

Understanding variation in microbial community composition across space and time

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Abstract

Microbes control vital ecosystem processes like carbon storage and nutrient recycling. A fundamental inquiry in microbial ecology is understanding how community structure varies over space and time. In this study, we ask the questions: “how much variation in microbial community structure can be attributed to time or space?”

To answer this question, we utilized a meta-analysis approach, in which we used tables of microbial taxon abundances (outlines number of unique species in each sample) in environmental samples from three published studies with high resolution in both space and time. We calculated similarity in community composition as the inverse Bray-Curtis pairwise distance between all pairwise combinations of samples within each study, as well as between each independent sampling event in space or in time per dataset.

Across all studies, communities varied with time and space and exhibited a time and distance decay relationship with community similarity; this rate of decline is often referred to the rate of species turnover. In bacterial and fungal communities of several landscapes, space was observed to be more important than time in shaping microbial community composition. These results suggest that over time and space, microbial community structure becomes less similar, which may be due to seasonal variation, presence of unique taxa in each landscape, dispersal barriers, or climatic gradients. These findings will be used to ecologically forecast how microbial communities will respond to disturbances and will be incorporated into Earth system models in the future.

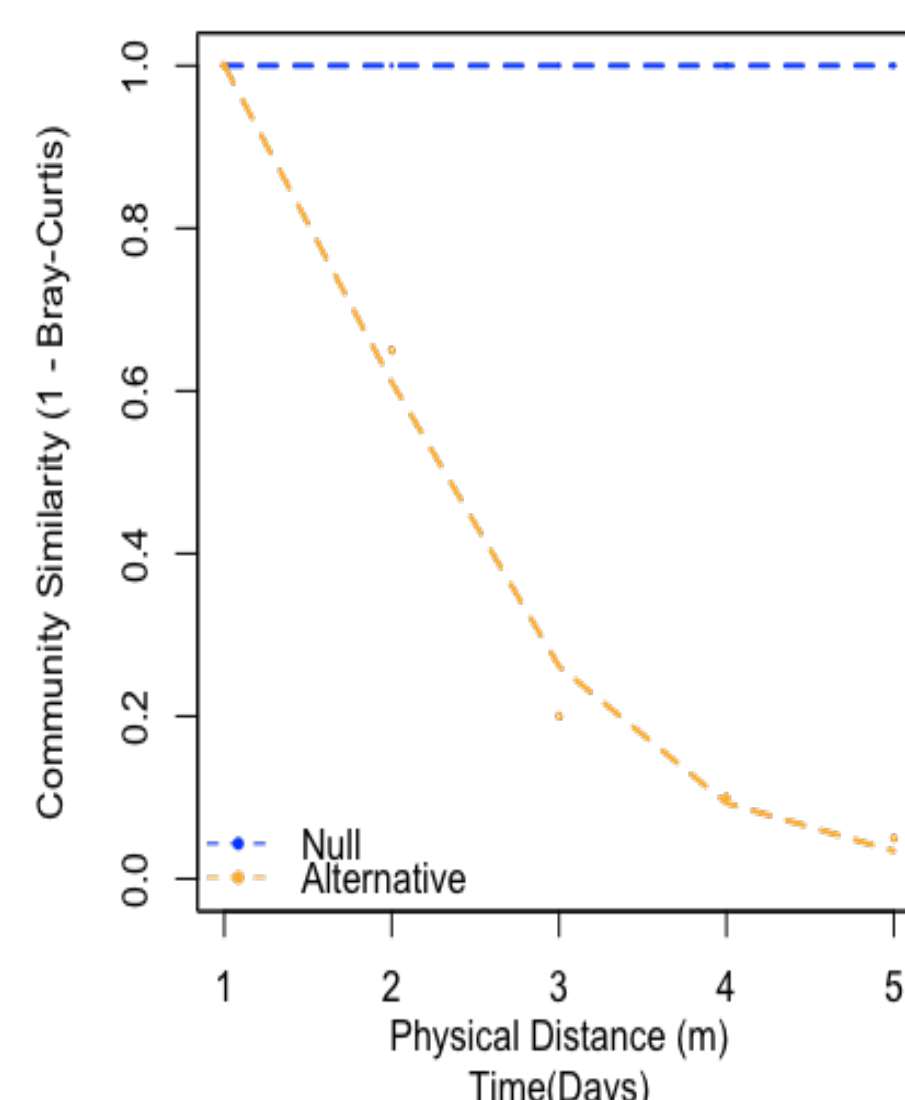
Background

- Microbes, the most abundant organism on earth, control vital ecosystem processes like carbon storage and nutrient recycling, yet little is known about them.
- To accurately forecast how microbes respond to disturbances, a better understanding of their temporal and spatial dynamics is required.
- Specific taxa can be identified by sequencing a specific region on the ribosome and clustering at 97% sequence similarity.
- We conducted a meta-analysis to determine how much variation in microbial community structure can be attributed to time or space.

Can we determine whether space or time is more important in shaping microbial community composition?

Hypotheses

- Microbial communities may not vary across time or space.
- Alternatively, a time-decay or distance-decay relationship with community similarity may be observed if communities become less similar over time or across space.



Methods

Collected data from literature for meta-analysis

Calculate pairwise distances for time & space

Calculate community similarity using Bray-Curtis

Calculate pairwise distances for community similarity

Develop a linear model, test significance of each predictor, & calculate effect sizes on microbial community variation

Three studies with high-resolution in space and time:

- Fungal U.S. Pine Soil
- Fungal Global Soil
- Bacterial Streams

Datasets

We compiled bacterial and fungal time-space series and microbial taxon abundances (OTU tables) from 3 studies, spanning global and regional scales. OTU tables outline the number of unique species in each sample. These studies include Shade et al., 2013, Talbot et al., 2014, and Tedersoo et al., 2014.

Pairwise Distance Matrix of Space or Time	Sample 1	Sample 2	Sample 3
Sample 1	0	37.5	44.9
Sample 2	37.5	0	504.1
Sample 3	44.9	504.1	0

Pairwise-Distance Matrices

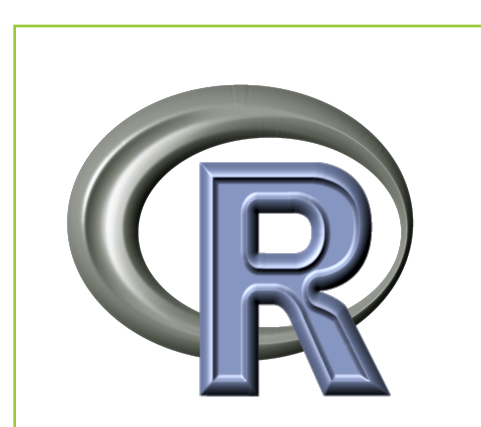
- Pairwise distance matrices were calculated for space and time predictors to quantify the length in time or distance in space between independent sampling events using a Euclidean algorithm or the geosphere package within R.

- Bray-Curtis is a polar ordination technique which quantifies dissimilarity. A Bray-Curtis pairwise distance matrix was derived from microbial taxon abundances in each sample using the vegan package within R. Community dissimilarities were converted to similarities by subtracting from one.

Pairwise Distance Matrix of Community Similarity	Sample 1	Sample 2	Sample 3
Sample 1	1	0.009	0.095
Sample 2	0.009	1	0.001
Sample 3	0.095	0.001	1

Statistical analyses

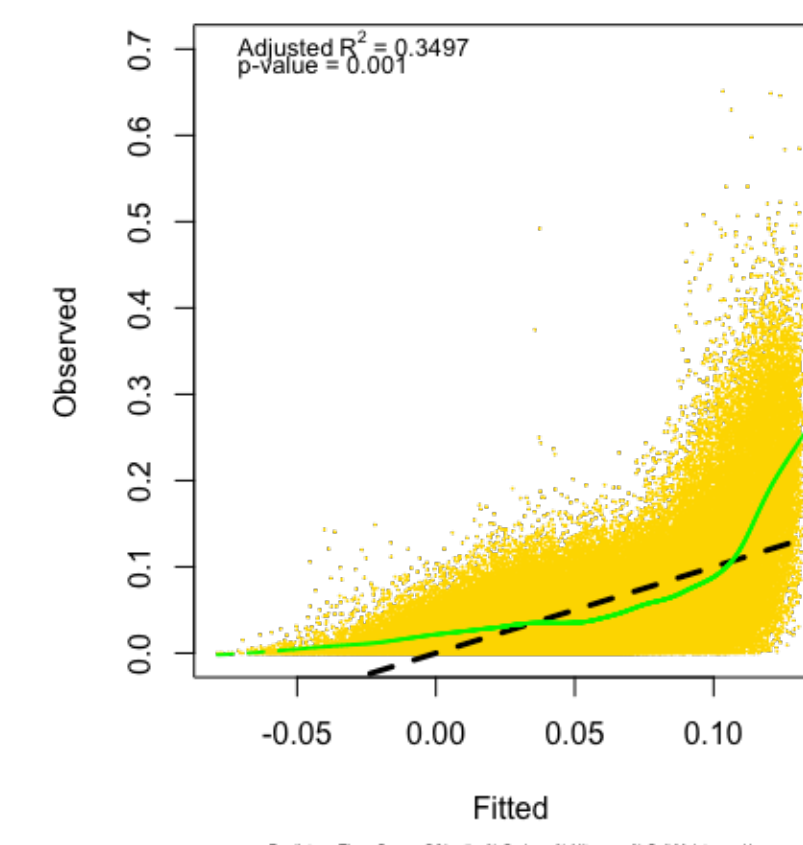
- We evaluated the decay of community similarity over time (time-decay) or over space (distance-decay) by plotting inverse Bray-Curtis pairwise distances against independent sampling events in time and space.
- To estimate the significance of the predictor on community similarity, we employed the several statistical tests, including the Mantel Test, variation inflations, and PERMANOVA from the ecodist, cor, and vegan packages, respectively, within R.
- The linear regression model was determined using multiple regression on matrices using the ecodist package within R.
- The effect sizes were determined by calculating the range of distances in space and time and fitting the regression model with averages of all predictors aside from the predictor tested at hand.



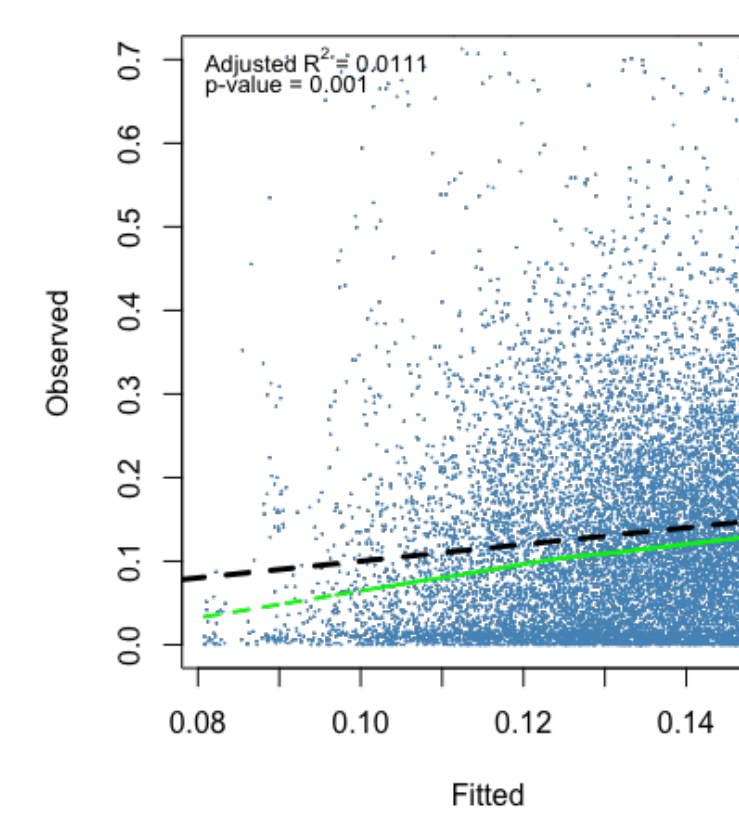
Results

Regression between species turnover predicted by combined spatial and temporal model

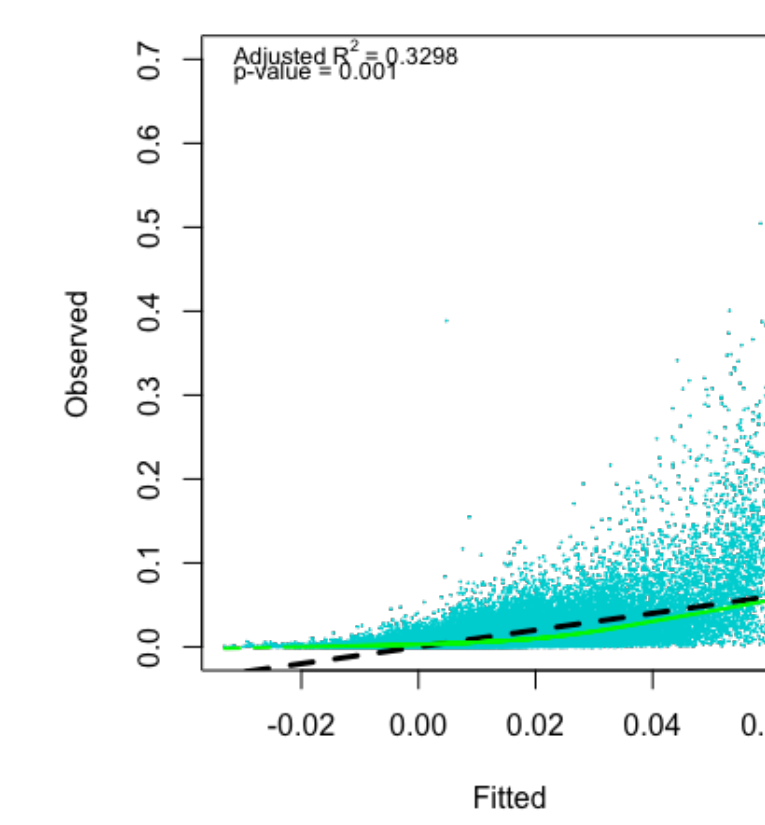
U.S. Pine Soil ITS



Streams 16S

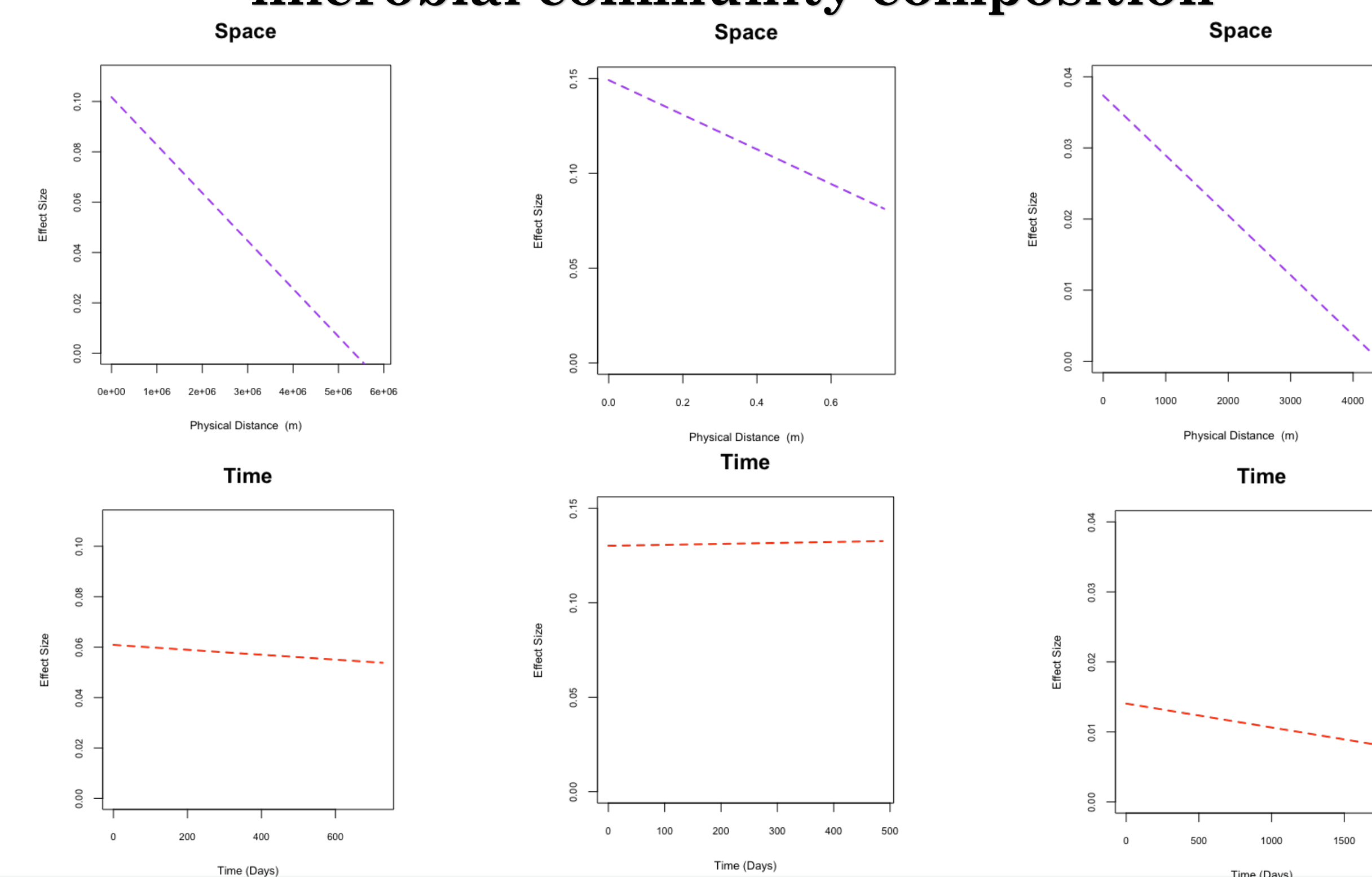


Global Soil ITS



Dashed line indicates 1:1 line. Green line indicates regression line.

Space is more important than time in shaping microbial community composition



Conclusions & Future Work

These results suggest space has a greater effect on microbial community composition than time, which may be caused for several reasons:

- Endemism (a species which is only found in a given region or location and nowhere else in the world)
- Presence of dispersal barriers between places with similar environments
- Climatic gradients (temperature changes along each spatial gradient)

Future work will be focused on using this data to ecologically forecast microbial community composition at NEON data sites.

References

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- Talbot, J. M. et al. Endemism and functional convergence across the North American soil mycobiome. Proc. Natl. Acad. Sci. 111, 6341–6346 (2014).
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