

Recommendation by the Subject Editor

Let me apologize for not getting feedback to you more promptly. This was due to different reasons. First, it has been extremely difficult to find two reviewers for this ms. Several reviewers declined to do it but I have been trying with patience until we got the two reviews discussed below. As it turned out, I believe the final reviewer's comments were useful. The second reason is due to me and my schedule, and not due to the Oikos editorial process.

We would like to thank both the subject editor and the reviewers for their in-depth, constructive comments. Reviews of this quality are worth waiting for. Line and page numbers in the replies refer to the copy of the document with track changed, which we submitted as "main text".

Your manuscript entitled "Interactions retain the co-phylogenetic matching that communities lost" has now been seen by 2 referees, whose comments are attached below. Both reviewers agree the paper present an interesting analysis to understand co-diversification between parasites and small mammals. Both mention that the paper is concise and goes to the point and the introduction is clear. Yet, there are several aspects that need to be substantially improved before we move forward this ms. Specifically, reviewers feel

that what the methods are actually doing needs to be explained more clearly (see comments about Figure 1 and several comments from both reviewers);

We agree with the reviewers. We have expanded the text, specifically from page 7 line 158 to page 7 line 172. We are confident that these additions will greatly clarify how *PACo* operates, and how it frames the interpretation of the results. We have also clarified the description of other methodological points, even if the phylogenetic analyses seemed to be the main source of strife for both reviewers (this includes notably page 7 line 174 to page 8 line 179)

authors have to clarify more which is the delineation of the different spatial scales. For example, as mentioned by one of the reviewers, how well matching at the local scale reflects matching at the regional scale rather than the absolute signal itself

We have done so both in the methods (see page 5) and during the discussion of the results (see page 8 line 182 to line 193). Note that this does not affect our results.

the interpretation of the analysis need to be sharpened, otherwise the ms. is going to be quite difficult to understand for the Oikos reader.

We apologize for overestimating our own ability to describe a complex subject as concisely as possible. We have expanded on the discussion and implication of the results at several places (most notably on page

12, lines 274 to 290) in the “Results and Discussion” section, and hope that it will make for a better and clearer read for the novice and expert alike.

My major concern is that both reviewers mention explicitly problems with the clarity of the methods. For example one of the reviewers explicitly states “... The key finding (lines 221-223) sounds very interesting, but even after much re-reading, I don’t fully understand how it emerges from the analyses here.” Could authors make an effort to make the connection between main findings and methods more clear? Both reviewers make points to improve the clarity of the ms., from suggestions to draw cartoons to a more clear explanation of the PACo method and how the results would compare against a randomization test of a null model.

As mentioned in a previous responses, we have greatly expanded the description of the methods. We hope that the revised manuscript is sufficiently clear.

At this stage, I strongly recommend authors to explain better the methods used in this ms. and make a better connection between methods and the main results. This includes making some figures more clear and introducing in the ms. point by point all the reviewer’s suggestions. Should further work allow you to address these comments and criticisms by doing a major revision, we would be happy to look at a revised manuscript.

Reviewer 1

This manuscript uses phylogenetic network properties to assess the signal of host-parasite interactions across different spatial scales. I like the general approach that it may be clearer to interpret differences in network matching signal (e.g., how well matching at the local scale reflects matching at the regional scale), rather than the absolute signal itself. The manuscript overall is concise and to the point. In interpreting my comments, please keep in mind that this work is a bit outside my area of expertise, although I do work in other ways on phylogenetic methods and spatial species interactions.

Lines 44-48: This sounds like an important point, but I can’t understand it (though I admittedly haven’t read most of those references). What are these “constraints”?

We have clarified and expanded this paragraph (page 3 lines 51 to 60). Briefly, the additional level of constraint is the fact that species interactions need to have a phylogenetic structure not only in the tree of the species establishing them, but also in the tree of species receiving them; furthermore, both trees should have matching shapes.

Data, and line 141: Where did the rodent and flea phylogenies come from? What does “rendered ultrametric” entail? (Divergence time estimation is a huge and complex field...) The details of phylogeny estimation are probably irrelevant here, but it would be good to be reassured that well-supported trees are used.

We have clarified the data provenance and subsequent manipulation at page 4 line 97 and page 7 line 174 to page 8 line 179.

The explanation of continental/regional/local networks on page 5 is pretty clear, but a cartoon or simple figure could help. It might also be a good way to explain the expectations on lines 145-156, which I had more trouble following.

We have expanded the first paragraph of the results to describe the predictions in more detail (page 8 lines 182 to 192). We do hope that this makes the cartoon unnecessary, though we are not vehemently opposed to adding it should the reviewer or editor request it be added to the revised version of the manuscript.

I also had trouble grasping the PACo method (lines 130-142). It seems that this is the method all the analyses are based on, so explaining it clearly is essential for a reader to interpret the results. Again, a small network picture might be very helpful for explaining what this method does, what its properties are, and what it means for a result to be “significant.”

We have greatly expanded this section (see the entirety of page 7).

While reading all of the results, I kept wondering how they would compare against a randomization test of a null model. For example, if many fake local networks are generated randomly from regional networks, what uncertainties would be attached to each point in Figure 2? Or maybe this is how significance testing with PACo works (e.g., lines 162-163)?

We apologize for not making immediately clear that PACo does indeed rely on permutations to assess significance. This has been clarified at page 7 lines 158 to 165.

When interpreting the number of sites that exhibit various results (lines 162-163, 219, Fig 2), how should spatial autocorrelation shape our interpretation? For example, do the results carry more weight if “significant” sites are not close to one another?

We understand where this comment comes from, and agree with the underlying idea. Unfortunately, different locations can have phylogenetic matching for a variety of reasons and we wish not to speculate too deeply on the diversification history of this system. What’s more, we are not confident that the current data allow to investigate this question to sufficient depth. For example, the site in the United Kingdom has *probably* been less connected to the rest of the system, but we cannot be certain this is the case. In addition, the sampling was also not spatially planned in a way to address this

question rigorously. In the end, we feel that a discussion of what spatial autocorrelation would mean would be too speculative for our liking. While we acknowledge that it is an interesting avenue for future study, we respectfully decline to address it here and hope that the reviewer is sympathetic to this decision.

Lines 183 and 185: That should be Fig 3AB, not Fig 2AB.

This is correct, and had been modified accordingly.

In Figure 1, it is hard to distinguish open from closed circles. Using different shapes would help.

We apologize for what the journal software did to our figures. The revised version has higher resolution files in a different format, which should make the differences between shapes clearer.

Lines 230-233: This made me wonder if the loss of signal at the smaller spatial scale could be due to lower sample size, i.e., fewer species present. Perhaps line 133 is saying that this isn't the case, but again, I don't really know what PACo is doing.

As we mention in the manuscript, the local and regional networks have the exact same species, so changes in richness has to be ruled out as an explanation for this scale transition. From the continental to regional scale, this is indeed possible, although Fig. 3B shows that this does not affect contribution at the interaction scale. However, it is true that the effective sample size in PACo is the number of interactions. For this reason, the reported signal was corrected to allow network comparison, and we now mention this explicitly on page 7 lines 166 to 172.

Lines 233-235: This feels like over-reaching. This work has assessed, at best, this particular host-parasite interaction, not "potential species interactions" as a whole.

Valid point. We have toned this sentence down.

Reviewer 2

Poisot and Stouffer present the results of a cross-scale analysis of co-diversification between parasites and small mammals. The introduction of this paper is clear and brings up some interesting issues at the interface of macro-evolution and ecology. However, I had a difficult time following the delineation of the different spatial scales, which is central to the study. This was made more difficult by the very low contrast between colors and the poor resolution of figure 1.

We apologize for the poor resolution of the figures in the version that was sent to the reviewers, and have uploaded higher resolution figures in the revision.

In addition, it wasn't clear to me how the analyses were interpreted. This was exacerbated by the lack of supplemental materials, which are referenced in the paper but were not online. Overall, I think the paper has some potentially interesting findings, but the definitions, analyses, and interpretation need more explicit description to make it easier to interpret the study within the broader context of literature on community assembly.

We have greatly expanded the definition of methods and how they should frame our reading of the results. We respectfully decline the invitation to re-frame this paper more explicitly within the context of community assembly, which does not seem germane to our narrative. This being said, we added a call for a future investigation of this explicit question at page 12 lines 286 to 290.

36-38: I had some difficulty understanding the 'cascade up' part of this sentence. I think you're trying to get a lack of predictability, but I'm a bit lost on the specifics.

The reviewer is indeed correct, and we have clarified this distinction in the revised version.

54: does

Changed.

71: matching

Changed.

106-114: I had difficulty understanding how regions were delineated and what the total number of regions were in the dataset. Ideally (from an ecological perspective), regions would correspond to distinct environmental areas with little movement between areas. The definition used here seems to be largely separate from an ecological definition of a region.

We have sought to clarify this part in the revised manuscript (see notably page 8 lines 182 to 193). Though we agree that definition put forth by the reviewer is correct in some context, it does not apply to the phenomena that we are aiming to quantify because it seems to define regions as parts of the landscape with a common environment, and not as an admittedly more abstract scale of observation and interpretation of ecological processes. As such, we feel that our use of continental/regional/local is more appropriate and accurate, and have therefore opted to keep the wording as it is.

146-148: Since the interaction described here is an antagonistic one I'm not sure how community assembly would favor co-occurrence. Where does the selection

come in? If it's just that specialist parasites can only occur on the suitable host I would refer to that as environmental filtering.

Parasites fundamentally need hosts to survive, so we expect a positive association within a pair. We have clarified this notion in the text (page 8 lines 184 to 186), and also removed the word selection, which can be problematic if interpreted strictly as natural selection. Though this was not the case here, we thank the reviewer for pointing out this possible point of confusion.

148 on the contrary?

Corrected.

160: The terminology 'ecological mechanisms' is confusing in this context. Wouldn't a species interaction (like parasite and host) qualify as an ecological mechanism? Perhaps abiotic variance or something related to community assembly would be a better term to differentiate between historical processes and factors that influence local assembly.

Thank you again for highlight this potential ambiguity. To better highlight what we meant, we have modified the text (page 9 line 206) to clarify that we are discussing mechanisms of filtering at this point. The reviewer will notice that this does indeed include abiotic variance.

162-166: It's not clear to me how these results are to be taken. What percentage would have to show matching to demonstrate that local interactions trump co-evolution at local or regional scales? The hypotheses for this paper are explicit, which is great, but the cutoffs on how to interpret the data are not described. Are the differences in phylogenetic matching between scales local and regional scales 'significantly different' (both biologically and statistically)?

This is a problem for most methods of co-phylogenetic matching, in that the meaning of absolute values of the output is not easy to interpret biologically. That being said, the fact that the amount of co-phylogenetic signal can be doubled when moving from the local to the regional network (Fig. 3A) is evidence of biological relevance. We have attempted to make the logic of this point easier to follow in the revised manuscript (page 12 lines 283 to 285).

173-174: I think there is a word missing here

Corrected.

181: I think this needs addition explanation on the mechanism vs. measure front.

We would be willing to do so should the reviewer clarify what was the specific issue in this sentence.

196: partners

Corrected.

207-210: Is this result significant (statistically)?

Yes, very strongly so. We now state this explicitly in the manuscript to avoid future readers asking the same question.

Fig. 1: The colors do not provide good contrast. It is not really possible to see patterns because of the poor color choices. Also the quality of this image is not good.

We have re-uploaded high-resolution versions of the figures. Unfortunately, some to all of the decrease in image quality is related to the journal software for creating the PDF for review.