Mapping Soil Microbiological Biodiversity Using Simulated CHIME Hyperspectral Data

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Abstract
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Challenge

Microbial communities play a pivotal role within forest ecosystems, serving as linchpins for the overall health, structure, and sustainability of these vital environments. While recent advances in molecular research offer a promising means to study these often-neglected communities, they come with significant cost and labour demands, making large-scale assessments challenging. However, there is a glimmer of hope on the horizon. The emergence of spaceborne hyperspectral sensors in recent years has presented an innovative solution to bridge the gaps in our data. These sensors enable the extrapolation of environmental DNA (eDNA)-based microbial profiles across expansive regions. For instance, the impending launch of the next-generation CHIME satellite, known as the Copernicus Hyperspectral Imaging Mission for the Environment, will cater to the surging demand for hyperspectral data needed for expanding our understanding of microbial diversity based on eDNA analysis. CHIME promises to transform the field of biodiversity monitoring, especially in the context of microbial communities. It will empower researchers to identify thousands of taxonomic units directly from modest soil, water, or plant samples. Despite this groundbreaking capability, our understanding of the spatial distribution of microbiological biodiversity, and its critical contribution to ecosystem function, remains limited due to the scarcity of in-situ observations.

Methodology (1200 – 1500 characters incl. spaces)

In this study, our main goal was to assess whether CHIME data could effectively estimate soil alpha diversity. To achieve this, we initially created simulated hyperspectral imagery data using the AVIRIS-NG product, matching the band specifications of CHIME data. We resampled the AVIRIS reflectance data to resemble CHIME bands, considering theoretical Gaussian spectral response functions (equating to 210 bands with 10 nm bandwidth). We then removed bands affected by atmospheric water vapor absorption, resulting in a final CHIME-like spectral setup of 157 bands. For validating our retrieval models, we used CHIME-like reflectance spectra obtained from the original AVIRIS-NG data at the same locations where field measurements were taken. Furthermore, to showcase our mapping process, we spatially resampled the images to the expected CHIME spatial resolution of 30 meters using a cubic convolution algorithm. This allowed us to create realistic CHIME maps displaying estimated soil alpha diversity metrics.

To estimate soil alpha diversity, we employed a Partial Least Square Regression (PLSR) model, which considers the variability in both the explanatory and dependent variables. PLSR establishes a linear relationship between a set of dependent variables (in this case, in-situ measured soil alpha diversity) and a set of predictor variables (represented by CHIME spectral reflectance data simulated from AVIRIS-NG data).

Expected results (1200 – 1500 characters incl. spaces)

The study's findings reveal that hyperspectral data obtained from a simulated CHIME satellite can accurately estimate soil alpha diversity. It resulted in a root mean square error (RMSEcv) of 18.43, 21.05, and 20.16, along with cross-validated coefficient of determination (R2CV) values of 0.56, 0.30, and 0.58 for functional richness, Shannon index, and phylogenetic diversity, respectively. Additionally, when we compared these findings to our prior results using DESIS image spectroscopy data on the same dataset, it became evident that the simulated CHIME data significantly enhanced the accuracy of the estimated alpha diversity metrics (see Table 1).

Outlook for the future (800 - 1000 characters incl. spaces)

This study illustrates how spaceborne next-generation CHIME hyperspectral data can be harnessed to accurately predict potential microbial functions. By generating maps and models of significant value to the field of forest ecology and management, this approach holds the potential to revolutionize the utilization and expansion of environmental DNA (eDNA) point-based information. It introduces groundbreaking solutions to tackle ecological challenges on a global scale, thereby opening up new horizons for the conservation and sustainable management of forest ecosystems.

Table1 : Comparison of Estimated Soil Alpha Diversity Metrics from DESIS and Simulated CHIME Data

Alpha Diversity Metrics	R^2_{cv}	
	Simulated CHIME spectra	**DESIS**
Shannon	0.30	0.24
Functional Richness	0.58	0.38
Phylogenetic Diversity	0.56	0.40

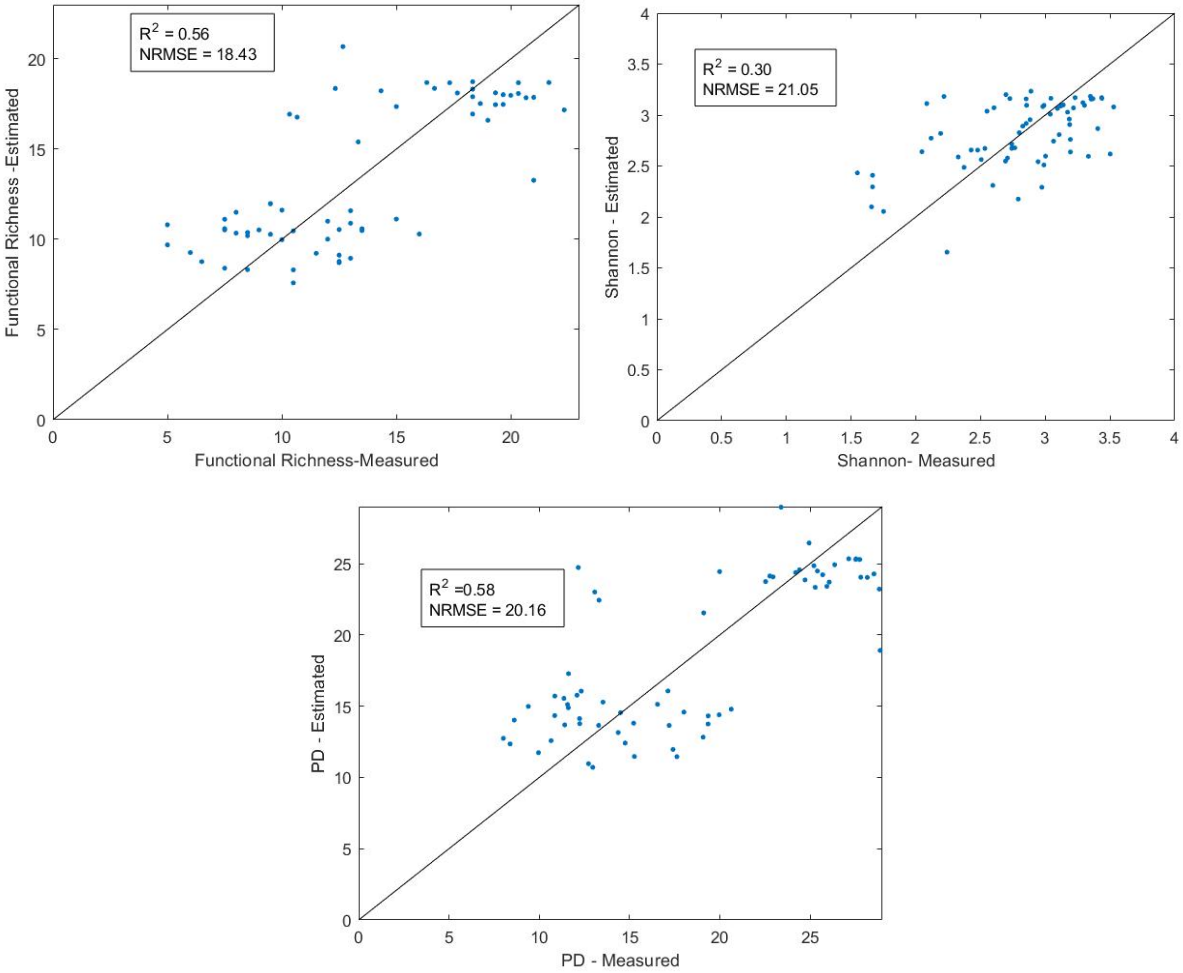

Figure 1: Scatter plot for measured and estimated soil fungi alpha diversity metrics (Shannon, functional richness, and PD.