Look at the README file on that directory it has links to more information on the biohpc site. You can pretty much follow the example and run a job.

The main idea is that you can split jobs into different smaller tasks and have the cluster run them.

https://biohpc.cornell.edu/lab/cbsubscb\_SLURM.htm#general contains details:

Steps to follow:

1. \*\*Create account\*\* at https://biohpc.cornell.edu//login\_bio.aspx

2. Check if your user password works on biohpc : https://biohpc.cornell.edu//login\_bio.aspx

3. Log in to the BioHPC Cluster: you can access with your user in terminal via ssh e.g. ssh dg663@cbsurobbins.biohpc.cornell.edu

4. Submit an Interactive Job: So now you will need to use slurm to submit jobs. There are examples on this directory: /local/workdir/slurm\_starter\_pack

4.1. Submitting jobs using 'sbatch' command:

sbatch -N 1 --mem=8000 -p regular /programs/bin/slurm\_screen.sh # here node N1, memory 8000 MB on regular partition.

OR

Submit: sbatch --mem=1000 -p regular --wrap="echo 'Hello SLURM\!'"

4.2. Check job status: squeue -u $USER like squeue -u dg663 and output will look like

JOBID PARTITION NAME USER ST TIME NODES NODELIST(REASON)

1729160 short slurm\_sc abc123 R 0:02 1 cbsubscb13

4.3. Copy node from above like (cbsubscb13)

4.4. Check the job status using sacct command: sacct -j 680 #replace 680 with job number assigned in 4.1. above

4.5. SSH into the assigned node: use SSH to access the node where your job is running. Eg. ssh cbsubscb13 #node name from 4.3. step

4.6. Check for Active Screen Sessions: screen -ls and you would see something like:

There is a screen on :

99274..cbsubscb13 (Detached)

4.7. Attach to the screen session: screen -r 99274..cbsubscb13

4.8. \*\*Start R\*\* in the Screen session: Once inside the screen session, start R by typing:

R

Now you are in R mode and can execute your R commands interactively.

4.9. Detach and Reattach to screen as needed: If you need to leave the screen session but want to keep it running, you can detach by pressing Ctrl + A followed by D.

To reattach later, use the screen -r command as shown above.

4.10. Exit and clean up: Exit using q() or type "exit".

NOW run in R

1. Log in to the BioHPC Cluster: ssh dg663@cbsurobbins.biohpc.cornell.edu (NEED YOUR PASSWORD TO LOGIN)

2.

\* General Information:

The cluster consists of 16 compute nodes. All these nodes are part of the BioHPC Cloud, with all the software and tools available in the Cloud also available on the cluster nodes

SSH is a Secure Shell Protocol to send commands to a computer over an unsecured network.

cat file name to view file through ssh

end to exit

mkdir works