

Scheduling Jobs on a Supercomputer





Website: www.rc.colorado.edu

Documentation: https://curc.readthedocs.io

Helpdesk: rc-help@colorado.edu



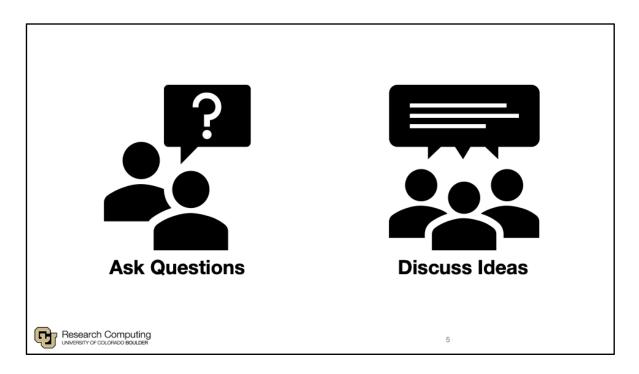




https://github.com/ResearchComputing/scheduling_a_job_o n_a_supercomputer_rc_shortcourse



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This workshop is meant to be empowering and information-rich – to help you get the most out of your HPC workflow.

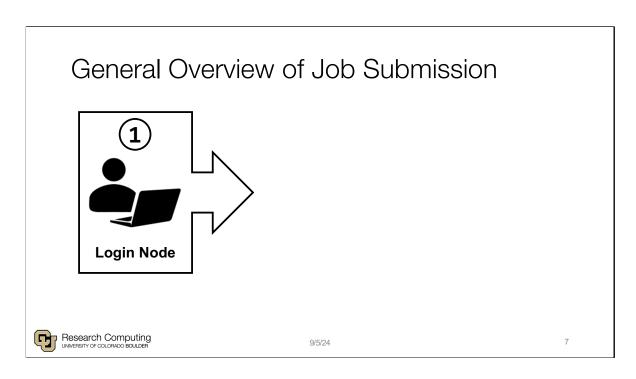
Feel free to ask questions during the presentations and to discuss ideas/thoughts during breaks and the hands-on portion of the workshop.

Session Overview

- Overview of Jobs Submissions
- Resource Requests
- Interactive & Batch Jobs
- Monitoring jobs



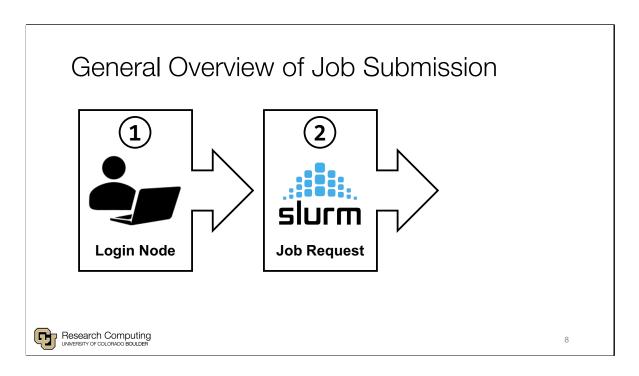
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A job submission consists of three general steps:

- 1. Log onto a CURC Login Node (ssh, OnDemand)
- *Warning/Reminder*

Software cannot be accessed/run from a login node. You must run your applications from a compute node. But, in order to run on a compute node, you must first request the system resources through a "job"

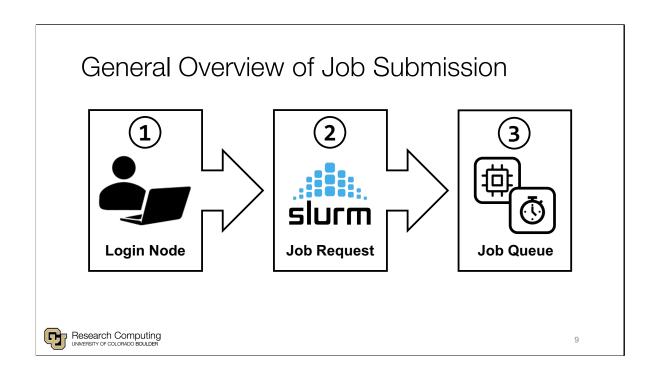


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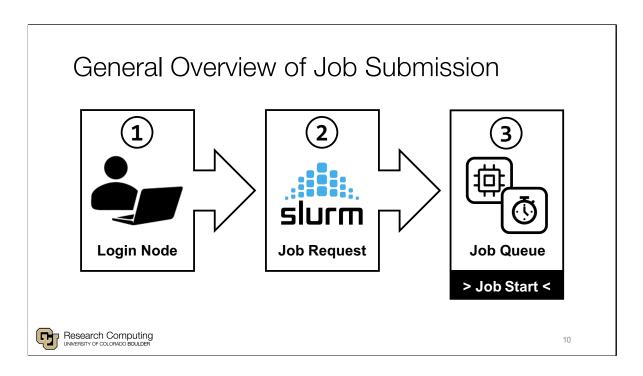
- 1. Log onto a CURC Login Node (ssh, OnDemand)
- *Warning/Reminder*

Software cannot be accessed/run from a login node. You must run your applications from a compute node. But, in order to run on a compute node, you must first request the system resources through a "job"

2. Job requests are submitted to SLURM, our system's Job Scheduler which manages how and when system resources are allocated to user submitted jobs.



3. Jobs do not run immediately but instead wait in a SLURM managed queue. A job's placement in the queue is dependent on multiple factors. We will discuss a few of the most common factors, but a general rule to follow is that the more resources a job requests the longer it will wait in the queue.



Once SLURM determines they system is ready, it will start the job. As we will discuss, quite a few factors influence how long a submitted job waits on the queue. But, in general, the more resources you request the longer your job will have to wait in the queue.

SLURM – Job Scheduler

- Simple Linux Utility for Resource Management
- Allocates compute resources to users through Jobs
- 2 Types of Jobs
 - Batch Jobs
 - Interactive Jobs

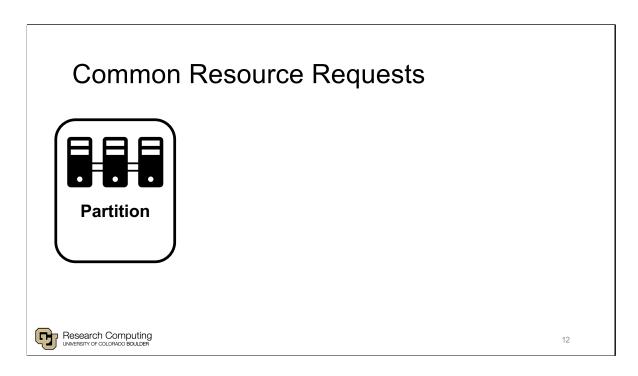


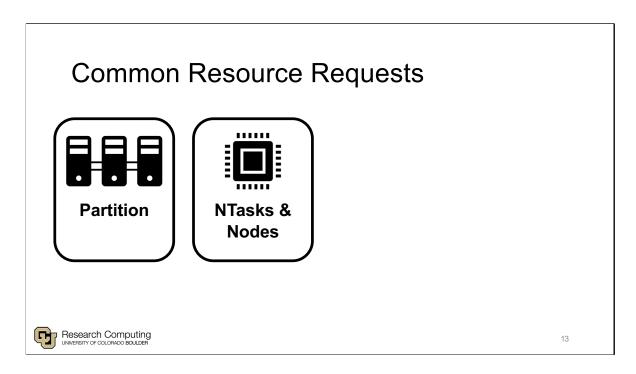


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Slurm manages our system's shared resources and ensures they are equitably shared amongst CURC users.

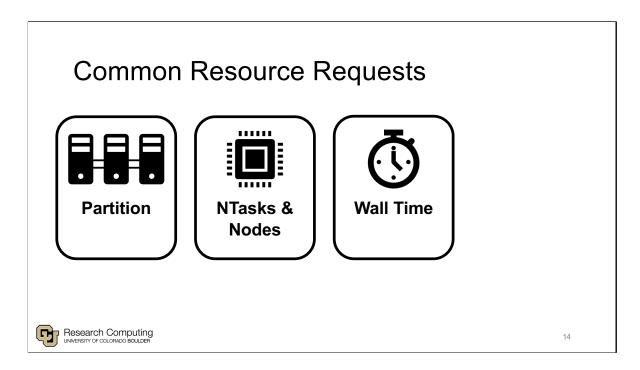
In the next section we will discuss common resources a job can request and then cover the two types of jobs we support (Batch and Interactive).





Ntasks – How many CPU cores your job is requesting

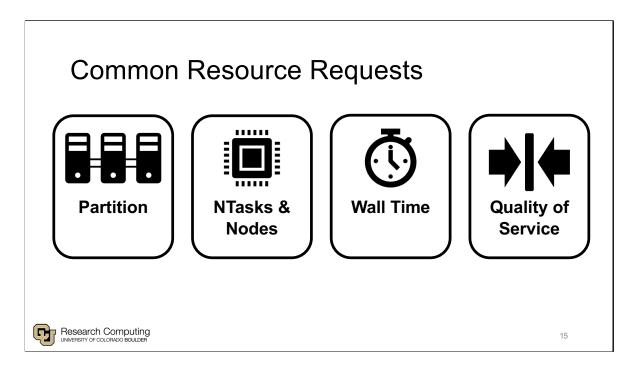
Nodes – How many nodes your job will run across (typically 1, but can be more)



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Wall Time – How much time your job needs to run on the system (can be a few minutes, a few hours, to multiple days)

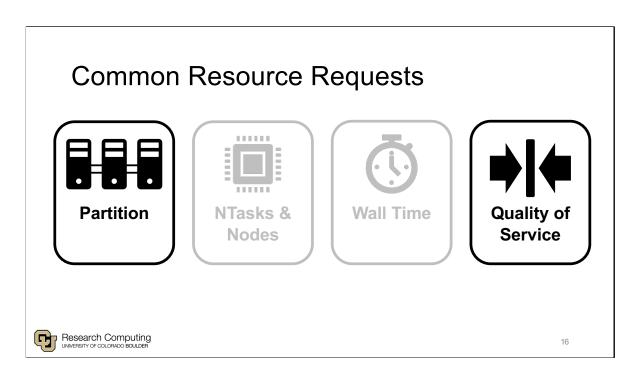


Ntasks – How many CPU cores your job is requesting

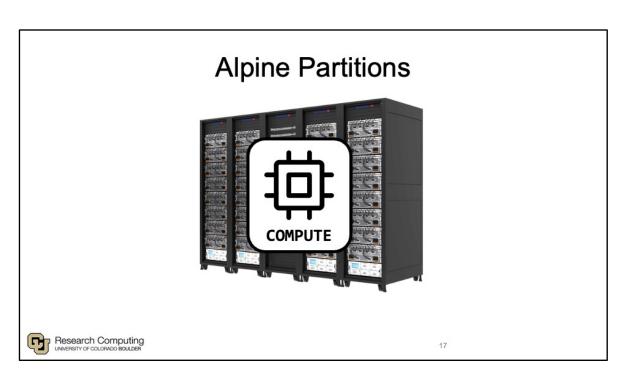
Nodes – How many nodes your job will run across (typically 1, but can be more)

Wall Time – How much time your job needs to run on the system (can be a few minutes, a few hours, to multiple days)

Quality of Service (QOS) – Defines additional job constraints – i.e. limits to how much your job can request.



What resources and how many you can request is heavily dependent on what partition and qos you select. We will now provide a general overview of our primary partitions and qos's.

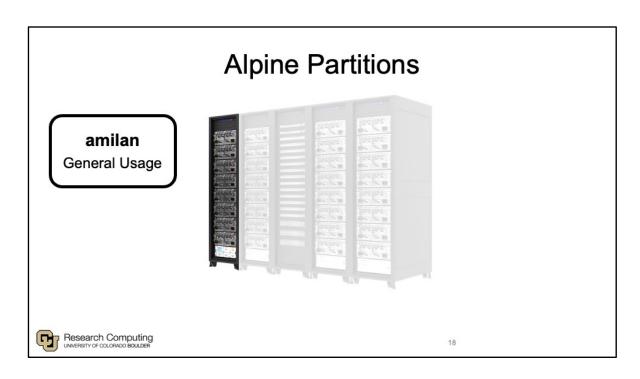


Compute nodes are organized into partitions – logical groups of similarly spec'd hardware.

Partitions make it easier to request specific resources and ensure a more consistent user experience.

The Alpine Cluster has four primary partitions.

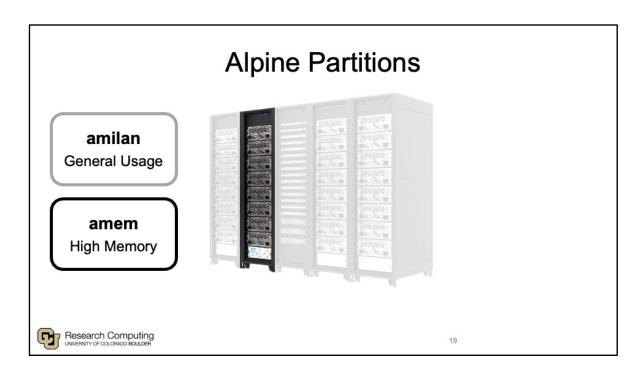
Detailed Information on Alpine Hardware: https://curc.readthedocs.io/en/latest/clusters/alpine/alpine-hardware.html



amilan:

285 Nodes 64 CPU Cores per Node 3.75 GB of RAM per CPU (240 GB total)

Detailed Information on Alpine Hardware: https://curc.readthedocs.io/en/latest/clusters/alpine/alpine-hardware.html



amem:

22 Nodes

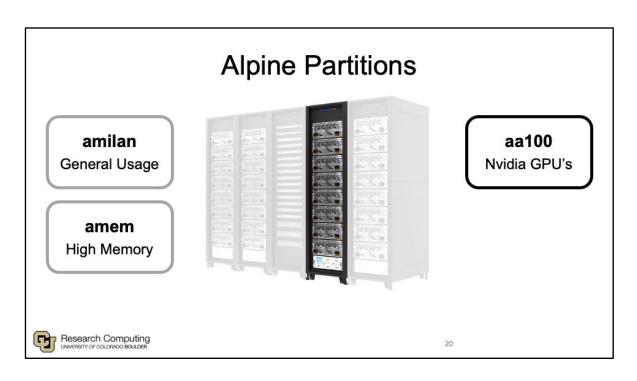
48 CPU Cores per node (12)

64 CPU Cores per node (10)

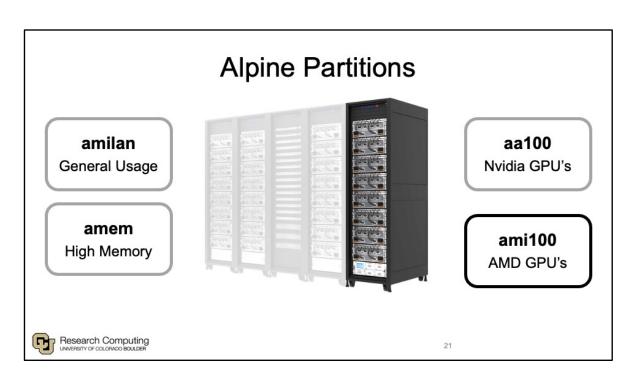
21.5 GB of RAM per CPU (1 TB total)

Detailed Information on Alpine Hardware:

https://curc.readthedocs.io/en/latest/clusters/alpine/alpine-hardware.html



aa10012 Nodes64 CPU Cores per Node3.75 GB of RAM per CPU (240 GB total)3 GPU's per Node (Nvidia A100)



ami100 8 Nodes 64 CPU Cores per Node 3.75 GB of RAM per CPU (240 GB total) 3 GPU's per Node (AMD MI100)

Detailed Information on Alpine Hardware: https://curc.readthedocs.io/en/latest/clusters/alpine/alpine-hardware.html

QoS	Description	Max wall time	Max jobs/user	Max nodes/user
normal	Default QoS	24 H	1000	128



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The normal qos is the default qos for all submitted jobs

QoS	Description	Max wall time	Max jobs/user	Max nodes/user
normal	Default QoS	24 H	1000	128
0	For jobs needing longer wall times	7 D	200	20



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The long qos provides a subset of amilan nodes to run longer jobs.

Please note! The long qos has fewer resources than normal and may have a longer wait time in the queue.

QoS	Description	Max wall time	Max jobs/user	Max nodes/user
normal	Default QoS	24 H	1000	128
long	For jobs needing longer wall times	7 D	200	20
mem	High-memory jobs	7 D	n/a	12



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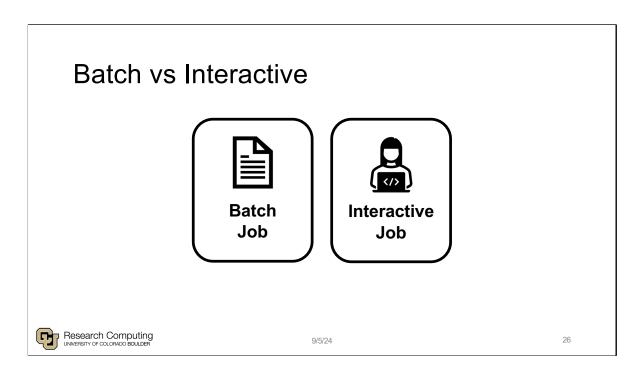
The mem gos is specifically for jobs that run on the amem partition.

QoS	Description	Max wall time	Max jobs/user	Max nodes/user
normal	Default QoS	24 H	1000	128
long	For jobs needing longer wall times	7 D	200	20
mem	High-memory jobs	7 D	n/a	12
testing	For jobs submitted to testing partitions	1 H	1	n/a



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The testing gos supports the different testing partitions, ensuring that users can quickly access resources for testing their workflows. Keep in mind the stringent constraints – this partition is not intended for running regular jobs.



Now that you have a general idea of what resources you plan to request, you will need to consider the type of job you are wanting to schedule. A batch job or an interactive job.

Batch vs Interactive

- Runs a job script
- No need for user input
- Best for tested workflows and long/big jobs



Batch Job





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Batch Job



Interactive Job

- Terminal or GUI
- Requires active user input
- Best for development and exploration



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Interactive jobs

acompile

- · Quick access to resources
- Limit of 4 CPUs for up to 12 hours
- Focused on compiling/building software and small workflows

sinteractive

• Request any partition, more resources, and longer walltime

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- Subject to standard wait times (not immediate access)
- · Focused on GUI-based software



Running an interactive job

- Here we will run a Python script using an interactive job
- First request resources:

```
$ sinteractive --partition=atesting --qos=testing --time=00:10:00 --ntasks=1
```

 When the job starts you will be put on a compute node and you can execute your commands:

```
$ module load anaconda
$ python my_very_cool_script.py
```

• To quit:

\$ exit



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Batch Jobs

- Batch Jobs are jobs you submit to the scheduler that are run later without supervision
- A job script is simply a script that includes **SLURM directives** (resource specifics) ahead of any commands.



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Anatomy of a job script

```
#!/bin/bash

## Directives
#SBATCH --<option>=<value>

## Software
module load <software>

## User scripting
<command>
```



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Directives in a job script



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Common directives

```
· Partition - A collection of compute nodes
```

```
• --partition=<partition_name>
```

• Quality of service (QoS) – System defined constraints for a job (more on this later!)

```
--qos=<qos>
```

· Allocation – Account to "charge to"

```
• --account=<account name>
```

· Number of nodes to run on

```
• --nodes=<nodes>
```

· Number of cores to run on

• --ntasks=<number-of-tasks>



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Common directives

Wall time – How long you want to run on these resources

```
• --time=<wall time>
```

Job name

```
• --job-name=<jobname>
```

· Output - Where all output that would be written to the terminal should go

```
• --output=<name>
```

· Send an email when events happen in the job

```
--mail-type=<type>
```

· Email address to send updates to

```
• --mail-user=<user>
```



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Example job script

```
#!/bin/bash
     ## Directives
                                           # Number of requested tasks/cores
     #SBATCH --ntasks=1
     #SBATCH --time=0:01:00
                                           # Max run time
     #SBATCH --partition=amilan
                                          # Specify Alpine CPU node
     #SBATCH --output=test_%j.out
                                           # Rename standard output file
     ## Software
                                           # Purge all existing modules
     module purge
     ## User commands
     echo "This is a test of user $USER"
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```

Output files are important for debugging and verifying a job has completed successfully. Always include a --output directive!

The output file is created in directory job was run unless specified in your -- output directive.

If the directive --output is not provided, then a generic file name will be used (slurm xxxxxx.out).

Software job script example

```
#!/bin/bash
      ## Directives
      #SBATCH --ntasks=1
                                               # Number of requested tasks/cores
      #SBATCH --time=0:01:00
                                              # Max run time
      #SBATCH --partition=amilan # Specify Alpine CPU node #SBATCH --output=test_%j.out # Rename standard output file
      ## Software
      module purge
                                                 # Purge all existing modules
      module load anaconda
                                                  # Load Anaconda
      conda activate <my-conda-environment> # Activate CONDA environment
      ## Run Python script
      python my_cool_script.py
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```

Software can be loaded using the software module system or by accessing user installed software in their /projects directory.

https://curc.readthedocs.io/en/latest/compute/modules.html

Be careful not to run GUI or other software that requires user interaction!

Submitting a Job script

sbatch <job_file> <other-directives>

• Command to submit a job to the SLURM job scheduler



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- If we created the job script "my_first_job.sh" then we would submit it as follows:

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```
sbatch /path/to/my_first_job.sh
```



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sbatch <job_file> <other-directives>

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```

• Modify slurm directives in the batch script:

```
sbatch /path/to/my_first_job.sh --ntasks=12
```



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Checking your jobs

- squeue: Monitor your jobs status in queue and while running:
 - By default, shows all jobs in queue can specify using:

```
$ squeue -u <username>
$ squeue -p <partition>
```

- sacct: Check back on usage statistics of previous Jobs
 - By default, only checks all jobs from the start of the current day can specify using:

```
$ sacct -u <username>
$ sacct --start=MM/DD/YY -u <username>
$ sacct -j <job-id>
```



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Checking your jobs

 To check the percentage of CPU and memory usage of a job after it completes, use seff

```
$ module load slurmtools
$ seff <job number>
```

• To see general statistics for your submitted jobs, use jobstats

```
$ module load slurmtools
$ jobstats <username> <# of days>
```



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Thank you!

- Documentation: curc.readthedocs.io/
- <u>Trainings with Center for Research Data and Digital Scholarship (CRDDS)</u>: https://www.colorado.edu/crdds/
- Helpdesk: rc-help@colorado.edu
- Consult Hours (Tuesday 12:00-1:00 in-person, Thursday 1:00-2:00 virtually)



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Survey and feedback

https://tinyurl.com/curc-survey18





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