



Improving the simulation of CO₂ fluxes integrating microbial biodiversity into a simple soil organic carbon model

Elisa BRUNI¹, Stefano MANZONI², Jorge CURIEL³, Leticia Perez IZQUIERDO³, Tijana MARTINOVIC⁴, Mathieu SANTONJA⁵, Bertrand GUENET¹

¹Laboratoire de Géologie, École Normale Supérieure, CNRS, PSL Univ., IPSL, Paris, France

²Stockholm University, Stockholm, 10691, Sweden

³BC3-Basque Centre for Climate Change, 48940, Leioa, Spain

⁴Institute of Microbiology of the Czech Academy of Sciences, Prague, Czech Republic

⁵Aix Marseille Univ, Avignon Univ, CNRS, IRD, IMBE, Marseille, France

Numerous models have been developed to simulate and predict the dynamics of soil organic carbon (SOC) stocks and greenhouse gas (GHG) fluxes at site and regional scales.

While ‘classical’ SOC models typically assume first-order kinetics to describe the decomposition patterns of conceptual SOC pools, there has been a recent shift towards incorporating microbial activity due to its significant role in SOC decomposition. However, microbial explicit SOC models usually treat microbial biomass as a single pool, although microbial diversity is understood as a crucial predictor of SOC respiration. In fact, kinetic parameters of different microbial communities are poorly constrained, and representing diversity likely adds too much complexity for large-scale model simulations.

In this study, we incorporate a simple rate modifier to capture the influence of microbial functional diversity on SOC decomposition, into a state-of-the-art SOC model. The aim is to assess whether microbial functional diversity is a determining factor for capturing the dynamics of CO₂ emissions in a forest site following a disturbance event (e.g., cutting and logging) that reduced microbial diversity and altered the soil environmental conditions. To achieve this, we rely on standard rate modifiers to account for changes in environmental conditions and we integrate the microbial diversity rate modifier to account for microbial community changes. With this new model parameterization, we then compare the simulated CO₂ dynamics to the default model simulations without diversity effects.

Finally, we discuss whether the inclusion of the simple rate modifier dependent on microbial functional diversity enhances the ability of the linear kinetics model to depict CO₂ dynamics in the aftermath of a disturbance event, without adding complexity to the model structure.