Biogeosciences

Discussions

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Interactive comment on "Diffusion based modelling of temperature and moisture interactive effects on carbon fluxes of mineral soils" *by* Fernando E. Moyano et al.

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Moyano et al. compare several versions of SOM turnover models with a comprehensive set of observations of varying temperature and soil moisture. They show that explicitly accounting for diffusion, compared to using empirical formulation of the temperature/moisture rate modifiers, improves fit and understanding of SOM decomposition. This result is interesting to the soil model developers and biogeoscientists studying SOM turnover and consequences at soil core to larger scales. The paper contains a strong validation by a good agreement with independent data. The clarity of the discussion on reasons for the good validation fit, interactions with initial pools, and different

resulting temperature sensitivities can be improved.

With an extension of discussion and some more clarifications in the discussion, the paper could be published. Nevertheless, I suggest several additional tasks with this model and data, that would help the community.

General comments:

First, while the paper already contains three different structural versions of decomposition, I suggest including another version of an inverse Michaelis-Menten dynamics for depolymerization (but not for DOM uptake), where the non-linear term is in enzymes instead of the substrate ($F = V C\_P * C\_E/(K + C\_E)$). This would broaden the application of conclusions of this study, because the inverse formulation is used by many microbial models since suggested by Schimel and Weintraub 2003.

Second, the study describes a decoupling between depolymerization and microbial uptake at low diffusion rates, I assume by accumulating OM in the dissolved pool. Are the fluxes correlated again for the same treatment, if you aggregate over say two weeks? The decoupling is a challenging fact for upscaling studies, that often assume the DOM pool in quick quasi steady state with decomposition and microbial uptake. For low moisture the decomposed flux was almost not taken up and respired (Fig. 9). Would this also be true with two separate DOM pools after longer time? I would appreciate an extended discussion on this topic.

The model used enzyme pools split to locations but a simplified diffusion limited rate multiplier for DOM. What is the reasoning for this decision, and what are the expected consequences for using a rate modifier for enzymes too?

There is an interesting differentiation between parameterized temperature sensitivity (E_a) and an apparent predicted one, the latter one also depending on partitioning of the pools (P13l20ff). What are the reasons and consequences here. The paper would profit from an extended discussion here.

Specific comments:

p5l10: The choice of the wording "particulate" suggests to OM floating together with the DOM. I assume instead that C_P comprises litter and residues also sitting on surfaces. When using "polymeric" it conveys a different connotation and still the "P" can be used as acronyms.

p7l10: The model assumes enzyme production to be modeled similar to growth respiration as a fraction of uptake, instead similar to maintenance respiration as determined by microbial biomass. What are the reasons for this formulation ?

p8l4ff: The wording here suggests, that all the processes have the same temperature sensitivity, i.e. same E_a. I suggest adding another index to E_a that this parameter varies between processes.

P8l10: I assume there is only one set of parameters fitted to the entire data of all temperature and moisture treatments. Would be nice to state that here. Please, also state the number of fitted parameters, and add the initial partitions to Table 1. The fitted parameter vector in a ~20 dimension space is quite challenging for a gradient based search. Did you check global convergence by starting from more states, maybe more random distributed as just the one described for p11l30. What are the most important correlations in parameter estimates?

P8l10: model calibration open questions: How were enzyme pools initialized? What were the values of fractions for particulate, dissolved and microbial pool, how do they compare to usual concentration of DOM and microbial biomass? I assume they were equal for all moisture and temperature treatments, right?

P3l20: Citation of the kinetic respiration analysis (Wutzler 2011) is not appropriate in this context. I assume you wanted to refer to: Wutzler T & Reichstein M (2008) Colimitation of decomposition by substrate and decomposers - a comparison of model formulations. Biogeosciences, 5, 749-759 10.5194/bg-5-749-2008

Fig 4: There seem to be two groups of observations, a higher branch and a lower one. Why is this? Is it ok to fit a single smoother to this data?

Technical comments:

The grammar of the paper needs to be re-checked, e.g. p9L18, p9L25, p13L19.