ANSYS on the CFAM Cluster

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There are two methods by which the CFAM cluster can be accessed from a PC. The first is through a terminal emulator and the second is through a graphical user interface (GUI). If you aren't comfortable with a command line interface, the GUI may be more familiar.

You can also access the cluster with a command line interface via a terminal window on a Mac or Linux machine.

See Lynda.com for tutorials regarding the command line interface.

1 Terminal Emulator

KiTTY and PuTTY are two popular terminal emulators through which you can access the cluster. No GUI is available through these.

Both are available for download for free. See kitty.9bis.com or putty.org.

After downloading, enter cfam-cluster.engr.unr.edu for the Host Name and 22 for the Port. A terminal window will open and ask for your login. Enter your NetID and hit enter, then enter your password and hit enter

ategory:				
Session	*	Basic options for your KITTY session		
Logging Scripting		Specify the destination you want to conn	ect to	
Terminal		Host Name (or IP address)	Port	
- Keyboard		cfam-cluster.engr.unr.edu	22	
Bell		Connection type:		
Features		🔘 Raw 🔘 Telnet 🔘 Rlogin 💿 SS	H 🔘 ADB	
Window		🔘 Serial 🔘 Cygterm		
Appearance Behaviour		Load, save or delete a stored session		
···· Benaviour	=	Saved Sessions/New Folder		
Selection	-			
Colours		Default Settings		
Connection		cfam	Load	
Data			Save (d)	
···· Proxy ···· Telnet				
Rlogin			Delete	
			New folder	
··· Serial				
Cygtem	-			
Open				
<u>.</u>				
Start				
Cancel				
About				
Check Update		Close window on exit:		
		Close window on exit. Always O Never O Only on other oth	1	

Figure 1: Kitty Configuration Window



Figure 2: Kitty Terminal Window

At this point you will have access to the cluster via the command line. See below for some basic command line instruction or try Lynda.com for in-depth instruction.

2 Graphical User Interface

Through X2Go client, the cluster can be accessed with a GUI. This allows you to open the same interfaces to which you're accustomed with the power of the cluster's computational power.

You can find X2Go, free to download online. See wiki.x2go.org or simply search "X2Go." After downloading, open the client and start a new session. For the host, enter cfam-cluster.engr.unr.edu, for the login, enter your NETID, for SSH port, enter 22 and for the Session type, select XFCE.

Click the New Session icon to enter your password

/ Session pre	ferences - New session	? ×				
Session	Connection Input/Output Media Shared folders					
Jession nam	Session name: New session					
1.0	<< change icon					
~						
Path: /						
Server						
Host:	cfam-duster.engr.unr.edu					
Login:	yournetid					
SSH port:	22	·				
Use RSA/D	Use RSA/DSA key for ssh connection:					
Try auto login (via SSH Agent or default SSH key)						
Kerberos 5 (GSSAPI) authentication						
Delegation of GSSAPI credentials to the server						
Use Pr	oxy server for SSH connection					
Session ty						
XFCE	Command:					
	OK Cancel	Defaults				

Figure 3: X2Go Session Startup Window

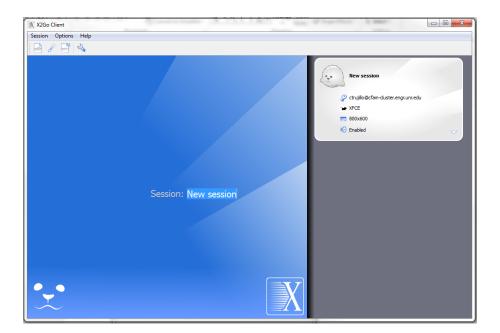


Figure 4: X2Go Startup

This will open a GUI window where you can access any files or programs on the Cluster.

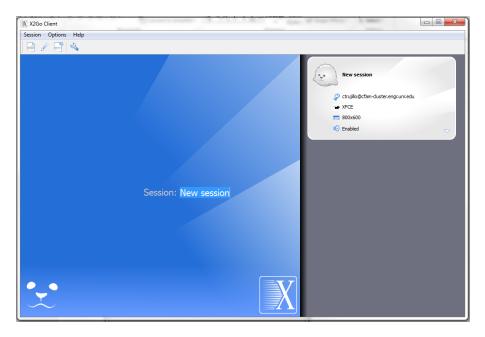


Figure 5: Password Entry

3 ANSYS on Linux

Running ANSYS on the HPC cluster requires at least a bit of background knowledge working with the Linux command line. As mentioned, the command line must be accessed through a terminal emulator - either with PuTTY, KiTTY or with the terminal emulator available on the Desktop of the GUI when accessing the cluster through X2Go.

To start open a terminal window. With X2Go, click the icon on at the bottom of the desktop. This will open a terminal window from which you can enter commands to run the programs you need.



Figure 6: Terminal Emulator Icon

One of the basic concepts to master in Linux is navigating the directory (or folder) structure. From the terminal window, the ls command displays the contents of the current directory. The cd command allows you to change the directory. To enter a directory within your current directory just type cd <name_of_directory>. It's simpler if directories don't

have spaces in their names. To navigate up a directory, use $cd \ldots$ and to navigate up two directories, $cd \ldots$...

4 Submitting Jobs

Jobs can be submitted through a terminal window either in X2Go or through the terminal emulator on your PC. You can submit Fluent jobs or Workbench jobs. If you need the Fluent and Workbench GUIs, you must access the cluster via X2Go.

Be sure to check your usage limitations before running a job. The first place to look is Ganglia, which shows which nodes of the cluster are being used. This can be accessed by typing cfam-cluster.engr.unr.edu into your browser window and clicking the "Ganglia Cluster Monitor" link.

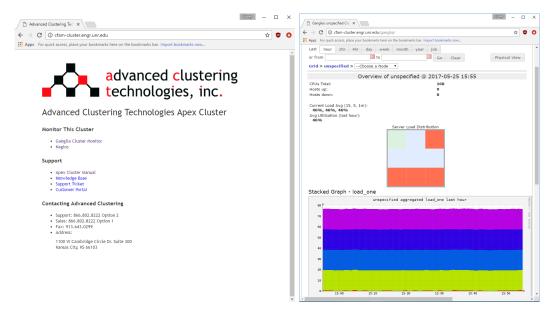


Figure 7: Accessing Ganglia

You will also want to check with the system administrator to verify what your permissions and priority are.

4.1 Submitting Interactive Fluent Jobs

The first step is to navigate to the folder where your case and data files are saved. Then you will need to submit the job

You need several nested commands to run a job using the Fluent GUI. The first is **salloc**, which allows another command to be executed on a reserved node or group of nodes. The form of the salloc command is as follows:

```
salloc --exclusive -N# -w nodelist command
The input arguments we'll use are as follows:
```

- --exclusive mandates that only your job can be on the nodes that you specify with -w. This means you can't share nodes with other jobs.
- \bullet -N# Specifies the number of nodes where # is the number. For example, -N2 would specify two nodes
- -w nodelist tells the cluster which nodes to reserve. For example -w highmem01,node01 would specify high memory node 1 and standard node 1. The number of nodes specified with -N should match the number of nodes in your nodelist.
- For the command, we'll use will be srun with the Fluent executable which will be explained below.

The **srun** command allows interactive jobs to be run. This means that your job won't run passively but you can specify changes in the Fluent GUI while once your job allocation is granted. The form of the srun command is as follows:

```
srun --x11 -N# <Executable>
```

- the --x11 argument activates a plugin that allows a GUI to be used
- -N# specifies the number of nodes (#). This must be specified in the salloc as well as srun
- The <Executable> in our case will be the Fluent command-line executable, described below.

The current location for the Fluent executable is /opt/ansys17-2/v172/fluent/bin/fluent. If you enter only that line into the terminal emulator , the Fluent Launcher should appear:

Fluent Launcher		+ - • ×
ANSYS		Fluent Launcher
Dimension 2D 3D Display Options Display Mesh Afte Workbench Color ACT Option Load ACT	Options Options Double Precision Meshing Mode Use Job Scheduler er Reading Processing Options Scheme Serial Parallel per Machine File Solver Processes 110 - GPGPUs per Machine 	hosts1234hi12.cnf
Show Fewer Options General Options Version 17.2.0	Vone	ronment
Working Directory /home/ctrujillo Fluent Root Path	70/0	✓ 🗳
/opt/ansys17-2/v1		▼ 2
	OK Default Cancel Help	•

Figure 8: Fluent Launcher

However, you cannot submit a job through the launcher with salloc - you must bypass the Fluent Launcher to submit a Fluent job successfully. To do this, you must specify all the settings in the command line that you would usually specify in the Launcher. To see all available options, type /opt/ansys17-2/v172/fluent/bin/fluent -help in the terminal window.

A typical Fluent Executable with arguments might look like: /opt/ansys17-2/v172/fluent/bin/flue -r17.2.0 3ddp -t36 -pinfiniband -mpi=pcmpi -cnf=highmem01,node03 -nm -ssh

- -r17.2.0 specifies the version
- 3ddp specifies a 3-dimensional simulation with double precision

- -t36 specifies the number of cores. This number will be evenly divided among reserved nodes. Each node has ten cores, but they're hyper-threaded so you can specify up to double the number of cores. It is recommended that you don't specify more than 18 cores here since you'll need at least one core leftover as the host.
- the interconnect: use -pinfiniband, which will specify that the fastest available connections between nodes be used
- -mpi=pcmpi specifies the MPI which dictates how data is passed between nodes
- -cnf=highmem01, node03 specifies to use high-memory node 1 and standard node 3.
- -nm allows Fluent to load faster by not displaying the mesh
- -ssh specifies to Fluent the kind of Linux cluster being used.

For example, you may enter the following in a single line in the terminal emulator of X2Go:

```
salloc --exclusive -N2 -w highmem01, node03 srun --x11 -N2
/opt/ansys17-2/v172/fluent/bin/fluent -r17.2.0 3ddp -t36 -pinfiniband -mpi=pcmpi
-cnf=highmem01,node03 -nm -ssh
```

Where:

- The salloc command allocates node resources to your job
 - The --exclusive argument ensures that no other jobs will share the nodes you specify
 - The first -N2 argument specifies the number of nodes to the salloc command
 - -w highmem01, node03 specifies which nodes will be used for the salloc command
 - The **srun** command allows an interactive job to be run
 - * The --x11 argument allows the GUI to be used
 - * The second -N2 argument specifies the number of nodes to the srun command
 - * /opt/ansys17-2/v172/fluent/bin/fluent launches Fluent
 - \cdot -r17.2.0 specifies the Fluent Version
 - · 3ddp specifies a 3D and double precision simulation
 - \cdot -t36 specifies 36 cores are used
 - · -pinfiniband specifies the fastest interconnect between nodes
 - -mpi=pcmpi specifies the MPI which dictates messaging between nodes
 - \cdot -cnf=highmem01, node03 specifies to Fluent which nodes are used. This was already specified to the cluster with the -w command but it must be re-specified to Fluent.
 - \cdot -nm loads Fluent without displaying the mesh, which saves time.
 - -ssh specifies to Fluent the kind of Linux cluster being used.

- 4.2 Submitting Passive Jobs through the Command Line
- 4.3 Submitting Workbench Jobs with the GUI