


Article

Three-Dimensional Quantification of Copepods Predictive Distributions in the Ross Sea: First Data Based on a Machine Learning Model Approach and Open Access (FAIR) Data

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Abstract: Zooplankton is a fundamental group in aquatic ecosystems representing the base of the food chain. It forms a link between the lower trophic levels with secondary consumers and shows marked fluctuations in populations with environmental change, especially reacting to heating and water acidification. Marine copepods account for approx. 70% of the abundance of zooplankton and are a target of monitoring activities in key areas such as the Southern Ocean. In this study, we have used FAIR-inspired legacy data (dating back to the 1980s) collected in the Ross Sea by the Italian National Antarctic Program at GBIF.org. Together with other open-access GIS data sources and tools, it allows one to generate, for the first time, three-dimensional predictive distribution maps for twenty-six copepod species. These predictive maps were obtained by applying machine learning techniques to grey literature data, which were visualized in open-source GIS platforms. In a Species Distribution Modeling (SDM) framework, we used machine learning with three types of algorithms (TreeNet, RandomForest, and Ensemble) to analyze the presence and absence of copepods in different areas and depth classes as a function of environmental descriptors obtained from the Polar Macroscope Layers present in Quantartica. The models allow, for the first time, to map-predict the food chain per depth class in quantitative terms, showing the relative index of occurrence (RIO) in 3Dimensions and identifying the presence of each copepod species analyzed in the Ross Sea, a globally-relevant wilderness area of conservation concern. Our results show marked geographical preferences that vary with species and trophic strategy. This study demonstrates that machine learning is a successful method in accurately predicting the Antarctic copepod presence, also providing useful data to orient future sampling and the management of wildlife and conservation.

Keywords: machine learning; Antarctic copepods; species distribution models (SDMs); Ross Sea; open source; FAIR data



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1. Introduction

In the Anthropocene of the finite Earth, there are just a few large wilderness areas left, often occurring in remote areas difficult to access. The Ross Sea (Figure 1), a remote portion of the Southern Ocean, is one of those areas, which remained virtually pristine until the early 1900s when sealing and whaling started, as well as in 1996 when commercial fishery started the exploitation of Antarctic krill (*Euphausia superba*) and toothfish (*Dissostichus mawsoni*) [1]. The impact of these fisheries in the pristine waters is disputed, e.g., described

as ‘low’ by FAO [2], with more relevant impacts described by Ainley [1]. Recent reports show a substantially triplicated effort since the late 1990s in Antarctic krill fishing (at least in the FAO areas 48, 58, and 88), while toothfish extraction remained stable over the years [2]. In the meantime, the area has been attributed a massive industrial footprint and a subsequent trophic cascade due to the earlier whaling and sealing [3]. After the iterative submission of a formal marine protected area proposal by New Zealand and the USA in 2012—supported by Germany—the Ross Sea was declared protected by the Commission for the Conservation of Antarctic Marine Living Resources members in October 2016. The “Ross Sea region Marine Protected Area” (RSRMPA) was founded on December 1 2017 and will last for the following 35 years [4]. The Commission for the Conservation of Antarctic Marine Living Resources parties also agreed on the Conservation Measure 91-05 (2016), where priorities for scientific research and monitoring activities were clearly stated. Fisheries in those areas are usually ‘experimental’ but ongoing, with some areas being ‘no-take’ zones. While the state of the atmosphere or low-temperature maintenance is not given any consideration, the RSRMPA was designed to protect whole ecosystems’ function and structure as well as trophic interactions, including areas considered important to the life cycle of toothfish and krill, hence its enormous extension of more than 2 million km². However, despite the long history of exploration of the Ross Sea, which extends to more than a century [5], samples and data are still few, especially considering the extent of the area to be monitored for the RSRMPA, which automatically implies high logistic costs regardless of the specific scientific target, as well as more effort and data collection. Moreover, some of the relevant existing data are not shared or available to the public (i.e., the Commission for the Conservation of Antarctic Marine Living Resources reports), may exist but are not digitally available or well-documented with metadata, and hence not truly accessible, or simply lack a robust research design for wider inference [6].

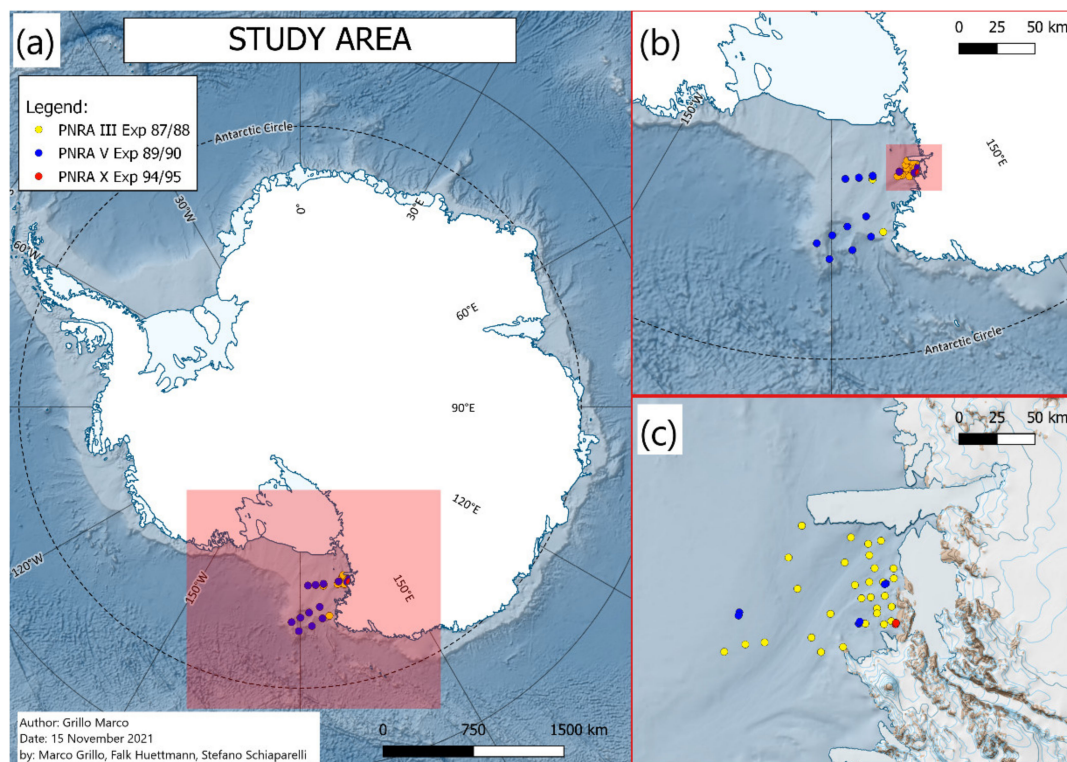


Figure 1. Study area. (a) Stations sampled in the Ross Sea area. (b,c) Stations sampled in the Terra Nova Bay area.

Paradoxically, this also applies to fishery target species such as the Antarctic toothfish *Dissostichus* for which ecological information is still incomplete [1,7,8], and specific spa-

tial population models are constantly being developed and refined within the RSRMPA boundaries [9–11].

For this remote and largely pristine area, it is thus mandatory to continue existing monitoring programs, establish new ones, mobilize potentially available legacy data, and use them well based on transparent and repeatable science. This is specifically relevant in the case of food chain structure and dynamics through the 3D structure of the water column, a widely attempted but rarely achieved target in oceanography. Here we pursue model predictions with the latest machine learning methods to achieve those goals for one of the last and most remote wilderness areas in the world. In this context, the study of zooplankton—a fundamental ecological component for all aquatic ecosystems—is especially relevant. From a trophodynamic point of view, these organisms represent a fundamental link between the microbial loop and higher consumers in marine food webs such as cnidarians, crustaceans, fish, seabirds, and even mammals [10,11].

Zooplankton communities are also sensitive to environmental changes to which they react, for instance biogeographical shifts [12], hence representing a good environmental indicator [13] to pinpoint any environmental changes, namely global and man-made climate-driven changes [14,15].

A major component of zooplankton assemblages is that of copepods. These crustaceans generally represent 70% of the entire mesozooplankton biomass and are also important in terms of secondary production and the grazing rate [16–19]. Here, copepods consist of over 302 [17] (<https://copepodes.obs-banyuls.fr/en/loc.php?loc=4>, accessed on 1 March 2022) species whose distribution was recently reassessed [18].

Copepods react strongly to changes in environmental conditions triggered by climate change such as modifications of the stratification of the water column and water acidification [19] by changing their distribution and life cycle [20].

In order to predict these distributional changes, we employ prediction-based inferences using machine learning and species distribution models (SDMs) [21]. Species distribution models represent a loose term for an approach to empirical ecological models that predict the presence or absence of one or more species in relation to environmental descriptors [22] and can provide models of habitat suitability on large spatial scales. SDMs are known to perform very well when using Machine Learning and Artificial Intelligence (AI) methods [21]. Specifically, when linked with open-access data, these models become powerful tools for the management and conservation of biodiversity and the environment [23,24]. In this investigation, we focus on the lower levels of the planktic food chain by using copepods' grey literature, "legacy data" previously digitalized [25], to provide the first 3D assessment of key Ross Sea species to help document the state of the art for RSRMPA's understanding and functioning. Despite being present for over 40 years, ML/AI is still widely underused in ecology despite its potentially great help in obtaining powerful data mining and predictions for inferencing.

Specimens analyzed in this work are present in the collections of the Italian National Antarctic Museum (section of Genoa) stored in 96% Ethanol with MNA codes in the range of 12279–13006.

Here we try to provide progress on wilderness areas, their best available information, and their ecological processes in a quantitative fashion explicit in space and time, making the best use of available field samples provided online to the public and using open-access tools.

2. Materials and Methods

The dataset of the copepods analyzed in this study derives from the Ross Sea sector. The study area is a large portion of northwestern Antarctica, spanning from the Drygalski Ice Tongue in Terra Nova Bay (TNB) to the continental slope surrounding the Central Basin (Figure 1).

Our copepod data are based on Bonello [25] and are available at <https://www.gbif.org/dataset/b212e93b-7800-4b05-8e2d-5f26798f5002>, accessed on 1 May 2020, where

they can be freely downloaded from the Global Biodiversity Information Facility (GBIF) website using the RGBIF package of the R program (R Core Team, 2020). Instead, the presence/absence matrix with relative environmental descriptors is available at <https://zenodo.org/record/6389676#.YmesgdpByUk>, accessed on 29 March 2022.

Specimens were obtained in the framework of three different Antarctic Expeditions of the Italian National Antarctic Program (PNRA), namely the III (1987-88), V (1989-90), and the X (1994-95), and were the subject of previous publications [26–33]. The list of species is reported in Table 1.

Table 1. Species list. AphiaID from the World Register of Marine Species (WORMS, <https://www.marinespecies.org>).

Family	Species	Worms Aphia ID	Trophic Guild
Acartiidae	<i>Paralabidocera antarctica</i> (Thompson I.C., 1898)	345234	Phytoplankton feeder [34]
Aetideidae	<i>Aetideopsis antarctica</i> (Wolfenden, 1908)	341236	Phyto- and zooplankton feeder [35]
	<i>Aetideopsis minor</i> (Wolfenden, 1911)	254600	Phyto- and zooplankton feeder [35]
	<i>Gaetanus tenuispinus</i> (Sars G.O., 1900)	237965	Phyto- and zooplankton feeder [35]
Augaptilidae Calanidae	<i>Haloptilus ocellatus</i> Wolfenden, 1905	342624	Zooplankton feeder [36]
	<i>Calanoides acutus</i> (Giesbrecht, 1902)	342434	Phytoplankton feeder [18,37]
	<i>Calanus propinquus</i> Brady, 1883	342435	Phytoplankton feeder [18,37]
Clausocalanidae	<i>Microcalanus pygmaeus</i> (Sars G.O., 1900)	104513	Phyto- and zooplankton feeder [37]
Euchaetidae	<i>Ctenocalanus vanus</i> Giesbrecht, 1888	104510	Phytoplankton feeder [37]
	<i>Paraeuchaeta antarctica</i> (Giesbrecht, 1902)	344974	Zooplankton feeder [37]
	<i>Paraeuchaeta exigua</i> (Wolfenden, 1911)	345051	Zooplankton feeder [36]
Harpacticidae	<i>Paraeuchaeta similis</i> (Wolfenden, 1908)	345055	Zooplankton feeder [36]
	<i>Harpacticus furcifer</i> Giesbrecht, 1902	293136	Phytoplankton feeder [38]
Heterorhabdidae	<i>Heterorhabdus austrinus</i> Giesbrecht, 1902	343728	Zooplankton feeder [39,40]
Lucicutiidae	<i>Lucicutia ovalis</i> (Giesbrecht, 1889)	104609	Phytoplankton feeder [41]
Metridinidae	<i>Metridia gerlachei</i> Giesbrecht, 1902	344689	Phyto-, zooplankton [37] and suspension feeder [36]
	<i>Metridia curticauda</i> Giesbrecht, 1889	104628	Suspension feeder [36]
Oithonidae	<i>Oithona frigida</i> Giesbrecht, 1902	344712	Phytoplankton feeder [42]
	<i>Oithona similis</i> Claus, 1866	106656	Phytoplankton feeder [42]
Oncaeidae	<i>Oncaea curvata</i> Giesbrecht, 1902	344719	Zooplankton feeder [36]
	<i>Triconia conifera</i> (Giesbrecht, 1891)	128957	Zooplankton feeder [36]
Rhincalanidae	<i>Rhincalanus gigas</i> Brady, 1883	220837	Phyto- and zooplankton feeder [37]
Scolecitrichidae	<i>Scolecithricella minor</i> (Brady, 1883)	104811	Phyto- and zooplankton feeder [36]
	<i>Racovitzanus antarcticus</i> Giesbrecht, 1902	104784	Phyto- and zooplankton feeder [36]
	<i>Scaphocalanus subbrevicornis</i> (Wolfenden, 1911)	104802	Phyto- and zooplankton feeder [36]
Stephidae	<i>Stephos longipes</i> Giesbrecht, 1902	345365	Phytoplankton feeder [37]

During the III and V Antarctic expeditions, copepods were sampled using a multi net Eznet-BIONESS [43], coupled with a multiparameter probe to acquire the environmental descriptors on-site [44,45].

The zooplankton sampling was carried out from 5 January 1988 to 21 February 1988, between 72° S and 75° S of latitude and 163° E and 173° E of longitude during the III expedition. Instead, the V expedition sampled organisms from 25 November 1989 to 12 January 1990, between 62° S and 75° S and 161° E and 177° W.

During the X PRNA expedition, sampling was carried out using the Working Party II (WP2—UNEP FAO) net. This type of net was used for horizontal and vertical sampling. Both sampling modalities provided a filtration of 200 μm . The sampling depths varied from 200 m deep to the surface, depending on the bottom depth of the different sampling points [26]. All the samples collected during the three campaigns were stored in a 4% buffered solution and seawater. Specimens now present in the collections of the Italian National Antarctic Museum are stored in 96% Ethanol.

The dataset used was constructed from published campaign reports from 1990, 1992, and 2002 [26,27,29,32,33,44,45], recently made available in the Global Biodiversity Information System (GBIF) by Bonello [25].

In this paper, among all the information available from the dataset, only the bibliographic basisOfRecord has been used.

We used OpenSource QGIS [46], R [47], ESRI ArcGIS (10.4), and Qantarctica [48] to explore, visualize, and map data and model predictions with basemaps. We used the projection of geographic WGS84 in latitude and longitude for data exploration and handling, and the stereographic Antarctic projection WGS 84/ Antarctic Polar Stereographic EPSG: 3031 for the map display.

To obtain the values of the environmental descriptors present on the Polar Macroscope Layer [48], the points with the presence and absence data were superimposed from the attribute table using the “extract multiple values in points” (GIS) function. The final table obtained at the end of the process was used to model the distribution of copepods with machine learning and its subsequent modeling and representation on Quantartica. We used a point lattice of 1km to derive a prediction grid that we scored with each of the ML methods. The environmental descriptors used are available from open-access sources and are reported in the online resource “Environmental descriptors” (Annex A).

We used the Ocean Data View [49] and R program (BIOMOD2 package, [47]) for initial exploration models, draft 1, and then fine-tuned model surfaces with the Salford Predictive Modeler (SPM).

Three predictive distribution models were created using the TreeNet, RandomForest, and a combined Ensemble (compare with Hardy [50] for Alaska, Meissner [51] for Iceland, and Huettmann and Schmid [52] for Antarctica) in SPM. From the algorithms, a Relative Occurrence Index (RIO) was obtained for the lattice to show the most suitable habitats for the copepods. Furthermore, for each model, four depth classes were analyzed: 0–750 m combined, and then also three stratified zones: 0–10 m, 11–70 m, and 71–750 m. These depth strata followed biological reasoning and allowed the use of data availability groups.

The division into the four depth classes was based on the knowledge of species biology and eventually driven by the number of real occurrences (i.e., “good sample size”) that the copepods had within these layers. Working in this way, it was possible to proceed with the setting of the chosen algorithms and the subsequent predictive analyses (Figure 2).

The RIO is an index concerning the “occurrence” category and can assume values between 0 and 1 [53,54].

The RIO for these analyzed points was extracted to evaluate how the predictions correspond to the independent field data and for the respective four depth classes investigated. The accuracy of the selected models is given by the area under the curve of the Relative Operating Characteristic (ROC) (Table 2).

Table 2. Classification table of the models used according to the ROC [55,56].

Algorithm	ROC (%) Range	Class
TreeNet	0–49	Poor
RandomForest	50–70	Good
Ensemble	71–100	Very good

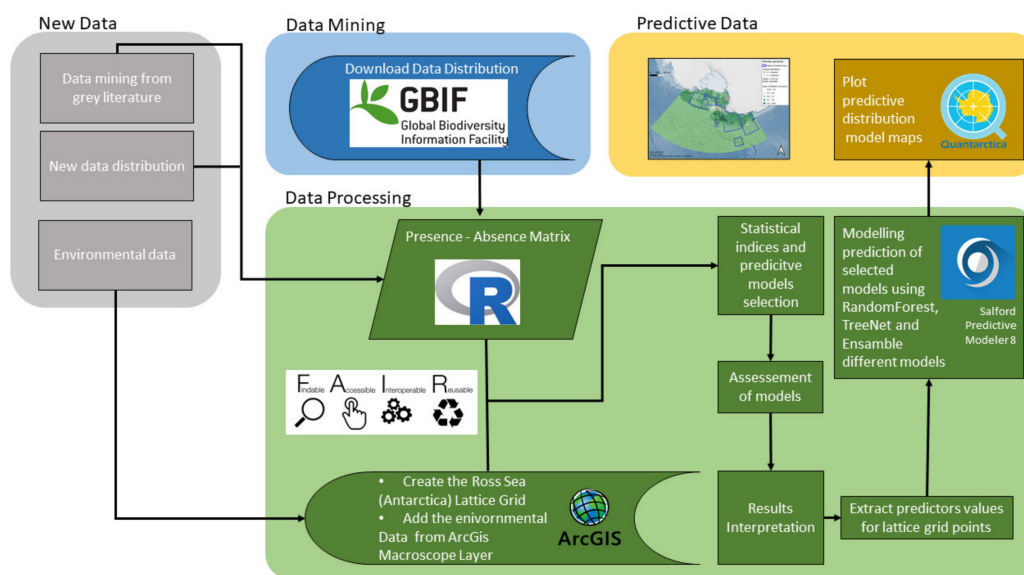


Figure 2. Workflow of the data analysis. This workflow represents the work steps that led to the species distribution models. This diagram shows data mining, data processing, new data, and predictive data.

In this way, it was possible to obtain a three-dimensional quantitative spatial assessment, that is, the neritic and oceanic provinces and water column were analyzed. The RIO values for the Ensemble maps were obtained by averaging the respective index values of the TreeNet and RandomForest algorithms.

Based on the sample number per species (Table 3), the depth classes to be evaluated were chosen. For the species *Calanaoides acutus*, *Calanus propinquus*, *Ctenocalanus vanus*, *Metridia gerlachei*, *Oithona similis*, *Oncaea curvata*, *Paraeuchaeta antarctica*, and *Rhincalanus gigas*, all the depth classes were analyzed, while for the remaining species, only one depth bin was used, i.e., 0–750 m. Instead, *Aetideopsis minor*, *Gaetanus tenuispinus*, *Harpacticus furcifer*, *Microcalanus pygmaeus*, and *Scolecithricella minor* were merged into a single category, namely “Other copepods”, due to the extremely low number of occurrences. Presumably, those species are rare and not detected much in the whole water layer. This grid was scored in SPM using the pattern created from the points of the presence/absence matrix. Within this matrix, two values, 0 (absent species) or 1 (present species), have been assigned, which represents the relative index of occurrence that a given point contains a forecast of the RIO.

Table 3. Species list with sample size and ROC accuracy for both models: Red (poor), yellow (good), and green (very good).

Species	Sample Size (# of Occurrences)				TreeNet ROC (%)			RandomForest ROC (%)				
	0–750 [m]	0–10 [m]	11–70 [m]	71–750 [m]	0–10 [m]	11–70 [m]	71–750 [m]	0–750 [m]	0–10 [m]	11–70 [m]	71–750 [m]	
<i>A. antarctica</i>	30	0	0	30	83			47				
<i>A. minor</i>	1	0	0	1								
<i>C. acutus</i>	534	71	144	319	66	70	69	67	64	60	64	59
<i>C. propinquus</i>	242	28	55	159	66	73	73	60	63	70	69	55
<i>C. vanus</i>	125	8	22	95	82	83	84	76	75	58	76	71
<i>G. tenuispinus</i>	2	0	0	2								
<i>H. ocellatus</i>	5	0	2	3	73				87			
<i>H. furcifer</i>	1	1	0	0								
<i>H. austrinus</i>	6	3	0	3	78				88			
<i>L. ovalis</i>	3	2	0	1	49				38			
<i>M. curticauda</i>	7	1	1	5	83				94			
<i>M. gerlachei</i>	579	58	104	417	67	65	58	66	66	60	53	65

Table 3. Cont.

Species	Sample Size (# of Occurrences)				TreeNet ROC (%)				RandomForest ROC (%)			
	0–750 [m]	0–10 [m]	11–70 [m]	71–750 [m]	0–750 [m]	0–10 [m]	11–70 [m]	71–750 [m]	0–750 [m]	0–10 [m]	11–70 [m]	71–750 [m]
<i>M. pygmaeus</i>	1	0	0	1					79			
<i>O. frigida</i>	68	1	3	64	81							
<i>O. similis</i>	231	55	52	124	84	84	87	79	79	78	80	73
<i>O. curvata</i>	214	55	43	116	83	84	85	76	77	82	83	68
<i>P. antarctica</i>	185	8	11	166	72	52	89	63	65	8	52	59
<i>P. exigua</i>	119	8	5	106	80	75		73	68	53		66
<i>P. similis</i>	3	0	0	3	60				0			
<i>P. antarctica</i>	24	19	1	4	91				62			
<i>R. antarcticus</i>	53	13	1	39	93				91			
<i>R. gigas</i>	32	8	12	12	94	81	89	96	93	82	84	95
<i>S. subbrevicornis</i>	9	4	0	5	91				93			
<i>S. minor</i>	4	0	0	4								
<i>S. longipes</i>	37	3	1	33	85				77			
<i>T. conifera</i>	19	0	0	19	96				80			
Other copepods	9	1	0	8	84				42			

3. Results

We were able to compile, for the first time, a value-added data cube, explicitly in time and space, consisting of copepod species and environmental predictors to be used for model predictions of copepods for the Ross Sea wilderness area. Our field data consist of twenty-six species with sample sizes, relative ROC (Table 3), and RIO values (Supplementary File S2).

Most of the ROCs obtained showed 70% higher accuracy in the depth classes investigated, which means that the analyzed models perform well with moderate accuracy. Specifically, the highest ROCs occur in the species *Triconia conifera* (96%, 0–750 m—TreeNet) and *Rhincalanus gigas* (96%, 71–750 m—TreeNet) followed by *Scaphocalanus subbrevicornis* (93%, 0–750 m—TreeNet), *Racovitzanus antarcticus* (93%; 0–750 m—TreeNet), and *Paralabidocera antarctica* (91%; 0–750 m—TreeNet). Meanwhile, the lowest ROC values occur in the species *Aetideopsis antartica* (47%; 0–750 m—RandomForest), *Ctenocalanus vanuus* (58%; 0–10 m—RandomForest), *Lucicutia ovalis* (49% and 38% in TreeNet and RandomForest, respectively), *Paraeuchaeta antarctica* (8%; 0–10 m—RandomForest), *Paraeuchaeta similis* (0%; 0–750 m—RandomForest), and “Other copepods” (42%; 0–750 m—RandomForest).

We were also able to create the first ensemble models for this study area, with data and maps provided in Supplementary Files S1 and S2.

The model diagnostics are presented in Supplementary File S5.

This is the first time for the Ross Sea, using publicly available legacy data with the help of machine learning, that we were able to obtain different accurate forecast surfaces for the different algorithms and depth classes.

The use of an RIO index enabled us to generalize and categorize the different areas according to their occupation by copepod species.

Below, two predictive maps are shown as examples with relative RIO values for *T. conifera* (Figure 3) showing the highest ROC value and an Ensemble map for a predatory copepod *Paraeuchaeta exigua* (Figure 4).

In Figure 3, the presence of this copepod has been analyzed up to the maximum sampled depth (750 m), that is, the water column from the epipelagic layer to the batipelagic layer has been studied using the TreeNet algorithm. It can be noted that the *T. conifera* is originally present in some coastal stations. For habitat suitability, it can be noted that the RIO index has medium-low values over the entire study area but presents high values in the area in front of the Ross Ice Shelf, in the Terra Nova Bay zone, and near the coast.

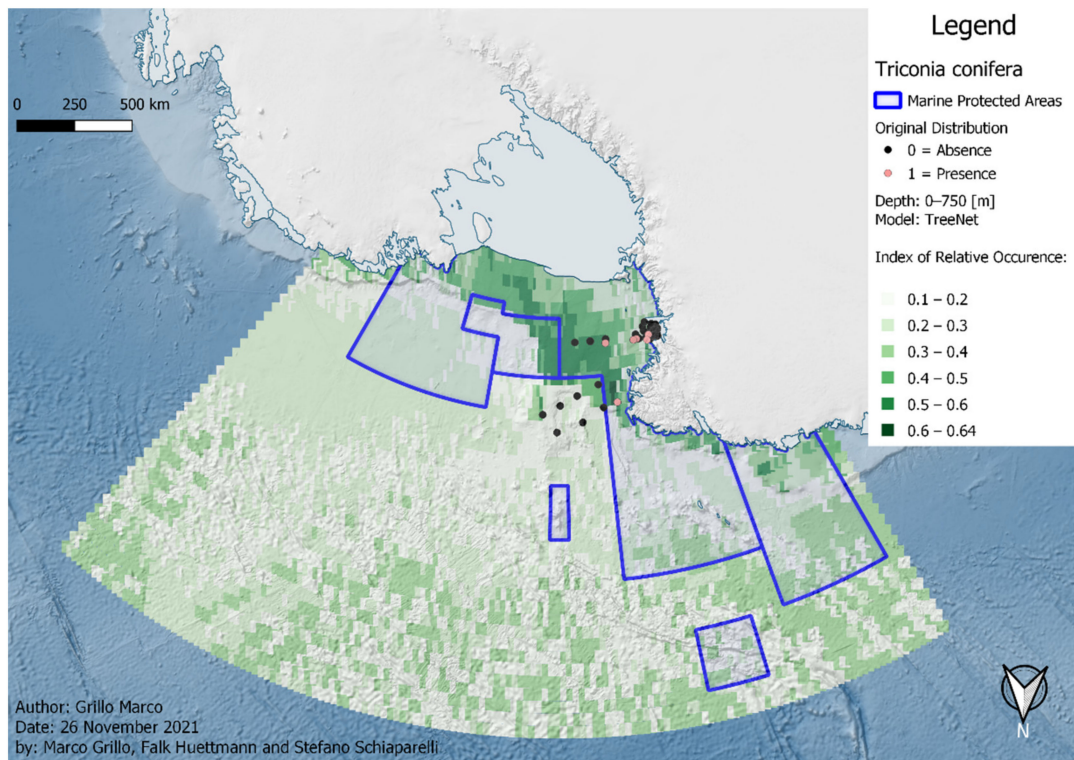


Figure 3. Presence/absence points of raw survey location shown over a predicted lattice grid distribution using the TreeNet algorithm for the depth class 0–750 m of the copepod *Triconia conifera*. For details, see legend.

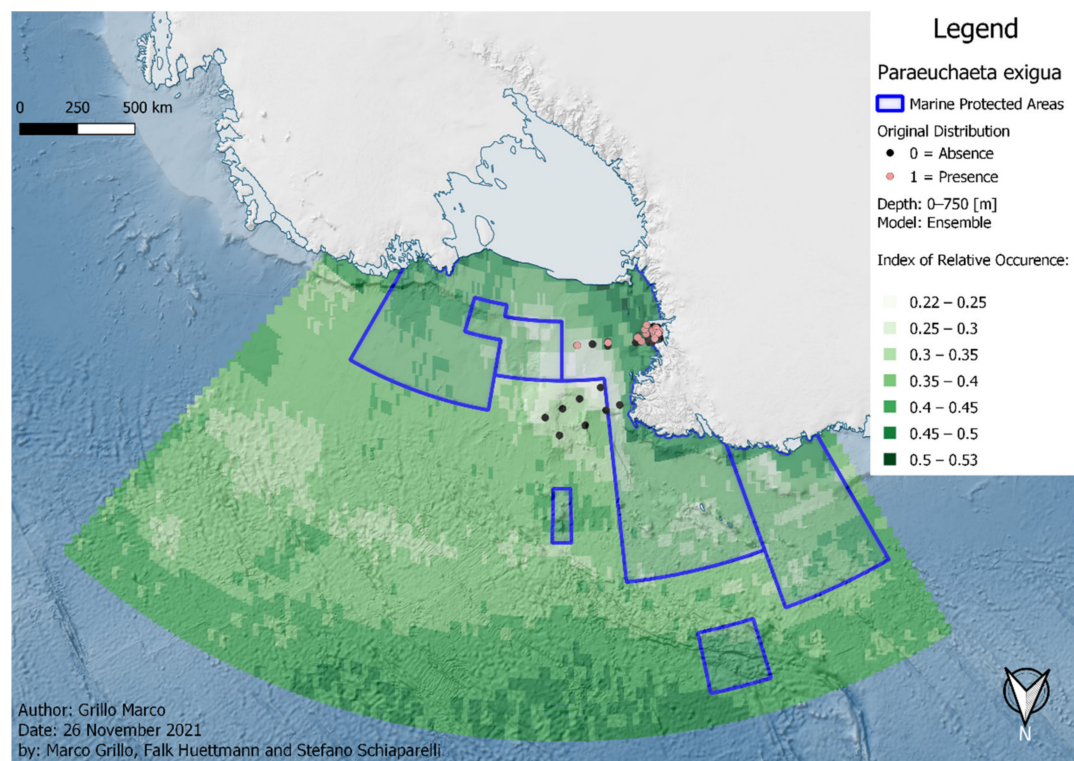


Figure 4. Presence/absence points of raw survey location shown over a predicted lattice grid distribution using the Ensemble algorithm for the depth class 0–750 m of the copepod *Paraeuchaeta exigua* (Wolfenden, 1911). For details, see legend.

This cyclopoid has high RIO values in the general protection zones near the Ross Ice Shelf and medium-low values in the special research zone, Krill research zone, and sub-Antarctic general protection zones.

In Figure 4, we can see the distribution predicted with the Ensemble method of the copepod *Paraeuchaeta exigua*, analyzing the 0–750 m water layer. The original distribution is mainly concentrated in the Terra Nova Bay area and two more pelagic stations. The predicted distribution shows the mean RIO values throughout the Ross Sea area. High values were found in the neritic province, in sub-Antarctic areas, and along the coast. The lowest values can be found in the Pennell Bank area. Furthermore, in all marine protected areas, it can be seen that the RIO index has medium values.

4. Discussion

The Ross Sea, one of the main basins of the Southern Ocean, encompasses several marine protected areas, which were established to conserve marine biodiversity, ecological structure, and all the habitats present within it [57]. In 2017, the whole area was declared the “Ross Sea region Marine Protected Area” (RSRMPA) [58]. It is one of the largest MPAs and the wildest and most remote. It is important for mankind and global well-being as it steers and indicates many oceanic and atmospheric processes on a wider, sometimes global, scale.

Thus, in this area, it is necessary to define the present and future conservation actions based on sound species distributional data in the best possible research framework that is transparent and repeatable. In this work, we related the environmental descriptors obtained in the Ross Sea Area by Polar Macroscopic Layers (present in Quantarctica) and the presence/absence of copepod species sampled during Antarctic Expeditions undertaken in the 1980s to the middle of the 1990s. These “legacy data” enabled obtaining, for the first time, a 3D representation (i.e., with horizontal and vertical distributions) of species distribution models for twenty-six Antarctic copepods. This effort was achieved thanks to the availability of zooplankton samples obtained through an Eznet-BIONESS multinet, a sampler that allows collecting samples at different depths of the water column all shared via GBIF.org online.

Compared to CPR, which only samples the surface layer, the Eznet-BIONESS multinet has the ability to simultaneously sample multiple depth classes, in this way offering a unique view of occurrences of copepod species through the whole water column. Thanks to this unique opportunity, we were able to produce an SDM relative to *Metridia gerlachei*, a very abundant Ross Sea calanoid, whose habitat suitability has never been studied before. The same was possible for other less common species, which were also modeled for the first time ever.

Knowing the potential distribution of these organisms is important due to the ecological key role played by copepods in the water column, where they result in being the most abundant component of the Antarctic mesozooplankton fraction in terms of biomass [26,59–61]. They represent the link between microzooplankton (i.e., bacterioplankton, protozooplankton, and phytoplankton) and secondary consumers [11]. The latter is important for ecological as well as economic reasons. Gaining a better understanding of the geographic distribution of copepods and their sensitivity to environmental descriptors is thus of particular importance to studying their potential geographic distribution and, possibly, predicting their influence on higher trophic levels.

This process, however, is still hampered by our limited understanding of single species ecologies, which are also greatly differentiated as a consequence of adaptation to different pelagic habitats. The definition of a trophic niche was thus also considered in the development of the SDMs. It is described in Hutchinson [62] as a “hypervolume with n-dimensions”, where the latter is characterized by environmental descriptors, which allow an organism to persist in a particular habitat. This definition allows a quasi-quantitative analysis to determine the trophic niches occupied by a species through computational analyses (e.g., [63,64]).

However, most studies of species distribution models in Antarctica have been conducted for secondary consumers, top predators, and species of commercial interest (e.g., [52,65,66]). Thus far, very few works have been carried out on organisms that occupy the lowest trophic levels of marine food networks, despite their acknowledged paramount ecological role.

The first species distribution models of Antarctic copepods were carried out by Pinkerton [67] analyzing the surface distribution of the cyclopoid *Oithona similis* based on Continuous Plankton Recorder data (CPR). In that study [67], predictions from the Boosted Regression Trees models with R software (*gbm* library) for *Oithona similis* presence distribution data were performed. The distribution modeled by us showed hotspots of occurrence (presence data) in the subantarctic region and an opposite situation, i.e., with lower occurrences, in the Ross Sea shelf areas. This is in complete accordance with the spatial models predicted by Pinkerton [67] where *Oithona similis* has a high probability of presence in the circumpolar belt between 54° and 64°S, then gradually decreasing towards the north and even more towards the south.

Our data, for this unique copepod species previously modeled, are concordant with Pinkerton's [67] predictions. In fact, by comparing the results obtained in the 0–10 m layer (Figure S71, Supplementary File S1) and Figure 11 in Pinkerton [67], it can be seen that the copepod in question has a very similar distribution. Our Ensemble, TreeNet, and RandomForest models data showed predicted values slightly lower (Supplementary File S2) than Pinkerton's data. Within our models, Ensemble and TreeNet have lower values compared to RandomForest.

As can be seen in Figure 5, observations with 100 sample sizes have generally good accuracy. This is mainly given by the biology and ecology of the copepod species and how they are distributed three-dimensionally in the water column.

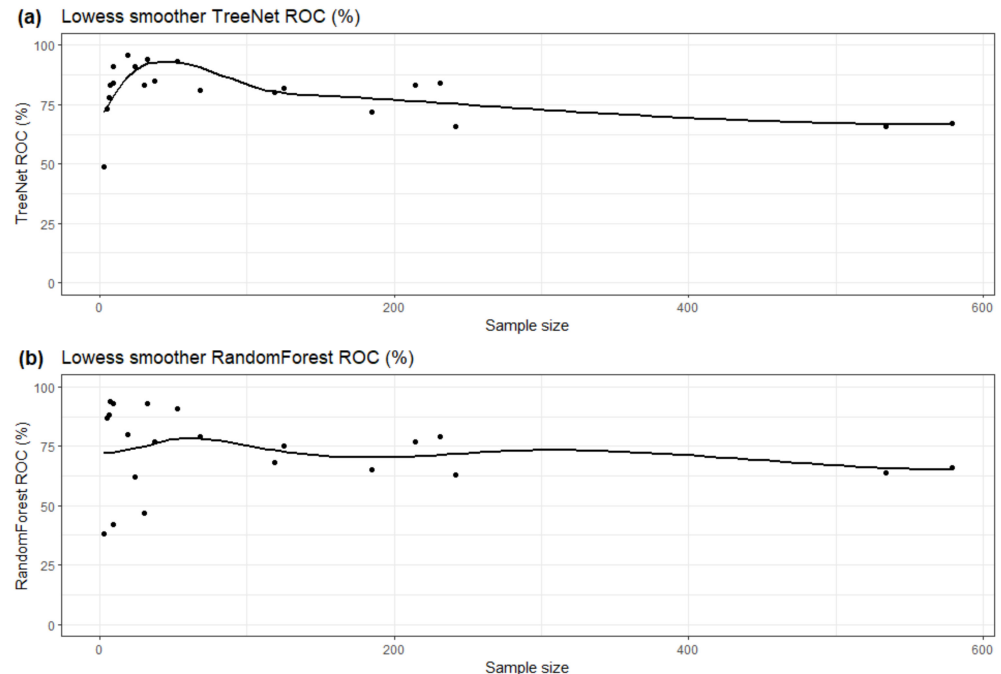


Figure 5. Evaluation of the quality of the TreeNet (a) and RandomForest (b) models underlying the Sample size and relative ROC values.

In this paper, we went further and modeled the distribution of *O. similis* for the whole 0–750 m layer (Figures S68–S70, Supplementary File S1). This showed that in the RandomForest and Ensemble models, this copepod assumes average presence values over the entire Ross Sea area, especially in the coastal areas and the oceanic province, whereas,

in the TreeNet model, the presence values are average only in the coastal areas and tend to decrease when moving north.

This was conducted for all the other considered species.

For example, *M. gerlachei*—the most abundant calanoid in the Ross Sea pelagic ecosystems [68]—represents an important reference baseline to also model higher trophic levels.

Our data show that *M. gerlachei* was present in all coastal stations analyzed. As Figures S54–S57 (Supplementary File S1) show, *M. gerlachei* is present in the Ross Sea area, Marine Protected Areas, and throughout the analyzed water column (0–750 m). This species has hotspots of occurrence values in neritic provinces, coastal habitats, subantarctic areas, and the Pinnacled Bank area.

In fact, *M. gerlachei* is a copepod targeted by *Pleuragramma antarctica* (Boulenger, 1902), a very abundant pelagic nototheniid in the High-Antarctic Zone that plays a very important role in marine food webs [69]. In turn, *P. antarctica* is an important resource for Antarctic apex predators such as birds, seals, and whales [70] as well as for other nototheniids [71]. *M. gerlachei* represents up to 11.4% of the stomach contents of prey biomass *Granata* [72] of this nototheniid. Moreover, in this study, we highlight the 3D SDMs of other relevant copepod species provided such as *Oncaea conifera*, *Oithona similis*, *Paralabidocera antarctica*, *Stephos longipes*, and *Harpacticus furcifer*, copepods that are part of the diet of *P. antarctica* [72].

As can be seen from the attached maps in Supplementary File S1, most that feed on the organic material suspended in the water column (suspensory) copepods are present in areas characterized by high abundances of phytoplankton, organic matter, and nutrients such as upwelling areas, frontal areas, and polynyas. This is confirmed in our occurrence data, with only a slight shift in geographic occurrences. In more detail, i.e., by examining not only the general trophic groups but instead the single species ecology, several peculiarities can be highlighted. Single species distribution models per depth bin are reported in Supplementary File S1 (Figures S1–S133).

Our findings are manifold and present many new data, patterns, and predictions allowing more research and inferencing. The most important result of our study thus far likely relies on the fact that for all examined species, the modeled distributional hotspots, based on presence data, are already within the RSMMPA (i.e., zones titled RS-GPZi, RS-GPZii, RS-GPZiii, RS-SRZ, RS-KRZ) [58]. This likely means that the current limits of the RSMMPA allow for the protection of the lower levels of the trophic web, at least for the adult copepods, but likely also for previous life stages such as eggs, nauplii, and copepodites stages.

Our data and metadata are released in compliance with the FAIR (findability, accessibility, interoperability, and reusability) principles [73]. The production of three-dimensional predictive maps was possible thanks to the initial digitalization of “grey literature” data [25], here “reused” to produce 3D distributional maps. By applying the FAIR principle, distributional data acquired during these old PNRA Antarctic expeditions were thus recycled and reused, allowing a closer look. This greatly improves our understanding of pelagic copepod biodiversity and helps in increasing the accuracy of the selected models. These data will remain searchable, accessible, and reusable to the maximum extent possible [74] and represent a permanent window of the Ross Sea structure of copepod diversity in the 1980s and early 1990s.

In conclusion, future advances will work to develop abundance distribution models using ML and AI applications in an attempt to predict the Ross Sea standing crop in an even more quantitative fashion as a monitoring tool for this remote wilderness area of relevance for mankind. These future models will be useful to quantitatively identify the areas or hotspots of abundance located in the Ross Sea area and understand which environmental descriptors regulate this phenomenon.

Supplementary Materials: The following supporting information can be downloaded at: <https://www.mdpi.com/article/10.3390/d14050355/s1>, File S1: Maps. File S2: Predicted data. File S3: GIS predictor set and raster. File S4: Raw species presence_absence data with environmental descriptors. File S5: Details models.

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