

Quantifying the Variation in Bacterial Diversity between Lake Michigan Beaches using Next Generation Sequencing

Gina Kuffel^{1,2}, Vinicio Reynoso^{1,2}, April Williams^{1,2}, Catherine Putonti^{1,2,3}

1 Bioinformatics Program, Loyola University Chicago, Chicago, IL 60626

2 Department of Biology, Loyola University Chicago, Chicago, IL 60626

3 Department of Computer Science, Loyola University Chicago, Chicago, IL 60611

Advances in the amount of data which can be generated by next-generation sequencers provide us with a unique opportunity to assess not only the microbial members present within environmental samples, but also the genes being expressed. High-throughput sequencing was conducted using the Illumina Genome Analyzer System for 3 samples collected from near shore waters at different Lake Michigan beaches including 57th St. Beach, Montrose Beach, and Loyola Beach. Recently, we have developed a new software suite specifically for the mapping of short reads. Using this tool, we performed an extensive analysis of the different beach samples, identifying what species and genic regions were present. Comparisons of the results from each beach were conducted. In addition, we have compared these results to those obtained from culturing samples in the laboratory and 16S sequencing of colonies. Herein, we present the preliminary results of our study.