

Running RepeatMasker in SGE mode is much faster but involves more steps. Depending on what you're doing, it may be preferred.

No need to migrate to a qlogin for this exercise.

We will use the same files as in the original RepeatMasker tutorial for this example.

```
#-----#
```

SETTING UP FOR THE RUN

```
#-----#
```

This method was developed by friend of the lab, Robert Hubley, one of the maintainers of RepeatMasker as a favor to us.

1] Create a new folder for your SGE run

```
'cd /lustre/work/<your username>
```

```
'mkdir sge_test'
```

```
'cd sge_test'
```

You'll need a setup file for this work. Borrow this one from my home directory:

```
'cp /home/daray/generic.sge.daray.sh .'
```

```
#!/bin/bash
```

```
#$ -V
```

```
#$ -cwd
```

```
#$ -S /bin/bash
```

```
#$ -N <your job>.SGE
```

```
#$ -o $JOB_NAME.o$JOB_ID
```

```
#$ -e $JOB_NAME.e$JOB_ID
```

```
#$ -q omni
```

```
#$ -pe sm 1
```

```
#$ -P quanah
```

```
cd <path to this folder>
```

```
/lustre/work/daray/software/generateSGEClusterRun_Chewie_S.pl \
```

```
-nolow \
```

```
-twoBit <yourgenome.2bit> \  
-batch_count <integer> \  
-lib <your library>
```

```
#-nolow is optional, if you want to skip analyzing simple repeats  
#-twoBit, note that the genome must be in twobit format. To convert, use  
/lustre/daray/software/faToTwoBit.  
#faToTwoBit <input .fa> <output.2bit>  
#-batch_count, how many batches do you want to break your job into. High number,  
faster... If there are processors available.  
#-lib or -species, or nothing. -lib = your custom library, -species = use a species library  
in RepeatMasker's files, nothing = use all of rebase  
#Also note that there are several flavors of this setup script to run, depending on your  
needs. All are in my /lustre/work/daray/software directory.
```

```
#change the permissions  
chmod u+x qsub.sh doLift.sh
```

```
#When this script is done, 'sh qsub.sh'.  
#When those are done, qsub doLift.sh'.
```

Convert your genome, if necessary and change this file as necessary for your data.

Save the file with a new file name.

```
#-----#
```

RUNNING REPEATMASKER IN SGE MODE

```
#-----#
```

Pretty simple. Just run the modified 'generic' script as a qsub and you will see a new directory pop up as well as some new files.

New directory – RMPart

New files – doLift.sh, qsub.sh

qsub.sh is just a list of files to submit to the queue.

doLift.sh is a script to compile all of the individual batch runs into a final set of files similar to those output by a standard RepeatMasker run.

RMPart is the folder where all of the action happens. Each of the X number of batches is deposited here.

Once the setup script is run, you will need to submit all of the batch jobs:

```
'sh qsub.sh'
```

Once all of those are done, you will need to submit doLift as a qsub.

```
'qsub doLift.sh'
```

Most of the resulting files will be the same as the ones output by regular RepeatMasker runs but there are a couple that are new. They're pretty self-explanatory.