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Spatial and temporal representation of marine fish occurrences available online

--Manuscript Draft--

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Abstract:	<p>Despite the 243,000 species of marine species described by 2022, our knowledge about the biodiversity in the oceans is still incomplete. This may have a negative and detrimental effect for the conservation of marine ecosystems under the current anthropization of our biota and the fast-paced climate and global change scenario. However, a large number of online repositories cataloging, storing and distributing biodiversity information hosting taxonomic information and species occurrence data have emerged recently. FishBase, the Global Biodiversity Information Facility (GBIF) and the Ocean Biodiversity Information System (OBIS) are part of these publicly available repositories representing a variety of sources that have exploded in number. However, despite the incredible accumulation of biodiversity records, not all the information is really useful, nor does it represent any new knowledge regarding global species richness patterns.</p> <p>In this study we evaluated the spatial and temporal representativeness of the records of marine fishes (order Actinopterygii) available in the GBIF and OBIS global repositories. We provide a methodological framework based on a set of non-parametric estimators to calculate species richness from incidence data, using hexagonal grids as sampling units overlaid on the marine bioregions worldwide.</p> <p>Using standard ecological and spatial analysis tools, we identify regions that are adequately represented in terms of available records and therefore have more reliable data, as well as regions with few records that do not represent current species richness. We overlap these results with the location of marine protected areas and fishing exploitation zones to understand the anthropogenic effect on marine ichthyofauna. We additionally evaluate hypotheses regarding the taxonomic, geographic, and temporal distribution of information biases to deepen our current understanding of public records of species occurrences worldwide.</p> <p>Considering that more than 40 years of information was analyzed, the results showed that on a global scale, the primary data on marine fish available on GBIF and OBIS platforms are still far from being representative and complete. Only 1.14% of the records were useful for our analyses. In addition, we found that the information seems to be biased towards coastal areas, regions close to developed countries and areas where there is a large fishing activity. Finally, the best represented species and families are those with a small body size, which use shallow habitats and have commercial cultural value.</p>
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Valdivia, February 2, 2023

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Dear Editor-in-Chief,

We hereby submit a manuscript entitled: "*Spatial and temporal representation of marine fish occurrences available online*" authored by Vanessa Pizarro, Andrea Castillo, Andrea Piñones and myself.

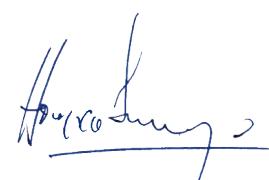
The marine ecosystem is among the least explored of our biota and understanding the spatial distribution of its biodiversity is essential to produce adequate protection planning nowadays. Several ecoinformatics tools have now been developed for such task with sometimes uncertain outcome; vast knowledge is produced at some locations while other are left unsampled. This work tackles precisely on this issue and seeks to provide a description of how marine fish diversity has been collected and stored in publicly available repositories such as OBIS and GBIF. By using a combination of spatial analyses and more classic diversity evaluation, we have identified the current state of the art among fish biodiversity inventories. We identify gaps, associated sample efforts and potential determinants e.g. life history features. Finally, an assessment on the incidence of protection areas and cultural values upon fish species richness is also provided.

We believe that this manuscript is of great interest for your audience as it addresses a unifying theme across biogeography and ecoinformatics by building on prominent contributions in the field, current effort to index our biota, so that we may pinpoint where efforts should be placed for conservation.

We hope that you find the manuscript compelling and would appreciate its prompt evaluation.

Thank you in advance for the consideration,

Sincerely,


 horacio@ecoinformatica.cl

Associate Editor: I agreed with both reviewers that recommend Major Revision of the manuscript. However, these intensive comments implied that substantial revisions were needed.

Reviewer #1

A potentially useful contribution, albeit very descriptive. However, in its current form there are too many issues with the analyses for it to be publishable. The English expression also needs substantial work.

== General comments.

1. The hexagons used are not equal area and are therefore not comparable spatial units. The analyses are therefore incorrect and need to be redone.

Indeed, we realized this and have completely redone the analysis using a Cylindrical Equal Area projection. This now bases our analyses on equal area grids. A description of the procedure were included in section 2.2.1 *Spatial Representativeness Analysis*; page 7.

2. It is possible the polygon data have also been incorrectly reported (Table 1), although I am unable to locate the geographic polygon data plotted in Fig 1 to check this (it appears not to be available from Costello *et al.*, 2017).

Thanks for this comment, we have now revisited the number of polygons, names and identification of them. Table 1 shows this revision and coincides with Costello et al (2017)'s bioregions (see <https://doi.org/10.1038/s41467-017-01121-2>). We have also corrected the reference in the text and added to the manuscript ref list.

3. The SRI index is subject to issues when the denominator is low. Consider (1 / 2) vs (100 / 200) - these have the same ratio but the number of missing taxa is very different. The authors need to place the work in the context of Marcer *et al.*, (2022, <https://onlinelibrary.wiley.com/doi/full/10.1111/ecog.06025>) which is a much more thorough analysis of data, albeit not focusing on marine fish species.

Respuesta:

We appreciate this comment as it shows that we did not fully convey the meaning of the SRI index. While we recognize the need to account for the absolute gap, or missing spp, the objective of SRI is not associated with identifying the absolute magnitude of the information gap. Indeed, this index only indicates the relative magnitude of this gap. However, following your suggestions, we have decided to generate a new category for those cases where only one species per cell is recorded. In these situations the SRI index indicates that the cell is "adequately" sampled. To correct this error, we created the category "Insufficient Records" (see section 2.2.1 in page 7).

4. The Chao2 index requires incidences. How were these handled? I assume each record was treated as a unit of 1? Or were the hexagons used to define the incidences?

As explained in page 7, incidence were based on the record number in hexagonal cells.

5. It is unclear why the average of the richness estimators is used. It would perhaps be better to simply calculate the Chao2 (or Chao1) and then also take into account the

confidence intervals. And perhaps consider the ICE index instead as it uses more than just singletons and doubletons. See for example <https://github.com/AnneChao/SpadeR>

The recent literature reviewed here, on how to evaluate large data repositories for estimating species richness (see Mora et al., 2008; Troia & McManamay, 2017), show that different parametric and non-parametric methods usually generate different results in calculating species diversity, as these methods consider different attributes of the data (Walther & Morand, 1998; Gotelli & Colwell, 2001). One way to solve this is to use an estimator-averaging approach, which is argued to be statistically more accurate than a single model (Mora et al., 2008).

See additionally the work by Gotelli & Colwell, 2001: (<https://doi.org/10.1046/j.1461-0248.2001.00230.x>) and Walther & Morand, 1998 (<https://doi.org/10.1017/S0031182097002230>) who consider an average of different diversity indexes as well.

6. The wrong reference has been cited for the marine bioregions. It should be Costello et al. (2017) Nat Comm, not Costello & Chaudhury (2017).

Respuesta: Thank you for this remark. We have indeed realized this error. We now cite the correct reference.

== Specific comments

7. P2, L18. What is a hands on concept?

We apologize for the lack of clarity here. We checked the manuscript by native speaker and added a clarification. We mean, concepts related to "species inventory", "taxonomic inventory" or "completeness of the inventory", terms used in contemporary studies to emphasize the need to record the diversity of species in a given ecosystem or for a given taxon. We have incorporated this clarification. (Page 3, 2nd paragraph)

8. P3, L14. Amon?

Respuesta: Thank you for this remark, we fixed this typo.

9. S2.2.1. These hexagons are not equal area if they are constrained to be 1x1 degrees. Indeed the maps in the supp mat show they are not equal area so therefore the analyses using the hexagons are not valid. As the meridians of longitude converge towards the poles the true area of each hexagon approaches zero, so there are many more hexagons at latitude -80 compare with latitude -10. This needs to be corrected.

The projection of the grid is corrected to "cylindrical equal area", so that now the grid does have hexagonal cells of equal area. This methodological modification has been incorporated in section 2.2.1 Spatial Representativeness Analysis.

10. P4, L34. Why give the formula for the mean? Or are the authors trying to make the analysis look more complex than it really is?

We apologize that displaying the formula produces the wrong impression here. We just believe that a succinct description of the index may help some users to better understand the index.

11. P5. Just say the SRI is the ratio of observed to expected. And why not also the difference? Otherwise one suffers from the low denominator problem, e.g. is 1/2 as important as 100/200? (see also general comments).

The objective is only to know the degree of representativeness of the cell, that is, whether or not the observed richness corresponds to the expected richness, instead of how many species are missing to reach the expected richness levels. However, we have now considered this observation by identifying cells that have only one observation. We additionally note that SRI only considers cells that are sampled "adequately", as we have now created an additional category to evidence these cases.

12. P5, L6-12. Assignment of a continuous scale to such arbitrarily defined classes does not really help. Why is it that $SRI=0.599999$ is incomplete but 0.6000001 is complete, for example? Just use the observed values.

While somehow subjective, we do believe that, in this case, categories are more useful to broadly understand how the data is distributed. Using a continuous scale of values or simply the observed values could be overwhelming as there are large differences for biodiversity hotspot areas. Particularly in areas where richness indices are very low. The categorization intends to standardize the information in order to emphasize the bias in the data, particularly for certain geographic areas. This additionally highlights the large information gaps on a global scale.

13. P5, L16. "asses"

Respuesta: Thank you for this remark, we fixed this error.

14. S2.2.3. This is a long-winded description of a spatial intersection.

Respuesta: Thanks for your comment.

15. P6, L3. "Just about" -> "Approximately"

Respuesta: Thank you for this remark, we fixed this error.

16. Fig 1 caption. Describe the normalisation used. It is not given in Table 1. The bioregions are not defined in Costello & Chaudhary (see general comments).

The reference to the work of Costello et al., (2017) has been corrected. Panel "A" delivers the ecoregion number information that can be collated in Table 1. Table 1 has been corrected to deliver all information plotted in Figure 1: Species richness (panel B); family richness (panel C); Proportion of occurrence records by bioregion area (panel D); and Shannon index (panel E).

17. Table 1. Given the level of detail in Fig 1, the bioregion data are not sufficiently accurate to support a precision of 1 km². Report to the nearest thousand km². Please ensure the areas have been calculated using geodesic methods if the data have not been projected into an equal area coordinate system first.

Table 1, specifically the column "Area (km2)" has been corrected as suggested by the reviewer. In addition, the projection of the hexagonal grid to cylindrical equal area has also been corrected, and the values for each column have been updated.

18. Fig 2. The colour scheme used suggests a false dichotomy between the upper and lower classes. A continuous colour scheme should be used, e.g. from light to dark.

Thank you for this remark. The colors have been corrected following the suggestions of the second reviewer for a color palette that is visible to people with color blindness (Rochinni et al., 2023, <https://doi.org/10.1016/j.ecoinf.2023.102045>).

19. P6, L7. I don't know what is meant by this: "We used hexagonal grids that fit the geographic reality of marine ecosystems". Hexagonal grids are very useful because each hexagon's centroid is equidistant to its six nearest neighbours, unlike with rectangular tessellations. Hexagons also work better than square cells when tessellating data on a spheroid.

We mean that hexagons fit better by their geometric shape to the shape of marine bioregions, which are not exact squares. In other words, hexagonal cells fit much better to the shapefile boundaries of marine bioregions, which are not perfect polygons, they do not have right angles. The idea of using hexagonal cells is drawn from the work of Costello et al., (2017) (<https://doi.org/10.1038/s41467-017-01121-2>), here the possibility of delimiting bioregions using this grid shape is explored.

20. P12, L20. I am not sure of the relevance of this para. The example studies are presented as a shopping list without being integrated. Are all needed?

The purpose of this paragraph is to inform the reader about the various studies that have been carried out, which include different taxa and methodologies. The objective here is to contextualize and show that the systematic evaluation of large data repositories is a highly relevant topic, especially if the final objective is to generate inputs for biodiversity conservation. We have slightly corrected this paragraph to reflect this idea (Page 18).

21. P13, L14. This is incomplete. "the greater the overestimation of the index than richness". In any case, as the resolution becomes coarser one expects to see SR increase, or at least never decrease due to how it is calculated.

The larger the grid, the larger the area covered by the cell and the more species are, hence, considered. This, in turn, increases the value of SRI locally. So, using a lower grid resolution, will indicate that bioregions have better sampled areas as records may be accumulated in a very small area compared to the large size of a cell. Conversely, using a higher grid size resolution (e.g. $1^\circ \times 1^\circ$) captures these very localized variations of the data. We have modified this paragraph so that this idea is properly conveyed (Page 19, line 19).

22. P13, L18. What is a thick grid? And why would hexagons also not suffer from this issue? Any regular tessellation will have this issue.

We refer to a low resolution grid. We have changed the word "thick" to "lower resolution". As we have already mentioned, a low resolution grid could be underestimating the SRI index by covering a large area when the records are clustered in more localized areas. This is especially true in coastal areas given the nature of the records hosted by GBIF and OBIS (opportunistic and citizen science records). On the other hand, we believe that a hexagonal shaped cell is better suited to the irregular shape of coastal areas, a methodology we adopt from Costello et al., (2017).

23. Fig 5. Why fit a straight line to what is clearly a curvilinear relationship? And if the dotted line is just to show a negative relationship then it is redundant as this is obvious. If significance is needed then see the first point in this comment.

Thank you, we have eliminated such line in the figures

24. P25, L7. This github repo is not available.

We apologize, it is now available.

Reviewer #2:

This is a well written and structured paper. I have some major points to be considered by the authors.

25. THE NEED FOR THIS STUDY: The pressing need for this study is not explained in detail or, at least, lacks a clear aim statement. Further, I would enlarge a bit the intro part on sampling effort which is, in my view, the most important spatial bias in species and diversity distribution mapping.

Respuesta:

While we understand the comments brought up by this reviewer, we believe to have clearly stated the context of the main concern in the introduction. The main idea behind this manuscript is that the large data accumulation of biodiversity information has not necessarily included an enlargement of our knowledge of biodiversity. In other words, we seem to have a fair amount of biased data providing a partial representation of our biota.

A large part of such discussion is related to developing a common framework to describe biodiversity in itself, and another part of the discussion is related to how we have sampled our biota from a macroecological perspective. This is extensively presented through the work of Yang et al (2013), Hortal et al (2008), Mora et al (2008), García-Rosello et al (2015) and Troia and McManamay (2017).

26. CARTOGRAMS: I strongly suggest in this paper the use of cartograms to represent in just one image both species diversity (as colour) and sampling effort (as a distortion of objects).

e.g.:

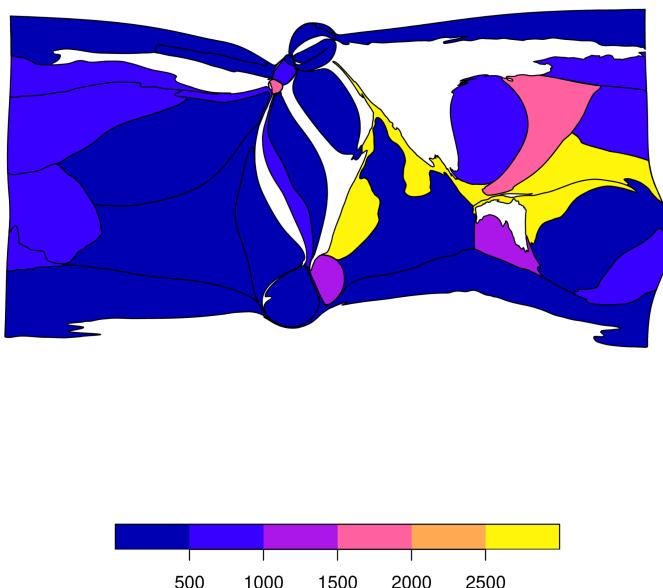
- Diffusion-based method for density-equalizing maps. Michael T. Gastner and M. E. J. Newman in PNAS

- Sampling biases shape our view of the natural world. Alice C. Hughes, Michael C. Orr, Keping Ma, Mark J. Costello, John Waller, Pieter Provoost, Qinmin Yang, Chaodong Zhu and Huijie Qiao in ECOGRAPHY

This would be one of the manners to represent spatial bias together with information on diversity. Showing uncertainty is mandatory in this type of paper.

See also the cartogram R package @: <https://CRAN.R-project.org/package=cartogram>

We tried to generate meaningful cartograms of Costello et al (2017)'s bioregion using species richness as colors and sampling effort as distortion. Unfortunately, we were not able to generate a representation of richness that will spark more information. We include here the best candidate for you to evaluate. The result is horrendous, and believe that this may be due to the fact that deformed marine bioregions completely shadows the shape of continents that help us understand the picture. We hence believe that we better stick to traditional representations.



27. Counts of records, species, families and Shannon diversity for each bioregion: they should be put as an infographic. The information provided as a table is too much. Translate Table 1 to an infographic or a graph and be put the complete table as supplementary material.

We have decided to keep the table as it allows us to evaluate the most succinct representation of the information used in this manuscript. It also provides lookup table to identify bioregions through their ID.

28. Spatial Representativeness Index: I definitively disagree with the colour ramp used to show the spatial representativeness.

See e.g.: <https://doi.org/10.1016/j.ecoinf.2023.102045> and change the colour ramp appropriately. Further, the table is complex and useless in my view.

All color palettes have been changed following the suggestions in Rocchini et al. (2023).

29. Protected area overlap and SRI: the same things I stated for the representation of counts apply here. This is also true for the overlapping FAO fishery exploitation areas and SRI grid.

We have decided to present our results on FAO fishery exploitation and protected areas in tables, as marine protected areas only represent an extremely small fraction of bioregions. Generating maps of this does not make much sense as it is poorly represented at a global scale. Regarding the FAO areas, the delimitations of these areas are not the same as the bioregions (they are totally different shapefiles), we believe that plotting this information on a map could be confusing for the reader. Our work already has two scales of analysis (bioregions and grids), we do not want to further complicate the information we are trying to communicate.

30. Records accumulation rate for each bioregion across the four decades analyzed: change red and blue with colours visible to everyone. This is also true for the map of slope values and for Spatial representativeness index (SRI) mapping of cells of different size.

All color palettes have been changed following the suggestions in Rocchini et al. (2023).

31. Why in the log relationships linear patterns are shown? I am clearly seeing a strong decay related to other types of functions to be used here.

Respuesta:

Thank you for this remark. We have now removed trend lines.

32. Compliments and thanks for the use of LaTeX which, as usual, renders everything more simple to read. I appreciated a lot the use of symbols for \ref to subsections, which is really straightforward.

Thank you very much for your comments and encouragement.

--Very minor:

33. Remove the final point in affil 4 after Chile.

Respuesta: Thank you for this remark, we fixed this typo.

34. Keywords in alphabetical order

Respuesta: Thank you for this remark, we fixed this error.

Spatial and temporal representation of marine fish occurrences available online

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¹⁸ Abstract

Despite the 243,000 species of marine species described by 2022, our knowledge about the biodiversity in the oceans is still incomplete. This may have dreadful and detrimental effect for the conservation of marine ecosystems under the current anthropization of our biota and the fast pacing climate and global change scenario.

However, a large number of online repositories cataloging, storing and distributing biodiversity information hosting taxonomic information and species occurrence data have emerged recently. FishBase, the Global Biodiversity Information Facility (GBIF) and the Ocean Biodiversity Information System (OBIS) are part of these publicly available repositories representing a variety of sources that have exploded in number. However, despite the incredible accumulation of biodiversity records, not all the information is really useful, nor does it represent any new knowledge regarding global species richness patterns.

In this study we evaluated the spatial and temporal representativeness of the records of marine fishes (order Actinopterygii) available in the GBIF

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July 4, 2023

and OBIS global repositories. We provide a methodological framework based on a set of non-parametric estimators to calculate species richness from incidence data, using hexagonal grids as sampling units overlapped on the marine bioregions worldwide.

Using standard ecological and spatial analysis tools, we identify regions that are adequately represented in terms of available records and therefore have more reliable data, as well as regions with few records that do not represent current species richness. We overlap these results with the location of marine protected areas and fishing exploitation zones to understand the anthropogenic effect on marine ichthyofauna. We additionally evaluate hypotheses regarding the taxonomic, geographic, and temporal distribution of information biases to deepen our current understanding of public records of species occurrences worldwide.

Considering that more than 40 years of information was analyzed, the results showed that on a global scale, the primary data on marine fish available on GBIF and OBIS platforms are still far from being representative and complete. Only 1.14% of the records were useful for our analyses. In addition, we found that the information seems to be biased towards coastal areas, regions close to developed countries and areas where there is a large fishing activity. Finally, the best represented species and families are those with a small body size, which use shallow habitats and have commercial cultural value.

Keywords: Species Richness-Ecoinformatics, Spatial-and-Teporal Representativeness-Ecological Information Biases, Marine Fish, Ecological Information Biases-Spatial and Temporal Representativeness, Ecoinformatics-Species Richness

1. Introduction

Currently, the more than 243,000 species included in the World Register of Marine Species database ([WORMS, 2022](#)) suggests that only 11 to 78% of all marine species have been discovered revealing a striking picture of vastly incomplete knowledge that may have serious implications for marine conservation ([Luypaert et al., 2020](#)). Moreover, ongoing climate change represents one of the greatest threats to biodiversity ([Malhi et al., 2020; Turner et al.,](#)

2020) and has already been documented to modify the distribution of marine species (Lenoir et al., 2020). Some of the described effects considers the invasion of non-native species leading to massive species turnover that may lead to the local extinction of large proportions of species (Cheung et al., 2009).

While species richness is often used to represents diversity patterns, species richness is, in itself, an aggregate variable subsuming the variety of life (Marquet et al., 2004). Hence, several attempts have focused on the development of more encompassing indices sparking interesting scientific debates to describe ecological heterogeneity (Tuomisto, 2011; Moreno and Rodríguez, 2011; Daly et al., 2018). However, scientific literature seem to have opted to shift focus to the consequences of biodiversity loss by fostering the usage of new terminology to provide hands-on concepts such as species inventory, taxonomic inventory or inventory completeness designed to convey sharper messages to policy makers summarizing the richness of biodiversity (Pereira et al., 2013; Butchart et al., 2010). Still, while scientists have debated the use of biodiversity terminology, species richness provides a succinct, and easy-to-handle description of the variability across several other quantities describing ~~biodiversity—the biota~~ in space and time (Appeltans et al., 2012), and is ~~, together with other diversity indices,~~ an essential feature to understand how diversity changes under the impact of natural and anthropogenic factors on biomes, regions and ecosystems (Troia and McManamay, 2017; Magurran and McGill, 2011).

Likewise, biodiversity can also be assessed through life history traits, which are modulated by both evolutionary factors and the variation in habitats and ecosystems (Neigel, 1997; Hutchings and Baum, 2005). We now know that biodiversity is more likely an expression of the heterogeneity of such life history traits. Alò et al. 2021, for example, shows that while some of the fish diversity is certainly due to environmental processes, a large fraction of such richness variance is also determined by evolved life history traits

related, for example, to migratory habits. Therefore, evaluating how life history traits impact richness metrics should deepen our understanding of fish diversity patterns.

While still short of having a robust and standardized biodiversity infrastructure ([Heberling et al., 2021](#)), a great diversity of online repositories with taxonomic information and species occurrences data exist. Among the most important databases hosting marine information are FishBase, a platform that hosts information on the taxonomy of fish, their ecology, trophic information, habitat and history of uses dating back to more than 250 years ([Froese and Pauly, 2000](#)); the Global Biodiversity Information Facility (GBIF), a platform that stores and allows for the free access to species occurrence records from around the world. GBIF is currently one of the repositories hosting the largest amount of such data in the world ([Telenius, 2011](#); [GBIF: The Global Biodiversity Information Facility , 2021](#)); and finally Ocean Biodiversity Information System (OBIS), which houses data on the occurrence and abundance of species from exclusively marine environments ([OBIS: Ocean Biodiversity Information System, 2021](#)). Records entered in these repositories are often used for research related to biodiversity assessment, taxonomic reviews, red listing of threatened species, species distribution, and generation of ecological niche models, among others ([Yesson et al., 2007](#)). GBIF currently offers more than 1.62 billion occurrence records and OBIS more than 63 million, which increase considerably each year ([GBIF: The Global Biodiversity Information Facility , 2021](#); [OBIS: Ocean Biodiversity Information System, 2021](#)).

The records of both platforms come from a wide variety of sources collected following different methodologies at different temporal and spatial scales introducing a great variety biases ([Beck et al., 2014](#); [Zizka et al., 2020](#)). ~~Amon~~ Among these, three main types of biases have been described: (i) taxonomic, this occurs when some species and/or families are better sampled than other rarer species ([Chandler et al., 2017](#)); (ii) geographic, when data

input is unevenly distributed across geographic regions and may prove to obscure inter-region comparisons (Yang et al., 2013; Yesson et al., 2007); and
3 (iii) temporal, which may be prevalent when comparing different time periods as data coverage is unevenly distributed over time (Chandler et al., 2017;
Yang et al., 2013). While these biases introduce some uncertainty regarding
6 reliability of species richness descriptions obtained from online platforms (Beck et al., 2014; García-Roselló et al., 2015), they have largely been used to provide an extensive overview of macro-ecological patterns of distribution
9 not available otherwise (Mora et al., 2008; Troia and McManamay, 2017).

Still, identifying how sampling effort is distributed across space and time
~~will help is a necessary step~~ to interpret biodiversity patterns and reduce
12 biases ~~as understanding the distribution of our biota is essential to design protection efforts~~. This may be achieved through different weighting schemes for records in areas with sufficient sampling that provide a more reliable contribution compared to underrepresented regions (Phillips et al., 2009; Hortal et al., 2008; Yang et al., 2013).

We here assessed the spatial and temporal representativeness of marine
18 fish records available in the global GBIF and OBIS repositories at the level of marine bioregions in order to pinpoint the location of records that best quantify the diversity of marine fishes. The result is a spatial representativeness analysis that we then overlay on marine conservation areas (UNEP-WCMC and IUCN, 2022) and fisheries exploitation areas (FAO, 2014) to learn whether marine conservation efforts, as well as large fisheries, are located in areas of high species richness or in areas of insufficient data coverage.
24

Finally, we also analyzed the potential effect that some attributes could have on the incidence of more records in global database repositories. Specifically, we evaluated three hypotheses related to body size, habitat depth and commercial use. The underlying hypotheses are that a better representation in the online platforms may be due to the over sampling of larger fish, caused
27 by its easy identification; that shallow areas provide easy access to sampling;
30

and economic and commercial interest have elicit a larger representation of culturally relevant species among online biodiversity repositories.

³ 2. Methods

2.1. Species data

We use all recorded occurrences from the order Actinopterygii hosted in
6 GBIF and OBIS repositories ([GBIF.org, 2021](#); [OBIS.org, 2021](#)). Following
Alò et al. (2021), evolutionarily older taxa, such as Cephalaspidomorpha, were
excluded from this analysis. The libraries *rgbif* and *robis* of the statistical
9 package R were used for data extraction (Chamberlain, 2017; Provoost and
Bosch, 2020; R Core Team, 2018). To minimize errors associated with the
public usage of GBIF and OBIS repositories, we curated the dataset following
12 Zizka et al. (2020) and filtered the dataset by the columns labeled “scientific name”, “family”, “year”, “Longitude” and “Latitude”. We retained all
taxonomic information down to the species level. Any record with NA values
15 was removed. We also removed any duplicated record with identical latitude
and longitude as well as any record collected before 1980 (see Alò et al.,
2021; García-Roselló et al., 2015). Each record was further assigned to a ma-
rine bioregions following Costello et al. (2017). Spatial data wrangling and
18 plotting was performed with the aid of the following libraries: *sf*, *dplyr*, and
cartography (Giraud and Lambert, 2016; Pebesma, 2018; Wickham et al.,
21 2021). We finally labeled and removed any exotic species record using the
distribution() function provided by the *rfishbase* library (Boettiger et al.,
2012; Froese and Pauly, 2021). To limit our analysis to species occurring
24 within their native range each record was checked against the classification
of FAO fisheries area for consistency (FAO, 2014).

2.2. Data Analysis by Bioregion

27 Once the database was cleaned, a subset of the data was created for each
of the 30 bioregions. For each bioregion, a count of records, species and

families was made, and the Shannon diversity index was calculated using the *vegan* library in R (Oksanen et al., 2020).

3 2.2.1. *Spatial Representativeness Analysis*

To assess the spatial representativeness of the data, bioregions were gridded into hexagonal cells of equal area to maximize fit to bioregions areas using
6 a cylindrical equal area projection and the World Geodetic System of 1984
Alò et al. (2021). These $1^\circ \times 1^\circ$ hexagonal lattice yielded ~~60,853~~57,067 cells
9 in total. We evaluated, in the appendix, two additional spatial resolutions,
of 5° and 10° lattice with a total of ~~3,021 and 958~~029 and 953 cells respectively,
12 in order to analyze different biodiversity macropatterns (Tittensor et al., 2010). The expected species richness (S_{exp}) was computed as the average
between three non-parametric richness estimators so that $S_{exp} = \frac{1}{3} \sum_i^3 S_i$,
where S_i is Chao2 (S_{chao}), Bootstrap ($S_{bootstrap}$) and Jackknife 1 ($S_{jackknife1}$)
(see Magurran and McGill, 2011, for individual definition of indices). Such
15 averaging seeks to minimize biases and potential errors of under- or over-estimation by using a single richness estimator following the work of (Mora et al., 2008; Troia and McManamay, 2017).

18 We then produced a spatial representativeness index (SRI) by comparing the observed richness (S_{obs}) per cell to S_{exp} (Troia and McManamay, 2017).

$$SRI_i = \frac{S_{obs}}{S_{exp}},$$

21 , $SRI_i = \frac{S_{obs}}{S_{exp}}$. This index indicates the degree of representativeness of records to quantify the actual species richness in each cell (i). Its value ranges from 0 to 1, where 0 represents an unsampled cell and 1 represents a fully sampled one(Eq. ??).

24 Because SRI somehow shows how databases depict the actual species richness, we may further classify SRI into four classes labeled by the levels of species richness knowledge they represent. Some cell may show very *few*

knowledge with $SRI \in (0, 0.60)$. Conversely, others may show to have a *sufficient* species diversity knowledge level for a complete representation of
3 species diversity if $SRI \in (0.60, 0.85)$. While others, in turn, will have an *adequate* representativeness level if $SRI \in (0.85, 1.00)$. Cells with one or no
records were also considered as an independent class, as well as cells with a
6 single record in order to identify those cells with insufficient records for SRI
estimation.

2.2.2. Temporal Representativeness Analysis

9 We generated plots of cumulative records over time to analyze the temporal distribution of data records for each bioregions. Accumulation curves
for the 30 bioregions were calculated based on the observation records and
12 the year of collection. We ~~asses~~assess the completeness of the sample by
evaluating the final 10% tip of the curve using a linear fit after rescaling
S to create statistically comparable slope units. Slopes close to 0 indicate
15 sufficiently sampled bioregions, while slopes closer to one are indicative of
insufficient sampling efforts across time.

2.2.3. Gap Analysis

18 We overlaid the spatial representativeness map (§2.2.1) with shapefiles
of Marine Protected Areas (MPA) ([UNEP-WCMC and IUCN, 2022](#)) and
fishing exploitation areas reported by ([FAO, 2014](#)). The superposition of
21 these layers allowed us to calculate the extent of protection offered by MPA
for each bioregions on a cell basis, and the extent of cells in designated
fishing zones. This exercise allows to jointly assess the relationship between
24 two opposing human impacts and current uncertainties about marine fish
diversity.

2.2.4. Bias Assessment

27 The evaluation of potential biases generated by body size, habitat depth
and cultural value of species (§2.1) was assessed from the fishbase database

([Froese and Pauly, 2021](#)). Size frequencies were determined using 80 cm intervals and ranges of habitat depth were determined according to the classification of oceanic layers (i.e. epipelagic = 0 - 200 m, mesopelagic = 200 - 1,000 m, and bathypelagic= 1,000 - 4,000) ([Costello et al., 2010](#)). Parametric correlation analysis was employed describe the relationship between the frequency of representation, using a logarithmic transformation, and the body size and habitat depth, while a simple pie chart shows the frequency of cultural values associated to the data.

All data and scripts are available (see Appendix A).

3. Results

3.1. Records by Bioregions

~~Just about~~ [Approximately](#) 1.14% of the total published occurrences in the order Actinopterygii were retained in our analysis. That is, from the 71,670,596 downloaded records off the GBIF and OBIS repositories, 820,004 were considered useful (see Appendix A). This subset consisted of 10,371 species in 361 families. The most represented families in our dataset are Scombridae, Pleuronectidae and Gadidae with 103,762, 57,018 and 52,079 records respectively. The species with the largest representation frequency are *Hippoglossoides platessoides*, *Mola mola* and *Coryphaena hippurus* with 30,885, 21,042 and 21,089 records.

The analysis at bioregion level (Table 1) shows a large variability. The count of records varies across three orders of magnitudes, that is from 2.68×10^5 records in the Caribbean Sea and Gulf of Mexico (11) down to 1.02×10^2 in the Black Sea (2). The bioregion with the largest species richness and diversity index is the the Indo-Pacific Seas and Indian Ocean (13) with 2.95×10^3 recorded species and a Shannon index of 6.93 followed by the Coral Sea bioregion (16) with 2.93×10^3 species and a Shannon index of 6.75. Likewise, the Coral Sea also presents the largest number of families. It is interesting to note that, while being the largest bioregion (i.e. in km^2), the

Table 1: Counts Area (1,000 km²) and counts of records, species richness, families family richness and Shannon diversity for each bioregion. The largest values are for each column is highlighted in bold.

ID	Bioregion	Area (km ²)	Records	Species	Families	Shannon	1	Inner Baltic Sea
2	Black Sea	537	102	72	30	2.46	2	Black Sea
3	NE Atlantic	2,053	87,377	310	104	3.90	3	NE Atlantic
4	Norwegian Sea	1,132	3,046	93	35	2.16	4	Norwegian Sea
5	Mediterranean	2,859	12,532	372	101	3.39	5	Mediterranean
6	Arctic Seas	10,276	2,506	114	23	2.99	6	Arctic Seas
7	North Pacific	12,974	78,070	839	156	4.50	7	North Pacific
8	North American boreal	8,001	9,709	162	48	2.99	8	North American boreal
9	Mid-tropical N Pacific Ocean	32,685	9,310	615	127	4.59	9	Mid-tropical N Pacific Ocean
10	South-east Pacific	21,952	386	615	127	4.59	10	South-east Pacific
11	Caribbean and Gulf of Mexico	8,427	268,066	1,703	209	4.49	11	Caribbean and Gulf of Mexico
12	Gulf of California	6,184	7,639	885	148	5.93	12	Gulf of California
13	Indo-Pacific seas and Indian Ocean	37,090	16,967	2,947	215	6.93	13	Indo-Pacific seas and Indian Ocean
14	Gulfs of Aqaba, Aden, Suez, Red Sea	830	926	352	72	5.51	14	Gulfs of Aqaba, Aden, Suez, Red Sea
15	Tasman Sea	3,592	1,003	380	120	5.36	15	Tasman Sea
16	Coral Sea	7,658	40,107	2,929	249	6.75	16	Coral Sea
17	Mid South Tropical Pacific	23,418	6,083	811	123	5.18	17	Mid South Tropical Pacific
18	Offshore and NW North Atlantic	16,012	130,994	897	190	3.46	18	Offshore and NW North Atlantic
19	Offshore Indian Ocean	31,076	1,263	337	116	4.06	19	Offshore Indian Ocean
20	Offshore W Pacific	10,291	6,363	1,839	232	6.81	20	Offshore W Pacific
21	Offshore S Atlantic	41,435	11,960	990	188	3.79	21	Offshore S Atlantic
22	Offshore mid-E Pacific	13,815	687	79	37	3.04	22	Offshore mid-E Pacific
23	Gulf of Guinea	3,325	6,816	384	138	3.95	23	Gulf of Guinea
24	Argentina	2,665	8,701	115	52	2.83	24	Argentina
25	Chile	1,739	250	100	54	4.36	25	Chile
26	Southern Australia	3,824	15,643	1,011	201	5.75	26	Southern Australia
27	Southern Africa	4,371	19,954	1,142	210	4.16	27	Southern Africa
28	New Zealand	6,293	426	53,879	558	154	28	New Zealand
		1,767	869	182	6.46	30	Southern Ocean	
					62,161,808	8,996	294	57
						3.98		

ID	Bioregion	Area	Records	Species	Families	Shannon
1	Inner Baltic Sea	415	8,902	72	30	2.46
2	Black Sea	537	102	37	22	3.21
3	NE Atlantic	2,053	87,377	310	104	3.90
4	Norwegian Sea	1,132	3,046	93	35	2.16
5	Mediterranean	2,859	12,532	372	101	3.39
6	Arctic Seas	10,276	2,506	114	23	3.90
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13	Indo-Pacific seas and Indian Ocean	37,090	16,967	2,947	215	6.93
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15	Tasman Sea	3,592	1,003	380	120	5.36
16	Coral Sea	7,658	40,107	2,929	249	6.75
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26	Southern Australia	3,824	15,643	1,011	201	5.75
27	Southern Africa	4,371	19,954	1,142	210	4.16
28	New Zealand	6,293	426	53,879	558	154

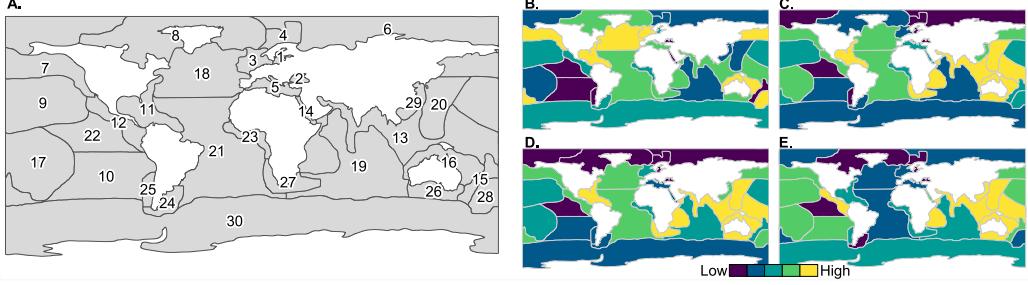


Fig. 1: Marine bioregions and spatial diversity distribution used in this study. **A.** The 30 marine bioregions from Costello et al. (2017) used in this study. Number are identification labels in Table 1. **B.** Records by bioregion; **C.** Overall species richness across bioregions; **D.** Family richness; **E.** Average Family richness (see §2.2.1); and **E.** Shannon diversity index. Note that values in **B-E C-E** have been normalized for display purposes. See Table 1 for actual values.

Southern Ocean show the fewest number of records and the lowest number of species and families across all bioregions. Black Sea (2) and Norwegian 3 (4) are the bioregions with lowest number of record and Shannon index value respectively. Fig. 1 illustrates the location of the 30 marine bioregions and their respective richness and diversity values.

6 3.2. Geographic Analysis

Fig. 2 shows the cell classification according to SRI (§2.2.1). As expected, no bioregion is completely sampled at the 1° scale resolution. In 9 fact, at this resolution scales, large empty regions with no records are observed. The bioregions with the largest area classified as *Adequate* are the Northeast Atlantic (3) (38.637.53%), the Caribbean and Gulf of Mexico (11) 12 (22.829.26%) and the Inland Baltic Sea (1) (21.824.37%). It should be noted that such cells mainly correspond to are mostly correspond from coastal areas in the northern hemisphere. On the other hand, the bioregions that 15 present a greater surface without records correspond to the Southeast Pacific (10) (97.596.3%), the Arctic Sea (6) (94.9%), and the Southern Ocean (30) (95.7%)and the South Pacific, Mid Tropical (17) (93.993.7%). While 18 the bioregions with the larger surface with sufficient records are the Gulf of

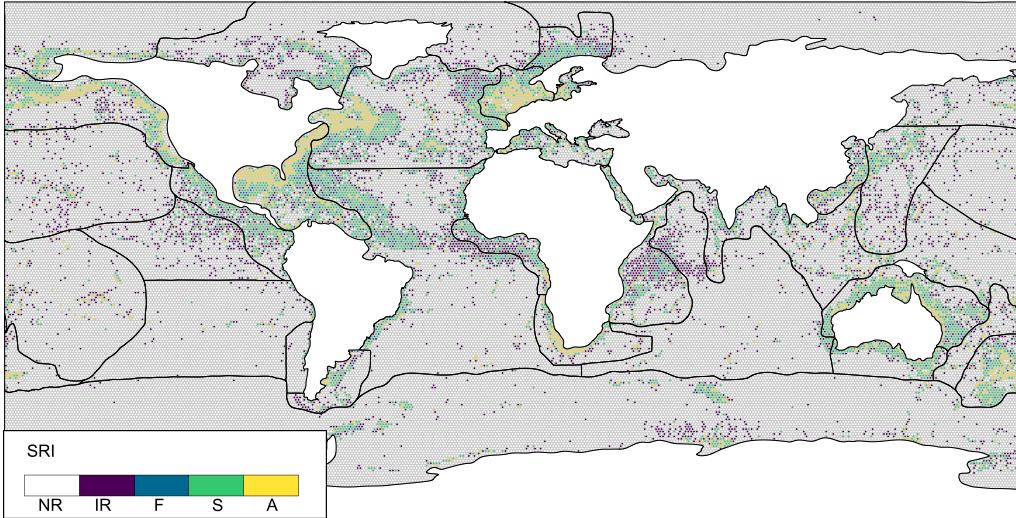


Fig. 2: Spatial Representativeness Index (SRI) in 1° hexagonal lattice. Values in the table below indicates the surface area as a percentage of each bioregion for every SRI category (see §2.2.1). **ID** is the identification number given to each bioregion (Table 1). **A** are cells with an adequate representativeness of species richness (i.e. $SRI > 0.85$). **S** are cells considered as having a sufficient representativeness (i.e. $SRI \in (0.60, 0.85)$). **F** cells are cells with few records and are thus not considered to be representative of actual species richness (i.e. $SRI \in (0, 0.6)$). **NR** as cells with no records ($SRI = NA$).

Guinea (23) (32%), the Norwegian Sea (4) (22.3%), and the Gulf of California (12) (21.6%). Additional results for $5^{\circ} \times 5^{\circ}$ and $10^{\circ} \times 10^{\circ}$ spatial resolution grids are available in Appendix B.

3.3. Temporal Analysis

Bioregions show similar trends of data accumulation across the four decades analyzed here (Fig. 3). While a significant increase is apparent in the time period between 2005 and 2010, such increase is not significant for 14 out the 30 bioregions. The Caribbean and Gulf of Mexico (11) is the bioregion with the largest increases in data contribution to the dataset, while the Black Sea (2) is the bioregion with the lowest rate of data contribution in the 40 years span between 1980 and 2020. (See Appendix C for further analysis).

We categorize the slopes of the final 10% of each accumulation curves in

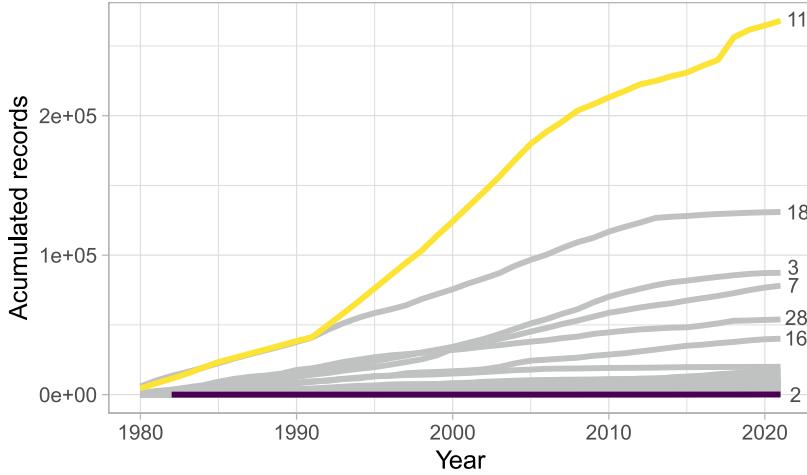


Fig. 3: Records accumulation rate for each bioregion across the four decades analyzed. The blue line is the accumulation of fish records in the Caribbean and Gulf of Mexico bioregion (11) and the red line shows the accumulation rate in the Black Sea (2). Numbers as the end of each timeseries correspond to the bioregion ID in Table 1.

Fig. 4. Fourteen bioregions show a slope less than 1. The Mediterranean Sea (5) stands out with the lowest slope value (0.47), while the Black Sea (2) is the bioregion with the steepest final slope (3.13).

3.4. Gap analysis and fishing exploitation areas

Most PAs are concentrated in the North Atlantic bioregions close to the European continent (Table 2). The largest incidences of PAs across bioregions are for the Northeast Atlantic (3) followed by the Inner Baltic Sea (1) ($n=296$) and the Mediterranean Sea (5) ($n=214$) with 734, 296 and 214 PAs respectively. However, the bioregions with the largest area covered by protected areas are the Coral Sea (16), the northeast Atlantic (3) and New Zealand (28) covering a 37.3, 17.4 and 16% of their respective areas. Regarding the sampling level of these bioregions, the Northeast Atlantic (3), the offshore and northwest of the North Atlantic (18), and the Mediterranean Sea (5), Offshore Indian Ocean (19); Gulf of Aqaba, Aden, Suez, Red Sea (14); and Coral Sea (16) are the bioregions with the highest number of PAs

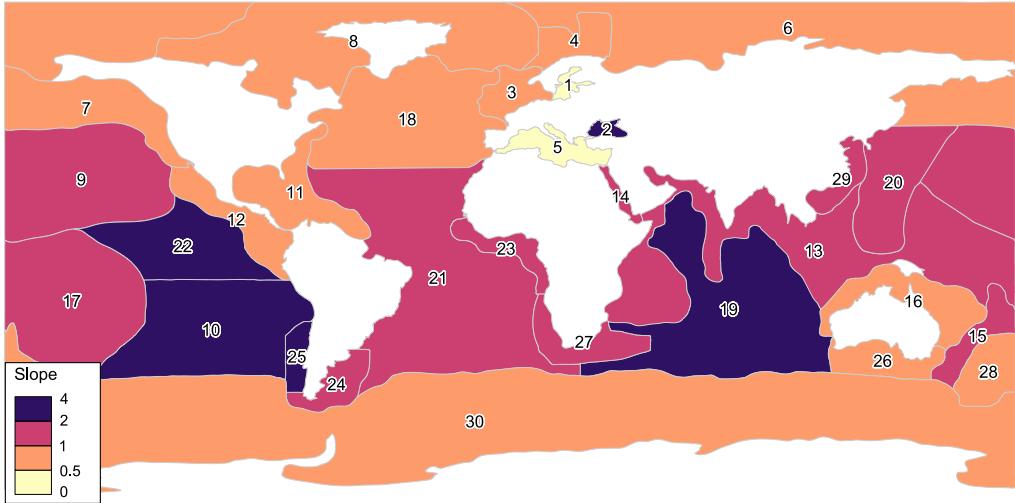


Fig. 4: Graphical representation of the slope values of the species accumulation curve for each bioregion. The slope corresponds to the final 10% of the species accumulation curve. See §2.2.2 for details regarding the analysis.

and which also have more than 50% of their area sampled as *Adequate*. While Indo-Pacific seas and Indian Ocean bioregion have over 80% of its protected area without any data among the analyzed databases (i.e. *NR*). inside of their protected areas (83, 63.8 and 59.8% respectively). While the Arctic Seas (6), North American boreal (8) and Mid South Tropical Pacific are the bioregions with protected areas with the highest percentage of cell with no records (86.2%, 83.8% and 81.2%). (See Appendix D).

FAO areas with the largest area categorized as *Adequate* correspond to the northwest Atlantic (20.98%), Northeastern part of the Pacific Ocean (11.78%), and Western part of the Atlantic Ocean (11.41%) (Table 3). These FAO areas correspond to regions of the Pacific Ocean (North Pacific, North West Pacific, Mid-tropical N Pacific Ocean and Indo-Pacific seas and Indian Ocean, as well the Gulf of California and Caribbean and Gulf of Mexico). Largest FAO areas with *NR* correspond to the Antarctic part of the Pacific Ocean, the Antarctic part of Atlantic Ocean and Southeastern part of the Atlantic Ocean in the Southern Ocean, Offshore S Atlantic and

Table 2: Results of overlapping Marine Protected area overlap Areas and SRI grid. “ID” is the identification number given to each bioregion. “PA num” is the number of protected areas (PA see Table 1 for bioregion names). “P”, Area corresponds to the percentage of the surface area covered by PA marine protected areas. “A>50% NR” is the number percentage of protected areas cells with more than 50% No Records; IR is the percentage of its surface area classified as Adequate. “NR>80%” cells with Insufficient records; F is the number percentage of PAs classified cells with a surface area larger than 80% Few records; S, the percentage of classified cells with No Records Sufficient records, and A, the percentage of classified cells with Adequate records. The highest values are for each column is highlighted in bold face.

ID	PA num	Area	% area	NR	A>50%	IR	NR>80%	F	S	A
1	296	0.03	12.89	2.38	92	4.30	73	5.22	49.08	39.01
2	10	12.89	1.23	26.71	2	27.61	1	10.49	35.19	0.00
3	734	9.74	17.36	3.23	614	1.35	5	0.94	40.86	53.62
4	7	0.15	5.01	11.16	0	19.63	1	5.18	56.69	7.34
5	214	0.09	1.66	5.71	104	6.77	12	11.20	47.95	28.37
6	2	5.01	0.20	86.16	0	5.97	1	0.02	4.65	3.20
7	32	0.00	0.16	26.48	27	4.24	1	1.26	23.77	44.25
8	7	1.23	0.15	83.82	1	7.77	3	0.62	6.70	1.11
9	27	0.69	3.79	69.58	14	15.77	2	0.00	6.40	8.25
10	2	17.36	0.69	73.51	0	24.58	1	0.00	0.80	1.11
11	97	0.28	0.45	20.13	47	6.25	7	3.44	29.98	40.21
12	7	0.83	0.28	0.33	0	1.23	0	8.85	61.35	28.25
13	165	0.45	2.56	50.52	63	11.94	29	0.88	25.17	11.50
14	2	0.25	0.21	8.87	1	0.00	0	1.59	25.65	63.88
15	16	4.06	13.83	57.18	0	15.27	1	0.00	7.29	20.26
16	86	16.00	37.29	3.10	22	0.49	3	1.10	35.52	59.79
17	13	0.20	4.06	81.19	4	11.43	3	0.00	3.07	4.31
18	197	4.91	131	35.87	6	16.63	0	0.77	25.64	21.09
19	8	2.78	0.83	11.88	0	0.74	3	0.00	4.34	83.04
20	122	2.56	0.09	34.06	29	9.68	2	6.85	35.31	14.10
21	40	3.79	0.07	51.06	1	19.35	2	0.38	21.35	7.86
22	1	0.16		41.98		27.54		0.00	1	23.22
23	2	13.83	0.03	9.92	0	4.92	0	7.98	61.33	15.85
24	8	0.21	0.28	40.86	4	20.64	1	0.24	23.97	14.29
25	3	0.07	0.00	65.27	1	0.50	1	0.05	1.29	32.89
26	125	0.28	9.74	30.04	19	12.83	0	6.89	38.62	11.63
27	45	1.45	39	16.78	1	5.75	0	0.15	18.71	58.62
28	76	0.00	16.00	45.36	39	2.25	10	0.00	13.71	38.67
29	19	37.29	0.25	20.49	1	17.05	1	2.68	42.50	17.29
30	11	1.66	2.78	64.05	0	7.12	7	4.89	19.86	4.08

Southern Africa.

3.5. Evaluation of Biases

³ We evaluated biases for body size, habitat depth, and cultural value for 10,371 marine fish species identified in our database (§3.1).

3.5.1. Body size

⁶ The range 0-80 cm is the most frequently occurring size length. Three species stand out with the highest numbers of records, *Scomber scombrus*, *Lagodon rhomboides* and *Mallotus villosus* with 20,995, 19,563 and 13,609 records respectively. These species are distributed mainly in the Northeast Atlantic (3) and Offshore and Northwest North Atlantic (18) bioregions. While the families that accumulate the greatest number of records correspond to Sparidae, Scombridae and Labridae with 24,837, 21,719 and 21,035 records. These families are mainly distributed in the Caribbean Sea and Gulf of Mexico and the Northeast Atlantic.

15 3.5.2. Habitat depth

The most frequent depth range is between 0-838 m (i.e. epipelagic and mesopelagic zones), and the species with the highest number of records are *Mola mola*, *Coryphaena hippurus* and *Lagodon rhomboides* with 21,089, 21,042 and 19,563 occurrences in the databases. These species are distributed mainly around the Caribbean Sea and Gulf of Mexico (11) bioregions, as well as the following bioregions: Offshore and NW North Atlantic (18) and the South Atlantic Coast (21). The families that accumulate a greater number of records correspond to Scombridae, Gadidae, Sparidae with 63,572, 38,876 and 30,041 records. These are mostly distributed in the northern hemisphere. That is, the Caribbean and the Gulf of Mexico (11), Offshore and NW of the North Atlantic (18) and part of the South Atlantic Ocean Coast (21) bioregions.

Figure 5 shows that body size and habitat depth have a negative correlation with the frequency of records.

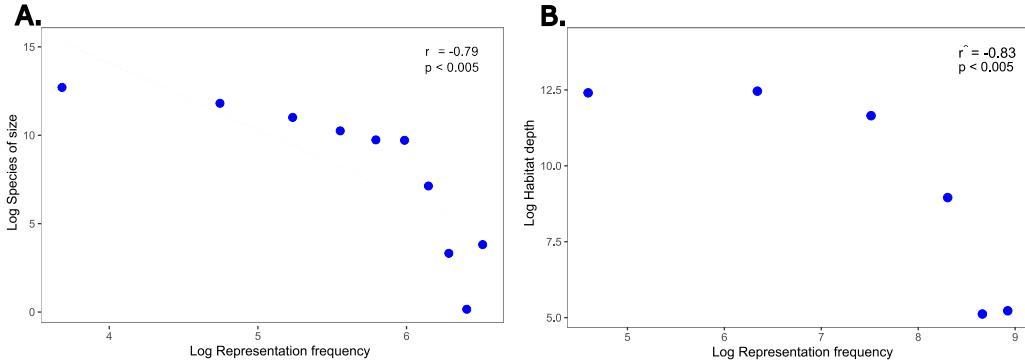


Fig. 5: **A.** Relationship between marine fish representation frequency ($\log_{10} a$) in GBIF and OBIS and habitat depth. **B.** Relationship between the frequency of representation of marine fishes ($\log_{10} a$) in GBIF and OBIS and the size of the species. The dotted line is only there to highlight the negative trend between variables.

3.5.3. Cultural value

Finally, when analyzing the most frequent cultural value represented across our dataset (Fig. 6), “Commercial” use of the species emerges as the most important with a 73.4% among records, followed by the category “No interest” (5.03%), and “Subsistence fishing” (3.08%).

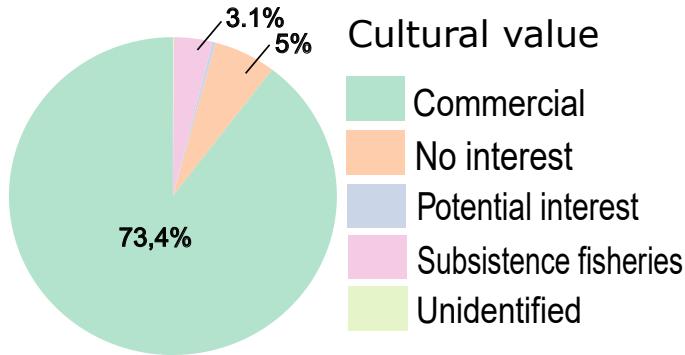


Fig. 6: Frequency of marine fish representation in GBIF and OBIS according to importance of cultural use.

4. Discussion

Our work provides a methodological framework based on a set of non-parametric estimators to quantify the potential number of species from incidence data (Chao et al., 2009). We used hexagonal grids that fit the geographic reality of marine ecosystems, and we placed special emphasis on cleaning the occurrence data in their taxonomy (Jin and Yang, 2020) and any potential input errors associated with large and massive datasets (Zizka et al., 2020). This led us to focus on only evaluating marine species in the order Actinopterygii (Alò et al., 2021).

Publicly accessible occurrence records are growing rapidly, partly due to the significant advances in ecoinformatics (Lenoir et al., 2020; Oliver et al., 2021). These databases harbor a growing variety of sources, including museum specimens, field observations, acoustic and visual sensors, and citizen science efforts (Amano et al., 2016). However, despite the incredible accumulation of biodiversity records, not all the data is really useful, nor does it represent new insights into the distribution of species (Bayraktarov et al., 2019; Zizka et al., 2020). That is why a systematic evaluation of the integrity and coverage of this information is required (Troia and McManamay, 2017).

There is an extensive bibliography that evaluates the record quality available for different taxonomic groups. Some examples are: legumes on a global scale (Yesson et al., 2007), lepidoptera from Great Britain and woody plants in Panama (Chao et al., 2009), global marine biodiversity (Tittensor et al., 2010), vascular plants in China (Yang et al., 2013), marine fish on a global scale (Mora et al., 2008; García-Roselló et al., 2015), freshwater fish in the USA (Troia and McManamay, 2017; Pelayo-Villamil et al., 2018), and terrestrial mammals on a global scale (Oliver et al., 2021), among many others. Assuming that not all data available in these repositories are useful for biodiversity analyses, several efforts have proposed parametric and non-parametric estimators for data cleaning and species richness analysis, ModestR (García-Roselló et al., 2013), KnowBr (Lobo et al., 2018), and RWizard

(Guisande and Lobo, 2019) among these.

Regarding the units of analysis, here we estimate the species richness at the grid level in order to obtain more uniform results on the distribution of occurrences and avoid overestimating the SRI for marine bioregions (Pelayo-Villamil et al., 2018). In addition, we evaluated two additional grid sizes ($5^\circ \times 5^\circ$ and $10^\circ \times 10^\circ$), and like other studies, our results show that the coarser the resolution used, the greater the overestimation ~~of the index than richness, and, conversely is, in terms of area. That is, the richness index will indicate that a large area is, indeed, well sampled when in reality, the occurrence records could in fact be groups in a very small area. On the contrary, the finer the analysis scale, the more localized and deficient the sampling is~~ (Tittensor et al., 2010; García-Roselló et al., 2015; Meyer et al., 2015; Troia and McManamay, 2016, 2017). In view of the above, we recommend using grids that really allow observing macro-ecological patterns, especially in coastal regions, which may be underrepresented when using ~~thick and lower resolution or~~ square grids (Pelayo-Villamil et al., 2018).

Considering that more than 40 years of data were analysed, our results demonstrated that on a global scale, the primary marine fish data available on the GBIG and OBIS platforms are still far from being representative and complete. Compared with other studies evaluating the same taxonomic group (Mora et al., 2008; García-Roselló et al., 2015), although we obtained similar macroecological patterns, only 1.14% of the records extracted from both repositories were useful for our analyses. The large percentage of the occurrences presented input errors or did not have the necessary data to generate a reliable analysis (Yesson et al., 2007; García-Roselló et al., 2014).

We also found evidence of strong information biases in the records explored. On the one hand, when analyzing the families and species with the greatest representation, they coincide with groups of fish of commercial interest, demonstrating the existence of **taxonomic bias** of the data (Melo-Merino et al., 2020). This is the case of the families Scombridae,

Pleuronectidae and Gadidae, which include species of nutritional importance such as tuna, cod, haddock, among others (Cohen et al., 1990). The same
3 is true for the species with the largest number of records, *H. platessoides* (Pleuronectidae), *C. hippurus* (Coryphaenidae), and *M. mola* (Molidae), the first two are species exploited by the fishing industry, with the exception of
6 sunfish (*M. mola*) which has a wide distribution and is mostly associated with scientific and recreational interest (Pope et al., 2010).

The unequal contribution of data at the spatial level is another factor that
9 must be considered to work with data available on ecoinformatic platforms. There is a clear preference for certain regions and/or ecosystems as a result of ~~geographical bias~~geographical bias. The literature indicates that the
12 highest data contribution rates correspond to developed countries (Yesson et al., 2007; Chandler et al., 2017), and those coastal regions with better road connectivity (Chandler et al., 2017; Melo-Merino et al., 2020). This
15 information uncertainty is also particularly prevalent in under-sampled marine habitats, such as the deep sea (Webb et al., 2010). Our results coincide with what is described in the literature, regardless of the size of the grid that
18 was used to generate the analysis, the bioregions that include the Atlantic, the Caribbean and the Gulf of Mexico, and the Baltic Sea are the regions with the highest number of area sampled as *Adequate* associated mainly with
21 coastal areas. However, the number of cells with insufficient data to generate a unbiased diversity analysis, is also worrisome. For instance, our results show that these cells are distributed in more internal areas of the bioregions, zones where sampling is likely to be more difficult. While the bioregions that include the South and Southeast Pacific (including the southern coast of South America), the Southern Ocean, and the Arctic Seas are the regions
27 with the least spatial representativeness of records, the proportion of cells without records (*NR*) exceeds 90%. This large area without samples will make any attempt to describe species richness and distribution highly unreliable in these bioegions (Yang et al., 2013; Troia and McManamay, 2017).

The marine regions that include the water column, the seabed and the sub-soil beyond the limits of jurisdiction of countries cover almost half of the
3 Earth's surface and support a great abundance and diversity of life (Visalli et al., 2020). Even so, when examining the marine ichthyofauna occurrence data, these represent the least sampled areas.

6 Finally, the ~~time-bias~~ time bias of the data is also present in our study. Diametric differences in species identification and sampling methodologies over the decades have resulted in the production of databases of variable quality.
9 However, the current era is characterized by more accurate data thanks to improvements in individual capture and identification tools (Costello et al., 2015; Jin and Yang, 2020). For these reasons our approach considers occurrence records since 1980, however, the coverage of occurrence data is uneven over time when comparing between marine bioregions. Despite evaluating more than four decades of data, still 46% of marine bioregions have insufficient sampling efforts. Not surprisingly, the Caribbean and Gulf of Mexico
12 (11) bioregion is the region with the largest input of data, demonstrating once again that geographic sampling bias has strong effects on spatial predictions
15 of species richness (Yang et al., 2013). Future sampling efforts should focus on ~~those bioregions corresponding to bioregions at~~ low or equatorial latitudes, areas where biogeographic studies show that marine biodiversity is
18 concentrated (Costello et al., 2017).
21

All the biases that we have described, added to the inherent problems in data capture, foster and deepen various information gaps that affect
24 the effective spatio-temporal quantification of biodiversity (Magurran and McGill, 2011). In this study, we have overlapped our estimates of species richness with the global marine protected areas declared up to the beginning
27 of the year 2022 (UNEP-WCMC and IUCN, 2022), and the areas of fishing exploitation reported by the FAO (FAO, 2014). This exercise demonstrates ~~how important it is to have the importance of~~ public databases that
30 can faithfully reflect the taxonomic and biogeographical knowledge avail-

able for each region of the world (Pelayo-Villamil et al., 2018). Our results indicate that ~~Northeastern Atlantic (3) bioregion~~ ~~North West Pacific~~ ~~bioregion (19)~~ has the largest ~~number of protected areas (n=734), of which the vast majority (n=614) have over 50% of their area Adequate sampled.~~ ~~However, area covered by marine protected areas. However, its percentage of adequately sampled cells is low compared to other bioregions. This latter result is of certain concern as this bioregion is not considered a marine biodiversity hotspot, compared to~~ ~~considered a conservation hotspot among other bioregions such as~~ the Coral Sea ~~and New Zealand bioregions, which have a larger area protected by marine conservation areas (Ramírez et al., 2017)~~ ~~–(16), a bioregion with a relatively large percentage of adequately sampled cells (Ramírez et al., 2017).~~ However, we found a low proportion of well-sampled cells in both regions, demonstrating the existence of important information gaps, at least for fish of the order Actinopterygii. We emphasize the need to correct these information gaps so that conservation efforts that seek the implementation of new marine protection areas can have reliable data so as not to underestimate the biodiversity of species (Sala et al., 2021).

In the same way, by overlapping the bioregions with the fishing exploitation zones, we determined that the North Pacific (7) North West Pacific (29), Mid-tropical N Pacific Ocean (9) and Indo-Pacific seas and Indian Ocean (13) bioregions, as well the Gulf of California (21) and Caribbean and Gulf of Mexico (11) are the regions with the highest representation of the data and where fishing activity is concentrated. According to (Kroodsma et al., 2018), the area corresponding to the central Atlantic and Northeast Pacific present little intense fishing effort, while the regions associated with the Northeast Atlantic, the Northeast Atlantic (Europe) regions, and the Northwest Pacific are known to have a huge fishing development and that is where fishing efforts are concentrated worldwide. The southeastern Atlantic Ocean (FAO area 47 and 88), part of the Pacific Ocean (FAO area 88) and Antarctica (FAO area 48 and 88) are the regions with the highest percentage of cells without

records ($NR = >93\%$). When compared with the findings of (Kroodsma et al., 2018), these areas agree with the “holes” without fishing effort data,
3 which is explained by the geographical remoteness and the lack of technological development necessary for the fisheries to extend to new domains (Visalli et al., 2020). This limits both the exploitation of marine resources and the
6 collection of data.

The hypotheses that we evaluated in this work were necessary to understand what the data collection trends have been and to be able to take future
9 actions to correct the biases described. Our first hypothesis about the size of the body of the fish was rejected. Small fish species (0-80 cm) are the ones that accumulate the largest number of records, among which *S. scombrus*
12 (Scombridae), *L. rhomboides* (Sparidae), *M. villosus* (Osmeridae), are <50 cm species that stand out for presenting the largest number of records, and, in addition, they are distributed in the best sampled regions (Mediterranean
15 Sea, Gulf of Mexico and the Caribbean, and the Atlantic Ocean). The size of the fish is inversely proportional to the abundance and, therefore, to the frequency of human use, both scientific and commercial (Pauly and Palomares,
18 2005). This difference in the sampling effort generates an evident overrepresentation of the smaller species and therefore deepens the taxonomic bias. The hypothesis about the depth of the habitat is accepted, at less depth
21 there is a greater representation of species of marine fish. The pelagic zone has a high concentration of data and effectively corresponds to shallow regions and therefore easily accessible, which generates all the conditions for
24 data collection (Melo-Merino et al., 2020). It has been pointed out that the concentration of species decreases as the depth of the ocean increases, however, it is precisely these areas that have been least sampled and where there
27 is the greatest probability of discovering new species (Costello et al., 2017). This demonstrates the need to concentrate efforts on the deeper regions of the water column (mesopelagic, bathyal, and abyssal) for a more equitable
30 representation of marine ecosystems. Finally, the hypothesis of the use of

the species is also accepted. The species of marine fish that have a more beneficial or lucrative use for humans are better represented in the analyzed databases. We believe that this is related to the fact that the fishing industry is one of the main sources of information for platforms such as OBIS (Zhang and Grassle, 2002).

Today, marine ecosystems and their biodiversity face the great challenges of climate change and the impact of human activity, especially those species considered key food resources for survival (Hollowed et al., 2013; Ramírez et al., 2017; O'Hara et al., 2021). It is necessary to focus and strengthen the study of those areas with very few or no records, since the descriptions of the geographic ranges of the species and their temporal dynamics are fundamental measures for the evaluation of the real state of biodiversity (Lenoir et al., 2020; Oliver et al., 2021). Having more reliable data will allow effective conservation actions to be implemented.

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Table 3: Results of overlapping FAO fishery exploitation areas and SRI grid. The surface area corresponding to each bioregion, and the percentage of surface area of each classification. Area is in thousands of km^2 ; NR is the percentage of cells with *No Records*; IR is the percentage of cell with *Insufficient Record*; F is the percentage of classified cells with *Few* records; S, the percentage of classified cells with *Sufficient* records, and A, the percentage of classified cells with *Adequate* records. The highest values are for each column is highlighted in bold.

FAO Area Name	Area	NR	F	S	A	Arctic Ocean	9.24	89.81	4.74	3.29	2.16
Northwestern part of the Atlantic Ocean	6.28	42.48	16.91	19.62	20.98						
Northeastern part of the Atlantic Ocean	14.35	62.85	13.42	14.02	9.71						
Western part of the Atlantic Ocean	14.65	43.56	22.37	22.66	11.41	Eastern					
Central part of the Atlantic Ocean	14.19	64.17	20.43	10.07	5.34						
Mediterranean Sea and the Black Sea	2.99	57.82	19.07	12.75	10.36						
Southwestern part of the Atlantic Ocean	17.70	85.60	7.08	5.42	1.91						
Southeastern part of the Atlantic Ocean	19.07	93.34	2.13	1.61	2.93						
Antarctic part of the Atlantic Ocean	12.48	95.31	2.38	1.63	0.68	Western					
part of the Indian Ocean	29.42	79.15	10.42	4.87	5.56	Eastern part of the					
Indian Ocean	31.21	87.57	5.24	5.16	2.04	Antarctic and Southern of the					
Indian Ocean	12.75	90.02	5.23	3.13	1.62	Indian Ocean					
Northwestern part of the Pacific Ocean	21.54	80.43	10.87	6.02	2.67	Northeastern part of the Pacific					
	7.63	68.73	8.53	10.96	11.78	Northeastern part of the Pacific Ocean					
	78.69	9.77	6.88	4.66	Eastern Central part of the Pacific Ocean	48.25	85.09				
	9.01	3.47	2.43	Southwestern part of the Pacific Ocean	27.64	87.72	4.79	4.88			
	2.61	Southeastern part of the Pacific Ocean	30.80	92.85	4.89	1.33	0.92				
		Antarctic part of the Pacific Ocean	10.23	95.61	2.28	0.71	1.40				

FAO Area Name	Area	NR	IR	F	S	A
Arctic Sea	4,085.78	93.22	3.13	0.29	2.61	0.75
Northwestern part of the Atlantic Ocean	873.55	31.19	11.66	5.69	29.37	22.08
Northeastern part of the Atlantic Ocean	3,222.88	66.29	12.54	2.55	13.63	4.99
Western part of the Atlantic Ocean	1,285.13	30.84	13.09	7.91	35.60	12.55
Eastern Central part of the Atlantic Ocean	1,207.71	52.61	24.09	3.44	18.37	1.19
Mediterranean Sea and the Black Sea	308.53	46.39	15.43	5.24	24.77	8.17
Southwestern part of the Atlantic Ocean	1,730.57	82.49	5.85	1.69	8.55	1.42
Southeastern part of the Atlantic Ocean	1,765.33	89.92	4.19	0.15	2.13	3.61
Antarctic part of the Atlantic Ocean	2,310.48	93.31	2.80	0.20	2.93	0.76
Western part of the Indian Ocean	2,620.90	72.45	16.11	1.03	8.51	1.89
Eastern part of the Indian Ocean	3,028.72	85.40	4.69	0.82	7.39	1.70
Antarctic and Southern of the Indian Ocean	1,977.29	85.71	7.76	0.56	4.33	1.64
Northwestern part of the Pacific Ocean	2,259.45	73.55	12.40	0.94	10.32	2.79
Northeastern part of the Pacific Ocean	967.54	55.13	12.65	1.34	16.26	14.62
Western Central part of the Pacific Ocean	2,963.11	70.45	12.56	0.43	11.58	4.98
Eastern Central part of the Pacific Ocean	4,140.60	79.36	11.30	0.31	6.94	2.09
Southwestern part of the Pacific Ocean	3,096.68	85.04	4.42	0.97	6.40	3.17
Southeastern part of the Pacific Ocean	2,997.11	91.16	6.00	0.10	2.30	0.44
Antarctic part of the Pacific Ocean	2,361.33	93.47	4.57	0.21	1.42	0.33

Appendix A. The database

Table A.4 below shows the data loss for each criterion that we have used
3 to clean our database. We downloaded 71,670,596 records from ~~GBIG~~~~GBIF~~ and OBIS. Only 820,004 records were useful for our analyses.

Database state	Number of records
Original records from GBIF and OBIS	71,670,596
Data curation (following Zizka et al. (2020))	5,380,439
Taxonomically filtered data	5,007,322
Deletion of data outside the native range	820,004

Table A.4: Criteria for filtering occurrence data from GBIF and OBIS using bioregions.

Files of the 10,371 marine fish species and their attributes (body size,
6 habitat depth, and cultural value) from FishBase may be found in the GitHub
project page of this manuscript: http://github.com/vapizarro/stp_fishes

Appendix B. Grids resolutions

9 For spatial representation analysis we evaluated two additional spatial
resolutions ($5^\circ \times 5^\circ = 3,021$ cells, and $10^\circ \times 10^\circ = 958$ cells). Table ??-B.5
contains the results of this analysis for these grids. We have also mapped
12 these results (see Figure B.7), to understand how the effect of spatial reso-
lution on the evaluation of biodiversity macropatterns. Finally, we also plot
the frequency of cells for each SRI category for the three grid sizes (R1= $1^\circ \times$
15 1° ; R5= $5^\circ \times 5^\circ$; R10= $10^\circ \times 10^\circ$) to understand how the data is distributed
in our analyses (see Figure B.8)

Appendix C. Bioregions slopes

18 We evaluated the slopes of the last 10% of the accumulation curves of
each bioregion in our temporal representation analysis. Table C.6 shows the
result for each bioregion.

$5^\circ \times 5^\circ$ $10^\circ \times 10^\circ$ NR F S A NR F S A 1 19.38 3.52 22.18 54.92 0.17 0.00 0.00
 99.83 2 10.22 67.79 22.00 0.00 0.24 79.80 13.41 6.55 3 14.17 5.86 3.68 76.30
 17.26 0.00 1.65 81.09 4 8.11 18.15 49.78 23.96 24.40 0.00 56.89 18.71 5 17.61
 11.41 51.06 19.91 0.76 21.01 29.87 48.37 6 72.22 13.59 7.01 7.18 57.95 14.53
 10.67 16.85 7 22.68 19.18 30.95 27.26 7.23 5.57 42.67 44.52 8 28.29 32.88
 28.34 10.49 10.75 38.44 49.14 1.68 9 38.10 36.07 20.03 5.80 8.97 49.76 30.88
 10.39 10 70.33 14.72 8.21 6.73 55.39 17.91 15.12 11.58 11 15.36 0.00 37.46
 47.18 3.84 0.00 10.04 86.11 12 21.88 17.33 49.92 10.87 2.44 9.04 53.22 35.30
 13 15.01 34.79 32.35 17.85 8.84 25.58 48.64 16.94 14 8.31 0.00 62.35 29.35
 66.52 0.00 0.00 33.48 15 17.06 37.36 29.94 15.64 3.42 15.88 66.66 14.04 16
 18.45 16.45 30.57 34.53 18.82 0.00 17.13 64.06 17 56.51 15.47 15.27 12.75
 10.25 25.29 48.27 16.19 18 15.10 27.12 37.68 20.17 16.20 14.33 29.37 40.10
 19 64.31 20.32 8.07 7.30 36.75 34.23 22.00 7.01 20 12.21 47.20 33.32 7.27
 10.74 40.12 35.84 13.30 21 44.88 19.20 24.68 11.23 22.43 23.33 30.03 24.21
 22 20.76 44.23 35.01 0.00 15.95 28.49 52.89 2.67 23 4.42 33.22 54.38 7.97
 18.89 27.78 46.90 6.43 24 19.18 39.23 28.34 13.25 20.90 22.41 21.87 34.82 25
 70.95 3.80 11.03 14.22 53.42 0.00 33.72 12.86 26 30.23 1.16 44.14 24.46
 27.42 0.00 32.14 40.44 27 17.67 20.53 37.77 24.02 10.57 18.38 41.56 29.48 28
 25.40 11.73 20.42 42.45 14.84 0.00 30.51 54.65 29 4.47 14.81 47.69 33.03
 20.81 0.00 65.06 14.13 30 72.92 11.70 9.40 5.98 44.37 22.69 25.57 7.37

ID	R1 ($1^\circ \times 1^\circ$)					R5 ($5^\circ \times 5^\circ$)					R10 ($10^\circ \times 10^\circ$)				
	NR	IR	F	S	A	NR	IR	F	S	A	NR	IR	F	S	A
1	18.49	15.13	5.04	36.97	24.37	0.00	16.67	0.00	33.33	50.00	16.67	16.67	0.00	33.33	33.33
2	68.75	19.79	1.04	10.42	0.00	10.00	40.00	10.00	30.00	10.00	40.00	0.00	0.00	40.00	20.00
3	15.74	6.54	3.39	36.80	37.53	3.57	3.37	0.00	17.86	75.00	0.00	0.00	0.00	10.00	90.00
4	46.35	22.34	7.93	22.13	1.25	28.13	9.38	6.25	40.63	15.63	30.77	15.38	0.00	23.08	30.77
5	42.39	14.75	4.92	27.87	10.07	14.29	3.57	0.00	32.14	50.00	16.67	8.33	0.00	8.33	66.67
6	94.96	2.21	0.13	1.87	0.83	82.13	5.64	0.31	6.58	5.33	62.65	13.25	1.20	10.84	12.05
7	63.24	11.24	0.87	14.46	10.19	17.09	9.40	3.42	29.06	41.03	7.69	7.69	2.56	35.90	46.15
8	79.52	11.27	0.89	7.17	1.15	43.93	11.56	4.05	32.37	8.09	32.69	11.54	3.85	40.38	11.54
9	88.74	8.71	0.00	1.57	0.99	28.74	22.99	2.87	38.51	6.90	7.69	9.62	21.15	38.08	13.46
10	96.31	2.41	0.04	0.88	0.36	70.87	15.75	0.79	7.09	5.51	51.28	15.38	2.56	20.51	10.26
11	23.82	8.42	5.65	32.85	29.26	8.62	0.00	0.00	18.97	72.41	0.00	10.53	0.00	5.26	84.21
12	35.59	21.61	2.45	35.59	4.76	14.29	4.76	2.38	47.62	30.95	5.88	11.76	0.00	17.65	64.71
13	67.52	15.80	1.01	12.00	3.67	13.76	12.84	7.34	44.95	21.10	9.46	6.76	2.70	44.59	36.49
14	45.83	10.83	2.50	30.83	10.00	46.15	0.00	0.00	7.69	46.15	25.00	0.00	0.00	0.00	75.00
15	74.52	13.06	0.00	7.07	5.35	20.00	6.67	6.67	40.00	26.67	37.50	12.50	0.00	37.50	12.50
16	36.68	10.95	3.84	34.65	13.88	5.77	7.69	3.85	28.85	53.85	10.53	0.00	0.00	21.05	68.42
17	91.36	4.90	0.00	1.57	2.17	47.93	19.01	0.00	20.66	12.40	25.00	8.33	0.00	36.11	30.56
18	48.29	16.27	3.78	22.06	9.61	6.50	7.32	7.32	43.09	35.77	10.26	5.13	0.00	28.21	56.41
19	90.40	6.93	0.06	2.27	0.35	53.45	18.39	3.45	17.82	6.90	31.48	12.96	1.85	35.19	18.52
20	63.61	17.35	1.43	13.56	4.04	8.20	8.20	9.84	44.26	29.51	15.00	5.00	0.00	45.00	35.00
21	74.78	9.63	2.84	11.48	1.27	34.68	13.51	3.15	28.38	20.27	21.21	9.09	0.00	27.27	42.42
22	76.12	18.00	0.00	5.10	0.78	33.33	6.17	16.05	43.21	1.23	9.09	4.55	9.09	59.09	18.18
23	34.65	32.02	2.89	24.41	6.04	25.93	0.00	14.81	51.85	7.41	0.00	18.18	0.00	36.36	45.45
24	63.07	17.89	1.38	13.53	4.13	25.93	7.41	3.70	51.85	11.11	20.00	10.00	0.00	50.00	20.00
25	88.02	4.96	0.83	5.37	0.83	52.63	10.53	0.00	21.05	15.79	42.86	0.00	0.00	28.57	28.57
26	60.93	7.04	2.41	22.41	7.22	27.27	12.12	0.00	30.30	30.30	16.67	0.00	0.00	33.33	50.00
27	66.84	10.35	0.70	8.07	14.04	27.78	16.67	0.00	22.22	33.33	7.69	7.69	0.00	23.08	61.54
28	59.84	9.17	2.13	17.67	11.19	30.19	7.55	1.89	30.19	30.19	30.00	10.00	0.00	25.00	35.00
29	41.96	19.87	2.84	26.81	8.52	15.00	10.00	5.00	40.00	30.00	12.50	12.50	0.00	37.50	37.50
30	93.74	3.49	0.20	1.97	0.59	69.45	11.02	38.00	10.52	8.01	42.29	16.57	2.86	22.29	16.00

Table B.5: Surface area as a percentage of each bioregion (ID) for every SRI category for each of the three grid sizes (R1= $1^\circ \times 1^\circ$; R5= $5^\circ \times 5^\circ$; R10= $10^\circ \times 10^\circ$). **Amount Values** show the surface area as a percentage of data **Adequate** each bioregion for every SRI category (see §2.2.1). ID is the representation-identification number given to each bioregion (Table 1). A are cells with an adequate representativeness of species richness (“A”); i.e. SRI = 0.60–0.85; Amount of data can be ≥ 0.85 . S are cells considered **Sufficient** (S); i.e. SRI = 0.85–1.00; Amount of data can be ≥ 0.85 . F are cells considered **Frivolous** (F); i.e. SRI = 0.00–0.60; Amount of data can be ≥ 0.85 .

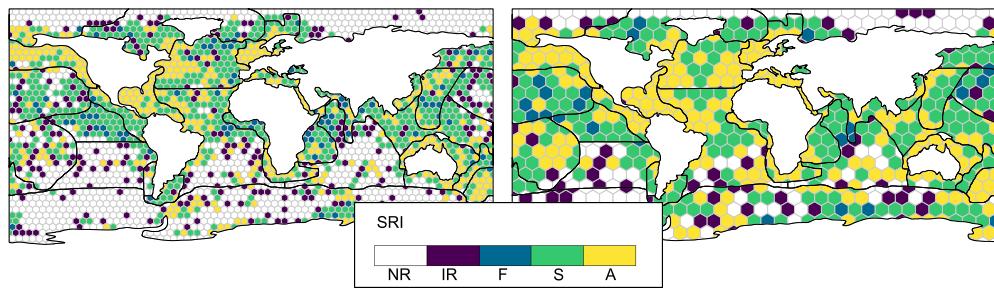


Fig. B.7: Spatial representativeness index (SRI) mapping of cells of size: $A=5^\circ \times 5^\circ$; $B=10^\circ \times 10^\circ$. The categorization of the cells corresponds to the level reached by the SRI, where SRI $\hat{>} 0.85$: Amount of data *Adequate* for the representation of species richness (“A”); SRI=0.60-0.85: Amount of data can be considered *Sufficient* (“S”); SRI=0-0.60: Amount of records *Few* (“F”); and SRI = NA: cells with no records (“NR”).

Appendix D. Supplementary Material: GAP Analysis

We plotted the percentage of surface with marine protected areas of each
³ bioregion (Fig D.9), and the percentage of cells of each FAO Area for each category of SRI value (Fig D.10).

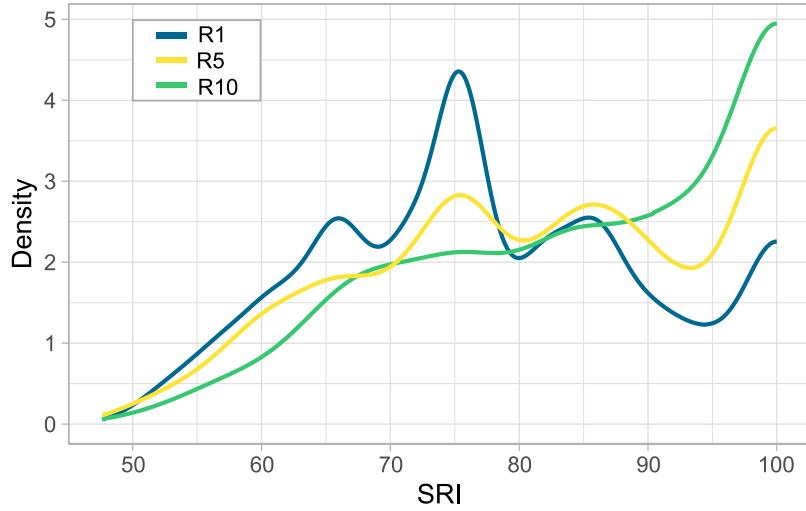


Fig. B.8: Density probability distribution of SRI in three grids of different sizes: R1 = $1^\circ \times 1^\circ$ (blue line); R5 = $5^\circ \times 5^\circ$ (red line); and R10 = $10^\circ \times 10^\circ$ (yellow line).

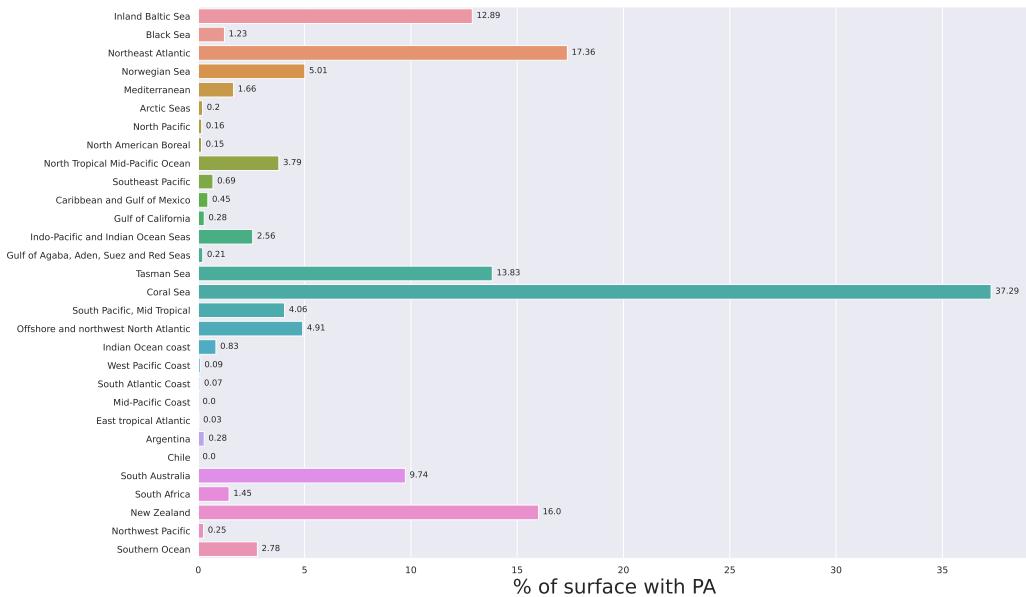


Fig. D.9: Percentage of surface with marine protected areas by bioregions.

Bioregion	Slope
1	0.35
2	1.16
3	1.79
4	0.91
5	1.76
6	0.65
7	4.44
8	1.37
9	6.18
10	4.87
11	10.37
12	7.57
13	32.86
14	4.90
15	6.78
16	21.62
17	10.10
18	6.59
19	12.44
20	23.21
21	11.70
22	1.85
23	4.42
24	3.49
25	2.12
26	7.74
27	12.29
28	4.82
29	14.08
30	2.74

Table C.6: Final slope (10%) of the accumulation curves for each bioregion

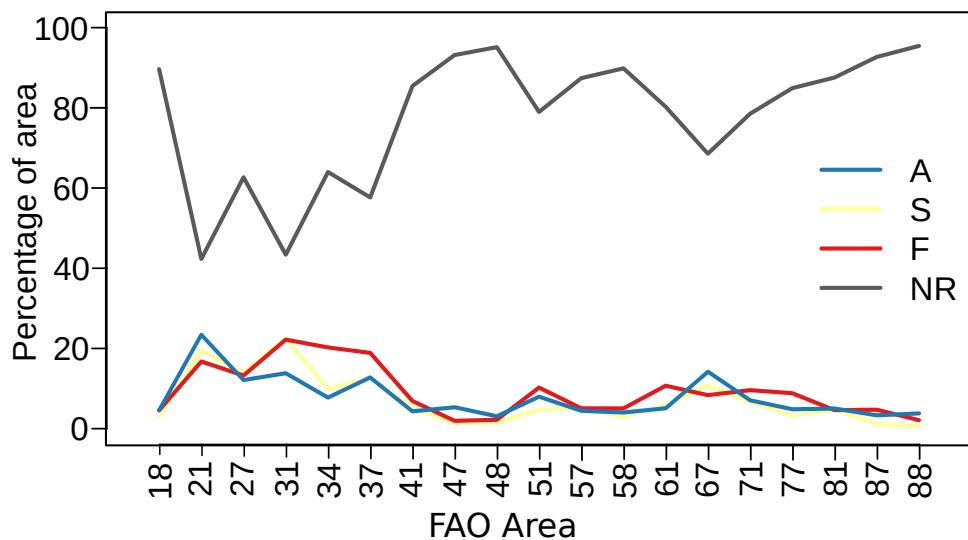


Fig. D.10: Percentage of cells of each FAO Area for each category of SRI value. Amount of data *Adequate* for the representation of species richness (“A”); SRI=0.60-0.85: Amount of data can be considered *Sufficient* (“S”); SRI=0-0.60: Amount of records *Few* (“F”); and SRI = NA: cells with no records (“NR”).

```
This is pdfTeX, Version 3.141592653-2.6-1.40.24 (TeX Live 2022)
(preloaded format=pdflatex 2023.3.8) 4 JUL 2023 16:27
entering extended mode
  restricted \write18 enabled.
  %&-line parsing enabled.
**pizarro_etal_ecoinf_r2.tex
./Pizarro_etal_EcoInf_R2.tex
TeXLive2e <2022-11-01> patch level 1
L3 programming layer <2023-02-22> (c:/TeXLive/2022/texmf-
dist/tex/latex/elsarti
cle/elsarticle.cls
Document Class: elsarticle 2020/11/20, 3.3: Elsevier Ltd
(c:/TeXLive/2022/texmf-dist/tex/latex/l3kernel/expl3.sty
Package: expl3 2023-02-22 L3 programming layer (loader)
(c:/TeXLive/2022/texmf-dist/tex/latex/l3backend/l3backend-pdfTeX.def
File: l3backend-pdfTeX.def 2023-01-16 L3 backend support: PDF output
(pdfTeX)
\l_color_backend_stack_int=\count185
\l_pdf_internal_box=\box51
)) (c:/TeXLive/2022/texmf-dist/tex/latex/l3packages/xparse/xparse.sty
Package: xparse 2023-02-02 L3 Experimental document command parser
) (c:/TeXLive/2022/texmf-dist/tex/latex/etoolbox/etoolbox.sty
Package: etoolbox 2020/10/05 v2.5k e-TeX tools for LaTeX (JAW)
\etb@tempcnta=\count186
)
\@bls=\dimen140
(c:/TeXLive/2022/texmf-dist/tex/latex/base/article.cls
Document Class: article 2022/07/02 v1.4n Standard LaTeX document class
(c:/TeXLive/2022/texmf-dist/tex/latex/base/size12.clo
File: size12.clo 2022/07/02 v1.4n Standard LaTeX file (size option)
)
\c@part=\count187
\c@section=\count188
\c@subsection=\count189
\c@subsubsection=\count190
\c@paragraph=\count191
\c@ subparagraph=\count192
\c@figure=\count193
\c@table=\count194
\abovecaptionskip=\skip48
\belowcaptionskip=\skip49
\bibindent=\dimen141
) (c:/TeXLive/2022/texmf-dist/tex/latex/graphics/graphicx.sty
Package: graphicx 2021/09/16 v1.2d Enhanced LaTeX Graphics (DPC,SPQR)
(c:/TeXLive/2022/texmf-dist/tex/latex/graphics/keyval.sty
Package: keyval 2022/05/29 v1.15 key=value parser (DPC)
\KV@toks@=\toks16
) (c:/TeXLive/2022/texmf-dist/tex/latex/graphics/graphics.sty
Package: graphics 2022/03/10 v1.4e Standard LaTeX Graphics (DPC,SPQR)
(c:/TeXLive/2022/texmf-dist/tex/latex/graphics/trig.sty
Package: trig 2021/08/11 v1.11 sin cos tan (DPC)
) (c:/TeXLive/2022/texmf-dist/tex/latex/graphics-cfg/graphics.cfg
File: graphics.cfg 2016/06/04 v1.11 sample graphics configuration
)
```

```

Package graphics Info: Driver file: pdftex.def on input line 107.
(c:/TeXLive/2022/texmf-dist/tex/latex/graphics-def/pdftex.def
File: pdftex.def 2022/09/22 v1.2b Graphics/color driver for pdftex
))
\Gin@req@height=\dimen142
\Gin@req@width=\dimen143
)
\c@tnote=\count195
\c@fnote=\count196
\c@cnote=\count197
\c@ead=\count198
\c@author=\count199
\@eadauthor=\toks17
\c@affn=\count266
\absbox=\box52
\elsarticlehighlightsbox=\box53
\elsarticlegrabsbox=\box54
\keybox=\box55
\Columnwidth=\dimen144
\space@left=\dimen145
\els@boxa=\box56
\els@boxb=\box57
\leftMargin=\dimen146
\@enLab=\toks18
\@sep=\skip50
\@@sep=\skip51
(./Pizarro_etAl_EcoInf_R2.spl) (c:/TeXLive/2022/texmf-
dist/tex/latex/natbib/nat
bib.sty
Package: natbib 2010/09/13 8.31b (PWD, AO)
\bibhang=\skip52
\bibsep=\skip53
LaTeX Info: Redefining \cite on input line 694.
\c@NAT@ctr=\count267
)
\splwrite=\write3
\openout3 = `Pizarro_etAl_EcoInf_R2.spl'.

\appnamewidth=\dimen147
) (c:/TeXLive/2022/texmf-dist/tex/latex/multirow/multirow.sty
Package: multirow 2021/03/15 v2.8 Span multiple rows of a table
\multirow@colwidth=\skip54
\multirow@cntb=\count268
\multirow@dima=\skip55
\bigstrutjot=\dimen148
) (c:/TeXLive/texmf-local/tex/latex/aries/setspace.sty
Package: setspace 2000/12/01 6.7 Contributed and Supported LaTeX2e
package
Package: `setspace' 6.7 <2000/12/01>
) (c:/TeXLive/2022/texmf-dist/tex/latex/amsmath/amsmath.sty
Package: amsmath 2022/04/08 v2.17n AMS math features
\@mathmargin=\skip56
For additional information on amsmath, use the `?' option.
(c:/TeXLive/2022/texmf-dist/tex/latex/amsmath/amstext.sty

```

```
Package: amstext 2021/08/26 v2.01 AMS text
(c:/TeXLive/2022/texmf-dist/tex/latex/amsmath/amsgen.sty
File: amsgen.sty 1999/11/30 v2.0 generic functions
\@emptytoks=\toks19
\ex@=\dimen149
)) (c:/TeXLive/2022/texmf-dist/tex/latex/amsmath/amsbsy.sty
Package: amsbsy 1999/11/29 v1.2d Bold Symbols
\pmbraise@=\dimen150
) (c:/TeXLive/2022/texmf-dist/tex/latex/amsmath/amsopn.sty
Package: amsopn 2022/04/08 v2.04 operator names
)
\inf@bad=\count269
LaTeX Info: Redefining \frac on input line 234.
\uproot@=\count270
\leftroot@=\count271
LaTeX Info: Redefining \overline on input line 399.
LaTeX Info: Redefining \colon on input line 410.
\classnum@=\count272
\DOTSCASE@=\count273
LaTeX Info: Redefining \ldots on input line 496.
LaTeX Info: Redefining \dots on input line 499.
LaTeX Info: Redefining \cdots on input line 620.
\Mathstrutbox@=\box58
\strutbox@=\box59
LaTeX Info: Redefining \big on input line 722.
LaTeX Info: Redefining \Big on input line 723.
LaTeX Info: Redefining \bigg on input line 724.
LaTeX Info: Redefining \Bigg on input line 725.
\big@size=\dimen151
LaTeX Font Info: Redeclaring font encoding OML on input line 743.
LaTeX Font Info: Redeclaring font encoding OMS on input line 744.
\macc@depth=\count274
LaTeX Info: Redefining \bmod on input line 905.
LaTeX Info: Redefining \pmod on input line 910.
LaTeX Info: Redefining \smash on input line 940.
LaTeX Info: Redefining \relbar on input line 970.
LaTeX Info: Redefining \Relbar on input line 971.
\c@MaxMatrixCols=\count275
\dotsspace@=\muskip16
\c@parentequation=\count276
\dspace@=\count277
\tag@help=\toks20
\row@=\count278
\column@=\count279
\maxfields@=\count280
\andhelp@=\toks21
\eqnshift@=\dimen152
\alignsep@=\dimen153
\tagshift@=\dimen154
\tagwidth@=\dimen155
\totwidth@=\dimen156
\lineht@=\dimen157
\@envbody=\toks22
\multlinegap=\skip57
```

```

\multlinetaggap=\skip58
\mathdisplay@stack=\toks23
LaTeX Info: Redefining \[ on input line 2953.
LaTeX Info: Redefining \] on input line 2954.
) (c:/TeXLive/2022/texmf-dist/tex/latex/hyperref/hyperref.sty
Package: hyperref 2023-02-07 v7.00v Hypertext links for LaTeX
(c:/TeXLive/2022/texmf-dist/tex/generic/ltxcmds/ltxcmds.sty
Package: ltxcmds 2020-05-10 v1.25 LaTeX kernel commands for general use
(HO)
) (c:/TeXLive/2022/texmf-dist/tex/generic/iftex/iftex.sty
Package: iftex 2022/02/03 v1.0f TeX engine tests
) (c:/TeXLive/2022/texmf-dist/tex/generic/pdftexcmds/pdftexcmds.sty
Package: pdftexcmds 2020-06-27 v0.33 Utility functions of pdfTeX for
LuaTeX (HO
)
(c:/TeXLive/2022/texmf-dist/tex/generic/infwarerr/infwarerr.sty
Package: infwarerr 2019/12/03 v1.5 Providing info/warning/error messages
(HO)
)
Package pdftexcmds Info: \pdf@primitive is available.
Package pdftexcmds Info: \pdf@ifprimitive is available.
Package pdftexcmds Info: \pdfdraftmode found.
) (c:/TeXLive/2022/texmf-dist/tex/latex/kvsetkeys/kvsetkeys.sty
Package: kvsetkeys 2022-10-05 v1.19 Key value parser (HO)
) (c:/TeXLive/2022/texmf-dist/tex/generic/kvdefinekeys/kvdefinekeys.sty
Package: kvdefinekeys 2019-12-19 v1.6 Define keys (HO)
) (c:/TeXLive/2022/texmf-dist/tex/generic/pdfescape/pdfescape.sty
Package: pdfescape 2019/12/09 v1.15 Implements pdfTeX's escape features
(HO)
) (c:/TeXLive/2022/texmf-dist/tex/latex/hycolor/hycolor.sty
Package: hycolor 2020-01-27 v1.10 Color options for hyperref/bookmark
(HO)
) (c:/TeXLive/2022/texmf-dist/tex/latex/letltxmacro/letltxmacro.sty
Package: letltxmacro 2019/12/03 v1.6 Let assignment for LaTeX macros (HO)
) (c:/TeXLive/2022/texmf-dist/tex/latex/auxhook/auxhook.sty
Package: auxhook 2019-12-17 v1.6 Hooks for auxiliary files (HO)
) (c:/TeXLive/2022/texmf-dist/tex/latex/hyperref/nameref.sty
Package: nameref 2022-05-17 v2.50 Cross-referencing by name of section
(c:/TeXLive/2022/texmf-dist/tex/latex/refcount/refcount.sty
Package: refcount 2019/12/15 v3.6 Data extraction from label references
(HO)
) (c:/TeXLive/2022/texmf-
dist/tex/generic/gettitlestring/gettitlestring.sty
Package: gettitlestring 2019/12/15 v1.6 Cleanup title references (HO)
(c:/TeXLive/2022/texmf-dist/tex/latex/kvoptions/kvoptions.sty
Package: kvoptions 2022-06-15 v3.15 Key value format for package options
(HO)
))
\c@section@level=\count281
)
\@linkdim=\dimen158
\Hy@linkcounter=\count282
\Hy@pagecounter=\count283
(c:/TeXLive/2022/texmf-dist/tex/latex/hyperref/pd1enc.def

```

```
File: pdlenc.def 2023-02-07 v7.00v Hyperref: PDFDocEncoding definition
(HO)
Now handling font encoding PD1 ...
... no UTF-8 mapping file for font encoding PD1
) (c:/TeXLive/2022/texmf-dist/tex/generic/intcalc/intcalc.sty
Package: intcalc 2019/12/15 v1.3 Expandable calculations with integers
(HO)
) (c:/TeXLive/2022/texmf-dist/tex/generic/etexcmds/etexcmds.sty
Package: etexcmds 2019/12/15 v1.7 Avoid name clashes with e-TeX commands
(HO)
)
\Hy@SavedSpaceFactor=\count284
(c:/TeXLive/2022/texmf-dist/tex/latex/hyperref/puenc.def
File: puenc.def 2023-02-07 v7.00v Hyperref: PDF Unicode definition (HO)
Now handling font encoding PU ...
... no UTF-8 mapping file for font encoding PU
)
Package hyperref Info: Hyper figures OFF on input line 4177.
Package hyperref Info: Link nesting OFF on input line 4182.
Package hyperref Info: Hyper index ON on input line 4185.
Package hyperref Info: Plain pages OFF on input line 4192.
Package hyperref Info: Backreferencing OFF on input line 4197.
Package hyperref Info: Implicit mode ON; LaTeX internals redefined.
Package hyperref Info: Bookmarks ON on input line 4425.
\c@Hy@tempcnt=\count285
(c:/TeXLive/2022/texmf-dist/tex/latex/url/url.sty
\Urlmuskip=\muskip17
Package: url 2013/09/16 ver 3.4 Verb mode for urls, etc.
)
LaTeX Info: Redefining \url on input line 4763.
\XeTeXLinkMargin=\dimen159
(c:/TeXLive/2022/texmf-dist/tex/generic/bitset/bitset.sty
Package: bitset 2019/12/09 v1.3 Handle bit-vector datatype (HO)
(c:/TeXLive/2022/texmf-dist/tex/generic/bigintcalc/bigintcalc.sty
Package: bigintcalc 2019/12/15 v1.5 Expandable calculations on big
integers (HO
)
))
\Fld@menulength=\count286
\Field@Width=\dimen160
\Fld@charsize=\dimen161
Package hyperref Info: Hyper figures OFF on input line 6042.
Package hyperref Info: Link nesting OFF on input line 6047.
Package hyperref Info: Hyper index ON on input line 6050.
Package hyperref Info: backreferencing OFF on input line 6057.
Package hyperref Info: Link coloring OFF on input line 6062.
Package hyperref Info: Link coloring with OCG OFF on input line 6067.
Package hyperref Info: PDF/A mode OFF on input line 6072.
(c:/TeXLive/2022/texmf-dist/tex/latex/base/atbegshi-ltx.sty
Package: atbegshi-ltx 2021/01/10 v1.0c Emulation of the original atbegshi
package with kernel methods
)
\Hy@abspage=\count287
\c@Item=\count288
```

```
\c@Hfootnote=\count289
)
Package hyperref Info: Driver (autodetected): hpdftex.
(c:/TeXLive/2022/texmf-dist/tex/latex/hyperref/hpdftex.def
File: hpdftex.def 2023-02-07 v7.00v Hyperref driver for pdfTeX
(c:/TeXLive/2022/texmf-dist/tex/latex/base/atveryend-ltx.sty
Package: atveryend-ltx 2020/08/19 v1.0a Emulation of the original
atveryend pac
kage
with kernel methods
)
\Fld@listcount=\count290
\c@bookmark@seq@number=\count291
(c:/TeXLive/2022/texmf-dist/tex/latex/rerunfilecheck/rerunfilecheck.sty
Package: rerunfilecheck 2022-07-10 v1.10 Rerun checks for auxiliary files
(HO)
(c:/TeXLive/2022/texmf-dist/tex/generic/uniquecounter/uniquecounter.sty
Package: uniquecounter 2019/12/15 v1.4 Provide unlimited unique counter
(HO)
)
Package uniquecounter Info: New unique counter `rerunfilecheck' on input
line 2
85.
)
\Hy@SectionHShift=\skip59
) (c:/TeXLive/2022/texmf-dist/tex/latex/xcolor/xcolor.sty
Package: xcolor 2022/06/12 v2.14 LaTeX color extensions (UK)
(c:/TeXLive/2022/texmf-dist/tex/graphics/graphics-cfg/color.cfg
File: color.cfg 2016/01/02 v1.6 sample color configuration
)
Package xcolor Info: Driver file: pdftex.def on input line 227.
(c:/TeXLive/2022/texmf-dist/tex/latex/graphics/mathcolor.ltx)
Package xcolor Info: Model `cmy' substituted by `cmy0' on input line
1353.
Package xcolor Info: Model `hsb' substituted by `rgb' on input line 1357.
Package xcolor Info: Model `RGB' extended on input line 1369.
Package xcolor Info: Model `HTML' substituted by `rgb' on input line
1371.
Package xcolor Info: Model `Hsb' substituted by `hsb' on input line 1372.
Package xcolor Info: Model `tHsb' substituted by `hsb' on input line
1373.
Package xcolor Info: Model `HSB' substituted by `hsb' on input line 1374.
Package xcolor Info: Model `Gray' substituted by `gray' on input line
1375.
Package xcolor Info: Model `wave' substituted by `hsb' on input line
1376.
) (c:/TeXLive/texmf-local/tex/latex/aries/subfig.sty
Package: subfig 2005/06/28 ver: 1.3 subfig package
(c:/TeXLive/2022/texmf-dist/tex/latex/caption/caption.sty
Package: caption 2022/03/01 v3.6b Customizing captions (AR)
(c:/TeXLive/2022/texmf-dist/tex/latex/caption/caption3.sty
Package: caption3 2022/03/17 v2.3b caption3 kernel (AR)
\caption@tempdima=\dimen162
\captionmargin=\dimen163
```

```
\caption@leftmargin=\dimen164
\caption@rightmargin=\dimen165
\caption@width=\dimen166
\caption@indent=\dimen167
\caption@parindent=\dimen168
\caption@hangindent=\dimen169
Package caption Info: elsarticle document class detected.
(c:/TeXLive/2022/texmf-dist/tex/latex/caption/caption-elsarticle.sto
File: caption-elsarticle.sto 2020/08/22 v2.0 Adaption of the caption
package to
the elsarticle document class (AR)
))
\c@caption@flags=\count292
\c@continuedfloat=\count293
Package caption Info: hyperref package is loaded.
)
\c@KVtest=\count294
\sf@farskip=\skip60
\sf@capttopadj=\dimen170
\sf@capskip=\skip61
\sf@nearskip=\skip62
\c@subfigure=\count295
\c@subfigure@save=\count296
\c@lofdepth=\count297
\c@subtable=\count298
\c@subtable@save=\count299
\c@lotdepth=\count300
\sf@top=\skip63
\sf@bottom=\skip64
) (c:/TeXLive/2022/texmf-dist/tex/latex/base/inputenc.sty
Package: inputenc 2021/02/14 v1.3d Input encoding file
\inpenc@prehook=\toks24
\inpenc@posthook=\toks25
) (c:/TeXLive/2022/texmf-dist/tex/latex/lineno/lineno.sty
Package: lineno 2023/01/19 line numbers on paragraphs v5.1
\linenopenalty=\count301
\output=\toks26
\linenoprevgraf=\count302
\linenumbersep=\dimen171
\linenumberwidth=\dimen172
\c@linenumber=\count303
\c@pagewiselinenumber=\count304
\c@LN@truepage=\count305
\c@internallinenumber=\count306
\c@internallinenumbers=\count307
\quotelinenumbersep=\dimen173
\bframerule=\dimen174
\bframesep=\dimen175
\bframebox=\box60
\linenoams@ams@eqopen=\count308
LaTeX Info: Redefining \\ on input line 3131.
) (c:/TeXLive/2022/texmf-dist/tex/latex/blindtext/blindtext.sty
Package: blindtext 2012/01/06 V2.0 blindtext-Package
(c:/TeXLive/2022/texmf-dist/tex/latex/tools/xspace.sty
```

```

Package: xspace 2014/10/28 v1.13 Space after command names (DPC,MH)
)
\c@blindtext=\count309
\c@Blindtext=\count310
\c@blind@countparstart=\count311
\blind@countxx=\count312
\blindtext@numBlindtext=\count313
\blind@countyy=\count314
\c@blindlist=\count315
\c@blindlistlevel=\count316
\c@blindlist@level=\count317
\blind@listitem=\count318
\c@blind@listcount=\count319
\c@blind@levelcount=\count320
\blind@mathformula=\count321
\blind@Mathformula=\count322
\c@blind@randomcount=\count323
\c@blind@randommax=\count324
\c@blind@pangramcount=\count325
\c@blind@pangrammax=\count326
)
Package hyperref Info: Option `bookmarksopen' set `true' on input line
36.
Package hyperref Info: Option `pdftoolbar' set `true' on input line 36.
Package hyperref Info: Option `pdfmenubar' set `true' on input line 36.
Package hyperref Info: Option `colorlinks' set `true' on input line 36.
Package hyperref Info: Option `pdffitwindow' set `true' on input line 36.
(./Pizarro_etAl_EcoInf_R2.aux)
\openout1 = `Pizarro_etAl_EcoInf_R2.aux'.

```

```

LaTeX Font Info:     Checking defaults for OML/cmm/m/it on input line 50.
LaTeX Font Info:     ... okay on input line 50.
LaTeX Font Info:     Checking defaults for OMS/cmsy/m/n on input line 50.
LaTeX Font Info:     ... okay on input line 50.
LaTeX Font Info:     Checking defaults for OT1/cmr/m/n on input line 50.
LaTeX Font Info:     ... okay on input line 50.
LaTeX Font Info:     Checking defaults for T1/cmr/m/n on input line 50.
LaTeX Font Info:     ... okay on input line 50.
LaTeX Font Info:     Checking defaults for TS1/cmr/m/n on input line 50.
LaTeX Font Info:     ... okay on input line 50.
LaTeX Font Info:     Checking defaults for OMX/cmex/m/n on input line 50.
LaTeX Font Info:     ... okay on input line 50.
LaTeX Font Info:     Checking defaults for U/cmr/m/n on input line 50.
LaTeX Font Info:     ... okay on input line 50.
LaTeX Font Info:     Checking defaults for PD1/pdf/m/n on input line 50.
LaTeX Font Info:     ... okay on input line 50.
LaTeX Font Info:     Checking defaults for PU/pdf/m/n on input line 50.
LaTeX Font Info:     ... okay on input line 50.
(c:/TeXLive/2022/texmf-dist/tex/context/base/mkii/supp-pdf.mkii
[Loading MPS to PDF converter (version 2006.09.02).]
\scratchcounter=\count327
\scratchdimen=\dimen176
\scratchbox=\box61
\nofMPsegments=\count328

```

```

\nofMParguments=\count329
\everyMPshowfont=\toks27
\MPscratchCnt=\count330
\MPscratchDim=\dimen177
\MPnumerator=\count331
\makeMPintoPDFobject=\count332
\everyMPToPDFconversion=\toks28
) (c:/TeXLive/2022/texmf-dist/tex/latex/epstopdf-pkg/epstopdf-base.sty
Package: epstopdf-base 2020-01-24 v2.11 Base part for package epstopdf
Package epstopdf-base Info: Redefining graphics rule for `'.eps' on input
line 4
85.
(c:/TeXLive/2022/texmf-dist/tex/latex/latexconfig/epstopdf-sys.cfg
File: epstopdf-sys.cfg 2010/07/13 v1.3 Configuration of (r)epstopdf for
TeX Liv
e
))
Package hyperref Info: Link coloring ON on input line 50.
(./Pizarro_etAl_EcoInf_R2.out) (./Pizarro_etAl_EcoInf_R2.out)
\@outlinefile=\write4
\openout4 = `Pizarro_etAl_EcoInf_R2.out'.

Package caption Info: Begin \AtBeginDocument code.
Package caption Info: subfig package v1.3 is loaded.
Package caption Info: End \AtBeginDocument code.

Overfull \vbox (40.57777pt too high) has occurred while \output is active
[]

Overfull \hbox (2.61108pt too wide) has occurred while \output is active
[]
[]

[1

{c:/TeXLive/2022/texmf-var/fonts/map/pdftex/updmap/pdftex.map}] [2]
Overfull \hbox (2.70287pt too wide) in paragraph at lines 104--105
[]\OT1/cmr/m/n/12 While species rich-ness is of-ten used to rep-re-sents
di-ver
-sity pat-tterns, species
[]

[3] [4] [5] [6] [7] [8]
<Fig_1.pdf, id=363, 562.56793pt x 155.87297pt>
File: Fig_1.pdf Graphic file (type pdf)
<use Fig_1.pdf>
Package pdftex.def Info: Fig_1.pdf used on input line 163.
(pdftex.def) Requested size: 390.0pt x 108.05907pt.

LaTeX Warning: No positions in optional float specifier.
Default added (so using `tbp') on input line 170.

```

```
[9 <./Fig_1.pdf>] [10]
<Fig_2.pdf, id=415, 615.92346pt x 327.82932pt>
File: Fig_2.pdf Graphic file (type pdf)
<use Fig_2.pdf>
Package pdftex.def Info: Fig_2.pdf used on input line 228.
(pdftex.def) Requested size: 390.0pt x 207.58403pt.

Overfull \hbox (6.52367pt too wide) in paragraph at lines 235--236
[]\OT1/cmr/m/n/12 Bioregions show sim-i-lar trends of data ac-cu-mu-la-
tion acr
oss the four decades
[]
```

```
[11] [12 <./Fig_2.pdf>]
<Fig_3.pdf, id=437, 361.35pt x 216.81pt>
File: Fig_3.pdf Graphic file (type pdf)
<use Fig_3.pdf>
Package pdftex.def Info: Fig_3.pdf used on input line 239.
(pdftex.def) Requested size: 312.00119pt x 187.20062pt.
<Fig_4.pdf, id=441, 617.40819pt x 315.87735pt>
File: Fig_4.pdf Graphic file (type pdf)
<use Fig_4.pdf>
Package pdftex.def Info: Fig_4.pdf used on input line 248.
(pdftex.def) Requested size: 390.0pt x 199.52914pt.
[13 <./Fig_3.pdf>]
```

```
\LaTeX Warning: No positions in optional float specifier.
Default added (so using `tbp') on input line 265.
```

```
\LaTeX Warning: `h' float specifier changed to `ht'.
```

```
[14 <./Fig_4.pdf>] [15] [16]
<Fig_5.pdf, id=480, 550.31795pt x 188.47154pt>
File: Fig_5.pdf Graphic file (type pdf)
<use Fig_5.pdf>
Package pdftex.def Info: Fig_5.pdf used on input line 397.
(pdftex.def) Requested size: 390.0pt x 133.56552pt.
[17 <./Fig_5.pdf>]
```

```
! \LaTeX Error: File `old_Figs/Fig6' not found.
```

```
See the \LaTeX manual or \LaTeX Companion for explanation.
Type H <return> for immediate help.
```

```
...
```

```
1.408 ...phics[width=.65\textwidth]{old_Figs/Fig6}
```

```
I could not locate the file with any of these extensions:
.pdf,.png,.jpg,.mps,.jpeg,.jbig2,.jb2,.PDF,.PNG,.JPG,.JPEG,.JBIG2,.JB2,.e
ps
Try typing <return> to proceed.
If that doesn't work, type X <return> to quit.
```

```
[18] [19] [20] [21] [22] [23] [24] [25] [26] [27]
Underfull \hbox (badness 1701) in paragraph at lines 812--819
[]\OT1/cmr/m/n/12 GBIF.org, 2021. Occurrence down-load. URL:
[] []\$ \OT1/cmtt
/m/n/12 https : / / www . gbif .
[]
```

```
Underfull \hbox (badness 1354) in paragraph at lines 812--819
\OT1/cmtt/m/n/12 org / occurrence / download / 0039590-
[]210914110416597$[][]\O
T1/cmr/m/n/12 , doi:[] []\$ \OT1/cmtt/m/n/12 10 . 15468 /
[]
```

```
[28] [29] [30] [31] [32] [33] [34]
```

```
Package lineno Warning: Linenumber reference failed,
(lineno) rerun to get it right.
```

```
[35]
```

```
\LaTeX Warning: No positions in optional float specifier.
Default added (so using `tbp') on input line 1375.
```

```
<Fig_AB.pdf, id=907, 638.19527pt x 190.37975pt>
File: Fig_AB.pdf Graphic file (type pdf)
<use Fig_AB.pdf>
Package pdftex.def Info: Fig_AB.pdf used on input line 1471.
(pdftex.def) Requested size: 386.10214pt x 115.17863pt.
```

```
\LaTeX Warning: `h' float specifier changed to `ht'.
```

```
<Fig_B8.pdf, id=908, 337.33296pt x 216.81pt>
File: Fig_B8.pdf Graphic file (type pdf)
<use Fig_B8.pdf>
Package pdftex.def Info: Fig_B8.pdf used on input line 1478.
(pdftex.def) Requested size: 312.00119pt x 200.53949pt.
```

```
\LaTeX Warning: `h' float specifier changed to `ht'.
```

```
\LaTeX Warning: `h' float specifier changed to `ht'.
```

```
[36]
```

```
] [37]
```

```
! \LaTeX Error: File `FigS3' not found.
```

```
See the \LaTeX manual or \LaTeX Companion for explanation.
Type H <return> for immediate help.
```

```
...
```

```
l.1537 ...ludegraphics[width=1.0\textwidth]{FigS3}
```

```
I could not locate the file with any of these extensions:  
.pdf,.png,.jpg,.mps,.jpeg,.jbig2,.jb2,.PDF,.PNG,.JPG,.JPEG,.JBIG2,.JB2,.e  
ps  
Try typing <return> to proceed.  
If that doesn't work, type X <return> to quit.
```

```
LaTeX Warning: `h' float specifier changed to `ht'.
```

```
! LaTeX Error: File `FigS4' not found.
```

```
See the LaTeX manual or LaTeX Companion for explanation.
```

```
Type H <return> for immediate help.
```

```
...
```

```
l.1545 ...ludegraphics[width=.95\textwidth]{FigS4}
```

```
I could not locate the file with any of these extensions:
```

```
.pdf,.png,.jpg,.mps,.jpeg,.jbig2,.jb2,.PDF,.PNG,.JPG,.JPEG,.JBIG2,.JB2,.e  
ps
```

```
Try typing <return> to proceed.
```

```
If that doesn't work, type X <return> to quit.
```

```
LaTeX Warning: `h' float specifier changed to `ht'.
```

```
[38 <./Fig_AB.pdf>] [39 <./Fig_B8.pdf>] [40]  
(./Pizarro_etAl_EcoInf_R2.aux)
```

```
LaTeX Warning: Label(s) may have changed. Rerun to get cross-references  
right.
```

```
Package rerunfilecheck Info: File `Pizarro_etAl_EcoInf_R2.out' has not  
changed.
```

```
(rerunfilecheck) Checksum:  
1E1EFC31C2C5FF077ACDF2C5DF498563;3347.  
)  
Here is how much of TeX's memory you used:  
13151 strings out of 476024  
210181 string characters out of 5794017  
1918382 words of memory out of 5000000  
33259 multiletter control sequences out of 15000+600000  
520616 words of font info for 61 fonts, out of 8000000 for 9000  
1141 hyphenation exceptions out of 8191  
75i,10n,79p,2201b,725s stack positions out of  
10000i,1000n,20000p,200000b,200000s  
{c:/TeXLive/2022/texmf-dist/fonts/enc/dvips/cm-super/cm-super-  
ts1.enc}<c:/TeX  
Live/2022/texmf-  
dist/fonts/type1/public/amsfonts/cm/cmbx10.pfb><c:/TeXLive/2022
```

```
/texmf-
dist/fonts/type1/public/amsfonts/cm/cmbx12.pfb><c:/TeXLive/2022/texmf-di
st/fonts/type1/public/amsfonts/cm/cmex10.pfb><c:/TeXLive/2022/texmf-
dist/fonts/
type1/public/amsfonts/cm/cmmi10.pfb><c:/TeXLive/2022/texmf-
dist/fonts/type1/pub
lic/amsfonts/cm/cmmi12.pfb><c:/TeXLive/2022/texmf-
dist/fonts/type1/public/amsfo
nts/cm/cmmi6.pfb><c:/TeXLive/2022/texmf-
dist/fonts/type1/public/amsfonts/cm/cmm
i8.pfb><c:/TeXLive/2022/texmf-
dist/fonts/type1/public/amsfonts/cm/cmr10.pfb><c:
/TExLive/2022/texmf-
dist/fonts/type1/public/amsfonts/cm/cmr12.pfb><c:/TeXLive/2
022/texmf-
dist/fonts/type1/public/amsfonts/cm/cmr17.pfb><c:/TeXLive/2022/texmf-
dist/fonts/type1/public/amsfonts/cm/cmr7.pfb><c:/TeXLive/2022/texmf-
dist/fonts/
type1/public/amsfonts/cm/cmr8.pfb><c:/TeXLive/2022/texmf-
dist/fonts/type1/publi
c/amsfonts/cm/cmss8.pfb><c:/TeXLive/2022/texmf-
dist/fonts/type1/public/amsfonts
/cm/cmssbx10.pfb><c:/TeXLive/2022/texmf-
dist/fonts/type1/public/amsfonts/cm/cms
y10.pfb><c:/TeXLive/2022/texmf-
dist/fonts/type1/public/amsfonts/cm/cmsy7.pfb><c
:/TeXLive/2022/texmf-
dist/fonts/type1/public/amsfonts/cm/cmsy8.pfb><c:/TeXLive/
2022/texmf-
dist/fonts/type1/public/amsfonts/cm/cmti10.pfb><c:/TeXLive/2022/texm
f-dist/fonts/type1/public/amsfonts/cm/cmti12.pfb><c:/TeXLive/2022/texmf-
dist/fo
nts/type1/public/amsfonts/cm/cmti7.pfb><c:/TeXLive/2022/texmf-
dist/fonts/type1/
public/amsfonts/cm/cmtt10.pfb><c:/TeXLive/2022/texmf-
dist/fonts/type1/public/am
sfonts/cm/cmtt12.pfb><c:/TeXLive/2022/texmf-dist/fonts/type1/public/cm-
super/sf
rm1000.pfb><c:/TeXLive/2022/texmf-dist/fonts/type1/public/cm-
super/sfrm1200.pfb
>
Output written on Pizarro_etAl_EcoInf_R2.pdf (40 pages, 14552853 bytes).
PDF statistics:
 1091 PDF objects out of 1200 (max. 8388607)
 948 compressed objects within 10 object streams
 162 named destinations out of 1000 (max. 500000)
 212 words of extra memory for PDF output out of 10000 (max. 10000000)
```