

## Introduction

- The East Helena Superfund site was created by the EPA in response to the severe pollution from the lead smelter that operated in the area from 1888 to 2001.
- Soil remediation was conducted in this area, pictured in Figure 1.1, to attempt to reduce lead pollution in the surrounding environment.
- Our research was conducted in these areas to understand the effects that this pollution, and in turn, the recovery process, has had on the soil microbiome.
- **Hypothesis:** The areas in which remediation was conducted will have greater microbial diversity than the non-remediated sample sites due to the introduction of non-contaminated soil.

## Methods

- Soil samples were gathered from different locations around the East Helena smelter site varying in remediation levels on February 28, 2022.
- DNA was extracted and subsequently quantified from our samples.
- Nanopore Technology was used to sequence DNA to provide microbial composition in each of the twelve samples.



Figure 1.1 The stars located on the map represent approximate areas where sampling occurred. Numbers in legend indicate barcodes in Figure 1.2.

## Results

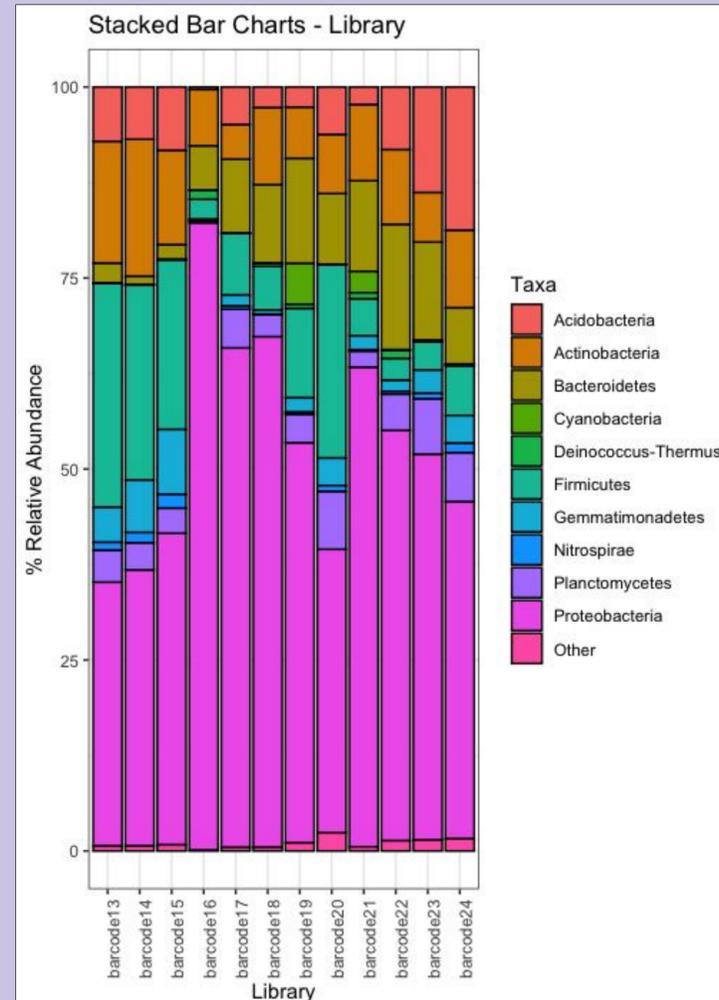


Figure 1.2 Bar chart indicating the relative abundance of bacterial phyla found in each location.

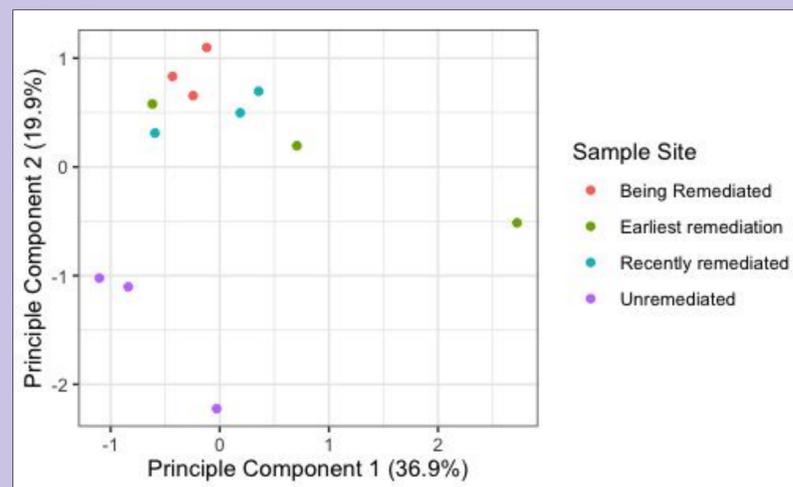


Figure 1.3 Principle Component Analysis plot showing the variation in our samples along two dimensions.

## Results (Continued)

Genus Present:	Sample Site:
<i>Bacillus</i>	Being Remediated, Recently Remediated, Earliest Remediation
<i>Paenibacillus</i>	Being Remediated
<i>Bradyrhizobium</i>	Being Remediated, Earliest Remediation
<i>Gemmatimonas</i>	Being Remediated
<i>Nitrospira</i>	Being Remediated, Earliest Remediation
<i>Noviherbaspirillum</i>	Unremediated, Recently Remediated
<i>Variovorax</i>	Unremediated
<i>Clostridium</i>	Unremediated, Recently Remediated
<i>Sphingomonas</i>	Unremediated, Earliest Remediation
<i>Pseudarthrobacter</i>	Unremediated
<i>Flavisolibacter</i>	Recently Remediated
<i>Massilia</i>	Unremediated, Recently Remediated
<i>Variovorax ginsengisoli</i>	Unremediated
<i>Roseomonas vinacea</i>	Earliest Remediation
<i>Skermanella</i>	Earliest Remediation
<i>Rubellimicrobium</i>	Recently Remediated
<i>Microvirga</i>	Earliest Remediation

## Conclusion

- Based on Figure 1.2, our evidence shows differences in microbial population composition between the four sites.
- Future research with increased sample sizes is needed to evaluate the potential correlation between remediation efforts and soil microbiome diversity.

## Acknowledgments

A special thanks to Dr. Ashley Beck, Sarah Harmon, and Blake Sexton for their continued guidance and support throughout the entirety of our research project.