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Earth System Science Data Discussions

Interactive comment on "Distribution of known macrozooplankton abundance and biomass in the global ocean" *by* R. Moriarty et al.

R. Moriarty et al.

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We would like to thank Anonymous Referee #1 for their understanding of this work and its application in global ocean modeling. Their thoughtful comments and careful reading of the manuscript, is fully appreciated.

General comments

Referee #1: I liked the effort done in this paper to compile data on macrozooplankton, a compartment often forgotten. We must keep in mind that macrozooplankton is collected with various kinds of nets, depth integration, tow types (oblique, vertical), seasons, years...bringing large sources of variability. It is a mess and the work done here has to be acknowledged. The other point we must keep in mind is that this compilation

is mainly done to help calibrate global models, thus we are looking for "the best we can" accurate world map of the average distribution of macrozooplankton. I hope this effort will push others to add their own data and improve the dataset as well as highlighting macrozooplankton in such models.

Referee #1:Yet, I have two general interrogations: 1) You mixed data from the rawKRILLbase and the COPEPOD datasets. The rawKRILLbase includes data on Euphausia superba and two salps whereas COPEPOD includes data on salps, doliolids, pyrosomes, ctenophores, cnidaria...(line 21 p192). When mapping the abundance there is a big shift between the Southern Ocean and the rest of the world, the Southern Ocean (rawKRILLbase) being a few orders of magnitude less abundant (fig. 4). This un-natural shift doesn't seem to be mentioned and explained in the manuscript. If I understand well you mixed abundance of three species only on one side, and of the whole community on another side, didn't you? I think this should be stated and argued further in the manuscript. How much of the total abundance these three species represent?

Author Response: We agree this was not sufficiently explained. We have added the following clarification in Section 3.3.2 (Page 14, lines 374-383): "In Table 3b there is a difference of two orders of magnitude between the biomass values for 40 to 90°N and 40 to 90°S. This may be explained by differences in the type of data in the datasets associated with each of these regions. The rawKRILLBASE data, three species, is most of the data in the Southern Ocean while the COPEPOD data, representative of the entire macrozooplankton community, is found throughout the global ocean. The rawKRILLBASE data is composed of three species are the predominant macrozooplankton species in the Southern Ocean and can make up 90% of the biomass (Witek et al., 1985). Depending on temporal and spatial scales Euphausia superba and Salpa thompsoni/Ihlea racovitzai are estimated to account for between 30 and 90% of the biomass in the Southern Ocean. Both species have bloom capabilities and patchy distributions and relatively high biomass in the Southern Ocean."

Referee #1: 2) I don't understand why you used so few data points for the biomass.

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Biogeochemical models work in carbon (or nitrogen or...) units, so the biomass appears much more useful than the abundance. There is already a large variability in the dataset (different nets, depth...) and I think that using generic relations to convert to biomass will add only a minor source of variability compared to others. The dataset will be more valuable if it proposes a large coverage of biomass estimates (as for abundance).

Author Response: We realize how valuable a large coverage of biomass estimates would be and we agree that carbon values are much more useful than abundance values. There are no published generic relations for the conversion of macrozooplankton abundance to biomass. At the onset of this project we bulk converted abundance to biomass, using a generic relationship, our best estimation from all the data available to us, and the numbers were unrealistically high, as we show below. We used the database of conversion factors that were used to generate the biomass data (this data can be found as supplementary material in the Macrozooplankton abundance and biomass dataset) and calculated the median (x μg/individual, n=y) and mean (z μg/individual) conversion factors. We then converted the gridded abundance dataset from abundance to biomass. The results can be seen in Table 1 below, which also includes a more conservative estimate. We have not included this type of conversion in the analysis as we feel the conversion factors are too general, and the large deviation of the bulk conversions from the species specific conversions show the former would severely distort the results.

Table 1: Mass conversions and the resultant global annual average biomasses.

[please insert Table 1]

Groups such as the ICES Working Group on Zooplankton Ecology have been trying to assemble a comprehensive listing of conversions for years. A group of scientists, experts in the field, find this effort overwhelming, and the differences due to regions, seasons and life stage (length to body composition) make the equations hugely vari-

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able. These variations are important considerations and you can see from the figures presented below (Figures 1a-d & 2a-d) that, in this instance, region seems particularly important. A blanket global conversion, without a better conversion estimate, is not the best way to convert abundance to biomass. Even using what we thought was a conservative value, e.g. 1.8 mg C/ind (Figure 1b & 2b) we see quite high values in the northern hemisphere. Without valid conversion equations from abundance (number of macrozooplankton per sample) to biomass (mass of biomass to sample) there is a need for length frequency data, mass data and carbon data. In the majority of cases this data is not available for macrozooplankton species or the entire macrozooplankton size class or cohort of species.

[please insert Figure 1]

Figure 1: Frequency distributions of macrozooplankton biomass: (a) species-specific conversion of abundance to biomass, (b) conversion of abundance to biomass using a conservative carbon mass (1.8 mg C ind-1, see Table 1), (c) conversion of abundance to biomass using the median value (3 mg C ind-1) for carbon mass (see Table 1) and (d) conversion of abundance to biomass using the mean value (53 mg C ind-1) for carbon mass. Median and mean values for C ind-1 are calculated from body mass data (Hirst, 2003; Moriarty, 2009) and from and body mass conversion data (this dataset).

[please insert Figure 2]

Figure 2: Global distributions of macrozooplankton biomass (ug C l-1): species-specific abundance to biomass conversion coverage and associated 'blank' regions where conversion of data was not possible, (b) abundance to biomass conversion coverage using a conservative carbon mass (1.8 mg C ind-1, see Table 1), (c) abundance to biomass conversion coverage using the median value (3 mg C ind-1) for carbon mass (see Table 1) and (d) abundance to biomass conversion coverage using the mean value (53 mg C ind-1) for carbon mass. Median and mean values for C ind-1 are calculated from body mass data (Hirst, 2003; Moriarty, 2009) and from and body mass conversion data (this

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dataset).

We have added text to the manuscript summarizing the points made above (Section 3.2.2 Page 12, lines 318-332): “Carbon values are a much more useful measurement than abundance data, however there are no published generic relations for the conversion of macrozooplankton abundance to biomass. This type of conversion has not been included in the analysis as the conversion factors are too general, and the large deviation of the bulk conversions from the species-specific conversions show the former would severely distort the results. Efforts to assemble a comprehensive listing of conversions for macrozooplankton by groups such as the ICES Working Group on Zooplankton Ecology has been ongoing for years. A group of scientists, experts in the field, find this effort overwhelming, and the differences due to regions, seasons and life stage (length to body composition) make the equations hugely variable. A blanket global conversion, without a better conversion estimate, is not the best way to convert abundance to biomass. Without valid conversion equations from abundance (number of macrozooplankton per sample) to biomass (mass of biomass to sample) there is a need for length frequency data, mass data and carbon data. In the majority of cases this data is not available for macrozooplankton species or the entire macrozooplankton size class or cohort of species”.

Referee #1: I think the manuscript needs more argumentation on these two points that leave the reader feeling bewildered.

Author Response: In relation to the first point we have added test to Section 3.3.2 (Page 14, lines 374-383) to provide a better explanation of the shift between data in the Southern Ocean and the rest of the world. This explicitly states differences in the datasets as the reason for the major shift between regions in terms of biomass. In relation to the second point we have added a summary explanation to Section 3.2.2 (Page 12, lines 318-332) in order to provide more background on this issue. We hope that to have addressed both these points above and in the manuscript.

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Specific comments

2.1 Dataset Referee #1: The dataset was easily available and I was able to reproduce the figures shown in the manuscript and to make others (I have done this with Matlab R2011a without any problem). The depth binning is 0-10, 10-20, 20-30. . . or 0-10, 0-20, 0-30? The unzipped MarEDat20120216Macrozooplankton.nc file is big (1.4GB); it is strange because the zipped one is only 2.3Mb. When I extract all data from it, my *.mat (matlab) file is only 10Mb. Is it only on my computer (Win7, same problem when unzipping with both WinRAR and 7zip)? You should check your *.nc file. (The data I have are 4D 360x180x33x12 matrix for abundance, biomass, number of observations. . .there is a total of 14 data 4D matrix).

Author Response: We have added a Section 2.4 that explains about the file formats. We did not use the latest NetCDF version 4 for the gridded file, which is compressed by default, but which is not widely used yet. The unzipped gridded file is therefore 360 $\times$ 180 $\times$ 33 $\times$ 12 $\times$ 14 entries, which includes all the land and missing values in the ocean, and is indeed a rather large file.

Referee #1: I didn't find the original data points, only the gridded ones.

Author Response: Both gridded and the original datasets are available at http://doi.pangaea.de/10.1594/PANGAEA.777398. The original data points are in the five Excel sheets corresponding to the datasets that are documented in Section 2.1.

2.2 Other comments Referee #1: Line12-15, p192: you didn't follow the advice of the data owner, could you explain your choice?

Author Response: The data owners requested that we use the raw data and not the standardized data. The data owners may want to publish the standardized data in the future. This sentence has been rewritten to make its intended meaning clearer. It now reads 'The krill and salp density data taken from the rawKRILLBASE are used in their raw form, i.e. the data owners have standardized these densities to a common

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sampling method but have stipulated that the standardized data may not be used as part of our study.'

Referee #1: Line25-27, p193: see above, I have difficulties to understand this choice.

Author Response: Please see response, in regard to bulk conversion from abundance to biomass, under General comments above.

Referee #1: Line20, p194: zero values of abundances could be transformed in log+1? Line9-10, p195: if they are real values why removing them? You used both the mean (which is sensitive to outliers) and the median, which is a robust statistics.

Author Response: I wish to respond to both comments immediately above together. As this manuscript is part of a wider effort to publish a global ocean plankton biomass database and an ESSD special issue - MAREDAT: Towards a world atlas of marine plankton functional types - the authors decided upon standardized statistical methods across all papers intended for the special issue. In both cases, transformation of the data and the exclusion of outliers, these actions were carried out across all datasets submitted to the special edition. All authors agreed that some form of outlier exclusion was necessary even if those outliers could be real. Chauvenet's criteria was used in order to retain as many data points as possible while still identifying extremely high biomass values. In all datasets only data at the high end of the biomass distribution was discarded therefore no special transformation was used to retain zero values. To clarify this point we have changed "outliers" to "high outliers" in the first sentence of Section 2.3

Referee #1: Line12-14, p196: Do you have a reference for this? I'm a little bit surprised there is a decline in macrozooplankton sampling activity.

Author Response: We have added "(Fig. 2b)" as a reference for this statement. This result is surprising but there could be any number of reasons for this, some of which I have mentioned in the manuscript (Sections 3.2.1 and 3.2.2).

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Referee #1: Line9-10, p198: the general trend is high biomass in the tropics...you have very few biomass data from 30S to 60N, so can you really say this?

Author Response: I have deleted this sentence and a similar sentence from the abstract (Page 2, Line 19-20)

References. Hirst, A. G., Roff, J. C., and Lampitt, R. S.: A synthesis of growth rates in marine epipelagic invertebrate zooplankton, Advances in Marine Biology, 44, 1-142, 2003.

Moriarty, R.: Respiration rates in epipelagic macrozooplankton: a dataset, PANGAEA, 2009.

Witek, Z., Kittel, W., Czykieta, H., Zmijewska, M. I., and Presler, E.: Macrozooplankton in the southern Drake Passage and in the Bransfield Strait Antarctica during BIOMASS-SIBEX Dec. 1983-Jan. 1984, Polish Polar Research, 6, 95-116, 1985.

Interactive comment on Earth Syst. Sci. Data Discuss., 5, 187, 2012.

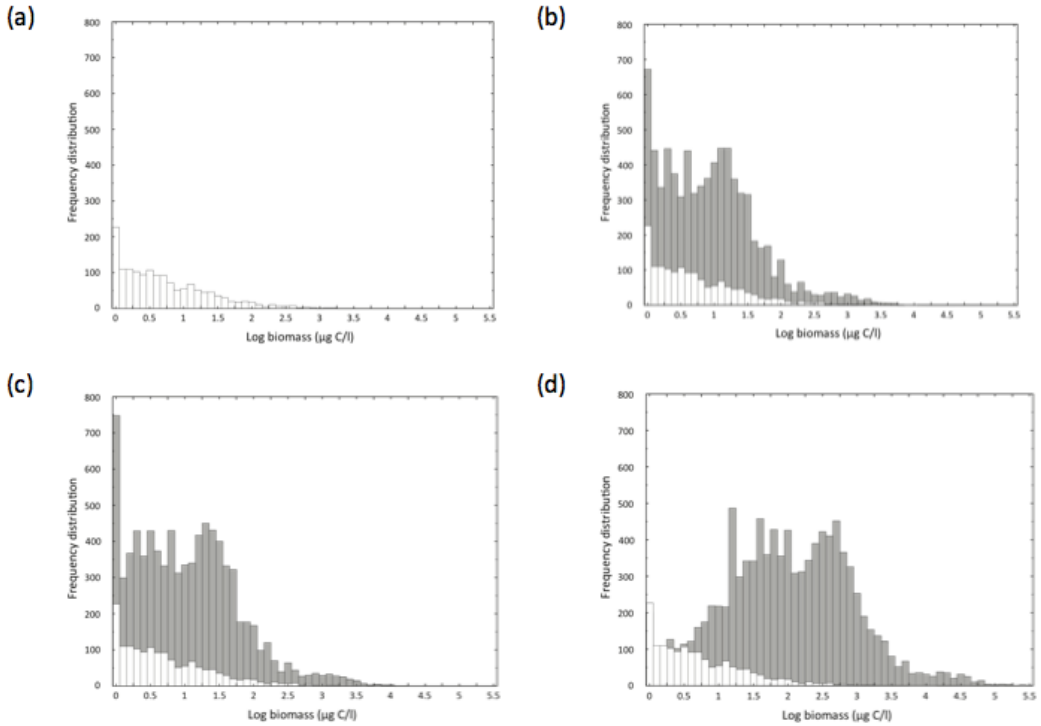

Fig. 1. Figure 1:Frequency distributions of macrozooplankton biomass (see text for full caption).

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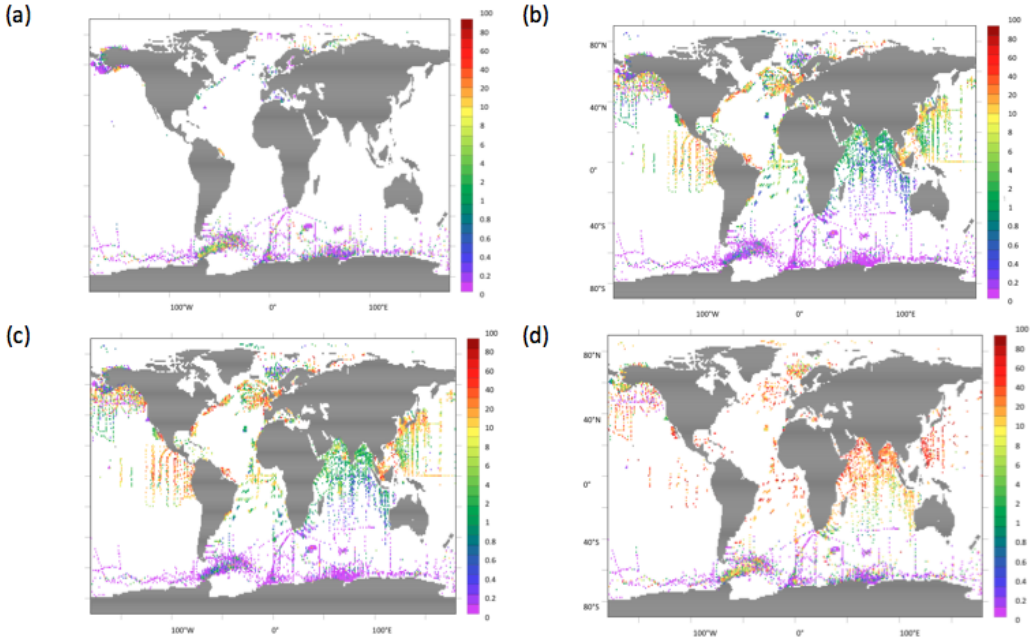

Fig. 2. Figure 2: Global distributions of macrozooplankton biomass (ug C l-1) (see text for full caption).

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			%	ug	Global annual average biomass (ug C l^{-1})	
Species specific carbon mass – as presented in the manuscript						
					Mean	8.4
					Median	0.15
					Stdev.	63.4
Conservative carbon mass						
	Wet	% of wm	100	200000	Mean	32.4
	Dry	% of wm	3	6000	Median	1.1
	Carbon	% of dm	30	1800	Stdev.	216
	# ind l^{-1}	multiplied by		1800 ug C ind^{-1}		
Median carbon mass						
	Carbon				Mean	54
	# ind l^{-1}	multiplied by		3000 ug C ind^{-1}	Median	1.8
					Stdev.	360
Mean carbon mass						
	Carbon				Mean	954
	# ind l^{-1}	multiplied by		53000 ug C ind^{-1}	Median	31.8
					Stdev.	6360

Note: wm is wet mass, dm is dry mass, cm is carbon mass and Stdev. is standard deviation.

Fig. 3. Table 1: Mass conversions and the resultant global annual average biomasses.

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