

Factors affecting soil fungal diversity in the Sierra Nevadas

Lei Yu (1) Judy A. Chung (2) T. Rodd Kelsey (3), Edward Smith (3), Sydney I Glassman (2)

(1). Genetics, Genomics & Bioinformatics Program, University of California, Riverside (2). Department of Microbiology and Plant Pathology, University of California, Riverside (3). The Nature Conservancy, 555 Capitol Mall, Suite 1290, Sacramento, CA 95814, USA.



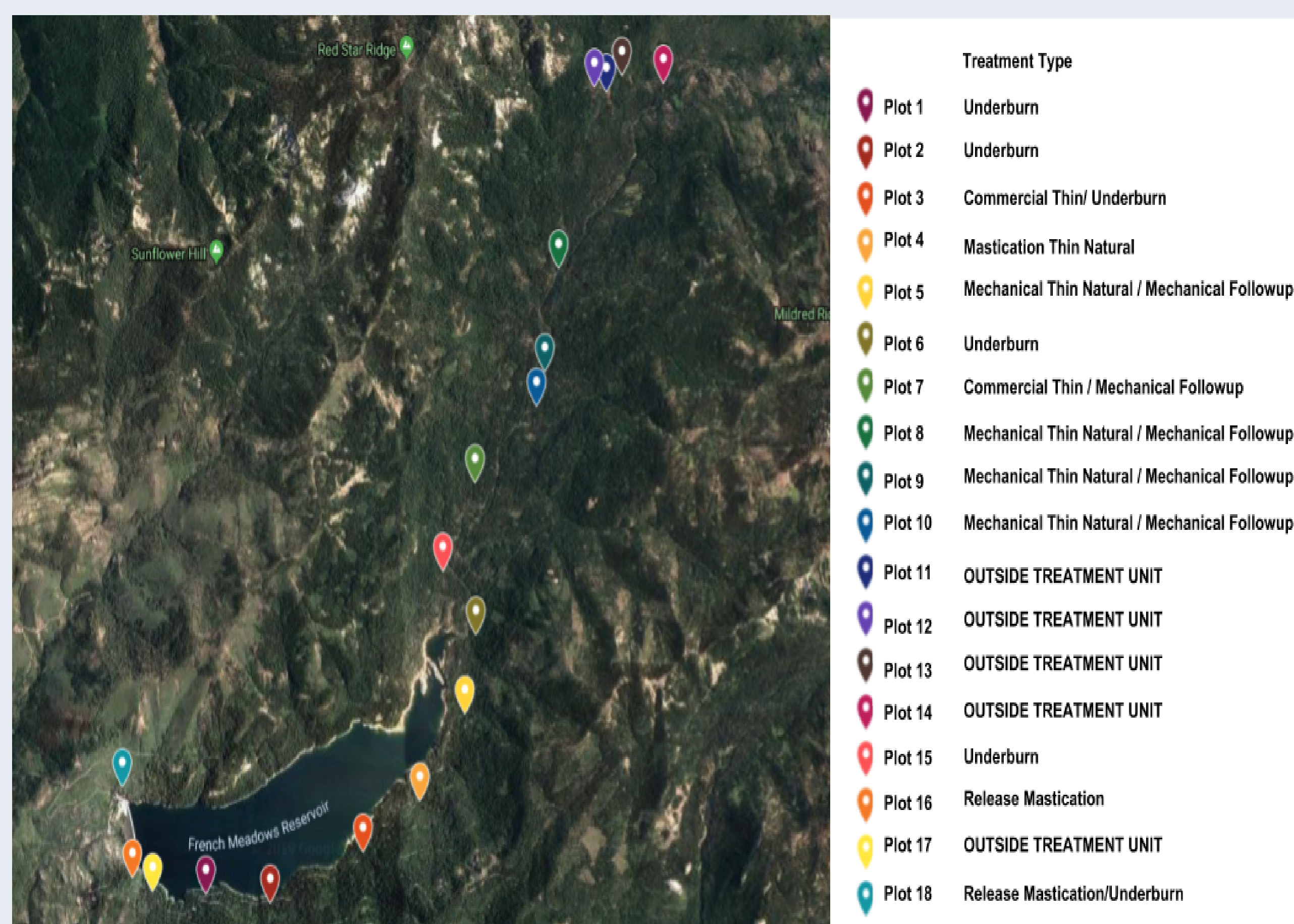
Introduction

We examined factors affecting soil fungal diversity in the Sierra Nevada Mountain range in CA, USA. In this project, we ask:

- 1. What are the factors (soil chemistry, slope, aspect, vegetation, etc) affecting soil fungal diversity in Sierra Nevadas?
- 2. Can we manage for fungal species richness and composition? In particular we are interested in ectomycorrhizal fungi, symbiotic associates of tree roots. Over the next 5 years, we will be testing how various forestry practices including prescribed fires, mastication, mechanical/commercial thin affect soil fungal diversity by comparing to control plots not undergoing treatment.

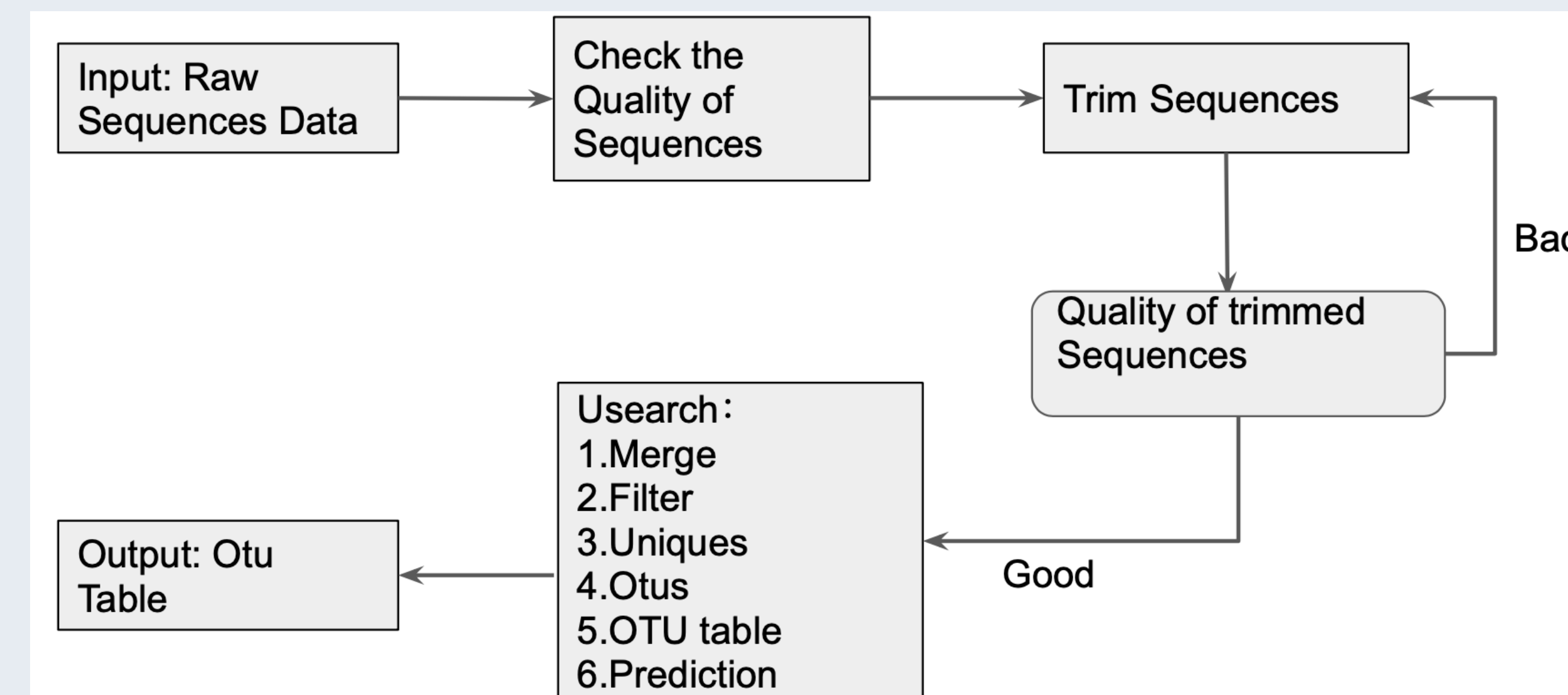
Methods: Sampling

We set up 18 plots dominated by mixed conifer trees in Tahoe national Forest in the middle fork of the American River. We selected a center point and collected 4 samples in each of the cardinal directions 5m from the center in each of the 18 plots. 1. Soil was collected, 2mm sieved, shipped overnight on ice to the lab; 2. DNA was extracted with MoBio Power Soil Kits and ITS1 amplicons were amplified with ITS1F-2 primer pair and sequenced with Illumina MiSeq.



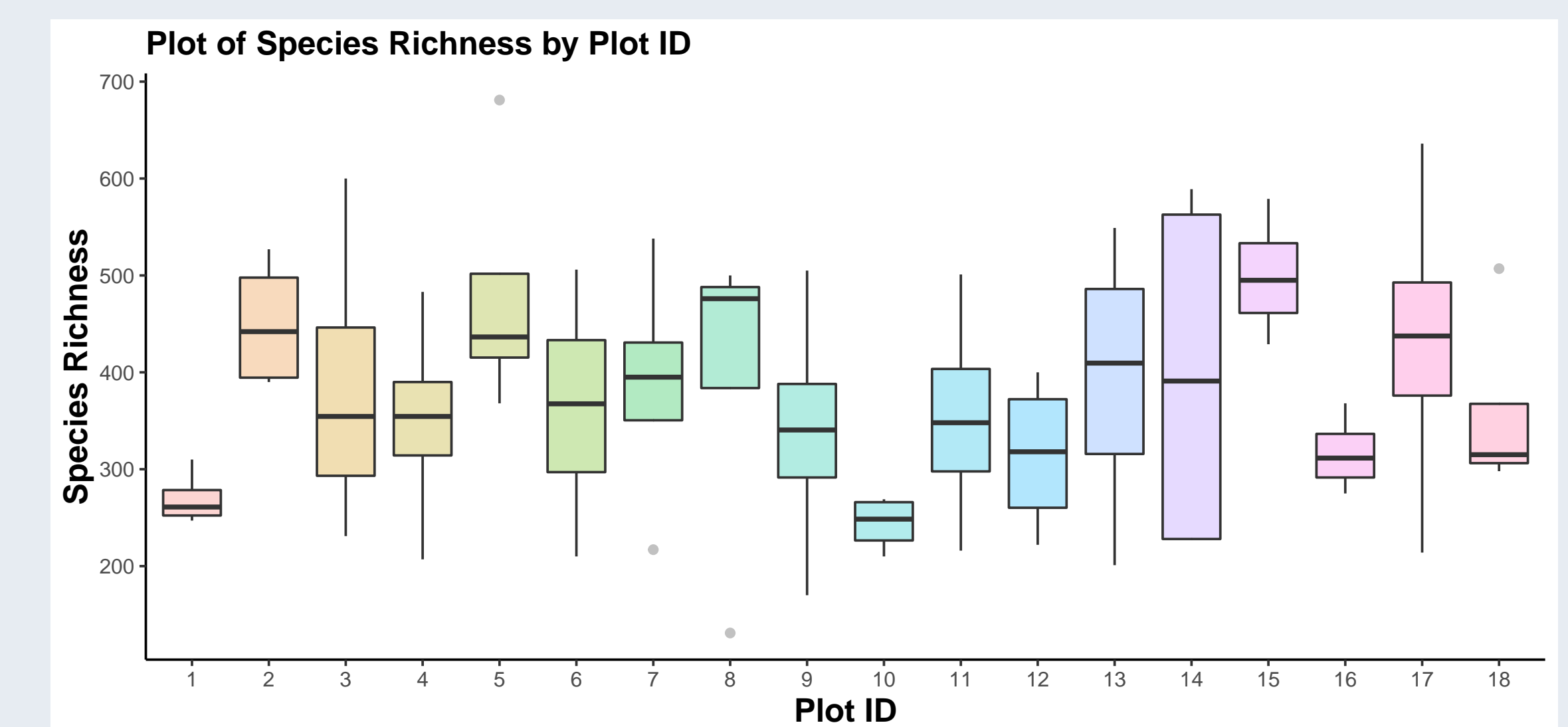
Methods: Bioinformatics

We mainly use *Usearch* to deal with the raw sequencing dataset. The pipeline is shown below:



Result: Species Richness

The Figure shows the statistics of species richness in each plot.

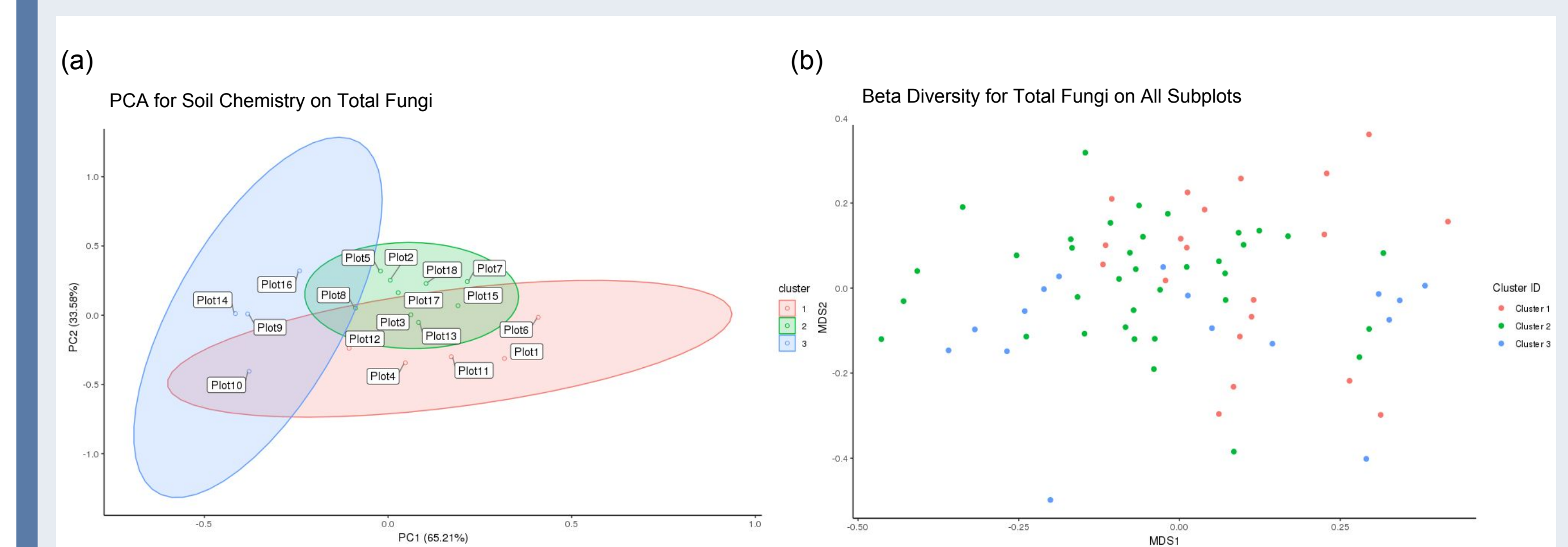


Methods: Statistics

From the OTU table, we can compute the Alpha diversity for each plot. We also collect the soil chemistry and vegetation data near each plot. Note the factors from soil chemistry as F_c , factors from vegetation data as F_v and note species richness as R . Then we do general linear regression to find the key factors which significant effecting the diversity of samples. $E(R) = \omega_c F_c + \beta_c$ and $E(R) = \omega_v F_v + \beta_v$. The importance for each factors can be shown in ω_c and ω_v . Then we operate PCA for on soil chemistry data and cluster plot 1 to 18 into three clusters which can be see as communities and do the Beta diversity analysis based on Bray-Curtis dissimilarity.

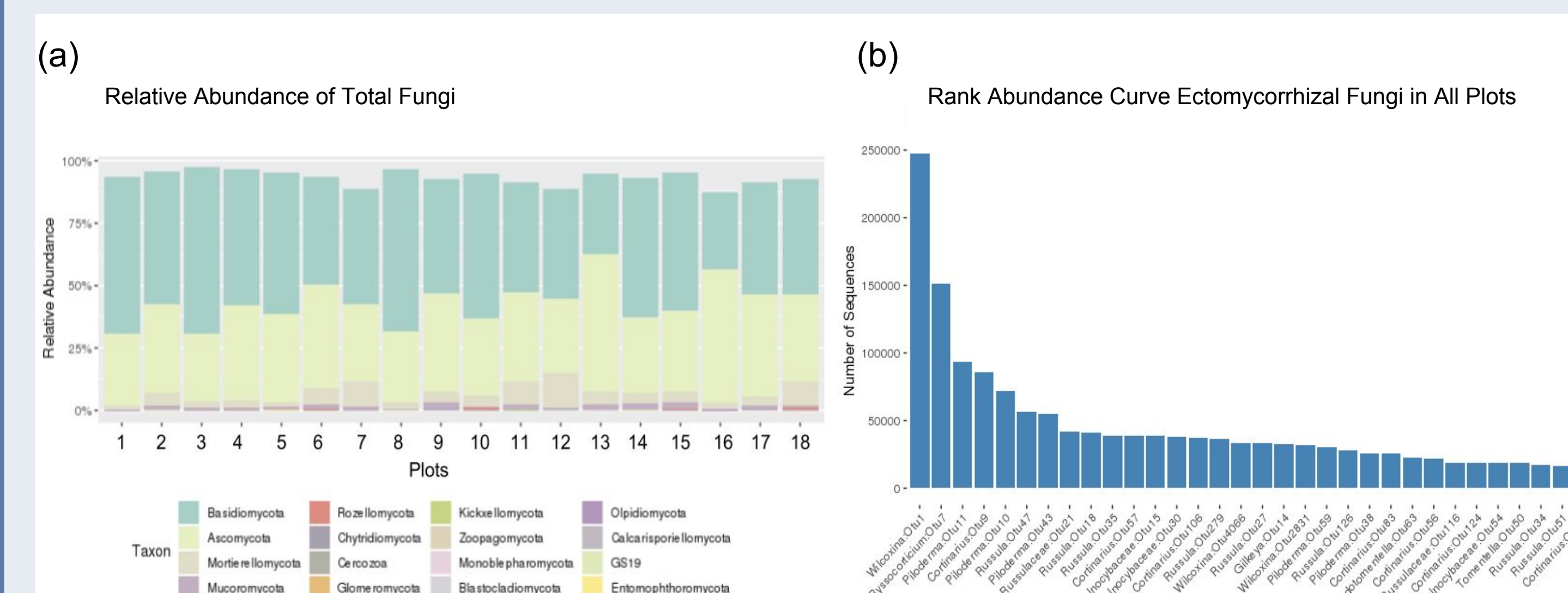
Result: PCA Clustering and Beta Diversity

(a) shows the result of classification of plots using PCA on soil chemistry data and (b) shows the beta diversity of every subplot.



Result: Taxonomy Abundance

(a) focuses the relative distribution of different fungal phyla in total samples and (b) focuses on the distribution of ectomycorrhizal fungi.



Conclusion

- Alpha Diversity: Soil chemistry environment have much more affects on the species richness of total fungi. And the key factors includes the content of Organic Matter, Calcium, NO_3N , Sulfur.
- Beta Diversity: There is no significant differences between clusters and there may show diversities after treatments on each plot.
- Future work: 1. Test effects on ectomycorrhizal fungi only; 2. Test effects of forestry treatments of fungal richness and composition

Contact

E-mail: lyu062@ucr.edu

Github: https://github.com/YULEITSINGTAO/TNC_project