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Interactive comment on “Metabolic tradeoffs and heterogeneity in microbial responses to temperature determine the fate of litter carbon in a warmer world” *by* Grace Pold et al.

Anonymous Referee #3

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This modeling experiment explored the implications of inter-taxon variability in CUE to emergent community CUE, taxonomic diversity, microbial biomass, and litter decay. Although framed within a climate change context, the work is relevant within any temperature-response system.

Overall, the work is interesting and timely but results and conclusions were sometimes overstated. Simulations are not the same as observations and at best provide possibilities when all underlying assumptions are accepted as adequate to the goals of the project.

Abstract: the next-to-last sentence was an important summary of the work, but it was inverted and complex to unpack. Consider rewording and maybe dividing into two sentences.

The 2nd paragraph of the introduction was a good synopsis of the state-of-art for estimating CUE and logical argument for a more flexible approach.

The 3rd paragraph of the introduction makes a case for taxonomic variation in extracellular enzyme production with temperature that may affect growth efficiency, but it takes a couple of reads to understand this point. Consider revising to clarify. Also, the final sentence links rapid growth to more enzyme production, which seems counter-intuitive given that increased costs associated with producing more enzymes reroute resources from growth. This point needs more support.

The rationale for the third of the selected suite of simulations isn't clear. Is there some reason why bacteria and fungi might have opposite responses to temperature? This adds complexity to the work that needs justification.

Did the last 5000 of 6000 iterations approximate steady-state?

How many of the outputs were omitted due to unrealistically high litter accumulation? Was there any obvious reasons why this happened, such as too little biomass or constrained enzyme production? This might be an interesting result.

Line 114: what is "biomass-weighted CUE?

Why were richness and diversity calculated on different sets of data? they cannot be compared for insights to evenness, for example on line 138.

Line 135: I didn't understand the statement. Was the dampening effect a result of extending the microscale model across a macroscale environment? The next line suggests not but refers to the current study instead of the citation.

Line 138: minor issueâĂŤMBC is listed as 0.15 in text but 0.16 in table 2. Richness and diversity were not calculated on the same data, so this comparison is questionable.

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Lines 140-144: Although the explanation for these patterns is logical, cause-and-effect relationships are problematic given the complexity of this model, non-linear relationships among variables, and variations in drivers.

Line 162: minor issueâĂŤis the word in parentheses “positive”?

Figure 1 wasn’t easy to understand, especially the dots. Were they output or illustrative of some specific information? Didn’t figures 1G and 1H contrast fungi and bacteria? The revisions were better, but still confusing.

Lines 182-4: The responses of kinetic parameters to temperature aren’t consistent among the available studies, and most studies report only apparent activities. So, this statement is more speculative than it seems.

Paragraph around line 190: Maybe I missed it but some of this information would help the reader better understand the purpose of some of the selected simulation treatments if provided earlier in the modeling description.

Line 224-5: This sentence seems to conflate competition with CUE and enzyme costs, but this idea seems like it would be limited to differential responses of taxa rather than a generic response of all taxa to temperature. Right? In any case, the results of DEMENT are not necessarily proof of concept for the real world. Line 234: simulations show the results of a possible synergy within a modeling context, only.

Lines 246-9: Again, why were these scenarios chosen?

Line 260: An alternative sensitivity analysis targeting individual model characteristics defining differences between fungi and bacteria would have been appropriate, nor would it take thousands of simulations to explore.

Line 267-8: This would be a good place to remind readers of the differences in fungi and bacteria that might explain this result.

Line 290: Fitting between a range of -48 to +178% doesn’t seem impressive, particu-

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larly given some of the omissions. What about the omitted simulations?

Line 291-3: This is the clearest, simple statement of the study results, and its buried here.

Lines 301-3: Although interesting, this statement only adds another level of confusion. This paragraph isn't needed.

Fig. 2. Were the temperature responses of soil bacteria isolates on the 4 different media indistinguishable? Ditto for the soil community responses.

Fig. 3. How did continuous and discrete compare to heterogeneous or homogeneous? The revisions helped.

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