

## 1. Complete Program Installation

\* See [\[\[Installation\]\]](#)

## 2. Configure Program Input

\* See [\[\[Configuration\]\]](#)

## 3. Start Your 1st Pipeline

- To start your pipeline, pass your [\[\[Configuration\]\]](#) file path \$CONFIG\_PATH to the [biolockj](#) command:

```
biolockj $CONFIG_PATH
=====
BioLockJ JAR: /projects/afodor_research/apps/BioLockJ/dist/BioLockJ.jar BioLockJ
Config File: /projects/afodor_research/apps/BioLockJ/resources/test/config/hpc/
testKraken.properties BioLockJ started successfully!
=====
```

- Verify [biolockj](#) command output is accurate:
- BioLockJ JAR file path is valid
- BioLockJ [\[\[Configuration\]\]](#) file path is valid
- Verify message "BioLockJ started successfully!" is printed.

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## 4. Check Pipeline Status

- Check pipeline progress by tailing the pipeline Java log file with [blj\\_go](#) and [blj\\_log](#):

`blj_go` # Go to your newest pipeline `blj_log` # Tail pipeline log file \* Verify java is running:

```
ps -u $USER psu PID TTY TIME CMD 16499 pts/45 00:36:21 java 188510 pts/45
00:00:00 bash ... * If running modules on the cluster, check status of BioLockJ scripts on
the job queue (command depends on job queue implementation):
```

```
qstat -u $USER Req'd Req'd Elap Job ID Username Queue Jobname SessID NDS TSK
Memory Time S Time
```

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```
530799.cph-m1.uncc.edu msioda cph_shor 04.0_PearMergeRe 44312 1 8 64gb 01:00:00 C
00:19:23 530800.cph-m1.uncc.edu msioda cph_shor 04.1_PearMergeRe 36453 1 8 64gb
01:00:00 D 00:05:22
```