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From enzyme to Earth system: linking soil community function and composition to constrain the magnitude of the terrestrial biosphere CO₂ sink

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When microscopic organisms such as bacteria, fungi and unicellular algae are assembled into communities they can exert a profound effect on the chemical composition of the atmosphere and modify climate at the Earth's surface. This is because microbial processes drive global photosynthesis, organic matter decomposition and nutrient cycling. However, modelling and scaling microbial physiology at the global scale and predicting the function of microbial communities to global change is an enormous scientific challenge. Here I present some ideas about how a multi-functional enzyme-based approach could help us constrain estimates of the CO₂ sink strength of the terrestrial biosphere. I also discuss how this approach could lead to new insights into the spatial regulation of microbial community function and diversity as soil and plant properties vary.