SRM SUPERCOMPUTER CENTER

USER GUIDE FOR "ANSYS"

SRM INSTITUTE OF SCIENCE AND TECHNOLOGY

Kattankulathur – 603 203

Introduction:

In our SRM HPC Cluster, we are using PBS Pro – Portable Batch System Professional. It is designed to manage the distribution of batch jobs and interactive sessions across the available nodes in the cluster.

Batch System:

The batch system allows the users to submit their jobs by requesting the resources (nodes, processors, memory) that they need. PBS Pro is handling these jobs on a First-Come, First-Served basis.

Login (Linux):

If you are using Linux os, then simply open you're Terminal, type

```
ssh -X username@ipaddr_of_server
```

Example Login page:



Submitting a job:

All users must submit their job via queuing system only using the command qsub.

```
Example for a script file: qsub.sh
```

APDL Script file:



#PBS –**N** <job name> - Specifies the name of the job that will appear in the job queue.

#PBS -q <queue name> - Specifies that the job should be run in the named queue.

#PBS -j oe - Specifies PBS to join standard output and standard error together in the output file.

PBS_O_WORKDIR - Contains the name of the directory from which the user submitted the PBS job.

PBS_NODEFILE	-	Name of the file that contains a list of the HOSTS
provided for the job.		
mapdl	-	Name of the executable file.
-р	-	Denotes the license type.
-np	-	Requesting the number of cores required for the job.
-b	-	Batch mode.
-dir	-	Working directory
-i	-	Input file

NOTE: The input file format should be in .inp

FLUENT Script file:

#!/bin/bash #PBS -N AnsysFluent #PBS -q work-01 #PBS -l select=1:ncpus=7:mpiprocs=7 #PBS -j oe				
cd \$PBS_0_WORKDIR cat \$PBS_NODEFILE > ./pbsnodelist CORES=`cat ./pbsnodelist wc -l`				
# Run fluent "fluent" 3d -t7 -g -i input.txt				

fluent	-	Name of the executable file
3d/2d/2ddp	-	Indicates the version of the solver
-t	-	Total number of cpus required by this job
-g	-	No graphics (Batch mode)
-i	-	Specifies the input file name

INPUT FILE (Sample for Fluent):

```
; Read case file
rc example.cas
; Initialize the solution
/solve/initialize/initialize-flow
; Calculate 50 iterations
it 50
; Write data file
wd example50.dat
; Calculate another 50 iterations
it 50
; Write another data file
wd example100.dat
; Exit Fluent
exit
yes
```

Once job submission script is ready to submit, and then use the command qsub to submit a job to the queuing system.

#qsub your_script.sh

Example: qsub qsub.sh

After submitting a job, an ID will be generating for that particular job. We can see that job ID by using a **qstat** command.

To Display the available job queue:

qstat -q - It will display all available queue for job.

To view all the node status:

\$pbsnodes -aSj

This command gives you the status of all the compute nodes in this server.

Queuing System:

There are 4 types of queue available,

res-4
 res-2
 work-01
 short

Their corresponding maximum Wall time will be 30 days for each job.

Deleting Job:

A queuing/running job can be delete by using following command,

#qdel <jobID>

Example:

#qdel 238

(Where 238 is the job ID, that can be obtained from qstat command)

CONTACT US:

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