

Interactive comment on “Comparing models of microbial-substrate interactions and their response to warming” by D. Sihi et al.

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General comments Sihi and co-authors present a nice study examining soil C dynamics projected by a series of simple models that make different assumptions about heterotrophic respiration and enzyme production. At a high level their findings could be interpreted as: 1) Forward Michaelis-Menten (M-M) models are crazy 2) Reverse Michaelis-Menten models look more reasonable and 3) Reverse models approximate first-order models so why bother with these silly microbial models that are a pain to parameterize and run?

I think this paper has more to offer, however, and my suggestions are intended to give the paper broader insight and appeal.

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The discussion around Model 4 (P 10885) may be the most interesting nuance of the paper, but I wonder if one has to invoke an optimized enzyme production model to get this same result? Could an empirical function between temperature and turnover accomplish the same goal? What if a larger (or temperature sensitive) K_m value was chosen (implying a lower affinity for substrates with increased temperatures)? More importantly, how do we quantify the “real” μ value that should be used for Model 4, if that’s the important value to differentiate between first order and microbial explicit models? What determines the cost of enzyme expenditures, and how may it be different in different soils.

There are really two underlying modeling frameworks being used, the forward and reverse M-M kinetics (currently models 1 & 3 respectively). Overlaying these basic structures the authors increase model complexity by adding maintenance respiration (Model 2), and enzyme production optimization (Model 4), but the order of these additions makes it unclear how maintenance respiration effects the reverse M-M model or how optimizing enzyme production may modify results from the forward model? I wonder if it makes more sense to restructure the results so we’re able to: A) Compare forward vs. reverse configuration (these could be models 1a and 2a); then B) Layer on maintenance respiration costs (models 1b & 2b); and finally, C) Add Enzyme production optimization (models 1c & 2c).

The model simulations nicely compare results of the models evaluated here, but given the choice to modify parameters to achieve the same initial and final values of CUE, M, and S (P 10869, L 21) it’s unclear how much the results in Fig 2 emerge because of the parameter values chosen vs. differences in model structure. Is there some a priori reason to expect these predefined responses of CUE, and substrate pools to warming? I realize that Fig. 4 and section 4.2 tries to address this concern, but it’s too derived to make much intuitive sense (beyond forward M-M models seem really wacky)- but that’s a point already made in Fig. 2 and elsewhere (Wang et al. 2014).

Would it be more illustrative to explore the parameter space that allows each model to

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hit the same initial conditions, but then potentially diverge in their responses to warming? This would provide more of a sensitivity analysis for the respective models, and illustrate potential issues with equifinality in the more complicated model (#4). Such considerations seem important, because I would assume that different parameterizations may project either an increase or decrease in microbial biomass, but currently only one set of parameters are used for each model (e.g. Model 3, discussed in the middle of page 10870).

Specific comments Introduction: There are so many clauses in the text that they become distracting to the main message being communicated. I understand this is highly editorial, but I'd recommend using more direct, precise language throughout the manuscript to directly convey the authors' intent.

Paragraph starting on P 10859, L 19-30: I'm not sure these features are unique to microbial models alone. (see Frey et al 2013 cited here, which uses CENTURY). Moreover, much of the partitioning of respiration fluxes could be done in first-order and microbial models. Separately, it's somewhat misleading to cite Hagerty et al. 2014, which is an observation based paper that doesn't really deal with models (the topic of the sentence here). Finally, it seems odd to cite Schimel 2013, which is a non-peer reviewed opinion / summary of Wieder et al. (2013).

The paragraphs at end of the Introduction and beginning of the Materials & Methods section are nearly identical and summarize the modifications to the basic "German model". I appreciate the clear organization, but wonder if some redundancy can be removed.

Methods: I really appreciate Figure 1, which nicely summarizes the model modifications being investigated here. Is it worth adding Fig. 1b that shows the first-order model (#5) used too? Alternatively, this could be described more completely in the text (is it just a two pool model with SOM and microbial biomass (that doesn't do anything?)

Model 3 is a reverse Michaelis-Menten models, which has been proposed and used

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in other microbial explicit models (e.g. Schimel & Wientraub 2003), as opposed to the forward configuration used by Allison et al 2010, on which the German model is built. References to models and the theory behind forward vs. reverse Michaelis-Menten models are likely relevant here.

Results: The 'knife edge' results are mentioned in both results and discussion, but I'm not really clear what this refers to? Is it obvious is any of the display items? If not, could it be- it's such a strongly visual phrase it seems like it should be obvious in a figure?

In Table 3 and results I'm not clear of the utility of the short times scale steady-state solution for M? Is this just to show that the forward models (#1 & 2) aren't stable & oscillate over short times scales (as evident in Fig 2b)? I'm also curious what causes the shift in the steady state equation for M in model 3 over longer times scales? It's also not clear what part of Table 3 is being reference in the results (P 10868, L 10-12), specifically what's independent of 'M', steady state S pools? This is generally true of other microbial explicit models (see Wang et al. 2014). I'd suggest dropping the shorter times scale M response to focus on the longer time scale dynamics, or spend time discussing both.

The authors never refer to Fig. 3 in the results, but I assume the first paragraph on P 10871 refers to these results?

I wonder if the lack of apparent changes of Q10 in the first order model (#5) are an artifact of the analysis done here, or the very simplified model structure being considered (see Koven et al. 2015).

Discussion: The beginning of the discussion reads too much like the introduction. In my mind, the discussion should highlight key finding of the work presented here, not a literature review on microbial models.

I wonder if you really need the nuances of maintenance respiration and CUE to get a reverse Michaelis-Menten model to approximate a first order model? Just looking at

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equation 9, if K_m is small (relative to M [P 10866, L 23]) then $D = V_{max} * S$ (basically eq. 14).

Material in the Appendix is frequently referred to in the discussion; however, it's not really clear what part of the Appendix readers should direct their attention. Moreover, it's not really clear if or how the mathematical derivations in the Appendix are (or are not) used in the main display items and results of the paper. If the material in the Appendixes are being used for simulations presented they should be clearly referenced in the main text. In my mind the Appendixes should NOT be used as a large parenthetical to house fancy mathematical derivations that don't inform the larger manuscript.

I appreciate the need to use simple models like this to understand the mathematical dynamics of microbial explicit models, but how much do we lose by using such a simple model that it doesn't really represent soil C dynamics at large spatial, or long temporal scales? There's some of this at the end of the discussion, but greater introspection into how this study may inform ecosystem scale models (or larger) that are used for soil C projections would be helpful.

Technical Corrections

P 10858, L 5-6 This sentence is somewhat awkward and doesn't seem grammatically correct.

P 10858, L 6 I'd recommend modifying the beginning of this sentence by adding 'often' or some other qualifier. For example: "A second phenomenon 'often' incorporated in microbial decomposition models"

P 10859, L 29 Wieder et al. 2014a doesn't deal with microbial models (as implied by the text in the sentence. A better reference may be Wieder et al. 2015, Geoscientific Model Development.

L 10860, L 6 What are "dynamical consequences"?

I appreciate thorough documentation supplied in the Appendix, but to aid in reader
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understanding can specific parts of the Appendix be referred to in the main body of the text where appropriate (e.g., sections 2.1.3 & 2.1.4)? Were A1, A2... etc. referred to in the text? (see also P 10873 L 23 and P 10874 L 10)

P 10869, L1-2 this statement is not obviously supported by results presented in this paper.

Figure 3: It's not immediately obvious to what model this figure refers? The green color chosen is painful to look at.

P 10873 L 23: It's nice that the authors derived a reverse M-M model (from the forward configuration), but it seems like a lot of work to replace a term in the denominator of an established model seem like a lot of work. I'm not sure how much the derivation is warranted in the Appendix.

Paragraph beginning on P 10875, L 10 should reference Fig 3.

P 10877 L 17-19 This sentence is completely unsubstantiated and should be qualified & reference or removed.

P 10877 L 20-21 This seems like completely throw away sentence that should be removed since no discussion of experiments and observations are used or discussed earlier in the paper.

References (not already in the discussions manuscript):

Koven et al. (2015) Biogeosciences, 12, 5211-5228, doi:10.5194/bg-12-5211-2015

Wieder et al. (2015) Geoscientific Model Development 8, 1789-1808, doi:10.5194/gmd-8-1789-2015

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