Abstract

Microbial communities are diverse across time and space. In environmental microbiomes, this diversity plays a role in several functions of microbial communities, including nutrient cycling, nitrogen fixation and carbon sequestration. Determination of microbial diversity across landscapes can help us to better understand the roles that function within the microbiome.

Methods

From the original thirteen sampling sites, six sites and eight samples were selected for sequencing. There were five from September 2020 and three from April 2021. The raw reads were then mapped to reference genomes with the software MIDAS. The results from this mapping were inconclusive, which is believed to be due to the human-centric nature of the database.

Results

We were successful in determining taxonomical inferences of the samples and in calculating the Shannon-Weiner Diversity Index values for the sampling sites. The taxonomical inferences were determining using the ribosomal S11 single copy core gene.

In this study, microbial samples were taken from a series of thirteen pools in Cold Creek, a breeding place for highly diverse amphibian populations in the Santa Monica mountains.