

Interactive comment on “The SUPECA kinetics for scaling redox reactions in networks of mixed substrates and consumers and an example application to aerobic soil respiration” by Jinyun Tang and William J. Riley

Anonymous Referee #2

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In this paper, the authors go through many different formulations of enzyme kinetics in an attempt to ‘scale’ kinetics from a single enzyme system to a metabolic network consisting of 10’s to 100’s of reactions. The paper doesn’t have a good introduction and there is little motivation for why it’s so critical to be able to ‘scale’ enzyme reaction kinetics other than it’s computationally intensive to simulate a bunch of equations instead of one. Reducing dimensionality will always make life easier, but it’s not clear that anyone in a real world modeling situation would even be in a position to try to translate kinetics for 10’s to 100’s of reactions for soil organic matter decomposition to a reduced set of reactions. In a real network, there will be feedbacks between reactions,

C1

but all are considered independent in this manuscript.

The authors quickly jump into kinetic equation after equation with no clear goal and minimal to non-existent links between models/equations. There are many blatant mistakes throughout the paper, terms without definition or basis are used repeatedly, and logical errors exist in many places. The authors never even clearly articulate why what they are presenting is better than anything else. The manuscript is incredibly hard to follow as well. It may be possible for the authors to distill some of this down into a coherent compelling message, but in its current form it’s not publishable.

Pg. 7, line 12: This doesn’t make sense. The whole idea is to consider a network of interactions, each with their own kinetics. Gardner, O’Neill, and Iwasa, among other did seminal work on aggregating model dynamics and establish good rules of thumb for when aggregation is reasonable. The problem the authors of this manuscript are trying to address is one of aggregation, not scaling. Furthermore, their expressions are incorrect. A sum can be expressed as the number of terms in the sum multiplied by the mean of the sum. In their case, each term is a product of a rate constant and a concentration, which means that it’s impossible to make their substitution. At a given instant, it can work, but as soon as concentrations change their expression is invalid. Furthermore, there’s no way to average the nonlinear interaction between enzyme and substrate for multiple reactions. I tried looking up the partition principle and didn’t find anything, and the analogies with Dalton’s and Newton’s laws don’t make any sense.

Pg. 3, line 23: Wieder, not wider

Pg. 6, line 2: dissociation

Pg. 6 line 7: r-K selection is only briefly mentioned in the Klausmeier and Litchman (2008) paper.

Pg. 7, eq. 2: Both terms are negative but dissociation should be positive

Pg. 8, line 1: I have no idea what the nonsingularity principle is, and again, searching

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for it give no results. The expression is really conservation of mass anyway.

Pg. 8, line 12: I don't know what this means. Furthermore, the only difference between the two sides of the equation is that the r.h.s. just moves the half saturation constant around. They appear equal and there is no basis for why they wouldn't be. Litchman and Klausmeier (2008) don't even mention Monod kinetics. It is unacceptable to incorrectly use references to justify assumptions or manipulations.

Pg. 9, line 3: When is it even reasonable to enzyme concentration approach infinity?

Pg. 9, line 5: There is no paper that I can find that matches the Murdock reference, and one published in the same year is completely unrelated. This is a very disturbing pattern of misrepresentation of the literature. I basically can't follow the rest of page 9 and I have no idea what parametric sensitivity is.

Starting in section two, the 'derivations' seem to be ok, but they are trivial algebra. It's easy to start with any reaction diagram, assume quasi steady state and derive equations. However, they still seem to be retaining more dynamics than is typical because the substrates/reactants A and B are changing over time.

Pg. 17, lines 2-3: I have no idea what this sentence means.

Pg. 17, line 15 (and appendix): I have no idea what their 'first order closure approach' is. The appendix isn't really a help here.

Pg. 19: The problem with trying to average over a bunch of nonlinear interactions seems to render this derivation incorrect.

Data examples and figures: By this point, I am totally lost and quite skeptical of whether their derivations are correct. The comparisons with data are poorly motivated and described so it's not possible to even know what we should be taking away from the exercise and why.

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