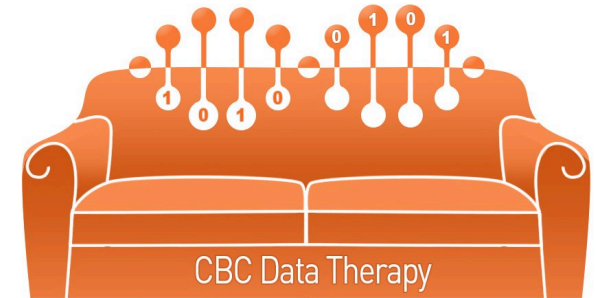


CBC Data Therapy

High-Performance Computing Basics

Xanadu Cluster



UConn
UNIVERSITY OF CONNECTICUT



Development of models begins at small scale.

Working on your laptop is convenient, simple.

Actual analysis, however is slow.



“Scaling up” typically means a small server or fast multi-core desktop.

Speed exists, but for very large models, not significant.

Single machines don't scale up forever.





For the larger problems/models, a different approach is required



High-performance computing (HPC)

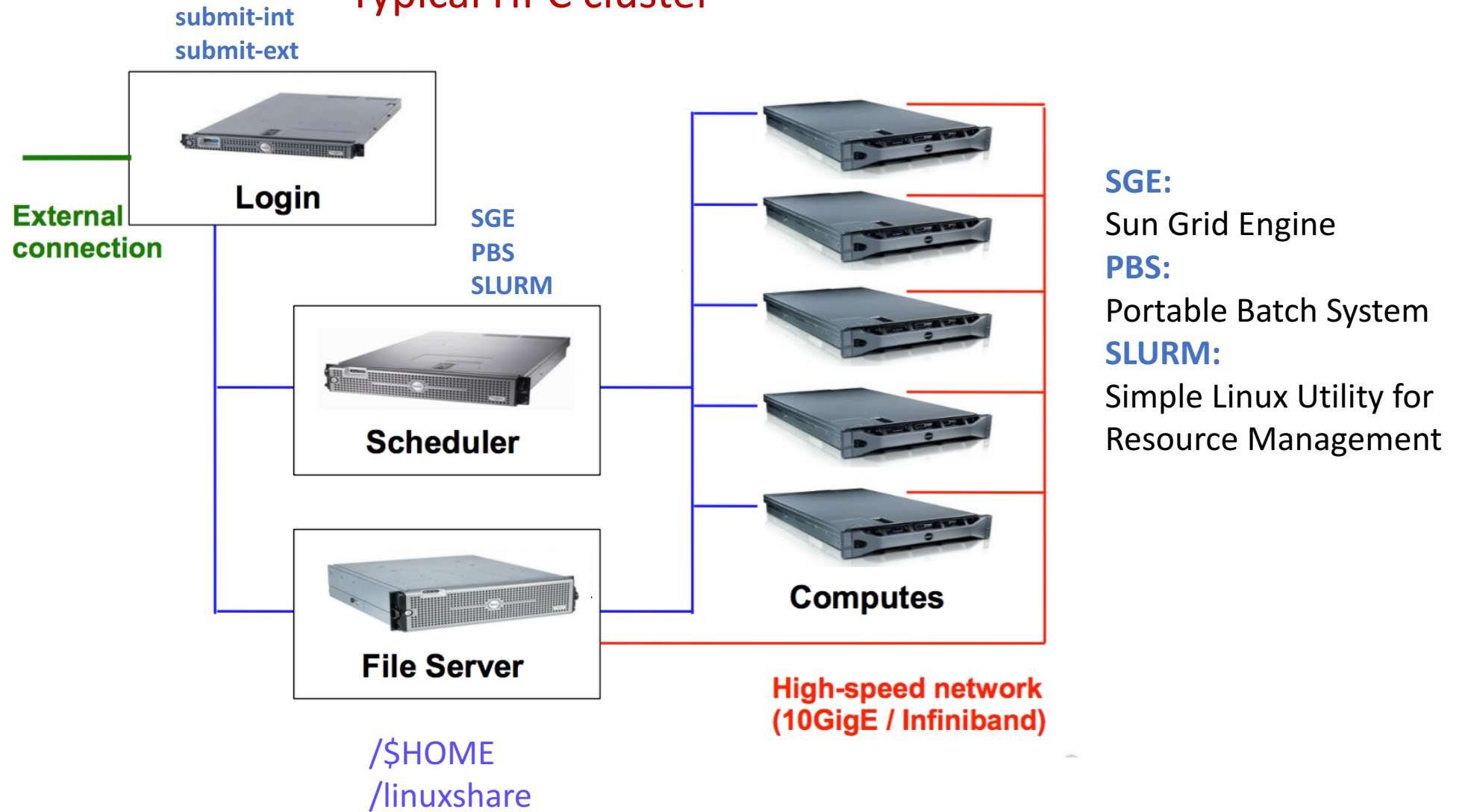
High-Performance computing involves mainly distinct computer processors working together on the same problem/calculation.

Large problem/calculations are divided into smaller parts and distributed among the many computers.

HPC is a cluster of quasi-independent computers which are coordinated by a central scheduler.

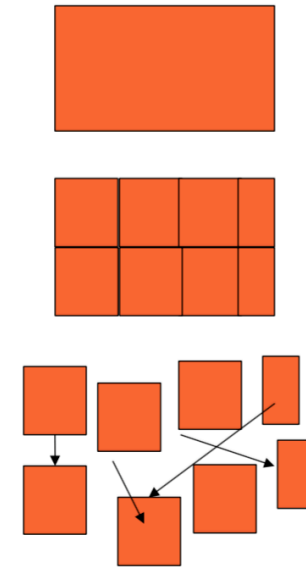


Typical HPC cluster



Performance comes at a price: **Complexity**

- Applications must be written specifically to take advantage of distributed computing
- Debugging becomes more of a challenge



Applications must be written specifically to take advantage of distributed computing.

- Explicitly split your problem into smaller “chunks”
- “Message passing” between processes



In Summary

- Why HPC

- A huge number of computational and memory requirements
- Cannot be afforded by a PC efficiently
- Speeds and feeds are the keywords

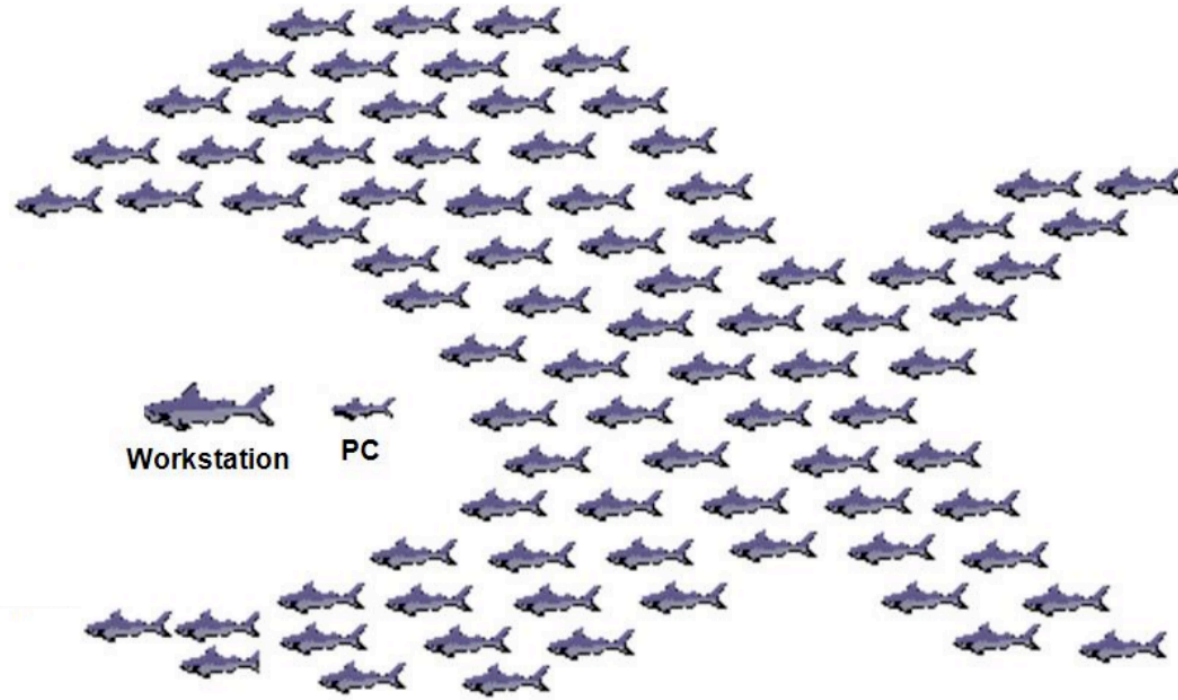
- Who uses High-Performance Computing

- Research institutes, universities and government labs
 - Weather and climate research, bioscience, energy, military etc.
- Engineering design: more or less every product we use
 - Automotive, aerospace, oil and gas explorations, digital media, financial simulation
 - Mechanical simulation, package designs, silicon manufacturing etc.

- Similar concepts

- Parallel computing: computing on parallel computers
- Super computing: computing on world 500 fastest supercomputers





Cluster

Parallel Computing on a Large Number of Servers is More Efficient than using Specialized Systems



HPC at UCONN

BBC (Storrs): SGE - Research and Teaching

HPC1 (UCH) : PBS - Advanced Research

Xanadu (UCH): SLURM - Advanced research

The screenshot shows the 'Contact Us' page of the UCONN Computational Biology Core website. The header includes the UCONN logo and 'UNIVERSITY OF CONNECTICUT'. Below the header, it says 'INSTITUTE FOR SYSTEMS GENOMICS' and 'Computational Biology Core'. A search bar is present with the text 'Search this site...'. The navigation menu includes 'Home', 'People', 'Hardware', 'Software', 'Databases', 'Resources', 'Data Therapy Sessions', 'FAQ', and 'Contact Us'. The main content area is titled 'Contact Us' and contains the following sections:

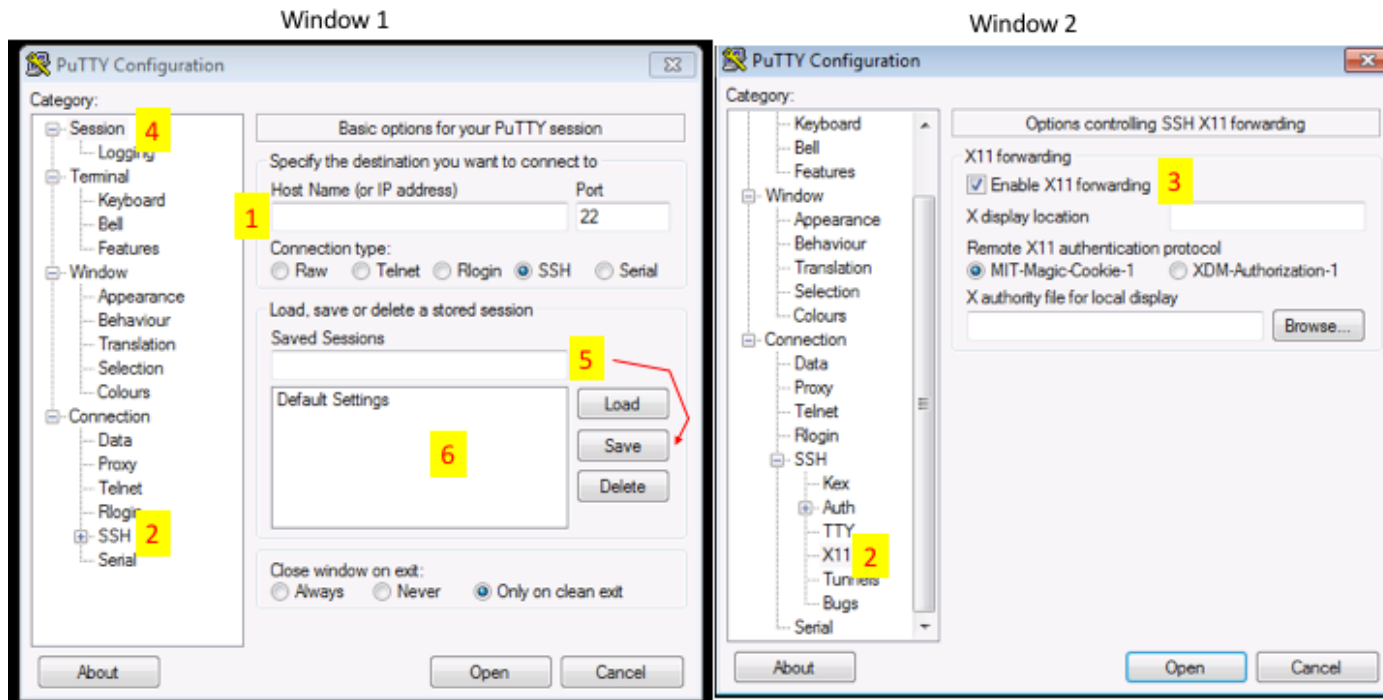
- Account and Support Requests**: A paragraph explaining the form's purpose: 'Please use this form to request an account, add software to either cluster, general bioinformatics/technical support, configure a virtual machine, or request additional cloud storage.'
- Inquiry Selection ***: A dropdown menu with the selected option 'Account Request (UCHC cluster)'.
- About You**: A section with two input fields for 'Name *', labeled 'First' and 'Last'.
- Status ***: A list of radio button options: 'Undergraduate Student', 'Graduate Student', 'Postdoctoral Researcher', 'Faculty', and 'Other' (with an adjacent input field).



Connecting to Xanadu

Mac : Terminal : `ssh username@xanadu-submit-ext.cam.uhc.edu`

Windows : Putty



Open Putty it will open window1.

1. Provide host name e.g. username@xanadu-submit-ext.cam.uhc.edu
2. Expand SSH tab and select X11 (shown in window2)
3. Enable X11 forwarding by selecting it. (window2)
4. Scroll up the left panel and select Session.(window1)
5. Name your session e.g. BBC_cluster and click save tab to save.
6. Your session name should appear in saved sessions. Double click on your session name to connect to server with SSH session.

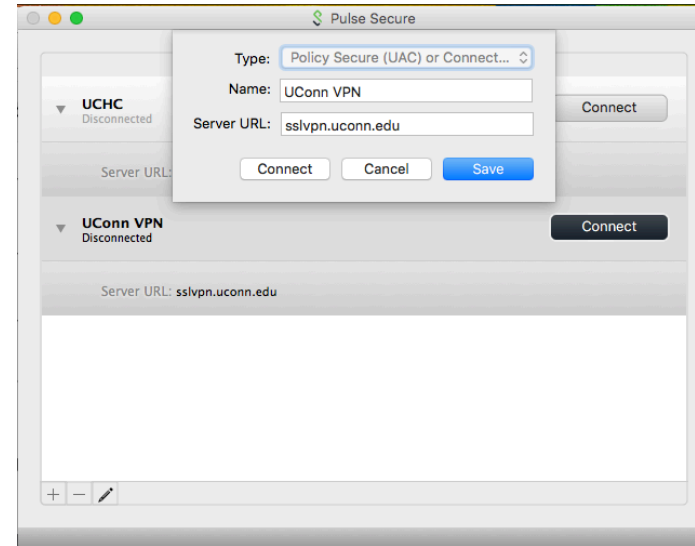


Login: From outside the network

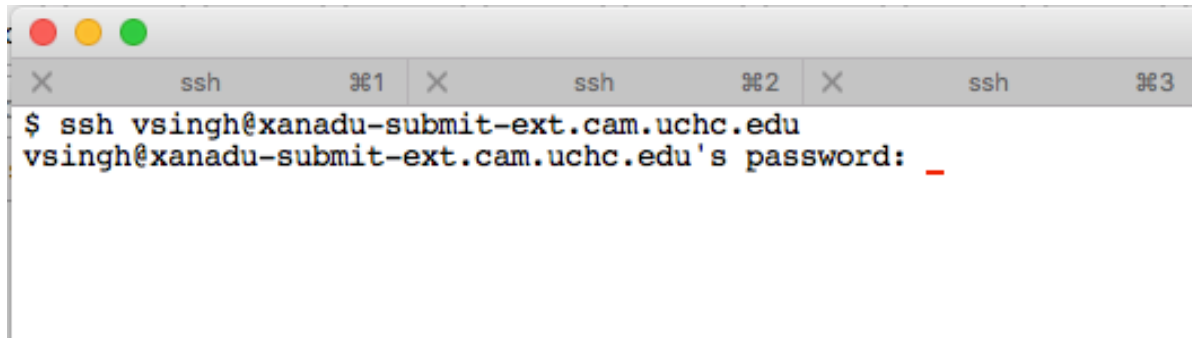
Use VPN (Open Pulse secure)



1. Open Pulse secure
2. Add new connection
3. Set Server URL to : sslvpn.uconn.edu
4. Save
5. Connect and login with NetID and Passwd



Login: (using terminal on mac)



```
ssh %1 ssh %2 ssh %3
$ ssh vsingh@xanadu-submit-ext.cam.uchc.edu
vsingh@xanadu-submit-ext.cam.uchc.edu's password: _
```

Logged on ext-submit node:

```
$ ssh vsingh@xanadu-submit-ext.cam.uchc.edu
vsingh@xanadu-submit-ext.cam.uchc.edu's password:
Last failed login: Thu Jun  1 17:04:42 EDT 2017 from d88h208.public.uconn.edu on ssh:notty
There were 3 failed login attempts since the last successful login.
Last login: Thu Jun  1 09:11:14 2017 from 137.99.88.208
xanadu-submit-ext ~ $ _
```



Common Linux commands

<code>pwd</code>	: Present Working directory
<code>cd destination</code>	: Change directory to destination
<code>cd</code>	: Change directory to \$HOME
<code>ls</code>	: List contents of directory
<code>cp source/file destination/file</code>	: Copy file from source in destination folder
<code>mv source/file destination/file</code>	: Move file from source to destination folder
<code>mv name name2</code>	: Rename file from name to name2
<code>touch filename</code>	: Create an empty file with name filename
<code>mkdir directory</code>	: Make directory
<code>rm file</code>	: delete file
<code>rm -r directory</code>	: delete file with its content
<code>~</code>	: Home directory
<code>cat</code>	: Read contents of file
<code>less</code>	: Contents of file, scroll, q to quit it
<code>head -10 file</code>	: first 10 lines of file
<code>tail -10 file</code>	: Bottom 10 lines of file

Resources: http://linuxcommand.org/writing_shell_scripts.php



Common Linux commands to edit file

```
vi filename
esc i
esc q !
esc w q !
esc dd
```

```
: Open file in vim to edit
: Insert or edit file
: quit file without saving changes
: Save and quit file
```

version 1.1
April 1st, 06

vi / vim graphical cheat sheet

Dvorak

Esc normal mode	~ toggle case	! external filter	@ play macro	# prev ident	\$ eol	% goto match	^ "soft" bol	& repeat is	* next ident	(begin sentence) end sentence	{ begin parag.	}	end parag.
\ goto mark	1	2	3	4	5	6	7	8	9	0 "hard" bol	.	misc	.	misc
" reg. spec	< un-indent	> indent	P paste before	Y yank line	F "back" find ch	G eof/ goto ln	C change to col	R replace mode	L screen bottom	? find (rev.)	+ next line			
' goto mk, bol	reverse	repeat cmd	p paste after	y yank	f find char	g extra cmds	c change	r replace char	l →	/ find	= auto-format			
A append at eol	O open above	E end WORD	U undo line	I insert at bol	D delete to eol	H screen top	T back 'till	N prev (find)	S subst line	"soft" bol down				
a append	o open below	e end word	u undo	i insert mode	d delete	h ←	t 'till	n next (find)	s subst char	- prev line				
ex cmd	Q ex mode	J join lines	K help	X back-space	B prev WORD	M screen mid'l	W next WORD	V visual lines	Z quit	bol/ goto col				
repeat	q record macro	j ↓	k ↑	x delete char	b prev word	m set mark	w next word	v visual mode	Z extra cmds	\ not used!				

motion moves the cursor, or defines the range for an operator

command direct action command, if red, it enters insert mode

operator requires a motion afterwards, operates between cursor & destination

extra special functions, requires extra input

Q commands with a dot need a char argument afterwards

bol = beginning of line, eol = end of line, mk = mark, yank = copy

words: `quux(foo, bar, baz)`
WORDS: `quux(foo, bar, baz)`

Main command line commands ('ex'):
:w (save), :q (quit), :q! (quit w/o saving)
:e f (open file f)
:%s/x/y/g (replace 'x' by 'y' filewide)
:h (help in vim), :new (new file in vim)

Other important comands:
CTRL-R: redo (vim),
CTRL-F/-B: page up/down,
CTRL-E/-Y: scroll line up/down,
CTRL-V: block-visual mode (vim only)

Visual mode:
Move around and type operator to act on selected region (vim only)

Notes:
(1) use "x before a yank/paste/del command to use that register ('clipboard') (x=a..z,*) (e.g.: "a%s to copy rest of line to reg 'a')
(2) type in a number before any action to repeat it that number of times (e.g.: 2p, d2w, 5l, d4j)
(3) duplicate operator to act on current line (dd = delete line, >> = indent line)
(4) ZZ to save & quit, ZQ to quit w/o saving
(5) zt: scroll cursor to top, zb: bottom, zz: center
(6) gg: top of file (vim only), gf: open file under cursor (vim only)

For a graphical vi/vim tutorial & more tips, go to www.viemu.com - home of ViEmu, vi/vim emulation for Microsoft Visual Studio



Software/tool/packages on cluster

Environment Modules:

The Environment Modules package provides for the dynamic modification of a user's environment via modulefiles.

```
module avail                : List modules that are available
module load modulefile     : Loads the module to user environment
module list                 : List modules that are loaded
module unload modulefile   : unloads module from user environment
module display modulefile  : Displays information on module
swap [modulefile1] modulefile2 :Switch loaded modulefile1 with modulefile2.
```



Xanadu Resources

Partitions

```
xanadu-submit-ext ~ $ sinfo
```

PARTITION	AVAIL	TIMELIMIT	NODES	STATE	NODELIST
general*	up	infinite	4	mix	xanadu-[20-22,25]
general*	up	infinite	13	idle	xanadu-[01-11,23-24]
xeon	up	infinite	11	idle	xanadu-[01-11]
amd	up	infinite	4	mix	xanadu-[20-22,25]
amd	up	infinite	2	idle	xanadu-[23-24]
himem	up	infinite	4	idle	xanadu-[30-33]

```
xanadu-submit-ext ~ $
```




```
xanadu-submit-ext ~ $ sinfo -N -l
```

```
Thu Jun 1 22:40:35 2017
```

NODELIST	NODES	PARTITION	STATE	CPUS	S:C:T	MEMORY	TMP_DISK	WEIGHT	AVAIL_FE	REASON
xanadu-01	1	general*	idle	36	2:18:1	257676	15620	1	(null)	none
xanadu-01	1	xeon	idle	36	2:18:1	257676	15620	1	(null)	none
xanadu-02	1	general*	idle	36	2:18:1	257676	15620	1	(null)	none
xanadu-02	1	xeon	idle	36	2:18:1	257676	15620	1	(null)	none
xanadu-03	1	general*	idle	36	2:18:1	257676	15620	1	(null)	none
xanadu-03	1	xeon	idle	36	2:18:1	257676	15620	1	(null)	none
xanadu-04	1	general*	idle	36	2:18:1	257676	15620	1	(null)	none
xanadu-04	1	xeon	idle	36	2:18:1	257676	15620	1	(null)	none
xanadu-05	1	general*	idle	36	2:18:1	257676	15620	1	(null)	none
xanadu-05	1	xeon	idle	36	2:18:1	257676	15620	1	(null)	none
xanadu-06	1	general*	idle	36	2:18:1	257676	15620	1	(null)	none
xanadu-06	1	xeon	idle	36	2:18:1	257676	15620	1	(null)	none
xanadu-07	1	general*	idle	36	2:18:1	257676	15620	1	(null)	none
xanadu-07	1	xeon	idle	36	2:18:1	257676	15620	1	(null)	none
xanadu-08	1	general*	idle	36	2:18:1	257676	15620	1	(null)	none
xanadu-08	1	xeon	idle	36	2:18:1	257676	15620	1	(null)	none
xanadu-09	1	general*	idle	36	2:18:1	257676	15620	1	(null)	none
xanadu-09	1	xeon	idle	36	2:18:1	257676	15620	1	(null)	none
xanadu-10	1	general*	idle	36	2:18:1	128532	15620	1	(null)	none
xanadu-10	1	xeon	idle	36	2:18:1	128532	15620	1	(null)	none
xanadu-11	1	general*	idle	36	2:18:1	128532	15620	1	(null)	none
xanadu-11	1	xeon	idle	36	2:18:1	128532	15620	1	(null)	none
xanadu-20	1	general*	mixed	32	4:8:1	128745	15620	1	(null)	none
xanadu-20	1	amd	mixed	32	4:8:1	128745	15620	1	(null)	none
xanadu-21	1	general*	mixed	32	4:8:1	128745	15620	1	(null)	none
xanadu-21	1	amd	mixed	32	4:8:1	128745	15620	1	(null)	none
xanadu-22	1	general*	mixed	32	4:8:1	257760	15620	1	(null)	none
xanadu-22	1	amd	mixed	32	4:8:1	257760	15620	1	(null)	none
xanadu-23	1	general*	idle	32	4:8:1	257760	15620	1	(null)	none
xanadu-23	1	amd	idle	32	4:8:1	257760	15620	1	(null)	none
xanadu-24	1	general*	idle	32	4:8:1	249696	15620	1	(null)	none
xanadu-24	1	amd	idle	32	4:8:1	249696	15620	1	(null)	none
xanadu-25	1	general*	mixed	32	4:8:1	209380	15620	1	(null)	none
xanadu-25	1	amd	mixed	32	4:8:1	209380	15620	1	(null)	none
xanadu-30	1	himem	idle	32	4:8:1	515792	15620	1	(null)	none
xanadu-31	1	himem	idle	32	4:8:1	515792	15620	1	(null)	none
xanadu-32	1	himem	idle	32	4:8:1	515792	15620	1	(null)	none
xanadu-33	1	himem	idle	32	4:8:1	515792	15620	1	(null)	none



Partition: general

```
xanadu-submit-ext ~ $ sinfo -N -l -p general
```

```
Thu Jun 1 22:41:40 2017
```

NODELIST	NODES	PARTITION	STATE	CPUS	S:C:T	MEMORY	TMP	DISK	WEIGHT	AVAIL	FE	REASON
xanadu-01	1	general*	idle	36	2:18:1	257676	15620	15620	1	(null)		none
xanadu-02	1	general*	idle	36	2:18:1	257676	15620	15620	1	(null)		none
xanadu-03	1	general*	idle	36	2:18:1	257676	15620	15620	1	(null)		none
xanadu-04	1	general*	idle	36	2:18:1	257676	15620	15620	1	(null)		none
xanadu-05	1	general*	idle	36	2:18:1	257676	15620	15620	1	(null)		none
xanadu-06	1	general*	idle	36	2:18:1	257676	15620	15620	1	(null)		none
xanadu-07	1	general*	idle	36	2:18:1	257676	15620	15620	1	(null)		none
xanadu-08	1	general*	idle	36	2:18:1	257676	15620	15620	1	(null)		none
xanadu-09	1	general*	idle	36	2:18:1	257676	15620	15620	1	(null)		none
xanadu-10	1	general*	idle	36	2:18:1	128532	15620	15620	1	(null)		none
xanadu-11	1	general*	idle	36	2:18:1	128532	15620	15620	1	(null)		none
xanadu-20	1	general*	mixed	32	4:8:1	128745	15620	15620	1	(null)		none
xanadu-21	1	general*	mixed	32	4:8:1	128745	15620	15620	1	(null)		none
xanadu-22	1	general*	mixed	32	4:8:1	257760	15620	15620	1	(null)		none
xanadu-23	1	general*	idle	32	4:8:1	257760	15620	15620	1	(null)		none
xanadu-24	1	general*	idle	32	4:8:1	249696	15620	15620	1	(null)		none
xanadu-25	1	general*	mixed	32	4:8:1	209380	15620	15620	1	(null)		none

```
---xanadu-submit-ext ~ $
```



Partition: himem

```
xanadu-submit-ext ~ $ sinfo -N -l -p himem
```

```
Thu Jun 1 22:42:13 2017
```

NODELIST	NODES	PARTITION	STATE	CPUS	S:C:T	MEMORY	TMP_DISK	WEIGHT	AVAIL_FE	REASON
xanadu-30	1	himem	idle	32	4:8:1	515792	15620	1	(null)	none
xanadu-31	1	himem	idle	32	4:8:1	515792	15620	1	(null)	none
xanadu-32	1	himem	idle	32	4:8:1	515792	15620	1	(null)	none
xanadu-33	1	himem	idle	32	4:8:1	515792	15620	1	(null)	none



Composing a script for cluster

Script:

1. Resource request

- number of CPUs,
- computing expected duration,
- amounts of RAM or disk space, etc

2. Job commands

- describe **tasks** that must be done, software which must be run



Resource request:

```
#!/bin/bash
#SBATCH --job-name=myscript
#SBATCH -n 1
#SBATCH -N 1
#SBATCH --partition=general
#SBATCH --mail-type=END
#SBATCH --mail-user=first.last@uconn.edu
#SBATCH -o myscript.out
#SBATCH -e myscript.err
```

#SBATCH --job-name=myscript Is the name of your script

#SBATCH -n 1 Request number of cores for your job

#SBATCH -N 1 This line requests that the cores are all on node.

Only change this to >1 if you know your code uses a message passing protocol like MPI. SLURM makes no assumptions on this parameter -- if you request more than one core (-n > 1) and your forget this parameter, your job may be scheduled across nodes ; and unless your job is MPI (multinode) aware, your job will run slowly, as it is oversubscribed on the master node and wasting resources on the other(s).

#SBATCH --partition=general This line specifies the SLURM partition (in this instance it will be the general partition) under which the script will be run

#SBATCH --mail-user=first.last@uconn.edu Email which the notification should be sent to

#SBATCH --mail-type=END Mailing options to indicate the state of the job. In this instance it will send a notification at the end

#SBATCH -o myscript.out Specifies the file to which the standard output will be appended

#SBATCH -e myscript.err Specifies the file to which standard error will be appended



more on Resource request:

```
#!/bin/bash
#SBATCH --time=10-01:00:00 # days-hh:mm:ss
#SBATCH --job-name=masurca_KG
#SBATCH --mail-user=user@uconn.edu
#SBATCH --mail-type=ALL
#SBATCH --comment=dataset_wuith_jump_libraries
#SBATCH --ntasks=1
#SBATCH --cpus-per-task=8
#SBATCH --mem-per-cpu=10240 # 10GB
or #SBATCH --mem=100G
#SBATCH -o filterGTF-%j.output
#SBATCH -e filterGTF-%j.error
```



Job commands:

They are regular linux/module commands

```
echo "Hello World"
```

Final script:

```
#!/bin/bash
#SBATCH --job-name=myscript
#SBATCH -n 1
#SBATCH -N 1
#SBATCH --partition=general
#SBATCH --mail-type=END
#SBATCH --mail-user=first.last@uconn.edu
#SBATCH -o myscript.out
#SBATCH -e myscript.err

echo "Hello World"
```

save the script as `myscript.sh`



Script submission and other commands

<code>sbatch myscript.sh</code>	: Submit script for execution
<code>squeue</code>	: Status of Jobs currently running on cluster (all users)
<code>squeue -j jobIDNUMBER</code>	: Status of job with jobIDNumber
<code>squeue -u UserID</code>	: Status of all the jobs submitted by user
<code>scancel jobID_number</code>	: Delete job with jobID_number
<code>scancel -u UserID</code>	: Delete all the jobs of a user



Script for Array jobs

```
#!/bin/bash
#SBATCH --mail-user=user@uconn.edu
#SBATCH --mail-type=ALL
#SBATCH --ntasks=1
#SBATCH --time=00:15:00
#SBATCH --mem=1G
#SBATCH --array=1-1002%100
#SBATCH --output=fastqc_%A_%a.out
```

This line will create 1002 jobs, but it instructs slurm to limit the total number of simultaneously running jobs to 100. This avoids swamping the queue, and shares bursting level with others in the group

This will create 1002 files to catch stdin, stdout and stderr for each respective job in the array. If the array job ID is 23678, we will find 1002 files starting with fastqc_23678_1.out ... fastqc_23678_1002.out

```
cd /NGSseq/data
module load fastqc/0.11.5

echo "SLURM_JOBID: " $SLURM_JOBID
echo "SLURM_ARRAY_TASK_ID: " $SLURM_ARRAY_TASK_ID
echo "SLURM_ARRAY_JOB_ID: " $SLURM_ARRAY_JOB_ID

arrayfile=`ls | awk -v line=$SLURM_ARRAY_TASK_ID '{if
(NR == line) print $0}'`

fastqc $arrayfile
```

Start: Slurm job ID and increase with each array job
Slurm job ID
Array job ID : 1-1002

This will list all the files from the directory (/NGSseq/data) and then pick up one file at a time and then run it through [fastqc](#) application.



Thank you

