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Linking soil microbial biodiversity to soil carbon dynamics

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Carbon emissions from soil are large contributors to the global carbon cycle, but depend on processes occurring at a small scale. Carbon cycling in the soils is mediated by plant roots, soil fauna, and microorganisms including fungi and bacteria. Sophisticated molecular analytical techniques have been developed to characterize soil microbial communities, resulting in discovery of new microbial species that are not yet culturable in the laboratory. The unculturable fraction of soil microbial communities make for a large data gap since we are not able to characterize their activity, and even less so their role in the microbial community. As a result, soil carbon models cannot be readily parameterized from the bottom up—essentially, we cannot quantify functions at low taxonomic level and then scale up to the community level. In this numerical study, we aim to explore how soil carbon model predictions are affected by microbial diversity as characterized *in silico* by distribution of traits.

The resilience of soil microbial communities is related to distance to the surface and diversity. Diverse microbial communities that are closer to the surface, experiencing regular temporal fluctuations in environmental conditions are more resilient to disturbances than microbial communities deeper down in the subsurface. However, forest management practices and extreme climate conditions impose conditions that may be hitherto unforeseen. This makes prediction of response of soil microbial communities to new disturbances and soil carbon respiration thereof to be uncertain. In this contribution, we developed a microbial process network incorporating diverse organic matter compounds, and bacterial and fungal species characterized by distributions of trait values (including co-variations and trade-offs). With this framework, we explore if soil microbial diversity is a good predictor for soil carbon stocks and study diversity effect on community-level responses to disturbance and variations in environmental conditions. These results will assist in the development of a rate expression to capture the contribution of soil microbial community composition to carbon dynamics in soil.