

Picard

If you want to run Picard's Mark Duplicates on Lonestar, do roughly this:

```
module load picard
# "picard" is not the name of the tool; picard is a collection of java .jar files that do things, so we have to
figure out where they are and which ones they are, like this:
ls $TACC_PICARD_DIR
# Now to run Mark Duplicates, do something like:
java -Xmx2g -jar $TACC_PICARD_DIR/MarkDuplicates.jar INPUT=all.bowtie.sorted.bam OUTPUT=all.bowtie.sorted.dedup.
bam METRICS_FILE=all.bowtie.sorted.dedup.bam.metrics ASSUME_SORTED=TRUE
```

The output metrics file is required and worth screening before you go further.

Picard is also installed on fourierseq at /usr/local/genome/bin and the jar files are in fourierseq user's paths.

General syntax for using picard jar files:

```
java -Xmx4g -jar /usr/local/genome/bin/jarfilename
```

Find picard document [here](#)