Biomedical Research Computing Facility Users Home

Welcome to the Biomedical Research Computing Facility (BRCF) Users wiki! Formerly known as the Research Computing Task Force (RCTF), the BRCF now has an official organizational home in the Center for Biomedical Research Support (CBRS).

> ***Our mission: Biomedical Research Computing Facility (BRCF) "PODs" (small compute clusters) provide a standard hardware, software and storage architecture, suitable for local, interactive biomedical research computing, that can be efficiently managed.***

Upcoming Maintenance

POD maintenance schedule for May 2024

- ***All BRCF research POD and the EDU pod: 8am - 6pm Tuesday May 21***

Python version updates

After the January 2024 maintenance JupyterHub Python version is now 3.9 on all compute servers. Python 3.9 is also available on the command line by calling it explicitly: i.e., **python3.9**; the default command line **python3** version is still 3.8.

Many Python packages were also updated, in both the Python 3.8 and 3.9 command line environments as well as in the JupyterHub Python 3.8 environment. Please contact us at rctf-support@utexas.edu if you experience Python-related issues.

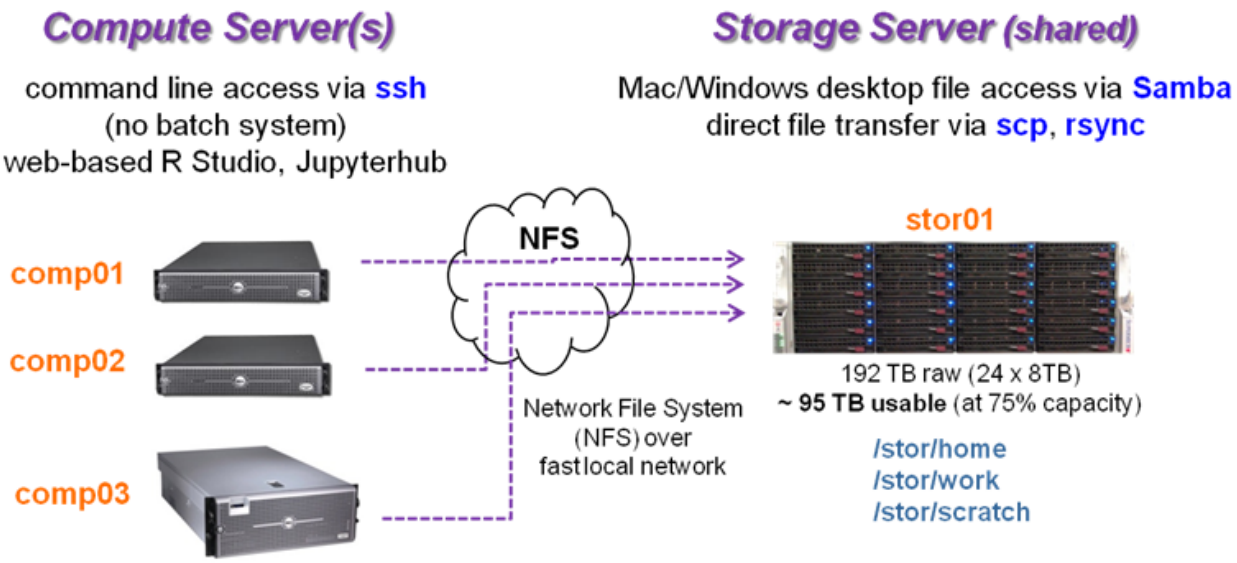
See this Wiki page for more information about Python on BRCF pods: About Python and JupyterHub server

Quick links

Architecture Overview

BRCF provides local, centralized storage and compute systems called PODs. A POD consists of one or more ***compute servers*** along with a shared ***storage server***. Files on POD storage can be accessed from any server within that POD.

A graphic illustration of the BRCF POD Compute/Storage model is shown below:



Features of this architecture include:

- A large set of Bioinformatics software available on *all* compute servers
  - interactive (non-batch) environment supports exploratory analyses and long-running jobs
  - web-based R Studio and JupyterHub servers implemented on all compute servers
- Storage managed by the high-performance **ZFS** file system, with
  - built-in data integrity, superior to standard Unix file systems
  - large, contiguous address space
  - automatic file compression
  - RAID-like redundancy capabilities
  - works well with inexpensive, commodity disks
- Appropriate organization and management of research data
  - weekly backup of Home and Work to spinning disk at the UT Data Center (UDC)
  - periodic archiving of backup data to TACC's **ranch** tape archive system (~yearly)
- Centralized deployment, administration and monitoring
  - OS configuration and 3rd part software installed via the **Puppet** deployment tool
  - global BRCF user and group IDs, deployable to any POD
  - self-service Account Management web interface
    - http://rctf-account-request.icmb.utexas.edu/
  - OS monitoring via **Nagios** tool
  - hardware-level monitoring via Out-Of-Band Management (OOBM) interfaces
    - IMPI, iDRAC

BRCF Architecture goals

The Biomedical Research Computing Facility (BRCF) is a core facility in UT's Center for Biomedical Research Support (CBRS), under the Office of the Vice President of Research. Our small compute clusters, known as "PODs", provide a standard hardware, software storage architecture, suitable for local research computing, that can be efficiently managed.

The BRCF grew out of the earlier Research Computing Task Force (RCTF) working group of IT-knowledgeable UT staff and students from CSSB, GSAF and CCBB. Today OurTeam consists of staff from Molecular Biosciences, CBRS, and the College of Natural Sciences Office of Information Technology (CNS-OIT).

Broadly, our goals are to supplement TACC's offerings by providing extensive local storage, including backups and archiving, along with easy-access non-batch local compute.

Before the BRCF initiative, labs had their own legacy computational equipment and storage, as well as a hodgepodge of backup solutions (a common solution being "none"). This diversity combined with dwindling systems administration resources led to an untenable situation.

The Texas Advanced Computing Center (TACC) provides excellent computation resources for performing large-scale computations in parallel. However its batch system orientation is not well suited for running smaller, one-off computations, for developing scripts and pipelines, or for executing very long-running (> 2 days) computations. While TACC offers a no-cost tape archive facility (**ranch**), its persistent storage offerings (**corral**, global **work** file system) can be cumbersome to use for collaboration.

The BRCF POD architecture has been designed to address these issues and needs.

- Provide adequate local storage (spinning disk) in a large, non-partitioned address space.
  - Implement some common file system structures to assist data organization and automation
- Provide flexible local compute capability with both common and lab-specific bioinformatics tools installed.
  - Augment TACC offerings with non-batch computing environment
  - Be robust and "highly available" (but 24x7 uptime *not* required)

- Provide automated backups to spinning disk and periodic data archiving to TACC's **ranch** tape system.
- Target the "sweet spot" of cost-versus-function commodity hardware offerings
  - Aim for rolling hardware upgrades as technology evolves
- Provide centralized management of POD equipment
  - Automate software and configuration deployment and system monitoring
  - Make it easy to deploy new equipment

Recent Changes

R version updates

After the August 15, 2023 maintenance the default R version is **R 4.3.1** both for RStudio Server on all compute servers, and on the command line. See About R and R Studio Server for more information.

OS upgrade changes

In March 2023, the BRCF completed upgrading the Operating System (OS) software on all our POD servers. See this page for important information about how this change may affect you: Winter 22-23 OS Upgrades.

Change to SSH key access

After the Tuesday June 28, 2022 maintenance, remote SSH access to POD compute servers ***no longer uses non-standard port 222***. Instead, uses standard port 22, so no port (**-p**) option is required in the **ssh** command.

Recently Updated

POD Resources and Access
May 05, 2024 • updated by Anna M Battenhouse • view change
Biomedical Research Computing Facility Users Home
May 05, 2024 • updated by Anna M Battenhouse • view change
GPU servers
May 01, 2024 • updated by Anna M Battenhouse • view change
POD Software Information
May 01, 2024 • updated by Anna M Battenhouse • view change
About X-Windows applications
Apr 21, 2024 • created by Anna M Battenhouse
About R and R Studio Server
Mar 27, 2024 • updated by Anna M Battenhouse • view change
Archive
Mar 22, 2024 • created by Anna M Battenhouse
FAQ
Mar 22, 2024 • updated by Anna M Battenhouse • view change
GSAF Fourierseq users
Mar 12, 2024 • updated by Anna M Battenhouse • view change
NVIDIA GPU servers
Mar 07, 2024 • updated by Anna M Battenhouse • view change
POD Resources and Access
Mar 04, 2024 • updated by Sean Provost • view change
About Python and JupyterHub server
Jan 21, 2024 • updated by Anna M Battenhouse • view change
AMD GPU servers
Nov 19, 2023 • updated by Anna M Battenhouse • view change
Livestrong and Hopefog pod AMD servers
Nov 19, 2023 • updated by Anna M Battenhouse • view change
The Educational POD
Oct 10, 2023 • updated by Anna M Battenhouse • view change

Navigate space

Recent space activity

Anna M Battenhouse
POD Resources and Access updated May 05, 2024 view change
Biomedical Research Computing Facility Users Home updated May 05, 2024 view change
GPU servers updated May 01, 2024 view change
POD Software Information updated May 01, 2024 view change
About X-Windows applications created Apr 21, 2024

Space contributors

- Anna M Battenhouse (7 days ago)
- Sean Provost (69 days ago)
- Eric J Rostetter (501 days ago)
- Carlos Villarreal (772 days ago)
- Marci Anne Coleman (1109 days ago)
- ...