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Interactive comment on “Benthic communities in the deep Mediterranean Sea: exploring microbial and meiofaunal patterns in slope and basin ecosystems” by K. Sevastou et al.

Anonymous Referee #1

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For Methods: It was not indicated in Methods, how many samples from each expedition / habitat / depth range were examined. Is it possible, that distinctions in dissimilarities (and number of taxa) between habitats, depth ranges, etc. were caused by different number of examined animals or samples (smaller number is supposed to lead to higher dissimilarity within an area)? Did you try to examine correlation between distance between samples (within area, depth range, habitat) and dissimilarity values within these ranges? Can it be that some portion of dissimilarities is explained by this factor?

Table 2. I understand Table 2 not completely. What do overlapping lines mean?

Table 2 and Figure 3. You have depths less than 1500 m (even less than 500 m)

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in Basins. Unfortunately, I am not familiar with bathymetry of the Mediterranean, but how can it be? Normally, depth of basins is more than 2000 m. May be, you mean some rises or seamounts, not basins? In this case, I believe, these habitats should be separated from basins.

Tables 4 and 5. I do not understand, to what applies signs “*” and “***” in this table? They stay in headings for rows, but not in some certain values of dissimilarity. How can I understand, which difference between dissimilarities was statistically significant?

Figures 4 and 5. Number of taxa / genera depends on number of samples or number of examined individuals. That is why, I believe, that it is not correct to use indicators “Number of taxa” and “Number of genera”. It seems to me, in this case, it would be better to use average values (for each area, depth range, habitat) of estimated number of taxa for samples of 200 individuals for nematodes and for some number of individuals for major taxa.

Interactive comment on Biogeosciences Discuss., 9, 17539, 2012.

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9, C7278–C7279, 2013

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