Introduction to NERSC Resources



LBNL CSA Summer Program June 9, 2022 Helen He NERSC User Engagement Group

Some Logistics

- Users are muted upon joining Zoom (can unmute to speak)
- Please change your name in Zoom session
 - to: first_name last_name
 - Click "Participants", then "More" next to your name to rename
- Click the CC button to toggle captions and View Full Transcript
- GDoc is used for Q&A (instead of Zoom chat)
 - <u>https://tinyurl.com/4h8ss95k</u>
- Slides and videos will be available on the Training Event page and CSASP CS Summer Program page
 - <u>https://www.nersc.gov/users/training/events/introduction-to-nersc-resources-jun2022/</u>
 - <u>https://cs.lbl.gov/careers/summer-student-and-faculty-program/2022-csa-summer-program/</u> <u>m/summer-program/</u>
- Apply for a training account if no NERSC account or MFA not setup yet
 - <u>https://iris.nersc.gov/train</u>, and use the 4-letter code "e1wR"





Outline

- NERSC and Systems Overview
- NERSC Online Resources
- Connecting to NERSC
- File Systems and Data Management / Transfer
- Software Environment / Building Applications
- Running Jobs
- Data Analytics Software and Services
- Hands-on: Compiling and Running Jobs on Cori







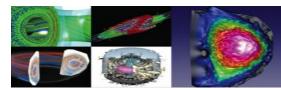
NERSC and Systems Overview

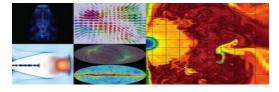




NERSC is the Mission HPC Computing Center for the DOE Office of Science

- NERSC deploys advanced HPC and data systems for the broad Office of Science community
- NERSC staff provide advanced application and system performance expertise to users
- Approximately 8,000 users and 800 projects
- Over 2,000 publications cite using NERSC resources per year
- Founded in 1974, focused on open science
- Division of Lawrence Berkeley National Laboratory







ASCR	Advanced Scientific Computing Research
BER	Biological & Environmental Research
BES	Basic Energy Sciences
FES	Fusion Energy Sciences
HEP	High Energy Physics
NP	Nuclear Physics
SBIR	Small Business Innovation Research

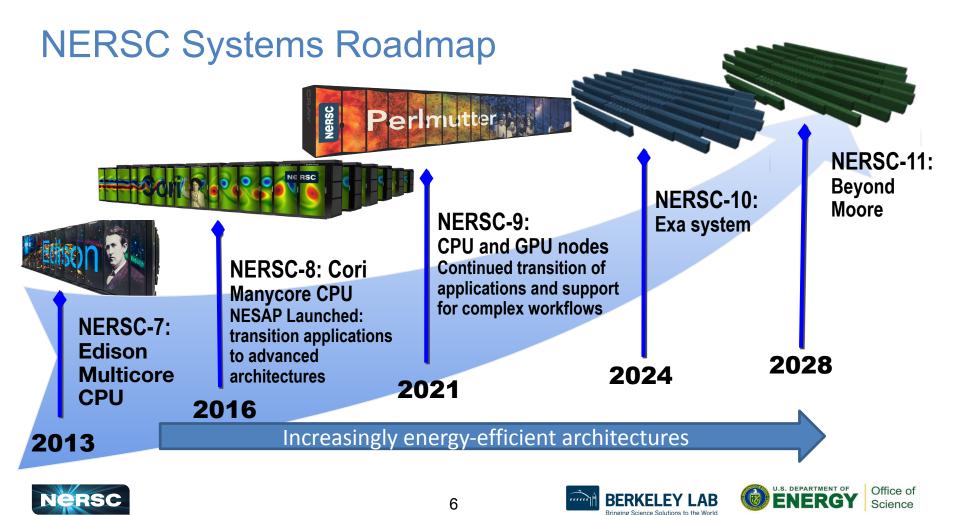






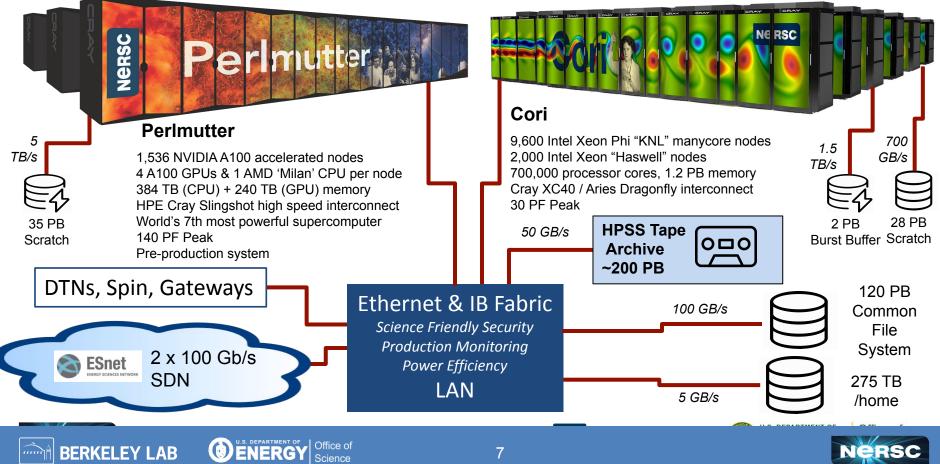
Office of

Science



NERSC Systems

BERKELEY LAB







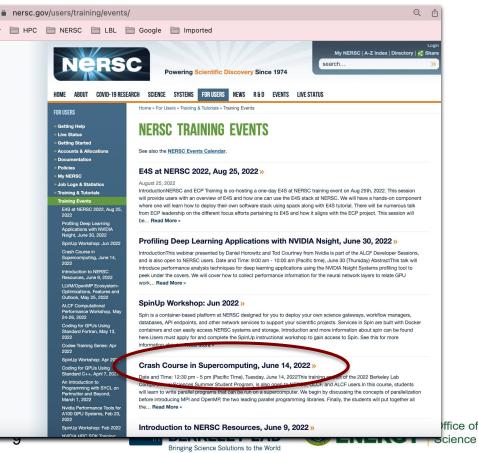
NERSC Online Resources





Classic NERSC Page

- https://www.nersc.gov
- Science, News, Publications
- Contact Us
- Live Status (MOTD) <u>https://www.nersc.gov/live-status/</u> <u>motd/</u>
- NUG (and Slack)
- Training Events
 <u>https://www.nersc.gov/users/train</u>
 <u>ing/events/</u>





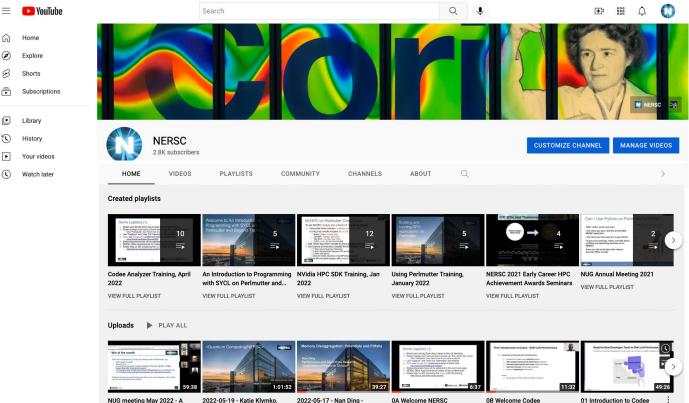
NERSC YouTube Channel

look at the Annual NERSC

9 views · 1 day ago

Daan Camps, Jan Balewski ...

34 views · 2 days ago



Memory Disaggregation:...

52 views · 3 weeks ago

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21 views · 3 weeks ago

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https://www.youtu be.com/c/NERSC Training-HPC

Training sessions and other NERSC events presentations are archived on youtube, with professional captions



tools Shift Left Performance

12 views · 3 weeks ago

CC

User Slack; User Appointments

slack

Lincoln Bryant Today at 10:11 AM hi folks. I'm trying to figure out what filesystems are attached to perlmutter and also accessible via Globus. On Cori we used /global/cscratch1 for our job input/output via the NERSC Cori globus endpoint. Can anyone point me to the equivalent for Perlmutter? Maybe I missed something blindingly obvious in the docs..

2 replies

Wileam Phan (LBNL) 5 minutes ago

Use the SPSCRATCH environment variable, according to https://docs.nersc.gov/filesystems/perlmutter-scratch/

docs.nersc.gov Perlmutter scratch - NERSC Documentation NERSC Documentation



Jean Sexton 2 minutes ago

I have not yet seen pscratch accessible from globus, some people use the CFS project directories, since those are visible from cori/dtn/globus/perlmutter https://docs.nersc.gov/systems/perlmutter/#transferring-data-tofrom-perlmutter-scratch

Using Perlmutter - NERSC Documentation NERSC Documentation

👍 1 😅



https://www.nersc.gov/users/NUG/

https://docs.nersc.gov/getting-start ed/#appointments-with-nersc-usersupport-staff



1 Choose Appointment
GPU Basics (30 minutes)
KNL Optimization (30 minutes)
Cori File Systems (30 minutes)
Using GPUs in Python (30 minutes)
Containers (30 minutes)
NERSC 101 (30 minutes)
Checkpoint/Restart jobs with MANA (30 minutes)
Spin (30 minutes)
Appentra Codee (30 minutes)

NERSC Docs

Technical Documentations https://docs.nersc.gov

- **Getting Started** https://docs.nersc.gov/getting-started/
- IRIS
- Systems
- Connecting
- Environment
- Development
- **Running Jobs**
- Applications
- Analytics
- Machine Learning •

Performance

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	Getting Started -	 NERSC Documentation 	Merse_	Resources	_20210603 - Google Slides
■ NERSC Documentation			Q Search		
Welcome to NERSC					Table of contents
VEICOTTE LO TILINGC					What is NERSC?
					NERSC Users Group (NUG)
Welcome to the National Energy Resea	rch Scientific Computing	g Center (NERSC)!			Computing Resources
					Cori
About this page					Storage Resources
This document will guide you through the bas	sics of using NERSC's superco	mputers, storage systems, and	services.		Community File System (CFS)
ó, Tip					HPSS (High Performance Storage System) Archival Storage
U					NERSC Accounts
Be sure to check out the slides and video reco	ordings from the New User Tra	aining here.			Connecting to NERSC
					Software
					Computing Environment
What is NERSC?					Compiling/ building software
NERSC provides High Performance Cor	mouting and Storage fac	ilities and support for res	earch sponsored by and of		Running Jobs
interest to, the U.S. Department of Ener				f	Interactive Computing
supporting all six Office of Science pro		. ,	1 1 0		Debugging and Profiling
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Tree View of NERSC Docs Topics

https://gitlab.com/NERSC/nersc.gitlab.io/-/blob/main/mkdocs.yml

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1	nav:
2	- Home: index.md
3	 Getting Started: getting-started.md
4	- Tutorials:
5	– tutorials/index.md
6	- Accounts:
7	- accounts/index.md
8	– Passwords: accounts/passwords.md
9	– Policy: accounts/policy.md
10	– Collaboration Accounts: accounts/collaboration_accounts.md
11	- Iris:
12	- iris/index.md
13	- Users: iris/iris-for-users.md
14	- PIs and Project Managers: iris/iris-for-pis.md
15	- ERCAP and Iris Guide for Allocation Managers: iris/iris-for-allocation-managers.md
16	- Systems:
17	- systems/index.md
18	- Perlmutter:
19	- Using Perlmutter: systems/perlmutter/index.md
20	– System: systems/perlmutter/system_details.md
21	– Interconnect: systems/perlmutter/interconnect/index.md
22	– Running Jobs: systems/perlmutter/running-jobs/index.md
23	 Finding and using software: systems/perlmutter/software/finding-software.md
24	– Timeline: systems/perlmutter/timeline/index.md
25	- Cori:
26	- systems/cori/index.md
27	- Interconnect: systems/cori/interconnect/index.md
28	- KNL Modes: systems/cori/knl_modes/index.md
29	- Timeline:

78	- Development:
79	- Compilers:
80	- development/compilers/index.md
81	- Base Compilers: development/compilers/base.md
82	– Compiler Wrappers (recommended): development/compilers/wrappers.md
83	- NPE: development/compilers/npe.md
84	- Build Tools:
85	– Autoconf and Make: development/build-tools/autoconf-make.md
86	 CMake: development/build-tools/cmake.md
87	- Spack: development/build-tools/spack.md
88	- Programming Models:
89	- development/programming-models/index.md
90	- MPI:
91	- development/programming-models/mpi/index.md
92	 Cray MPICH: development/programming-models/mpi/cray-mpich.md
93	 Open MPI: development/programming-models/mpi/openmpi.md
94	 Intel MPI: development/programming-models/mpi/intelmpi.md
95	- OpenMP:
96	 development/programming-models/openmp/index.md
97	 Tools for OpenMP: development/programming-models/openmp/openmp-tools.md
98	- OpenACC:
99	 development/programming-models/openacc/index.md
100	- CUDA:
101	development/programming-models/cuda/index.md
102	 UPC: development/programming-models/upc.md
103	- UPC++: development/programming-models/upcxx.md
104	 Coarrays: development/programming-models/coarrays.md
105	- SYCL:
106	 development/programming-models/sycl/index.md
107	 Kokkos: development/programming-models/kokkos.md
108	 Raja: development/programming-models/raja.md
109	- Languages:

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Science





• IRIS: NERSC Account Management and Reporting:

https://iris.nersc.gov

- Account info
- Change password
- Change contact info
- SSH Keys, MFA
- Check usage info

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Help Portal

https://help.nersc.g

- Submit tickets (as
- Request forms:
 - Quota Increase Ο
 - Reservations, Ο
- Allocation (ERCAP)

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(LNCAP) Requests	Open a Ticket Unresolved Tickets		
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MyNERSC

https://my.nersc.gov

- Dashboard
- Jobs
- Center Status
- File Browser
- Service Tickets
- Data Dashboard
- Jupyter Hub
- Links to other useful pages

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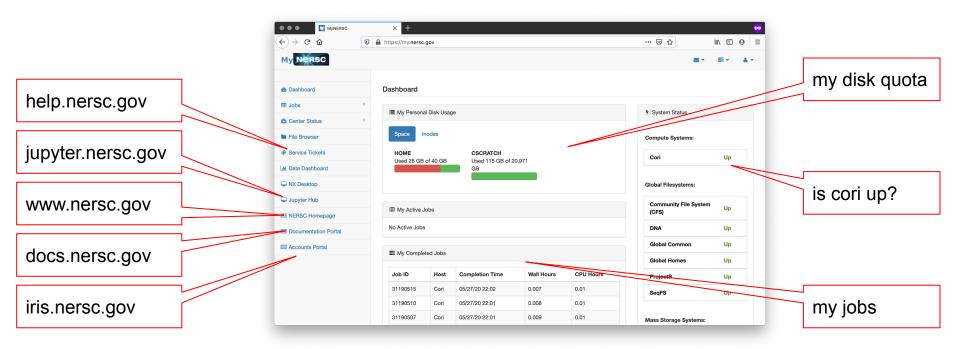








https://my.nersc.gov Leads You to All Sites









Cori GPU Documentation

https://docs-dev.nersc.gov

- GPU nodes
 - Hardware info
 - Slurm access
 - Usage
 - Software
 - Compilers
 - Math libraries
 - Python
 - Shifter
 - Profiling
 - Examples

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G 🔣	Usage - NERSC Develo	pment System Documentation	
NERSC Developme	nt System Documentation	Q Search	GitLab/NERSC/docs-dev 0 Stars - 2 Forks
NERSC Development System	Heres		 Table of contents
Documentation	Usage		CPUs
Home			GPUs
Cori GPU nodes 🗸 🗸	CPUs		SSD
Introduction	CPUS		005
Hardware Info	Using the CPUs on the GPU nodes is similar to using	, 'normal' compute nodes on Cori. CPU	
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Usage			
Software >			
Examples	GPUs		
Help	In a batch job submitted with sbatch , GPUs can be	accessed with or without srup. Howev	ver in
Storage Systems >			
	normal shell commands. For example:		-9
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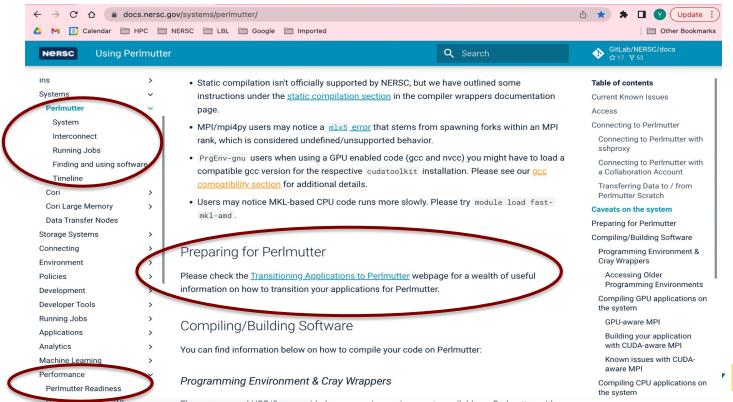




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Perlmutter Documentation

https://docs.nersc.gov/systems/perlmutter



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Selected Perlmutter Training Events

https://www.nersc.gov/users/training/events/

- <u>Using Perlmutter</u>, Jan 2022
- Nvidia HPC SDK, Jan 2022
- Nvidia Performance Tools, Feb 2022
- <u>Codee Training</u>, Apr 2022
- Coding for GPUs with Standard C++, Apr 2022
- Coding for GPUs with Standard Fortran, May 2022
- Programming with SYCL, Mar 2022
- <u>LLVM/OpenMP Ecosystem</u>, May 2022
- OpenMP Offload, Sept 2021
- <u>3-part OpenACC training series</u>, Apr-Jun, 2020
- <u>9-part CUDA training series</u>, Jan 2020 Sept 2021
- GPU for Science, Jul 2020
- Data Analytics in Python on GPUs with NVIDIA RAPIDS, Apr 2020











Connecting to NERSC





Multi-Factor Authentication (MFA) and sshproxy

- NERSC password + OTP ("One-Time Password")
 - OTP obtained via the "Google Authenticator" app on your smartphone
 - Alternative/backup option: Authy on desktop https://authy.com/
- MFA is used in login to NERSC systems, web sites, and services
 - Setup MFA <u>https://docs.nersc.gov/connect/mfa/</u>
- sshproxy.sh creates a short-term certificate
 - Run sshproxy.sh once, then you can ssh to NERSC systems for the next 24 hours before being asked for password+OTP again
 https://docs.persc.gov/connect/mfa/#sshproxy/
 - <u>https://docs.nersc.gov/connect/mfa/#sshproxy</u>





SSH and MFA Examples

<laptop>\$ ssh elvis@cori.nersc.gov

Login connection to host cori01	:
Password + OTP:	

. . .

		۴×
Login		
	Login	Login

You will login to one of the login nodes (12 on Cori).

To allow X-forwarding to access visualization programs, use the "-Y" flag: localhost% ssh -Y elvis@ cori.nersc.gov e/elvis> module load matlab e/elvis> matlab <MATLAB starts up>



3



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Connecting to NERSC: NX

- NERSC recommends using NX instead of SSH X-forwarding since NX is faster and more reliable
- NX is a service for Accelerated X
- NX also has the benefit of long lasting terminal sessions that can survive between lost internet connections
 - Can reconnect later, even from a different location or computer
- Download and install the Client software: NoMachine
 - <u>https://docs.nersc.gov/connect/nx</u>
 - Works on Window/Mac/Linux







NoMachine

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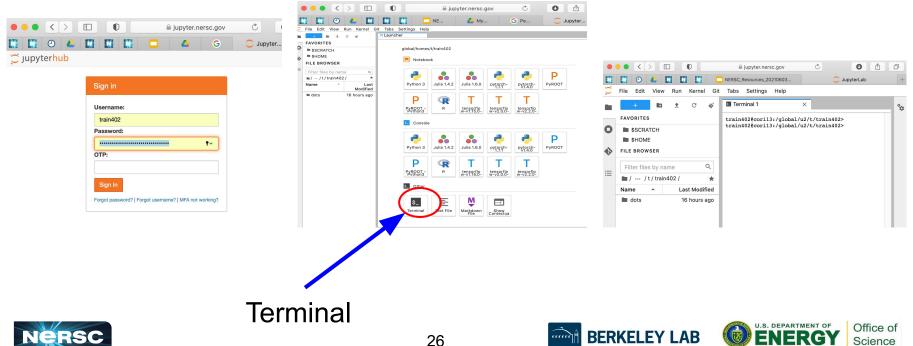




Office of Science

Terminal in Jupyter

You can access Cori from any web browser, via https://jupyter.nersc.gov



Bringing Science Solutions to the World

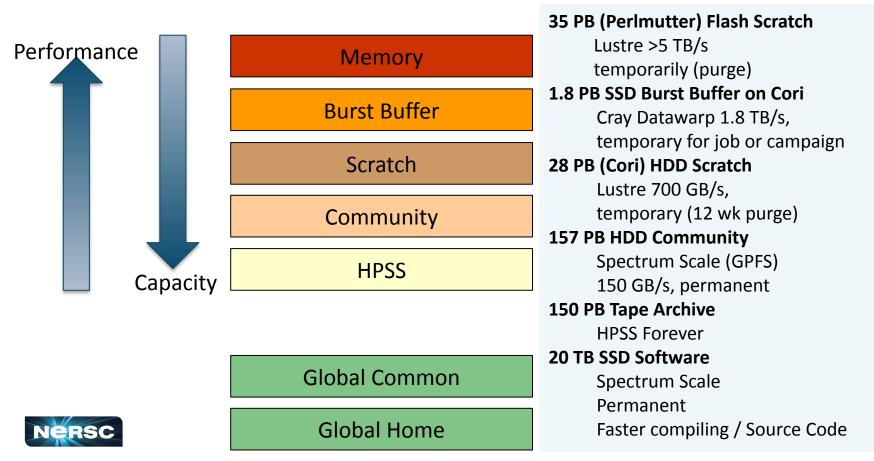


File Systems and Data Management / Transfer





Simplified NERSC File Systems



Global File Systems

Global Home

- Permanent, relatively small storage
- Mounted on all platforms
- NOT tuned to perform well for parallel jobs
- Quota cannot be changed
- Snapshot backups (7-day history)
- Perfect for storing data such as source code, shell scripts

Community File System (CFS)

- Permanent, larger storage
- Mounted on all platforms
- Medium performance for parallel jobs
- Quota can be changed
- Snapshot backups (7-day history)
- Perfect for sharing data within research group





Local File Systems

Scratch

- Large, temporary storage
- Optimized for read/write operations, NOT storage
- Not backed up
- Purge policy (12 weeks)
- Perfect for staging data and performing computations

Burst Buffer

- Temporary storage
- High-performance SSD file system
- Perfect for getting good performance in I/O-constrained codes
- (Support is reduced)









HPSS: Long Term Storage System

- High-Performance Storage System
- Archival storage of infrequently accessed data
- Use hsi and htar to put/get files between NERSC computational systems and HPSS
- https://docs.nersc.gov/filesystems/archive/







Software Environment and Building Applications





Software

- Cray supercomputers OS is a version of Linux
- Compilers are provided on machines
- Libraries: many libraries provided by vendor and by NERSC
- Applications: NERSC compiles and supports many software packages (such as chemistry and materials sciences packages) for our users
- DOE Extreme-scale Scientific Software Stack (E4S): open-source projects, including xSDK, dev-tools, math-libraries, compilers, and more





Modules Environment

- Modules are used to manage the user environment
 - <u>https://docs.nersc.gov/environment/#nersc-modules-environment</u>

module	
list	To list the modules in your environment
avail avail -S	To list available modules To see all available modules: % module avail To see all available netcdf modules: % module avail -S netcdf
load/unload	To load or unload module
show/display	To see what a module loads
whatis	Display the module file information
swap/switch	To swap two modules For example: to swap architecture target from Haswell to KNL % module swap craype-haswell craype-mic-knl
help	General help: <pre>\$module help Information about a module: \$ module help PrgEnv-cray</pre>





Default Loaded Modules

yunhe@cori08:~> module list Currently Loaded Modulefiles:

- 1) modules/3.2.11.4 2) darshan/3.3.1 3) craype-network-aries
- 4) intel/19.1.2.254
- 5) craype/2.7.10

6) cray-libsci/20.09.1

7) udreg/2.3.2-7.0.3.1 3.16 g5f0d670.ari 8) ugni/6.0.14.0-7.0.3.1_6.4__g8101a58.ari 9) pmi/5.0.17 10) dmapp/7.1.1-7.0.3.1_3.21_g93a7e9f.ari

11) gni-headers/5.0.12.0-7.0.3.1 3.9 gd0d73fe.ari

12) xpmem/2.2.27-7.0.3.1_3.10__gada73ac.ari 13) job/2.2.4-7.0.3.1 3.17 g36b56f4.ari 14) dvs/2.12 2.2.224-7.0.3.1 3.14 gc77db2af 15) alps/6.6.67-7.0.3.1 3.21 gb91cd181.ari 16) rca/2.2.20-7.0.3.1 3.18 g8e3fb5b.ari 17) atp/3.14.9 18) perftools-base/21.12.0 19) PrgEnv-intel/6.0.10 20) craype-haswell 21) cray-mpich/7.7.19 22) craype-hugepages2M

4) Compiler 6) Cray Scientific Libraries 19) Programing Environment 20) Target architecture Driver 21) MPI Libraries

Cori uses Tcl module Perlmutter uses LMOD







Cross-Compile is Needed

- Cori: Haswell compute nodes and KNL compute nodes
- All Cori login nodes are Haswell nodes
- We need to cross-compile
 - Directly compile on KNL compute nodes is very slow
 - Compile on login nodes; Executables run on compute nodes
- Recommend to build separate binaries for each architecture (Cori Haswell, Cori KNL, Perlmutter CPU, Perlmutter GPU) to take advantage of optimizations unique to processor type
 - Haswell binaries do run on KNL
 - All other binaries are not compatible among each other





Software Environment

- Available compilers: Intel, GNU, Cray
- Use compiler wrappers to build. It calls native compilers for each compiler (such as ifort, mpiicc, etc.) underneath.
 - Do not use native compilers directly.
 - ftn for Fortran codes: ftn my_code.F90
 - cc for C codes: cc my_code.c
 - CC for C++ codes: CC my_code.cc
- Compiler wrappers add header files and link in MPI and other loaded Cray libraries by default
 - Builds applications dynamically by default. Can add "-static" to build statically if chosen





Building Simple Test Program (1)

- To build on Cori Haswell:
 - Using default Intel compiler:

ftn -o mytest mytest_code.F90

 Using Cray compiler: module swap PrgEnv-intel PrgEnv-cray ftn -o mytest mytest_code.F90





Building Simple Test Program (2)

- To build on Cori KNL
 - Using default Intel compiler

module swap craype-haswell craype-mic-knl cc -o mytest mytest_code.c

 Using Cray compiler module swap PrgEnv-intel PrgEnv-cray module swap craype-haswell craype-mic-knl cc -o mytest mytest_code.c





Building Applications on Perlmutter

- User environment and instructions are still evolving
- Building for Perlmutter CPU similar to Cori
- More info on building for Perlmutter GPU
 - <u>https://docs.nersc.gov/systems/perlmutter/#compilingbuilding-software</u>
- More info on porting and optimizing for GPU on Perlmutter Readiness page
 - <u>https://docs.nersc.gov/performance/readiness/</u>
 - Basic GPU concepts and programming considerations, programming models, running jobs, machine learning applications, libraries, profiling tools, IO, case studies, …







Running Jobs





Jobs at NERSC

- Most are parallel jobs (10s to 100,000+ cores)
- Also a number of "serial" jobs
 - Typically "pleasantly parallel" simulation or data analysis
- Production runs execute in batch mode
- Our batch scheduler is **SLURM**
- Typical run times are a few to 10s of hours
 - Limits are necessary because of MTBF and the need to accommodate 7,000 users' jobs





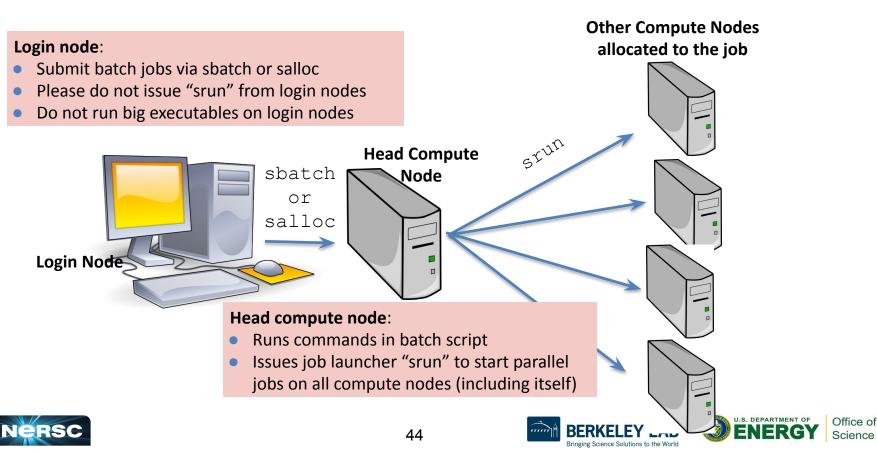
Login Nodes and Compute Nodes

- Login nodes (external)
 - Edit files, compile codes, submit batch jobs, etc.
 - Run short, serial utilities and applications
 - Cori has Haswell login nodes
- Compute nodes
 - Execute your application
 - Dedicated resources for your job
 - Cori has Haswell and KNL compute nodes
 - Binaries built for Haswell can run on KNL nodes, but not vice versa





Launching Parallel Jobs with Slurm



My First "Hello World" Program

my_batch_script:

#!/bin/bash
#SBATCH -q debug
#SBATCH -N 2
#SBATCH -t 10:00
#SBATCH -t 10:00
#SBATCH -L SCRATCH
#SBATCH -J myjob
srun -n 64 ./helloWorld

To run via batch queue

% sbatch my_batch_script **To run via interactive batch** % salloc -N 2 -q interactive -C haswell -t 10:00 <wait_for_session_prompt. Land on a compute node> % srun -n 64 ./helloWorld

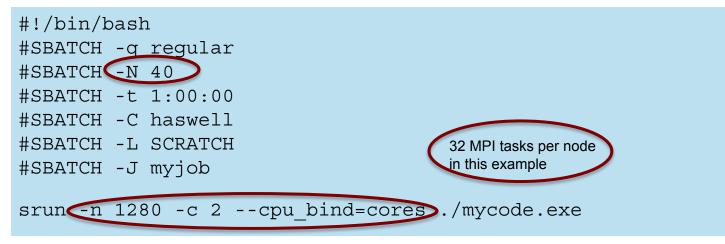
45







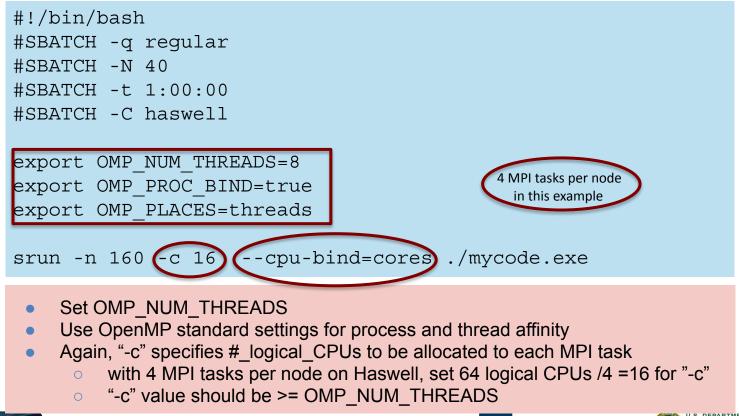
Sample Cori Haswell Batch Script - MPI



- There are 64 logical CPUs (the number Slurm sees) on each node
- "-c" specifies #_logical_CPUs to be allocated to each MPI task
- --cpu-bind is critical especially when nodes are not fully occupied



Sample Corl Haswell Batch Script - Hydrid **MPI/OpenMP**









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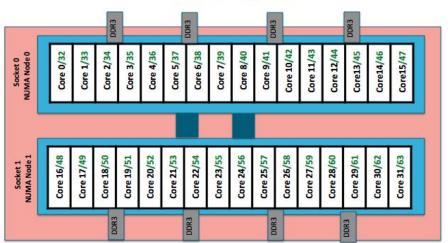
Process / Thread / Memory Affinity

- Correct process, thread and memory affinity is critical for getting optimal performance on Cori Haswell and KNL
 - Process Affinity: bind MPI tasks to CPUs
 - Thread Affinity: bind threads to CPUs allocated to its MPI process
 - Memory Affinity: allocate memory from specific NUMA domains
- Both -c xx and --cpu-bind=cores are essential, otherwise multiple processes may land on the same core, while other cores are idle, hurting performance badly
- Pay special attention on KNL, usually we waste (or aside for OS) 4 cores on purpose, to allow number of logical cores distributed evenly for each MPI rank
- <u>https://docs.nersc.gov/jobs/affinity/</u>





Cori Haswell Compute Nodes



Cori Phase1 Compute Node

To obtain processor info:

Get on a compute node: % salloc -N 1 -C ...

Then: % numactl -H or % cat /proc/cpuinfo or % hwloc-ls

- Each Cori Haswell node has 2 Intel Xeon 16-core Haswell processors
 - 2 NUMA domains (sockets) per node, 16 cores per NUMA domain. 2 hardware threads per physical core.
 - NUMA Domain 0: physical cores 0-15 (and logical cores 32-47)
 NUMA Domain 1: physical cores 16-31 (and logical cores 48-63)
- Memory bandwidth is non-homogeneous among NUMA domains









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Cori KNL Example Compute Nodes

- A Cori KNL node has 68 cores/272 CPUs, 96 GB DDR memory, 16 GB high bandwidth on package memory (MCDRAM)
- Default mode is: quad, cache

Core #	-	0	1	2	3	 16	17	18	 33	34	35		50	51	52	 65	66	67
1562557	Г	0	1	2	3	 16	17	18	 33	34	35		50	51	52	 65	66	67
HW Thread		68	69	70	71	 84	85	86	 101	102	103	**	118	119	120	 133	134	135
#		136	137	138	139	 152	153	154	 169	170	171	***	186	187	188	 201	202	203
		204	205	206	207	 220	221	222	 237	238	239	***	254	255	256	 269	270	271

Arrangement of Hardware Threads for 68 Core KNL

• A quad,cache node (default setting) has only 1 NUMA node with all CPUs on the NUMA node 0 (DDR memory). MCDRAM is hidden from the "numactl -H" result since it is a cache.





Sample Job Script to Run on KNL Nodes

Sample Job script (MPI+OpenMP)

#!/bin/bash -l

#SBATCH -N 2

#SBATCH -q regular

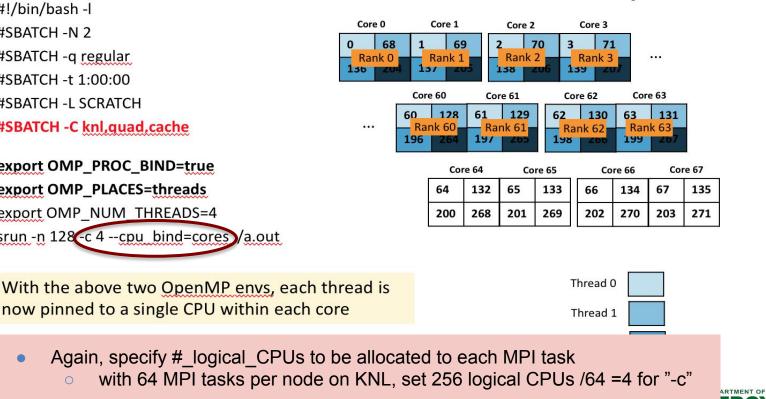
#SBATCH -t 1:00:00

#SBATCH - L SCRATCH

#SBATCH -C knl, guad, cache

export OMP PROC BIND=true export OMP_PLACES=threads export OMP NUM THREADS=4 srun -n 128-c 4 --cpu bind=cores/a.out

Process and thread affinity





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Use salloc to Run Debug and Interactive Jobs

- You can run small parallel jobs interactively on dedicated nodes
- Debug
 - Max 512 nodes, up to 30 min
 % salloc -N 20 -q debug -C haswell -t 30:00
- Interactive (highly recommend to use this!!)
 - Instant allocation (get nodes in 6 min or reject)
 - Max walltime 4 hrs, up to 64 nodes total on Cori per project

% salloc -N 2 -q interactive -C knl -t 2:00:00

- More information (such as how to find out who in your project is using)
 - <u>https://docs.nersc.gov/jobs/examples/#interactive</u>
 - <u>https://docs.nersc.gov/jobs/interactive/</u>





Use "shared" QOS to Run Serial Jobs

- The "shared" QOS allows multiple executables from different users to share a node
- Each serial job run on a single physical core of a "shared" node
- Up to 32 (Cori Haswell) jobs from different users depending on their memory requirements

#SBATCH	-q	shared
#SBATCH	-t	1:00:00
#SBATCH	m	nem=4GB
#SBATCH	- C	haswell
#SBATCH	-J	my_job
./mycode	.x	

- Only available on Cori Haswell, charged by a fraction of a node used
- https://docs.nersc.gov/jobs/best-practices/#serial-jobs





Bundle Jobs

Multiple Jobs Sequentially: #!/bin/bash #SBATCH -q regular **#SBATCH -N 100** #SBATCH -t 12:00:00 #SBATCH -J my_job #SBATCH -J my_job.o%j #SBATCH -c my_job.o%j #SBATCH -L project,SCRATCH #SBATCH -C haswell

srun -n 3200 ./a.out srun -n 3200 ./b.out srun -n 3200 ./c.out

- Request largest number of nodes needed
- <u>https://docs.nersc.gov/jobs/examples/#</u> <u>multiple-parallel-jobs-sequentially</u>

Multiple Jobs Simultaneously: #!/bin/bash #SBATCH -q regular **#SBATCH -N 9** #SBATCH -t 12:00:00 #SBATCH -J my_job #SBATCH -J my_job.o%j #SBATCH -c my_job.o%j #SBATCH -L project

srun -n 44 -N 2 -c2 --cpu-bind=cores ./a.out & srun -n 108 -N 5 -c2 --cpu-bind=cores ./b.out & srun -n 40 -N 2 -c2 --cpu-bind=cores ./c.out & wait

- Request total number of nodes needed
- No applications are shared on the same nodes
- Make sure to use "&" (otherwise run in sequential) and "wait" (otherwise job exit immediately)
- <u>https://docs.nersc.gov/jobs/examples/#multiple-parallel-jobs-simultaneously</u>

Dependency Jobs

cori% sbatch job1 Submitted batch job 1655447

```
cori06% sbatch --dependency=afterok:5547 job2
or
cori06% sbatch --dependency=afterany:5547 job2
```

https://docs.nersc.gov/jobs/example s/#dependencies

cori06% sbatch job1 submitted batch job 1655447

cori06% cat job2 #!/bin/bash #SBATCH -q regular #SBATCH -N 1 #SBATCH -t 1:30:00 **#SBATCH -d afterok:1655447** #SBATCH -C haswell srun -n 16 -c 4 ./a.out



cori06% sbatch job2



Job Arrays

#!/bin/bash
#SBATCH -q regular
#SBATCH -N 1
#SBATCH -t 1:00:00
#SBATCH --array=1-10
#SBATCH -L SCRATCH
#SBATCH -C haswell

cd **test_\$SLURM_ARRAY_JOB_ID** srun ./mycode.exe

- Better managing jobs, not necessary faster turnaround
- Each array task is considered a single job for scheduling
- Use \$SLURM_ARRAY_JOB_ID for each individual array task

https://docs.nersc.gov/jobs/examples/#job-arrays









Use Workflow Management Tools

- These tools can help data-centric science to automate moving data, multi-step processing, and visualization at scales.
- Please do not do below!

```
for i = 1, 10000
srun -n 1 ./a.out
```

It is inefficient and overwhelms Slurm scheduler

- Available workflow tools include: GNU parallel, Taskfarmer, Fireworks, Nextflow, Papermill, etc.
- One usage case is to pack large number of serial jobs into one script
- https://docs.nersc.gov/jobs/workflow-tools/





GNU Parallel Is Better Than Shared QOS

elvis@cori07:~> module load parallel

```
elvis@cori07:~> seq 1 5 | parallel -j 2 'echo \
> "Hello world {}!"; sleep 10; date'
Hello world 1!
Thu Jun 11 00:21:00 PDT 2020
Hello world 2!
Thu Jun 11 00:21:00 PDT 2020
Hello world 31
Thu Jun 11 00:21:10 PDT 2020
Hello world 4!
Thu Jun 11 00:21:10 PDT 2020
Hello world 5!
Thu Jun 11 00:21:20 PDT 2020
elvis@cori07:~>
```

- Packed jobs have massively reduced total queue wait
 - Can also pack single-node tasks into multiple node jobs
- No risk of Slurm overload
- Run combinations of tasks in parallel and sequence
- Easy input substitution
 - If you need it, *much* more power is available
- Superior to task arrays, too
- <u>https://docs.nersc.gov/jobs/workflow/</u> <u>gnuparallel/</u>







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NERSC Job Script Generator

Select the QoS you request for your job.

https://my.nersc.gov/script_generator.php

Dashboard	Jobscript Generator
III Jobs 🗸 🗸	
Jobscript Generator	Job Information
Completed Jobs	This tool generates a batch script template which also realizes specific process and thread binding configurations.
E Cori Queues	Machine #//bin/bash
Zueue Backlog	Select the machine on which you want to submit your job. #SBATCH -N 150 #SBATCH -C knl
Center Status <	Cori - KNL #SBATCH -q regular #SBATCH -t 02:30:00
File Browser	Application Name #OpenMP settings:
Service Tickets	Specify your application including the full path. export OMP_NUM_THREADS=8 export OMP_PLACES=threads
Service fickets	export OMP_PROC_BIND=spread
III Data Dashboard	Job Name
🖋 PI Toolbox	Specify a name for your job. #run the application: srun -n 1200 -c 32cpu_bind=cores myapp.x
Jupyter Hub	
I NERSC Homepage	Email Address
Documentation Portal	Specify your email address to get notified when the job enters a certain state.
I Accounts Portal	
	Wallclock Time
	Specify the duration of the job.
	2 0 0 0
	hours minutes seconds
	Quality of Service
	Select the OoS you request for your job





Bringing Science Solutions to the World

Monitoring Your Jobs

- Jobs are waiting in the queue until resources are available
- Overall job priorities are a combination of QOS, queue wait time, job size, wall time request, etc.
- You can monitor with
 - **squeue**: Slurm native command
 - **sqs**: NERSC custom wrapper script
 - **sacct**: Query Completed and Pending Jobs
 - o <u>https://docs.nersc.gov/jobs/monitoring/</u>
- On the web
 - o <u>https://my.nersc.gov</u>
 - Cori Queues, Queue backlogs, Queue Wait Times (statistics data)
 - <u>https://www.nersc.gov/users/live-status/</u> □ Queue Look
 - <u>https://iris.nersc.gov</u> the "Jobs" tab





Cori Haswell Queue Policy (as of June 2022)

QOS	Max nodes	Max time (hrs)	Submit limit	Run limit	Priority	QOS Factor
regular	512/1932 ²	48	5000	-	4	1
shared ³	0.5	48	10000	-	4	1
interactive	64 <u>4</u>	4	2	2	-	1
debug	64	0.5	5	2	3	1
premium	1772	48	5	-	2	2 -> 4 ⁵
flex	64	48	5000	-	6	0.5
overrun	1772	4	5000	-	5	0
xfer	1 (login)	48	100	15	-	-
bigmem	1 (login)	72	100	1	-	1
<u>realtime</u>	custom	custom	custom	custom	1	custom
compile	1 (login)	24	5000	2	7.1	



Tips for Getting Better Throughput

- Line jumping is allowed, but it may cost more ("premium" QOS)
- Submit shorter jobs, they are easier to schedule
 - Checkpoint to break up long jobs, use variable time and "flex" QOS
 - Short jobs can take advantage of 'backfill' opportunities
- Make sure the wall clock time you request is accurate
 - Larger shorter jobs are easier to schedule than long smaller jobs
 - Many users unnecessarily request the largest wall clock time possible as default
- Check queue backlogs and queue wait times
 - <u>https://my.nersc.gov/backlog.php</u>
 - o <u>https://my.nersc.gov/queuewaittimes.php</u>





Running Jobs Considerations

- Running jobs on Perlmutter and instructions are still evolving
 - Running on CPU is similar to running on Cori Haswell
 - More examples for Running on GPU: <u>https://docs.nersc.gov/systems/perlmutter/running-jobs/</u>
- Remember to compile separately for each type of compute nodes
- Running jobs from global homes (\$HOME) is strongly discouraged
 - IO is not optimized
 - The global homes file system access on compute nodes is much slower than from \$SCRATCH
 - It may also cause negative impact for other users interactive response on the system
 - Consider to use shifter for large jobs using shared libraries







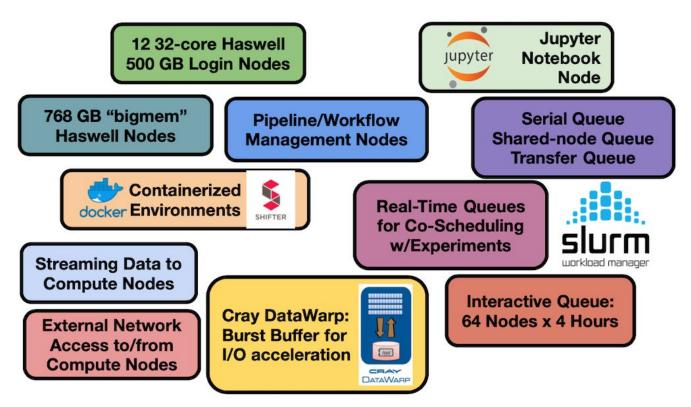


Data Analytics Software and Services





Cori's Data Friendly Features





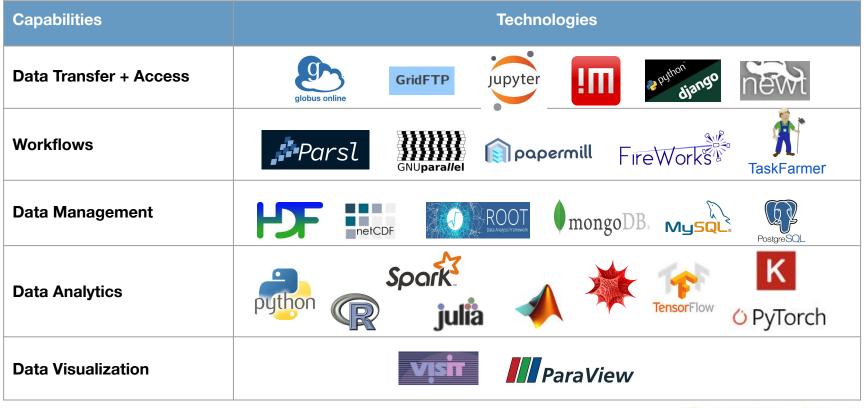




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Production Data Software Stack









Data Analytic Software Services

- Globus Online
- Science Gateways
- Databases
- Shifter
- Python
- Jupyter
- Machine Learning / Deep Learning
- Workflows
- And more ...







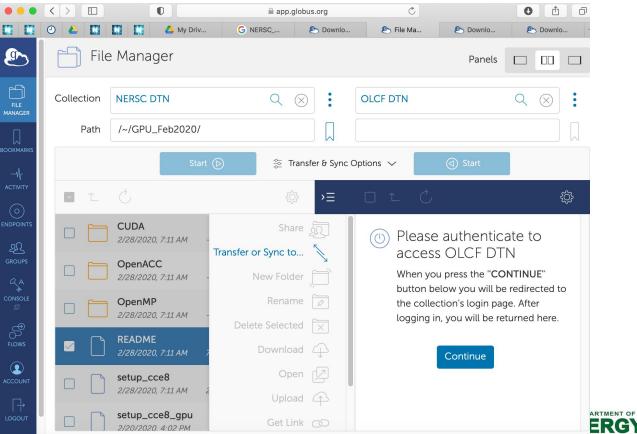
Globus Online: Move Data

- https://www.globus.org https://docs.nersc.gov/services/globus/
- The recommended tool for moving data in&out of NERSC
 - Reliable & easy-to-use web-based service:
 - Automatic retries
 - Email notification of success or failure
 - NERSC managed endpoints for optimized data transfers
 - NERSC DTN (dedicated data transfer system), NERSC Cori, NERSC Perlmutter, NERSC HPSS, etc.
 - Other Center has endpoints
 - Setup <u>Globus Connect Personal</u> to ease transfer between local system (such as laptop) and NERSC systems





Globus File Transfer Example





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Data Transfer General Tips

- Use Globus Online for large, automated or monitored transfers
- cp, scp, or rsync is fine for smaller, one-time transfers (<100 MB)
 - But note that Globus is also fine for small transfers
- Use give-and-take to share files between NERSC users
 - o % give -u <receiving_user> <file or directory>
 - o % take -u <sending_user> <filename>



Access for External Collaborators

- Web Portals
 - NERSC supports project-level public http access
 - Project specific area can be created:

/global/cfs/cdirs/<your_project>/www

- These are available for public access under the URL: http://portal.nersc.gov/cfs/<your project>
- Each repo has a /project space, can publish as above
- Special Science Gateways can be created.
 - Sophisticated ones can be made with SPIN <u>https://docs.nersc.gov/services/spin/</u>

https://www.nersc.gov/users/training/spin/ (SPIN workshop required)

• Details at: <u>https://docs.nersc.gov/services/science-gateways/</u>





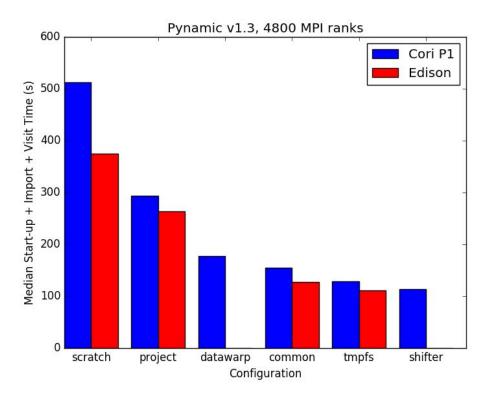




- NERSC R&D effort, in collaboration with Cray, to support Docker Application images
- "Docker-like" functionality on the Cray and HPC Linux clusters. Enables users to run custom environments on HPC systems.
- Addresses security issues in a robust way
- Efficient job-start & Native application performance



Shifter Accelerates Python Applications











Create an Image with Docker



Dockerfile

```
FROM ubuntu:14.04
MAINTAINER Shane Canon scanon@lbl.gov
# Update packages and install dependencies
RUN apt-update -y && \
        apt-get install -y build-essential
```

```
# Copy in the application
ADD . /myapp
# Build it
RUN cd /myapp && \
    make && make install
```

laptop> docker build -t scanon/myapp:1.1 .
laptop> docker push scanon/myapp:1.1











Use the Image with Shifter

```
#!/bin/bash
#SBATCH -N 16 -t 20
#SBATCH --image=scanon/myapp:1.1
module load shifter
export TMPDIR=/mnt
srun -n 16 shifter /myapp/app
```

cori> shifterimg pull scanon/myapp:1.1 cori> sbatch ./job.sl





Python

- Extremely popular interpreted language, continuing to grow
- Libraries like NumPy, SciPy, scikit-learn commonly used for scientific analysis
- Are used for ML/DL
- Python is fully supported at NERSC we use Anaconda Python to provide pre-built environments and the ability for users to create their own environments
- Guide to use Python on Perlmutter:
 - https://docs.nersc.gov/development/languages/python/using-python-perlmutter
- Do not use /usr/bin/python, instead: module load python

which already includes basic packages: numpy, scipy, mpi4py





Make Your Own Python Conda Environment

 To make a custom env module load python conda create -n myenv python=3.9 conda activate myenv conda (or pip) install your_custom_packages ###import antigravity conda deactivate myenv

https://docs.nersc.gov/development/languages/python/#how-to-ru
n-python-jobs-at-nersc





Options to Run Python Code in Parallel

https://docs.nersc.gov/development/languages/python/parallel-python/#how-to-u se-parallelism-in-python

- Multiprocessing, PyOMP
 - Single node only, process parallelism via a pool of workers
- Dask
 - Single or many nodes, framework to create a group of workers that execute tasks coordinated by a scheduler, nice visualization tools
- mpi4py
 - Single or many nodes, best performance when used together with a container (Docker/Shifter)
 - Do not pip install mpi4py or conda install mpi4py, follow instructions at <u>https://docs.nersc.gov/development/languages/python/parallel-python/#using-mpi4py-i</u> <u>n-a-shifter-container</u>







Interactive open-source web application



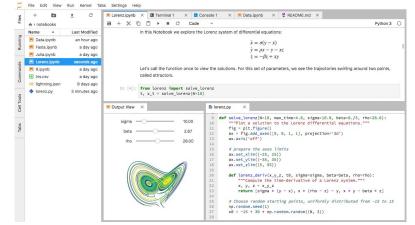
Allows you to create and share documents, "notebooks," containing:

Live code Equations Visualizations Narrative text Interactive widgets

Things you can use Jupyter notebooks for:

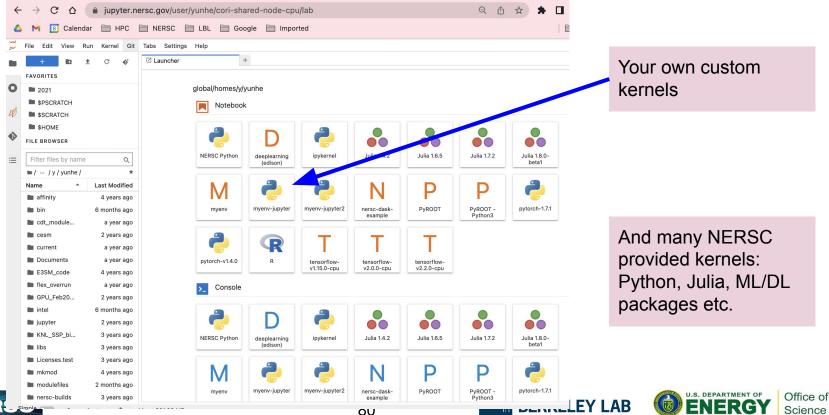
Data cleaning and data transformation Numerical simulation Statistical modeling Data visualization Machine learning Workflows and analytics frameworks Training and Tutorials

https://docs.nersc.gov/services/jupyter/





Available Jupyter Kernels



Bringing Science Solutions to the World

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Your Own Custom Jupyter Kernel

Most common Jupyter question:

"How do I take a conda environment and use it from Jupyter?"

Several ways to accomplish this, here's the easy one.

```
$ module load python
$ conda create -n myenv python=3.9 ipykernel <more-packages-to-install>
$ conda activate myenv
(myenv) $ python -m ipykernel install --user --name myenv-jupyter
```

Point your browser to jupyter.nersc.gov. (You may need to restart your notebook server via control panel). Kernel "myenv-jupyter" should be present in the kernel list.





Additional Customization

edit: \$HOME/.local/share/jupyter/kernels/myenv-jupyter/kernel.json The helper script is the most flexible approach for NERSC users since it easily enables modules.

```
"argv": [
 "/global/homes/y/yunhe/jupyter-helper.sh",
 "python",
 ``−m″,
 "ipykernel launcher",
                                           Meanwhile, in jupyter-helper.sh:
 "-f",
                                           #!/bin/bash
 "{connection file}"
                                           export SOMETHING=123
],
                                           module load texlive
                                           exec python -m ipykernel "$@"
"display name": "myenv-jupyter2",
"language": "python",
```





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Available Notebook Servers

← ▲		🛆 🔒 jupyter.nersc.gov/hul alendar 🛅 HPC 🗎 NERSC	D/home Q	🖞 🖈 🖨 🚺 💟 Update 🔅
ĊJ	upyter <mark>h</mark>	ub Home Token Services -	Documentation	train438 🕒 Logout
		Shared CPU Node	Exclusive GPU Node	Configurable GPU
	Perlmutter	start	start	start
	Cori	start		start
	Resources	Use a node shared with other users' notebooks but outside the batch queues.	Use your own node within a job allocation using defaults.	Use multiple compute nodes with specialized settings.
	Use Cases	Visualization and analytics that are not memory intensive and can run on just a few cores.	Visualization, analytics, machine learning that is compute or memory intensive but can be done on a single node.	Multi-node analytics jobs, jobs in reservations, custom project charging, and more.

Can request additional access for exclusive Cori CPU and shared Cori GPU nodes





NERSC Deep Learning Software Stack Overview

https://docs.nersc.gov/machinelearning/

Frameworks:

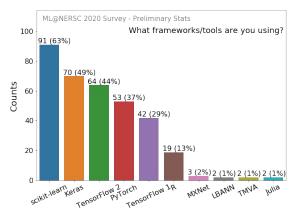


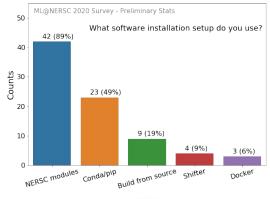
Distributed training libraries:

- Horovod
- PyTorch distributed
- Cray Plugin

Productive tools and services:

• Jupyter, Shifter





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How to Use NERSC DL Software Stack

- We have modules you can load which contain python and DL libraries
 - module load tensorflow/<version>
 - module load pytorch/<version>
- You can install your own packages on top to customize
 pip install --user MY-PACKAGE
- Or you can create your conda environments from scratch
 - conda create -n my-env MY-PACKAGES
 We also have pre-installed lupyter kernels
- We also have pre-installed Jupyter kernels





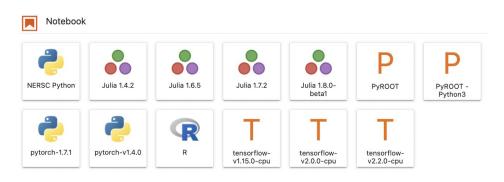
Jupyter for Deep Learning

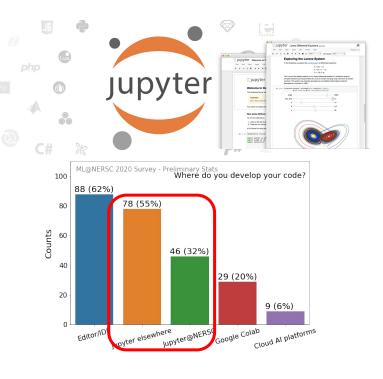
JupyterHub service provides a rich, interactive notebook ecosystem

- Very popular service with hundreds of users
- A favorite way for users to develop ML code

Users can run their deep learning workloads

- using our pre-installed DL software kernels
- using user custom kernels













Hands-on Exercises





Compiling and Running Jobs on Cori

- % ssh <user>@cori.nersc.gov
- % cd \$SCRATCH
- % git clone https://github.com/NERSC/intro-NERSC-resources.git
- % cd intro-NERSC-resources
- Follow
 - hello-exercise.README
 - matrix-example.README
 - xthi-exercise.README
- References
 - Running Jobs: <u>https://docs.nersc.gov/jobs/</u>
 - Interactive Jobs: <u>https://docs.nersc.gov/jobs/examples/#interactive</u>





Using Compute Node Reservations

- Existing NERSC users are added to "ntrain4" project
- Cori node reservations available from 2-3:30 pm today
- User reservations with --reservation=xxx -A ntrain4, where
 xxx is "intro hsw" or "intro knl"







