

Raw illumina reads: Forward, Reverse, Barcode

Import data: qiime tools import

Preprocessing:

- Demultiplexing (qiime demux)
- Cut adaptor contamination (qiime cutadapt)
- Denoise, cluster (dada2)

Sequences

Features table

Filtering (qiime2 tutorial – filtering data):

- Frequency-based?
- Contingency-based?

Phylogeny :  
Alignment (mafft)  
Tree (RAxML) :

- GTRGAMMA
- 100 Bootstr.

Diversity analyses  
Taxonomic analyses  
Biome analyses  
Etc.