QIIME2-DEBLUR PROCEDURE TO MAKE OTU TABLES

Start qiime2
source activate qiime2-2018.6

Go to qiime2 folder
```
cd qiime2
```

Make directory to work in
```
mkdir q2_"todaysdate"
cd q2_"todaysdate"
```

Make manifest file which shows path to data files
sample-id,absolute-filepath,direction
sample-1,$HOME/path/"name".fastq,forward
sample-2,$HOME/path/"name".fastq,forward
sample-1,$HOME/path/"name".fastq,reverse
sample-2,$HOME/path/"name".fastq,reverse

Import files
```
qiime tools import --type 'SampleData[PairedEndSequencesWithQuality]' --input-path manifest --output-path paired-end-demux.qza --source-format PairedEndFastqManifestPhred33
```

Denoise with Deblur
https://docs.qiime2.org/2018.6/tutorials/read-joining/

Join pairs
```
qiime vsearch join-pairs --i-demultiplexed-seqs paired-end-demux.qza --o-joined-sequences demux-joined.qza
```
**Can vary the --p-maxdiffs parameter (default is 10)*

View summary
```
qiime demux summarize --i-data demux-joined.qza --o-visualization demux-joined.qzv
```

Quality filter
```
qiime quality-filter q-score-joined --i-demux demux-joined.qza --o-filtered-sequences demux-joined-filtered.qza --o-filter-stats demux-joined-filter-stats.qza
```

Deblur
```
qiime deblur denoise-16S --i-demultiplexed-seqs demux-joined-filtered.qza --p-trim-length 250 --p-sample-stats --o-representative-sequences rep-seqs.qza --o-table table.qza --o-stats deblur-stats.qza
```

Export table
```
mkdir exported
qiime tools export table.qza --output-dir exported
qiime tools export rep-seqs.qza --output-dir exported
```

Convert biom to tab file
```
biom convert -i exported/feature-table.biom -o table.txt --to-tsv
```