# Parallel Matlab on HPC Cluster (Applied to Bresch Segmentation)

I attach 3 .m files:

cluster\_contour\_tracker.m effectively replaces switch\_contour\_tracker (should be put in same folder)

cluster\_generate\_scripts replaces generate\_pbs\_from\_full\_file\_mat and generate\_pbs\_mat

wrap\_pbs\_batch replaces the previous version (the difference is minimal, you will be basically working with it the exact same way as before).

You will need to configure Matlab on the cluster. This will need to be done once. The process is based on <https://hpcc.usc.edu/support/documentation/parallel-matlab/> but I have added much stuff on top of it.

Login to the cluster with –X terminal:

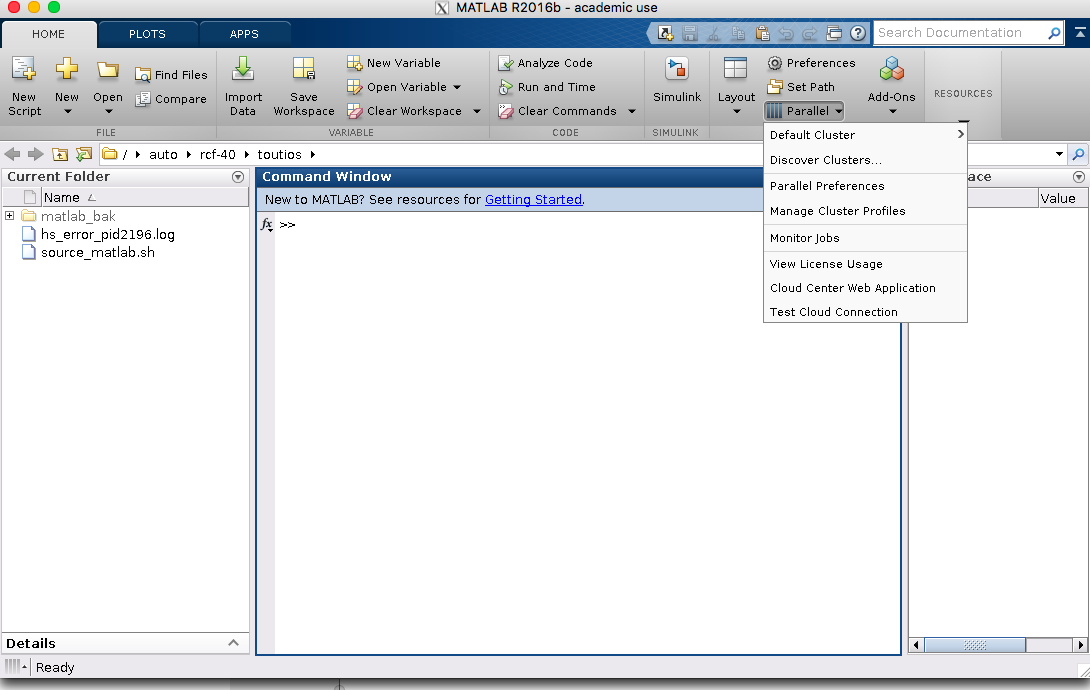
**ssh -X hpc-login2.usc.edu**

open matlab as:

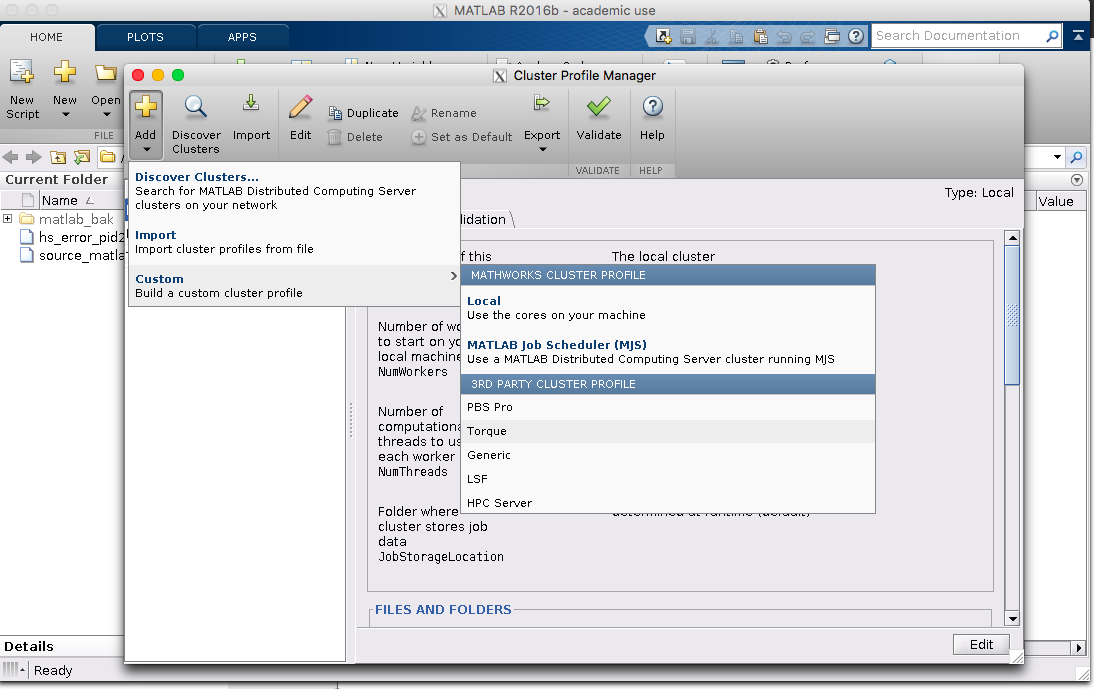
**source /usr/usc/matlab/default/setup.sh; matlab**

because of the –X this will open a full Matlab GUI. It will probably respond quite slowly, so be patient when you click something.

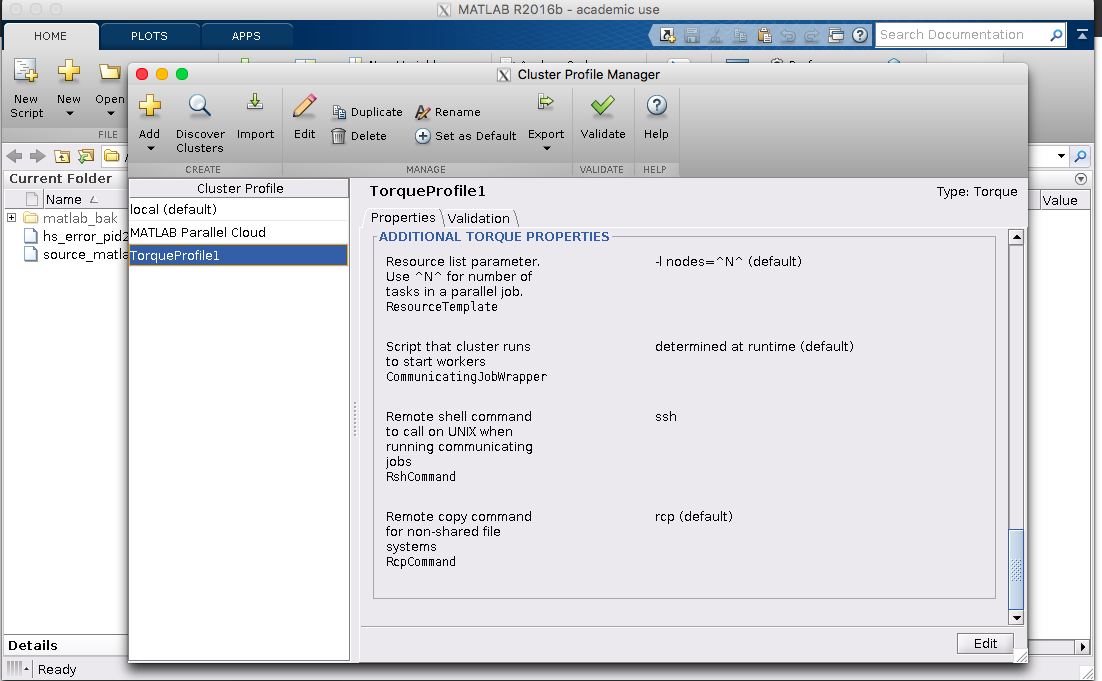
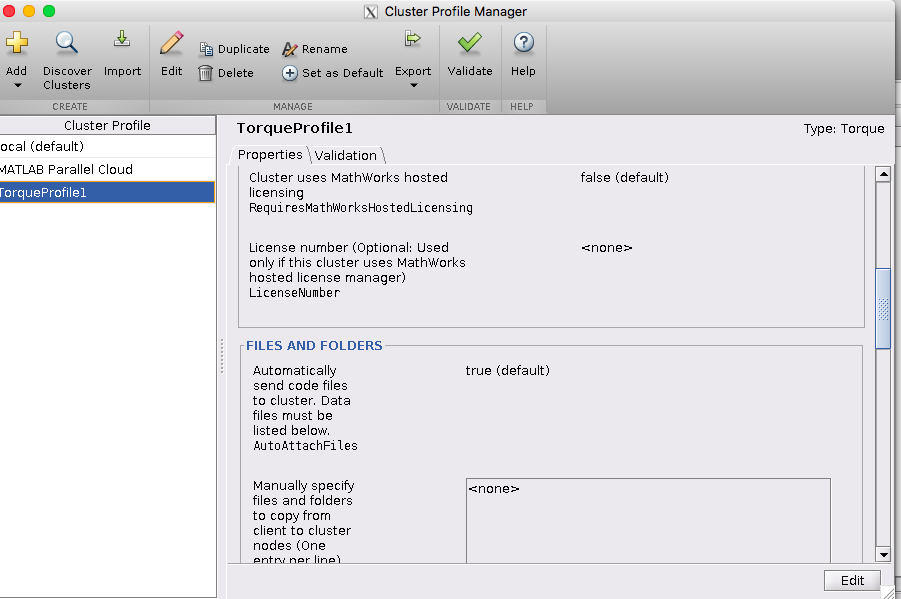
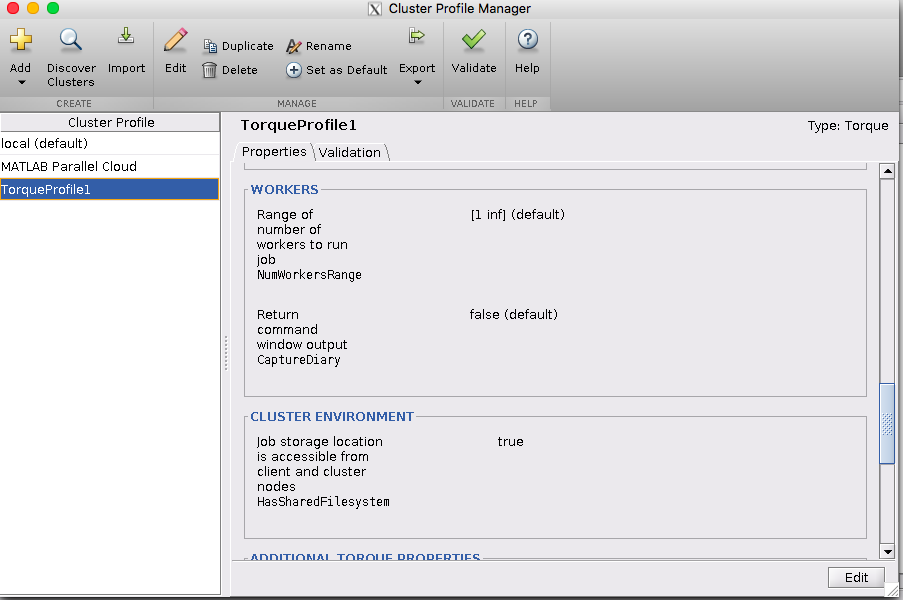
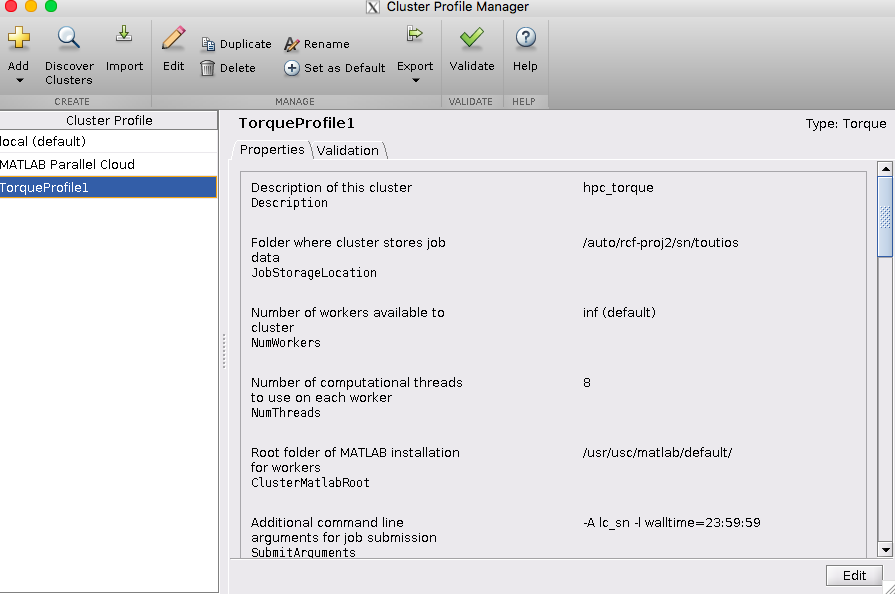
Click “Parallel” as shown, and select “Manage Cluster profiles”



In the window that opens do Add > Custom > Torque



You will have a new profile at the left column called something like “TorqueProfile1” (make a note of the name). You should select it and edit its properties. Click “Edit” at the bottom-right and fill the values as I show in the following screens (replace “toutios” by your username).



When you are done, close the window and quit Matlab. The exit the –X terminal.

If the name of the profile was not “TorqueProfile1” you should go to line 28 of cluster\_contour\_tracker.m and replace that name.

Now you can run wrap\_pbs\_batch as before. You will get a similar folder structure as before. The difference is that instead of a <script>.sh file you will have a <script>.m file. Upload everything to the cluster.

Now login normally.

**ssh hpc-login2.usc.edu**

You want to run the <script>.m. This is how I recommend doing it:

Start a screen session

**screen**

in the blank screen that opens start matlab (this will now be command line, since we don’t have the –X) again with

**source /usr/usc/matlab/default/setup.sh; matlab**

navigate to the script folder and execute it normally. As soon as it starts running you can press Control+a and then d to “detach” the screen. You will return to the first terminal. Now you can exit this terminal / close your laptop. The program will be running in the background. Check back in an hour or so, you should start getting \_track.mat files at the usual location.

At any time, you can do

**qstat -u <username>**

like before and see what is going on.

In case you want to return to the matlab terminal do:

**screen –r**

(you will have to detach again). You can google “screen cheat sheet”, it may be interesting.

NOTE: The code uses now 64 cores. This can be changed in line 64 of cluster\_generate\_scripts. You can have more cores and it theoretically should run faster, but you will have to wait more time in the queue (I tried 128 and did not notice faster overall results). This is a value you can experiment with.