

The authors provide a nice example of the role of spatial heterogeneity not only in resource transformation but also in the species interactions that will emerge in soils, which can be very different from the “average behavior” in which they are actually lumped. I think the contribution is clear, and the paper is well written. I have some comments that I hope can help this nice manuscript get published:

General comments:

General Comment 1: Framing and scope: the term "metabolic networks" implies a level of complexity that the model doesn't deliver, and the paper should reframe its contribution more precisely. The term metabolic networks carries a strong implication of either genome-scale modeling (Flux Balance Analysis, constraint-based approaches) or large-scale cross-feeding reconstructions (as described in the introduction). However, my understanding of what SHISHAMO actually models is better described as a resource transformation graph, species passing resources through space. There seems to be a gap between what the title implies and what the paper delivers, and maybe a clarification of the terminology might be helpful. Similarly, terms like resource dynamics give a sense that we are dealing with a dynamic model, and this is not the case, so maybe the authors can revise a bit the terminology and use a more precise language that reflects the static, geometric nature of the model.

General Comment 2: Positioning relative to existing models. The introduction lacks engagement with spatially explicit microbial models already in the literature (e.g., DEMENT model (Allison 2012) and similar), and the paper needs to clearly articulate what SHISHAMO uniquely offers. Models like DEMENT ask how trait diversity and enzyme kinetics drive decomposition rates, and SHISHAMO works specifically on network topology and spatial arrangement. This distinction is not clear, and the authors should at least acknowledge the existing body of literature to make the unique contribution of their model clear.

General Comment 3: The model description is quite short and lacks the explicit statement of their assumptions, such as that there is an assumed entire consumption of the resources within the disc, no uptake, etc. Figure 1 shows the model's details, but a written description would be helpful. Also, the authors should justify a bit more about the choices of the paper, for example, why a geometric snapshot of the system is sufficient to draw conclusions about the functioning of the metabolic network and resource transformation, and network functioning, especially if these imply a dynamic process. Additionally, some acknowledgment of the limitations in the interpretation of this model is needed in the discussion, especially keeping in mind how much the authors can generalize the outputs if

just a couple of scenarios are presented with one parameter combination. I believe there is an attempt at this in the future work section, but more detail is needed in my opinion.

General Comment 4: The authors present comparisons between simulation outputs and what are referred to as 'theoretical relationships' or a 'theoretical model' (e.g., Equation 1, Figure 4a). However, it is unclear to me what these theoretical relationships represent and where they come from, as their derivation is deferred entirely to the supplementary materials. On closer reading, Equation 1 appears to be an analytical solution derived from the model's own geometric assumptions under CSR, that is, a self-consistency check confirming that the stochastic simulation converges to its analytical expectation, rather than a validation against an independent theoretical framework or empirical data. This distinction is important and should be made explicit. The authors should clarify in the main text what the theoretical relationships are, what assumptions underlie them, and what the comparison with simulation output actually demonstrates. This concern is related to the lack of explicit model equations in the methods section (see General Comment 3): without a clear statement of the model's governing assumptions, it is difficult to see what the authors are actually doing.

General Comment 5: The paper does not define the biological identity of the entities referred to throughout as 'species.' It is never made clear whether S1, S2, and S3 are meant to represent individual bacterial taxa, functional groups, broader taxonomic groups, or metabolic guilds. This ambiguity is consequential rather than merely semantic. The parameterization choices, particularly the disc radius, which encodes the spatial range of interaction, and the cell densities used in simulations, are only interpretable if the biological level of organization is known. For individual bacterial cells, diffusion-based interaction ranges on the order of 10–50 μm are plausible; for functional groups distributed across soil aggregates, the relevant spatial scales would be fundamentally different. Furthermore, the paper's two main real-world examples point implicitly in different directions: the nitrification analogy in the discussion treats AOA/AOB and NOB as species, which are in reality broad functional guilds, while the eclipse dilemma is grounded in a synthetic community of individual species (*E. coli* and *S. enterica*). The paper moves between these framings without acknowledging the difference.

This lack of conceptual clarity also directly constrains the discussion of empirical validation. What data would be needed to confront the model depends entirely on what its entities represent. If species correspond to individual taxa, validation would require methods with species-level metabolic resolution, such as DNA-SIP, qSIP, or NanoSIMS combined with FISH, approaches that, while technically demanding, are increasingly available and have been used to detect taxon-specific carbon exchange interactions in soil.

If species correspond to functional groups, broader approaches such as PLFA-SIP may suffice. The authors should commit to a level of biological organization, justify their parameterization choices accordingly, and use this as the basis for a more concrete and realistic discussion of how the model might eventually be confronted with empirical data.

General comment 6: The discussion makes several claims that go beyond what the model actually demonstrates. For example, lines 310-311 suggest that the model integrates pore variability and could help improve larger-scale models, but SHISHAMO represents spatial heterogeneity only through the positions and clustering of bacterial discs. It does not model pore geometry, water films, or any physical soil structure, so the connection to pore variability is not justified and needs either a clearer argument or to be toned down.

More broadly, the discussion tends to present future possibilities rather than clearly stating what has actually been shown. The core contribution of the model, that spatial arrangement affects how metabolic networks function, is potentially valuable, but it is not new on its own. What SHISHAMO could add is a formal way to quantify how much spatial arrangement matters and under what network conditions. However, the current results only explore one parameter combination for the eclipse dilemma, so the broader claims in the discussion, such as lines 300-301 about making soil compartments in larger models more realistic, are not yet supported by the results. The authors should be more explicit about what has been demonstrated, what is plausible based on the results, and what remains speculative.

Related to this, the paper would benefit from at least a few sentences on the biological and ecosystem-level implications of its findings. For instance, if spatial arrangement can shift a metabolic network from competitive to mutualistic functioning, what does that mean for nutrient cycling, carbon storage, or greenhouse gas production in soils? Processes like aggregate disruption, tillage, or rewetting after drought all redistribute microorganisms in space, and the model suggests this could have consequences for how microbial networks function. Making this connection explicit would help clarify why quantifying spatial effects on metabolic networks matters beyond a mathematical exercise, and would strengthen the justification for the model in both the introduction and the discussion

Specific comments:

Line 36: The example of Kundu et al. (2019), and the motivation for part of the work, is quite off for a soil paper. The example highlights the complexity in the termite's gut. I wonder if there are not sufficient complex networks in soil systems that the authors can add that can be more fitting for a soil paper.

Line 159-162: For the eclipse dilemma, the authors mentioned the following example: "*Such metabolic interaction network has been described for interactions between populations of E. Coli and S. enterica*". I just wonder how relevant this dilemma is then for soils if they provide this example only. Would it be possible to add a soil analog to anchor the eclipse dilemma in their system of interest?

Equation 3: It seems that the area of the square is missing in the equation in order to actually get a percentage loss relative to the resource available. Maybe this is just a typo in the equation.

$$L(d, r) = -50 \times \frac{2r^2 \arccos\left(\frac{d}{2r}\right) - \frac{1}{2}d \cdot \sqrt{4r^2 - d^2}}{\pi r^2}$$

Line 253 "so" I believe it is a typo.