Protocols for 16S Analysis of Sanger Seq from University AZ Genetics Core

\*UAZ Genetics Core used EdgeBioSystems ExcelaPure PCR purification blocks and Applied Biosystems 3720 DNA Analyzer (DNA sequencing). Provide chromatograph and sequence files with no quality scores.

1. Obtain permission and downloads for *phred* (Ewing and Green 1998)
2. Create a folder for the chromatograph files (.ab1)
3. Install *phred*
4. Assign Q scores with *phred*
5. Convert Q scores to Ascii values and combine into fastq file (Python Script)
6. Quality trim reads using *fastp*
   1. Default sliding window: 4
   2. Front mean score=25
   3. Cuttail mean score=25
7. Upload fastq file to RDP Classifier