Reply on RC1

Chris H. Wilson and Stefan Gerber

Author comment on "Theoretical insights from upscaling Michaelis–Menten microbial dynamics in biogeochemical models: a dimensionless approach" by Chris H. Wilson and Stefan Gerber, Biogeosciences Discuss., https://doi.org/10.5194/bg-2021-108-AC1, 2021

RC1: In this study, the authors proposed a dimension-less reformulation of the scale transition method to analyze the effect of spatial heterogeneity on the mean-field description of SOC dynamics by the Michaelis-Menten kinetics. They showed that the ratio between mean microbial biomass and mean half-saturation parameter of the Michaelis-Menten kinetics can serve as the characteristic parameter to measure the strength of spatial heterogeneity and the non-linearity of the SOC dynamics of interest. They argue that such a result can help both theoreticians and empiricists to better interpret observed soil C decomposition dynamics, specifically respiration in their case.

Overall, I think this is a well-attempted study, and is clearly reported. I have some moderate to major suggestions for the authors to further improve the manuscript.

CHW: We thank the reviewer for taking the time to read our manuscript carefully and providing us with a constructively critical overall assessment. Please find our response to the review comments in italics below.

Idea-wise, the paper is very similar to the study by Chakrawal et al. (2020), except that the presentation here is simplified by introducing a characteristic parameter and normalization of the variances by the mean field approximation (making the variance corrections dimension-less in the analysis). However, I think the authors ignored the fact that some of the spatial heterogeneity can be considered in the nonlinear kinetics by recognizing that decomposition is at least a two-step process: (1) microbes approach the substrate (or vice versa), and (2) microbes assimilate the substrate. Consequently, the nonlinearity with the Michaelis-Menten kinetics emerge from the combination of two linear steps, and one thus should not be surprised to see that the mean-field Michaelis-Menten kinetics cannot upscale robustly. As shown in Tang and Riley (2019), conceptualizing microbial substrate uptake as a two-step processes enables the half saturation parameter to incorporate the spatial heterogeneity to some extent. I thus recommend the authors to clarify this.

CHW: The reviewer highlights an interesting point here vis a vis the derivation of the Michaelis-Menten kinetics. We agree that more detailed representations of decomposition can have utility in extending our biogeochemical models to smaller scales. The derivation present in Tang and Riley (2019) illustrates how microscale/pore-scale models can be developed that represent how soil moisture mediates diffusional transport of substrate to

microbial cells. However, Tang and Riley (2019) nonetheless represent the final uptake of that substrate as following Michaelis-Menten kinetics, which is non-linear. Put together, these processes define what they call "effective substrate affinity" (let's call this k_eff). All in all, k_eff is still a component in a non-linear dynamic and would be expected to vary substantially across space in any field setting. So, we therefore think that our analysis is especially pertinent for the scale transition at this level, and thus complements the microscale analysis of Tang and Riley (2019). In our view, Tang and Riley (2019) provide a very interesting mechanistic basis for incorporating variations in soil moisture into the substrate affinity portion of the non-linear kinetics. In fact, we are happy to extend our discussion of dimensionless analysis of the scale transition to a specific focus on the half-saturation/substrate-affinity parameter.

Additionally, in the "lessons for scientific inference", I would suggest the authors trying to discuss the relationship between their analysis and the parametric sensitivity analysis or uncertainty analysis that are very popular in the modeling community. Apparently, what the authors presented here and also in Chakrawal et al. (2020) are closely related to approaches like global sensitivity analysis that is used to understand the influence of parametric uncertainty on model performance. Has the authors here just rediscovered the global sensitivity analysis in a new context? And what can sensitivity or uncertainty analysis learn from the authors' study?

CHW: We agree this is a helpful way to strengthen our discussion. In brief, our analysis would be an ideal starting point for parameterizing a global sensitivity analysis (GSA), since it is framed in terms of dimensionless quantities and multiplicative effects which therefore do not depend on the choice of unit scales etc. Although our focus was on highlighting the qualitative insights possible with this setup, we do think that it would make sense particularly for intercomparison among systems with varying soils, hydrology, climate, plant and microbial communities where parameter values would be expected to vary considerably. With a more generic setup such as ours, it is easier to isolate which combinations of parameter values are likely to lead to significant scale transitions.

The second advantage is that the analysis can help understand GSA results. For example, results from GSA can be used to set up the hessian matrix and the variance/covariance factor for each of the variables. In other words, one can directly infer how the variability of a target variable is decomposed into the various factors.

If properly made, I believe the paper will become much more interesting to general readers. Particularly, I don't see an easy way to apply the authors approach to a model that is presented as numerical code, which technically could involve tens if not hundreds of equations, e.g. for a decomposition model that involves tens of microbial populations that I am work with, I don't see how I can apply the authors' method.

CHW: We believe that this is still a possibility and should actually also be done in more complex models. It is possible, even for a complex model to calculate the Hessian Matrix (for example from a sensitivity analysis), This may further help in evaluating and identifying the most crucial parameter and identify the variance/covariance structure in an efficient way, given the variability of the system. This will further help with the ultimate goal of integrating structures of co-location into models. We aim to expand this in our revision, and fits well with your prompt regarding the GSA.

Finally, how should one analyze the temporal heterogeneity blended with the spatial heterogeneity using the authors method?

CHW: This is an excellent question. Although we believe it is beyond the scope of this paper, our approach offers a template. The temporal tendency of the mean field can be expanded to include the scale transition terms arising from the variance-covariance matrix

and the Hessian, ideally in dimensionless form as in the present contribution. The components arising from the hessian matrix can be evaluated at any time. However, the coefficients of variation that result are much more difficult and may depend to a great degree on the specific problem. Ultimately, the details of how microbial dynamics develop over time and space in response to resources and environmental conditions that vary both predictably and unpredictably is not analytically tractable, and therefore no closed-form, time dependent function for the relevant covariances/coefficients of variation can be written down. In the extreme, responses to catastrophic disturbances lead to deep and transient alteration of the covariance structure for which there may not be a readily available solution. However, for smaller time horizons, absent catastrophic weather or geological events, we believe that empirical sampling of the correlations and variabilities can be used to gain insight into scale transition effects influencing observed gas exchanges.