

# **Response to reviewers: Estimating soil fungal abundance and diversity at a macroecological scale with deep learning spectrotransfer functions by Yang et al.**

We have addressed the topical editor's comment. Our response indicating the changes we made in our revision is in (in blue text and preceded by **Authors:**).

## **Topical Editor: Comments to the author**

I would like to thank you for the new version and the changes you made. The manuscript has been improved after addressing the comments from reviewers. However, I have a final comment. I did not find any discussion about the ranking of the prediction performances for the different soil fungal abundances. Figure 3 shows the different R<sup>2</sup> but why Mortierellomycota and Mucoromycota produced the largest R<sup>2</sup> while ACE produced the smallest ones? I think we need a paragraph in the discussion about this results ?

**Authors:** Regarding the predictability of the relative abundance of fungal phyla and diversity, we have revised the manuscript, as suggested by the editor, by including a new paragraph in the Discussion section (around lines 225–235) as follows: “...The spectro-transfer functions explained less than 60% of the variance in the two dominant phyla, the Ascomycota and Basidiomycota, representing 80% of the total fungal relative abundance. In comparison, the spectro-transfer functions could explain more than 70% of the variance in the Mortierellomycota and Mucoromycota, which were less abundant in soil. The reason for the different predictability might be the coarse phylum-level identity. Compared with the Mortierellomycota and Mucoromycotawere, the Ascomycota and Basidiomycota are more complex phylogenetic classifications and consist of more diverse taxa with different phenotypic traits. These taxa have distinct ecological functions and environmental preferences, which might have reduced the predictability of their relative abundance at the

phylum level. Classifying taxa with similar habitat preferences or studying at a finer taxonomic resolution might provide better predictability and understanding of soil fungal communities. The spectro-transfer function for the ACE index could only explain around 50% of the variance in diversity. The reason might be that local geography, environmental conditions, and difficult-to-proxy long-term natural selection and evolution affect community diversity.”

**Authors:** We also added a final sentence to the Conclusions (around line 320) as follows: “...We hope that our study will provide food-for-thought for further research on the measurement and estimation of fungal abundance and diversity. We believe that improvements will be possible as new technologies and methodologies develop that will also help to deepen our understanding of fungal biology and biogeography.”