**Effects of Composite Sampling on Diversity and Functional Potential of Microbial Communities in Soils**

**Request for Proposals**

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**Purpose**

Making science accessible to the general public, as well as the scientific community, is a goal of many organizations, including the National Ecological Observatory Network (NEON). One way that NEON is doing that is by providing open access to all of the data collected at its various sites across the United States. In order to provide high quality data, however, there must be standardized, consistent collection methodologies in place, along with a clear understanding of the strengths and weaknesses of said methodologies (Protocols & Standardized Methods, 2016). The goal of this study is to determine how changes to one of NEON’s sampling methods – specifically the soil microbial sampling methodology – may affect the ability of NEON data to measure long-term ecological changes at the continental scale. This will allow us to provide the most complete and accurate data possible.

**Background**

Genetic information is used to determine organism abundance and diversity in samples. Composite soil samples from a single site can be processed for this information much faster and more cheaply than individual samples from a single site, which makes compositing appealing for efficient data collection. However, we do not know whether this sampling method has a bias for (or against) particular taxa of microorganisms or if it excludes other valuable data. This study will compare specimens collected via compositing to specimens collected from the same location via individual sampling to determine the effects compositing has on the types of microorganism data we collect.

**Plan**

We will conduct microbial community analysis on 140 NEON metagenome samples. Each method has both metagenomic and marker gene data available for comparison. Each data set will be analyzed for three specific types of information. The metagenomic data will be analyzed for diversity (using multiple diversity indices), functional composition, and taxonomic composition. The marker gene data will be analyzed for diversity (also using multiple diversity indices), scale diversity, and taxonomic. In order to determine the data provided by each sampling method, we will run ordination statistical analyses on the datasets independently of one another The analyses will provide insight into the types of data collected by each sampling method as well as a basis for comparison between the two.

**Timeline**

* June 6-10: Format data for comparison and automate data retrieval process (MG-RAST API)
* June 13-June 24: Metagenomic analyses
* June 27-July 8: Marker gene analyses
* July 11-15: Final comparisons and conclusions

**Conclusion**

In addition to the value of knowing the applications and output of a particular sampling method, this study will provide NEON field scientists, as well as many other microbiologists, a low-cost, standardized process for microbe collection. This is turn gives the scientific community confidence in microbial ecology research and the benefits that that research provides: advances in health and medicine, increased accuracy in predictions of climate change to an area, etc.

# Works Cited

*Protocols & Standardized Methods*. (2016). Retrieved from NEON, Inc.: http://www.neonscience.org/science-design/protocols-standardized-methods