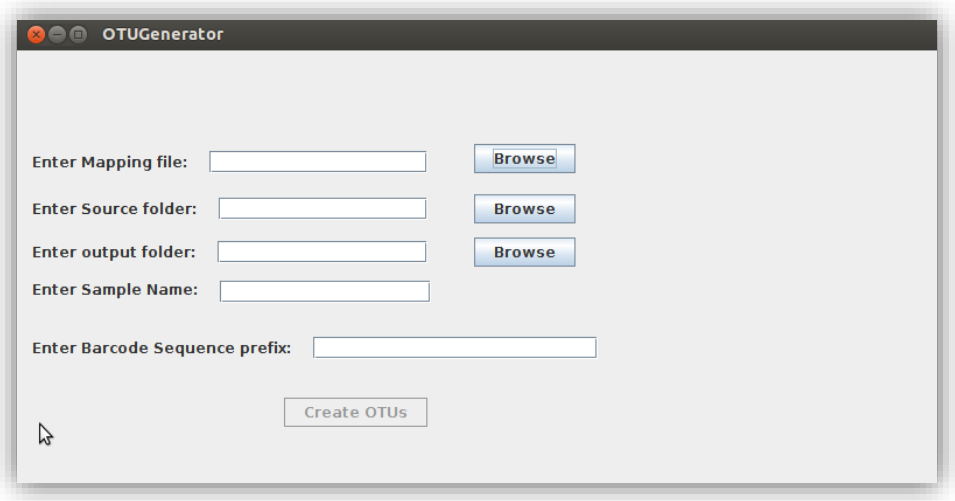
User Manual – OTUGenerator Software



This utility software facilitates joining of paired-end reads, creation of the seq.fna file and generation of OTU tables using open, closed and De Novo picking.

Note: Extract the .zip file which contains a folder with the files automat_qiime.py and the JAR file OTUGenerator.jar. This folder can be placed in any directory, however, make sure it contains both the files at all times.

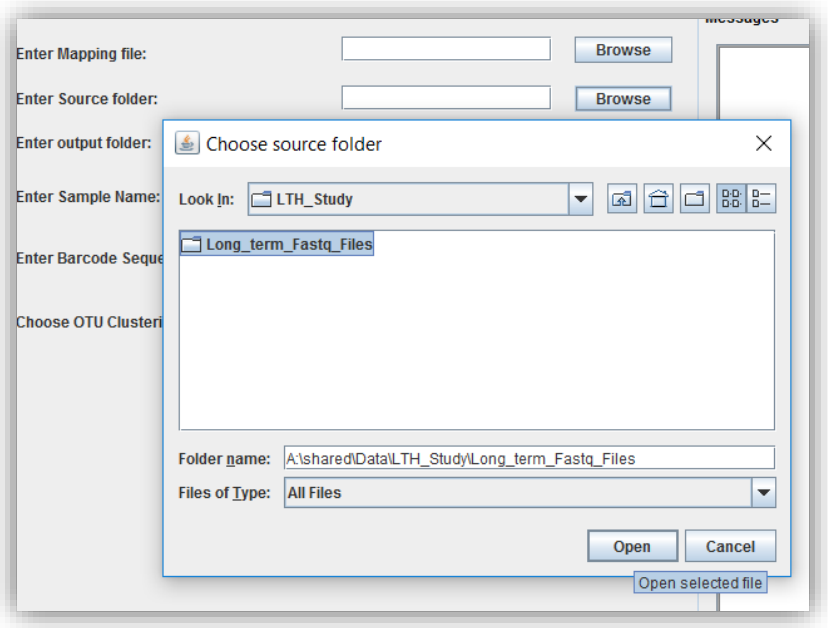
Step 1:

Locate the mapping file using the Browse button. The mapping file MUST contain a column named 'SampleID' and a column named 'Grouping' as shown below.

#SampleID	BarcodeSequence	LinkerPrimerSequence	Sample	Illumina Ba	Illumina Ba	Grouping

Step 2:

Locate the source folder which contains all the FastQ files and provide its path using the Browse button.



Step 3: Locate the output folder you would like the software to generate the OTU Tables and intermediate files in.

Step 4: Type in the sample name which is the common prefix of all fastq files (Illumina naming convention). Example shown below in red.

Step 5: Type in the barcode sequence prefix common to all fastq files. (Shown below in green)

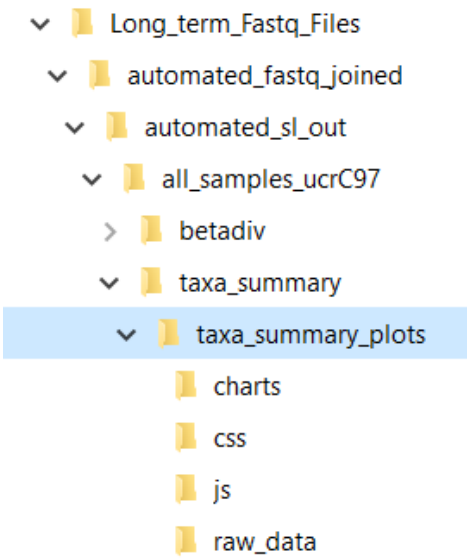
Sample fastq file name: 1-VM1-338rcbc1_S1_L001_R1_001.fastq

Step 6: Choose the desired OTU clustering technique from the drop down list.

Step 7: Click the button Create OTUs. All the outputs would be created in the output directory you mentioned in Step 3.

In the output directory, look for a folder named: “automated_fastq_joined”

This folder contains the following



The folder taxa_summary_plots contains plots showing graphs representing changes in abundancy of OTUs over samples.