

Submitting jobs without writing qsub scripts

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When you submit a job with `qsub`, you would normally put a few lines of PBS directives followed by your commands in a job submission script say, `job.qsub`, and then type `qsub job.qsub` on the command line. However, if you want to submit multiple jobs in parallel, and they are only slightly different from each other, creating as many `qsub` scripts as there are jobs can be frustrating.

In the example below, we used `seqtk` to randomly sample 1% of the reads from paired-end fastq files. We tried two different seeds (`-s100` and `-s500`) and, to keep pairing, the seed was the same for read files 1 and 2. The way each of these four jobs is submitted is by echo-ing (`echo`) and piping (`|`) commands to `qsub`, without needing a script to contain them.

```
echo "module load seqtk/1.0; seqtk sample -s100 /mnt/re-  
search/common-data/Examples/RNASeq-Model/data/ERR315325_1.fastq  
0.01 > ~/out1_r1.fq" | qsub -l walltime=00:30:00,mem=50mb -N out-  
1_r1
```

```
echo "module load seqtk/1.0; seqtk sample -s100 /mnt/re-  
search/common-data/Examples/RNASeq-Model/data/ERR315325_2.fastq  
0.01 > ~/out1_r2.fq" | qsub -l walltime=00:30:00,mem=50mb -N out-  
1_r2
```

```
echo "module load seqtk/1.0; seqtk sample -s500 /mnt/re-  
search/common-data/Examples/RNASeq-Model/data/ERR315325_1.fastq  
0.01 > ~/out2_r1.fq" | qsub -l walltime=00:30:00,mem=50mb -N out-  
2_r1
```

```
echo "module load seqtk/1.0; seqtk sample -s500 /mnt/re-  
search/common-data/Examples/RNASeq-Model/data/ERR315325_2.fastq  
0.01 > ~/out2_r2.fq" | qsub -l walltime=00:30:00,mem=50mb -N out-  
2_r2
```

It should be noted that, in the above examples, each job is as simple as a one-liner command. For larger jobs, writing a `qsub` script in the usual way would still be preferable.

More information about Singularity and how to use it can be found on the HPC Wiki (<https://wiki.hpcc.msu.edu/display/hpccdocs/Singularity>).