Usersguide of TUHEP cluster

Here is the usersguide of TUHEP cluster. Please read this document carefully before using the cluster and network in the office. If you have problems, please contact Zhenwei Yang (9498, zhenwei.yang@gmail.com).

Some important reminders:

1、Please close the tunet client or web-based logins in advance. If you forget it, please close them directly WITHOUT clicking "Disconnect" button. Otherwise, the whole network would be lost for several minutes.

2、The main purpose of TUHEP cluster is data analysis of HEP and other scientific calculations. The gate node is "hepfarm" (hostname), with ip 166.111.32.48 and domain name http://server.hep.tsinghua.edu.cn. The gate node is merely for login from outside, and no other services are provided. One cannot run any resource time/resource-consuming program either.
If one need to submit a job or run other analysis computing, please login the computing nodes, hepfarm21/22/23 (details followed in next page).

3、Disk quota is applied to hepfarm21/22/23. One cannot exceed 2GB in home directory. If you have large-size data, please put them in subdirectories of /projects.

4、Please change your password frequently for safety.

5、p2p applications are strictly banned both in the cluster and office. Net service in the office is only for research and teaching, and one cannot provide your account and password to others. Otherwise, your account would be banned.

6、Attention please, for important private data, especially codes, please backup by yourself. There's always potential risk of data lose.

Well, before going to next page, make sure again that you've read these reminders carefully.

一、 General introduction

1. The OS of the cluster is SLC58. The ip of gate node is 166.111.32.48, whith hostname hepfarm and domain name server.hep.tsinghua.edu.cn. One can login the gate through ssh. Currently there are 3 computing nodes:

   hepfarm21: 192.168.20.21
   hepfarm22: 192.168.20.22
   hepfarm23: 192.168.20.23

   each node has four 8-core CPU's and memory of 64 GB. The node hepfarm21 is also administration node, with 46 TB disk space mounted to /projects, which is shared to other nodes by autofs. User account is also shared to other nodes through autofs. To change password, please login hepfarm21 (see "Change Password and/or shell).
2. OpenPBS is installed. See "job submission" for details.
3. ROOT, Geant4, and LHCb software environment, etc., are provided.

二、 Login the cluster

First login the gate node, hepfarm, (i.e., server.hep.tsinghua.edu.cn):

ssh username@166.111.32.48 (ssh username@server.hep.tsinghua.edu.cn)

Then login any node, e.g., ssh username@hepfarm22

三、 Change password and/or shell

Login hepfarm21, and change your password using "passwd", and/or change your shell using "chsh". To make this change take effect in all nodes, issue the sudo command:

```
sudo make -C /var/yp
```

四、 Job submission

OpenPBS is installed in the cluster for job submission.

1. There are 3 queue, with the queue names "L", "M" and "S". CPU time limits for this 3 queue are 1 week, 3 hours and 20 miniutes respectively.
2. Each user can run maximally 4 "S" jobs, 3 "M" jobs and 2 "L" jobs simutaneously. However, totally only 8 jobs can be run at the same time for each user, other jobs would stay in the queue.
3. To submit a job, using "qsub", e.g.,

   qsub mytestjob.tcsh

   To scan the status of submitted job(s):

   qsub -n

   To delete submitted job:

   qdel <jobID>

   (jobID is the 1st number of your job shown by "qsub –n")
4. A simple job script as example:

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```
#!/bin/tcsh
#PBS -q M
#PBS -N jobKs2PiPi
#PBS -l nodes=1:ppn=1
cd /projects/lhcb/users/yangzw/pArun/Ks
source /projects/lhcb/sw/LbLogin.csh
SetupDaVinci v32r1p2
gaudirun.py Ks2pipi.py
```

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5. Comments for the job script example

First of all, the first 4 lines are essential, and the "#"'s here do NOT mean comments!!!

Line 1: to specify shell of the script.

Line 2: to specify the job queue. If the job is expected to be finished in 20 minutes, you may change the S queue: #PBS -q S

Line 3: to specify the job name.

Line 4: usually just keep it as this default format. PBS server would run your job in the most unoccupied nodes, and each job uses one CPU core. If you do want your job to be run in some specified node, like hepfarm22, change this line like this:

#PBS –l nodes=hepfarm22:ppn=1

Do NOT change the number "1" in "ppn=1", unless you are sure that your program support parallel computing!

Line 5 and later: to go to the working directory, set up enviroments and run your programs.

Reminders: the submitted job will be run in batch mode, please do not add "&" in the end of qsub command.

Frequently used job commands:

qsub <jobscript>: to submit a job
qstat -n : to scan submitted jobs
qdel <jobID> : to delete a job