Install QIIME2 and Complete Tutorial

The documentation can be found at https://docs.qiime2.org/2024.10/

Installation instructions:
https://docs.qiime2.org/2024.10/install/

Tutorial (Moving Pictures): You will need to download the metadata and the raw sequence files
https://docs.qiime2.org/2024.10/tutorials/moving-pictures/

ASSIGNMENT: Turn in fully commented QIIME2 code and a tutorial describing the analysis data and results.

1) Put all the QIIME2 code for the moving pictures tutorial into a **text fil**e and comment every line (#) explaining the purpose of the command or option.
2) In another file (**turn in a pdf**) make a tutorial with screenshots explaining each of the input data and the results from the analyses. These should be done as figures with figure legends with 2-3 per page depending on the size. (If the figure or table is too big, just show a portion of it. In addition to the result images, also include figures and explanations for the following:
   a. The metadata file
   b. The barcode file
   c. A .qza file including citations and provenance
   d. The rep-seq file – see below on how to export
   e. demux.qvz – what is this and what does it show?
   f. stats-dada2 – what is dada2 and what does this mean?
   g. table.qvz – interactive sample detail (change sampling depth; feature detail)

   h. (to export files from use
```
mkdir Rep-seqs
qiime tools export \
  --input-path rep_seq.qza \
  --output-path Rep-seqs/
```

Results:
       Beta-diversity plots: Show body-site for all four metrics. (antibiotic for one)
       Rotate the plots so you can see all three dimensions. Which metric explains the most variation on the first PC axis?

Alpha-diversity : Interpret body-site and antibiotic-usage results for both metrics.

Show and explain barplot analysis (genus or family level) and the taxonomic analyses.