



# Succession of Soil Microbial Communities in a Managed Conifer-Encroached Grassland



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## Introduction

Woody plant encroachment: a widespread phenomenon in grassland ecosystems either by human introduction or by natural spread in their native range (Archer et al. 2017)

- Conifers are one of the most common and prevalent groups of woody plant to encroach on grasslands (Strang and Parminter 1980; Griffiths et al. 2005)
- Shifts biomass distribution in the ecosystem - from mostly belowground roots in grasslands to primarily aboveground woody biomass in the encroachment area (Van Auken 2009)

Conifer encroachment not only rapidly change the vegetation and displaces grassland habitats, but it can also alter the soil microbial biomass and soil nutrients (Banning et al. 2011)

- Few studies have surveyed the changes in soil microbial community composition of conifer-encroached grassland



*Conifers actively encroaching the grassland at Rancho Corral de Tierra*

## Objectives

How do invasive trees impact soil microbial communities on a grassland?

- Examining whether invasive tree encroachment (*Pinus radiata* and *Hesperocyparis macrocarpa*) and tree removal treatment will alter the grassland soil microbial community

## Research Questions

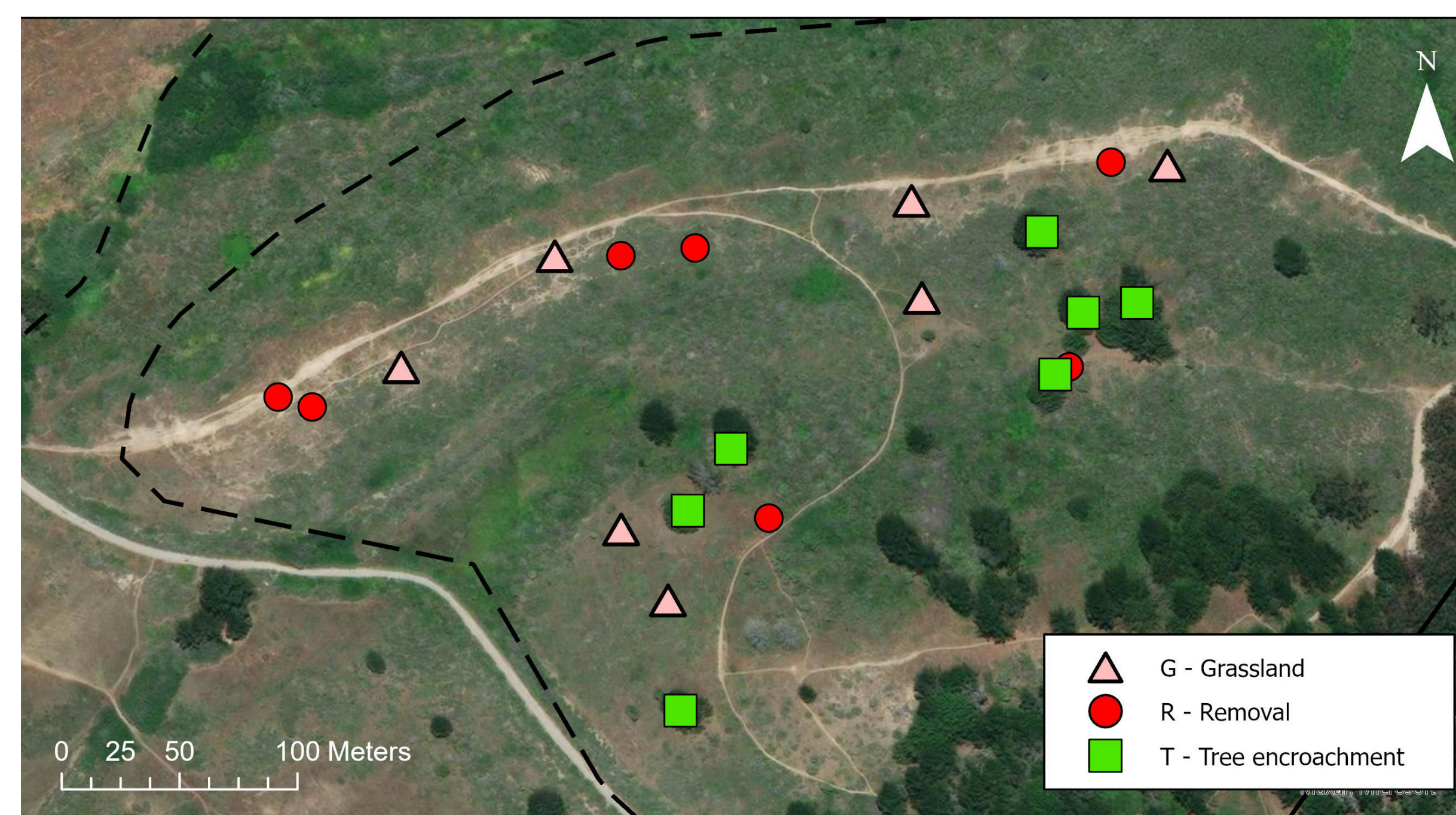
Is there a difference between soil microbial communities among pristine grassland, areas of active conifer encroachment, and areas of tree removal?

- Tree encroachment decrease the alpha diversity of grassland soil?
- Soil microbial community in tree removal sites resembles grassland sites or conifer encroachment sites?
- Environmental factors that may be responsible for altering the soil microbial community?

## Study Design

Study Site: Rancho Corral de Tierra in Montara, CA

- 7 replicates of each treatment
  - Grassland
  - Tree removal
  - Tree encroachment



*Map of sample plots*

I collected three soil samples from the top 15cm at three random directions one meter from the center of the plot and mixed well to generate one homogenized sample



*Soil sampling at a grassland plot (top left), removal plot (top right), tree encroachment plot (bottom left), and ruler showing the thick litter and litter layer at a tree encroachment plot (bottom left)*

## Soil Processing and Testing

Soil samples were tested for

- Soil moisture
- pH
- Total carbon
- Total nitrogen, soil nitrate, soil ammonium
- Soil texture

## Molecular Methods

To identify bacterial and fungal species from all three treatments, I extracted DNA from the soil samples using a commercial DNA extraction kit

*DNA extraction set up*



- Amplified the extracted DNA using the 16S 515F/806R and 5.8S-Fun/IT4-FUN primer sets to target bacteria and fungi
- Gel electrophoresis: Target DNA region was visible on the gel when compared to the DNA ladders

## Next Steps and Analysis

- Amplicon sequencing on the extracted DNA samples
- Raw reads from sequencing will be analyzed using QIIME 2 and grouped into amplicon sequence variants used to identify bacterial and fungal families, genera and/or species
- Statistical analysis (ANOVA) to determine whether there's a significant difference in soil microbial communities among grassland, areas of active conifer encroachment, and areas of tree removal

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