

Reviewer comments for egusphere-2024-3661

This paper sought to quantify the effect of multiple abiotic and biotic factors on Nup and NUE, which contribute greatly to the N cycle. Authors utilized a large-scale dataset using a model selection approach paired with a series of generalized mixed linear models. Interestingly, they found that Nup is primarily driven by abiotic factors such as N deposition, air temperature and precipitation, while NUE is driven by soil attributes such as pH, soil microbial stocks, and AMF presence. The authors also compared their results to eight different climate models included in the TRENDY models and claim that these models may be severely overestimating the Nup in ecosystems.

While I find some of their results insightful, particularly that Nup and NUE are driven by very different environmental factors, I am less convinced that their later result is as big as they claim. Mainly, that the TRENDY models are overestimating Nup to that large of degree when 5 out of the 7 models are very much in line with the estimates derived from this approach (Fig. S7). Thus, I do not think the claim that the TRENDY models is as large as the authors here are claiming. Rather, a more in-depth discussion about why there are two models that are so much higher would be much more useful.

Additionally, there is a lack of clarity regarding where this data came from. In the manuscript, it states that plot-level data was collected from 159 sites. But it unclear if these sites are or data were collected first-hand by the authors, if there were additional collaborators, if these are network sites, or if these was more of a meta-analysis approach in which this data was extracted from multiple published datasets. Also, in the manuscript itself, it does not mention how many datapoints total are included in this dataset, and that multiple points are coming from a single site. Where and how you attained the climatic data is very clear. However, I am confused about how you derived and interpret the AMF data, notably, what the percentages mean. Do they represent the maximum potential % colonization on roots or a likelihood of assassination? A little more clarity would ease interpretation of the data. Finally, looking at Fig. S8, you have severe data discrepancies in much of Africa, Russia, Australia, and the tropics in general. This leaves me very wary about your ability to scale up to the level that you do. It leads me to believe that the Nup differences are likely due to lack of data in those area rather than differences in how you model the biology. More discussion about this is needed in the interpretation of the results.

My last major concern is regarding the statistical analysis. While it is fairly clear how the analysis was performed, there are key details missing from the methods that are important. Importantly, the random effects structure (if any were included) is not discussed. Given that you have multiple points from a single site, data from a wide range of dates, and potentially some spatial autocorrelation, a mixed effect approach is most appropriate here. If there are random effects incorporated, this needs to be included into the methods – and if not, why? I think it would also be useful to present the variance inflation factor (VIF) scores here as well, as some variables may not be correlated, but overlap in the variance they explain. Also, a little more explanation on what “variable importance” would be useful for interpretation. Is it a derivative of R^2 ? Lastly, in terms of the upscaling approach, which I appreciate the amount of citations included here, I feel that there is still a lack of explanation for those who may be unfamiliar with this approach. Namely, if the validation ratio used here is standard, and what exactly is the parameter optimization approach

described in lines 460-461 (this can go in the supplement, but as written is it difficult to understand).

In terms of the writing, the flow of the manuscript is nice and easy to follow. However, I think a little more motivation and discussion is needed in the introduction. Specifically, the mechanisms in which the soil microbiota are important, the roles they play, and how the different types (AMF vs. microbes) influence the various processes. Then, the quick switch to a discussion about N deposition is abrupt and a little confusing. Overall, the first paragraph needs to be broken up into distinct topics and expanded. The results and discussion are structured nicely and in a way that makes sense. However, I think the methods could be more streamlined such as combining sections 4.1 and 4.2 into a single “data extraction” section. In general, the manuscript has grammar errors throughout that disrupt the flow of the reader.