# Bridges-2 Demo

#### CyberAccelerate ACCESS Workshop

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## **Bridges-2 Computing Cluster**

With an ACCESS account through NSF's ACCESS program, users can access various advanced computing resources.

Bridges-2, the flagship cluster offered by Pittsburgh Supercomputing Center (PSC), is one of these available resources.

Bridges-2 Information: <a href="https://www.psc.edu/resources/bridges-2">www.psc.edu/resources/bridges-2</a>

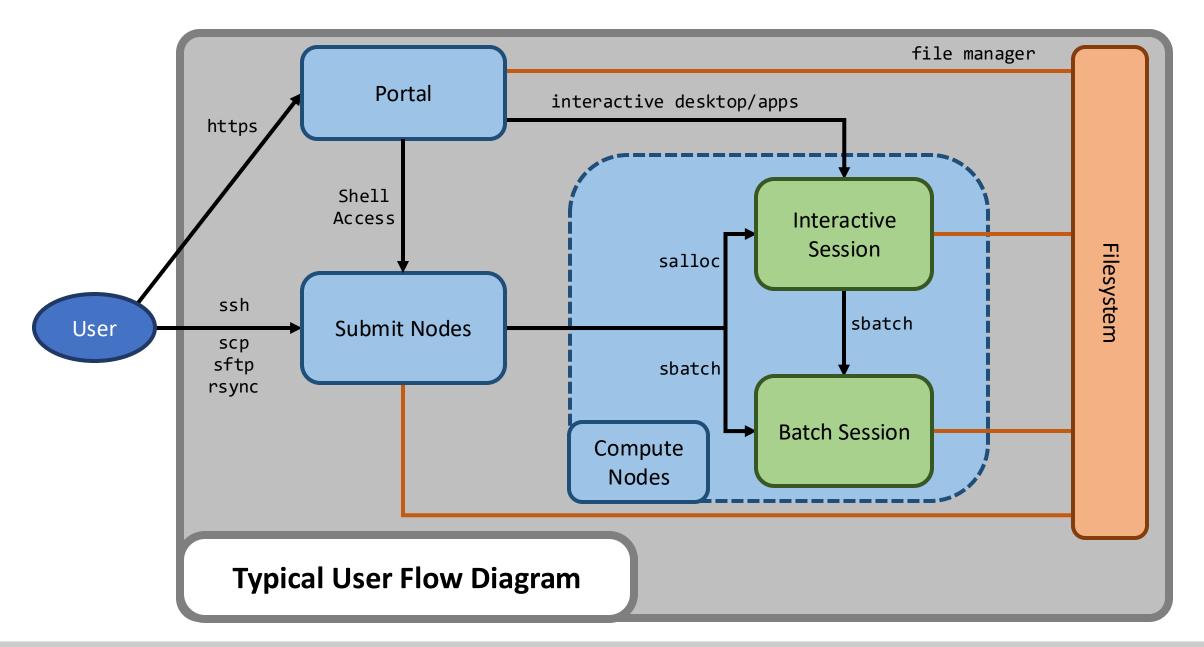
Bridges-2 User Guide: <a href="https://www.psc.edu/resources/bridges-2/user-guide">www.psc.edu/resources/bridges-2/user-guide</a>

Today's demo utilizes Bridges-2, but this is just one of the many compute resources available via the ACCESS program.







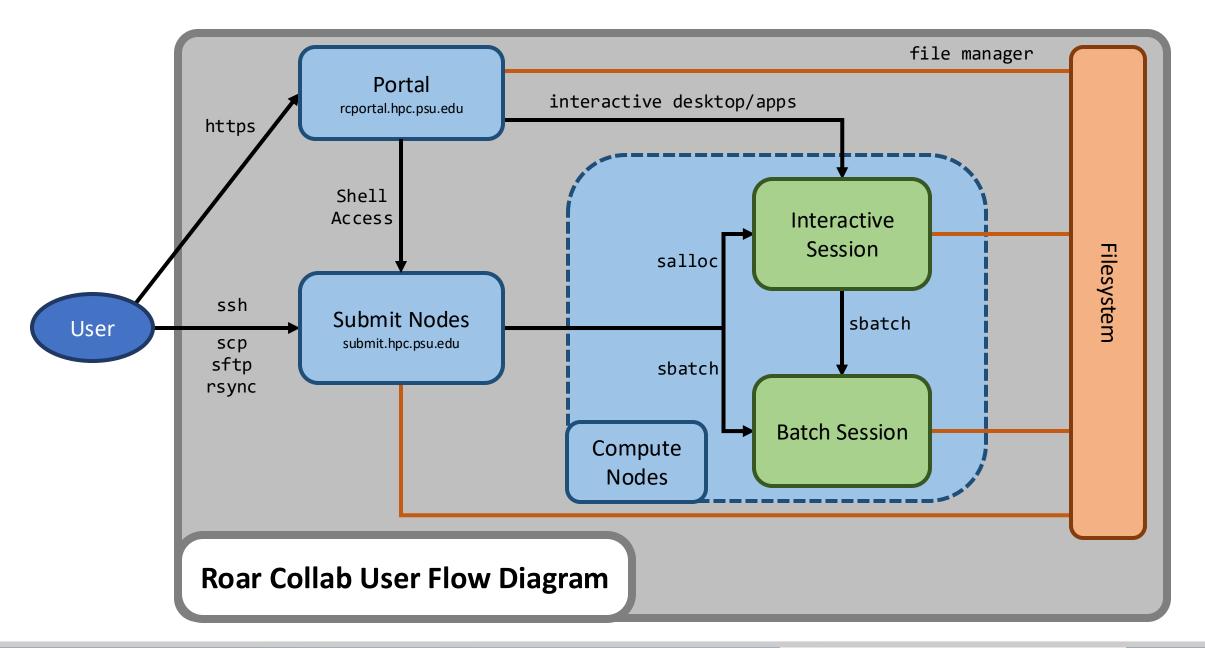










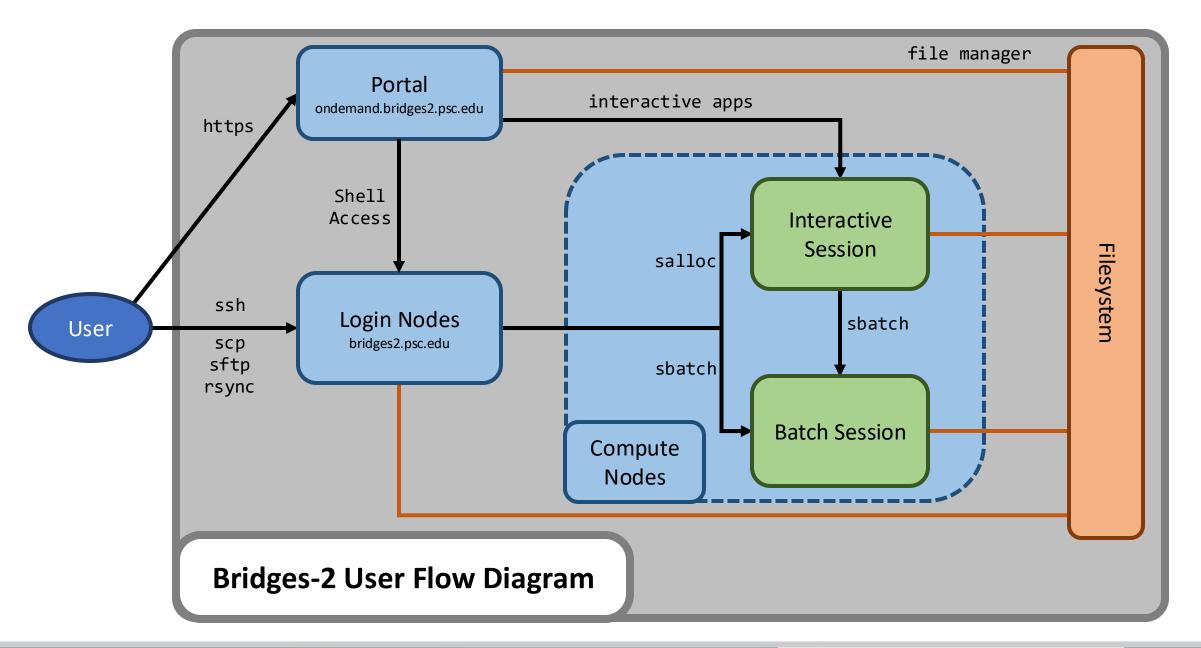










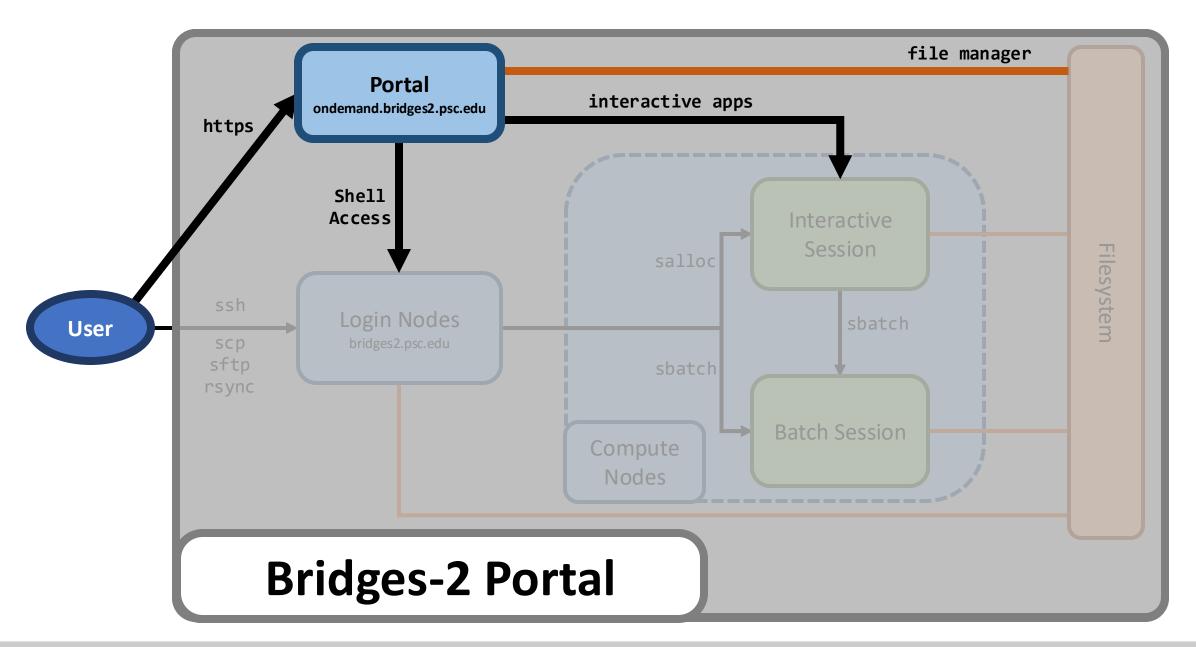




















## **Bridges-2 Portal**

The Bridges-2 Portal, powered by Open OnDemand (OOD), allows users to submit and monitor jobs, manage files, and run applications using just a web browser.

To access the Bridges-2 Portal, navigate to the following website in a web browser: <a href="mailto:ondemand.bridges2.psc.edu">ondemand.bridges2.psc.edu</a>

To log into the Bridges-2 Portal successfully, users must log in using valid PSC account credentials.









## **Bridges-2 Portal Menu Bar**

**Apps:** Lists all available Portal apps

Files: Provides a convenient graphical file manager and lists primary file locations

Jobs: Lists active jobs and allows use of the Job Composer

Clusters: Provides shell access to submit nodes on RC

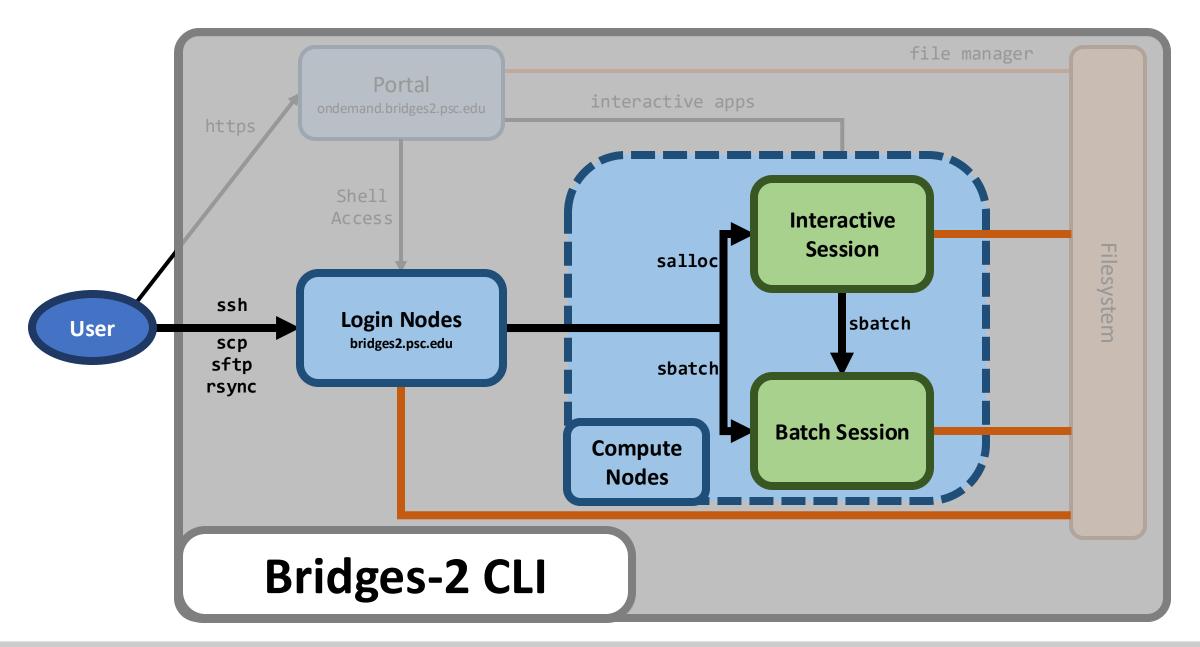
Interactive Apps: Provides access to Jupyter and RStudio interactive apps

My Interactive Sessions: Lists any active sessions

















## **Key Notation**

Green highlight identifies a **command** that can be run in a terminal session.

Light \$BLUE highlight with a dollar sign identifies a user environment variable.

Grey highlight identifies something within a file.

Angle brackets like **<this>** represent the need to insert a string. Replace **<this>** with the string, and do not keep the angle brackets.









## **Computing Environment Basics**

Data Storage and Data Transfer

Accessing and Utilizing Software

Performing Computational Tasks









## **Data Storage and Data Transfer**







## **Bridges-2 Data Storage**

#### **Data Storage and Data Transfer**

Accessing and Utilizing Software Performing Computational Tasks

Users can access personal, project-specific, and job-specific storage locations.

Storage	Quota	Backup Policy	Use Case
\$HOME	25 GB	Daily Snapshot	Batch scripts, source code, and parameter files
\$PROJECT	Project-dependent	No Backup	Primary project storage
\$LOCAL	Job-dependent	No Backup	Job-specific node-local storage
\$RAMDISK	Job-dependent	No Backup	Job-specific IO memory

The my\_quotas and projects commands provide further details on the available storage locations and the usage of those storage locations









## **Bridges-2 Data Transfer**

#### **Data Storage and Data Transfer**

Accessing and Utilizing Software Performing Computational Tasks

File transfer utilities like <a href="mailto:scp">scp</a>, <a href="mailto:stp">sftp</a>, and <a href="mailto:rsync">rsync</a> can be used with the bridges2.psc.edu hostname to transfer smaller files to/from Bridges-2.

Globus, a web-based file transfer tool, should be used for larger file transfers. With Globus, users can easily, reliably, and securely transfer data to/from Bridges-2.

Details on using Globus for file transfers to/from Bridges-2 are provided in the Bridges-2 User Guide.









## **Accessing and Utilizing Software**







#### **Software Stack**

**Accessing and Utilizing Software** 

Performing Computational Tasks

Software stacks often use Lmod to package available software.

Lmod is a useful tool for managing user software environments using **environment modules** that can be dynamically added or removed using module files.

Lmod alters environment variables, most notably the **\$PATH** variable.









#### **Lmod Commands**

Data Storage and Data Transfer

#### **Accessing and Utilizing Software**

Performing Computational Tasks

Command	Action
module avail	Lists all modules that are available to be loaded
<pre>module show <module_name></module_name></pre>	Shows the contents of a module
<pre>module spider <module_name></module_name></pre>	Searches the module space for a match
<pre>module load <module_name></module_name></pre>	Loads a module or multiple modules if given a space-delimited list of modules
module load <module>/<version></version></module>	Loads a module of a specific version
<pre>module unload <module_name></module_name></pre>	Unloads a module or multiple modules if given a space-delimited list of modules
module list	Lists all currently loaded modules
module purge	Unloads all currently loaded modules
module use <path></path>	Adds an additional path to \$MODULEPATH to expand module scope
module unuse <path></path>	Removes a path from \$MODULEPATH to restrict module scope







## **Performing Computational Tasks**







## **Shared Computing Systems**

Data Storage and Data Transfer
Accessing and Utilizing Software

**Performing Computational Tasks** 

The clusters are shared computational resources. To perform computationally-intensive tasks, users must request compute resources and be provided access to those resources to perform the tasks.

The request/provision process allows the tasks of many users to be scheduled and carried out efficiently to avoid resource contention.

Slurm (Simple Linux Utility for Resource Management) is often utilized as the job scheduler and resource manager for shared computing clusters.

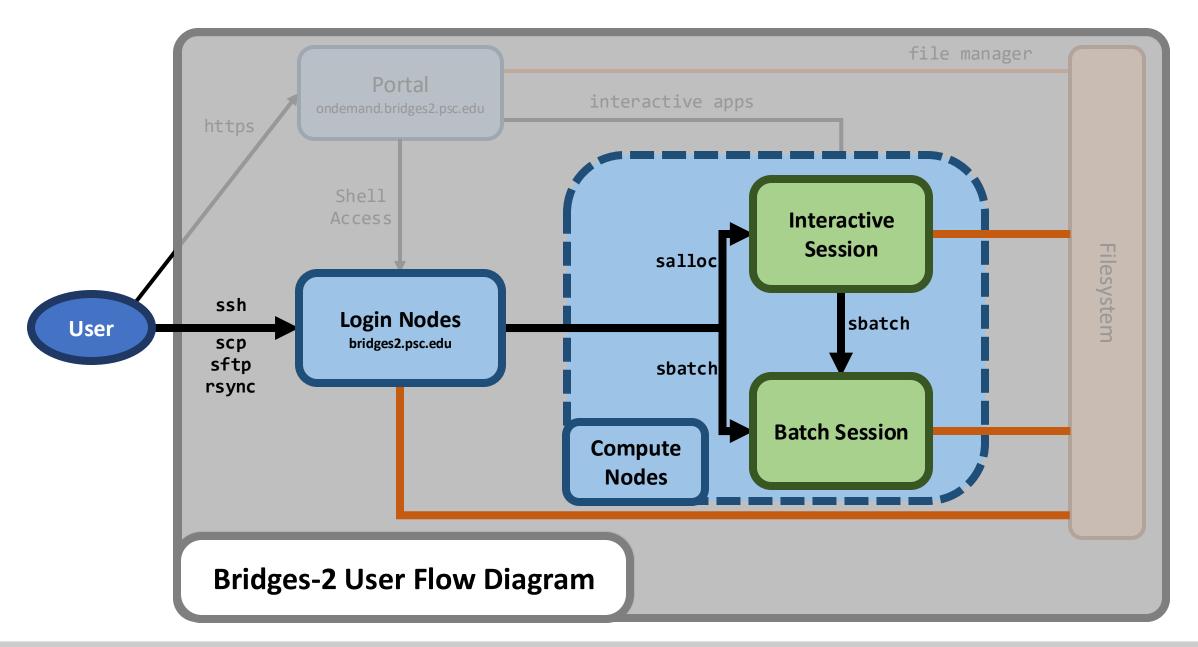
Slurm is rapidly rising in popularity and research computing cluster use Slurm. ICDS clusters (both RC and RR) and Bridges-2 all utilize Slurm.



















### **Slurm Job Submission**

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Requesting an interactive compute session can be accomplished using the salloc command.

Submitting a batch job with a submission script can be accomplished using the **sbatch** command.

Detailed information for each of these commands (<u>salloc</u>, <u>sbatch</u>) can be found in Slurm's documentation.









#### **Common Resource Directives**

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Directive	Description
-J orjob-name	Specify a name for the job
-A oraccount	Charge resources used by job to specified compute account
-p orpartition	Request a specific partition
-N ornodes	Request the number of nodes for the job
-n,ntasks, orntasks-per-node	Request the number of tasks for the job
-C orconstraint	Specify any required node features for job
mem ormem-per-cpu	Specify the memory required per node or CPU, respectively
-t ortime	Set a limit on the total run time of the job
requeue	Specify that the batch job should be eligible for requeuing
-e orerror	Instruct Slurm to connect the batch script's standard error to a non-default file
-o oroutput	Instruct Slurm to connect the batch script's standard output to a non-default file







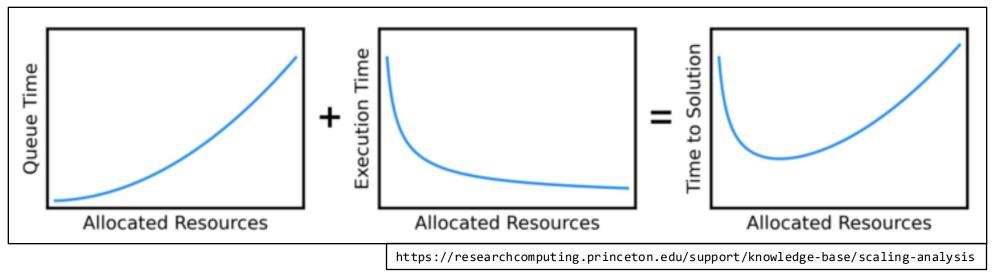
### **Time To Solution**

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Requesting more resources for a job will increase its time in the queue as it must wait longer for resources to be allocated.

Typically, parallelized code will see a reduction in overall runtime as more resources are requested.



The total time to solution is ultimately reduced when the job strikes a balance by requesting the minimal amount of resources needed to provide a reasonable speedup.









## Requesting Resources

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The goal of a resource request is to attain the necessary computational resources to complete a task while minimizing the time to solution.

An optimal resource request is the minimal amount of computational resources that allows a computational task to run to successful completion.

Let's examine 1 laptop-worth of resources as a reference. My laptop, for example, has a 12-core processor and 36 GB of RAM.

If a computational task can run on a laptop without crashing the device, then there is absolutely no need to submit a resource request larger than this.









# Bridges-2 Demo







## Access Login Node



Choose one of two options to initiate an interactive session on a submit node:

- From a terminal session, run the following command:
   ssh <userid>@bridges2.psc.edu
- Access ondemand.bridges2.psc.edu and from the banner select
   Clusters > Bridges-2 Shell Access

After completing the login process, the prompt will indicate that the interactive session is on a login node.









#### **Download Session Files**



Within the session on Bridges-2, navigate to either your \$\frac{\$HOME}{\text{directory with the following command:}}

cd OR cd \$HOME

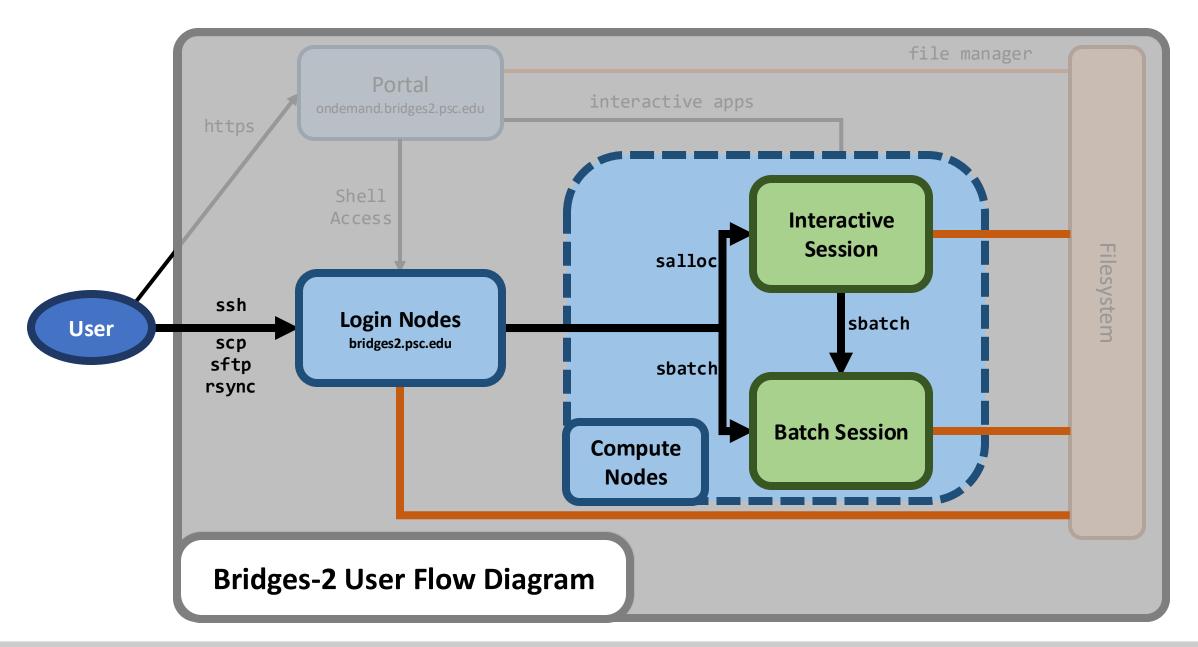
Download the session files and enter the directory with















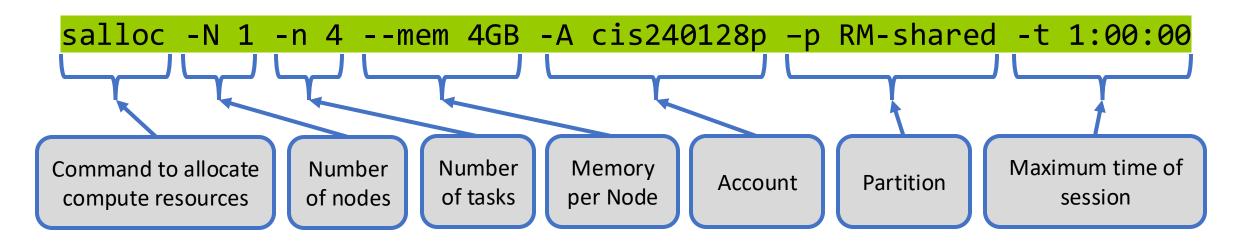




## **Interactive Compute Session**



To launch an interactive session on a compute node, run the following command on a login node:



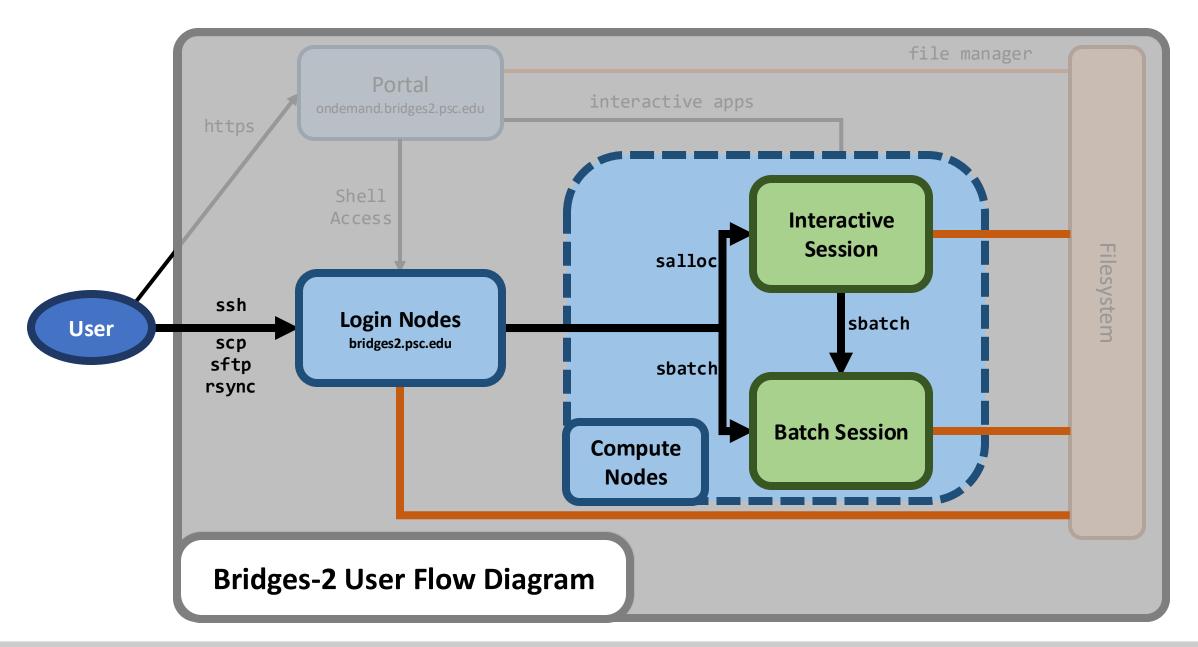
Note that the prompt changes from a login node type to a compute node type after the resources are granted.



















### **Submission Script Example**

```
#!/bin/bash
#SBATCH --job-name=pi serial
#SBATCH --account=cis240128p
#SBATCH --partition=RM-shared
#SBATCH --nodes=1
#SBATCH --ntasks=1
#SBATCH --mem=1G
#SBATCH --time=00:20:00
#SBATCH --output=out/slurm-%x.out
#SBATCH --error=out/slurm-%x.err
module load python numpy
echo "Job ID is $SLURM_JOB_ID."
echo "Executing on the machine: " $(hostname)
python pi serial.py > out/pi serial.out
```







### **Submission Script Example**

```
Shebang
#!/bin/bash
#SBATCH --job-name=pi serial
#SBATCH --account=cis240128p
#SBATCH --partition=RM-shared
                                                             Scheduler/
#SBATCH --nodes=1
#SBATCH --ntasks=1
                                                              Resource
#SBATCH --mem=1G
                                                              Directives
#SBATCH --time=00:20:00
#SBATCH --output=out/slurm-%x.out
#SBATCH --error=out/slurm-%x.err
module load python numpy
echo "Job ID is $SLURM JOB ID."
                                                             Job Payload
echo "Executing on the machine: " $(hostname)
python pi serial.py > out/pi serial.out
```









#### **Common Environment Variables**

Variable	Description
SLURM_JOB_ID	ID of the job
SLURM_JOB_NAME	Name of job
SLURM_NNODES	Number of nodes
SLURM_NODELIST	List of nodes
SLURM_NTASKS	Total number of tasks
SLURM_NTASKS_PER_NODE	Number of tasks per node
SLURM_QUEUE	Queue (partition)
SLURM_SUBMIT_DIR	Directory of job submission







## Filename Pattern Symbols

Both standard output and standard error are directed to the same file by default, and the file name is "slurm-%j.out", where the "%j" is replaced by the job ID.

Description
Job ID
Job name
Username
Hostname where the job is running
Job array's master job allocation number
Job array ID (index) number

The output and error filenames are customizable, however.

#### For example:

```
#SBATCH --output=%x-%j.out
#SBATCH --error=%x-%j.err
```









#### **Submit A Job**



Enter the *pi\_example* directory and launch a job:

cd pi\_example
sbatch submit-pi\_serial.slurm

The job will be placed in the job queue until it gains enough priority to be assigned compute resources.









#### **Monitor A Job**



Find out what node this job is running on with

squeue -u <userid>

A useful environment variable is the <a href="SQUEUE\_FORMAT">SQUEUE\_FORMAT</a> variable and can be set, for example, with the following command:

export SQUEUE\_FORMAT="%.7i %9P %35j %.8u %.2t %.12M %.12L %.5C %.7m %.4D %R"

Further details on the usage of this variable are available in Slurm's <u>squeue</u> documentation.

Another useful job monitoring command is: scontrol show job <jobid>

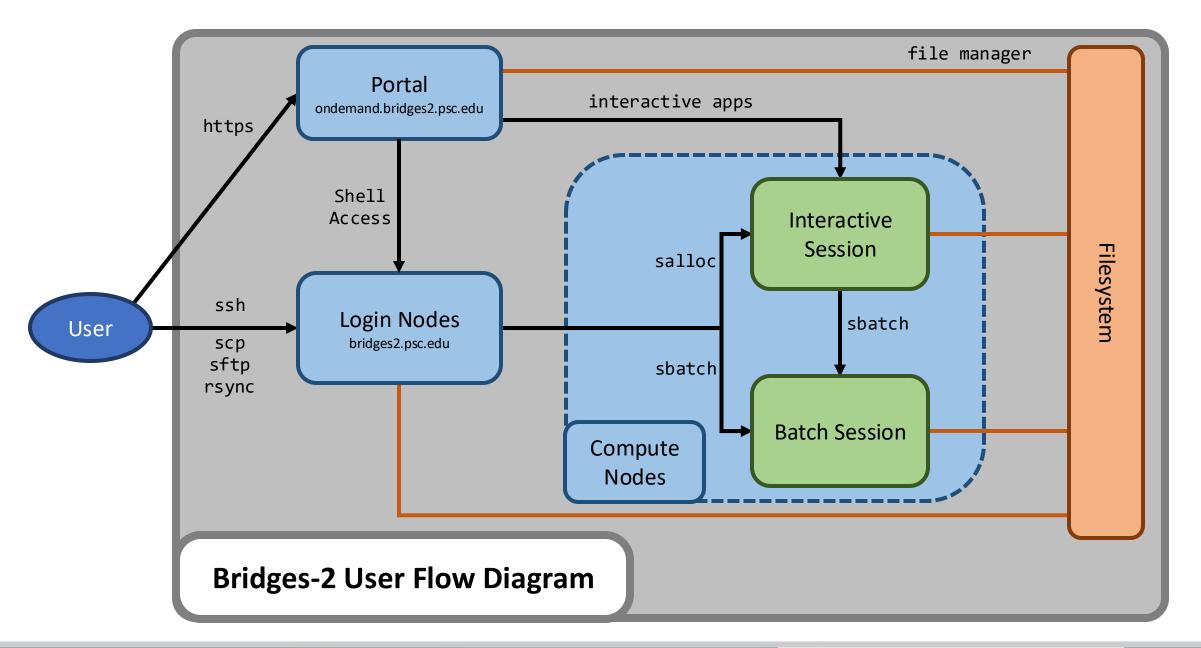
Cancel a job with: scancel <jobid>



















# **Bridges-2 User Guide**

www.psc.edu/resources/bridges-2/user-guide





