



Using Open OnDemand to Access CURC Resources

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Agenda

- XSEDE & the Transition to ACCESS
- About Open OnDemand
- How to Login to CURC resources
- Features of Open OnDemand
 - Using the Shell
 - File Transfer
 - Job Monitoring and Composer
 - Interactive Applications

XSEDE

- For the last 11 years or so XSEDE has been the primary organization that provided access to national Computing resources.
- Many large institutions and HPC centers have been using the XSEDE user portal for authenticating on their systems, including TACC, SDSC, PSC and many others.
- Earlier this year the announcement was made that XSEDE's funding was ending, and operations will cease.



ACCESS

- Beginning September 1st 2022, the ACCESS program will be taking over many functions that XSEDE was managing including:
 - Allocations
 - Support
 - Operations
 - Metrics
- <https://access-ci.org/>



Advanced Cyberinfrastructure Coordination Ecosystem:
Services & Support

The Effects of the Transition

- The XSEDE user Portal, the SSO hub, gsi-ssh will no longer work starting August 31st 2022.
- The institutions using these XSEDE functions will need to find alternatives.

However, the XSEDE username and password identities will turn into ACCESS identities with the same password.

How is CU-Boulder handling the change for RMACC?

- We have been exploring using Federated Authentication using CILogon.
 - Still planning on it but will take much more work.
 - As an interim workaround, we will enable existing XSEDE accounts to login via the web-based tool Open OnDemand using ACCESS authentication.



Open OnDemand



- Open OnDemand is an NSF-funded open-source HPC portal based on Ohio Supercomputing Center's original OnDemand portal. Open OnDemand provides an easy way for system administrators to enable web access to their HPC resources, including, but not limited to:
 - Plugin-free web experience
 - Easy file management
 - Command-line shell access
 - Job management and monitoring across different batch servers and resource managers
 - Graphical desktop environments and desktop applications

Open OnDemand at CURC

- We have had Open OnDemand working for six months at CU Boulder, but only for CU-Boulder users.
- In Mid-August 2022 we now have a version of Open OnDemand that accommodates existing XSEDE accounts as well as new ACCESS accounts (the default for RMACC users who register for accounts from mid-August forward).

Is this the Permanent Solution?

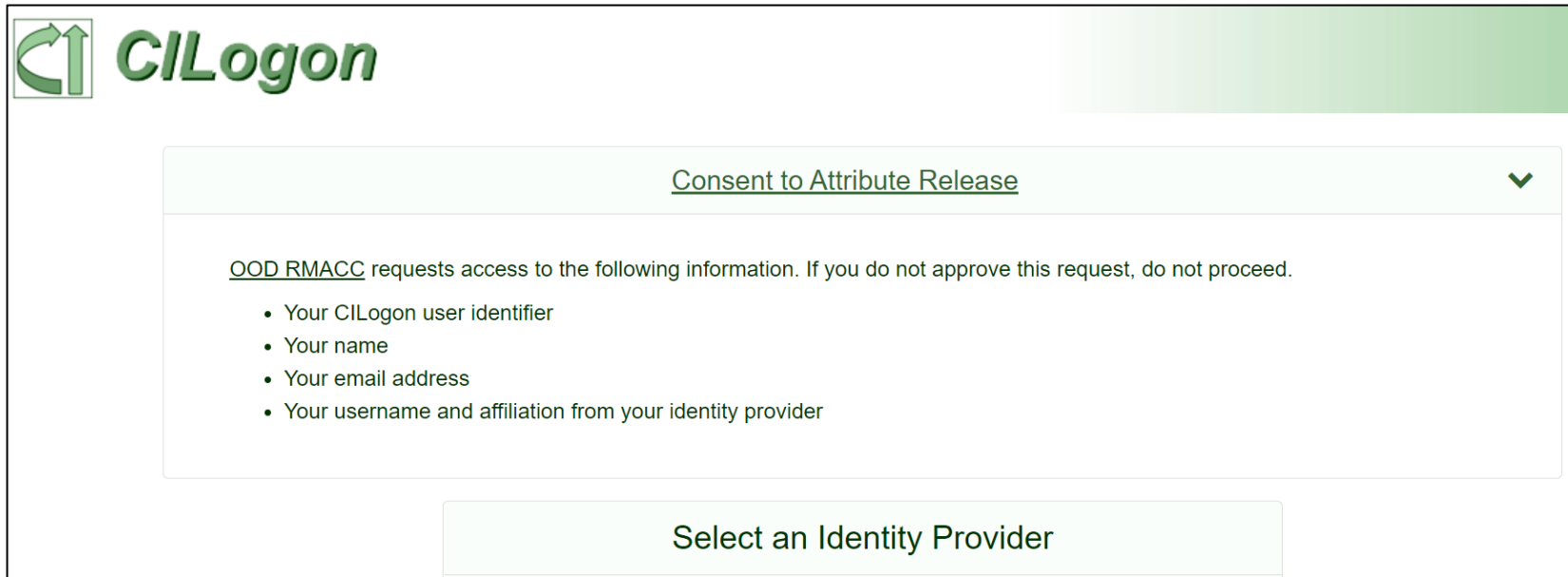
- Not necessarily
 - We are committing to having Open OnDemand available for all CURC users in the future with some minor tweaks
 - Hopefully, we can leverage CILogon and other tools to not rely on XSEDE/ACCESS accounts.
 - This would enable for CU, CSU and RMACC users would be able to use their own institutional accounts to logon. *If they use MFA!*
 - We would also like to provide access to login nodes, but figuring out that authentication is trickier than a web-based tool like Open OnDemand
- What we are showing today is the interim solution method so that RMACC users don't lose access when XSEDE ends.

Live Demo of Open OnDemand

<https://ondemand-rmacc.rc.colorado.edu>

Logging In

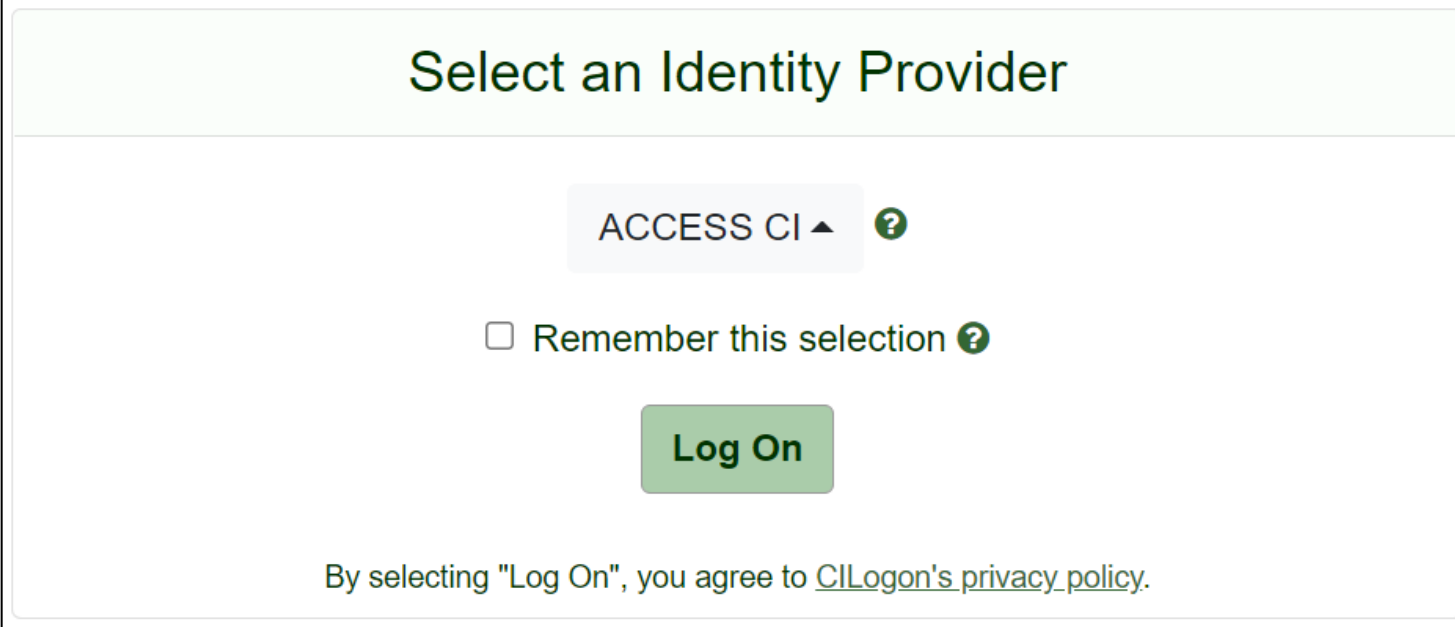
- Go to <https://ondemand-rmacc.rc.colorado.edu> using any web browser
- You will be re-directed to the CILogon sign-in page



The image shows a screenshot of the CILogon sign-in page. At the top left is the CILogon logo, which consists of a green square with a white 'C' and an upward arrow, followed by the text 'CILogon' in green. Below the logo is a green bar. In the center, there is a white box with a green border. At the top of this box is a green bar with the text 'Consent to Attribute Release' and a green checkmark. Below this bar, the text reads: 'OOD RMACC requests access to the following information. If you do not approve this request, do not proceed.' followed by a bulleted list: '• Your CILogon user identifier', '• Your name', '• Your email address', and '• Your username and affiliation from your identity provider'. At the bottom of the white box is a green bar with the text 'Select an Identity Provider'.

Logging In (con't)

- Next Select your identity provider.
 - If using an existing XSEDE account please select the ACCESS CI provider



The screenshot shows a web interface titled "Select an Identity Provider". It features a dropdown menu with "ACCESS CI" selected, accompanied by a small upward arrow and a help icon. Below this is a checkbox labeled "Remember this selection" with a help icon. A green "Log On" button is centered below the checkbox. At the bottom, a line of text states: "By selecting 'Log On', you agree to [CILogon's privacy policy](#)."

Logging In (con't)

- You will be redirected to the ACCESS login page
 - Use your XSEDE username and password
 - Example:
 - Username: dperkin6
 - Password *****

ACCESS

Login to CILogon

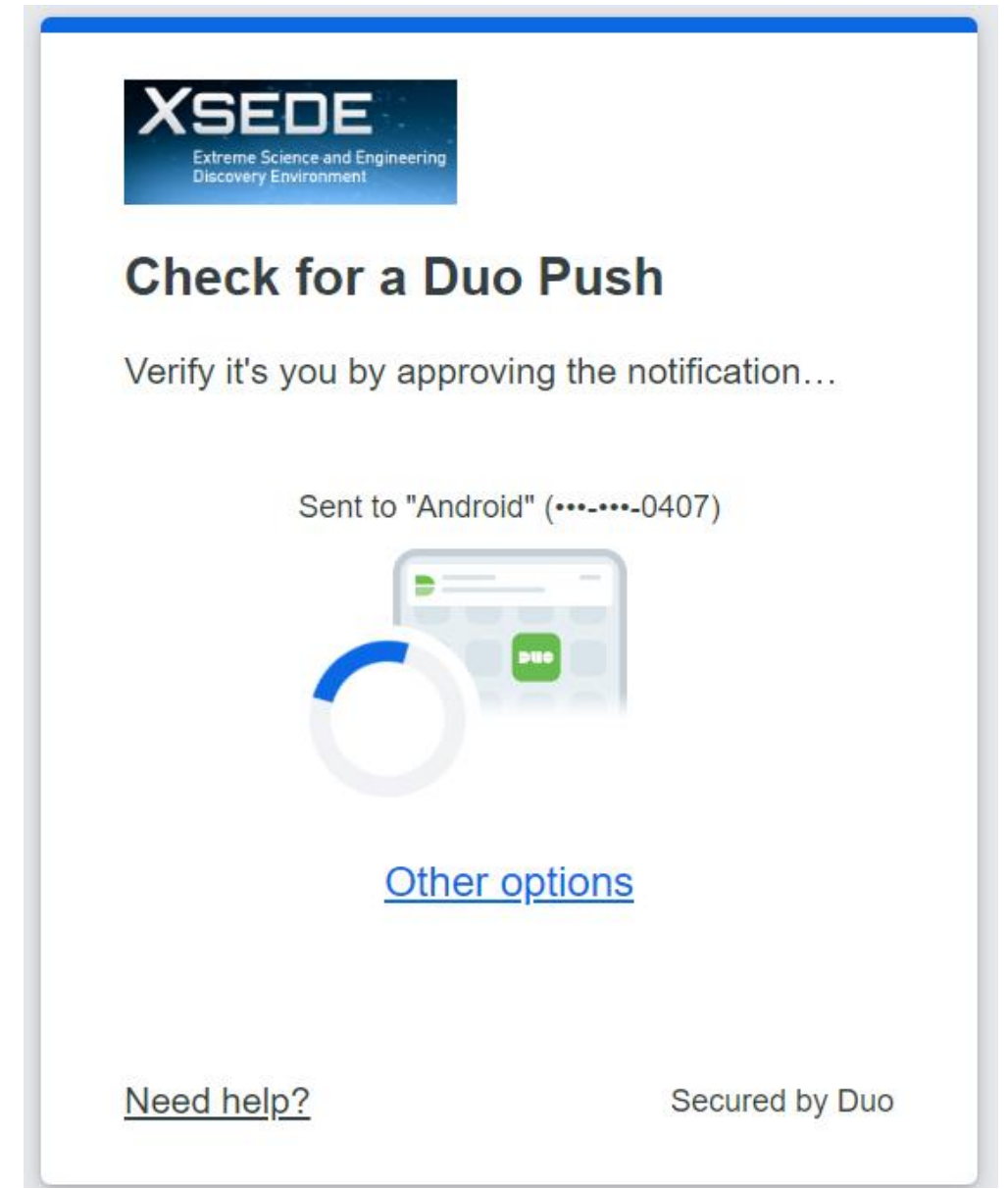
ACCESS Username

ACCESS Password

☐ Don't Remember Login

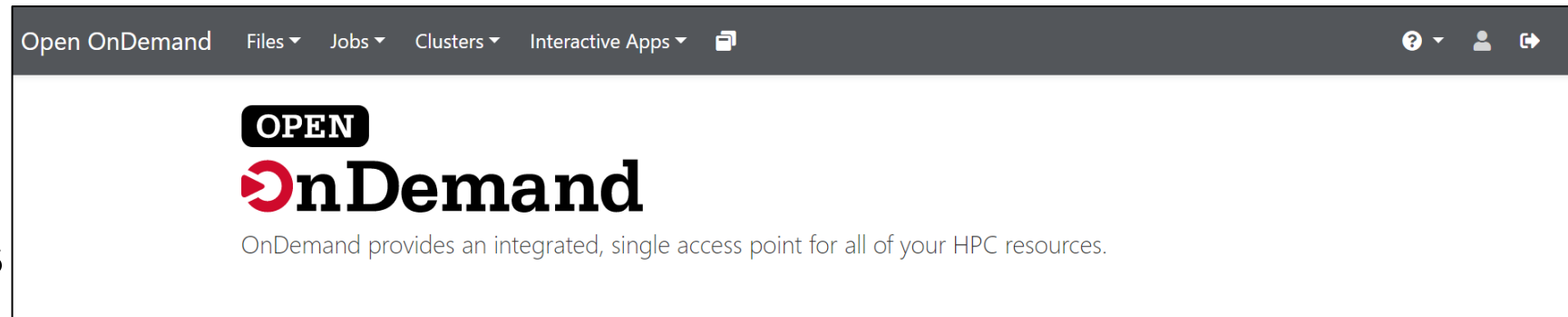
Logging In (con't)

- Multi-factor authentication (MFA) is a requirement for the security of our systems.
- You must have this enabled prior to attempting to login
- Once Duo is configured, you can accept the MFA and be logged in to RMACC Open OnDemand



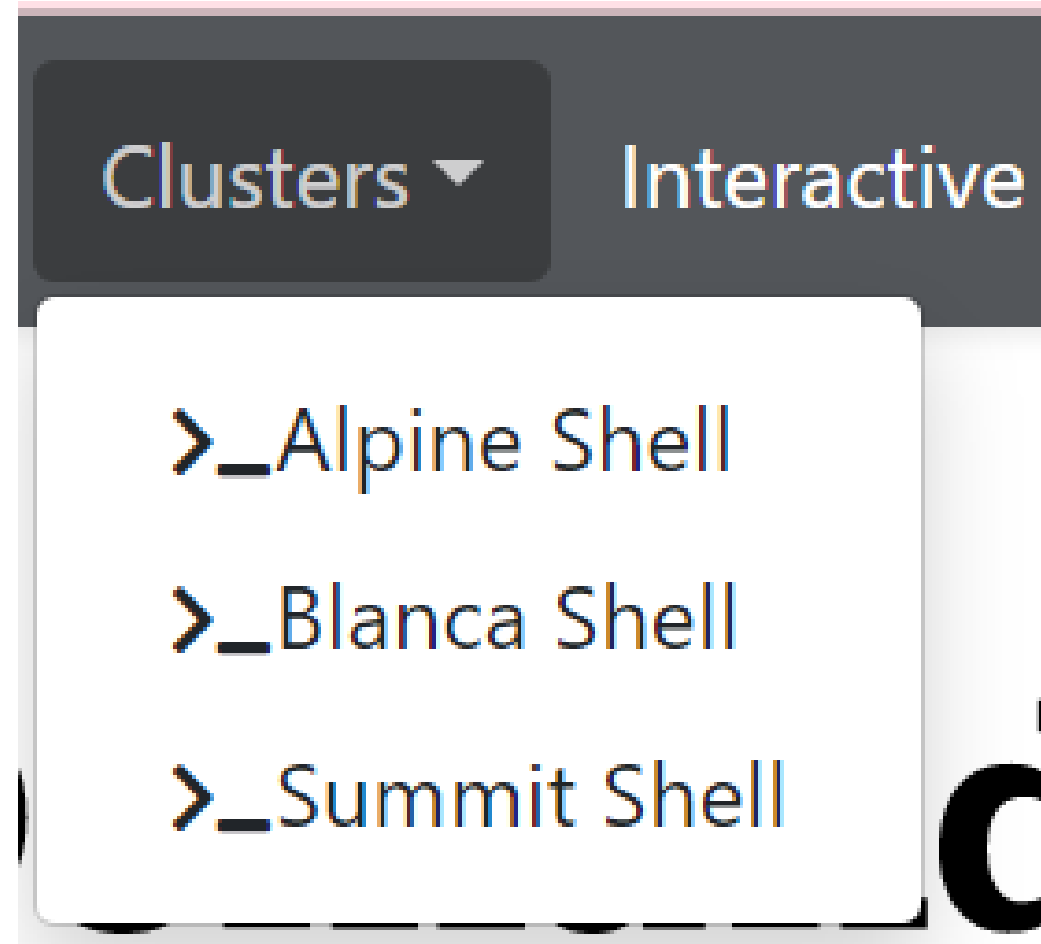
OnDemand Home Page

- Here, you'll notice several menu items on the top of the page including:
 - Files
 - Jobs
 - Clusters
 - Interactive Apps
- Along with
 - Help
 - Profile
 - Sign out



Clusters

- This option is to open a terminal (In your Web browser!) and acts very similarly as any native app or ssh client.
- Here you get to select which of CURC's HPC systems you wish to use.



Terminal

- Once open it looks very familiar if you have used CURC systems before and any Linux commands can be used just as you have before.

```
Password:
Last login: Wed Jun 29 11:00:51 2022 from 198.11.28.208
Welcome to CU-Boulder Research Computing.

* Website http://colorado.edu/rc
* Questions? rc-help@colorado.edu
* Subscribe to system announcements: https://curc.statuspage.io/
* Please type rc-help for the Acceptable Use Policy and a short help page.

You are using login node: login10

Recent changes:

* Alpine partition names have been changed (and simplified). As of the August 10, 2022 maintenance,
  users no longer need to include their institution suffix to request nodes on Alpine.
  Please use --partition=amilan, --partition=aa100, or --partition=ami100.
Welcome to University of Colorado Boulder Research Computing!

Full documentation is available in our user guide at
https://www.rc.colorado.edu/support/user-guide. If you have a question
that's not answered there, contact us at rc-help@colorado.edu.

A number of directories have been created for you already:

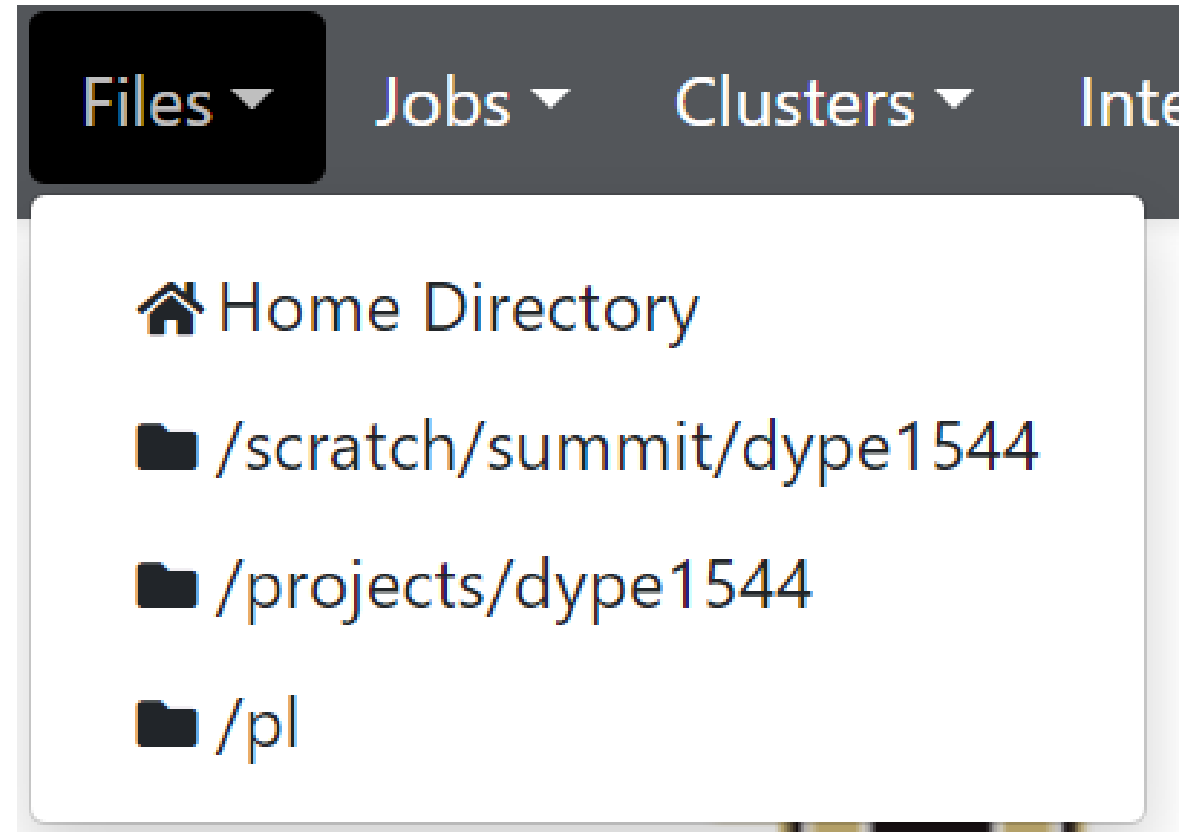
* `/home/$USER`, your home directory
* `/projects/$USER`, your project directory

Run the command `module avail` to see a list of available software.

To prevent this README from being displayed at login, edit your
`.bash profile` or `.login` files.
```

Files

- The files function allows you to navigate your files on the systems with a graphical interface
- Including your Home, Scratch, and Projects directories as well as access to the PetaLibrary



Files Management

- On the files page you can:
 - Upload data
 - Download files
 - Create new files
 - Edit files
 - Copy/move data
 - Delete files
 - Create directories

Open in Terminal New File New Directory Upload Download Copy/Move Delete

/ home / dype1544 / Change directory Copy path

☐ Show Owner/Mode ☐ Show Dotfiles Filter:

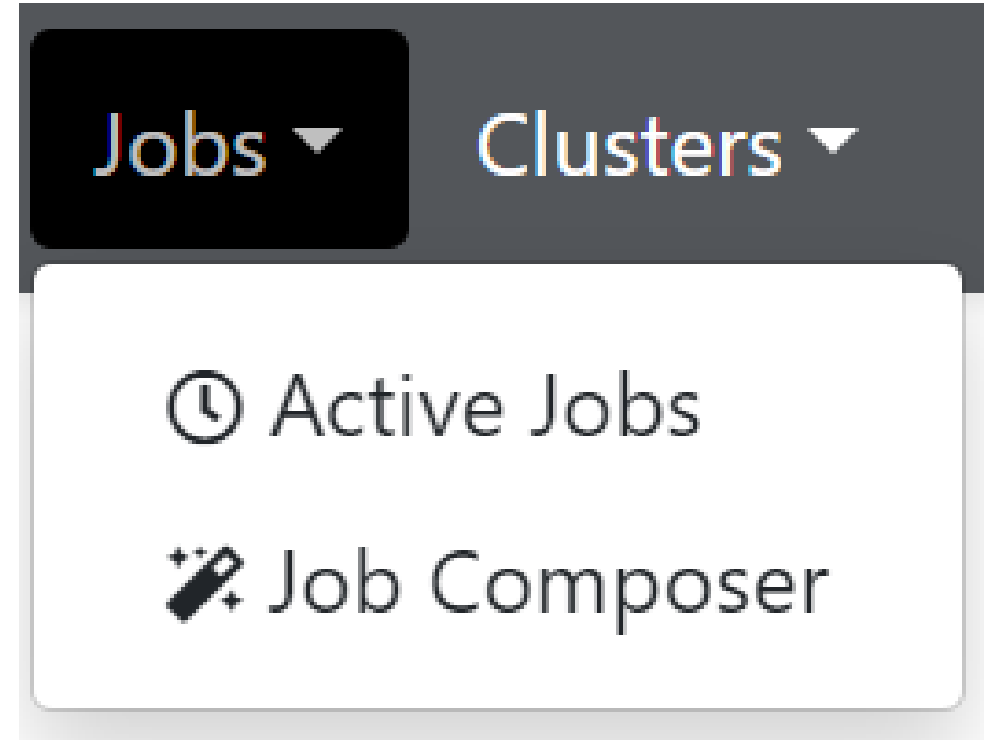
Showing 10 of 34 rows - 0 rows selected

	Type	Name	Size	Modified at
<input type="checkbox"/>	Folder	Desktop	-	12/8/2021 12:35:12 PM
<input type="checkbox"/>	Folder	Documents	-	12/8/2021 12:35:12 PM

One thing to note is that file upload is limited to file sizes of 10 GB or less

Jobs

- The Jobs section allows you to monitor active jobs (yours and all) By cluster
- It also includes a Job composer App



Active Jobs

All Jobs ▾

Alpine ▾

Active Jobs

Show

50 ▾

 entries

Filter:

	ID ▴ ▾	Name ▴ ▾	User ▴ ▾	Account ▴ ▾	Time Used ▴ ▾	Queue ▴ ▾	Status ▴ ▾	Cluster ▴ ▾	Actions ▴ ▾
<div>></div>	68970	d25r	jofa3453	ucb-general	00:00:00	aa100	<div>Queued</div>	Alpine	
<div>></div>	68999	d25k	jofa3453	ucb-general	00:00:00	aa100	<div>Queued</div>	Alpine	
<div>></div>	68998	d25k	jofa3453	ucb-general	00:00:00	aa100	<div>Queued</div>	Alpine	
<div>></div>	68997	d25k	jofa3453	ucb-general	00:00:00	aa100	<div>Queued</div>	Alpine	
<div>></div>	68996	d25k	jofa3453	ucb-general	00:00:00	aa100	<div>Queued</div>	Alpine	

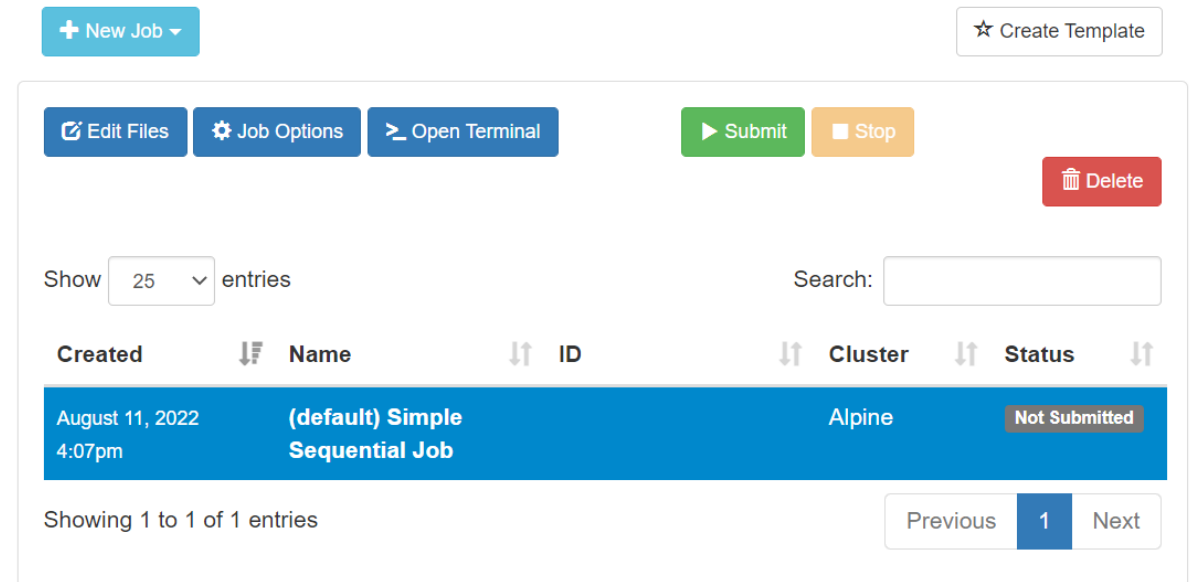
Active Jobs (con't)

- Here you'll see a list of jobs on the cluster(s)
- If you select one of them, you can see details about the job

▼	68991	s11k	jofa3453	ucb-general	00:00:00	aa100	Queued	Alpine
Queued s11k 68991								
Cluster				Alpine				
Job Id				68991				
Job Name				s11k				
User				jofa3453				
Account				ucb-general				
Partition				aa100				
State				PENDING				
Reason				Dependency				
Total Nodes				1				
Total CPUs				3				
Time Limit				1-00:00:00				
Time Used				0:00				
Memory				3830M				

Job Composer

- With the Job Composer, you can create a BATCH script and submit to the scheduler without needing to use the Command line!
- Available for you is a default template, but you can create your own template for you to use



The screenshot displays the Job Composer web interface. At the top left is a '+ New Job' button. At the top right is a 'Create Template' button. Below these are three buttons: 'Edit Files', 'Job Options', and 'Open Terminal'. To the right of these are 'Submit' and 'Stop' buttons, and a 'Delete' button with a trash icon. Below the buttons is a 'Show 25 entries' dropdown and a 'Search:' input field. A table lists job entries with columns: Created, Name, ID, Cluster, Status, and a 'Not Submitted' badge. The table contains one entry: 'August 11, 2022 4:07pm', '(default) Simple Sequential Job', 'Alpine', and 'Not Submitted'. At the bottom, it says 'Showing 1 to 1 of 1 entries' and has 'Previous', '1', and 'Next' navigation buttons.

Created	Name	ID	Cluster	Status
August 11, 2022 4:07pm	(default) Simple Sequential Job		Alpine	Not Submitted

Job Composer Options

Job Options

Name

(default) Simple Sequential Job

Cluster

Summit

Specify job script

main_job.sh

Files larger than 65KB are omitted for the job script field

Account

Account is an optional field. If not set, the account may be auto-set by the submit filter.

Job array specification

1-10

Job arrays are optional. e.g. 1-10

Save

Reset

Back

Job Composer Script


Submit Script


main_job.sh


Script contents:

```
#!/bin/bash
# JOB HEADERS HERE

echo "Hello World"
```

 Open Editor

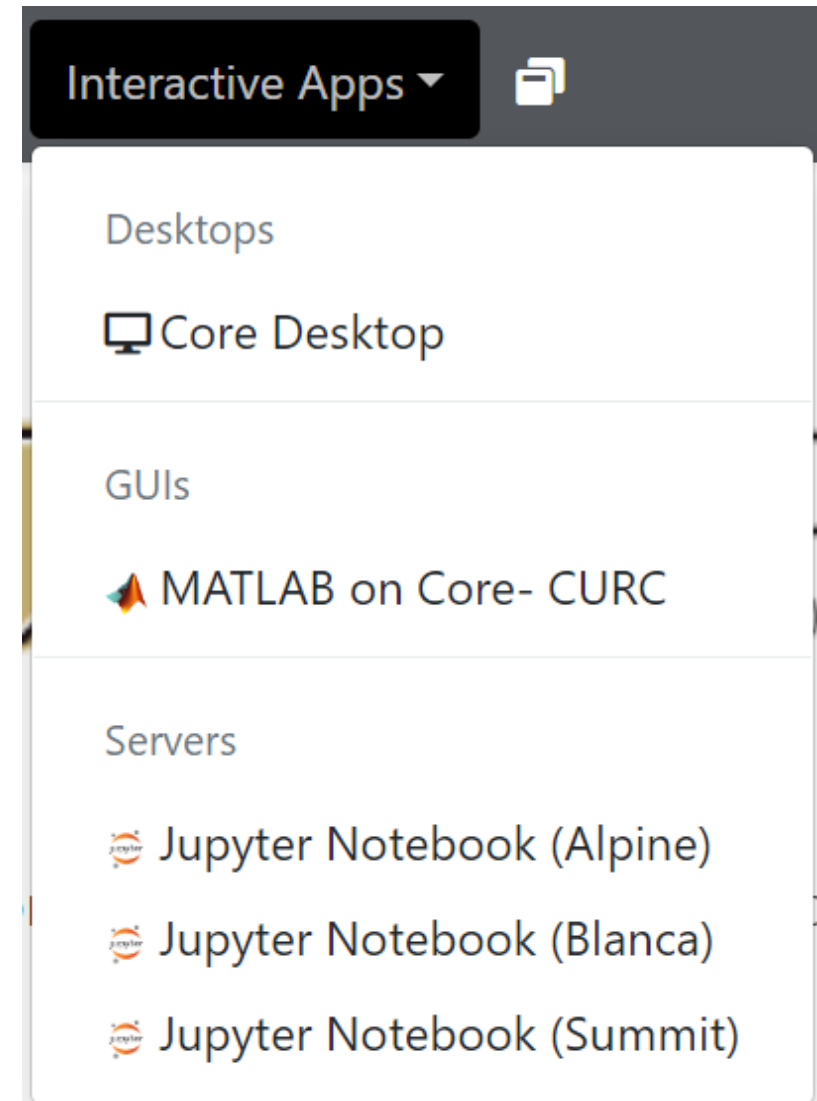
 Open Terminal

 Open Dir

- Once you've added all of the options for your job, you will see what the submit script for your job will look like.
- You can edit this file right here in Open OnDemand without needing to use vim, nano, or whatever text editor you are used to using.

Interactive Apps

- With interactive Applications, users can start using more user-friendly interfaces to work on the HPC systems
- These will include a Desktop, MATLAB, and Jupyter Notebook interfaces.
- ***Currently Only Jupyter is working***



Jupyter Notebooks

- To use Summit with a Jupyter Notebook, we need to start an interactive session.
- We can add information on
 - Slurm Account
 - What Partition we'd like
 - Hours that we want this to run
 - How many Nodes we'd like
- Once all that is done, click 'Launch' at the bottom of the screen

Home / My Interactive Sessions / Jupyter Notebook (Summit)

Interactive Apps

Desktops

Core Desktop

GUIs

MATLAB on Core-CURC

Servers

Jupyter Notebook (Alpine)

Jupyter Notebook (Blanca)

Jupyter Notebook (Summit)

Jupyter Notebook (Summit)

version: 2345bda

This app will launch a Jupyter Notebook server on one or more nodes.

Account

Partition

Number of hours

1

Number of nodes

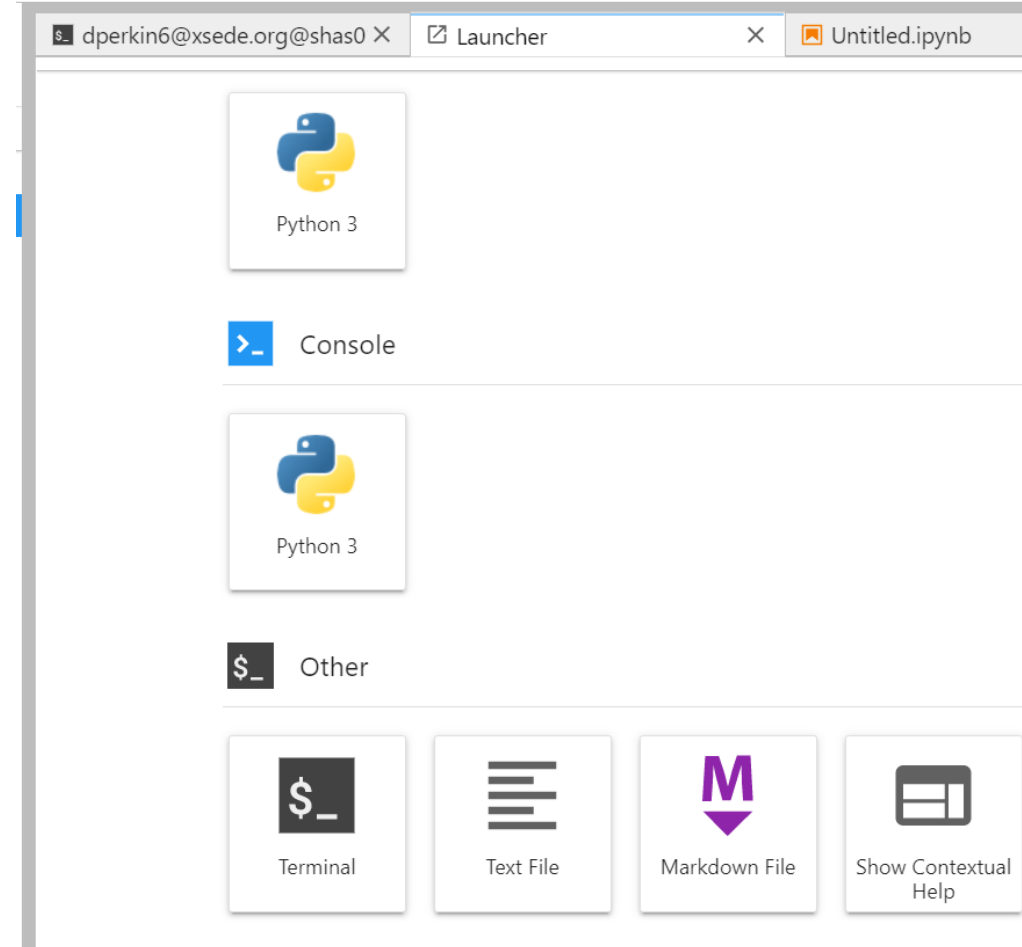
1

☒ Use JupyterLab instead of Jupyter Notebook?

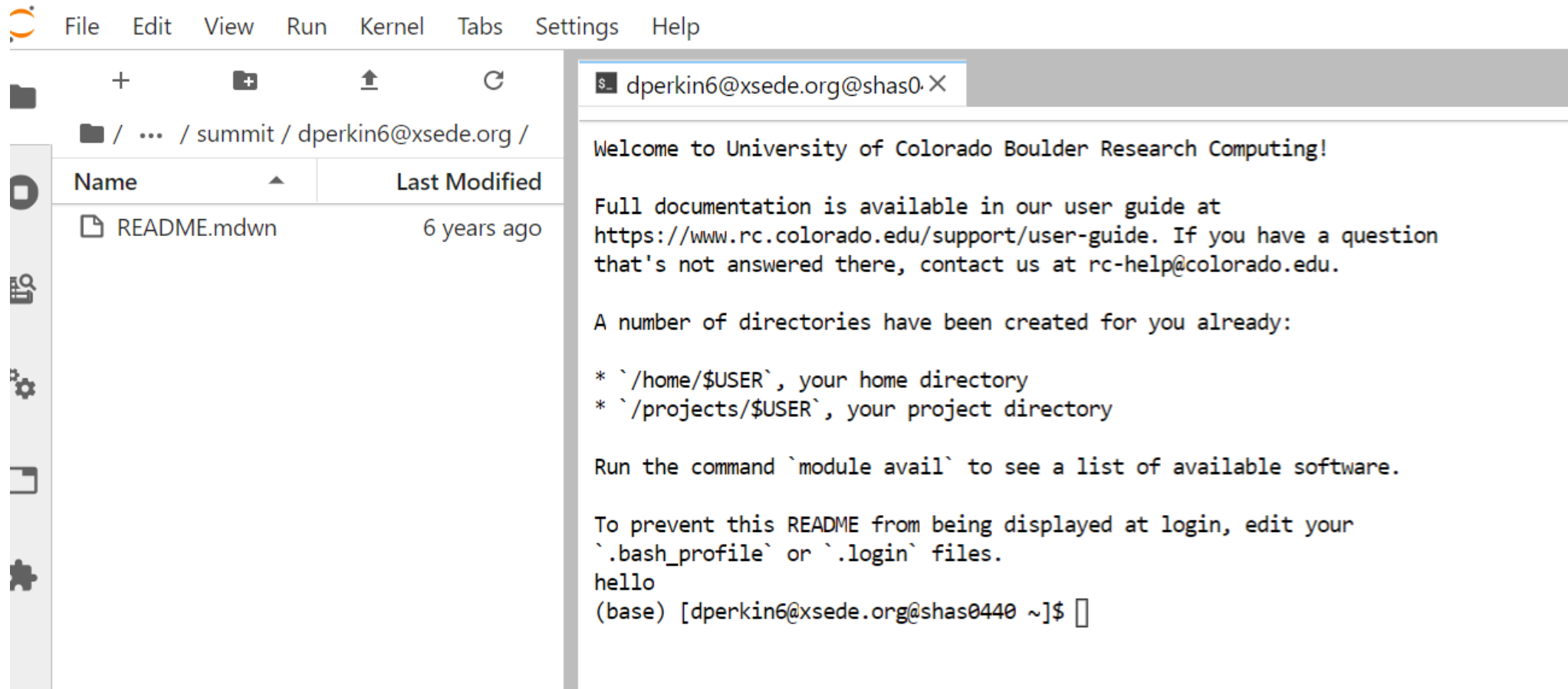
JupyterLab is the next generation of Jupyter with an IDE-like

Jupyter Notebooks Launcher

- It will take a few moments to start up once the resources are allocated, but once it is you will see the Launcher screen.
- Here we get to select a number of Applications including Notebooks, Console, or a Terminal app.



Terminal in Jupyter



The screenshot displays the JupyterLab interface. On the left, a file browser shows the directory structure: `/ ... / summit / dperkin6@xsede.org /`. A table lists files with columns 'Name' and 'Last Modified':

Name	Last Modified
README.mdwn	6 years ago

On the right, a terminal window titled `dperkin6@xsede.org@shas0` shows the following output:

```
Welcome to University of Colorado Boulder Research Computing!

Full documentation is available in our user guide at
https://www.rc.colorado.edu/support/user-guide. If you have a question
that's not answered there, contact us at rc-help@colorado.edu.

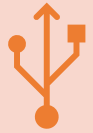
A number of directories have been created for you already:

* `/home/$USER`, your home directory
* `/projects/$USER`, your project directory

Run the command `module avail` to see a list of available software.

To prevent this README from being displayed at login, edit your
`.bash_profile` or `.login` files.
hello
(base) [dperkin6@xsede.org@shas0440 ~]$
```

Interactive Apps Wrap Up



Currently, using the terminal app in Jupyter Notebooks is the only command line interface that is working.



The other apps are coming as fast as we can get to them

Resources

- <https://curc.readthedocs.io/en/latest/access/rmacc.html>
- <https://ask.cyberinfrastructure.org/c/rmacc/65>
- rc-help@colorado.edu

Questions?

Please visit us at <https://www.colorado.edu/crdds/>