## Reviewer #1

### General comments

The manuscript by Wang et al describes model development within a specific peatland branch (SPRUCE) of the land component of the E3SM model, ELM. The manuscript displays a substantial work with both model development, parameter optimization/calibration, sensitivity analysis and analysis of implications for model simulations in comparison to older versions of the model. In total there are four model setups are run, with the new and old model structures as well as with default and optimized parameters.

The topic is relevant and the modelling approach is reasonable from a theoretical perspective, although I am a bit concerned over the amount of new parameters introduced (37 in total). The paper do discuss the problem of equifinality, however, I would like a deeper discussion on constricting the model parameters or parameter ranges, either through observations or theoretical reasoning.

Thank you for the overall encouragement.

We clarified the rationales behind the perturbation ranges of the parameters in the revised manuscript Sect. 2.7.1, lines 435 and 463-492, in response to "Specific comments – Section 2.2" below.

We added a Sect. 4.3.2 to the Discussion (revised manuscript lines 1062-1102) to discuss how to better constrain the model parameters or parameter ranges than the C-flux based optimization in the current study. Here is a brief summary of the discussion:

- The most sensitive and therefore important parameters to constrain are the uptake rate constants and half-saturation points in revised manuscript Eqs. 2-4 (original Eqs. 1-3). Experimental observations are concentrated in temperate regions and crop species and exhibit high cross-species uncertainty. Therefore, those observations are more useful for large-scale than site-scale simulations. In site-scale simulations where uncertainty is high, total plant NP uptakes, estimated from paired NPP and whole-plant C:N and C:P measurements, can be a reasonable proxy constraint. Well-validated qualitative understandings (e.g. mycorrhizal roots generally have higher rate constants for inorganic NP on a per unit fine root biomass basis than uncolonized roots) can be used to shrink the parameter search space.
- Other sensitive parameters are related to mycorrhizal colonization and their exchange of NP and C with the plant host. Past observations suggest these quantities range 0-100%, and the high uncertainty is supported by SPRUCE-observed colonization fractions (revised manuscript Fig. S10, original Fig. S8). On the other hand, large-scale environmental gradients are found to affect mycorrhizal activity. Therefore, multi-site model-data integration can be employed to capture the broad pattern while avoiding overfitting.
- Root morphological parameters are observed at SPRUCE and have global database available (e.g. the Fine-Root Ecology Database). Empirical data together with covarying

> relationships based on root economics theory can provide good constraints for ELM-MYCI in future extensions.

The analysis puts a lot of emphasis on the sensitivity of the different model setups, which is of course a sound approach, however, I feel that the analysis is sometimes overly complicated for a model setup such as this. The focus on sensitivity leads to a lot of relative figures where internal variables are compared to each other, e.g., N acquisition per GPP. While relative values can be informative, absolute values are also important for judging the performance of the model. A simple time-series or scatterplot comparing the different setups against observed data would help. That would also help the interpretation of other metrics such as the normalized values presented in figure 2. I would recommend to move some of the figures of sensitivity, e.g., Figure 7, to the supplementary materials and add a simple figure (time-series or scatterplot) showing absolute values in comparison to observational data.

Thank you for pointing out the problem.

The N acquisition per GPP figure (original Fig. 4) was a mistake – please see previous AC1: 'Correction on Fig. 4', Yaoping Wang, 12 Dec 2025 and we apologize for not having noticed it before submission. The figure was always intended to show absolute N and P acquisition values. The revised manuscript now has the correct original Fig. 4 (revised manuscript Fig. 6). The descriptions and caption in the original manuscript are correct.

We converted the original Fig. S5, which compared mean and temperature sensitivity enclosure-by-enclosure, into a time series plot (revised manuscript Fig. S7) that shows the raw annual observed and modeled data points with root mean squared error metric. Because there are 11 plots, multiple variables per plot, and four model setups, we found it more readable to display the time series in heat map format (like the original Fig. S6 [revised manuscript Fig. S8]). We edited the original Fig. S6 (revised manuscript Fig. S8) to also display root mean squared error like the revised manuscript Fig. S7.

We kept the original Fig. 1 (revised manuscript Fig. 2), because we want to disclose the uncertainty information, i.e. the denominators in the calculation of RAE (Eq. 4), to the reader. But we displayed the newly added Fig. 3, which shows out-of-sample evaluation on C fluxes (see below response to “Section 2.5.1” comment), in scatterplot format similar to the original Fig. 2 (revised manuscript Fig. 4). We kept the original Fig. 2 (revised manuscript Fig. 4), because the comparison can only be performed in normalized terms, as explained in the figure caption. We moved the original Fig. 7 into the SI (revised manuscript Fig. S12).

In general, the paper is well written with an easy structure which is easy to follow. I have reviewed the text and some of the supplementary materials and have some comments that I would like to see resolved. After some revision I think this paper is suitable for publication within GMD.

**Specific comments**

Section 2.2. This section is generally well written however, I feel like the conceptual idea should be helped by a simple conceptual diagram. Also, I believe that the parameter values should be displayed in the main text and not "hidden" in the supplementary materials. At least the 18 parameter values selected for calibration should be shown along with their default values, calibration ranges, and justification of ranges (if available).

Thank you for these suggestions. We added a simple conceptual diagram to illustrate the nutrient competition relationships between plants and soil decomposition in the original and modified models (Fig. 1 in the revised manuscript). We also moved the table of calibrated parameters from the SI into the main text Table 1. We described the parameter ranges and justifications in the revised manuscript Sect. 2.7.1, lines 435 and 463-492.

Section 2.5.1. The RAE is described here as a metric for calibrating the model and assess the optimal parameter combination. While I have not come across this metric before, it seems like a suitable metric to me. However, it is also used later as an evaluation metric (e.g., section 3.1.1), which seems like a breach of good calibration/validation practice. It is also unclear to me whether the same data was used for calibration and validation.

Thank you for pointing out the problem. The calibration and evaluation in the original Fig. 1 were done using RAE on the same data, but additional non-calibration data (observed annual maximum LAI, pretreatment peat CNP contents, pore water nutrient concentrations, resin-exchange nutrients) were used for model evaluation. We clarified the situation in the revised manuscript by splitting the original data description into a Sect. 2.5 Model calibration data and a Sect. 2.6 Model evaluation data.

To further mitigate the problem of calibration-validation overlap, we added post-calibration C fluxes for model evaluation (revised manuscript Fig. 3), and root mean squared error values for individual variables as an evaluation metric (revised manuscript main text Fig. 3, SI Figs. S7-S8). The post-calibration C fluxes data include aboveground NPP of the two tree species in 2022, the aboveground NPP of the shrubs in 2023, and the growing season NEE of the shrub-moss community in 2023. These new data are described in detail in the revised manuscript Sect. 2.6.1 and SI Sect. 1.3.

## Technical comments

L305 "are not overemphasized" is written twice.

Figure 4. The unit description on the y-axis lacks a closing bracket.

Thank you for noticing these two issues. They are fixed in the revised manuscript (line 453 and revised manuscript Fig. 6).

## Reviewer #2

This manuscript presents new representations of plant–mycorrhizal nutrient acquisition in ELMv2-SPRUCE and evaluates them against multiple carbon and nutrient cycling observations from the SPRUCE experiment. Testing whether the inclusion of mycorrhizal fungal nutrient uptake improves model performance in predicting peatland responses to environmental change, leveraging the extensive SPRUCE experimental datasets, is timely and important work. I commend the authors for the significant amount of work involved in modifying and evaluating an already complex land surface model. I have one major comment, primarily related to clarifying key modeling assumptions in the main text (currently placed largely in the SI), as well as several minor comments. Overall, I recommend the manuscript for publication once these points are addressed.

### Major comment

Methods are too concise relative to the importance of the new process representations. Right now, key assumptions and equations for the new modeling processes are mostly described in the Supplement (SI pp. 8–13), but they are central to interpreting the results. I think the main-text Methods should briefly summarize these model key assumptions and equations, so readers don't need to go back and forth from main text to SI for key model structure clarification. Examples that seem important enough to mention in the main text include:

- Mycorrhizal colonization is modeled as a function of soil inorganic N availability, rather than plant nutrient limitation status (as a lot of existing ecosystem/land surface models do), and does not include sensitivity to soil inorganic P. This is an important model assumption that needs to be mentioned in the main text, and maybe discussed a bit the implication of this assumption in the discussion.

- Mycorrhizal organic N uptake is restricted to litter pools, excluding SOM pools with fixed stoichiometry. This likely underestimates the magnitude of organic nutrient uptake and may also underestimate the potential feedback whereby extraction of organic nutrients reduces nutrient availability for microbial SOM decomposition. This limitation should be stated and briefly discussed;

- In addition, I have several concerns regarding the formulation in Eqs. S19–S20 describing the effects of litter N pool size on mycorrhizal organic N uptake (i) litter pool size appears to impose only an upper bound on uptake rather than scaling uptake rates directly with pool size like first-order decomposition models do; (ii) the constant value (0.0001) in S19 is not justified; and (iii) organic N extraction rates do not differ among pools (e.g., lignin-associated N vs more labile pools)

- Carbon allocation to nutrient acquisition is capped at 50% of current NPP per timestep. Empirical studies suggest that belowground C allocation often peaks later in the growing season, supported by non-structural carbohydrate accumulation towards the end of the growing season. Thus imposing a cap tied to instantaneous NPP could therefore lead to misplaced mycorrhizal N uptake seasonality. It would be helpful to clarify this

> assumption in the model description in main text and may briefly discuss how this assumption may affect the results.

This is not a request for new simulations, but rather a request to move key information into the main text and to acknowledge the implications of omitting or simplifying these mechanisms.

Thank you for these suggestions. We split the description of ELM-MYCI into a new Sect. 2.3 in the revised manuscript. The section now states (1) mycorrhizal colonization is modeled as a function of soil inorganic N availability only (revised lines 212-215), (2) mycorrhizal organic NP uptake is restricted to litter pools, and organic acquisition rates are only limited by 0.0001 * litter pool sizes and do not differ among pools (revised lines 253-259, 260-262), (3) nutrient acquisition is capped by 50% of NPP per time step (revised lines 235-238).

We added a Sect. 4.3.1 to the Discussion of the revised manuscript to discuss the limitations and implications of these assumptions. Here is a brief summary:

(1) Sensitivity to soil inorganic P should be added if extending the model to temperate or tropical regions. Sensitivity to plant nutrient status is mechanistically defensible but distinguishing it from the effect of sensitivity to soil inorganic nutrient is best tested in multi-site, multi-PFT simulations across a gradient of N and P availability.

(2) Restricting organic nutrient acquisition to plant litter pools may result in underestimation of the magnitude of this pathway, contributing to underestimated mineral nutrient limitation on heterotrophic respiration and overestimated nutrient limitation on plant growth.

(3) The lack of sensitivity to soil organic nutrient content or the recalcitrance of the plant litter pools may result in underestimation of the sensitivity of acquisition rates across environmental gradients. A Michaelis-Menten form sensitivity to soil organic nutrient content should be tested if extending the model to mineral soils, where substrate availability no longer outweighs enzyme availability. A Michaelis-Menten form sensitivity to directly absorbable small organic molecules, and sensitivity to the recalcitrance of the plant litter pools require improved classification of pools in the soil decomposition processes in ELMv2-SPRUCE. The 0.0001 upper bound should be viewed as a sanity upper bound to prevent unrealistically large hourly acquisition rates rather than a real upper bound on fungi-accessible organic matter.

(4) Capping the nutrient acquisition to 50% of NPP can result in underestimated late-growing season mycorrhizal uptake. In the real world, this could overestimate nutrient limitation on leaf expansion and underestimate NP limitation of the heterotrophic microbes. But the current ELMv2-SPRUCE framework has fixed stoichiometry and always determines nutrient limitation based on concurrent demands and supplies. Heterotrophs and mycorrhizal fungi are also not separated in current ELM-OLD or ELM-MYCI. Therefore, the impact on simulation result in the current ELMv2-SPRUCE is probably minor.

**Minor comments**:

Line 57: consider adding an intro sentence on what plant-mycorrhizal associations do before listing mycorrhizal types, like “mycorrhizal fungi deliver nutrients to plants in exchange for carbon”

Thank you for the suggestion. This has been added to line 66 of the revised manuscript:

“Mycorrhizal fungi deliver nutrients to plants in exchange for carbon, and have three broad classes …”

Line 94-95: regarding “excess flux mechanism is likely realistic at the microscopic level (Bunn et al., 2024)”, Bunn et al. (2024) do not provide support for surplus or “excess flux” mechanisms being locally regulated at the microscopic level, instead, they emphasize caution against reciprocal exchange interpretations. Surplus C concepts have been discussed primarily as ecosystem- and model-level frameworks (e.g., Prescott et al., 2020 Surplus Carbon Drives Allocation and Plant–Soil Interactions). Clarification or revision of this statement is needed.

Thank you for pointing out the issue. Please see updated statement in lines 103-106 of the revised manuscript:

“Compared to return-on-investment, the excess flux mechanism may better describe EcM and ErM exchanges with the host plant, because the reciprocity of EcM and ErM are more strongly affected by environmental, developmental, and physiological factors than the AM transfers (Bunn et al., 2024; Garcia et al., 2015). The drawback is a large number of parameters.”

Line 283–284: Do the ensemble simulations mentioned here correspond to the ~4000 ensemble members described later (Lines 290–291)? If so, it may improve clarity to introduce and describe these ensemble simulations before referencing them. Additionally, please clarify whether the parameter optimization refers to selecting the best-performing parameter set(s) from this ensemble.

Thank you for pointing out the issue. The ensemble simulations and the ~4000 ensemble members are the same. Parameter optimization refers to selecting the best-performing set from this ensemble. We improved those descriptions in the revised manuscript:

“…we used either optimized values obtained from 4000-member ensemble simulations that are described below, or…” (lines 425-426)

“… we ranked these parameter sets by relative absolute error (RAE) and selected the sample with the lowest RAE as the optimized parameter values …” (lines 438-440)

“We then perturbed those most sensitive 18 parameters in a 4000-member ensemble simulation, calculated the RAE in the same way as done for ELM-OLD, and selected the sample with lowest RAE as the optimized set of parameters.” (lines 496-498)

Figure 2: Could the authors clarify whether these dots correspond to modeled values from different years, soil temperatures, and $CO_2$ treatments all plotted together? As currently presented, it is unclear what quantities are being compared in this figure.

Thank you for pointing out the issue. Yes, they are all plotted together (different years and different soil temperatures are the same because the x-values are annual mean soil temperatures). We clarified this in the caption of Fig. 4 in the revised manuscript (original Fig. 2).

Future directions: Fungal necromass needs to be considered too. As ERM necromass for example is known to have high melanin% and is propoased to be recalcitrant to decomposition and contributed to the large SOC accumulation.

Thank you for pointing out the issue. We added necromass discussion to lines 1106-1108 of the revised manuscript:

"Explicit simulation of fungal and heterotrophic microbial biomass will enable separating mycorrhizal fungal from non-mycorrhizal respiration and the modelling of fungal necromass, which has different decomposability from saprotrophic residues due to higher melanin content, particularly in ErM fungi (Fernandez et al., 2019)."