**Prokka**

To get annotation of multiple files in one go:

#!/bin/sh

source /apps/profiles/modules\_asax.sh.dyn

module load anaconda/3-2020.02

for file in \*.fna; do tag=${file%.fna};

prokka --prefix "$tag" --locustag "$tag" --increment 10 \

--outdir "$tag"\_prokka --force --addgenes --genus Xylella --gcode 11 "$file"; done

**Pseudofinder (Annotate)**

python3 pseudofinder.py annotate --genome GENOME.GBF --outprefix PREFIX --database /PATH/TO/NR/nr --threads 16

**CheckM (For assessing the quality of genomes)**

#!/bin/bash

module load drep

checkm lineage\_wf -t 14 --reduced\_tree -x fasta ./ ./checkm