In this work, we consider whether spatial proximity and environmental factors influence the composition of microbial communities. We approach this question by applying two different measures of diversity to microbial communities sampled along the Atlantic seaboard. Using the sampling frequency considered, we find no correlation between spatial proximity and community composition. However, we do find strong evidence that salinity has a significant influence on the composition of microbial communities.

Sequencing of 16S rRNA genes directly from environmental samples has revolutionized our understanding of microbial diversity and provided valuable insights into the ecological roles of microbial communities. In this work we consider the influence of spatial proximity and environmental factors on the diversity of microbial communities along 15 samples from the Global Ocean Sampling (GOS) project that are situated along the Atlantic seaboard at an average interval of 320 km [1].

We characterize differences in microbial communities using two distinct diversity measures: the Bray-Curtis Index (BCI) [2] which quantifies differences in the number of taxa present in each community; and UniFrac [8], an extension of UniFrac which accounts for both community richness and evenness. These measures were generated for each of the 15 samples obtained from the GOS project.

UniFrac [8] characterizes the diversity of two microbial communities as the amount of divergent evolution that has occurred between them. This is achieved by using a phylogenetic tree to calculate the fraction of branch length that leads to descendents from a single community. Using the UniFrac-based diversity measure removes the need to define taxonomical units which can often be arbitrary.

We explain the UniFrac diversity measure using two examples. In these examples, there are two microbial communities identified by red squares and blue circles. The branches coloured purple are those that lead to descendents from a single community. UniFrac measures the amount of evolutionary divergence between these two communities by dividing the length of the purple branch by the total branch length of the tree. The example on the left shows two communities which have little evolutionary divergence and therefore a relatively low UniFrac distance. In contrast, the example of the right shows two communities that are maximally different as their lowest common ancestor is the root of the tree.

In this section we investigate if the 11 coastal samples along the Atlantic seaboard form a cline. We qualitatively approach this question by extending GenGIS [1] to support the visualization of tree structures with geography. To aid in the rapid assessment of spatial relationships, the tree topology is optimized to minimize the number of branch crossings which occur between leaf nodes. As such, each crossing indicates a discordance between geographical location and tree topology.

The image contains a UPGMA tree indicating the similarity of microbial communities under the weighted UniFrac diversity measure. This image clearly illustrates that there is little relationship between community similarity and geographical location. This result is consistent with the work of Fuhrman et al. [6] who identified a latitudinal cline where the richness of microbial life, although further research is needed to support this hypothesis.

We found no evidence supporting an Atlantic seaboard cline regardless of whether differences between microbial communities characterized by taxon-level differences (BCI) or evolutionary divergence (UniFrac). More generally, in our dataset where the distance between samples is on the order of several hundred kilometers, we found no correlation between spatial proximity and community composition. It would be interesting to investigate at what scale community composition and spatial proximity begin to strongly correlate.

The hypothesis that salinity is a major determinant of microbial community composition is strongly supported by our results. We also found limited evidence suggesting that pollution can influence the composition of microbial communities and recommend continued research be performed to further support this hypothesis. These conclusions are supported by both our weighted UniFrac analysis and our BCI analysis for all taxonomical ranks from and including class to genus.

We investigated whether or not environmental factors influence the composition of microbial communities by dividing our samples into different environmental types (as described in the Introduction).

For both BCI and weighted UniFrac we constructed control trees which indicate the relationships between the 15 GOS samples. Sequence jackknifing was performed to determine the robustness of each clade. Both community trees were similar.

1. The estuary samples are highly similar and distinct from samples found in the other environment types.
2. The Bay of Fundy sample is similar to the coastal samples.
3. The Halifax Harbour sample is distinct from all other samples. However, the low salinity of the Halifax Harbour clade suggest that this may be the result of sequencing bias.

The weighted UniFrac principal coordinates plot further clarifies the relationship between these environment types. It shows that all coastal samples along with the Bay of Fundy sample form a single cluster, that the two estuary samples form a second cluster, and that the Halifax Harbour sample is well isolated from all other samples. Similar results are obtained under BCI for all taxonomical ranks from and including class to genus.

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