A Brief Introduction to managing data science workloads on HPC

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Agenda

- Housekeeping on your host machine
- Useful slurm commands (getting to know the system)
- Requesting an interactive job
- Containers, port-forwarding, interactive example (jupyter)
- Containers, port-forwarding, batch example (jupyter)
- Discussion

Preparing your host machine

- Modify your ~/.ssh/config
- Copy your public ssh key to caviness

>> ssh-copy-id -i ~/.ssh/id_rsa.pub caviness

• ssh caviness

>> cat ~/.ssh/config

Host caviness

Hostname caviness.hpc.udel.edu

ForwardX11 yes

User <your udel username>

Useful Slurm Commands: sview

Sview (on log1n00) –										
Actions Options Query Help										
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	andr	nu interestin	rd			38	mix	ed	r00n[21-23,26-27,29,31-33,36-38],r01n[24-26,28-29,31-34,36,38-40,42-44],r03n[0	00-01,04,11-13,16,19,21,28]
	and i	Cececis_research	' Y			29	allo	cated	r00g03,r00n[24,30,34-35,40-44],r01n[21-23,27,37,41],r03g06,r03n[02-03,05-10,1	4,18,20,23]
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		▶ ecosys	no	up	7-00:00:00	53			r04n[00-23,50-76],r04s[00-01]	
			no	up	7-00:00:00	20			r00n[01-17,45-55],r01n[01-17,45-55]	
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		▶ icecube	no	up	7-00:00:00	29			r03n[29-57]	
		▶ it css	no	up	7-00:00:00	266			r00g[01-04].r00n[01-55].r01g[00-04].r01n[01-55].r02s00.r03n[00-57].r03g[00-08].	.r04n[00-76].r04s[00-01]
		▶ it nss	no	up	7-00:00:00	266			r00g[01-04],r00n[01-55],r01g[00-04],r01n[01-55],r02s00,r03n[00-57],r03g[00-08],	,r04n[00-76],r04s[00-01]
		∍ jayaraman lab	no	up	7-00:00:00	107			r00n[01-17,45-55],r01n[01-17,45-55],r04n[00-23,50-76]	
		▶ jneun	no	up	7-00:00:00	7			r04n[24-29,41]	
		▶ kirby	no	up	7-00:00:00	83			r00g01,r01g[00-01],r03n[29-57],r04n[00-23,50-76]	
		kuehl_group	no	up	7-00:00:00	99			r00n[21-44],r01n[21-44],r04n[00-23,50-76]	
		kukulka_lab	no	up	7-00:00:00	56			r00n[01-17,45-55],r01n[01-17,45-55]	
		lg-swap	no	up	30-00:00:00	1	idle		r02s01	
		▶ lianglab	no	up	7-00:00:00	53			r04n[00-23,50-76],r04s[00-01]	

Interactive Job: salloc

salloc -t hh:mm:ss -N <num_nodes> \\
-p <partition> -A <your_workgroup> \\
-J <jobname>

- -N, -p, -A are required
- There are plenty other features that may be useful to your workloads.. Run "man salloc" for a full list

* Wrap the command into a script with some logic for quick and easy interactive job allocations

./interactiveSession <time> <num_nodes>
<partition> <workgroup>

#!/bin/bash wall time=30 num nodes=1 partition="ececis research" account="ececis research" if [-z \${1+x}]; then echo "Using default value for walltime" else wall time=\$1 fi if [-z \${2+x}]; then echo "Using default value for number of nodes" else num nodes=\$2 fi if [-z \${3+x}]; then echo "Using default value for partition" else partition=\$3 if [-z \${4+x}]; then echo "Using default value for account" else account=\$4 fi echo "Time: \${wall time} minutes" echo "Number of nodes: \${num nodes}" echo "Partition: \${partition}" echo "Account: \${account}" echo "Are these values correct?" read -r -p "Are you sure? [y/N] " response response=\${response,,} # tolower if [["\$response" =~ ^ (yes|y)\$]] cmd="salloc --time 00:\${wall time}:00 -N \${num nodes} -p \${partition} -A \${account}" echo "Running command: \${cmd}" \${cmd} else echo "Exiting on user input" fi

>> cat interactiveSession

Containers, Port-forwarding, Front-end Applications Interactive Job: jupyter notebook example

- Connect to Caviness
 - >> ssh caviness
- Load the singularity package

>> vpkg_devrequire singularity

- Convert the jupyter docker image to singularity with singularity pull

>> singularity pull docker://jupyter/datascience-notebook:python-3.8.8

- Start up an interactive session

>> ./interactiveSession <time (min)> <num_nodes> <partition> <account>

- Launch container

>> singularity exec datascience-notebook_python-3.8.8.sif jupyter notebook

- In another shell, port forward to your running notebook

>> ssh -L 8888:localhost:8888 caviness
>> ssh -L 8888:localhost:8888 <compute-node>

Containers, Port-forwarding, Front-end Applications Batch Job Jupyter

- Connect to Caviness
 - >> ssh caviness
- Create batch script
- Run batch script

>> sbatch batch_jupyter

- Find the node the job is running on using squeue
 - >> squeue -u \$USER
- In another shell, port forward to your running notebook

>> ssh -L 8888:localhost:8888 caviness
>> ssh -L 8888:localhost:8888 <compute-node>

* On caviness, /opt/templates/slurm/ has batch script templates.. Use them, they're very detailed and they work >> cat batch_jupyter

#SBATCH -A "ececis_research"

#SBATCH -p "ececis_research"

#SBATCH -J "jupyter"

#SBATCH -N 1

#SBATCH -t 00:10:00

vpkg devrequire singularity

singularity exec datascience-notebook_python-3.8.8.sif
jupyter notebook

Useful Slurm Commands

Job Manipulation and Cluster configuration

Cancel a job	scancel <jobid></jobid>		
Cancel all of your jobs	scancel -u \$USER		
Get status of a job	squeue <jobid></jobid>		
Status of all of your jobs	squeue -u \$USER		
Job Status in more detail	scontrol show jobid -dd <job_id></job_id>		
Slurm accounting info for historical jobs	sacct -j <jobid> format=JobID,JobName,MaxRSS,Elapsed</jobid>		
Information on partitions	scontrol show partition		
Condensed view of node features	sinfo -o "%20N %10c %10m %25f %10G "		

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Questions

- The Caviness system is very well documented. Refer to <u>http://docs.hpc.udel.edu/</u> for more information on HPC tasks