

# Microbial Diversity Across Cold Creek

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## Abstract

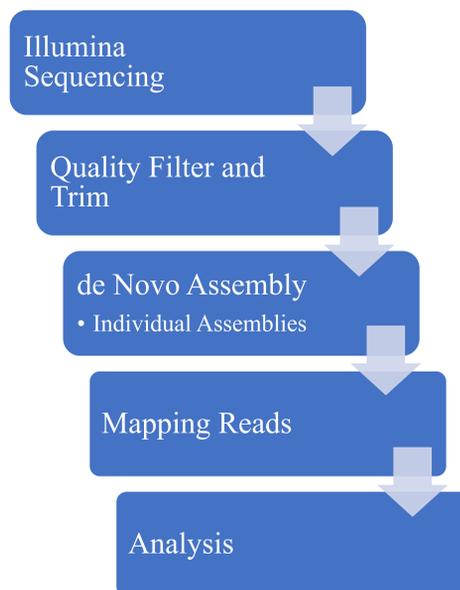
Microbial communities are diverse across time and space. In environmental microbiomes, this diversity plays a role in several functions of microbial communities, including nutrient cycling, nitrogen fixation and carbon sequestration. Determination of microbial diversity across landscapes can help us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



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.

## 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.



Given that environmental microbiomes are so diverse and contain several potential unknown species, we de novo assembled genomes using the raw reads from the eight samples with the Anvi'o software. (Murat Eren et al., 2015) After performing the quality filter, trim and individual assemblies, the reads were mapped to the assembled genomes. During the assembly process there were some issues regarding memory and co-assembly of all eight samples. To rectify the situation we did individual assemblies for all eight samples. With the individual assemblies, we inferred species abundances with the Anvi'o software. Finally, we analyzed the results to determine alpha diversity with the Shannon-Weiner Index.

## 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.

Table 1. Species Abundance across sampling locations for the ten most prevalent species.

	E1_1	E1_3	E6_1	E6_3	E9_1	E11_1	E12_1	E13_3
<i>Proteobacteria Alphaproteobacteria Rhizobiales Methylophilaceae Methylophilum</i> None			20.63	8.44	0.00	8.14	15.26	44.43
<i>Proteobacteria Alphaproteobacteria Rhodobacterales Rhodobacteraceae</i> None & None	16.39		3.02	0.00 & 4.24			6.27	4.28
<i>Actinobacteriota Acidimicrobia Acidimicrobiales Microtrichaceae ATN2 ATN2 sp003577145</i>			8.30	0.92	0.00	6.97		6.08
<i>Proteobacteria Gammaproteobacteria Steroidobacteriales Steroidobacteraceae ZC4RG30</i> None			20.08		0.00	43.10	18.96	24.18
<i>Bacteroidota Bacteroidia Cytophagales Cyclobacteriaceae ZC4RG29 ZC4RG29 sp003242315</i>	6.35		2.42	0.91	0.00	3.36	7.00	7.22
<i>Chloroflexota Anaerolineae Promineofilales Promineofilaceae CAADGU01 CAADGU01 sp014584575</i>			6.79		0.00 & 0.00	12.28	5.13	
<i>Actinobacteriota Actinomycetia</i> None None None None			20.44	2.37 & 0.79	0.00	14.49		
<i>Proteobacteria Gammaproteobacteria UBA6522 UBA6522 FEN-1219 FEN-1219 sp011054615</i>				4.35		8.77	3.55 & 3.75	15.62 & 18.32
<i>Nitrospirota Nitrospira Nitrospirales Nitrospiraceae Palsa-1315</i> None			16.31	1.30	0.00 & 0.00		5.42	
<i>Proteobacteria Gammaproteobacteria Xanthomonadales SZUA-36 JABDPF01 JABDPF01 sp013001885</i>			8.88	5.04	4.45		3.06	5.20

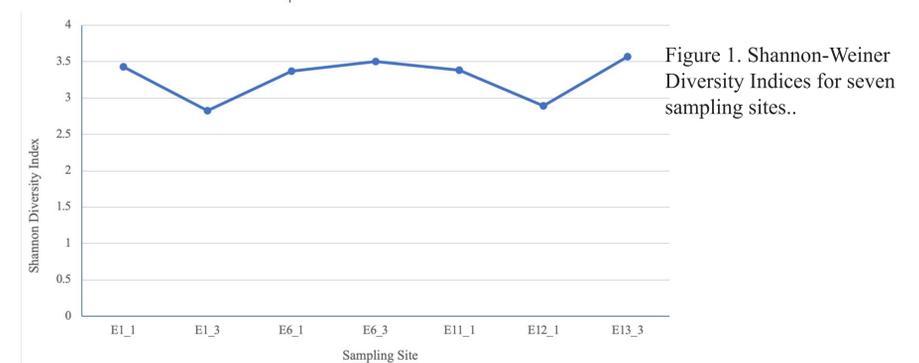


Figure 1. Shannon-Weiner Diversity Indices for seven sampling sites..

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Eren, A. M., Esen, Ö. C., Quince, C., Vineis, J. H., Morrison, H. G., Sogin, M. L., & Delmont, T. O. (2015). Anvi'o: an advanced analysis and visualization platform for omics data. *PeerJ*, 3, e1319.