**Notes to analyse the 16S rRNA gene (full length) sequencing data from Genewiz (Sanger sequencing)**

*Updated on 2018-06-15 (SE)*

**Before starting, make sure to have the following:**

1. The ab1 sequence files for each sample from Genewiz into a single folder.
2. The two python scripts for merging the paired sequences (forward and reverse): *mergeGenewizSeqs.py* and *mergeGenewizAb1\_SE.py*
3. *Note: In addition, you may need to install the biopython and numpy packages (if not installed already).*

**Then, open the terminal:**

1. Run the merging script:

*python mergeGenewizAb1\_SE.py*

1. *Merge all fasta\_merge files into a single fasta file by running:*

cat \*-merged.fasta > merged.fasta

1. To assign taxonomy, submit the *merged.fasta* file to the RDP classifier: <http://rdp.cme.msu.edu/classifier/hierarchy.jsp;jsessionid=00A6C6E30C2828C56401B137A8527881.radiant>

Or to the Silva classifier: [*https://www.arb-silva.de/aligner/*](https://www.arb-silva.de/aligner/)