

A CALL FOR COLLABORATION

Building a global database of soil microbial biomass and function: a call for collaboration**Gabriel R. Smith^{1,2,*}, Thomas W. Crowther², Nico Eisenhauer^{3,4} and Johan van den Hoogen^{2,*}**¹ Department of Biology, Stanford University, 371 Jane Stanford Way, Stanford, CA 94305, USA² Global Ecosystem Ecology, Institute of Integrative Biology, Department of Environmental Systems Science, ETH Zürich, 8092 Zürich, Switzerland³ German Centre for Integrative Biodiversity Research (iDiv) Halle–Jena–Leipzig, Deutscher Platz 5e, 04103 Leipzig, Germany⁴ Leipzig University, Institute of Biology, Deutscher Platz 5e, 04103 Leipzig, Germany

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Abstract

Global analyses are emerging as valuable complements to local and regional scale studies in ecology and are useful for examining many of the major environmental issues that we face today. Soil ecology has significantly benefited from these developments, with recent syntheses unearthing interesting, unexpected biogeographic patterns in belowground biotic communities. However, some questions still remain unanswered, and the accuracy of these studies is inevitably limited by the extent of the data they draw upon. This is a particular problem in global ecology because most datasets used exhibit geographic bias in sample distribution. Here, we work towards addressing this problem with an open call for collaboration on a planned global analysis of soil phospholipid fatty acid and potential enzyme activity measurements. We summarize the current extent of our dataset, outline the planned analyses, and provide information for prospective collaborators who would like to contribute or learn more.

Local and regional studies in ecology and environmental science form the foundations of biodiversity conservation and sustainable agriculture (Whittaker et al. 2005, Gonthier et al. 2014). Research at this scale allows us to rapidly gather information, perform experiments, and address system-specific concerns, which are priorities for scientists and policymakers alike. Manipulative field experiments help to build ecological theory (Simberloff & Wilson 1969), and effective management of environmental problems like the spread of invasive species depends on swift detection and response by on-the-ground experts (Pyšek & Richardson 2010). Resolving many of the concerns and questions relevant to communities both human and ecological is well-served by targeted, local investigation.

However, in the era of climate change, we are now also facing new, additional challenges. A number of our most pressing environmental issues today are global in scope, and these threats develop and change over long periods of time. Addressing these subjects with basic and applied science requires research coordination at larger temporal and spatial scales than before. Responding to the issue of temporal limitation in ecology, the United States National Science Foundation established a countrywide network of long-term ecological research sites in 1980 (Waide & Thomas 2012). In addition to supporting continued progress in this area, computational advances are now helping our community to rise to the challenges posed by large spatial scales. Global collaborative networks allow today's researchers to work simultaneously at

multiple scales, expanding regional knowledge while also furthering our understanding of the Earth as a unified system (Maestre & Eisenhauer 2019).

Progress in soil ecology has accelerated, thanks to these and other developments. Though our field has historically lagged behind aboveground research, recent years have seen an explosion of exciting work (Eisenhauer et al. 2017). Complementing our rapidly growing understanding of microscale species interactions in soil (Baveye et al. 2018), teams carrying out extensive field surveys and collaborative syntheses are helping to document and analyze the global distribution of the Earth's belowground biodiversity. We now have a vastly improved biogeographic understanding of many soil organisms, ranging from bacteria and fungi (Fierer & Jackson 2006, Talbot et al. 2014, Tedersoo et al. 2014, Bahram et al. 2018, Delgado-Baquerizo et al. 2018, Ramirez et al. 2018, Vetrovsky et al. 2019) to soil invertebrates (Bastida et al. 2019, van den Hoogen et al. 2019, Phillips et al. 2019), and researchers have also established databases specifically designed to facilitate further meta-analyses (Burkhardt et al. 2014). From these works, we have learned that soil life, which governs the dynamics of one of our planet's largest organic carbon pools (Jackson et al. 2017), exhibits fascinating, unexpected biogeographic patterns that differ markedly from those found above ground (Crowther et al. 2019).

However, major gaps remain in our understanding of soil ecosystems. Although molecular sequencing can show us the immense extent of belowground microbial biodiversity, abundance estimates based on sequence occurrence can only be semi-quantitative (Amend et al. 2010). Conversely, common methods of microbial biomass measurement like fumigation-extraction can estimate the total amount of carbon held in microbial

biomass (Serna-Chavez et al. 2013, Xu et al. 2013), but they cannot be used to characterize the composition of soil communities. Furthermore, while surveys of functional gene distributions can help us to constrain predictions of microbial functional potential (Bahram et al. 2018), they might not capture actual *in situ* ecosystem dynamics. Ultimately, all global analyses are necessarily limited by the data on which they are based, and a large proportion of work in this area relies heavily on samples from a few geographic regions (Cameron et al. 2018, Guerra et al. 2019).

To address these knowledge gaps, we here announce an open call for collaboration in developing and analyzing an extensive global dataset of soil phospholipid fatty acid (PLFA) and potential enzyme activity measurements. PLFA measurement allows differentiation of multiple microbial functional groups as well as the quantification of total microbial biomass (Frostegård et al. 1991), and potential enzyme activity assays provide measurements of *in situ* microbial community functioning (Caldwell 2006). Most importantly, both of these assays are widely used and time-tested, having been deployed by soil scientists and ecologists for decades. These methods can therefore offer new insights complementary to those provided by the metabarcoding methods commonly utilized in large-scale microbial surveys. Since PLFA and potential enzyme activity assays have been used for many years, a sufficiently comprehensive dataset might even allow for illuminating time-series analyses.

We have already collected over a thousand soil PLFA data points across all human-inhabited continents (Figure 1) and are now rapidly expanding our coverage of potential enzyme activity to match. However, the dataset still exhibits some of the same gaps found in other

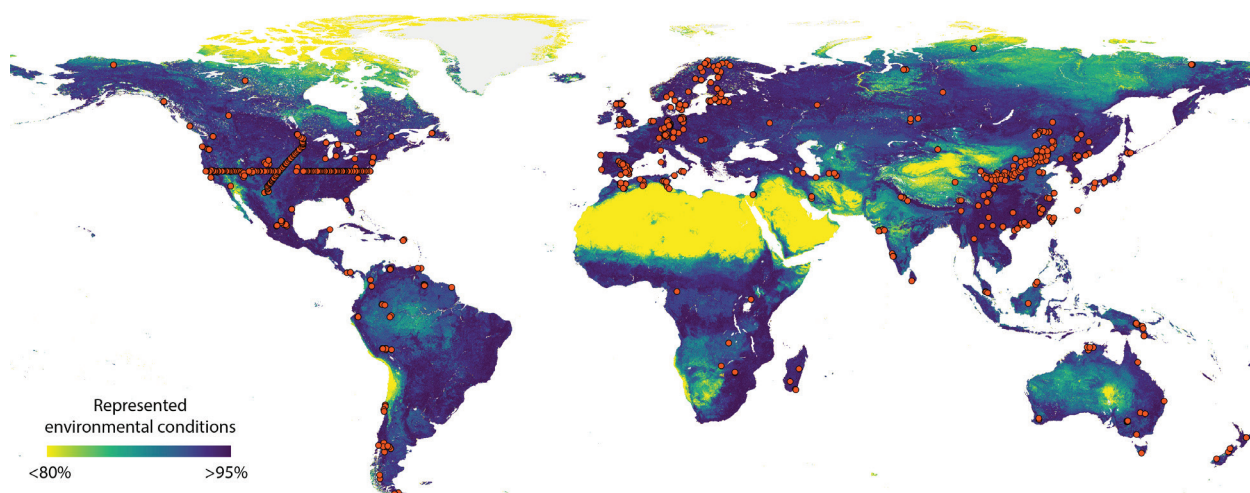


Figure 1. Sampling locations and underrepresented environmental conditions in the dataset as of 19 November, 2019. For each pixel, we measured the percentage of environmental conditions (e.g. climate, soil characteristics, topographic information, vegetation indices) captured by the current dataset. Hot deserts, tropical rainforests and sub-Arctic regions are the least represented.

global analyses (Cameron et al. 2018, Guerra et al. 2019): undersampling in Africa, Latin America, and large parts of Asia. These deficiencies need to be addressed not only because undersampling here hampers optimal modeling, but also because it means our team is missing scientists with expertise in these systems. We want to remedy this to the greatest extent possible by expanding our collaborative global network of researchers and sites.

We therefore wish to invite scientists and teams who have measured soil PLFA and/or potential enzyme activity in natural, unmanaged ecosystems, especially (but not exclusively) in the undersampled regions highlighted above, to collaborate with us on this project. Contributions of data, coupled with involvement at analysis and writing stages, will merit co-authorship on this and future projects. All who are interested or curious are encouraged to contact the corresponding authors, who can discuss specifics with prospective collaborators. The project will be open for contributions until 29 February, 2020, at which point the team will proceed to analysis and writing stages.

We hope that by working together, we will be able to gain new insight into the diversity, composition, and functioning of microbial life in soil and produce research of notable value. As a global team, we're excited to begin tackling questions out of reach for a single scientist or a single research group. We are eager to get started and look forward to establishing new collaborations to support this and future projects.

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