**Roary (To generate a core gene alignment)**

#!/bin/bash

# script to run roary

#

# load the module

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

module load roary/3.13.0

#

# run roary

roary -e --mafft -p 8 \*.gff

**RAxML (To create a phylogenetic tree with core gene alignment)**

#!/bin/bash

#

#  load the module

source /opt/asn/etc/asn-bash-profiles-special/modules.sh

module load raxml/8.0.24

#

#  put RAxML commands here

raxmlHPC-SSE3 -m GTRGAMMA -p 12345 -s core\_gene\_alignment.aln -n T1 -f a -x 123 -N 1000 -p 456