

High Performance Computing (HPC) on GACRC Sapelo2 Cluster

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Outline

- GACRC
- What is High Performance Computing (HPC)?
- What is a Cluster?
- How to Work on Cluster?



GACRC

- A high-performance-computing (HPC) center at the UGA
- Provide to the UGA research and education community an advanced computing environment:
 - HPC computing and networking infrastructure located at the Boyd Data Center
 - Comprehensive collection of scientific, engineering and business applications
 - Consulting and training services

Wiki: http://wiki.gacrc.uga.edu

Support: https://uga.teamdynamix.com/TDClient/Requests/ServiceCatalog?CategoryID=11593

Web Site: http://gacrc.uga.edu



What is High Performance Computing?



10 years later.....



1 worker

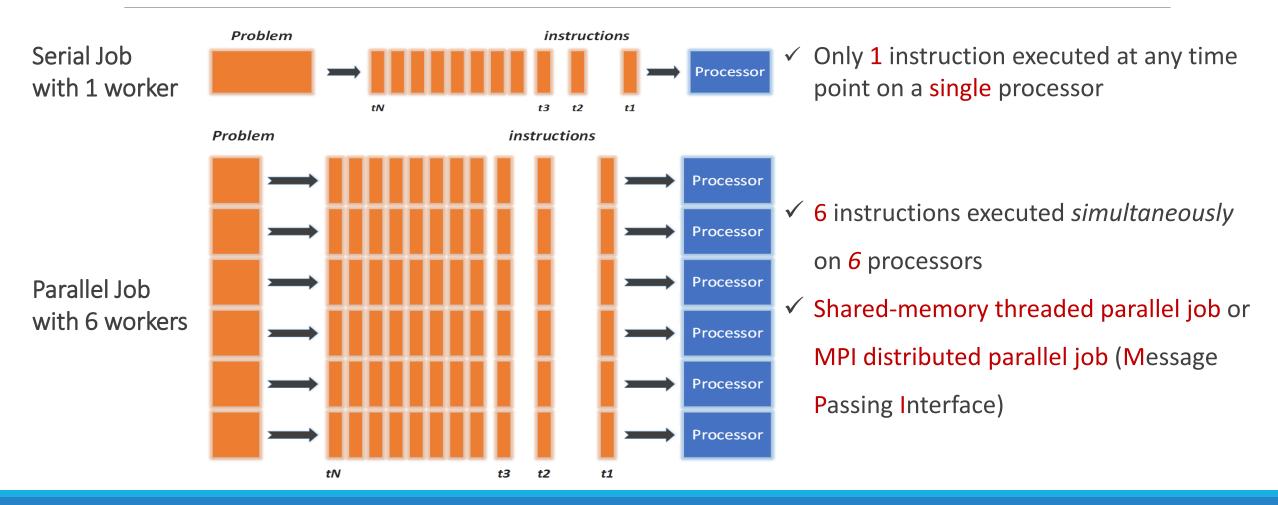


What is High Performance Computing? (cont.)





What is High Performance Computing? (cont.)

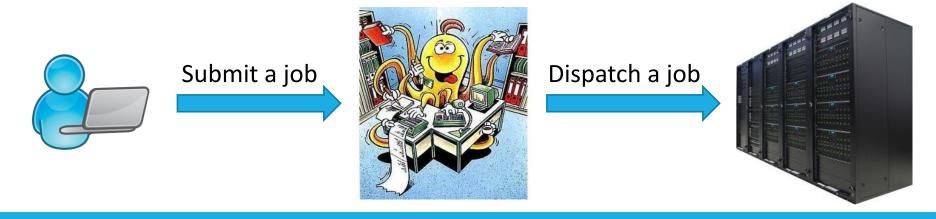


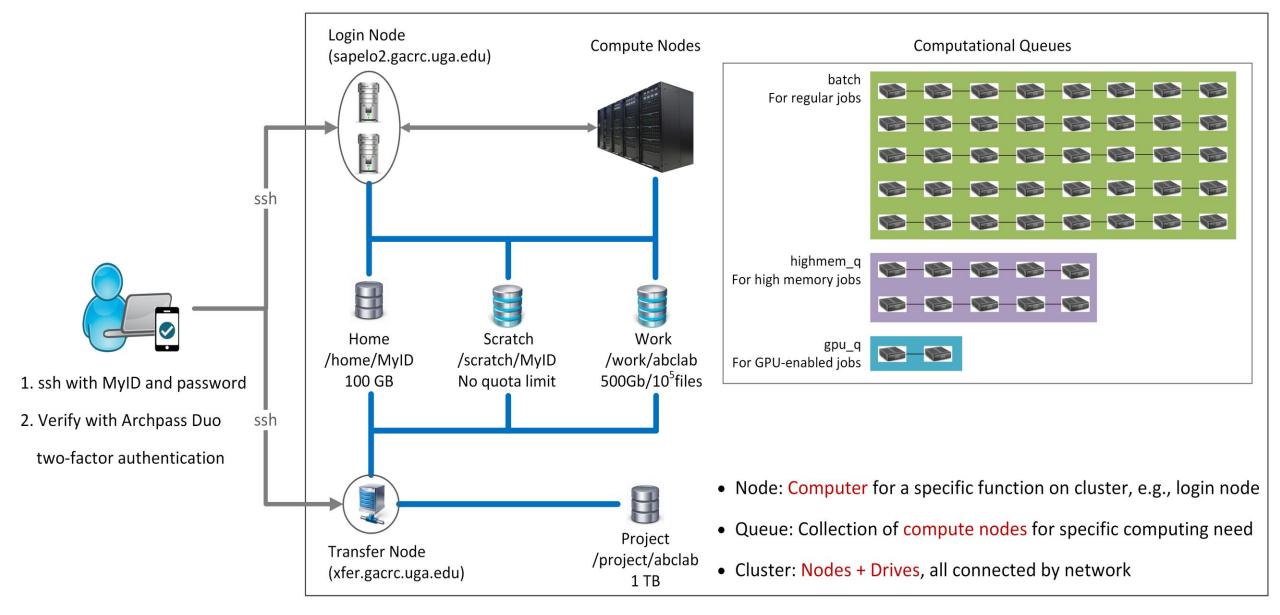


What is a Cluster?

When you work on cluster, 3 roles are working:

- You: Who submit a job
- Queueing System: Who dispatch your job to run on cluster
- Cluster: Who run your job





Please Note: You need to connect to the UGA network using VPN when accessing from outside of the UGA main campus.

UGA VPN: https://eits.uga.edu/access and security/infosec/tools/vpn/



Overview https://wiki.gacrc.uga.edu/wiki/Systems#Sapelo2

- Two Nodes:
 - Login node for batch job workflow: MyID@sapelo2.gacrc.uga.edu
 - 2. Transfer node for data transferring: MyID@xfer.gacrc.uga.edu
- > Five Directories:
 - 1. Home: Login landing spot; 100GB quota; Backed-up
 - 2. <u>Scratch</u>: High-speed storage for <u>temp files</u> needed for <u>current jobs</u>; NO quota; NOT backed-up
 - 3. <u>Work</u>: High-speed storage for <u>input files</u> needed for <u>repeated jobs</u>; per group quota of 500GB and max 100,000 single files; NOT backed-up
 - 4. <u>Project</u>: Temporary data parking; per group quota of 1TB; Backed-up (ONLY accessible from Transfer node!)
 - 5. Local Scratch: Local storage on each individual compute node; 200GB quota; NOT backed-up
- Four Computational Queues: batch, highmem_q, gpu_q, groupBuyin_q



Overview (cont.)

- To connect to cluster, you need to have a user account:
 - 1. Group PI request a user account for you: http://help.gacrc.uga.edu/userAcct.php
 - 2. You need to pass new user training: https://wiki.gacrc.uga.edu/wiki/Training
 - 3. We send you a welcome letter with detailed info about your Sapelo2 user account
- Once your account is provisioned, use SSH Secure Shell program to open connection: https://wiki.gacrc.uga.edu/wiki/Connecting



How to work on cluster?

Your job working space is global scratch folder /scratch/MyID/

Why?

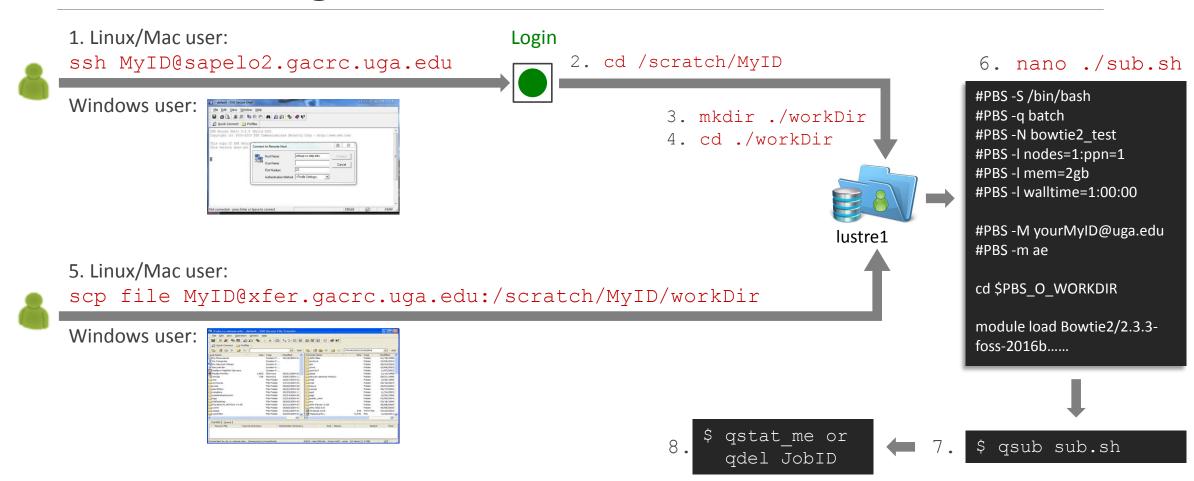
High-performance filesystem with the fastest I/O!



- How to access?
 - From Login node, cd /scratch/MyID
- What do you need?
 - Software! We installed ~1000 software on cluster for you. Check if the software you need is already installed at https://wiki.gacrc.uga.edu/wiki/Software
- What do you need to pay attention to?
 Clean up data you will not need after your job is finished!



Workflow Diagram



Useful Links

- GACRC Web: http://gacrc.uga.edu/
- GACRC Wiki: https://wiki.gacrc.uga.edu/wiki/Main_Page
- GACRC FAQ: https://wiki.gacrc.uga.edu/wiki/Sapelo2 Frequently Asked Questions
- GACRC Help: http://gacrc.uga.edu/help/
- GACRC Training: https://wiki.gacrc.uga.edu/wiki/Training
- GACRC User Account: https://wiki.gacrc.uga.edu/wiki/User Accounts
- GACRC Software: https://wiki.gacrc.uga.edu/wiki/Software

Thank You!