Geoscientific
Model Development
Discussions

Interactive comment on "Representing life in the Earth system with soil microbial functional traits in the MIMICS model" *by* W. R. Wieder et al.

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General comments

Building on a simple model structure with two explicit microbial groups, the authors tackle a multitude of simulation experiments of SOM dynamics both cross site and global. They compare their result to classical, microbial non-explicit models.

Exploration of the effect of different representations of microbial control on soil organic matter (SOM) dynamics is of high interest to the SOM modelling community and this paper has potentially a high impact.

Although the idea of using microbial traits in soil dynamic models is not entirely new, it deserves the attention by this paper and the community.

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My biggest concern is that due to the multitude of the objectives and simulations, each of the simulations/objective lacks detail. Methods and assumptions are not sufficiently clear. Therefore, I cannot follow several of the interpretations and conclusions.

One of the main conclusions is that representing microbial diversity by traits in SOM dynamic models is important and improves predictions. However, the model was never compared to a microbial explicit model without this diversity, e.g. with a lumped microbial biomass that influences litter and SOM decomposition. The conclusion that can be drawn is that predictions from this microbial explicit model differ from classical models. But as the paper says: "we already know that ..." (p 2024 L 24)

The step from microbial non-explicit to trait based is too big for properly relating observed difference in model predictions to microbial diversity. There are too many causes so that differences in results can be attributed to several features in addition to microbial diversity.

Method Section 2.2 is hard to follow, because several experiments are lumped into this single section. This is similar for the corresponding results section. Many details of are not sufficiently described: The model simulates microbial biomass to increase with litter inputs - why were they kept constant (p. 2017 L23)? How were the litter inputs distributed across depths? And how specifically were the parameters adjusted for depth (p2018 L13)? What varied in the bootstrap analysis (p. 2019 L2ff)?

Similar for Methods 2.3: E.g. How did you adjust parameter values to account for the 1m (p2019 L18)? Did you adjust litter inputs as well for the 1m constraint?

At several places, ad-hoc adjustments of the model parameters were necessary to match the results (e.g. p 2021 L 18ff). First, these parameter adjustments are described in the results section instead of the methods section and appendices. When reading the methods section first, I was confused about what had been done. In the results section the different adjustment are motivated and discussed. Nevertheless, they are quite ad-hoc and the specific values seem quite arbitrary tunings. I suggest to

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integrate such adjustments in a proper sensitivity study.

The adjustments were mainly necessary to modify the ratio of biomass in different microbial groups. For a trait-based model I would expect that those ratios arise because of competitions or some other emergent effect of the model instead of prescribing parameters.

A big part of the discussion on copiotrophic:oligotrophic ratio (p2021 14ff) is based on the N-addition scenario. However, the described corresponding scenario is an increase in soil litter input carbon (ANPP) instead (p2018 L25). The same scenario could result from increased CO_2 with opposite arguments to the litter quality and resulting parameters and stoichiometric effects on microbial groups.

There are a number of features in the global runs that only appear in the discussion rather than methods or results, which have a great influence: Specifically: 1) Litter quality parameters of lower and higher latitudes have been set differently 2) Parameterization partitioning of the different SOM pools (related to clay content) differs between low and high latitudes.

Again there are many causes of observed differences, and to my opinion it takes more scenarios or specific work to tease apart which of all those assumptions help/hinder the model fit.

Specific comments

Labels of equations A1 to A10 are difficult to follow. I suggest more semantics in Names e.g. dec_LIT_m (A1)

I would appreciate some more discussions in Appendix A1 on model features. E.g. Under which conditions is it viable to separate microbial uptake from different portions in the DOM, i.e. different LIT and SOM sources? (There are several completely independent Michaelis-Menten equations for the update.) What is the rationality of applying MM kinetics twice in the breakdown and uptake of SOM_c?

How were the empirical relationships clay content and Km or the partitioning of microbial turnover derived?

P 2017L 18 typo proscribed? Table B1: typo desorbsion rate?

When trying to the run the Git-Hub source-code, I could not find function quartz() (though it worked without it)

Interactive comment on Geosci. Model Dev. Discuss., 8, 2011, 2015.