Can we accurately predict the spatial distribution of soil microorganism presence-absence and relative abundance?

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Abstract

Soil microbes play a key role in shaping terrestrial ecosystems. It is therefore essential to understand what drives their distribution. While multivariate analyses have been used to characterise microbial communities and drivers of their spatial patterns, few studies have focused on predicting the distribution of amplicon sequence variants (ASVs). Here, we evaluate the potential of species distribution models (SDMs) to predict the presence-absence and relative abundance distribution of bacteria, archaea, fungi, and protist ASVs in the western Swiss Alps. Advanced automated selection of abiotic covariates was used to circumvent the lack of knowledge on the ecology of each ASV. Presence-absence SDMs could be fitted for most ASVs, yielding better predictions than null models. Relative abundance SDMs performed less well, with low fit and predictive power overall, but displayed a good capacity to differentiate between sites with high and low relative abundance of the modelled ASV. SDMs for bacteria and archaea displayed better predictive power than for fungi and protists, suggesting a closer link of the formers with the abiotic covariates used. Microorganism distributions were mostly related to edaphic covariates. In particular, pH was the most selected covariate across models. The study shows the potential of using SDM frameworks to predict the distribution of ASVs obtained from topsoil DNA. It also highlights the need for further development of precise edaphic mapping and scenario modelling to enhances prediction of microorganism distributions in the future.

Keywords: amplicon sequencing, species distribution model, topsoil, eDNA, bacteria, fungi, archaea, protis, cross, validation.

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