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Geoscientific
Model Development
Discussions

Interactive comment on "ORCHIMIC (v1.0), a microbe-driven model for soil organic matter decomposition designed for large-scale applications" *by* Ye Huang et al.

Anonymous Referee #2

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The authors provide a well-documented new ORCHIDEE-family model that introduces a number of features: explicit microbial biomass pool, dormancy, MFTs, coupled C and N dynamics, and mineral protection. The model reasonably reproduces CO2 fluxes and microbial biomass measurements. I have some comments and questions below that I hope are helpful.

p.4 L4 says that this model is embedded in the land model ORCHIDEE but it is also a zero-D model - wouldn't embedding in a land model make it at least 2-D? If you are not using the land model feature for this study, I would hesitate to say this.

p.4, L25 mentions fluxes that represent occlusion by macro-aggregates but it is not

clear from the model description which fluxes these would be (since there is not specifically an aggregate pool) in the way that, for example, adsorption is clearly labeled in the conceptual diagram. I would either be clear that aggregates are implicitly represented by the exchanges between the SOM pools or clearly define which exchange is meant.

p.5, L27 I'm fine with the implicit representation of cheaters, but I am curious how much coexistence you achieved between MFTs in the multiple MFT models. The same limitations that you describe with cheaters can apply, causing all but one MFT to quickly die off in spatially or temporally homogenous environments, e.g., zero-D simulation or constant environmental forcing, respectively.

p.9, L25 There is generally good attribution of where functional forms and parameters for equations come from, but there are a few places where it is unclear. For example, is Equation 15 taken from Parton et al. 1987 or somewhere else? Some of these very empirical forms need to be either cited or explained. Further into this, the water-modifying equations for decomposition (Eq 15) and uptake (Eq 28) look very different from one another. Why is that?

p.12, L2 I think there is a way to avoid performing the adjustment in Eq 32. It involves including total available C as a term in your uptake rate calculation (Eq. 31), but in order to get the multiple MFT competition to scale correctly, you would need something like [Tang and Riley, 2017]. I'm not recommending this for this paper, but something to think about for the future.

p.21, L29 No change in SOM after doubled inputs is a common observation with microbial models [Wang et al., 2013, 2015] because your microbial death rate (Eq 51) is linear. If it were density-dependent (i.e. BAd = dMFT*BAˆ2*dt), then you would likely see some response to increased inputs because microbial biomass would no longer be exactly proportional to inputs (see [Georgiou et al., 2017]). Not necessary to change your model, as many models use linear turnover, but I think it is important to acknowledge the potential importance of this choice to the model behavior somewhere in the text.

References:

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