QIIME 1.9

QIIME1 was installed as a virtual machine using the latest Virtual Box Image from the QIIME website (<http://qiime.org/install/virtual_box.html>) and using the latest Virtual Box Version (<https://www.virtualbox.org/>). The instructions for installation can be found at <http://qiime.org/install/install.html> .

Install Miniconda 4.7.12

Miniconda was first installed which can be found at <https://docs.conda.io/en/latest/miniconda.html>

Install dependencies

<https://github.com/conda-forge/matplotlib-feedstock>

QIIME2

The QIIME2 microbiome bioinformatics platform was used to perform the microbiome analysis of the 16S rRNA samples. All of the information pertaining the installation procedure can be found at <https://docs.qiime2.org>.

Installing QIIME2:

QIIME2 was installed as a virtual machine using the latest Virtual Box Image from the QIIME2 website (<https://docs.qiime2.org/2020.2/install/>) and using the latest Virtual Box Version (<https://www.virtualbox.org/>).

Data used in this study:

The sample data used for this study can be found at (<https://qiita.ucsd.edu/>). The sample data files are the V4 region of the 16S rRNA gene that were sequenced using Illumina MiSeq machine which generated paired sample files with dual index. These sequence sample files are in the FASTQ format. Additionally, there was sample metadata files generated by the researchers at the site of collection which described location, size and habitat of each specimen. The metadata sample files are in the .tsv format.

Importing Data into QIIME2

QIIME2 references:

Bolyen et al., 2019