hutlab load centos7/python3/biobakery\_workflows/3.0.0-beta-devel-dependsUpdate

conda install -c bioconda/label/cf201901 metabat2 (other version doesn’t work)

conda install -c bioconda checkm-genome

conda install -c bioconda assembly-stats

conda install -c bioconda fastani

For checkm to work on hutlab load, need to run: export SETUPTOOLS\_USE\_DISTUTILS=stdlib