JupyterHub at NCAR

The JupyterHub deployment that CISL manages allows "push-button" access to NCAR's Cheyenne supercomputing resource and the Casper cluster of nodes used for data analysis and visualization, machine learning, and deep learning.

It gives users the ability to create, save, and share Jupyter Notebooks through the JupyterLab interface and to run interactive, web-based analysis, visualization and compute jobs on Cheyenne and Casper. JupyterHub is an alternative to X11 access for interacting with those resources to run jobs as well as for using web-based interactive shell functionality without the need to install or use software such as SSH or PuTTY.

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Getting started

Use your web browser to go to jupyterhub.hpc.ucar.edu. Chrome and Firefox are recommended for all users.

Select Production.



Log in with your NCAR username and Duo two-factor authentication, just as you would when logging directly in to either system.

NCAR UCAR Computational & Information Systems Lab
Online documentation for NCAR JupyterHub is available here.
Sign in
Username:
Password:
Sign in

After you authenticate, you will be able to start a new default server or create a named server. (See following image.) You can have up to four named servers to use for accessing different compute resources.

Caution

Do not start a new server simply to run additional notebooks; a single server can support multiple notebooks at once. However, executing the same notebook file in multiple servers concurrently can lead to kernel failures and other errors.

Online documentation for NCAR JupyterHub is available here.					
		Start My Server			
Named Servers					
n addition to your default server, you may have additional 4 server(s) with names. This allows you to have more nan one server running at the same time.					
In addition to your default than one server running a	t server, you may ha at the same <mark>t</mark> ime.	ave additional 4 server(s) wit	th names. This allows you to have more		
In addition to your defaul than one server running a Server name	t server, you may ha at the same time. URL	ave additional 4 server(s) wit Last activity	th names. This allows you to have more Actions		
In addition to your default than one server running a Server name Name your server	t server, you may ha at the same time. URL Add New Ser	ave additional 4 server(s) wit Last activity	th names. This allows you to have more Actions		
In addition to your default than one server running a Server name Name your server Example1	t server, you may ha at the same time. URL Add New Ser	ave additional 4 server(s) wit Last activity rver 4 minutes ago	th names. This allows you to have more Actions start delete		

After starting a server, select the cluster you want to use. You can choose to work on a login node or a batch node on either Casper or Cheyenne.

Online documentation for NCAR JupyterHub is available here.				
NCAR HPC JupyterHub				
Cluster Selection				
Casper Login	*			
Casper Login				
Casper Batch				
Cheyenne Login				
Cheyenne Batch				

If you choose a login node, launching the server will take you to the web interface.

If you choose a batch node, use the form provided (images below) to specify your project code, set the necessary PBS job options, and launch the appropriate server. The name of your batch job will be STDIN.

For more information about the options, see:

- Submitting Cheyenne jobs with PBS
 Starting Casper jobs with PBS

Launch your job when ready. This job only gives you access to the JupyterLab instance. If you need more resources, you can launch another job or jobs from within JupyterLab.

Cluster Selection		
		Cluster Selection
Casper Batch	~	Cheyenne Batch ~
Enter Queue or Reservation (-q)		Enter Queue or Reservation (-q)
casper		share
Specify your project account (-A)		Specify your project account (-A)
Specify N node(s) (-! select=N)		Specify N node(s) (-i select=N)
1 Specify N CPUs per node (-I ncpus=N)		1 Specify N CPUs per node (-l ncpus=N)
1		1
Specify N MPI tasks per node (-I mpiprocs=N)		Specify N MPI tasks per node (-I mpiprocs=N)
1		1
Specify N threads per process (-I ompthreads=N)		Specify N threads per process (-I ompthreads=N)
1		1
Specify the Amount of memory / node in GB (MAX: 1494)		Specify the Amount of memory / node in GB
1		1
Specify X Number of GPUs / Node (-I ngpus=X)		Specify wall time (-I walltime=[[HH:]MM:]SS) (12 Hr Maximum)
0		02:00:00
Select GPU Type, X (-I gpu_type=X)		
none	~	Launch Server
Specify wall time (-I walltime=[[HH:]MM:]SS) (24 Hr Maximum)		
02:00:00		
Launch Server		

After launching the job, you will have access to multiple kernels in the web interface (image below) for working with various languages and applications.

Note that the "File browser" icon (upper-left of following image) allows you to explore your home directory only. To change to your scratch or work space, create soft links in your home directory to those locations.



Python environments and kernels

The JupyterLab dashboard provides access to Notebook and Console kernels, which are programming language interpreters. Available kernels, which change periodically as new releases are installed, include:

- Multiple Python 3 interpreters with varying package support including a basic install (Python 3), the Pangeo stack installed with conda (Pangeo), and the NCAR Python Library (NPL) that is also provided at the command-line by the conda environment module.
- R
- MATLAB Julia
- Three C++ interpreters with different standards compliance
- . A Bash interpreter that provides a shell environment

Related documentation

See these related CISL documentation pages for additional support:

- Jupyter and IPython
- Using Conda and Python