

Gatk4

To get the full list of available tools within GATK4 toolkit see [official web page](#).

How to use:

Available versions and modules:

| Version | Module |
|---------|---------------------|
| 4.2.6 | bioinfo/gatk4/4.2.6 |

Example:

```
#!/bin/bash
#$ -N test_job
#$ -cwd
#$ -q a12.q 1
module load bioinfo/gatk4/4.2.6
gatk --java-options "-Xmx8G" HaplotypeCaller -R reference.fasta -I input.bam -O output.vcf
```

Most tools can not use more than one thread so you need to send your jobs to the serial queue.



Multithread jobs

For tools that use multiple threads you need to make sure the tool uses the exact number of threads you requested. Multithread jobs must be sent to mpisingle parallel environment as this tools can not be used cross multiple nodes.