

How to make commands run in parallel

Say you have a job file:

```
#PBS HEADER

module load java
module load fastqc

fastqc file1.fq
fastqc file2.fq
```

This will run each line to completion before running the next – the steps are sequential. If you want both fastqc jobs to run at the same time, you can modify the file very slightly:

```
#PBS HEADER

module load java
module load fastqc

fastqc file1.fq &
fastqc file2.fq &

wait
```

The & says that this command can run in the background and the job will move to the next command as long as there is an available processor in your requested reservation. The “wait” is CRITICAL. If you forget it, the job will start all the commands in the background and then think it is done. “Wait” tells it to wait for all child processes to complete before moving forward.

You can do the same thing in the command line – by putting an & at the end of the line, you can automatically push jobs to the background (an alternative to running the command, ctrl-z, bg).