Macroinvertebrate Barcoding

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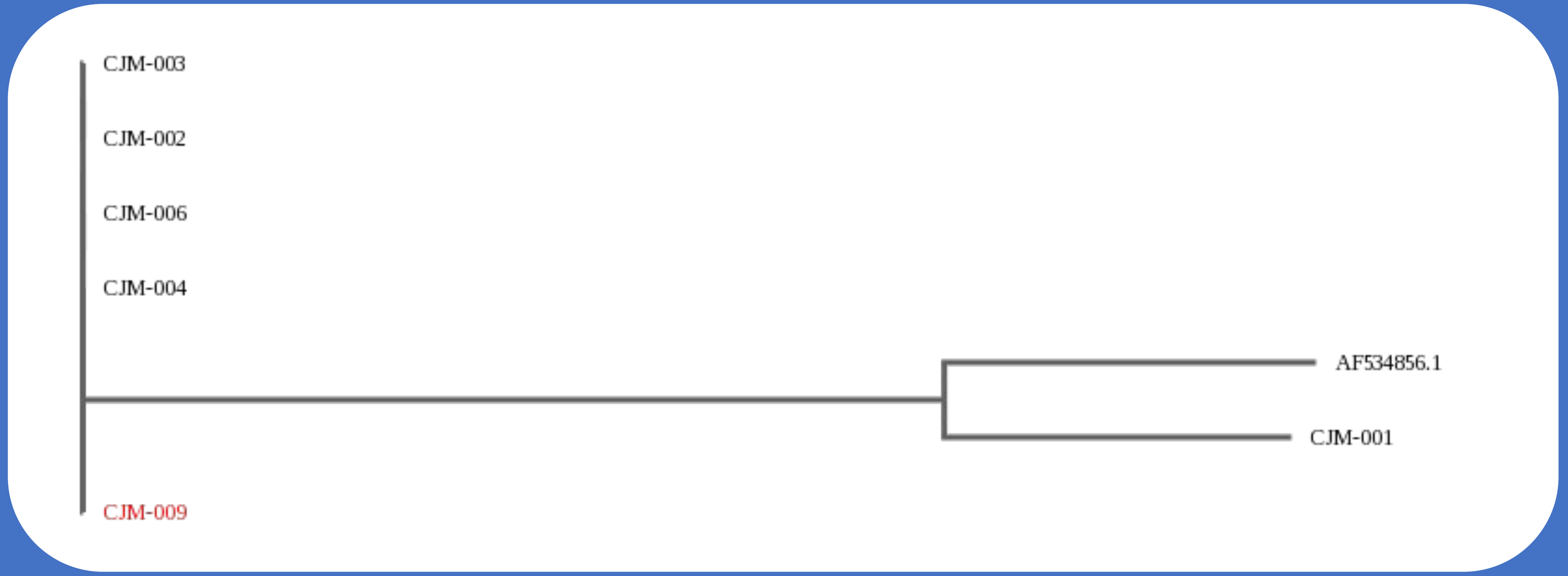
Abstract

The biodiversity of Massapequa Creek has been a concern for decades due to anthropogenic pollutants threatening its biological integrity. Collecting samples of macroinvertebrates from the Massapequa Preserve is expected to give a scope of the biodiversity in the preserve. The samples were collected manually and from a streambank in the Massapequa Preserve, and then barcoded with the assistance of Cold Spring Harbor Laboratories. The goal is to be able to gauge differences in the biodiversity of the Massapequa Preserve. Basic gear was used, such as latex gloves, waders, and sieves. The results gathered showed that 7 of the 9 samples that worked were the same species, and the other two samples were each different species. The results suggest that the area is dominated by that one species or that the species has a very large population. The other two samples show that other diversity is present, but is not as dominant in that area as the species that was repeated. Overall, the data supports that, while biodiversity is present in the Massapequa Preserve, it is fairly low, especially for a moist riverbank.

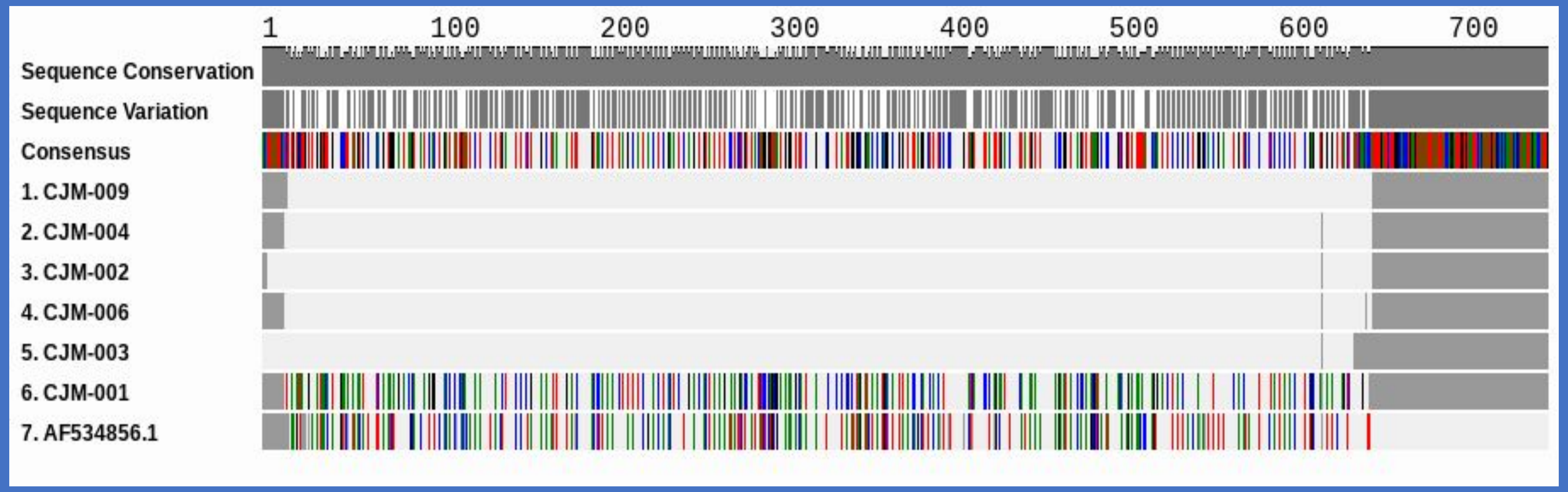
Introduction

This project's aim is to provide a small portion of information regarding Massapequa Preserves' biodiversity. It's important to regularly collect data on the status of biodiversity in ecological communities to define the status of that ecosystem and the threat of a species becoming endangered. In this study, organisms from Massapequa Preserves creek were collected and analyzed to find their identity as well as their possible relationships to other species.

ML-Tree



Alignment Viewer



Materials & Methods

Materials: Waders, nitrile gloves, a sieve, collection tubes containing ethyl alcohol

Method:

1. Locate a body of freshwater with a shallow entry point during late September and record its coordinates.

2. Put on chest high or waist high waders as well as nitrile gloves before entering the water.
Gather various materials, such as rocks, logs, sticks, soil, and aquatic plants, and sift through them.

3. The discovered macroinvertebrates were photographed, put into collection tubes filled with ethyl alcohol and labeled. The tubes were frozen at -20 degrees celsius.

4. DNA from the procedure was isolated, amplified, analyzed, and sequenced in accordance with Cold Spring Harbor Laboratory procedure.

Results

Many of our samples turned out to be the same genus of isopod crustacean, Proasellus. Out of our 7 samples, excluding CJM-007 and CJM-008 due to both samples' data being unusable, only 1 of our samples were not of the Proasellus genus. CJM-001 was identified as Eukerria Saltenesis, a subtropical earthworm closely related to Ripistes parasita, another oligochaete primarily found in the Palearctic region. It should also be noted that despite the fact CJM-009 was identified as being apart of the genus Proasellus, it's distant from other Proasellus samples on the ML tree.

Discussion

The results of this experiment provide two most likely outcomes: either the species that was sampled many times has a large population in the preserve, or they are simply the dominant species of that area. Since this one organism occupied more than half of the samples, and only two samples were of different species, it is possible that the area that was sampled had a fairly low biodiversity and was dominated by that species. The data did not necessarily support the hypothesis because the biodiversity sampled was very low, but the hypothesis was not properly designed anyway, as 10 possible samples is not nearly enough to accurately represent any level of biodiversity.