

Research Computing
Orientation for Courses

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UF Information Technology









Course use of HiPerGator The University of Florida Supercomputer for Research

- Course is allocated 32 cores, 256GB RAM, 2TB Blue storage,
 GPUs as needed
 - Design projects with this in mind
 - Time your work with this in mind
 - Use resources efficiently
- Support requests should go through course TA
 - If TA cannot solve the issue, the TA should open support requests
- By using your account, you agree to the AUP
 - http://www.rc.ufl.edu/about/policies/
 - No restricted data





HiPerGator Account Training

- Content and links at: <u>help.rc.ufl.edu/doc/New_user_training</u>
 - Page also has additional information for classes at the end



UFRC Help and Documentation

Welcome to the University of Florida Research Computing Help and Documer Site. General information, announcements, and purchase request forms are on our main web site. The information here is focused an information formation, services, and usage examples. Provide Feedback.



FOR NEW USERS

Guides to get you started with HPC est practices!

Getting Started | Training Videos | Trainings & Events | Interactive Development and Testing | Practical Storage Use



ACCESS

How to connect to HPG with Duo, authenticate multiple connections, or check account.

Multi-Factor Authentication | SSH Multiplexing | SSH Keys | Blocked Accounts | Federated Access and Login



HELP

Resources to ask questions, get support, or communicate directly.



INTERFACES

Guides for GUI/web interfaces you can run on HPG.

Jupyter (Python, R) | Galaxy Genomics

UF Information Technology

https://help.rc.ufl.edu/



For users with an account

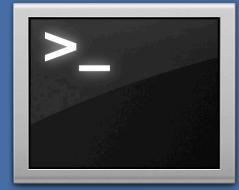
- If you already have a Research Computing account for research:
 - Make a folder for yourself at /blue/pre1234/<gatorlink>
 - When submitting jobs, add:
 - --account=pre1234 --qos=pre1234





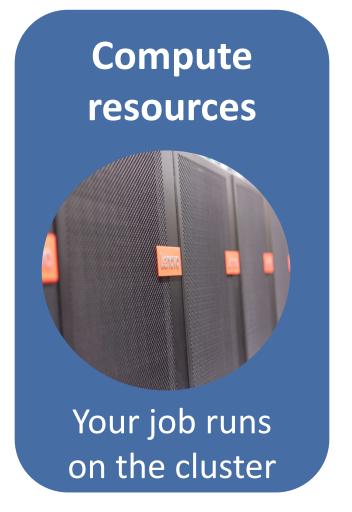
Cluster overview

User interaction



Login node (Head node)

SLURM Scheduler Tell SLURM what you want to do



Tools for working with HiPerGator

ssh client to connect to hpg.rc.ufl.edu



SFTP client to move files to/from your computer

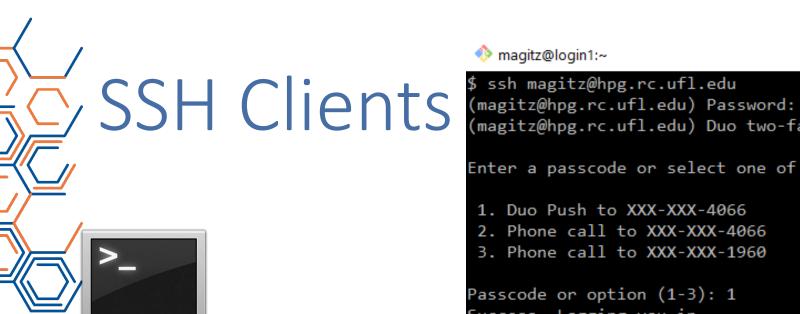
hpg.rc.ufl.edu



Text editor

Especially on Windows, be sure to convert DOS line breaks to Unix, and *don't use Word*





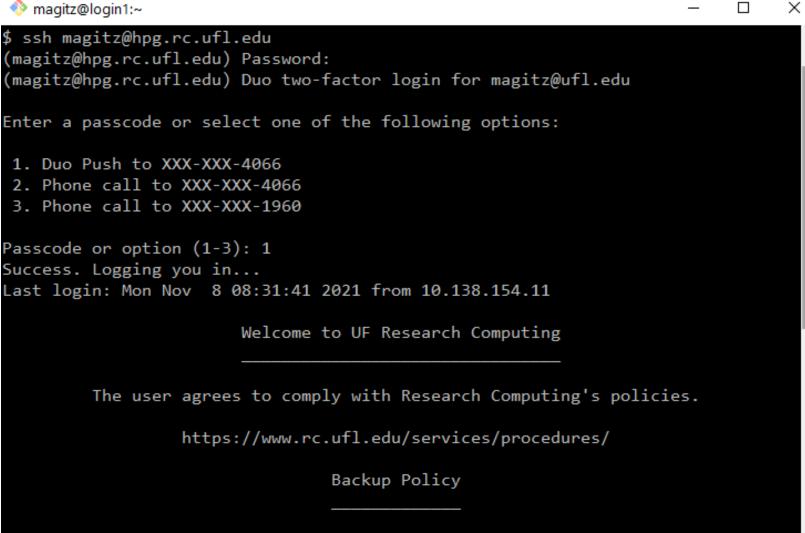
Mac/Linux: Terminal







Windows: Git Bash, MobaXterm, PuTTY, Bitvise



ssh user@hpg.rc.ufl.edu







npg.tlp - magitz@hpg.rc.ufl.edu:22 - Bitvise SSH Client —												×
Profile: hpg.tlp												
(*)	Login	Options	Terminal	RDP	SFTP	Service	s C2S	S2C	SSH	Notes	About	
	Server						Authentication					
Save profile	Host hpg.rc.ufl.edu						Userna	magitz	nagitz			
	Port 22 Enable obfuscation						Initial method		keyboard-interactive ∨			
Save profile as	Obfuscation keyword						Submethods bsdauth,pam			,pam,tot	p,pw,p\	
Carrier 1	Kerberos						Elevation De		Default	Default v		
Bitvise SSH	SPN											
Server Control	GSS/Kerberos key exchange											
Panel	Request delegation											
	gssapi-keyex authentication											
New terminal console	Prox	cy settings		<u>Host k</u>	ey mana	<u>qer</u>	Client k	ey man	<u>ager</u>		Е	<u>lelp</u>

Initial method: keyboard-interactive





ood.rc.ufl.edu

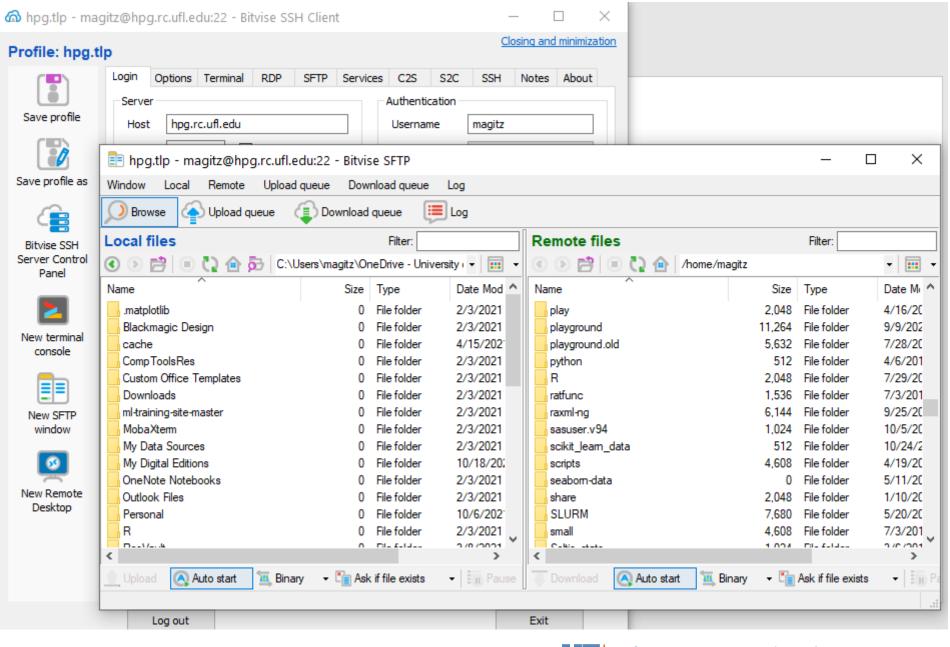






SFTP Client

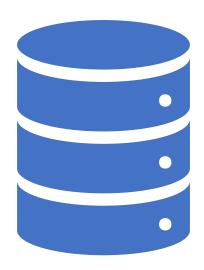






Storage on HiPerGator

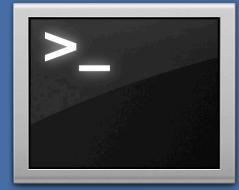
- •Home storage: /home/<user>
 - 40GB limit
 - Scripts, code, compiled applications
 - Do NOT use for job input/output
 - Week of snapshots at ~/.snapshot/
- •Blue storage: /blue/pre1234/<user>
 - 2TB limit per class
 - ALL input/output from jobs should go here
- All storage systems are for research and coursework data only
- Nothing is backed up
- All course accounts are deleted at the end of the semester





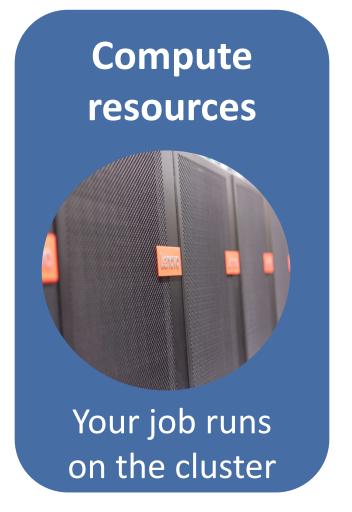
Cluster overview

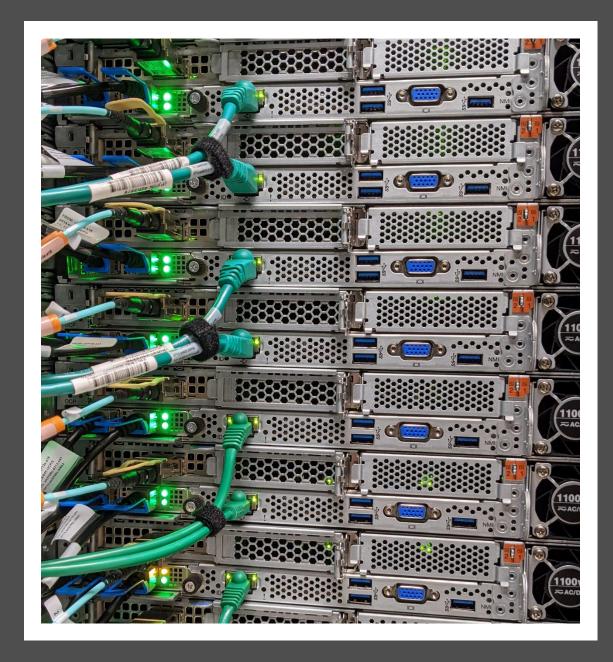
User interaction



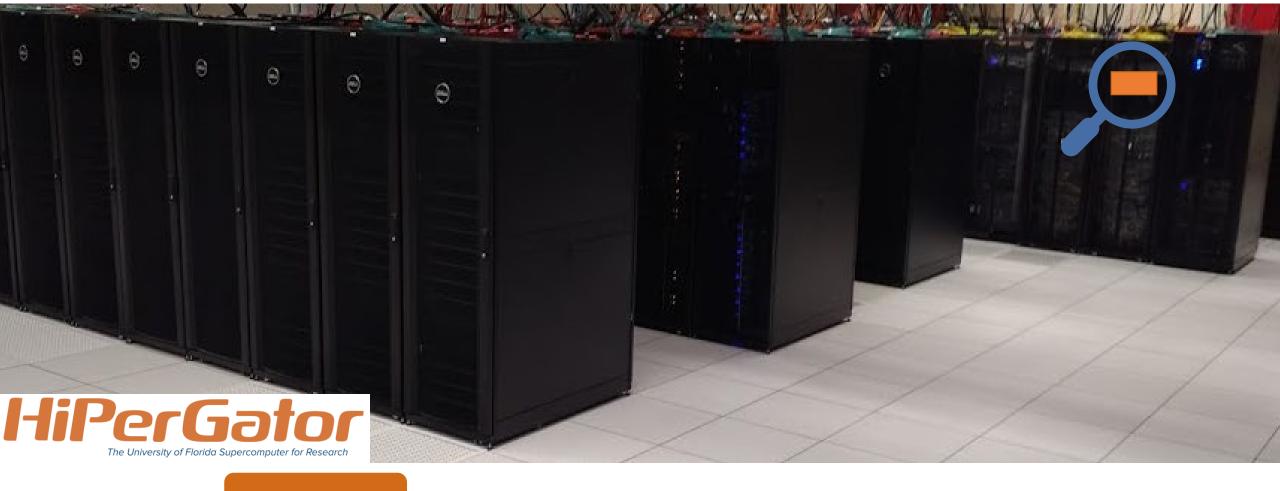
Login node (Head node)

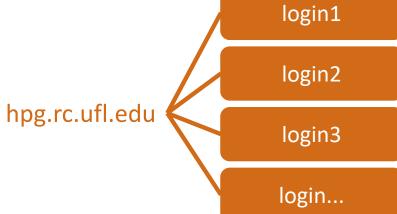
SLURM Scheduler Tell SLURM what you want to do











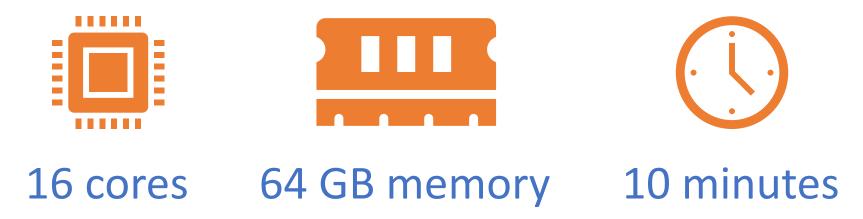


UF Information Technology



Appropriate use of login nodes

- Login nodes are for:
 - File and job management
 - Short-duration interactive testing and development
- Limit your use to **no more than**:





Resources

Development servers

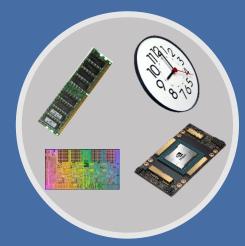


GPU Servers









Tell SLURM what you want to do





GUI servers



Batch compute resources





Jupyter Hub and on Demand

jhub.rc.ufl.edu ood.rc.ufl.edu



To setup link to the class blue directory, open a Terminal (File> New > Terminal) and run (e.g. for class ast4930):

ln -s /blue/ast4930 blue_ast4930



Jupyter and conda environments

Be careful with pip install

- Can lead to conflicting versions of packages
- pip installs packages in
 ~/.local/lib/python3.x/site-packages

Use conda/mamba

- Create isolated environments
- To use in Jupyter, create custom kernel folder. See help page.
- To use in script:

```
module purge; module load conda
conda activate my_env
python my_script.py
```

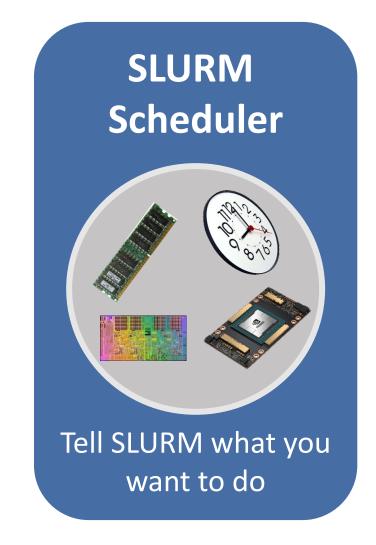
Script should start with:
#!/usr/bin/env python





Scheduling a job

- What resources does your job need?
 - How many CPUs you want and how you want them grouped?
 - How much RAM your job will use?
 - How long your job will run?
 - How many GPUs?
 - Also need the commands that will be run to do your work

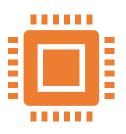


Basic SLURM job script

```
#!/bin/sh
#SBATCH --cpus-per-task=1
                                     # Run on a single CPU
#SBATCH --mem=1qb
                                     # Memory limit
   #SBATCH --time=00:05:00
                                     # Time: hr:min:sec
                                     # Job name
   #SBATCH --job-name=job test
   #SBATCH --mail-type=ALL
                                     # Mail events
   #SBATCH --mail-user=email address # Where to send mail
   #SBATCH --output=serial %j.out
                                     # Output and error log
   pwd; hostname; date # Print some information
   module load python # Load needed modules
   echo "Running plot script on a single CPU core"
   python /data/training/SLURM/plot template.py
                         # Print ending time
   date
```

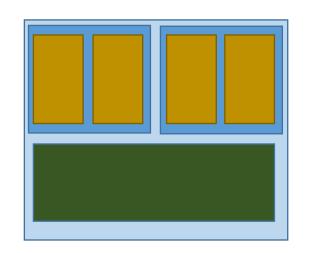


SLURM CPU Requests



For threaded applications (single node):

```
#SBATCH --nodes=1 # Physical servers
#SBATCH --ntasks=1 # MPI ranks or processes
#SBATCH --cpus-per-task=8
```









SLURM GPU Requests



```
#SBATCH --partition=gpu # required for GPUs #SBATCH --gpus=1
```

```
#SBATCH --gpus=a100:1 #Specify type
```

See: https://help.rc.ufl.edu/doc/GPU Access

Cluster partition (--partition, -p)

gpu

Select a specific cluster partition for job. (default = first available compute partition)

Generic Resource Request (--gres).

gpu:a100:1

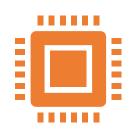
--gres: gpu:a100:1

This is the Generic resource request string to request GPU resources. See also https://help.rc.ufl.edu/doc/GPU_Access

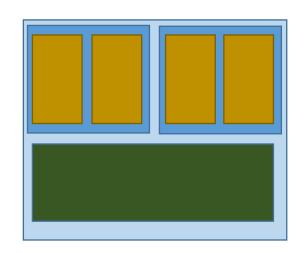


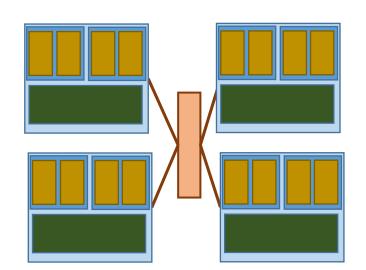


SLURM CPU Requests



- Parallel applications
 - OpenMP, Threaded, Pthreads
 - All cores on one sever, shared memory
 - MPI—Message Passing Interface
 - Can use multiple servers
 - See: help.rc.ufl.edu/doc/Sample SLURM Scripts

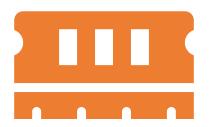








SLURM Memory Requests



- --mem=1gb (total memory)
- --mem-per-cpu=1gb (memory per core)
 - Can use mb or gb
 - No decimal values: use 1500mb, not 1.5gb

HPG 2.0

120

GB RAM

HPG 3.0

1000

GB RAM





SLURM Time Request



- Time: --time or -t
 - **■**120 (minutes)
 - **2**:00:00 (hh:mm:ss)
 - ■7-0 (days-hours)
 - -7-00:00 (days-hh:mm)
 - -7-00:00:00 (days-hh:mm:ss)



Quality of Service (--qos)

- Each group has two QOS options
 - Investment QOS: --qos=group
 - Burst QOS:
 - The burst capacity, available when idle resources are available on the cluster
 - --qos=group-b
- Users can choose higher priority, or larger pool of resources

Compute allocation

nvestment

Burst capacity (up to 9X investment)

Lower priority access to idle resources as available

SLURM

Note that multi-letter directives are double-dash:

```
sbatch: error: distribution type
--ntasks
'ail-type=ALL' is not recognized
```

- --mem-per-cpu
- Use either, but not both, space or =
 - ■--mail-user=magitz@ufl.edu 🗸
 - --mail-user magitz@ufl.edu 🗸
 - not: --mail-user= magitz@ufl.edu

Submit your job

```
[magitz@login3 SLURM_examples]$ sbatch single_job.sh
Submitted batch job 30592170

[magitz@login3 SLURM_examples]$ squeue --me

JOBID PARTITION NAME USER ST TIME NODES NODELIST(REASON)
30592170 hpg2-comp serial_j magitz R 0:30 1 c24b-s15
[magitz@login3 SLURM examples]$
```





- Applications
- Essentials
- ▶ Help
- ▶ Infrastructure
- Scheduler
- Services

Tools

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How To Get Help | Al Help | FAQ | Submit a Support Request | HiPerGator Metrics



INTERFACES

Guides for GUI/web interfaces you can run on HPG.

Jupyter (Python, R) | Galaxy Genomics Framework | OnDemand (Matlab, RStudio,...) | Conda and Jupyter Kernels | Running GUI Apps



SCHEDULER

How to schedule and manage jobs and resources on



SOFTWARE AND REFERENCE DATA

help.rc.ufl.edu

UF Information Technology



Training

▶ Scheduler

E Servicea Tools

Recent changes

Training Videos

Quick How Tos [add]

The following videos are designed to provide quick help for users on various topics, most are only a few minutes long.

Please let us know if there are additional topics that you feel would be useful for a quick help video.

In addition to the pre-recorded content, we also provide in-person training sessions. Visit the main training page for additional training information.

Connecting to HPG [edit

SSH From MacOS

SSH From Windows

Jupyter Hub

Open On Demand

Read Edit View history * More V Search UFRC

Data Transfer [odt]

SAMBA Access On MacOS

SAMBA Access On Windows

Globus Data Transfer

Globus Connect Personal

Globus Shared End-points

Other How Tos [adit]

File Restoring Snapshots

Automounted **Directories** Demo

SLURM Job Arrays Submitting **Purchase** Requests

Recorded Trainings [odt]

HIPerGator Account Training [adt]

All new HiPerGator users are required to take the HiPerGator Account training: Link and overview on this page.

Introduction to Research Computing and HIPerGator [edit

Intended for new users, this training provides a general overview of the UF Research Computing facilities and basic usage of HiPerGator.

This training is available in three parts:

- Part 1: Intro to UF Research Computing and HiPerGator®
- Part 3: Working with the SLURM Scheduler to run Jobs@

Or as a recording of the most recent Zoom session:

You can download a copy of the slides used from hereig.

Introduction to the Linux Command Line | judt|

This session will lead participants through some exercises that go over basic Linux commands such as moving around the file system, making directories, moving and copying files, etc. We will also go over some of the applications you can use on your computer to connect to and move files to and from HiPerGator. This session is largely aimed at users who are new to the Command Line.

This session is available as a pre-recorded video or zoom recording: (5)



The handout and files for the session are now located in a git repository here: https://github.com/UFResearchComputing/Linux_trainingtiff

The handout can be downloaded as a PDF file @.

The molecules folder used in the training is at /data/training/LinuxCLI/molecules

For those wishing to use this training outside of HiPerGator, the molecules folder is in the repository in the /data folder. There are also directions for non-HiPerGator use in the non-HiPerGator, mdi@ file or as a PDFig. The repository can be downloaded to you own computer

HIPerGator: SLURM Submission Scripts for MPI Jobs [add]

This session will go into depth on the details of scheduling MPI jobs on HiPerGator. Efficiently running MPI applications requires an understanding of both how to specify the needed resources as well as the layout and properties of the available hardware. This session will provide examples from several commonly used applications and provide guidelines for users to optimize their own runs.

This video is approximately 25 minutes and includes a demonstration.



The files used in this video are on the Sample_SLURM_Scripts page and on the cluster in /data/training/SLURM/

Recording of the October 6th, 2022 session # Note due to Hurricane Ian, this session includes both the non-MPI and the MPI content.

Running Graphical Applications on HiPerGator [adt]

Users can run applications with graphical user interfaces (GUI) on HiPerGator either using Open on Demand or using the gui module and submitting jobs from the command line.

This video provides and overview of Open on Demand, which offers many GUI applications: [5 min, 11 sec]

This video reviews launching additional GUI applications using the gui module to submit jobs from the command line: [5 min, 16 sec]

A recording of the most recent Zoom session, coving both Open on Demand and gui module is also available:

The GUI Programs page has additional information.

Running MATLAB on HiPerGator [adit]

Users walk through a hands-on examples using MATLAB at Research Computing. Participants will work with the MATLAB GUI, compiling code and submitting MATLAB jobs to the scheduler to run on the cluster.

This video is approximately 24 minutes and includes a demonstration.





