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Summary of Progress and Future Steps

The goal of this current project is to employ metagenomic analysis tools to construct genomes for and further characterize *Bifidobacterium infantis* (*B. infantis*)*,* a common colonizer of the human infant gut. *B. infantis* is capable of digesting human milk oligosaccharides (HMOs), which are the third most abundant solid component of human milk. Interestingly enough, HMOs cannot be independently digested by infants, and it seems as though HMOs are produced solely to sustain microbes such as *B. infantis.* Additionally, the presence of *B. infantis* in the infant gut has been positively associated with long-term human health. It is our hope to use publicly available infant gut metagenomes in order to assemble *B. infantis* genomes across populations around the world. In doing this, we intend to analyze the genetic variation between strains of the microbe, and further characterize the biogeographic stratification of *B. infantis.*

The past summer and fall semester were used to lay a foundation for this large project. Firstly, a list of papers with corresponding public metagenomic databases was compiled and cataloged. Next, papers discussing the more technical aspects of metagenomic assembly were read, and a series of helpful tools were noted down. In order to assess the quality of the public databases we collected, and to see if *B. infantis* could be found, the Web Basic Local Alignment Search Tool (WebBLAST) and the Joint Genome Institute’s Integrated Microbial Genomes & Microbiomes (IMG/M) systems were trialed. Though some search results were found using WebBLAST, it was determined that better and more reliable results would be collected through a different method.

Due to this, I met with Lauren Tso ‘20 to learn more about the computational tools she used to conduct metagenomic analysis for the Environmental influences on Child Health Outcomes (ECHO) project. I procured two files written in Python from her, and I am currently working on debugging and using the file. Firstly, in order to be able to work remotely through the lab’s computer, Hopper, I learned how to use my computer’s Terminal to connect to Hopper. I then downloaded miniconda for Python 3 onto Hopper, and proceeded to install all of the necessary tools. I also made a git repository for this project, and have been refamiliarizing myself with GitHub. Finally, I installed bowtie2 onto Hopper, and hope to begin using this program as well.

Clearly, this project is still in its infant stages, and there is lots of work to be done. My first order of business is to get Lauren’s files running in order to compile a list of metagenomes containing *B. infantis*. In order to familiarize myself with computational biology and bioinformatics using Python, I am taking a Coursera class titled “Biology Meets Programming: Bioinformatics for Beginners,” of which I have completed 25%. Concurrently, I hope to research bowtie2, and begin to use this program to see if it will be more useful for the purposes of this project. If this is not sufficient, I will attempt to write julia code to achieve the desired result. In addition, I plan on making a figure to encapsulate this work.

After this, the list of metagenomic assembly tools previously compiled will be consulted and reviewed in order to find a program or programs to be used to construct the individual *B. infantis* genomes. This will allow us to finally study the genetic variation between strains of *B. infantis,* and to see if there are any connections between the genetic variation and the location from which the strain was found. This has potential to illustrate the differences that arise between the gut microbiomes of infants from Westernized and non-Westernized lifestyles. Additionally, since *B. infantis* is not found in all infant guts due to many factors, this study can eventually allow us to observe whether the presence of *B. infantis* could be connected to genetic or environmental factors. The study of *Bifidobacterium infantis* through this project will be exciting and thrilling, and can help us understand the connection between this important infant gut microbe and long-term human health.