

Job Script Template

If you don't want to run jobs interactively, I've made a "job script" template for all of you to use!

[job_template.q](#)

Job scripts, or PBS batch scripts, are text files that have all of the job setup information for the batch system as well as any commands that you want to be executed. These job scripts are essentially shell scripts that have PBS directives, comments, and executable statements: # characters indicate a comment, #PBS headers indicate PBS directives, and blank lines can also be included for readability.

One example of what you can include in the template I've provided is:

```
#!/bin/bash

#PBS -l nodes=1:ppn=8
#PBS -l walltime=01:00:00
#PBS -M [INSERT YOUR EMAIL HERE]
#PBS -m aeb
#PBS -q hotel

### The lines above this comment set some parameters for the job script - Michelle:

### PBS -l nodes=#;ppn=# ==> denotes the amount of processing power you wish to use (#
nodes and # processor per node)
### PBS -l walltime=HH:MM:SS ==> denotes the amount of walltime you wish to allocate to
the job
### PBS -M x@ucsd.edu ==> if you put your email address here, you can get updates to yo
ur email
### PBS -m aeb ==> a: abort notifications, e: job ending notifications, b: job beginnin
g information
### PBS -q hotel ==> denotes where you'll be getting resources from (don't change this
line)

### PLACE ALL COMMANDS TO RUN ON A JOB BELOW THIS LINE ###

# this next line will allow me to load the samtools program
module load samtools

# this next line after this will allow me to grep the headers from a fasta file and outp
ut it
grep ">" example_file.fasta > headers.txt
```

Something to remember is that **job scripts will initialize in your home directory (/home/\$TSCC_USERNAME/)**! So if you want to run your scripts in another directory, you have to change into that directory at the beginning of the script, but below all of the PBS headers.

To actually run the script, you'd use the command:

```
qsub job_script_name.q
```

Here are some other useful things to know:

```
# view the status of all of your jobs  
qstat -u $TSCC_USERNAME  
  
# kill one of your jobs  
qdel $JOB_ID  
  
# hold one of your jobs (pause it)  
qhold $JOB_ID
```

I also made a post last week with some helpful information I've found for PBS commands and Bowtie commands (@22).

These websites are also helpful :-)

<https://www.osc.edu/supercomputing/batch-processing-at-osc/job-scripts>

<https://gif.biotech.iastate.edu/torque-pbs-job-management-cheat-sheet>

<https://www.weizmann.ac.il/chemistry/sites/chemistry/files/uploads/pbs-professional-cheat-sheet.pdf>