



University of Colorado **Anschutz Medical Campus**

# Overview of Alpine

*By AMC HPC and Research Computing*  
*11/25/2024*





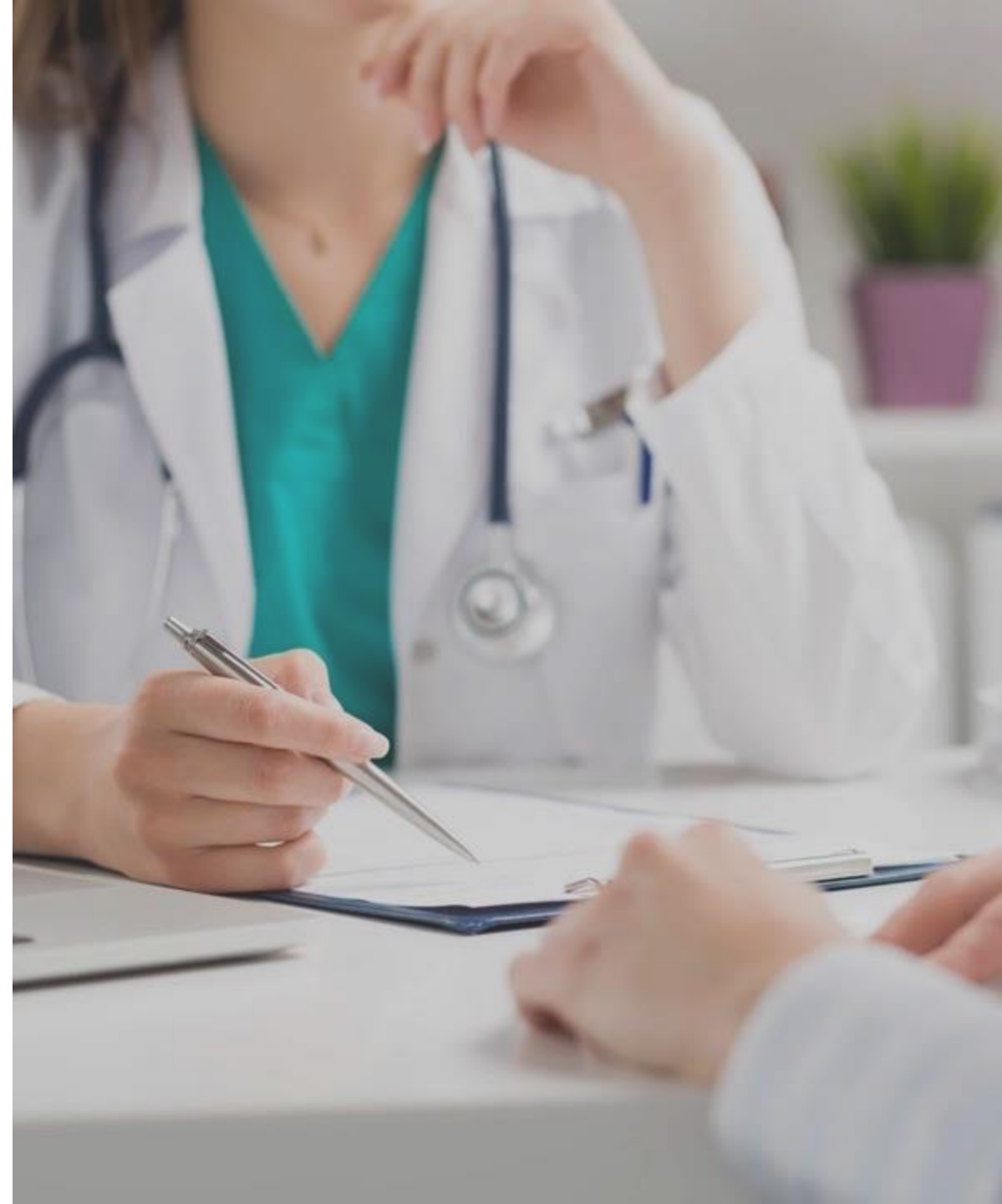
# I- Attending Team Members



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Anschutz Medical Campus

# Attending Team Members

- Kevin Fotso: Bioinformatics Technical Analyst.
- Maclean Sherren: Bioinformatics Technical Analyst.





# II- What is Alpine?

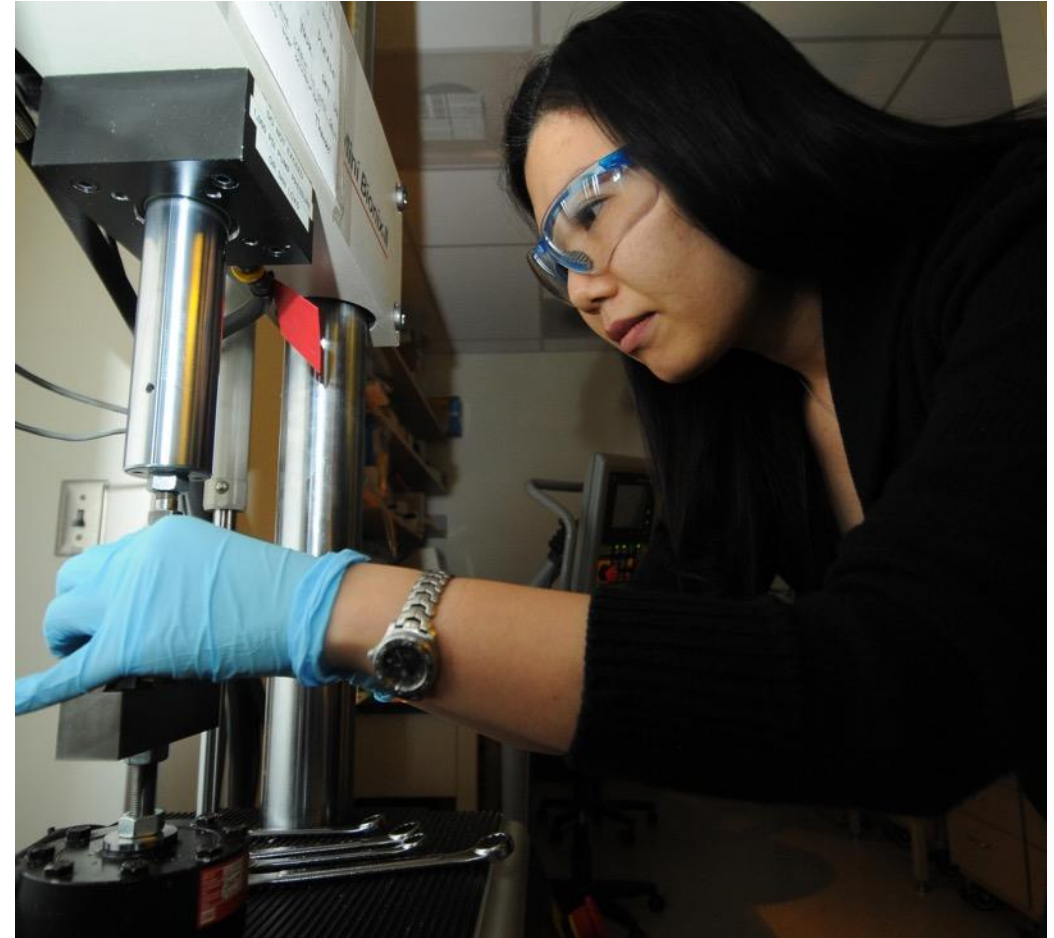


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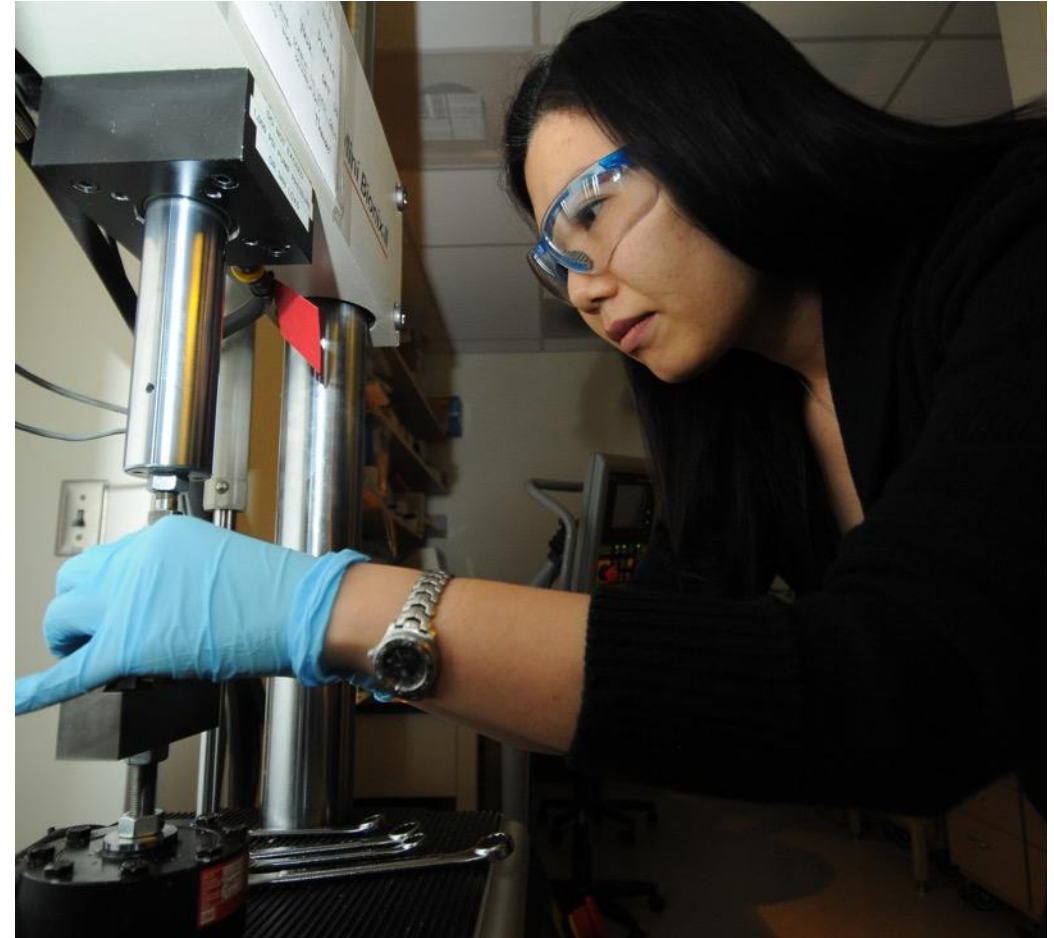
# What is Alpine?

Alpine is a supercomputing cluster funded by institutional contributions from the University of Colorado Boulder (UCB), the University of Colorado Anschutz Medical Campus (AMC), Colorado State University (CSU), and by National Science Foundation grants.



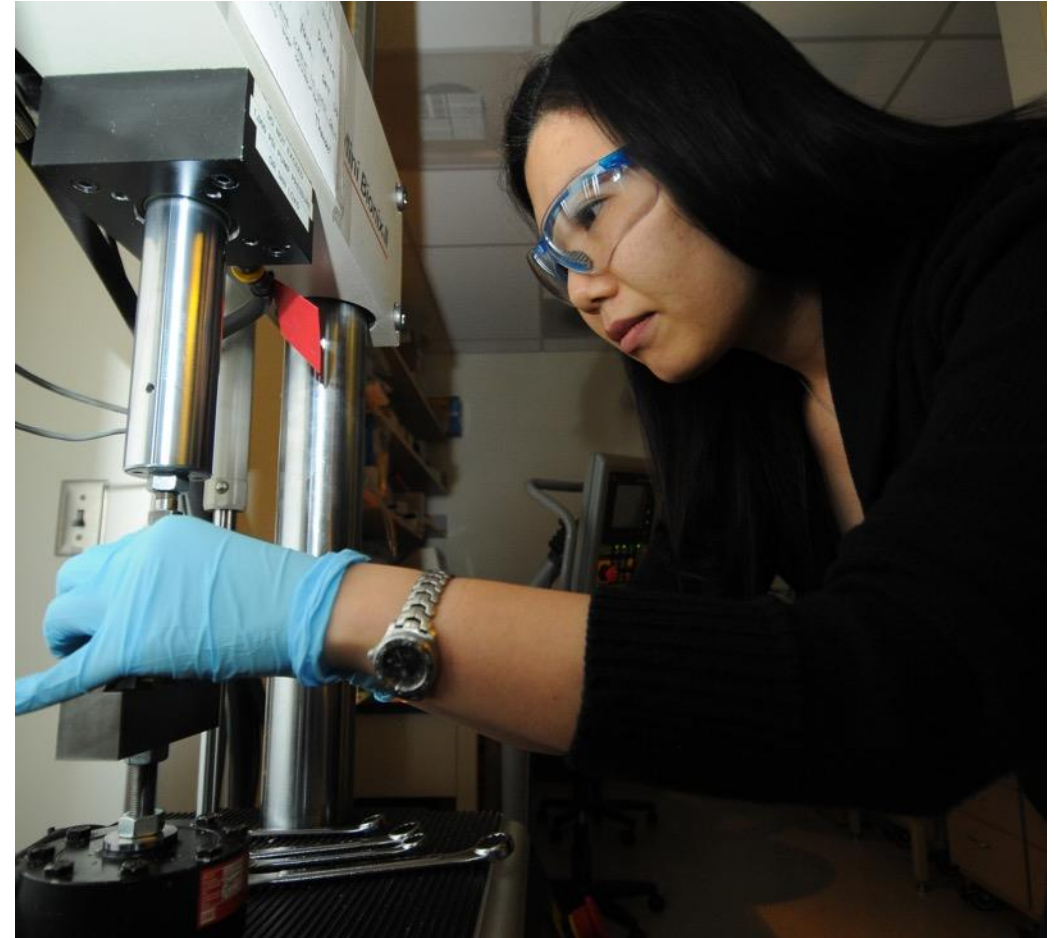
# What is Alpine?

It is available to any US-based researcher affiliated with UCB, AMC, CSU, and institutions that are members of the Rocky Mountain Advanced Computing Consortium (RMACC).



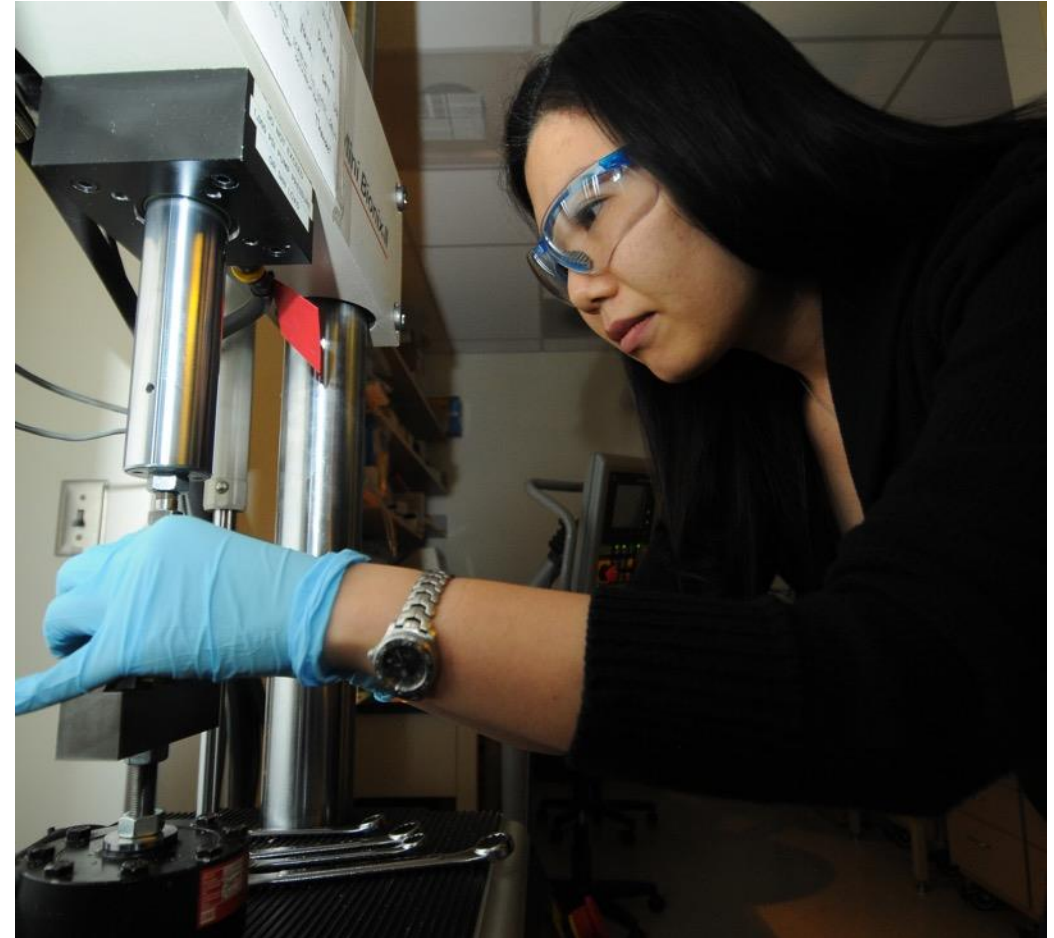
# What is Alpine?

- Alpine uses slurm as the scheduler to allocate resources for jobs.



# What is Alpine?

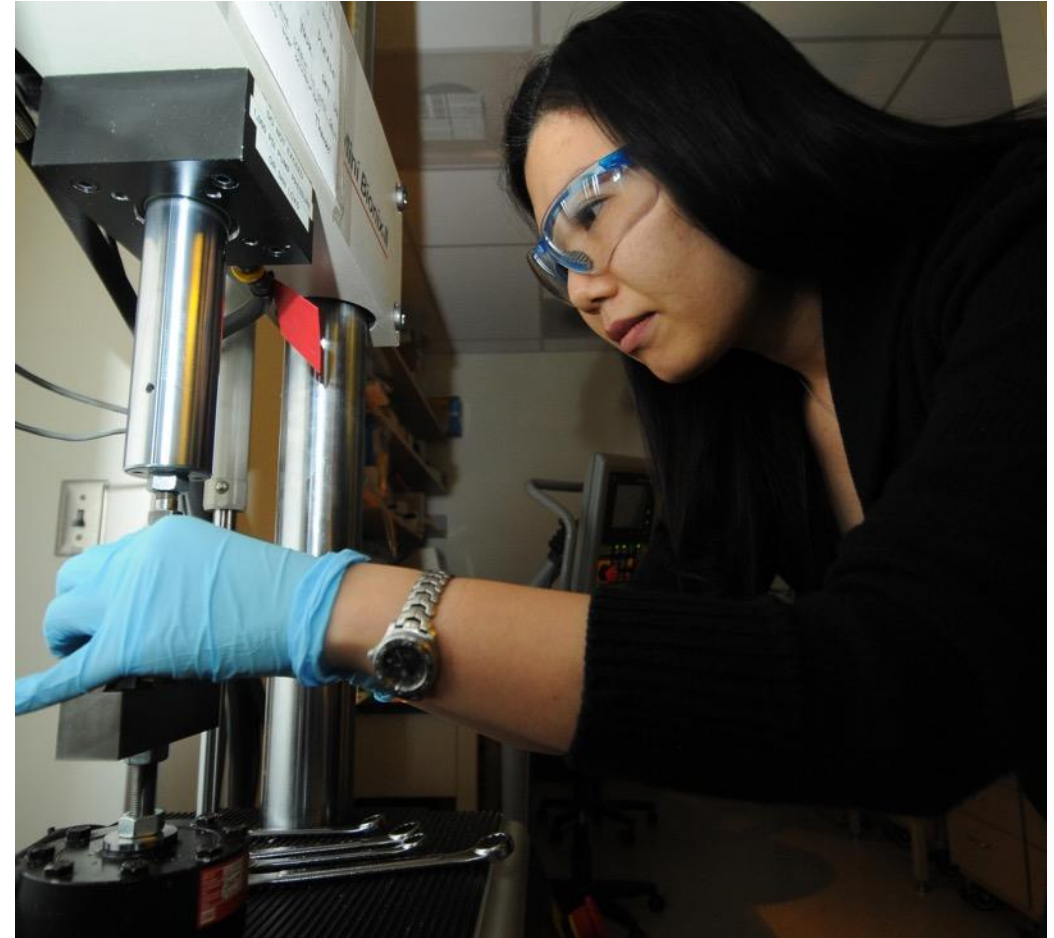
- Alpine uses slurm as the scheduler to allocate resources for jobs.
- Slurm is an open source, fault-tolerant, and highly scalable cluster management and job scheduling system for large and small Linux clusters.





# Terms of Usage

- Data will need to be in full compliance with term of service.
- No PHI data, no FERPA, no ITAR, no GDPR, no export control and data/software that comply with IRB requirements.
- No highly confidential data.
- More information here:  
<https://www.colorado.edu/rc/resources/petalibrary/tos>

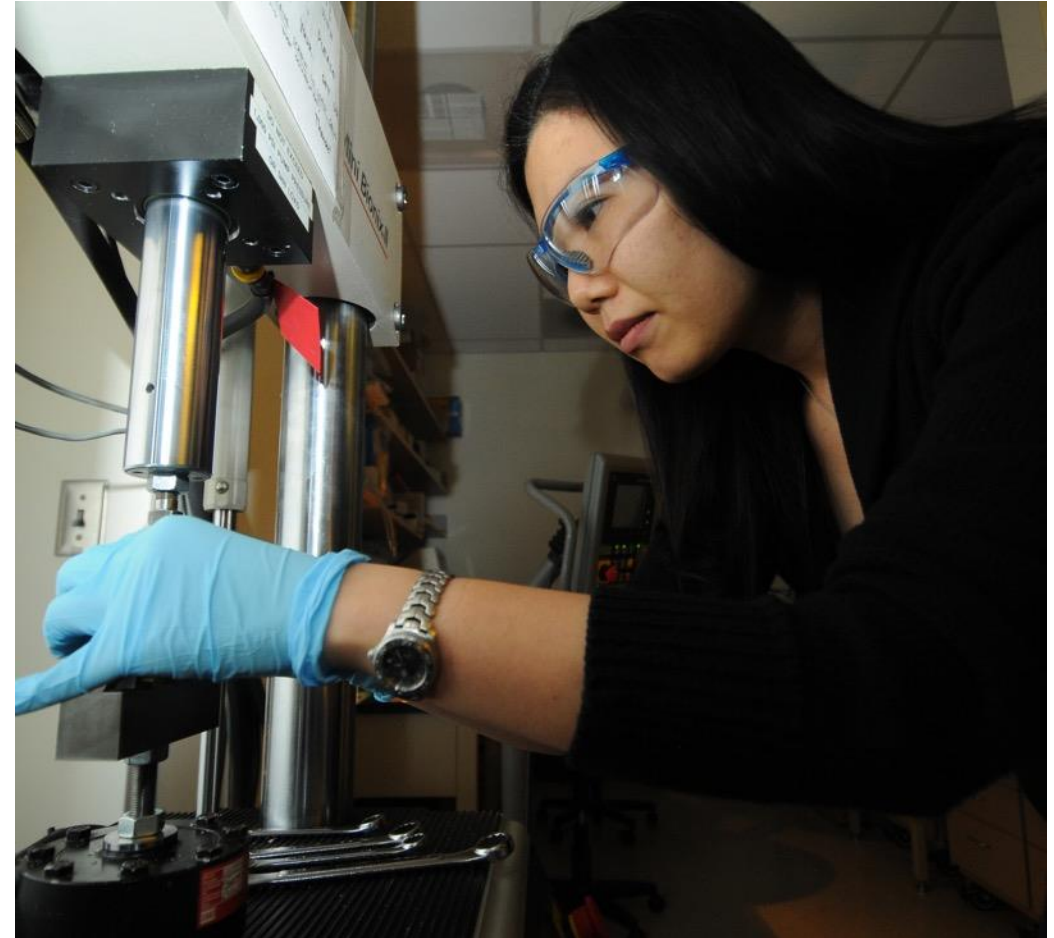


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- No highly confidential data.
- More information here:  
<https://www.colorado.edu/rc/resources/petalibrary/tos>
- Data classification:  
<https://www.cu.edu/security/data-classification>.
- HIPAA identifiers:  
<https://www.dhcs.ca.gov/dataandstats/data/Pages/ListofHIPAAIdentifiers.aspx>
- Alpine EUA form:  
[https://ucdenverdata.formstack.com/forms/alpine\\_eua\\_and\\_intake](https://ucdenverdata.formstack.com/forms/alpine_eua_and_intake)



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# Alpine EUA form



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## Anschutz Medical Campus Research Computing End User Agreement

### Introduction

This End User Agreement (EUA) is made by and between the Anschutz Medical Campus (CU Anschutz) High Performance Computing (HPC) system user and the Regents of the University of Colorado, a body corporate, for and on behalf of the University of Colorado Denver | Anschutz Medical Campus Office of Information Technology (OIT) concerning the use of University of Colorado Research Computing (CURC) systems housed at the University of Colorado | Boulder.

These systems include but are not limited to the use of Summit, Alpine, Blanca, CUMulus, and the PetaLibrary. These systems are not designed to support computing on data covered by regulatory requirements such as HIPAA, GDPR (e.g. UK Biobank), or FERPA data. This [page](#) highlights potential HIPAA identifiers. Finally, any credentials associated with PHI accounts such as the Health Data Compass Google credentials cannot be used on Alpine nor can the credentials and their corresponding keys and/or tokens be stored on Alpine. For more information about the Alpine HPC system and other services offered by CURC, please click [here](#).



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Source: [https://ucdenverdata.formstack.com/forms/alpine\\_eua\\_and\\_intake](https://ucdenverdata.formstack.com/forms/alpine_eua_and_intake)



# III- Alpine nodes

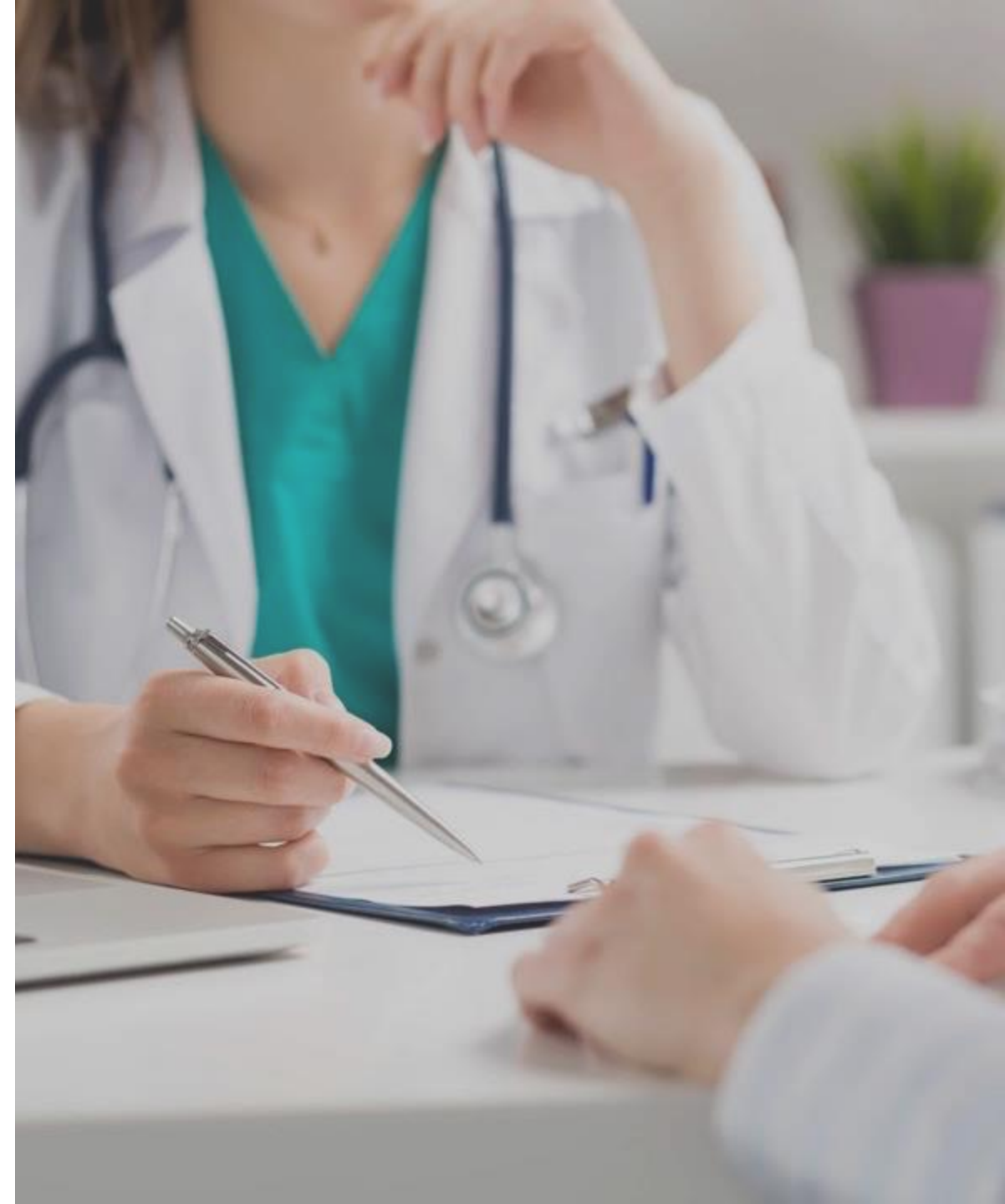


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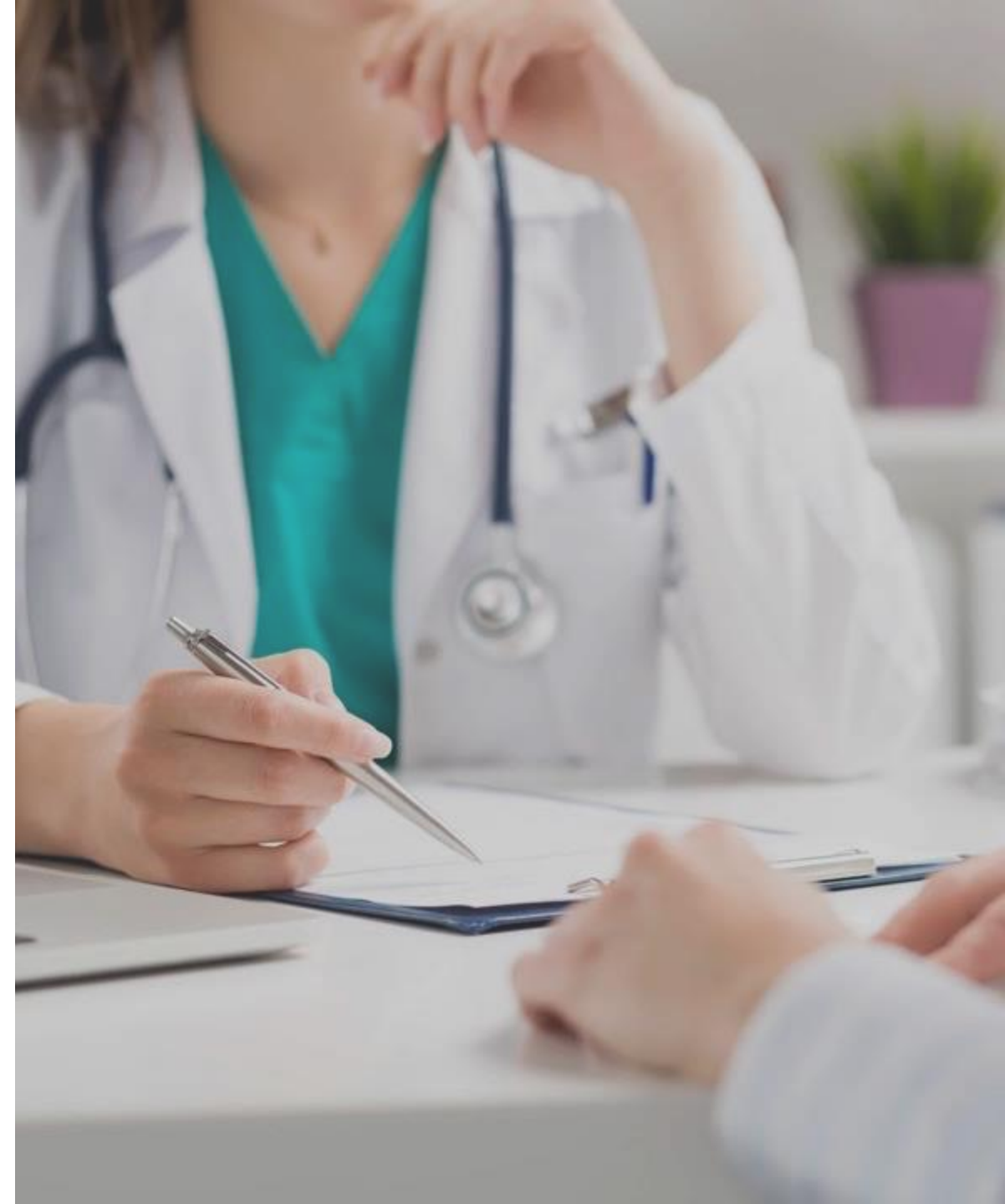
# Alpine nodes

- 389 nodes in total



# Alpine nodes

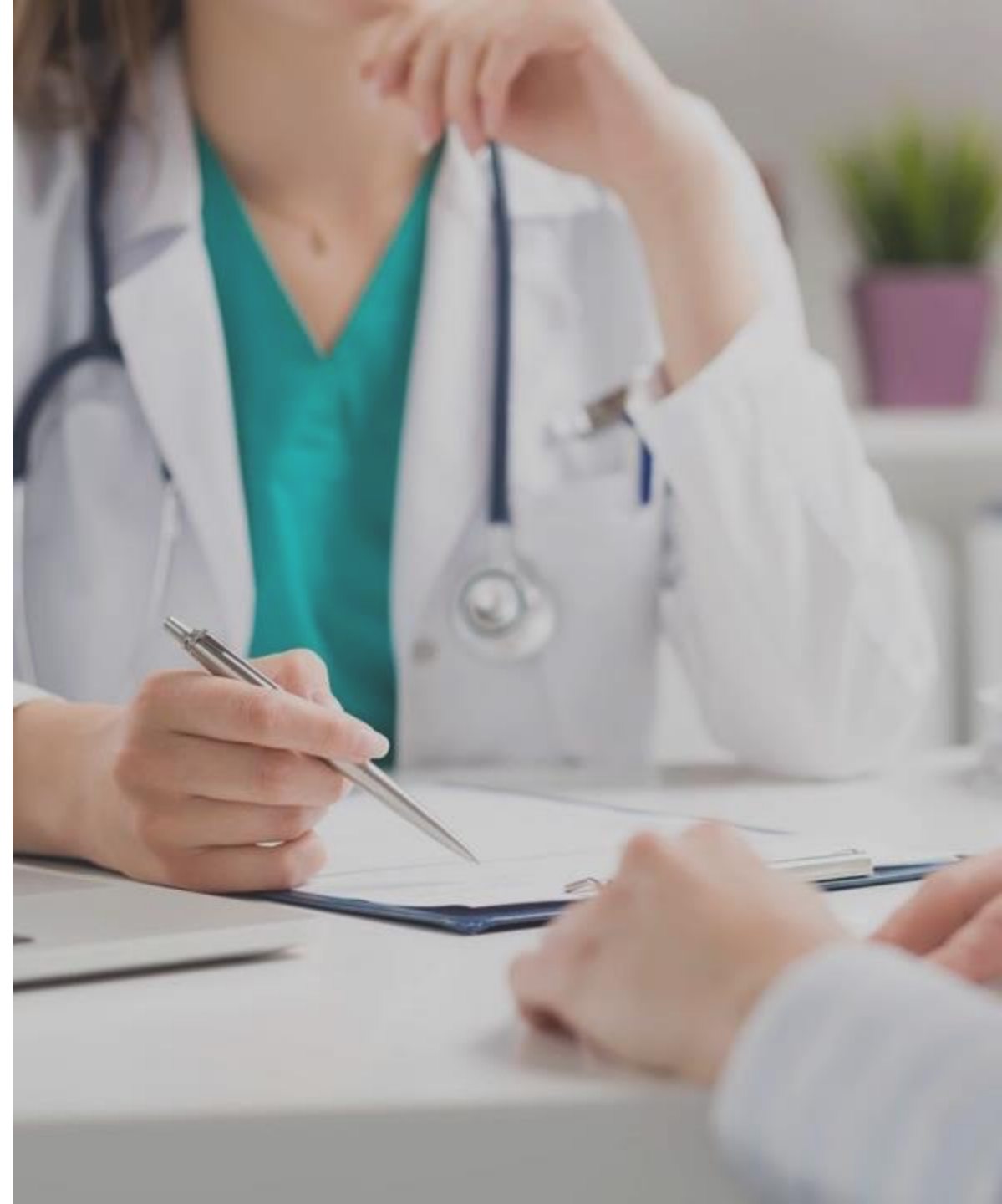
- 389 nodes in total
- 347 CPU nodes





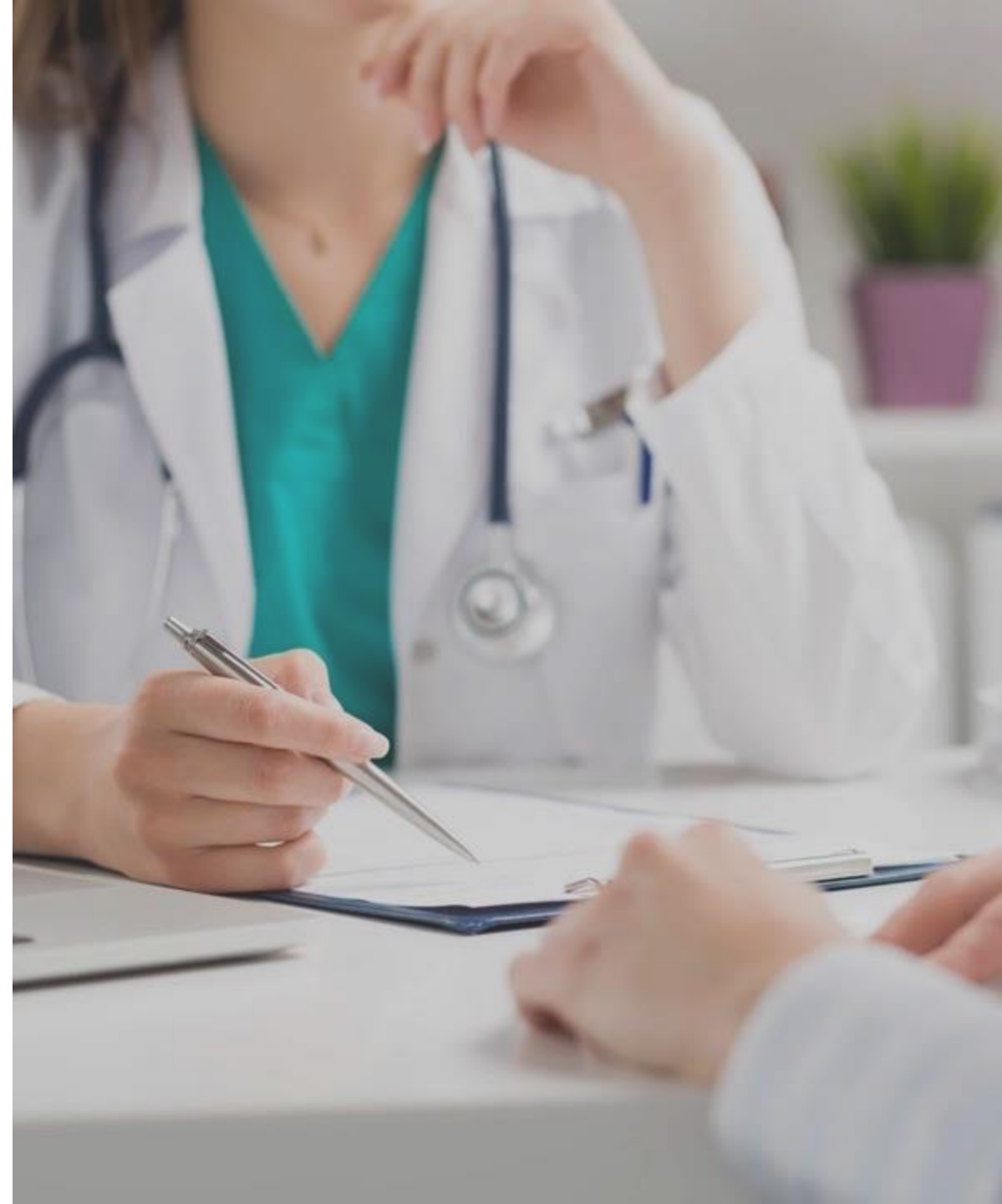
# Alpine nodes

- 389 nodes in total
- 347 CPU nodes
- 22 high memory nodes



# Alpine nodes

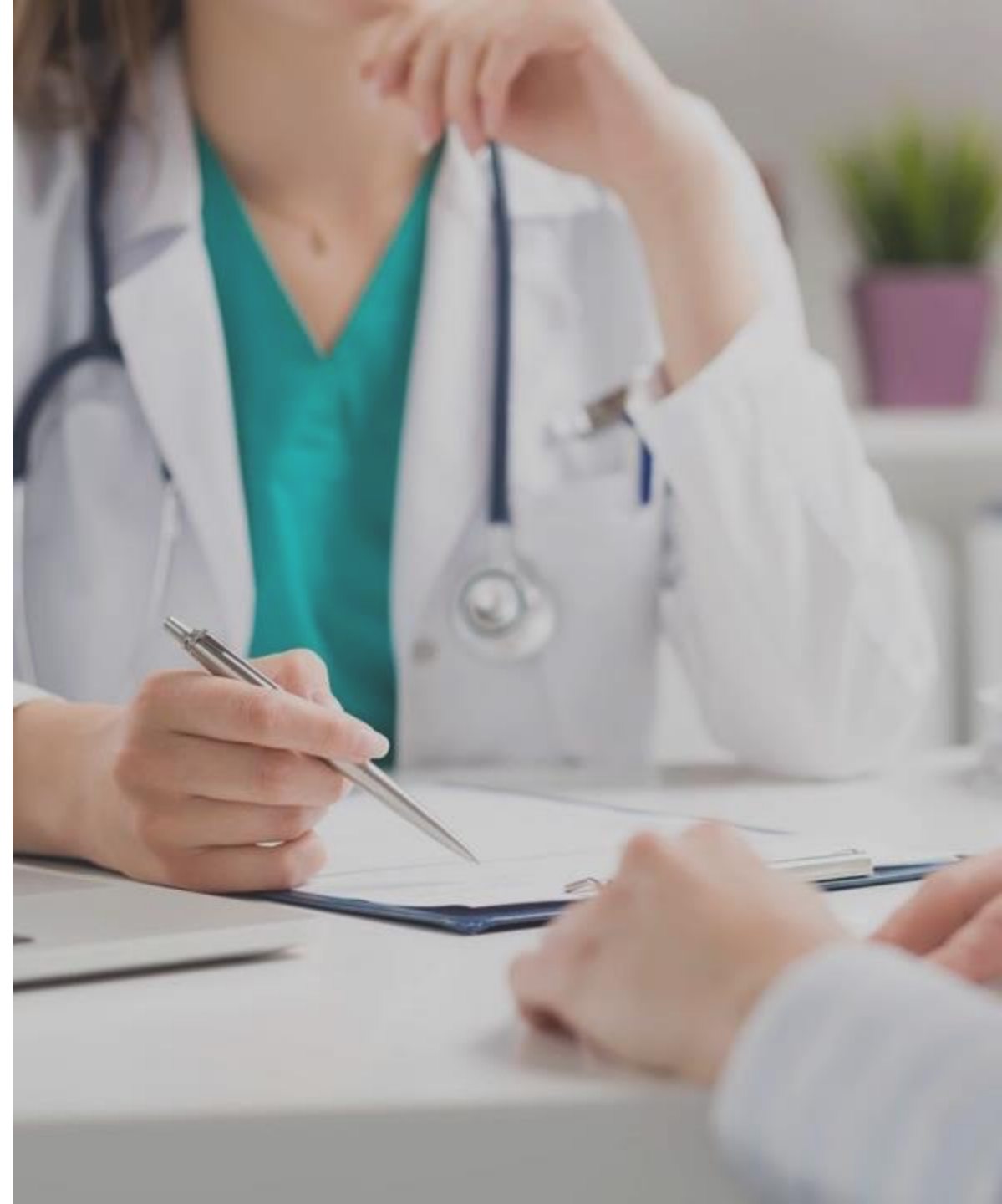
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- 347 CPU nodes
- 22 high memory nodes
- 8 NVIDIA A100 gpu nodes (40G global mem)





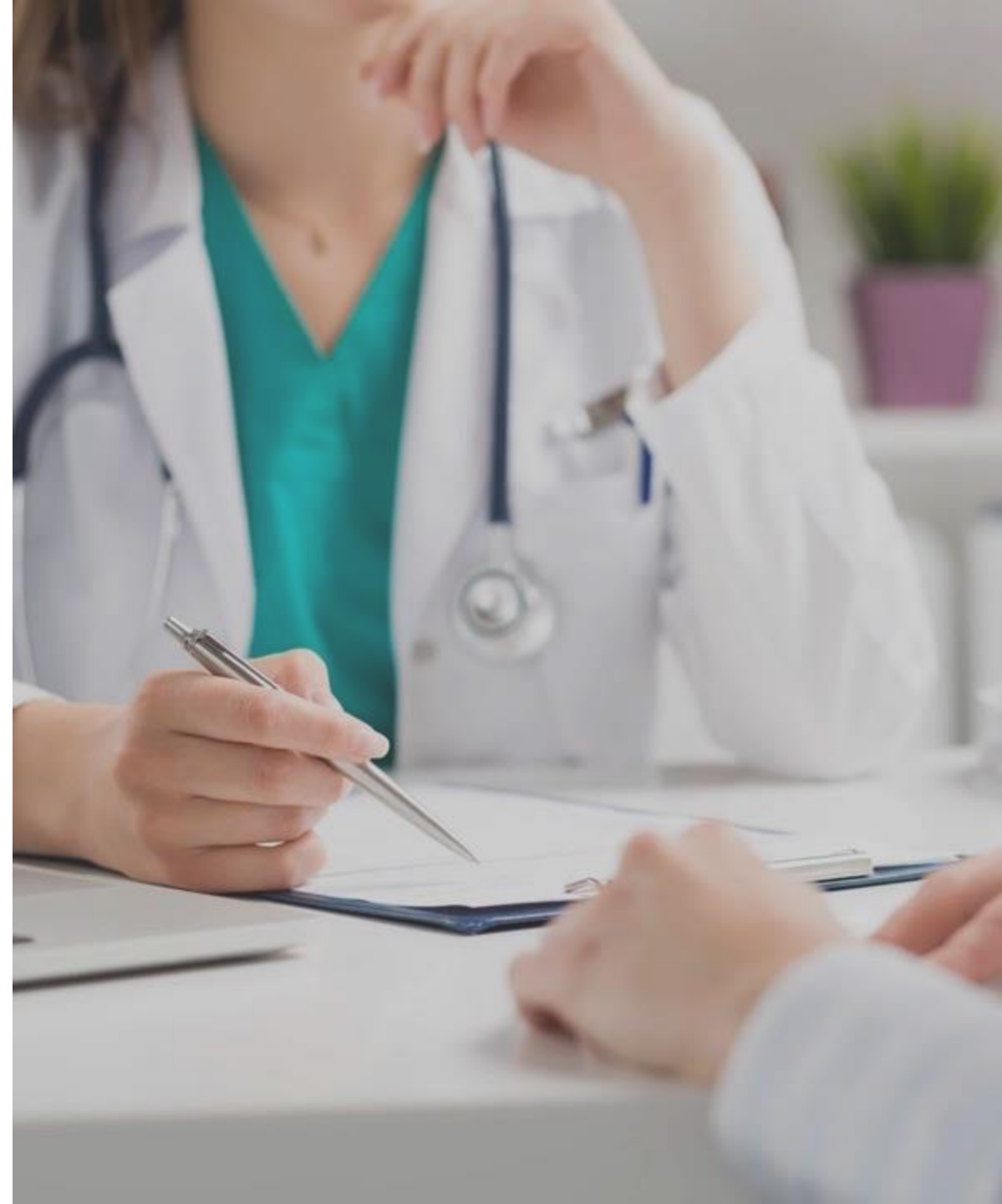
# Alpine nodes

- 389 nodes in total
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- 4 NVIDIA A100 gpu nodes (80G global mem)



# Alpine nodes

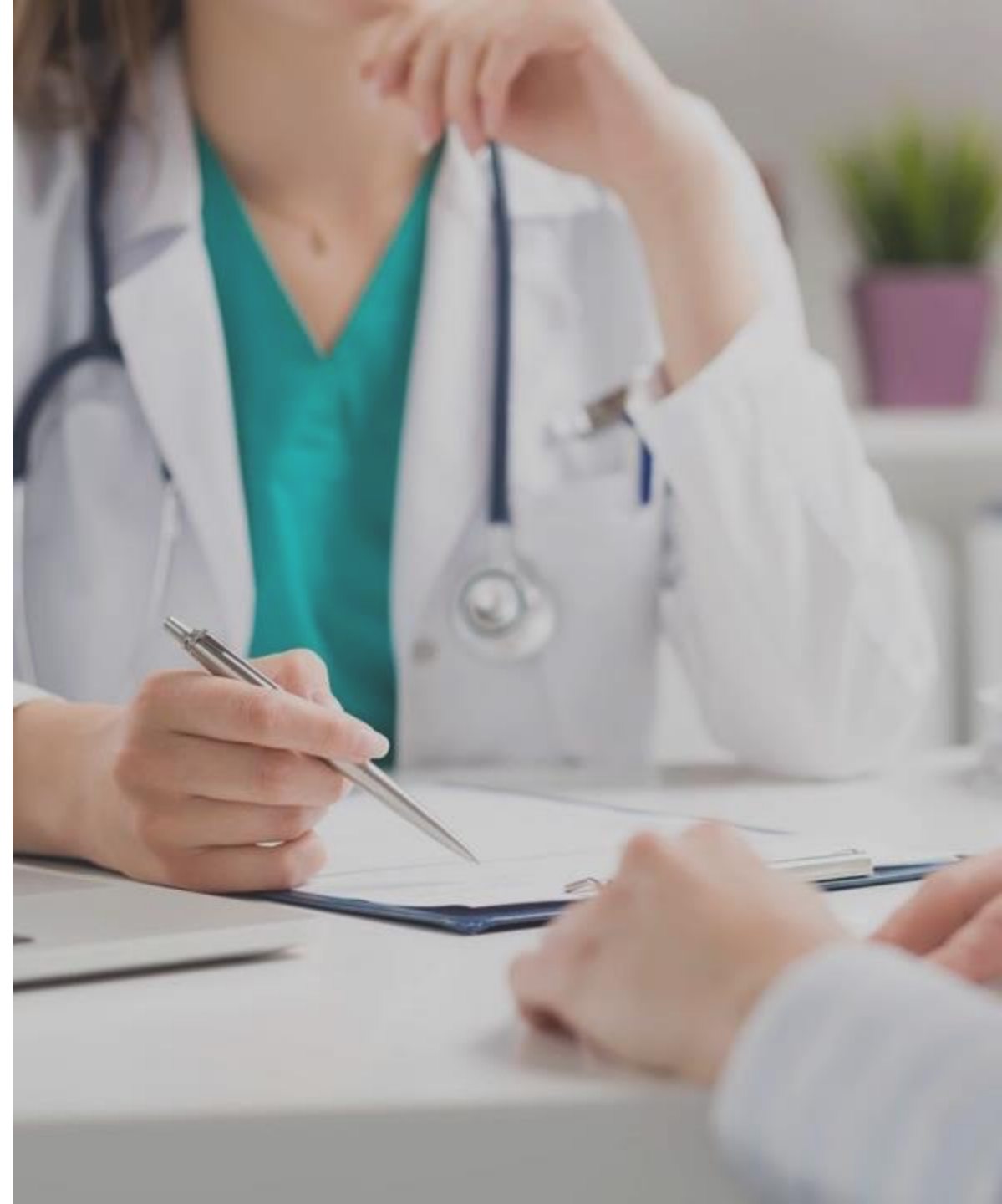
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- 347 CPU nodes
- 22 high memory nodes
- 8 NVIDIA A100 gpu nodes (40G global mem)
- 4 NVIDIA A100 gpu nodes (80G global mem)
- 8 AMD ami100 gpu nodes (32G global mem)





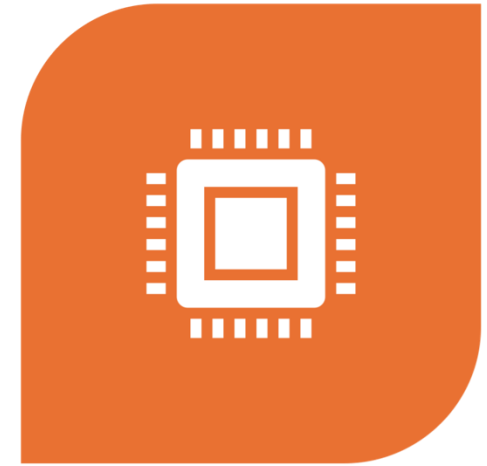
# Alpine nodes

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- 22 high memory nodes
- 8 NVIDIA A100 gpu nodes (40G global mem)
- 4 NVIDIA A100 gpu nodes (80G global mem)
- 8 AMD mi100 gpu nodes (32G global mem)
- Total of 22,180 cores



# CPU nodes

- AMD EPYC 7<sup>th</sup> generation
- 64 or 48 or 32 each
- HDR 100 Infiniband

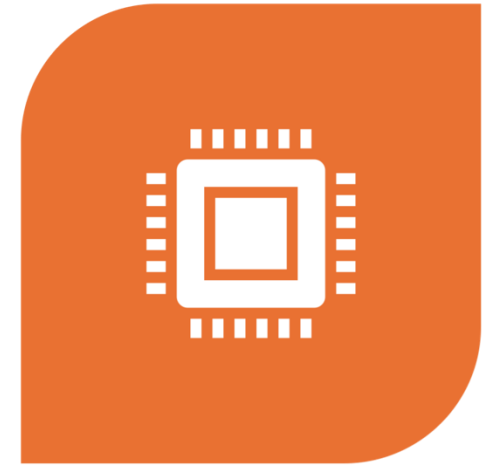


347 CPU NODES



# CPU nodes

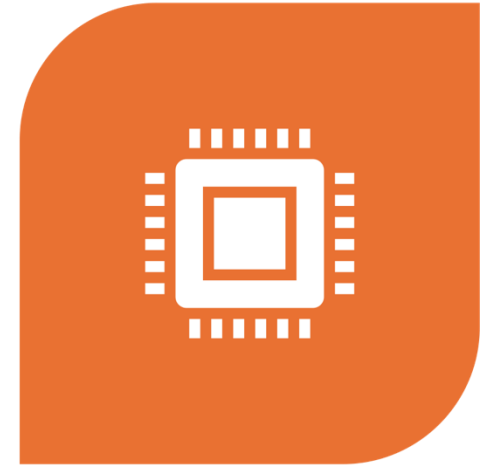
- AMD EPYC 7<sup>th</sup> generation
- 64 or 48 or 32 each
- HDR 100 Infiniband
- 240G memory



347 CPU NODES

# High mem nodes nodes on Alpine

- AMD EPYC 7<sup>th</sup> generation
- 64 or 48 cores each
- 2x25 Gb Ethernet +RoCE
- Up to 1TB RAM

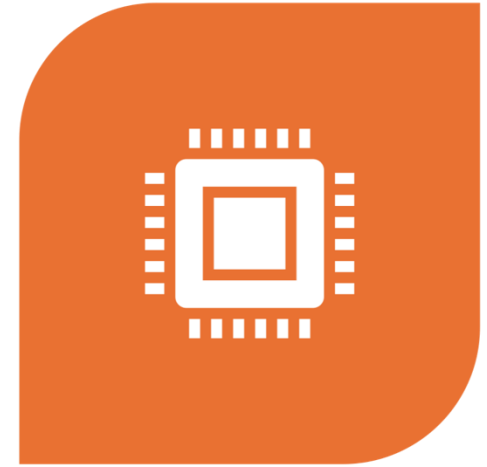


22 HIGH MEM NODES



# NVIDIA GPU nodes on Alpine

- aa100 gpu nodes with 3Xgpus per node
- 40GB or 80GB gpu global memory
- 64 cores each
- 2x25 Gb Ethernet +RoCE



12 NVIDIA GPU NODES (3  
GPU EACH)

# AMD GPU nodes on Alpine

- ami100 gpu nodes with 3Xgpus per node
- 32GB gpu global memory
- 64 cores each
- 2x25 Gb Ethernet +RoCE



8 AMD GPU NODES (3  
GPU EACH)



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# Upcoming nodes this Fall

- 12 CPU nodes
- 2X2TB high mem nodes
- NVIDIA 3XL40 gpu nodes with 3 gpus each



# IV- Data transfer methods

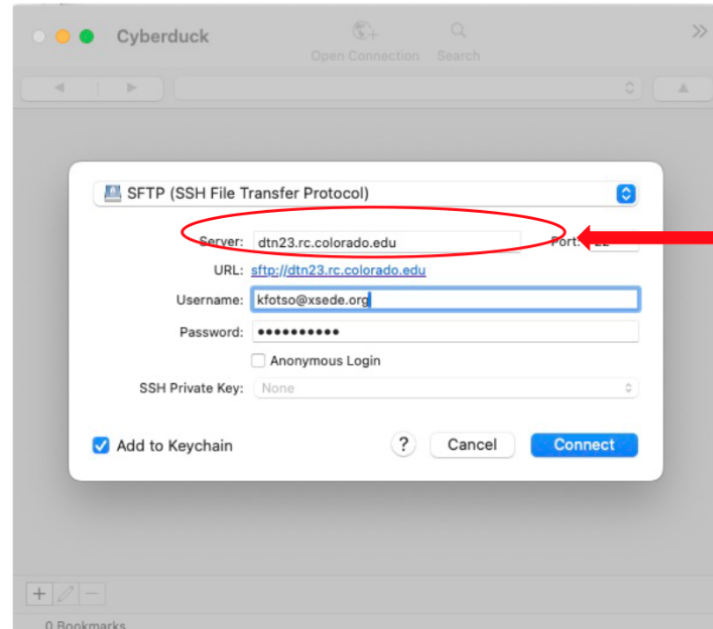


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# Data transfers

- Globus, scp, rsync, sftp, cyberduck, Filezilla etc ...

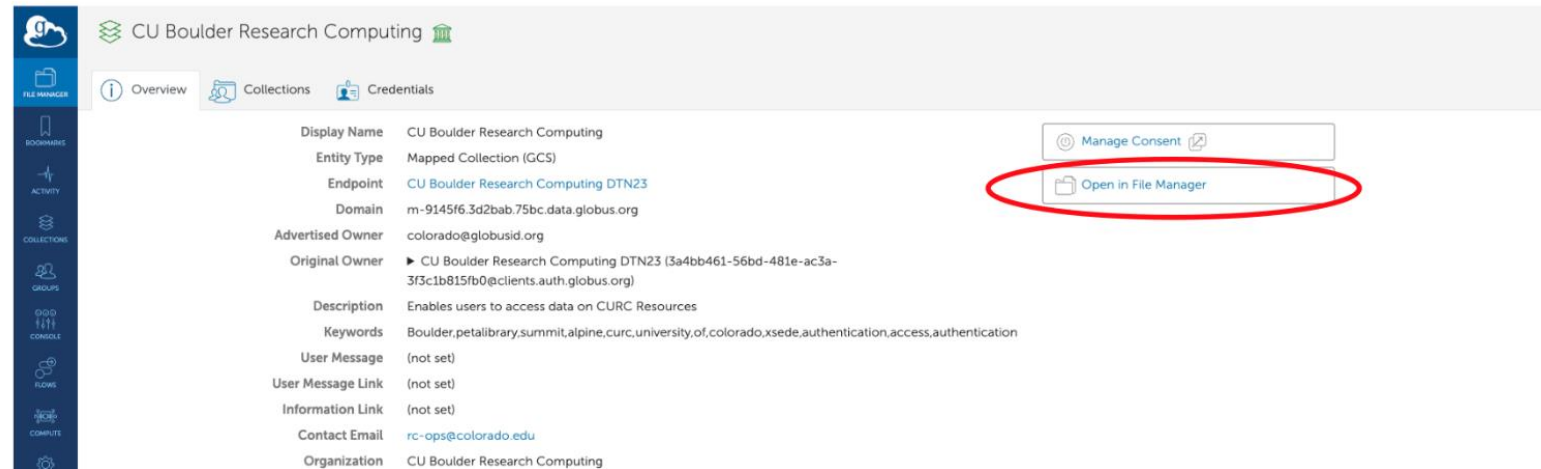


We point out to the Alpine data transfer node



# Data transfers

- Globus, scp, rsync, sftp, cyberduck, Filezilla etc ...



The screenshot displays the Globus interface for the 'CU Boulder Research Computing' collection. The left sidebar contains navigation icons for File Manager, Bookmarks, Activity, Collections, Groups, Console, Flows, and Compute. The main area shows the 'Overview' tab with a table of metadata. The 'Open in File Manager' button is highlighted with a red circle.

Property	Value
Display Name	CU Boulder Research Computing
Entity Type	Mapped Collection (GCS)
Endpoint	CU Boulder Research Computing DTN23
Domain	m-9145f6.3d2bab.75bc.data.globus.org
Advertised Owner	colorado@globusid.org
Original Owner	CU Boulder Research Computing DTN23 (3a4bb461-56bd-481e-ac3a-3f3c1b815fb0@clients.auth.globus.org)
Description	Enables users to access data on CURC Resources
Keywords	Boulder,petalibrary,summit,alpine,curc,university.of.colorado,xsede,authentication,access,authentication
User Message	(not set)
User Message Link	(not set)
Information Link	(not set)
Contact Email	rc-ops@colorado.edu
Organization	CU Boulder Research Computing

Buttons: Manage Consent, Open in File Manager



# V- Alpine storage



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# Storage overview

- Home filesystem (2G). Backed up + for hosting config files. (free)





# Storage overview

- Home filesystem (2G). Backed up + for hosting config files. (free)
- Project filesystem (250G). Backed up -> for package installation. (free)



# Storage overview

- Home filesystem (2G). Backed up + for hosting config files. (free)
- Project filesystem (250G). Backed up -> for package installation. (free)
- Scratch filesystem (10TB) (free)



# Storage overview

- Home filesystem (2G). Backed up + for hosting config files. (free)
- Project filesystem (250G). Backed up -> for package installation. (free)
- Scratch filesystem (10TB) (free)
- Petalibrary (optional and paid service).





# Scratch overview

- Scratch space (10 TB)
- GPFS filesystem
- Very suitable for parallel application + heavy I/O
- Data gets purged every 90 days!!





# VI- Petalibrary service



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# What is Petalibrary?

- An Alpine service that supports the paid storage, archival, and sharing of research data.





# What is Petalibrary?

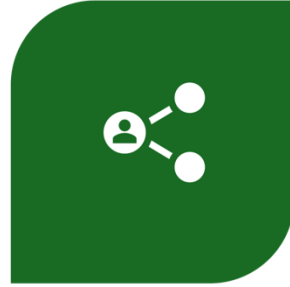
- An Alpine service that supports the paid storage, archival, and sharing of research data.
- It is available at a subsidized cost to any researcher affiliated with the University of Colorado System (Boulder, Anschutz, Denver, Colorado Springs)



# Preliminary conditions



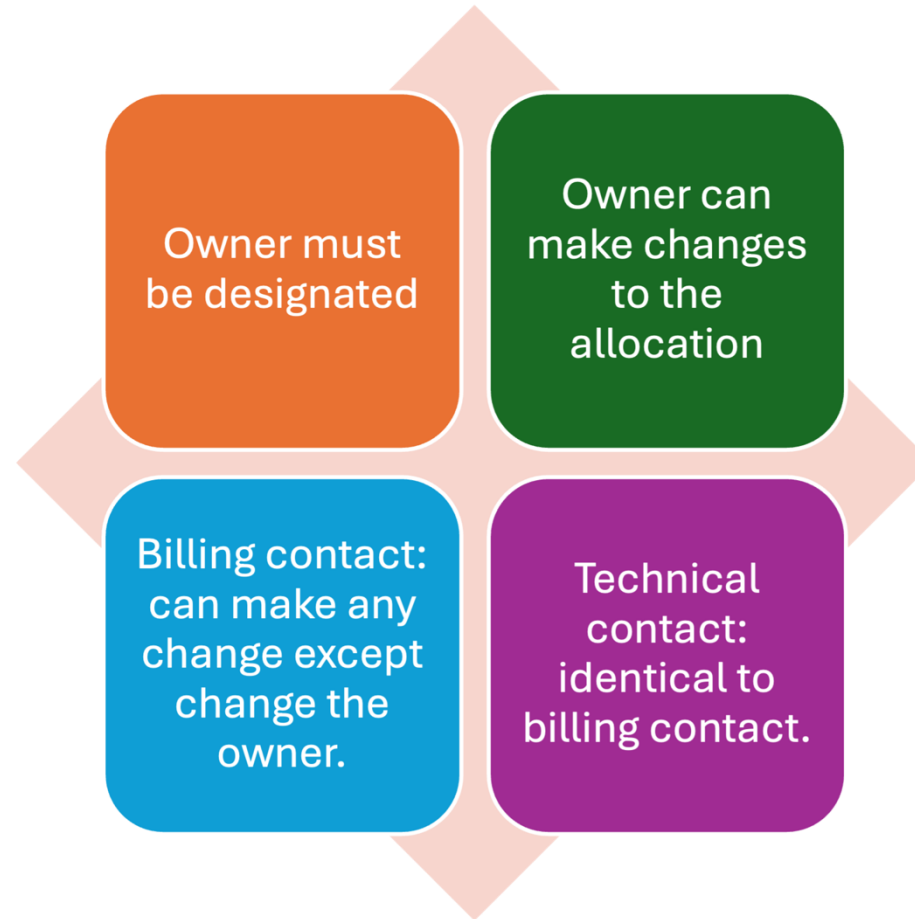
CREATION OF AN ACCESS  
GROUP



ALL MEMBER ADDED TO THE  
GROUP WILL NEED  
ACCESS/XSEDE ACCOUNTS.

```
/pl/active/<your_allocation_name>  
/pl/archive/<your_allocation_name>
```

# Preliminary conditions





# Application

- Application submitted here:  
<https://www.colorado.edu/rc/resources/petalibrary>
- The request form will need a speedtype: account# to which they plan to charge the allocation.



# Billing

- On active storage: \$48/TB/yr.
- ZFS Raidz2 allow for frequent read/write + parity.
- **It is the responsibility of the PI to estimate and foresee the PL allotment for the year.**



# Billing

- On archive storage: \$25/TB/yr.
- Tape-like storage for infrequently accessed data.
- Can be accessed from RC login node only and data transfer resources.
- Min size for any alloc is 1 TB.





# Billing

- On archive storage: \$25/TB/yr.
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- Min size for any alloc is 1 TB.
- **10,000 object (file/directory) limit.**



# Billing

- On archive storage: \$25/TB/yr.
- Tape-like storage for infrequently accessed data.
- Can be accessed from RC login node only and data transfer resources.
- Min size for any alloc is 1 TB.
- **10,000 object (file/directory) limit.**
- **Owner will get and pay for the space even if they do not use it.**



# Data redundancy



PL allocations are of single-copy nature.



All users should fill out the PL single copy acknowledgment.



Snapshots monitoring in place so that they are not missed unless on snapshot custom schedule





# Data replication solution

- Replicated PetaLibrary active+archive allocation.
- CURC **only takes data replication responsibility.**



# Data replication solution

- Replicated PetaLibrary active+archive allocation.
- CURC **only takes data replication responsibility.**
- Not subject to the **10,000 object (file/directory) limit.**



# Active+Archive replication

- Synchronization between active and archive happen every 15 min in theory but are not always guaranteed.
- Snapshots are also replicated from active to archive.
- The Boulder storage team maintains the second copy (e.g. archive) for you and you do not have direct access to it.
- \$73/TB/year total. **(NOT \$73 on top of the \$48/\$25 original rate!!)**





# VII- Examples of HPC tools on Alpine.



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# AlphaFold



Source: <https://alphafold.ebi.ac.uk/>

# Fragfold

- Fragment binding prediction
- High-throughput computational discovery of inhibitory protein fragments with AlphaFold

The screenshot shows the GitHub repository for FragFold, a public repository by user swanss. The repository has 2 branches, 0 tags, 2 watchers, 5 forks, and 14 stars. The main branch is selected. The file list shows a merge pull request #11 from swanss/fix\_install, merged 2 months ago with 54 commits. The files listed are: fragfold (added \_\_init\_\_.py, 2 months ago), input (updating column names in the dataframes and fixing the r..., 2 months ago), nextflow (change name of env to fragfold, 2 months ago), scripts (updating column names in the dataframes and fixing the r..., 2 months ago), .gitignore (updating column names in the dataframes and fixing the r..., 2 months ago), LICENSE.txt (Added pyproject.toml, instructions for installing as a pack..., 9 months ago), README.md (fix typo in variable name and add script for running the test, 2 months ago), install\_fragfold.sh (change name of env to fragfold, 2 months ago), and pyproject.toml (Fix pip install and bugs in install\_fragfold.sh/peak predicti..., 2 months ago). The README section is visible, titled "Fragment binding prediction with ColabFold". The right sidebar shows the repository's activity, including a Readme, MIT license, 14 stars, 2 watchers, 5 forks, and no releases or packages published. The contributors section shows 2 contributors, with swanss being the primary one.

**FragFold** Public

Watch 2 Fork 5 Star 14

main 2 Branches 0 Tags

Go to file Add file Code

swanss Merge pull request #11 from swanss/fix\_install b240282 · 2 months ago 54 Commits

fragfold	added __init__.py	2 months ago
input	updating column names in the dataframes and fixing the r...	2 months ago
nextflow	change name of env to fragfold	2 months ago
scripts	updating column names in the dataframes and fixing the r...	2 months ago
.gitignore	updating column names in the dataframes and fixing the r...	2 months ago
LICENSE.txt	Added pyproject.toml, instructions for installing as a pack...	9 months ago
README.md	fix typo in variable name and add script for running the test	2 months ago
install_fragfold.sh	change name of env to fragfold	2 months ago
pyproject.toml	Fix pip install and bugs in install_fragfold.sh/peak predicti...	2 months ago

README MIT license

## Fragment binding prediction with ColabFold

**About**  
No description, website, or topics provided.

Readme  
MIT license  
Activity  
14 stars  
2 watching  
5 forks  
Report repository

**Releases**  
No releases published

**Packages**  
No packages published

**Contributors** 2

swanss

Source: <https://www.biorxiv.org/content/10.1101/2023.12.19.572389v1> ;  
<https://github.com/swanss/FragFold>;



# Containers

- Apptainer/Singularity can now be built directly on the cluster
- Can be built either from a definition file or converted from a docker image.

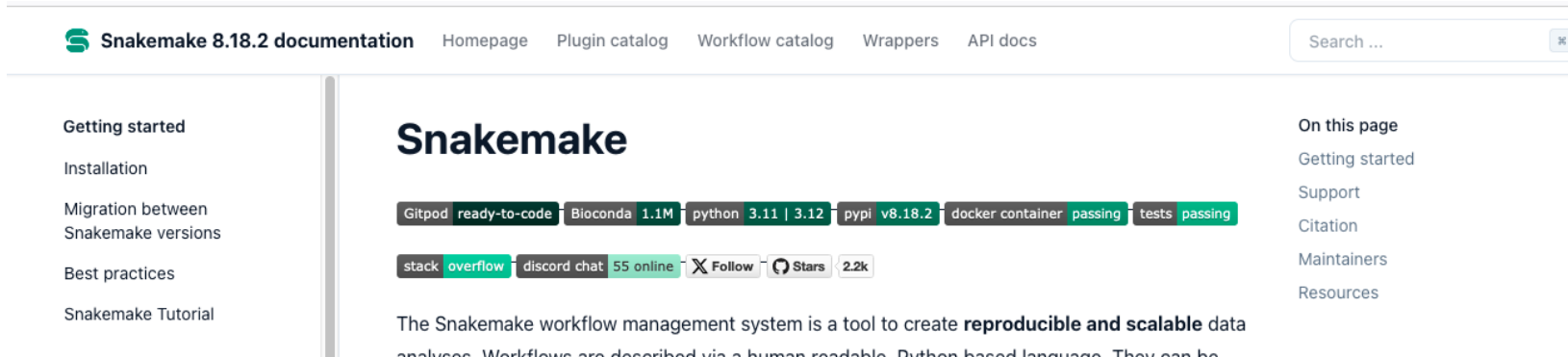


# Containers

- Apptainer/Singularity can now be built directly on the cluster
- Can be built either from a definition file or converted from a docker image.
- Available on all compute nodes.
- e.g: `apptainer build horovod_cuda.sif docker://horovod/horovod:latest`



# Snakemake




The screenshot shows the Snakemake 8.18.2 documentation homepage. The header includes navigation links: Snakemake 8.18.2 documentation, Homepage, Plugin catalog, Workflow catalog, Wrappers, and API docs. A search bar is located on the right. The left sidebar lists: Getting started, Installation, Migration between Snakemake versions, Best practices, and Snakemake Tutorial. The main content area features the title 'Snakemake' followed by a row of badges: Gitpod, ready-to-code, Bioconda, 1.1M, python, 3.11 | 3.12, pypi, v8.18.2, docker container, passing, tests, passing. Below this is another row of badges: stack, overflow, discord chat, 55 online, Follow, Stars, 2.2k. The text below the badges states: 'The Snakemake workflow management system is a tool to create **reproducible and scalable** data analyses. Workflows are described via a human-readable, Python-based language. They can be'.

- Workflow management software compatible with slurm

Source: <https://snakemake.readthedocs.io/en/stable/>





# Nextflow


 test-ci.sh


Fix integration tests


2 weeks ago


 README

 Code of conduct

 Apache-2.0 license








# nextflow

*"Dataflow variables are spectacularly expressive in concurrent programming"*

[Henri E. Bal](#) , [Jennifer G. Steiner](#) , [Andrew S. Tanenbaum](#)

 Nextflow CI

passing

release

v24.04.4

@nextflow

Published

Nature Biotechnology

install with

bioconda

license

Apache-2.0

Source: <https://github.com/nextflow-io/nextflow>

# Rstudio instances

- Dedicated Rstudio, Vscode, MATLAB or Jupyterlab instances.

Files ▾ Jobs ▾ Clusters ▾ Interactive Apps ▾ My Interactive Sessions

Home / My Interactive Sessions / RStudio Server (Presets)

**Interactive Apps**

- Desktops
  - Core Desktop (Presets)
- GUIs
  - MATLAB (Presets)
- Servers
  - Jupyter Session (Custom)
  - Jupyter Session (Presets)
  - RStudio Server (Custom)
  - RStudio Server (Presets)**
  - VS Code-Server (Custom)
  - VS Code-Server (Presets)

**RStudio Server (Presets)**

This app will launch [RStudio Server](#), an IDE for [R](#) on Alpine.

Before utilizing this application, please see the [RStudio section of the CURC documentation](#). This documentation includes important information regarding quitting an RStudio session. For more information on installing dependencies required by R packages, please see the [Installing dependencies for RStudio section](#) in our documentation.

Please note that the first time you launch RStudio it may take 15 minutes or more to create a [persistent overlay](#), if 1 core is used. For this reason, we recommend using 4 cores or more during your first launch of an RStudio session. Subsequent sessions will not require the creation of the persistent overlay; therefore 1 core may be sufficient.

RStudio Version

Rstudio 2023.03.0, R 4.2.2

Configuration

4 cores, 4 hours, 0 GPUs (Alpine)

**Launch**


\* The RStudio Server (Presets) session data for this session can be accessed under the [data root directory](#).

Source: [https://github.com/kf-cuanschutz/CU-Anschutz-HPC-documentation/tree/main/Rstudio\\_related\\_scripts](https://github.com/kf-cuanschutz/CU-Anschutz-HPC-documentation/tree/main/Rstudio_related_scripts)

# Distributed deep learning on multiple nodes

- Horovod on both NVIDIA & AMD gpus support

main 1 Branch 0 Tags  Add file Code

 **kf-cuanschutz** Update README.md ...

fddb90c · last month 🕒 19 Commits

README.md	Update README.md	last month
install_file.sh	Adding files associated with the installation	3 months ago
part2-install_horovod_amd_gpu.sh	Update part2-install_horovod_amd_gpu.sh	2 months ago
part3-load_rocm+horovod_.sh	File to load rocm and horovod related ENV	3 months ago
requirements.txt	Adding files associated with the installation	3 months ago
requirements_2.txt	Adding files associated with the installation	3 months ago

README

## AMD\_diversification

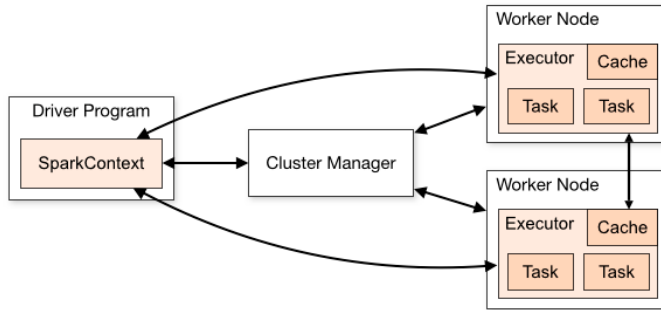
The scripts associated with this repository will allow you to adapt your pytorch GPU workflow on Alpine to AMD gpus.

Please follow the recommendation below in order to adapt your NVIDIA pytorch pipeline into AMD





# Hail & Sparcluster distributed computing



```
# Loading the hail module
module load hail
```

```
# We want the name of the nodes we requested
scontrol show hostname > $SLURM_SUBMIT_DIR/nodelist.txt
export SLURM_NODEFILE=$SLURM_SUBMIT_DIR/nodelist.txt
```

```
# We submit hail with the custom made slurm-spark-submit which was modified from: https://lobogit.unm.edu/CARC/tutorials/-/blob/master/spark/pbs-spark-submit
# The hail script was modified from https://hail.is/docs/0.2/install/other-cluster.html
#
```

```
python slurm-spark-submit \
--jars $HAIL_HOME/backend/hail-all-spark.jar \
--conf spark.driver.extraClassPath=$HAIL_HOME/backend/hail-all-spark.jar \
--conf spark.executor.extraClassPath=./hail-all-spark.jar \
--conf spark.serializer=org.apache.spark.serializer.KryoSerializer \
--conf spark.kryo.registrator=is.hail.kryo.HailKryoRegistrator hail-script.py --temp_dir $TMP
```



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Source: [https://github.com/kf-cuanschutz/Hail\\_support\\_cu\\_anschutz](https://github.com/kf-cuanschutz/Hail_support_cu_anschutz)

# Jobs in chain and job arrays with slurm

```
# Addressing the total number of files to be processed
actual_work_files=$((< "$scripts_dir/files_to_process.txt" wc -l)
total_work_files=$(( actual_work_files*2 ))

# Phase 1 FastQC Raw, no dependencies:
# Note: Job arrays have been added for that step.

# Producing the files to be processed for phase 1
ls $base_dir/Raw Sequences/NW_*.fastq.gz > arg_fastq_raw_tmp.txt
sort arg_fastq_raw_tmp.txt | uniq -u > arg_fastq_raw.txt

tmp1=$(sbatch --array=1-$total_work_files ${scripts_dir}/FastQC_Raw.sh $base_dir)
jid1='echo ${tmp1##* }'

# Setting up sbatch to avoid dependency error
alias sbatch='sbatch --export=NONE'

# Phase 2 Skewer_trim, dependency iid1
# RAW_DIR="/scratch/alpine/ /SEARCH-TB_base_dir/Raw Sequences"
# num_skewer_files=$((< "$RAW_DIR/arg_skewer_trim.txt" wc -l)
tmp2=$(sbatch --array=1-$total_work_files --dependency=afterany:$jid1 $scripts_dir/Skewer_trim.sh $base_dir)
```

# Bioinformatics modules on Alpine

```
-----  
alphafold/2.2.0  
alphafold/2.3.1 (D)  
bamtools/2.5.2  
-----
```

```
samtools/1.16.1  
sra-toolkit/3.0.0  
star/2.7.10b
```

```
plink2/2.00a2.3  
qiime2/2023.5  
qiime2/2024.2_amplicon
```





# Bioinformatics modules on Alpine

---

```
alphafold/2.2.0  
alphafold/2.3.1 (D)  
bamtools/2.5.2
```

---

```
samtools/1.16.1  
sra-toolkit/3.0.0  
star/2.7.10b
```

```
plink2/2.00a2.3  
qiime2/2023.5  
qiime2/2024.2_amplicon
```

---

```
cutadapt/4.2  
fastqc/0.11.9  
gatk/4.3.0.0
```

---

```
bowtie2/2.5.0  
bwa/0.7.17  
cellranger/7.1.0
```

```
nextflow/22.10.6  
nextflow/23.04  
picard/2.27.5
```



# Bioinformatics modules on Alpine

---

```
alphafold/2.2.0  
alphafold/2.3.1 (D)  
bamtools/2.5.2
```

---

```
samtools/1.16.1  
sra-toolkit/3.0.0  
star/2.7.10b
```

```
plink2/2.00a2.3  
qiime2/2023.5  
qiime2/2024.2_amplicon
```

---

```
cutadapt/4.2  
fastqc/0.11.9  
gatk/4.3.0.0
```

---

```
bowtie2/2.5.0  
bwa/0.7.17  
cellranger/7.1.0
```

```
nextflow/22.10.6  
nextflow/23.04  
picard/2.27.5
```

---

```
bbtools/39.01  
bcftools/1.16  
bedtools/2.29.1
```

---

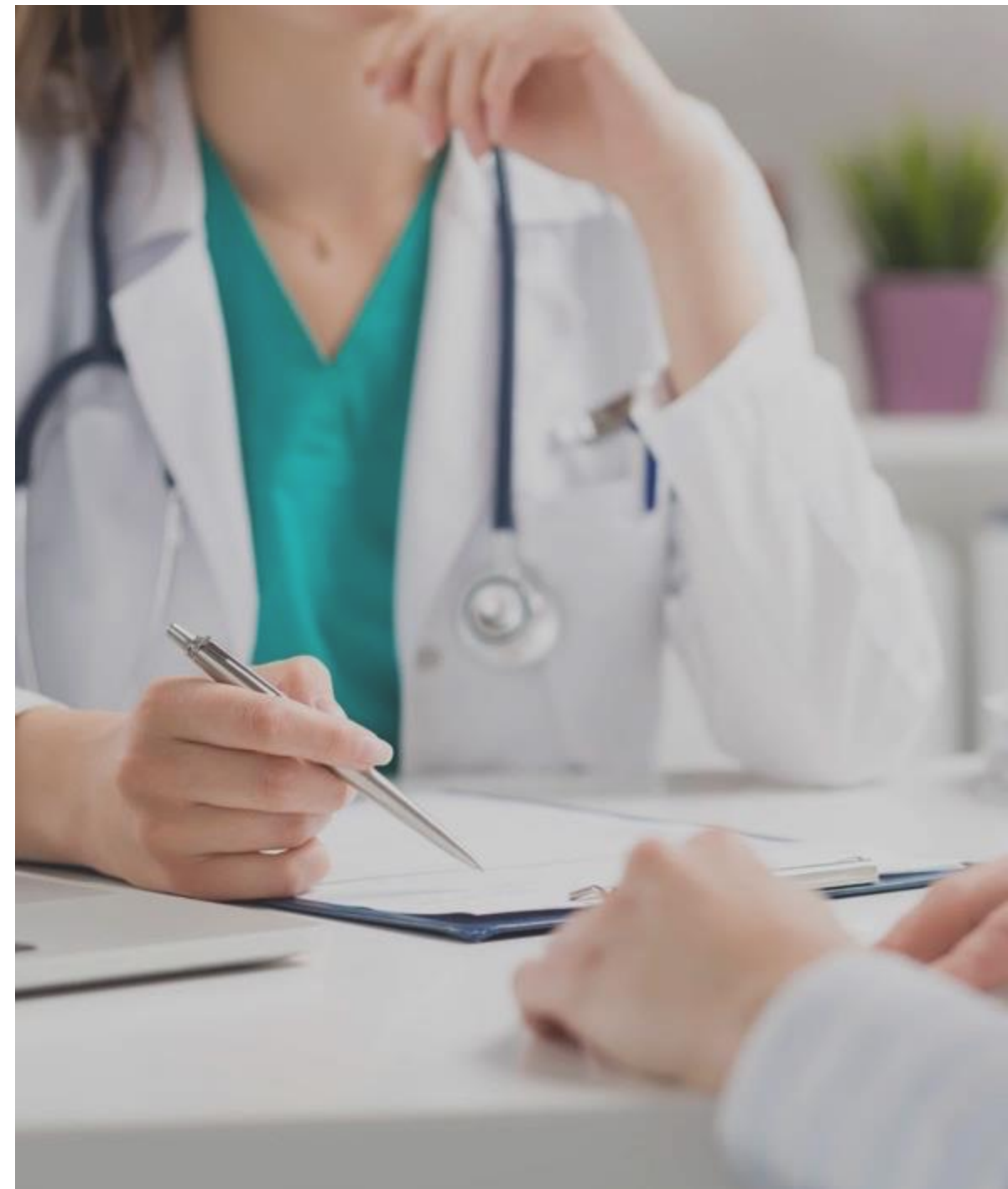
```
homer/4.11  
htslib/1.16  
multiqc/1.14
```

```
trimmomatic/0.39
```



# Many more ...

- We will work with you to build any publicly available module not discussed here.





# VIII- Workshops



University of Colorado  
Anschutz Medical Campus



# Workshops

- On many aspects of Research computing (Introduction to the cluster, Deep learning, parallel computing, Package installation etc ... )

1<sup>st</sup> workshop to get started



2<sup>nd</sup> workshop to get started



## VI- Lab workshops:

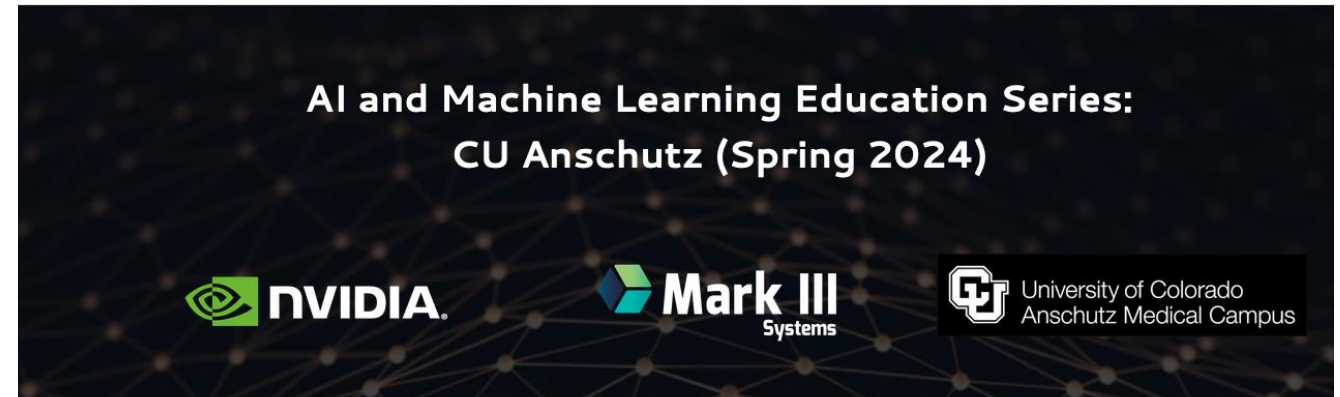
Workshops given to customized to labs that have been already given. Send an email to [rc-help@colorado.edu](mailto:rc-help@colorado.edu) to request a workshop.

- List of workshops:
  - [NVIDIA Mark III Sys workshop series \(05/04/23 to 06/22/23\)](#). Additional information can be found [here](#).
  - [Introduction to the Shell - Barocas lab](#)
  - [Introduction to Slurm - Barocas lab](#)
  - [Introduction to Alpine - Kalpathy-Cramer lab](#)
  - [Introduction to Slurm and Petalibrary - Lange lab](#)
  - [GPU partitions on Alpine Janani lab 090623](#)
  - [Alpine entry level workshop 090723](#)
  - [Immuno 6110 class 090723](#)
  - [Intro to spack part 1 10/17/23](#)
  - [Intro to Horovod part 1 10/24/23](#)
  - [Alpine entry level workshop 110223](#)
  - [Intro to GPU computing part 1 112823](#)
  - [Intro to GPU computing part 2 113023](#)
  - [Intro to GPU computing part 3 120423](#)
  - [Alpine for noobs workshop 120723](#)
  - [AMD\\_GPU\\_computing\\_022924](#)
  - [Alpine\\_entry\\_level\\_workshop\\_030524](#)
  - [NVIDIA Mark III Sys workshop series Spring 2024 \(01/25/24 to 05/02/24\)](#)

# Workshops

- NVIDIA collaborations with trainings in bioinformatics, Machine learning, containers, and LLMs.

HOME



NVIDIA and Mark III Systems would like to host an AI/Machine Learning Education Series for CU Anschutz and its greater community in Spring 2024. This bi-weekly education series is 100% virtual and will include both tutorials and virtual "rapid labs" for attendees delivered via Jupyter Notebook. There will be a series of sessions that will feature industry experts in Machine Learning, who will dive into current trends around AI/ML. We hope you can join us!

## AI/ML Education Series:

### Replays (Past Sessions):

Thursday, Jan 25th (12pm-1pm MT)

Introduction to Machine Learning and AI:  
What is it and why we do we need it?

**Speaker:** Data Scientist, Mark III

In this session, we'll cover the basics around what Machine Learning is, look at the different ML techniques and methods, examine what a typical ML project lifecycle looks like, and discuss some of the most commonly used example algorithms

Replay Session





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**THANK YOU**