



- ① Provide information about sequencing types and desired outputs, etc.
- ② Provide raw sequencing filenames/locations.
- ③ Quality control and read filtering (optional)?
- ④ Whole genome vs. targeted sequencing branch point. (Will tNGS be used?)
- ⑤ If tNGS, then may have to map reads instead of assemble, but maybe not.
- ⑥ Assemble reads with software appropriate for sequence type (unicycler).
- ⑦ Identify and curate exact target sequences. Build phylogenies for each and concatenated.
- ⑧ Determine ANI against database known NTM assemblies.
- ⑨ Make ABX susceptibility determinations based on appropriate existing methodology.
- ⑩ Estimate most likely species based on target/genomic phylogenies and/or ANI.
- ⑪ Semi-hard coded database of sequence targets (hsp65, rpoB, tlyC, etc.). Could be updatable.
- ⑫ Semi-hard coded database of antibiotic targets and rules. Could be updatable.
- ⑬ Hard coded database of NTM assemblies and pre-computed ANI comparisons.
- ⑭ Newick phylogeny outputs for use in any tree visualization program.
- ⑮ Phylogenetic tree images.
- ⑯ Reports for species, antibiotics, logs, intermediate files, etc.