Reply to Sara König :

In this paper, the authors present a mechanistic spatially-explicit model simulating microbial dynamics and carbon consumption in a realistic pore space with different moisture levels, integrating different microbial life and motility strategies. This allows to analyze trade-offs between such strategies in regard to resource use efficiency, and how those are shaped by pore space. It is well written and highly relevant in regard to ongoing developments of carbon cycle models. It also includes an extensive supplement with more simulation results and sensitivity analysis, which is very nice.

I very much like how you justify all your assumptions made. For many model applications, we do not have reliable data, but we still can learn a lot applying them based on assumptions – very good job! This is a nice example on how simplified mechanistic models can help to understand interactions and trade-offs, which cannot be easily observed in experiments and thus add up on experimental work. I hope to see more on your model in the future!

[answer] We sincerely thank the reviewer for this positive and encouraging assessment of our work. We appreciate the reviewer's recognition of the relevance of our mechanistic and spatially-explicit modeling approach.
We also thank the reviewer for acknowledging the extensive supplementary material and sensitivity analyses. We are pleased that these additional results were considered useful for supporting the robustness and transparency of the study.

1. *I am not convinced that your framework includes 'moisture regimes'. You do not change the water content dynamically, right?*

[answer] 1. The reviewer is correct that soil water content is not dynamically updated during the simulations. Instead, the model compares fixed soil moisture conditions represented by different static water-filled pore configurations. We agree that the term "moisture regimes" may be misleading, as it could suggest temporal moisture dynamics or wetting–drying cycles. **We therefore revised the manuscript to replace this expression with terms such as "moisture levels" or "soil" throughout the text. We also clarified in the manuscript that the study focuses on comparisons between fixed moisture states, while additional moisture levels were explored in the supplementary material.**

2. *In the methods part, you describe the concept first very general, but I am afraid that the different usages of cells might confuse a reader. I am not sure what you mean with the interactions among or between microbial cells which can occur within a spatial cell (#108ff). Each spatial cell is either be occupied by microbes or not, right? There are no differences in the amounts or whatever. So, what do you mean with interactions within the cell ?*

[answer] 2. We agree that, in the paper, the term 'cell' refers both to the spatial unit of the automaton and to the microbes. In the cellular automaton, each **grid unit** corresponds to a discrete microsite that can adopt a single state at a given time (e.g., microbe, organic resource, water-filled pore, air-filled pore, or solid phase). There is indeed no interaction within a cell.

Interactions occur between neighboring **spatial cells**, for example between microbes and adjacent resource. To clarify this point, we revised the manuscript accordingly. The sentence now reads:
(L108): In this study, each grid unit represents a microscopic spatial unit. Explicit spatial interactions can occur between microbes, as well as between microbes and organic substrates. The system is based on two coupled matrices of 100 × 100 cells (pixels).

3. *Can you explain why you have two matrices, but the 'state matrix' also includes 'resource' as a state? If I understand correctly, one overlying cell in the two matrices can include resources and microbes or water, correct? I do not understand than why the state matric even has resource as a state.*

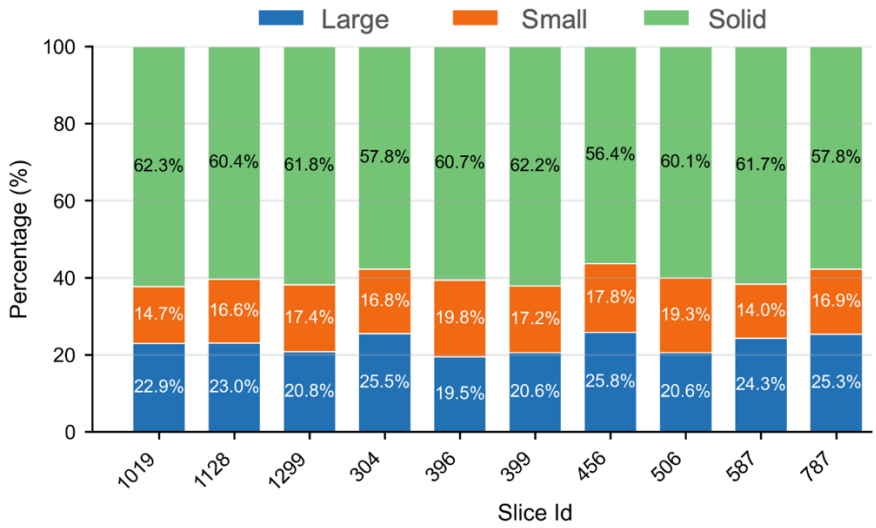
[answer] 3. We thank the reviewer for this question. The two matrices contain complementary information. The state matrix contains the *nature* of each grid unit, eg. microbe, organic resource, water, air, or solid phase. Thus, "resource" in the state matrix only refers to the type of occupancy of the spatial cell. The second matrix stores the *amount* of organic matter associated with each cell (when it applies, eg. for microbes and resources), expressed as resource "points". This matrix therefore represents the amount of carbon/energy available or stored within the corresponding spatial unit. **We have clarified this point in the Methods section**

4. *I would suggest to term the section 2.2 just 'initialisation', its confusing for me that you construct the state matrix with the resource distribution (related to my previous comment). However, very nice justification of your initialization!*

[answer] 4. Following the reviewer's recommendation, **we renamed Section 2.2 from "State matrix construction and resource distribution" to simply "Initialization".**

5. *Have you further analysed the ten regions you have randomly picked in regard to spatial characteristics? Is the fragmentation comparable, what about the total amount of the different states especially solid vs. empty of course?*

[answer] 5. We performed additional exploratory analyses on the ten selected regions to ensure that they displayed broadly comparable spatial characteristics, particularly regarding overall porosity and the relative proportions of the different spatial states. The selected regions were chosen to avoid major structural discrepancies that could dominate the observed microbial dynamics.



We also conducted preliminary comparisons between the porosity values derived from the original real soil images and those obtained from the extracted simulation matrices. Overall, the values were reasonably consistent. However, we chose not to include these analyses in the manuscript because the simulations are performed on 2D extracted matrices, whereas the original soil data are inherently 3D. We felt that direct quantitative comparisons between these datasets could be methodologically misleading and insufficiently rigorous within the scope of the present study.
As the main objective of this work was to investigate microbial strategy trade-offs within realistic pore-space configurations rather than to characterize soil structure itself, we opted to keep the focus on the microbial dynamics and model behavior.

6. *I know, short descriptions in figures are important, but I do not find the scenario names very intuitive. With 'Large + water saturated' I first of all think about large pores in general, or a larger amount of resources. Can you find more specific terms? Such as 'resource in large pores + water saturated'. I know, too long…*

[answer] 6. We agree that abbreviated labels such as "Large + water saturated" may initially appear somewhat ambiguous when taken out of context. **We changed the original terminology in the figures using resource in large pores + water saturated.**

7. *Moisture levels do not change during the simulations? This is basically also why empty pores stay empty, because they cannot be filled with water, so they can also not be occupied by microbes or resources, right? Can you please clarify*

[answer] 7. We thank the reviewer for this clarification request. Indeed, soil moisture conditions are fixed during each simulation and do not evolve dynamically over time (cf 1.). However, even under the "low-water" condition, a connected water film remains present within part of the pore network, allowing microbial cells and resources to be distributed and transported through accessible water-filled pathways. Empty air-filled pores therefore remain inaccessible during the simulation, whereas water-connected pores can host microbial activity and resource diffusion. As correctly pointed out by the reviewer, **lower moisture conditions reduce the fraction of accessible pore space and therefore spatial connectivity within the pore network. This limitation is a feature of the model and reflects real soil conditions under**

low moisture, where reduced water connectivity constrains microbial dispersal and substrate accessibility.
We clarified this point in the revised manuscript **(2.2.3)** to better explain the role of fixed moisture conditions and pore accessibility in the simulations.

8. *With the resource matrix, I get a little bit confused. Recourses do have different concentrations within a cell, so its not an on/off status? But microbes are either on or off, while growth basically means occupying neighboring cells? Is the cell chosen randomly? Note that one might argue that its not a CA anymore when you have continuous differences in the concentration of the resource, as you have an infinite number of possible states..*

[answer] 8. We agree that the distinction between the state matrix and the resource matrix was not sufficiently clear in the original manuscript and could lead to confusion regarding the nature of the cellular automaton framework. In the model, the state matrix remains fully discrete: each spatial cell can only adopt a finite set of states (e.g., microbial cell, resource, water, air, or solid phase). The resource matrix, in contrast, stores the quantity of organic matter associated with each spatial cell. This allows both microbial cells and resources to contain variable amounts of carbon/energy ("resource points"), which determine the extent to which microbial activity, maintenance, motility, and reproduction occur. Resource concentrations are therefore continuous (or quasi-continuous) variables superimposed onto the discrete cellular automaton structure.
We agree that this hybrid structure extends beyond a strictly classical cellular automaton with purely finite discrete states. However, the core framework remains based on cellular automaton principles, as the spatial dynamics still rely on discrete cells, local neighborhood interactions, and rule-based state transitions without the use of continuous differential equations.
To avoid confusion, we have substantially clarified the description of the coupled state and resource matrices in Section 2.1 of the revised manuscript.

9. *Have you tested different perception radii? (just out of curiosity)*

[answer] 9. In preliminary exploratory simulations, we tested different perception radii for mobile microbial cells. However, these analyses were not included in the final manuscript because they substantially increased the number of parameters and scenarios beyond the scope of the present study.
Informally, we observed that when the perception radius was very small, mobile cells behaved similarly to immobile cells because their ability to detect and actively target nearby resources was strongly limited. As the perception radius increased, mobile cells generally became more efficient at locating and exploiting resources, improving their competitive performance. However, beyond a certain threshold, larger perception distances became counterproductive: cells increasingly targeted distant resources that were costly to reach, leading to excessive motility costs and, ultimately, population collapse.
Although these preliminary observations were not analyzed, they suggest the existence of an optimal trade-off between perception capacity and motility cost, which could represent an interesting direction for future work.

10. *Maybe I am completely lost, but can you explain the number of 400 simulations? You have 10 images, each with 4 initial matrices, makes already 40 matrices which you run then 20 times. But you also have the different combinations of microbial densities and diversities, so I count more than 400 different simulations…*

[answer] 10. We thank the reviewer for carefully checking the simulation design and for pointing out this inconsistency. The reviewer is correct: the number of simulations reported in the manuscript was incorrect. **We corrected this error in the revised manuscript (4800).**

11. *Very good that you performed sensitivity analyses, however, can you briefly summarise the main outcome as it is also important for your choice of parameters?*

[answer] 11. We agree that a brief summary of the main outcomes of the sensitivity analyses is important to justify the parameter choices used in the study. We therefore added a short synthesis in the manuscript highlighting the main conclusions of the sensitivity analyses.
Overall, these analyses showed that microbial responses strongly depended on interactions between pore structure, moisture conditions and microbial traits. Importantly, no single parameter combination emerged as universally optimal across all simulated conditions. Instead, the results suggest that microbial performance arises from complex trade-offs between physiological traits and pore-scale environmental structure. These findings support the relevance of the selected parameter ranges while also indicating that the framework could be extended beyond the classical r/K dichotomy. We chose to focus specifically on r- and K-like strategies because they represent well-established ecological archetypes that provide a robust conceptual framework for exploring microbial trade-offs. Their widespread use in ecology makes them particularly suitable for investigating how different life-history strategies interact with pore-scale environmental heterogeneity.
We incorporated this clarification into the revised manuscript.

12. *Can you please add to the statistical analysis section what statistical tests you have actually performed?*

[answer] 12. We agree that the statistical analysis section required additional detail regarding the statistical tests that were performed. We therefore added some clarification in the revised manuscript. **Mean comparisons of CUE were analyzed using linear models (lm), with location of resources in pore size, moisture condition, and mobility as fixed factors. Analysis of variance (ANOVA) was then applied to the fitted models to assess the significance of the main effects and their interactions. Each time, Tukey Honest Significant Differences post hoc pairwise comparisons were performedto account for multiple comparisons.**
These additions have been included in the statistical analysis section of the manuscript.

13. *I miss a section on the technical realization of your model. Out of your Data availability statement I assume it is written in Python, is it based on any libraries or existing implementations, or did you use a specific coding environment for the spatial visualization? You might have a good reason, but why not share the code in a repository? I think it could be very interesting for many people, as there are many more applications thinkable.*

[answer] 13. We thank the reviewer for this valuable suggestion and for the interest shown in the technical implementation of the model.
The cellular automaton model itself was developed in R. Python was only used during the preprocessing stage to extract pore-space images and initialize the simulation matrices from the image data. The spatial simulations and visualizations were implemented using custom R scripts rather than relying on an existing cellular automaton framework or dedicated spatial modeling library. We agree that adding these technical details improves the transparency and reproducibility of the study.We also fully agree with the reviewer regarding the interest of making the model openly available. The code has been released on GitHub and is available at https://github.com/Maelmstr/soil-cellular-automaton.

14. *Regarding CUE – is it correct that the ratio is carbon assimilated as biomass / all carbon uptaken i.e. for growth, maintenance and motility? So, the costs for maintenance and motility do have an influence on this, and you have performed a sensitivity analysis because of this, where you observe indeed effects. But what would that mean for your study, if you would choose other parameters? Why did you choose exactly this parameter set?*

[answer] 14. In our framework, CUE is indeed calculated as the ratio between carbon retained as microbial biomass and the total carbon assimilated, that include the costs associated with growth, maintenance, and motility. Consequently, maintenance and motility costs directly influence microbial CUE, which is why these parameters were included in the sensitivity analysis. The parameter values used in the main simulations were first selected to ensure the emergence and persistence of viable microbial populations within the pore networks. Beyond this constraint, we specifically chose parameter combinations designed to represent different ecological strategies inspired by the classical r/K framework. Our objective was not to identify a universally optimal parameter set, but rather to test whether strategies resembling r- or K-type behaviors consistently performed better under particular pore-scale environmental conditions. As shown in the sensitivity analysis, alternative parameter combinations may indeed produce a greater range of CUE outcomes. In addition, some parameter combinations not explored in the main manuscript may be better suited to specific micro-environmental conditions or ecological contexts.
We therefore emphasize that the selected parameter sets should be viewed as representative ecological archetypes rather than definitive physiological values. The choice to focus on r- and K strategies was primarily methodological, as these strategies provide a well-established conceptual framework for investigating microbial trade-offs and spatial adaptation, as discussed in our responses to comments 9 and 11. **We have added this point to the discussion section of our manuscript.**

15. *You decided to treat the first 25 iterations as kind of warm-up phase for CUE, which I agree makes sense. However, I wonder how different the overall resource amount in the simulations are at this point in time, and if you need to relate the CUE to this when comparing the simulations. The 'initial' condition of resources is likely not the same anymore at time point 25, does this have an effect?*

[answer] 15. The first 25 iterations were treated as a stabilization or "warm-up" phase in order to reduce the influence of the random initial spatial placement of microbial cells on the calculated CUE values.
During these early iterations, the main process occurring in the simulations is the spatial redistribution of mobile cells toward accessible resource-rich areas. As shown by the population density curves, microbial populations rapidly increase during the first iterations, indicating that active resource exploitation already begins very early in the simulations.
Although the initial transient phase is excluded from the CUE calculations, the large majority of the simulation duration is still included in the analyses. We therefore expect the influence of this exclusion on the final CUE estimates to remain limited.
We agree with the reviewer that the resource distribution at iteration 25 is no longer identical to the initial condition. However, this was intentional: the objective was to evaluate microbial efficiency after the initial random spatial configuration had stabilized into a more ecologically meaningful organization shaped by microbial movement and local resource accessibility.
Importantly, this warm-up period was applied consistently across all simulations, allowing relative comparisons among treatments to remain valid while reducing stochastic effects associated with initial placement.

16. *In the discussion section, can you please elaborate on the effects of water dynamics – which would affect resource distribution and microbial distribution probably also for immobile cell, especially in context to your conclusions regarding the influence of pore size and connectivity (4.2)*

[answer] 16. To address this point, we expanded Section 4.2 to better explain how fixed moisture conditions shape microbial dynamics through changes in pore connectivity and water-film continuity.
Importantly, the spatial distribution of organic resources remains identical across moisture treatments (Fig. 1). Therefore, the differences observed between low-water and water-saturated conditions arise primarily from differences in water connectivity and pore accessibility rather than from differences in initial resource placement. We also clarified that moisture conditions influence the initial spatial distribution of microbial cells and their access to resources within the porous network. Under low-water conditions, microbial cells and dissolved substrates are restricted to the water film, reducing the fraction of accessible pore space.
We added the following clarification to the discussion: **It is important to note that moisture conditions also influence the initial spatial distribution and accessibility of microbial cells within the pore network. Under low-water conditions, only pores connected by the remaining water film can host microbial cells and allow resource diffusion which may have affected our results on the CUE. In contrast, the spatial distribution of organic resources remains identical across moisture treatments (Fig. 1), indicating that the observed differences in microbial dynamics and CUE primarily result from changes in resources accessibility and water connectivity.**

17. *When the conclusion is that motility patterns evolve from the resource availability, would this imply for models on larger scales that there should be no differentiation between motile and immobile cells but rather an optimization of resource usage with some lack phase?*

[answer] 17. Our interpretation is that the distinction between motile and immobile microbial strategies remains important, even at larger scales, because the benefits of motility are highly context-dependent. In our simulations, motility is not universally advantageous: its effectiveness depends strongly on pore connectivity, water-film continuity, tortuosity, and the energetic costs associated with movement.
Therefore, microbial access to resources cannot always be reduced to a simple optimization process independent of microbial traits. Instead, our results suggest that spatial structure determines when motility becomes beneficial or disadvantageous relative to immobile strategies.That being said, we agree that large-scale models may not need to explicitly simulate individual microbial movement. The effects highlighted here could potentially be represented indirectly through emergent parameters related to substrate accessibility, spatial connectivity, diffusion limitation, or temporal delays in resource exploitation.
Finally, although this raises interesting questions regarding the representation of microbial strategies in large-scale models, we consider that such broader modeling implications fall outside the scope of the present study. For this reason, we do not propose additional modifications to the manuscript on this point.

18. *You focus on carbon as a resource, but CUE is also affected by nitrogen. Can you discuss the limitations regarding this?*

[answer] 18. We fully agree that in natural systems, microbial carbon use efficiency is strongly influenced not only by carbon availability, but also by nitrogen (and other nutrients), which can constrain growth and alter allocation patterns.
In the present model, we consider a single resource type that we interpret as carbon. This resource is treated as a "complete" substrate in the sense that it is assumed to fulfill all microbial requirements for growth and maintenance. This simplification allows us to isolate the effects of spatial structure, pore connectivity, and microbial traits on carbon processing efficiency without introducing additional nutrient limitation constraints. We acknowledge that this represents an significant limitation of the current framework, as it does not explicitly account for nutrient stoichiometry or potential nitrogen limitation, which are known to affect microbial metabolism and CUE in soils.
However, extending the model to include multiple nutrient pools is a natural and relevant next step. In particular, we have considered the possibility of introducing a C:N stoichiometric constraint in future versions of the model, where resource quality and microbial uptake would depend on elemental composition and where stoichiometric imbalances could constrain microbial growth and metabolism. If N were readily available throughout the pore network, the results would likely remain similar to those obtained here. In contrast, heterogeneous spatial distributions of C and N substrates could generate local N limitations, which are known to reduce microbial carbon use efficiency (CUE) by increasing respiratory carbon losses associated with nutrient acquisition and maintenance costs. Such spatial mismatches between carbon and nitrogen availability could therefore lead to stronger spatial heterogeneity in microbial activity and CUE within a single simulation.
We have clarified this limitation and future direction in the revised discussion to better reflect the scope and assumptions of the current modeling approach.

19. *Another aspect is oxygen. A high consumption rate might reduce oxygen and thus limit resource consumption although there might be enough available.*

[answer] 19. We thank the reviewer for highlighting the potential role of oxygen limitation in regulating microbial activity and carbon use efficiency. **In the current version of the model, we did not simulate oxygen diffusion or oxygen-dependent constraints on microbial metabolism. As a result, oxygen limitation arising from high microbial respiration rates or restricted gas diffusion in water-filled pores is not represented.**
We acknowledge that this is a important simplification. **In natural soils, oxygen availability is strongly controlled by pore structure and moisture conditions: larger and better-connected pores tend to be more aerated and therefore support higher aerobic microbial activity, whereas oxygen diffusion is more restricted in smaller or water-filled pores, potentially limiting microbial respiration and substrate utilization even when carbon resources are available (e.g. Kravchenko et al., 2021b; Ceriotti et al., 2022).** In our simulations, the focus was intentionally placed on the role of pore-scale connectivity, water films, and substrate accessibility, rather than on redox limitations. We therefore assume that microbial activity is not constrained by oxygen availability, which may lead to an overestimation of resource utilization under highly water-saturated conditions compared to natural systems.

We have added this limitation to the discussion to clarify that oxygen dynamics represent an additional layer of realism that is not yet included in the current framework, but could significantly interact with pore structure and moisture in future model extensions.

All minor comments have been taken into account in the revised manuscript.

Reply to Anonymous Referee #2:

I have reviewed the manuscript "Microbial carbon use efficiency emerges from interactions between soil structure and life-history strategies" for publication in SOIL. In this article, the authors present a spatially explicit model based on a cellular automaton framework and use it to investigate the effects of soil pore structure, moisture and selected microbial traits on microbial CUE. They find that the configuration of the pore space is a dominant control on CUE, as it modulates the relative performance of traits such as microbial life-history strategy and motility.
The paper is well written and nicely illustrates the use of a relatively simple model to study processes and effects in the soil system at a scale that remains difficult to observe or manipulate directly. It thereby enhances our understanding of the system even in the absence of measured data, and it will be relevant for both future experimental and modelling work in the field. Therefore, the article should spark interest among many readers of SOIL and the special issue.

Below, I provide some comments to hopefully enhance the clarity of the text and to expand some aspects of the discussion. In particular, I would suggest a more explicit presentation of the processes and update rules of the cellular automaton to improve reproducibility. Otherwise, I have no major concerns regarding this study and I am looking forward to the final version of the article.

[answer] We thank the reviewer for this positive and encouraging assessment of our work, as well as for the constructive suggestion regarding the clarity of the cellular automaton description.
We fully agree that a more explicit presentation of the processes and update rules is important to improve readability and reproducibility of the model. In the revised manuscript, we have therefore expanded the methods section to provide a clearer and more detailed description of the cellular automaton framework.

> *L164ff. While this is a nice conceptual description of the automaton, it would be difficult for me to reproduce an update step based on the provided information. I strongly recommend providing a structured overview of all processes and rules being observed during one update/iteration, e.g., in a table or set of equations (at the very least, this should be included in the supplement). Of course, it would be optimal to make the underlying code accessible as well, if feasible.*

[answer] L164ff. We added a section in the supplements concerning this point. The model code has been made publicly available at https://github.com/Maelmstr/soil-cellular-automaton, ensuring full reproducibility and enabling further reuse and extension of the framework.

> *L175: In my opinion, this equation is not explicit enough. I suggest writing the actual equation/update rule using full notation.*

[answer] L175. We agree that the original formulation was too compact and could be improved in terms of mathematical clarity and explicitness. In the model, resource diffusion occurs along local concentration gradients, but is implemented as a threshold- and rate-limited process.
At each iteration i, resources diffuse when the resource content of a grid unit was above a threshold value. Fixed amounts of resources were distributed from resource grid units to neighbouring grid units with lower resource contents, up to a maximum diffusion rate. The update can therefore be written as:

$$Resource^{i+1}_{(resource\ x,y)} = Resource^{i}_{(resource\ x,y)} - \sum T^{i}_{(x,y)}$$

where $\sum_j T^{i}_{(x,y)\to j}$ denotes the total amount of resources transferred from cell (x,y) to neighboring cells during iteration i. This transfer is constrained by a diffusion threshold (donor eligibility, so that Ti(x,y) > 0 only if Resource(x,y) > Resource(neighbour) and a fixed diffusion rate (maximum transfer per neighbor), such that resource-rich cells lose a constant quantity to each eligible neighbor rather than a gradient-proportional amount.
This formulation explicitly reflects the stepwise and locally asymmetric redistribution process implemented in the cellular automaton. It also clarifies that diffusion leads to progressive homogenization of resource distributions without assuming instantaneous equilibrium.

L183ff: I am somewhat confused about the role of the resource matrix and its interaction with microbes. How exactly do (grid) cells that contain microbes accumulate resources? Do they simply "ingest" all available resource at their current location at each step, and the resulting microbial resource level is checked against the various thresholds? This should be clarified.

[answer] L183ff. In the model, microbial cells accumulate resources. **Microbial cells take up all resources that are present in the grid unit that they occupy. The resources arrive in the grid unit by diffusion or were already present when a motile microbial cell came to occupy the grid unit.**
At the end of each iteration, the total accumulated resource content stored in a microbial cell is used as an internal state variable ("resource points") that determines its physiological status. This accumulated pool is then compared to the predefined thresholds that govern microbial processes such as maintenance, survival, reproduction, or mortality.
We have clarified this mechanism in the revised manuscript to better distinguish between (i) spatial resource distribution in the environment and (ii) intracellular resource accumulation that drives microbial life-history transitions.

L188: What happens between maintenance and reproduction, so for Sd < x < Sr? Microbes could move I suppose, and they still lose carbon via maintenance?

[answer] L188. Indeed, in the range between the dormancy threshold and the reproduction threshold (i.e. Sd < x < Sr), microbial cells are in an active state. In this state, cells are able to perform metabolic activity, including movement (for motile cells), while still incurring maintenance costs that continuously reduce their internal resource pool. Therefore, microbial cells in this intermediate state remain active but do not reproduce, as their resource level is not sufficient to reach the reproduction threshold.

L191: Again, this equation could be improved. For example, in L175, "Resource" at a location xy was a function of iteration i, but here it is a function of microbial entities (parent, descendant) and iteration t. This should be harmonized and made more explicit, see my comments above. Also, how is the location of the descendant microbe chosen? Is overcrowding ever an issue?

[answer] L191. We agree that the notation should be harmonized with the rest of the manuscript, in particular with the resource and state updates defined at the cellular automaton level. We have revised this section to improve consistency in the use of indices and variables across equations.

$$Resource^{i+1}_{(parent\ x,y)} = Resource^{i}_{(parent\ x,y)} - Resource^{i+1}_{(descendant\ x,y)}$$

Regarding the reproduction mechanism, the location of the descendant cell is chosen randomly among the set of available neighboring cells that can be occupied (i.e., empty or otherwise permissible states depending on the model rules). If no suitable cell is available in the local neighborhood, reproduction does not occur during that iteration and is postponed until space becomes available. In practice, this situation is rare due to the spatial structure and occupancy dynamics of the cellular automaton.

L213: The study design could be described more clearly. Currently, I cannot confidently enumerate all the studied combinations.

[answer] L213: The study design was not sufficiently clear in its original form and there was a typo in the total number of simulation that were carried out. We have therefore revised Section 2.3 to more clearly describe the full factorial design of the simulations. In the revised manuscript, we now explicitly detail how the different levels of each factor are combined and how this results in the total number of simulations.

For each of the 10 pore-space images, four distinct initial conditions were generated by combining two moisture levels (water-saturated and low-water conditions) with two resource spatial distributions (resources located either in large pores or in small pores). This results in a total of 40 distinct initial matrices (= 10 images x 2 moisture levels x 2 resource distributions).

For each initial matrix, simulations were then performed under different microbial community configurations, combining two initial microbial densities (low: 23 cells, and high: 56 cells) and three microbial diversity treatments (r-strategists only, K-strategists only, and mixed r+K communities).

Each unique combination of initial matrix and microbial configuration was replicated 20 times and simulated over 200 iterations. This full factorial design resulted in a total of 4,800 simulations runs.

We hope that this revised description makes the experimental design clearer.

L218: Do you have a sense of the timescale of 200 iterations? Since the spatial scale is well defined and many of the processes have some constraints (diffusion, microbial growth, etc), I wonder if something can be said about the temporal dimension as well (and if there are potentially some mismatches that must be considered during interpretation).

[answer] L218. We thank the reviewer for this very relevant question regarding the temporal interpretation of the 200 iterations. We agree that, while the spatial scale of the model is explicitly defined, the temporal dimension is more difficult to directly translate into real-world units due to the discrete and rule-based nature of the cellular automaton framework. In our model, one iteration represents a generic update step that includes resource diffusion, microbial uptake, maintenance costs, movement, and reproduction. As such, it does not correspond to a single directly measurable unit of real time (e.g. hours or days), but rather to a composite step integrating multiple fast microbial processes.

Nevertheless, based on the typical timescales of microbial responses to substrate inputs in soils, and by comparison with previous modeling and experimental studies (e.g. Wiesenbauer et al., 2024), we estimate that the simulated period of 200 iterations may correspond to a short-term decomposition or growth phase on the order of a few days (likely less than ~10 days), during which an initial pulse of microbial growth and resource exploitation occurs.

Interestingly, this order of magnitude is also consistent with microbial doubling times reported for fast-growing bacteria such as *Escherichia coli*. Under favorable conditions, *E. coli* exhibits a doubling time of approximately 59 minutes (Nana et al., 2018). Since cells in our model can reproduce at most once per iteration, 200 iterations would correspond to roughly 200 hours, i.e. approximately 8 days, which remains consistent with our estimation of the time scale.

We acknowledge that this mapping remains approximate and should be interpreted qualitatively rather than as a strict quantitative conversion. Importantly, the goal of the model is to capture relative differences between scenarios rather than to reproduce an exact temporal scaling. **We have added this point to the discussion section.**

> *L220ff.: I greatly appreciate the amount of effort invested into performing the sensitivity analysis. It is unfortunate that all of it is hidden in the supplement. Of course, you cannot include all of these observations and discussions in the main text, but I would encourage you to summarize the most important results and implications at least briefly. As it stands, the outcome of the sensitivity analysis is barely mentioned again.*

[answer] L220ff. We agree that while a full presentation of all sensitivity results is best kept in the Supplementary Material, the main manuscript should still provide a clear synthesis of the key findings and their implications. As also suggested by the first referee, we have revised the discussion to include a more explicit summary of the most relevant outcomes of the sensitivity analyses. **Moisture conditions strongly modulate the relative performance of microbial strategies and microbial traits is a key determinant of CUE variability across simulations. In this work, we highlight that no single parameter combination emerged as universally optimal across all tested conditions, reinforcing the robustness of the observed patterns and supporting the general conclusions of the study.**

> *L246ff: I appreciate the transparency regarding the limitation of necromass recycling. You suggest that it should be kept in mind when interpreting model outcomes, yet you do not explore it much in the discussion. For example, do you expect this choice to favour certain traits more than others in your simulations (e.g., r vs K, mobile vs immobile)? How could this be addressed?*

[answer] L246ff: We thank the reviewer for this comment regarding the absence of explicit necromass recycling in the current model implementation and its potential implications for the interpretation of trait performance. In the present version of the model, necromass is not explicitly recycled back into the available resource pool, which represents a simplification of microbial carbon cycling in soils. We agree that this assumption may influence long-term resource availability and therefore potentially affect competitive outcomes between microbial strategies.
However, based on complementary analyses conducted with the CA we found that the main factor controlling microbial responses in the model is not microbial traits, but rather the rate at which necromass is reintroduced into the system (i.e., the recycling rate). In these analyses, variations in recycling intensity had a similar impact to differences in life cycle strategy (r vs K) or motility characteristics. This suggests that while the omission of explicit necromass recycling may influence absolute carbon dynamics, the relative differences between microbial strategies observed in the present study are likely robust, as they are mainly driven by spatial access to resources and pore-scale constraints rather than by secondary recycling pathways.
We acknowledge, however, that explicitly including necromass recycling and its spatial redistribution would be an important extension of the model. In particular, it could introduce ad-

ditional feedbacks between microbial mortality, resource regeneration, and pore-scale structure, which may further refine the emergent patterns observed here. We have clarified this limitation and its implications in the revised discussion.

> *L260: Please explicitly state all statistical analyses you performed. For example, you show the results of Tukey tests, but you do not specify the underlying analysis (I assume an ANOVA, but is it with a single factor of 4 levels or two factors with 2 levels each, and what are the results?).*

[answer] L260ff. We have revised the statistical analysis section to explicitly describe the full procedure and added details regarding the statistical tests that were conducted.

> *L264: Again, the correct interpretation of this equation is somewhat hindered by the lack of an explicit/rigorous notation (or perhaps just my confusion with the resource matrix). I would appreciate some clarification of the processes involved (e.g., "assimilation")*

[answer] L264. In the model, microbial carbon use efficiency (CUE) is computed at each iteration based on carbon fluxes at the level of the microbial community. The total carbon uptake by microbes, includes both the portion converted into biomass (growth) and the portion lost through respiratory processes (maintenance and metabolic costs).
CUE is therefore defined as:
CUE = (carbon allocated to biomass) / (total carbon uptake)

L389: While you provide a detailed and insightful discussion, I am missing a paragraph on the relation of your model to other cellular automata that have been used in this context, some of which you cite in the introduction. From a modelling point of view, do you identify certain advantages or disadvantages of your approach, and do any opportunities arise from these in combination with others? I would enjoy a few sentences on the matter.

[answer] L389. We agree that positioning our model more explicitly within the broader family of cellular automata (CA) approaches used in soil and microbial ecology helps clarify both its methodological contributions and limitations.
We have therefore added a short paragraph in the discussion comparing our framework with previously published CA-based models cited in the introduction. In particular, we now emphasize that the main advantage of our approach lies in its explicit representation of soil spatial structure and pore connectivity, allowing microbial processes and resource accessibility to emerge from local interactions at the microscale. At the same time, this simplified framework does not include several processes considered in more mechanistic models, such as explicit biochemical regulation or oxygen dynamics.

L501ff.: I assume that you reach these conclusions based on your sensitivity analyses? It would be worth pointing this out and elaborating a bit. As it stands, the central role of these parameters comes as a bit of a surprise after just the main text, at least for me.

[answer] L501ff. We agree that the importance of the parameters highlighted in the discussion should be more clearly linked to the results of the sensitivity analyses. **We have therefore**

revised this part of the manuscript to explicitly state that these conclusions are supported by the sensitivity analyses presented in the Supplementary Material.

> *L531ff.: I think you raise an important point here that could be elaborated a bit. While I understand the choice of focussing on the traditional r- and K-strategist distinction, I believe that the spatially explicit nature of your model enables a much more nuanced analysis of microbial traits. In particular, I took from your sensitivity analysis that the detailed interplay of several traits that may or may not align with this axis must be considered. One potential extension that I would emphasize is the role of extracellular enzymes and associated microbial traits, as a spatially explicit analysis of the return on investment could be very valuable (similar to motility).*

[answer] L531ff. We fully agree that one of the strengths of our model lies in its ability to resolve local interactions between microbial traits and heterogeneous resource distributions, which opens the door to more nuanced trait-based analyses. As suggested by the reviewer, our sensitivity analyses indeed indicate that microbial performance emerges from the interplay of multiple traits and environmental constraints, rather than from a single dominant axis. This supports the idea that spatial structure can modulate trait trade-offs in ways that are not fully captured by simplified categorical classifications such as r- and K-strategists.
We also agree that extending the framework to include additional functional traits, such as extracellular enzyme production, would be a highly relevant and promising direction. In particular, a spatially explicit representation of extracellular enzyme production and diffusion could help investigate the local return on investment associated with enzyme allocation strategies, similarly to what we explored here for motility.
At the same time, implementing such processes remains challenging because quantitative relationships between extracellular enzyme concentrations, enzyme activity, and microbial investment are still poorly constrained in soils. In particular, the actual quantities of extracellular enzymes produced by microorganisms and their links to measured enzymatic activities remain difficult to estimate empirically. **We have added a few sentences in the discussion to acknowledge both the relevance of this extension and the current limitations associated with its parameterization.**

Fig 1, Fig 2: I think a scale bar could be useful to make the size of the spatial domain immediately discernible from the figure.

[answer] We have added a scale to the figures, as well as a note regarding the scale of the matrix.

Fig 5, Fig 6: You focus on CUE as the key outcome, but I am curious whether you also looked at absolute carbon fluxes (e.g. respiration) per microbial group? This could also reveal interesting patterns. Along these lines, are all available resources typically depleted by the end of the simulations?

[answer] Fig 5 Fig 6. In our simulations, these variables were found to be very strongly correlated with total microbial population size and therefore provided limited additional insight beyond the CUE analyses presented in the manuscript. Because our objective was primarily to

investigate metabolic efficiency and trait-related trade-offs rather than total biomass production alone, we chose to focus on CUE as the central response variable.
Regarding resource depletion, in another work, we analyzed the fate of remaining resources at the end of the simulations. These analyses showed that resources tended to persist longer in smaller pores, even after microbial populations had strongly declined. This pattern is consistent with the idea of physical protection of organic matter in confined pore environments, where limited accessibility and pore tortuosity reduce microbial exploitation efficiency.

All comments regarding minor amendments have been incorporated into the manuscript.