALSE, marine_only = TRUE)
my_sp_mar301_400 <- wm_records_names(name = data_filtered$scientific_name[301:400], fuzzy = FALSE, marine_only = TRUE)
my_sp_mar401_500 <- wm_records_names(name = data_filtered$scientific_name[401:500], fuzzy = FALSE, marine_only = TRUE)
my_sp_mar501_600 <- wm_records_names(name = data_filtered$scientific_name[501:600], fuzzy = FALSE, marine_only = TRUE)
my_sp_mar601_700 <- wm_records_names(name = data_filtered$scientific_name[601:700], fuzzy = FALSE, marine_only = TRUE)
my_sp_mar701_726 <- wm_records_names(name = data_filtered$scientific_name[701:726], fuzzy = FALSE, marine_only = TRUE)
# Convert the returned data into a neat dataframe
my_sp_mar1_100 <- bind_rows(my_sp_mar1_100)
my_sp_mar101_200 <- bind_rows(my_sp_mar101_200)
my_sp_mar201_300 <- bind_rows(my_sp_mar201_300)
my_sp_mar301_400 <- bind_rows(my_sp_mar301_400)
my_sp_mar401_500 <- bind_rows(my_sp_mar401_500)
my_sp_mar501_600 <- bind_rows(my_sp_mar501_600)
my_sp_mar601_700 <- bind_rows(my_sp_mar601_700)
my_sp_mar701_726 <- bind_rows(my_sp_mar701_726)
# Join all dataframe together
df_list <- list(my_sp_mar1_100, my_sp_mar101_200, my_sp_mar201_300, my_sp_mar301_400,
                my_sp_mar401_500, my_sp_mar501_600, my_sp_mar601_700, my_sp_mar701_726)
```

```
my_sp_mar <- df_list %>% reduce(full_join, by='scientificname')
# If we want to obtain the list of marine species, we can use the following command
sp_list_mar <- my_sp_mar %>%
  dplyr::select(scientificname) %>%
  dplyr::distinct(.keep_all = TRUE) %>% # Remove duplicate rows
  dplyr::rename(Species = "scientificname")
# Export list of marine species
write.table(sp_list_mar, file ="Marine_SpList_Bijagos_iNat.txt", row.names = FALSE, col.names =
FALSE, quote = FALSE)
```

2. Obtain_matrix_marine_Sp_GBIF

```
#!/home/gareth/miniconda3/bin/perl
use strict;
use warnings;
my @spList;
my %table;
#Open the file containing the list of marine species or print an error message if it is not possible
open (LIST,"Marine_SpList_Bijagos_GBIF.txt") || die "Error: problem opening list file\n";
#Read the file line by line to the end of the file
while (my $line=<LIST>) {
        #Remove newline
        chomp $line;
        my $sp = $line;
        #print "$sp\n";
        #Push the species onto a new list
        push(@spList,$sp);
}
#Open the Matrix file containing all species or print an error message if it is not possible
open (MAT,"GBIF_data.csv") || die "Error: problem opening matrix file\n";
#Open the output file or print an error message if it is not possible
open (OUT, ">>Marine_Matrix_Bijagos_GBIF.csv") || die "Error: problem opening results file\n";
while (my $line=<MAT>) {
        #Remove newline
        chomp $line;
        # Split all the information by comma
        my @info = split(/,/,$line);
        # The species name will correspond to the 9th element of the list @info
        my $genus_sp = $info[9];
        #print "$genus_sp\n";
        # Join all remaining information
        my $rest_info = join(",", $info[0],
$info[1],$info[2],$info[3],$info[4],$info[5],$info[6],$info[7],$info[8],@info[10..$#info]);
        #print "$rest_info\n";
        #Create a hash containing as value the species name, and as key the remaining information
        $table{$rest_info} = $genus_sp;
        #print "$genus_sp - $rest_info\n";
}
# For each species of the list
for my $SP1 (@spList) {
        #print "$SP1\n";
        #For each entry from the "table" hash
        foreach my $inf (keys %table) {
                my $SP2 = $table{$inf};
                #print "$SP2\n";
                #If the two species names are equal
```

```
                if ($SP1 eq $SP2) {
                        #Print out the Species name and all of its associate information
                        print OUT "$SP2,$inf\n";
                }
        }
}
close(LIST);
close(MAT);
close(OUT);
```

2.1. Obtain_matrix_marine_Sp_iNat

```
#!/home/gareth/miniconda3/bin/perl
use strict;
use warnings;
my @spList;
my %table;
#Open the file containing the list of marine species or print an error message if it is not possible
open (LIST,"Marine_SpList_Bijagos_iNat.txt") || die "Error: problem opening list file\n";
#Read the file line by line to the end of the file
while (my $line=<LIST>) {
        #Remove newline
        chomp $line;
        my $sp = $line;
        #print "$sp\n";
        #Push the species onto a new list
        push(@spList,$sp);
}
#Open the Matrix file containing all species or print an error message if it is not possible
open (MAT,"iNat_data.txt") || die "Error: problem opening matrix file\n";
#Open the output file or print an error message if it is not possible
open (OUT, ">>Marine_Matrix_Bijagos_iNat.csv") || die "Error: problem opening results file\n";
while (my $line=<MAT>) {
        #Remove newline
        chomp $line;
        # Split all the information by tab
        my @info = split(/\t/,$line);
        # The species name will correspond to the 35th element of the list @info
        my $sp = $info[35];
        #print "$sp\n";
        # Join all remaining information
        my $rest_info1 = join(",", @info[0..34]);
        my $rest_info2 = join(",", @info[36..38]);
        #print "$rest_info2\n";
        my $rest_info = join ",", $rest_info1, $rest_info2;
        #print "$rest_info\n";
        #Create a hash containing as value the species name, and as key the remaining information
        $table{$rest_info} = $sp;
        #print "$sp - $rest_info\n";
}
# For each species of the list
for my $SP1 (@spList) {
        #print OUT "$SP1\n";
        #For each entry from the "table" hash
        foreach my $inf (keys %table) {
                my $SP2 = $table{$inf};
```

```
        #print "$SP2\n";
        #If the two SPs are equal
        if ($SP1 eq $SP2) {
            #print "$SP1 -- $SP2\n";
            #Print out the Species name and all its associate information
            print OUT "$SP2,$inf\n";
        }
    }
}
close(LIST);
close(MAT);
close(OUT);
```

3. Get_Marine_Matrix_FINAL_GBIF

```
library(dplyr)
library(tidyr)
library(tidyverse)
# Read the excel file
data <- read.csv(file = "Marine_Matrix_Bijagos_GBIF.csv", header = FALSE)
# Reorder Genus_Species column:
data_order <- data %>%
  relocate(V1, .after = V10)
# Read the matrix containing the header
data2 <- read.csv(file = "GBIF_data.csv", header = TRUE)
# Define colnames data, using the colnames from data2
colnames(data_order) <- colnames(data2)
# Export the complete FINAL dataframe
write.csv(data_order,file="Marine_Matrix_Bijagos_GBIF_FINAL.csv", row.names = FALSE)
```

3.1. Get_Marine_Matrix_FINAL_iNat

```
library(dplyr)
library(tidyr)
library(tidyverse)
# Read the excel file
data <- read.csv(file = "Marine_Matrix_Bijagos_iNat.csv", header = FALSE)
# Reorder Genus_Species column:
data_order <- data %>%
  relocate(V1, .after = V36)
# Read the matrix containing the header
data2 <- read.csv(file = "iNat_data.csv", header = TRUE)
# Define colnames data, using the colnames from data2
colnames(data_order) <- colnames(data2)
# Export the complete FINAL dataframe
write.csv(data_order,file="Marine_Matrix_Bijagos_iNat_FINAL.csv", row.names = FALSE)
```

4. Get_Taxonomy

```
library(cookbook)
library(dplyr)
#Read file containing the Species list
spList <- read.table("SpList_Bijagos.txt", header = FALSE, sep = "\t")
#Rename first column as "Species"
colnames(spList)[1] <- "Species"
#Get taxonomy information from WORMS
```

```
info <- get_worms_taxonomy(spList$Species)
#Keep only columns containing the taxonomic information
taxonomy <- info %>%
  select(kingdom,phylum,class,order,family,genus,valid_name)
#Save the taxonomy in a .txt file and a .csv file
write.table(taxonomy, file = "Taxonomy_Bijagos.txt", sep = "\t",
          quote = FALSE, col.names = FALSE, row.names = FALSE)
write.table(taxonomy, file = "Taxonomy_Bijagos.csv", quote = FALSE,
          sep = ",", row.names = FALSE, col.names = FALSE)
```

5. Get_IUCN_category

```
library(taxize) #search the IUCN status and distribution of species
library(tidyverse) #to arrange data
# Load the species list
data <- read.table("SpList_IUCN.txt", header = FALSE, sep = "\t")
# Rename first column as "Species"
colnames(data)[1] <- "Species"
# Get IUCN access
API = "84552858afd0ef8d4ff668b5ed49eae75e283100ca267a5aaab1ab15213b5668"
#https://apiv3.iucnredlist.org/, provide IUCN access
IUCN.list = iucn_summary(data$Species, distr_detail = TRUE, key = API)
IUCN.list
# Get the information in a list
IUCN_info <- iucn_status(IUCN.list) %>% as.data.frame() %>%
  rownames_to_column(var = "Species") %>%
  set_names(c("Species", "IUCN")) #Give names "Species" and "IUCN" to columns
# Export as a txt file
write.table(IUCN_info, file = "Species_Bijagos_IUCN_category.csv", sep = ",",
          row.names = FALSE, quote = FALSE)
```

6.1. Data_Tidying

```
library(readxl)
library(dplyr)
library(tidyr)
# Read the excel file containing the Final Table
matBij <- read_xlsx("1_Marine_Matrix_Bijagos_FINAL.xlsx")
# Keep only columns needed for analyses
matBij_filt <- matBij %>%
  select(Valid_Name,taxonRank,Locality,decimalLatitude,decimalLongitude,NationalPark_MPA,
       year,bibliographicCitation)
# Create a column containing a which Island belong each locality. This column
# will be named as Island
matBij_Island <- matBij_filt %>%
  mutate(Island = if_else(Locality %in% c("Baie de Escaramaca", "Binte", "Carache"),
                        "Carache", NA_character_)) %>%
  mutate(Island = if_else(Locality %in% "Baixio das Gaivotas",
                        "Gaivotas", Island)) %>%
  mutate(Island = if_else(Locality %in% c("Ilha de Adonga", "Sul de Adonga"),
                        "Adonga", Island)) %>%
  mutate(Island = if_else(Locality %in% "Bolama",
                        "Bolama", Island)) %>%
  mutate(Island = if_else(Locality %in% c("Banco de Bubaque", "Bijante", "Bruce",
                                        "Bubaque", "Bubaque hotel", "Casa Dora",
                                        "Escadinhas", "Ilha de Bubaque", "Porto de Bubaque",
                                        "Praia Bubaque", "Praia de Bijante",
                                        "Praia de Bruce", "Rio de Bruce", "Saldomar"),
```

```
                "Bubaque", Island)) %>%
mutate(Island = if_else(Locality %in% "Bubaque/Rubane",
                "Bubaque/Rubane", Island)) %>%
mutate(Island = if_else(Locality %in% "Ilha de Bubaque/Ilha de Soga",
                "Bubaque/Soga", Island)) %>%
mutate(Island = if_else(Locality %in% "Cabras",
                "Cabras", Island)) %>%
mutate(Island = if_else(Locality %in% c("Bane", "Acampamento Canhabaque", "Ambeno",
                          "Canhabaque", "Inorei", "Sul-oueste de Canhabaque"),
                "Canhabaque", Island)) %>%
mutate(Island = if_else(Locality %in% c("Canogo", "Ilha de Canogo"),
                "Canogo", Island)) %>%
mutate(Island = if_else(Locality %in% c("Caravela", "Ilha de Caravela"),
                "Caravela", Island)) %>%
mutate(Island = if_else(Locality %in% c("Canal Pedro de Cintra", "Ilha de Caravela/Ilha de Carache"),
                "Caravela/Carache", Island)) %>%
mutate(Island = if_else(Locality %in% "Cute/Uracane",
                "Cute/Uracane", Island)) %>%
mutate(Island = if_else(Locality %in% "Ilha de Cute/Ilha de Uno",
                "Cute/Uno", Island)) %>%
mutate(Island = if_else(Locality %in% "Edana",
                "Edana", Island)) %>%
mutate(Island = if_else(Locality %in% "Enu",
                "Enu", Island)) %>%
mutate(Island = if_else(Locality %in% "Enu/Uracane",
                "Enu/Uracane", Island)) %>%
mutate(Island = if_else(Locality %in% c("Bolanha de Abu", "Cuiane", "Abu",
                          "Acôcó", "Acuno", "Angaruma", "Annanoupa",
                          "An-oxan", "Anrumai", "Banco de Formosa",
                          "Formosa", "Galinhas", "Praia de Abu"),
                "Formosa", Island)) %>%
mutate(Island = if_else(Locality %in% c("Banco de Imbone", "Imbone", "Itchinhou"),
                "Imbone", Island)) %>%
mutate(Island = if_else(Locality %in% "Rio Ancabenoa Riname",
                "Imbone/Orango", Island)) %>%
mutate(Island = if_else(Locality %in% "Kéré",
                "Kéré", Island)) %>%
mutate(Island = if_else(Locality %in% c("Maio Hotel", "Banco Formosanorte",
                          "Bol Maio/Formosa", "Chedia", "Maio",
                          "Salina"),
                "Maio", Island)) %>%
mutate(Island = if_else(Locality %in% c("Rio de Ambuduco", "Ilha de Canogo/Ilha de Meneque"),
                "Meneque/Canogo", Island)) %>%
mutate(Island = if_else(Locality %in% c("Rio Anubudugui", "Ilha de Meneque/Ilha de Orangozinho"),
                "Meneque/Orangozinho", Island)) %>%
mutate(Island = if_else(Locality %in% c("Acapa-Imbone", "Adonga", "Ambuducu",
                          "Ancopado", "Anôr", "Atrás de Parque hotel Orango",
                          "Banco Atrás de Hotel", "Banco de Etinhoque",
                          "Banco de Porto de Eticoga", "Caranx", "Colonia",
                          "Costa de Etinhoque", "Entrada de Ancopado",
                          "Etiogo", "Ilha de Orango", "Orango-Grande",
                          "Ponta Amudo", "Praia de Ancopado", "Praia de Eticoga",
                          "Praia de Etimopa", "Praia de Orango", "Praia de Tartaruga",
                          "Rio de Acapa 2", "Hotel Orango", "Orango"),
                "Orango", Island)) %>%
mutate(Island = if_else(Locality %in% "Rio Ancopado",
```

```
                          "Orango/Imbone", Island)) %>%
  mutate(Island = if_else(Locality %in% "Ilha de Orango/Ilha de Canogo",
                          "Orango/Canogo", Island)) %>%
  mutate(Island = if_else(Locality %in% c("Ilha de Orangozinho", "Rio Amuia", "Rio Amuia2",
                                          "Uite"),
                          "Orangozinho", Island)) %>%
  mutate(Island = if_else(Locality %in% "Papagaios",
                          "Papagaio", Island)) %>%
  mutate(Island = if_else(Locality %in% "Poilão",
                          "Poilão", Island)) %>%
  mutate(Island = if_else(Locality %in% c("Ponta", "Nago", "Bol Formosa/Nago"),
                          "Ponta", Island)) %>%
  mutate(Island = if_else(Locality %in% c("Lama", "Rubane"),
                          "Rubane", Island)) %>%
  mutate(Island = if_else(Locality %in% c("Rubane/Canhabaque", "Ancanho"),
                          "Rubane/Canhabaque", Island)) %>%
  mutate(Island = if_else(Locality %in% "Ilha de Rubane/Ilha de Soga/Ilha de Bubaque",
                          "Rubane/Soga/Bubaque", Island)) %>%
  mutate(Island = if_else(Locality %in% "Soga",
                          "Soga", Island)) %>%
  mutate(Island = if_else(Locality %in% c("Unhocomo", "Urtrocano", "Etimbato"),
                          "Unhocomo", Island)) %>%
  mutate(Island = if_else(Locality %in% c("Unhocomozinho", "Acunda Lodge", "Ancante",
                                          "Ancante2", "Akassesse"),
                          "Unhocomozinho", Island)) %>%
  mutate(Island = if_else(Locality %in% c("Sul de Uno", "Uno"),
                          "Uno", Island)) %>%
  mutate(Island = if_else(Locality %in% c("Ilha de Uno/Ilha de Orango", "Uno/Orango"),
                          "Uno/Orango", Island)) %>%
  mutate(Island = if_else(Locality %in% c("Uracane", "Eguba"),
                          "Uracane", Island)) %>%
  mutate(Island = if_else(Locality %in% c("Canal Ninguin", "Canal de Uno"),
                          "Uracane/Uno", Island)) %>%
  mutate(Island = if_else(Locality %in% c("Meio", "Ambine Monca", "Praia Amindo Toze"),
                          "Meio", Island)) %>%
  mutate(Island = if_else(Locality %in% c("Cavalos", "Acampamento Tartarugas",
                                          "Praia Canal", "Praia Colonia"),
                          "Cavalos", Island)) %>%
  mutate(Island = if_else(Locality %in% "Ilha de Porcos",
                          "Porcos", Island)) %>%
  mutate(Island = if_else(Locality %in% c("Banco da Areia", "Canudé", "Etabou",
                                          "Hotel Cláudio", "Hotel Caranx", "João Vieira"),
                          "João Vieira", Island)) %>%
  mutate(Island = if_else(Locality %in% c("Angurman ecolodg", "Angurman ecolodg1",
                                          "Angurman ecolodg2"),
                          "Angurman", Island)) %>%
  mutate(Island = if_else(Locality %in% "Unknown",
                          "Unknown", Island)) %>%
  mutate(Island = if_else(Locality %in% "Amegue",
                          "NA", Island))
# Create a column containing if the locality belong (IN) or not (OUT) to a
# National Park or Marine Protected Area(MPA)
matBij_Park <- matBij_Island %>%
  mutate(IN_OUT = case_when(grepl("Non", NationalPark_MPA) ~ "OUT", .default = "IN"))
# Join the taxonomic information
```

```
txnm <- read.table("Taxonomy_Bijagos.txt", sep = "\t", encoding = "latin1") # read the file containing the taxonomy
colnames(txnm) <- c("Kingdom","Phylum","Class","Order","Family","Genus","Species") # define column names in the taxonomic matrix
colnames(matBij_Park)[1] <- "Species" # change the column name of the first column of the general matrix
matBij_tax <- merge(matBij_Park, txnm, all = TRUE) # merge the two matrices

# Join the IUCN category
IUCN <- read.table("Species_Bijagos_IUCN_category.txt", sep = "\t", header = TRUE)
matBij_tax_IUCN <- merge(matBij_tax, IUCN, all = TRUE)

# Reorder columns
matBij_FINAL <- matBij_tax_IUCN %>%
  relocate(Species, taxonRank, .after = Genus) %>%
  relocate(year, .before = Locality) %>%
  relocate(Island, .before = NationalPark_MPA) %>%
  relocate(bibliographicCitation, .after = last_col())

# Export Taxonomic Matrix and FINAL Matrix
write.csv(txnm, file = "Taxonomy_Matrix_Bijagos.csv", quote = FALSE, row.names = FALSE, fileEncoding ="UTF-16LE")
write.table(matBij_FINAL, file = "Marine_Matrix_Bijagos_ANALYSES.csv", sep = "\t", quote = FALSE, row.names = FALSE, fileEncoding ="UTF-16LE")
```

6.2. Data_Tidying

```
library(dplyr)
library(tidyr)
# Read the excel file containing the Tidied Table
matBij <- read.csv("Marine_Matrix_Bijagos_ANALYSES.csv")
# Join the Species commercial information
SpComm <- read.table("Comercial_Species.txt", sep = "\t", fileEncoding = "latin1")
colnames(SpComm) <- c("Species", "Commercial")
matBij_Comm <- merge(matBij, SpComm, all = TRUE)
# Reorder columns
matBij_Comm_FINAL <- matBij_Comm %>%
  relocate(Species, .after = Genus) %>%
  relocate(bibliographicCitation, .after = last_col())
# Export Taxonomic Matrix and FINAL Matrix
write.table(matBij_Comm_FINAL, file = "Marine_Matrix_Bijagos_ANALYSES_FINAL.csv", sep = "\t", quote = FALSE, row.names = FALSE, fileEncoding ="UTF-16LE")
```

7. Data_Analyses

```
library(dplyr)
library(tidyverse)
library(ggplot2)
library(ggrepel)  # modify label charts
library(RColorBrewer) # modify color in charts
library(patchwork) # combine separate plots
library(gridExtra)
library(grid)
library(ggridges)
library(lemon)
library(ggpubr)
library(viridis) # to modify colour of plots
```

```
# Load the FINAL table
data <- read.table("Marine_Matrix_Bijagos_ANALYSES_FINAL.txt", sep = "\t", header = TRUE,
                   encoding = "latin1", na.strings=c("","NA"))

# Number of records per Reference Type #
data_Ref <- data %>%
  select(year,Bibliographic_Type) %>%
  count(Bibliographic_Type) %>%
  mutate(fraction = n/sum(n)) %>% # Compute percentages
  mutate(ymax = cumsum(fraction)) %>% # Compute the cumulative percentages (top of each rectangle)
  mutate(ymin = c(0, head(ymax, n=-1))) # Compute the bottom of each rectangle

# Make the plot
hsize <- 2 # define the size of the donut plot
data_Ref <- data_Ref %>%
  mutate(x = hsize)
data_Ref$key <- paste0(data_Ref$Bibliographic_Type,' [',data_Ref$n,']') # define the label adding the n
value to the source type
ggplot(data_Ref, aes(x = hsize, y = n, fill = key)) +
  geom_col(color = "black") +
  geom_text(aes(label = n),
            position = position_stack(vjust = 0.5)) +
  coord_polar(theta = "y") +
  scale_fill_brewer(palette = "Paired") +
  xlim(c(0.2, hsize + 0.5)) +
  ggtitle("Number of Records per Source") +
  theme_void() +
  theme(plot.title = element_text(hjust = 0.5), legend.title = element_blank())

# Number of records per Reference Type and Year #
data_Ref_Year <- data %>%
  select(year,Bibliographic_Type) %>%
  count(year,Bibliographic_Type) %>%
  drop_na()

my_colors <- c("skyblue", "royalblue3", "olivedrab3", "green4",
               "lightpink", "red2", "sandybrown", "darkorange")

ggplot(data_Ref_Year, aes(x = year, y = Bibliographic_Type, fill = Bibliographic_Type)) +
  geom_density_ridges() +
  theme_classic() +
  ggtitle("Number of records over time per Source") + #set the graphic title
  labs(x = "", y = "") +
  scale_fill_manual(values = my_colors) +
  theme(plot.title = element_text(hjust = 0.5), #adjust title position to the middle
        axis.text.x = element_text(angle = 90, vjust = 0.5)) + #adjust x axis label
  theme(legend.position = "none")

# Number of records over time #
records <- data %>%
  select(year,taxonRank) %>%
  drop_na() %>% #remove columns where the year is not specified
  group_by(year) %>%
  summarise(n=n())

ggplot(data = records, mapping = aes(x = as.factor(year), y = n)) +
```

```
  geom_col(position = "dodge2", fill="powderblue", color="black", width = 0.8) +
  theme_classic() +
  scale_y_continuous(expand = c(0, 0), limits = c(0, 1280), breaks = c(0, 200, 400, 600, 800, 1000, 1200))
+
  theme(plot.title = element_text(hjust = 0.5), #adjust title position to the middle
        axis.text.x = element_text(angle = 90, vjust = 0.5)) + #adjust x axis label
  geom_text(aes(label = n), vjust = -0.5) +
  labs(x = "Year", y = "No. of records") + #set the name of each axis
  ggtitle("Number of records over time") #set the graphic title

# Number of records over time by Taxonomic Rank #
records_Rank <- data %>%
  select(year,taxonRank) %>%
  drop_na() %>% #remove columns where the year is not specified
  group_by(year,taxonRank) %>%
  summarise(n=n())

ggplot(data = records_Rank, mapping = aes(x = as.factor(year), y = n, fill=taxonRank)) +
  geom_col(color="black", width = 0.8) +
  scale_fill_brewer(palette = "Paired", name = "Rank",
                    breaks = c("Phylum", "Class", "Subclass",
                               "Infraclass", "Superorder", "Order",
                               "Superfamily", "Family", "Subfamily",
                               "Genus", "Species")) +
  theme_classic() +
  scale_y_continuous(expand = c(0, 0), limits = c(0, 1280), breaks = c(0, 200, 400, 600, 800, 1000, 1200))
+
  theme(plot.title = element_text(hjust = 0.5), #adjust title position to the middle
        axis.text.x = element_text(angle = 90, vjust = 0.5)) + #adjust x axis label
  labs(x = "Year", y = "No. of records") + #set the name of each axis
  ggtitle("Number of records by Taxonomic Rank over time") #set the graphic title

# Number of new records over time (Accumulation curves)  #
# SPECIES
data_AccSp <- data %>%
  filter(taxonRank == "Species") %>% #select only those identified until species level
  select(year,Species) %>% #keep only year and Species column
  drop_na() %>% #remove columns where the year is not specified (3 species)
  mutate(rec = 1) %>% #create a new column, all cells with 1
  group_by(Species) %>%
  arrange(year) %>% #order by year (oldest to newest)
  mutate("cm_count" = cumsum(rec)) %>% #compute the cumulative sum
  select(-rec) %>% # remove column that is not needed
  filter(cm_count < 2) #keep only the first entry for each species (first year when the species was found)

data_AccSp_year <- data_AccSp %>%
  group_by(year) %>%
  summarise(n=n()) %>% #obtain the number of each species reported by year
  mutate("cm_count" = cumsum(n)) %>% #get the cumulative sum
  select(-n) %>%
  mutate(Rank="Species")

# GENUS
data_AccGen <- data %>%
  select(year,Genus) %>% #keep only year and Genus column
  drop_na() %>% #remove columns where the year is not specified
```

```
  mutate(rec = 1) %>% #create a new column, all cells with 1
  group_by(Genus) %>%
  arrange(year) %>% #order by year (oldest to newest)
  mutate("cm_count" = cumsum(rec)) %>% #compute the cumulative sum
  select(-rec) %>% # remove column that is not needed
  filter(cm_count < 2) #keep only the first entry for each Family (first year when the Family was found)
data_AccGen_year <- data_AccGen %>%
  group_by(year) %>%
  summarise(n=n()) %>% #obtain the number of each species reported by year
  mutate("cm_count" = cumsum(n)) %>% #get the cumulative sum
  select(-n) %>%
  mutate(Rank="Genus")

# FAMILY
data_AccFam <- data %>%
  select(year,Family) %>% #keep only year and Family column
  drop_na() %>% #remove columns where the year is not specified
  mutate(rec = 1) %>% #create a new column, all cells with 1
  group_by(Family) %>%
  arrange(year) %>% #order by year (oldest to newest)
  mutate("cm_count" = cumsum(rec)) %>% #compute the cumulative sum
  select(-rec) %>% # remove column that is not needed
  filter(cm_count < 2) #keep only the first entry for each Family (first year when the Family was found)

data_AccFam_year <- data_AccFam %>%
  group_by(year) %>%
  summarise(n=n()) %>% #obtain the number of each species reported by year
  mutate("cm_count" = cumsum(n)) %>% #get the cumulative sum
  select(-n) %>%
  mutate(Rank="Family")

# Join all data together to Plot all information in one graphic
all_data <- bind_rows(data_AccSp_year, data_AccGen_year, data_AccFam_year)

ggplot(all_data, aes(x=factor(year), y = cm_count,
                     color = Rank, group = Rank)) +
  geom_line(size = 1) + #select line width
  labs(x = "Year", y = "No. of records") + #set the name of each axis
  ggtitle("Number of new records over time") + #set the graphic title
  theme_classic() +
  scale_y_continuous(expand = c(0, 0), limits = c(0, NA)) + #establish y axis limits
  theme(plot.title = element_text(hjust = 0.5), #adjust title position to the middle
        axis.text.x = element_text(angle = 90, vjust = 0.5)) #adjust x axis label

# Number of records in each Park over time #
records_Park_year <- data %>%
  select(year,NationalPark_MPA) %>%
  drop_na() %>% #remove columns where the year is not specified
  group_by(year,NationalPark_MPA) %>%
  summarise(n=n())

ggplot(data = records_Park_year, mapping = aes(x = as.factor(year), y = n, fill=NationalPark_MPA)) +
  geom_col(color="black", width = 0.8, show.legend = FALSE) +
  scale_fill_brewer(palette = "Set1") +
  theme_classic() +
  scale_y_continuous(expand = c(0, 0)) +
```

```
  theme(plot.title = element_text(hjust = 0.5), #adjust title position to the middle
        axis.text.x = element_text(angle = 90, vjust = 0.5)) + #adjust x axis label
  labs(x = "Year", y = "No. of records") + #set the name of each axis
  ggtitle("Number of records in each National Park over time") + #set the graphic title
  facet_wrap(~ NationalPark_MPA, scales = 'free') #split in different graphics by National Park


# Number of Class, Family, Order and Species records in each Park #
records_Park <- count(data,NationalPark_MPA)

# SPECIES
records_Sp_Park <- data %>%
  filter(taxonRank == "Species") %>% #select only those identified until species level
  select(NationalPark_MPA,Species) %>%
  mutate(rec = 1) %>% #create a new column, all cells with 1
  group_by(Species, NationalPark_MPA) %>%
  mutate("cm_count" = cumsum(rec)) %>% #compute the cumulative sum
  select(-rec) %>% # remove column that is not needed
  filter(cm_count < 2) #keep only the first entry for each species (first year when the species was found)

count_Sp_Park <- records_Sp_Park %>%
  select(-cm_count) %>%
  group_by(NationalPark_MPA) %>%
  summarise(count = n_distinct(Species))

# FAMILY
records_Fam_Park <- data %>%
  select(NationalPark_MPA,Family) %>%
  mutate(rec = 1) %>% #create a new column, all cells with 1
  group_by(Family, NationalPark_MPA) %>%
  mutate("cm_count" = cumsum(rec)) %>% #compute the cumulative sum
  select(-rec) %>% # remove column that is not needed
  filter(cm_count < 2) %>% #keep only the first entry for each species (first year when the species was found)
  drop_na() #remove columns where the Family is not specified

count_Fam_Park <- records_Fam_Park %>%
  select(-cm_count) %>%
  group_by(NationalPark_MPA) %>%
  summarise(count = n_distinct(Family))

# ORDER
records_Ord_Park <- data %>%
  select(NationalPark_MPA,Order) %>%
  mutate(rec = 1) %>% #create a new column, all cells with 1
  group_by(Order, NationalPark_MPA) %>%
  mutate("cm_count" = cumsum(rec)) %>% #compute the cumulative sum
  select(-rec) %>% # remove column that is not needed
  filter(cm_count < 2) %>% #keep only the first entry for each species (first year when the species was found)
  drop_na() #remove columns where the Family is not specified

count_Ord_Park <- records_Ord_Park %>%
  select(-cm_count) %>%
  group_by(NationalPark_MPA) %>%
  summarise(count = n_distinct(Order))
```

```
# Class
records_Class_Park <- data %>%
  select(NationalPark_MPA,Class) %>%
  mutate(rec = 1) %>% #create a new column, all cells with 1
  group_by(Class, NationalPark_MPA) %>%
  mutate("cm_count" = cumsum(rec)) %>% #compute the cumulative sum
  select(-rec) %>% # remove column that is not needed
  filter(cm_count < 2) %>% #keep only the first entry for each species (first year when the species was found)
  drop_na() #remove columns where the Family is not specified

count_Class_Park <- records_Class_Park %>%
  select(-cm_count) %>%
  group_by(NationalPark_MPA) %>%
  summarise(count = n_distinct(Class))

# Combine all plots together
pALL <- ggplot(records_Park, aes(x="", y=n, fill=NationalPark_MPA)) +
  geom_bar(width=1, stat="identity", color = "black") +
  coord_polar("y", start=0) +
  ggtitle("Total") +
  theme_void() + theme(plot.title = element_text(hjust = 0.5, vjust = -10)) +
  theme(legend.title = element_blank()) +
  geom_text(aes(label = n),
            position = position_stack(vjust = 0.5)) +
  scale_fill_brewer(palette = "Accent",
                    breaks = c("Área Marinha Protegida Comunitária de Urok",
                               "Parque Nacional do Grupo de Ilhas de Orango",
                               "Parque Nacional Marinho João Vieira e Poilão", "Non"))

pCl <- ggplot(count_Class_Park, aes(x="", y=count, fill=NationalPark_MPA)) +
  geom_bar(width=1, stat="identity", color = "black") +
  coord_polar("y", start=0) +
  ggtitle("No. Class") +
  scale_fill_brewer(palette = "Accent") +
  theme_void() + theme(plot.title = element_text(hjust = 0.5)) +
  theme(legend.position="none") +
  geom_text(aes(label = count), position = position_stack(vjust = 0.5))

pOrd <- ggplot(count_Ord_Park, aes(x="", y=count, fill=NationalPark_MPA)) +
  geom_bar(width=1, stat="identity", color = "black") +
  coord_polar("y", start=0) +
  ggtitle("No. Oder") +
  scale_fill_brewer(palette = "Accent") +
  theme_void() + theme(plot.title = element_text(hjust = 0.5)) +
  theme(legend.position="none") +
  geom_text(aes(label = count), position = position_stack(vjust = 0.5))

pFam <- ggplot(count_Fam_Park, aes(x="", y=count, fill=NationalPark_MPA)) +
  geom_bar(width=1, stat="identity", color = "black") +
  coord_polar("y", start=0) +
  ggtitle("No. Family") +
  scale_fill_brewer(palette = "Accent") +
  theme_void() + theme(plot.title = element_text(hjust = 0.5)) +
  theme(legend.position="none") +
```

```
  geom_text(aes(label = count), position = position_stack(vjust = 0.5))

pSp <- ggplot(count_Sp_Park, aes(x="", y=count, fill=NationalPark_MPA)) +
  geom_bar(width=1, stat="identity", color = "black") +
  coord_polar("y", start=0) +
  ggtitle("No. Species") +
  scale_fill_brewer(palette = "Accent") +
  theme_void() + theme(plot.title = element_text(hjust = 0.5)) +
  theme(legend.position="none") +
  geom_text(aes(label = count), position = position_stack(vjust = 0.5))

title <- textGrob("Number of records per National Park/Marine Protected Area",
                  gp=grid::gpar(fontsize=14, fontface='bold'))
nt <- theme(legend.position='none')
grid_arrange_shared_legend(pALL + nt, arrangeGrob(pOrd,pFam, pSp), ncol=2, top=title)

grid_arrange_shared_legend(pALL + nt, arrangeGrob(pCl,pOrd,pFam, pSp), ncol=2, top=title)

# Most recorded Phylum #
Phylum_abn <- count(data, Phylum)

Phylum_abn$key <- paste0(Phylum_abn$Phylum,' [',Phylum_abn$n,']')

MyPalette <- c("tan1", "black", "paleturquoise","deeppink", "chartreuse4", "darkorchid",
               "sienna4", "darksalmon", "gold", "plum1", "red3", "cornflowerblue")

ggplot(Phylum_abn, aes(x="", y=n, fill = reorder(key, n))) +
  geom_bar(stat = "identity", color = "black") +
  coord_polar(theta = "y") +
  labs(colour = NULL) +
  scale_fill_manual(values = MyPalette) +
  ggtitle("Most recorded Phylum") +
  theme_void() + theme(plot.title = element_text(hjust = 0.5)) +
  theme(legend.title = element_blank())

# Number of Species recorded per Phylum #
Phylum_abn_Sp <- data %>%
  filter(taxonRank == "Species") %>% #select only those identified until species level
  select(Phylum,Species) %>%
  group_by(Phylum) %>%
  summarise(count = n_distinct(Species)) #count number of different species belonging to each Phylum

Phylum_abn_Sp$key <- paste0(Phylum_abn_Sp$Phylum,' [',Phylum_abn_Sp$count,']')

MyPalette2 <- c("deeppink", "chartreuse4", "darkorchid",
               "sienna4", "darksalmon", "gold",
               "plum1", "red3", "cornflowerblue")

ggplot(Phylum_abn_Sp, aes(x="", y=count, fill = reorder(key, count))) +
  geom_bar(stat = "identity", color = "black") +
  coord_polar(theta = "y") +
  labs(colour = NULL) +
  scale_fill_manual(values = MyPalette2) +
  ggtitle("Number of Species recorded per Phylum") +
  theme_void() + theme(plot.title = element_text(hjust = 0.5)) +
  theme(legend.title = element_blank())
```

```r
# Number of records per Class (Phylum Chordata) #
Chord_abn_Class <- data %>%
  dplyr::filter(Phylum == "Chordata") %>%
  group_by(Phylum, Class) %>%
  count(Phylum, Class) %>%
  mutate(Class = if_else(Class %in% "Aves", "Reptilia (Aves)", Class)) %>%
  mutate(Class = if_else(Class %in% NA_character_, "Reptilia (Turtles)", Class))

ggplot(Chord_abn_Class, aes(x = Class, y = n, fill = Class)) +
  geom_bar(stat = "identity", width=0.8, color = "black") +
  scale_fill_brewer(palette = "Dark2", na.value = "grey") +
  coord_flip() +
  ggtitle("Most recorded Classes (Phylum = Chordata)") +
  labs(x = "Class", y = "Number of records") + #set the name of each axis
  theme_classic() + theme(plot.title = element_text(hjust = 0.5)) +
  scale_y_continuous(expand = c(0, 0), limits = c(0, 3100)) +
  theme(legend.position="none")

# Number of records per Class per Park (Phylum Chordata) #
Chord_abn_Class_Park <- data %>%
  dplyr::filter(Phylum == "Chordata") %>%
  select(Phylum,Class,NationalPark_MPA) %>%
  count(Class,NationalPark_MPA) %>%
  mutate(Class = if_else(Class %in% "Aves", "Reptilia (Aves)", Class)) %>%
  mutate(Class = if_else(Class %in% NA_character_, "Reptilia (Turtles)", Class))

ggplot(Chord_abn_Class_Park, aes(x = Class, y = n, fill = NationalPark_MPA)) +
  geom_bar(stat = "identity", width=0.8, color = "black") +
  coord_flip() +
  scale_fill_brewer(palette = "Accent", name = "National Park/Marine Protected Area",
                    breaks = c("Área Marinha Protegida Comunitária de Urok",
                               "Parque Nacional do Grupo de Ilhas de Orango",
                               "Parque Nacional Marinho João Vieira e Poilão", "Non")) +
  ggtitle("Number of records per Class in each National Park (Phylum = Chordata)") +
  labs(x = "Class", y = "Number of records") + #set the name of each axis
  theme_classic() + theme(plot.title = element_text(hjust = 0.5)) +
  scale_y_continuous(expand = c(0, 0))

# Number of Species records per Class (Phylum Chordata) #
Chord_abn_Sp <- data %>%
  dplyr::filter(Phylum == "Chordata") %>%
  filter(taxonRank == "Species") %>% #select only those identified until species level
  select(Phylum,Class,Species) %>%
  group_by(Class) %>%
  summarise(count = n_distinct(Species)) %>% #count number of different species belonging to each Phylum
  mutate(Class = if_else(Class %in% "Aves", "Reptilia (Aves)", Class)) %>%
  mutate(Class = if_else(Class %in% NA_character_, "Reptilia (Turtles)", Class))

ggplot(Chord_abn_Sp, aes(x = Class, y = count, fill = Class)) +
  geom_bar(stat = "identity", width=0.8, color = "black") +
  scale_fill_brewer(palette = "Dark2", na.value = "grey") +
  ggtitle("Number of Species per Class (Phylum = Chordata)") +
  labs(x = "Class", y = "Number of Species") + #set the name of each axis
  theme_classic() + theme(plot.title = element_text(hjust = 0.5)) +
```

```
  scale_y_continuous(expand = c(0, 0)) +
  theme(legend.position="none")

# Number of records per Class (Other Phyla) #
Abn_Class <- data %>%
  dplyr::filter(!Phylum == "Chordata") %>%
  group_by(Phylum, Class) %>%
  count(Phylum, Class)

mycolors <- colorRampPalette(brewer.pal(8,"Accent"))(16)

ggplot(Abn_Class, aes(x = Phylum, y = n, fill = Class)) +
  geom_bar(stat = "identity", width=0.8, color = "black") +
  scale_fill_manual(values = mycolors, na.value = "black") +
  coord_flip() +
  ggtitle("Numbebr of records per Phylum by Class (excluding Chordata)") +
  labs(x = "Phylum", y = "Number of records") + #set the name of each axis
  theme_classic() + theme(plot.title = element_text(hjust = 0.5)) +
  scale_y_continuous(expand = c(0, 0))

# Number of records per Class per Park (Other Phyla) #
Abn_Class_Park <- data %>%
  dplyr::filter(!Phylum == "Chordata") %>%
  select(Phylum,Class,NationalPark_MPA) %>%
  count(Phylum,Class,NationalPark_MPA)

ggplot(Abn_Class_Park, aes(x = Phylum, y = n, fill = Class)) +
  geom_bar(stat = "identity", width=0.8, color = "black") +
  scale_fill_manual(values = mycolors, na.value = "black") +
  coord_flip() +
  ggtitle("Number of records per Phylum by Class in each National Park (excluding Chordata)") +
  labs(x = "Phylum", y = "Number of records") + #set the name of each axis
  theme_classic() + theme(plot.title = element_text(hjust = 0.5)) +
  scale_y_continuous(expand = c(0, 0)) +
  facet_wrap(~ NationalPark_MPA, scales = 'free') #split in different graphics by National Park

# Number of Species per Class per Park (Other Phyla) #
Oth_ClSp_Park <- data %>%
  filter(!Phylum == "Chordata") %>%
  filter(taxonRank == "Species") %>% #select only those identified until species level
  select(NationalPark_MPA,Phylum,Class,Species) %>%
  mutate(rec = 1) %>% #create a new column, all cells with 1
  group_by(Species, Class, Phylum, NationalPark_MPA) %>%
  mutate("cm_count" = cumsum(rec)) %>% #compute the cumulative sum
  select(-rec) %>% # remove column that is not needed
  filter(cm_count < 2) #keep only the first entry for each species (first year when the species was found)

count_Oth_ClSp_Park <- Oth_ClSp_Park %>%
  select(-cm_count) %>%
  group_by(Phylum, Class, NationalPark_MPA) %>%
  summarise(count = n_distinct(Species))

ggplot(count_Oth_ClSp_Park, aes(x = Phylum, y = count, fill = Class)) +
  geom_bar(stat = "identity", width=0.8, color = "black") +
  coord_flip() +
  scale_fill_manual(values = mycolors, na.value = "grey") +
```

```
  ggtitle("Number of Species per Class per Phylum in each National Park (excepting Chordata)") +
  labs(x = "Phylum", y = "Number of Species") + #set the name of each axis
  theme_classic() + theme(plot.title = element_text(hjust = 0.5)) +
  scale_y_continuous(expand = c(0, 0)) +
  facet_wrap(~ NationalPark_MPA, scales = 'free') #split in different graphics by National Park

# Most studied Island #
Isl_abn <- count(data, Island)

# Most studied Island in terms of Species #
Isl_abn_Sp <- data %>%
  filter(taxonRank == "Species") %>% #select only those identified until species level
  select(Island,Species) %>%
  group_by(Island) %>%
  summarise(count = n_distinct(Species)) #count number of different species belonging to each Phylum

Total_ISL <- merge(Isl_abn, Isl_abn_Sp, all = TRUE)

## Find minimum and maximum values for each variable
tmp <- Total_ISL %>%
  drop_na() %>%
  summarise(across(c("count", "n"), ~list(min = min(.x), max=max(.x)))) %>%
  unnest(everything())

## make mapping from Records to Species
m <- lm(count ~ n, data=tmp)
## make mapping from Species to Records
m_inv <- lm(n ~ count, data=tmp)

## transform Records so it's on the same scale as Species.
## to do this, you need to use the coefficients from model m above
dat <- Total_ISL %>%
  mutate(n = coef(m)[1] + coef(m)[2]*n) %>%
  ## pivot the data so all plotting values are in a single column
  pivot_longer(c("count", "n"),
               names_to="var", values_to="vals") %>%
  mutate(var = factor(var, levels=c("count", "n"),
                      labels=c("Species", "Records")))

ggplot(dat, aes(x=as.factor(Island), y=vals, fill=var)) +
  geom_bar(position="dodge", stat="identity", width = 0.8) +
  ## use model m_inv from above to identify the transformation from the tick values of SPH
  ## to the appropriate tick values of CPH
  scale_y_continuous(sec.axis=sec_axis(trans = ~coef(m_inv)[1] + coef(m_inv)[2]*.x, name="Number of
Records"),
                     expand = c(0, 0)) +
  labs(y="Number of Species", x="Island", fill="") +
  theme_classic() +
  theme(legend.position="top", axis.text.x = element_text(angle = 90, hjust=0.95,vjust=0.2))

# IUCN species Categories in each Park #
IUCN_Sp_Park <- data %>%
  filter(taxonRank == "Species") %>%
  select(NationalPark_MPA,Species,IUCN) %>%
  mutate(rec = 1) %>% #create a new column, all cells with 1
  group_by(Species, NationalPark_MPA, IUCN) %>%
```

```
  mutate("cm_count" = cumsum(rec)) %>% #compute the cumulative sum
  select(-rec) %>% # remove column that is not needed
  filter(cm_count < 2) #keep only the first entry for each species (first year when the species was found)

count_IUCN_Sp_Park <- IUCN_Sp_Park %>%
  select(-cm_count) %>%
  group_by(NationalPark_MPA,IUCN) %>%
  summarise(count = n_distinct(Species))

IUCN_color <- c("red", "gray62", "darkorange", "green3",
                "greenyellow", "yellow", "grey99")

ggplot(count_IUCN_Sp_Park, aes(x = IUCN, y = count, fill = IUCN)) +
  geom_bar(stat = "identity", width=0.8, color = "black") +
  coord_flip() +
  scale_fill_manual(values = IUCN_color,
                    labels = c("Critically Endangered (CR)", "Data Deficient (DD)",
                               "Endangered (EN)", "Least Concern (LC)",
                               "Near Threatened (NT)", "Vulnerable (VU)",
                               "Not evaluated (NA)")) +
  ggtitle("Number of Species IUCN category in each National Park/Marine Protected Area") +
  labs(x = "IUCN category", y = "Number of Species", colour = "IUCN Category") + #set the name of each axis
  theme_classic() + theme(plot.title = element_text(hjust = 0.5)) +
  scale_y_continuous(expand = c(0, 0)) +
  facet_wrap(~ NationalPark_MPA, scales = 'free') +#split in different graphics by National Park
  guides(fill=guide_legend(title='IUCN Category'))
```

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