

## Referee 1

Many thanks for considering our manuscript for publication in Biogeosciences. The review helped a lot to improve our first version, and we hope that this revised version of the manuscript now fulfils the demands for publication.

We thank the reviewer for pointing out that the novelty of our work was not illustrated clear enough.

We corrected various sections throughout the manuscript as explained below:

### GENERAL COMMENTS & KEY CONCERNS:

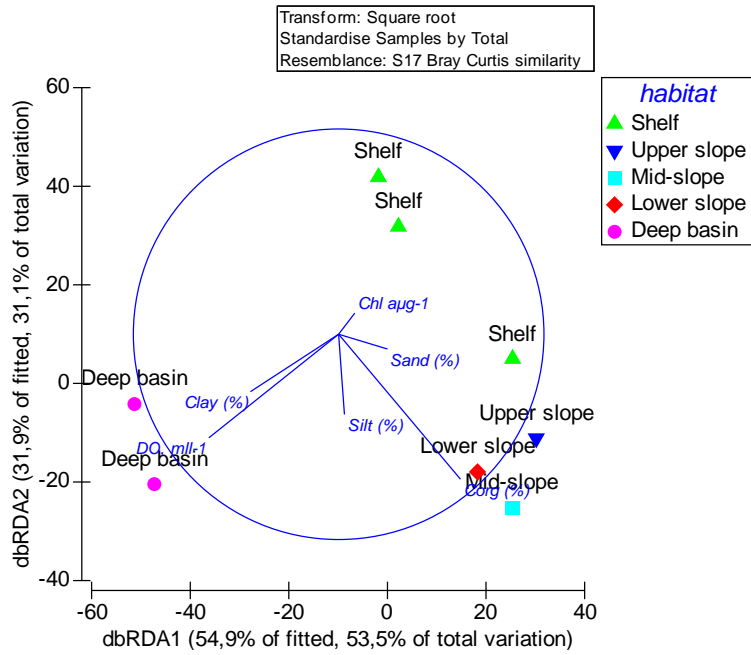
Comments: Whilst the strategy of the analyses has been explained, I have some questions regarding the tests that have been performed. There seems to be some redundancy (I have explained this in my in-text comments) and the BEST/BIOENV/DistLM analyses could be simplified I think. That being said, the authors have performed a substantial and deep-community analysis using the latest statistical procedures which is laudable

Reply: The detailed method explained clearly in methods however prior to DistLM.

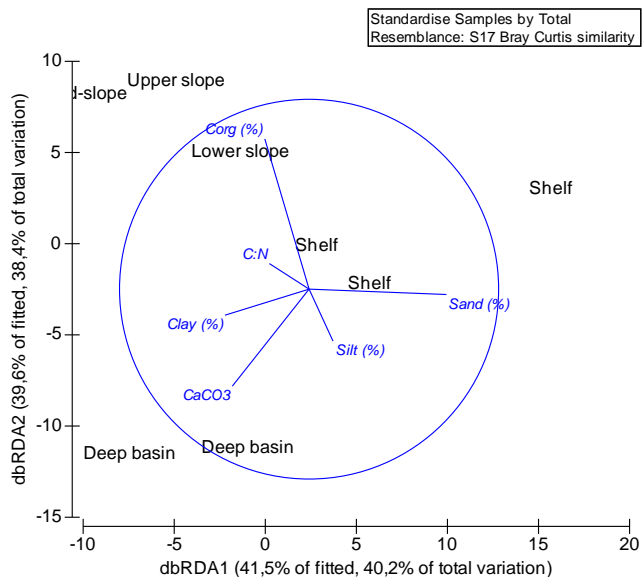
Analysis of collinearity was tested using draftsman plot and the associated standard product moment correlation coefficient between all pairs of variables and those with correlations ( $r^2$ ) > 0.9 were omitted from the model. For skewness natural logarithm transformation was applied to the response variable until assumptions were met by the best model.

The relationships of taxonomic and functional traits with environmental variables were examined by mean of the BIOENV procedure (Clarke and Ainsworth, 1993), which calculates rank correlations between a similarity matrix derived from biological data and matrices derived from the environmental variables, thereby defining a set of variables that 'best explain' the biotic structure.

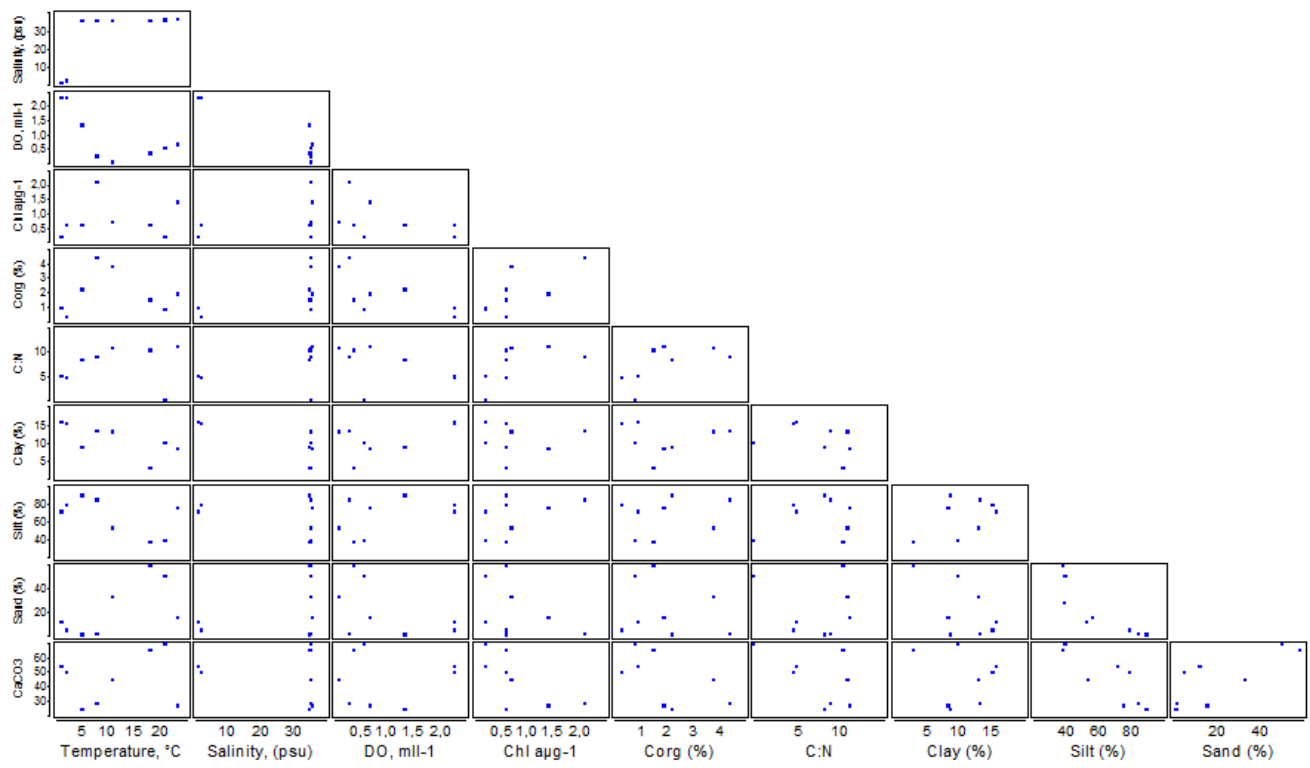
RELATE and stepwise distance-based linear model permutation test (DistLM, McArdle and Anderson, 2001) was performed to identify which set of environmental variables predict the multivariate variation to nematode species assemblages. The adjusted  $R^2$  was used as a selection criterion to enable the fitting of the best explanatory environmental variables in the model. Euclidean distance was used as resemblance measure in DISTLM procedures. Results were visualized with a distance-based redundancy analysis (dbRDA) (Anderson et al., 2008). Moreover the marginal test table and draftsman plot is added as supplementary data.



dbRDA based on taxonomic data



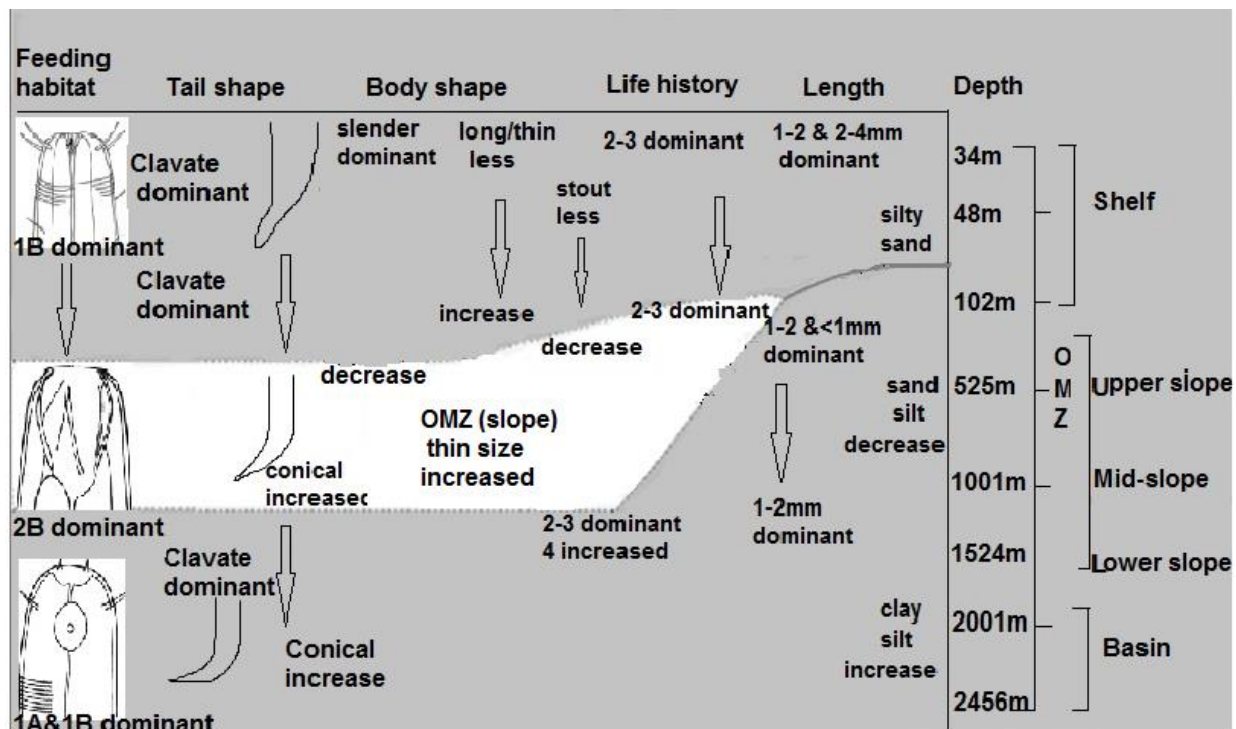
dbRDA based on taxonomic data



Draftsman plots

Comment: The schematic figure that is the real product of the manuscript does not get enough attention in my opinion. Many of the findings make their way into the figure but with little discussion. This scheme could attract quite a bit of attention, but is not as well presented as it could/should. The authors could dedicate more text to the reasoning behind it, what it tells us, and what the more general implications of it are. I would also work on how it looks at the moment, has much more potential to be an important figure in meiofauna OMZ and deep-sea ecology

Reply: Yes we agreed with the suggestion and it is improved accordingly. The new figure is prepared with well resolution and clear view. More text related to that added in the discussion and methodology. The schematic figure gives the whole summary of the pattern about the nematode community structure in the continental margin. This idea explains everything about the functional traits pattern and how they behave according to the different zones. The figure is given down under;



Schematic model

Comment: One last general comment I have is that the authors should come up with some clear hypothesis and questions from the start, which they then could answer in a logical sequence in the results and discussion. At the moment, it seems like the MS is a very descriptive piece of work and reads as if the authors have unleashed a suite

Reply: we agree with the reviewer about the questions and hypothesis however

Our study is from the Arabian Sea which is not studied in terms of nematode community. The first question which we posed may be general but important to answer from the Indian continental margin. The heterogeneity gradient which includes shelf, slope and basin acquire different conditions therefore it's important to know their impact on nematode community both structurally and functionally. The question is more specific and clearly adds the value to our study. However it is modified according to the reviewer's suggestion.

Other specific comments are discussed in the section below.

### Specific comments

Comment: this question is very general and has been answered in literature. The authors could specify with explaining what kind of heterogeneity they mean and were... specific gradient, location

Reply: The question is specific to Indian western continental margin however it is modified

Does heterogeneous gradient like shelf, slope and deep basin of western Indian continental margin affect marine nematode community structurally and functionally?

Comment: Study area description

Reply: Information related to the area characteristics,

Like; water masses, wind direction, monsoon seasons, upwelling and OMZ thickness, area.

Comment: Was there no upper sieve used (1mm, 500um, or 300um even?)

Reply: Samples were washed over a 300- $\mu$ m mesh and then sieved on a 32- $\mu$ m mesh and the retained meiofauna fractions then elutriated by the centrifugation-flotation technique. The following information is added to the method section.

Comment: Please make note that in Bongers and Bongers 1998 (Functional diversity of nematodes) monhysterids have been classified as having a c-p score 2. Often this is overlooked and they are regularly given score 1 as per Bongers 1990 and Bongers et al 1001.

Reply: We would like to thank reviewer for that however we have got two species belonging to Monhysteridea and they were assigned to the c-p 2 class (“general opportunists”) as advised by Bongers et al. (1995) and latter mentioned by Pape et al. (2013) and as such there were no nematodes belonging to c-p class 1 (“enrichment opportunists”).

Comment: Is there a reference/basis for this methodology; why are these values the ones to distinguish between functional groups of individuals?

Reply: Nematode specimens were measured and assigned to four length groups (< 1 mm, 1–2 mm, 2–4 mm, > 4 mm) and three shape categories (stout with a length–width ratio < 18, slender with a length–width ratio of 18–72 and long/thin with a length–width ratio > 72). The same procedure is given in literature (Schratzberger et al. 2007, Marine Environmental Research) however they deduced the length data from literature while we measure every adult specimen.

Comment: have the authors used relative abundance and presence-absence data - what is the logic behind it? And, which resemblance measure was used on the presence-absence data. The authors say similarity measure but in PRIMER there are 19 similarity measures available. This information should be included here.

Reply: When it comes to ecological abundance data collected at different sampling locations, the Bray-Curtis dissimilarity is one of the most well-known ways of quantifying the difference between samples. This measure appears to be very reasonable way of achieving this goal but it does not satisfy as it is based on the relative abundance. Since it is likely that many of the species will be singletons and hence the chances of a species being absent are quite high. It is extremely useful in situations where sampling has not been intensive and when overall similarity, independent of species numeric abundances, is all that is needed to compare locations. We sampled with box corer and therefore the chance of losing fauna is higher hence it is important to carry both type of measures (Sørensen's similarity index based on presence-absence)

Comment: Also when PCOs are compared? It is difficult to compare different MDS because they have no scale, one can infinitely rotate the scaleless axes and data to come to a different image... spacing between samples is based on resemblance distances... and these are heavily reliant on the resemblance measure, unless you decide to rank the data.

Reply: As per the suggestion the PCOs based on functional traits and taxonomic data were compared and the results were similar as the MDS had produced. However this phrase was deleted as it was not required as suggested by another referee. The PCOs based on taxonomic and functional data are given down under;

Comment: It would be interesting to discuss species level knowledge in terms of life styles and tolerances (this information may be available for some species) in the light of depth-gradient, zone differences, OMZ and their environmental characteristics more specifically

Reply: As it is known that we don't have much information available on nematode species life style and tolerance however whatever the info was available it is discussed in more detail now. Moreover there are some speculations on species behavior but it's difficult to relate them with OMZ life style until it is not observed in laboratory. However much of the information is discussed and compared specially with zone gradient and OMZ influence.

Comment: If an upper sieve was used, could this not have had as effect that the larger nematodes (mostly 2B) were excluded from any community analysis? Potentially the real community may have a higher percentage of larger/predatory/scavenging nematodes

Reply: We used 500 micron sieve and it is ideal way in order to retain the real fraction of meiofauna otherwise the counts of macro size nematode will be more. The length of marine nematodes is usually around 1-3 mm but sizes over 10 mm may be attained. The smallest adult nematodes (*Greeffiella Cobb, 1922*, a desmoscolecid) are shorter than 0.2 mm. Gambi et al. (2000) used 1000 mm mesh and a 20-mm mesh to retain the smallest organisms. However the predator nematodes were very less in the basin and they have increased in OMZ probably related to the availability of freshly dead organisms because they are capable of ingesting other animals.

Comment: For the deep sea, there is very little evidence of nematode-bacteria symbiosis, but they should probably be mentioned here... cf. Hope 1977 (gutless nematodes in the deep sea), Ingels et al 2011 (Plos ONE), Van Gaever et al 2006 (stilbonematids with ectosymbionts from the Darwin mounds), Bernhard et al 2000 (desmodorids with ectosymbionts from Californian deep sea) and Tchesunov et al (stilbonematids (ectosymbionts) and siphonolaimids (endosymbionts) in the deep Atlantic canyons), the latter gives some ecological insights into what advantages the symbioses could bring

Reply: A new modified paragraph is added on physiological and behavioural mechanisms (e.g., symbiosis with bacteria, which we also observed, and migration to “oxygen islands,” sensu Reise and Ax (1979) and Wetzel et al. (1995).

As suggested by the reviewer many sentences were rephrased and improved accordingly.