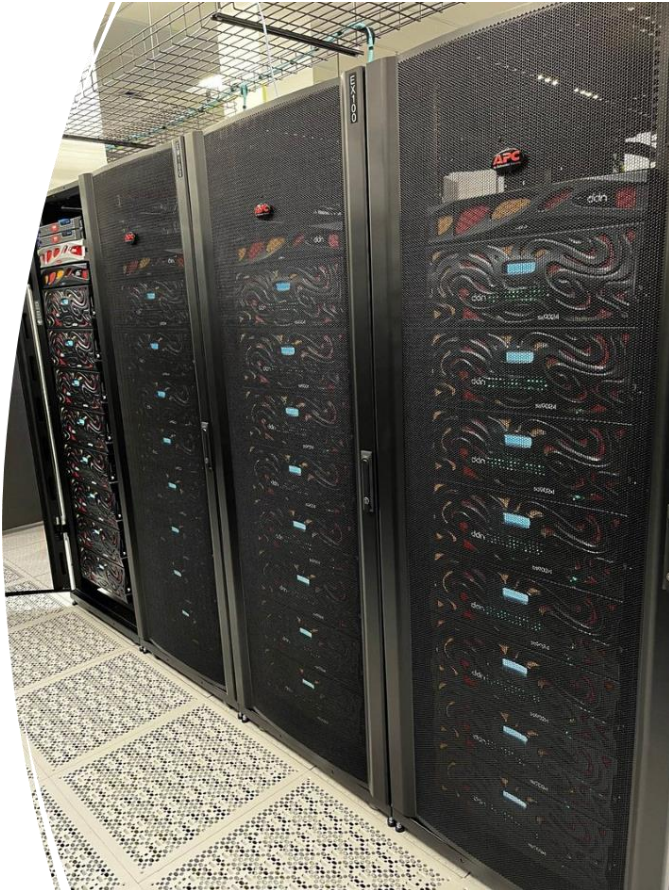


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BioHPC Post-downtime Update

New /project file system and storage roadmap



/home2

user profile

two backups per week



/work

important data

one backup per week



/project

scratch data

performance**



/archive

long term archive data

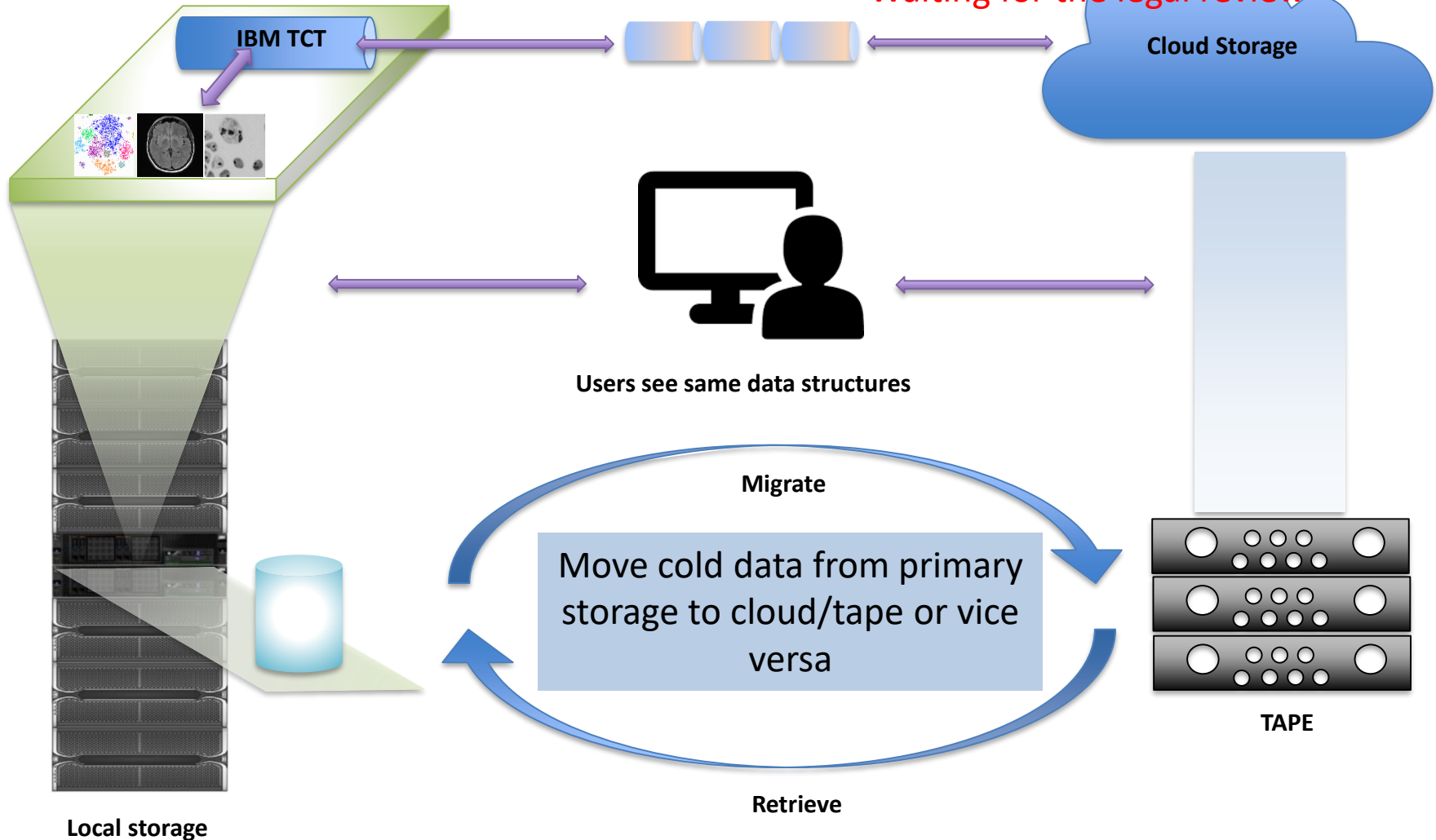
multiple tiers##

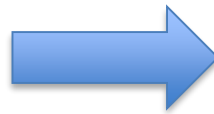
** 20 times faster than /work and /archive); No backup (but PI can request)

if data didn't R/W for one year, move to tape storage system; No backup (but PI can request)

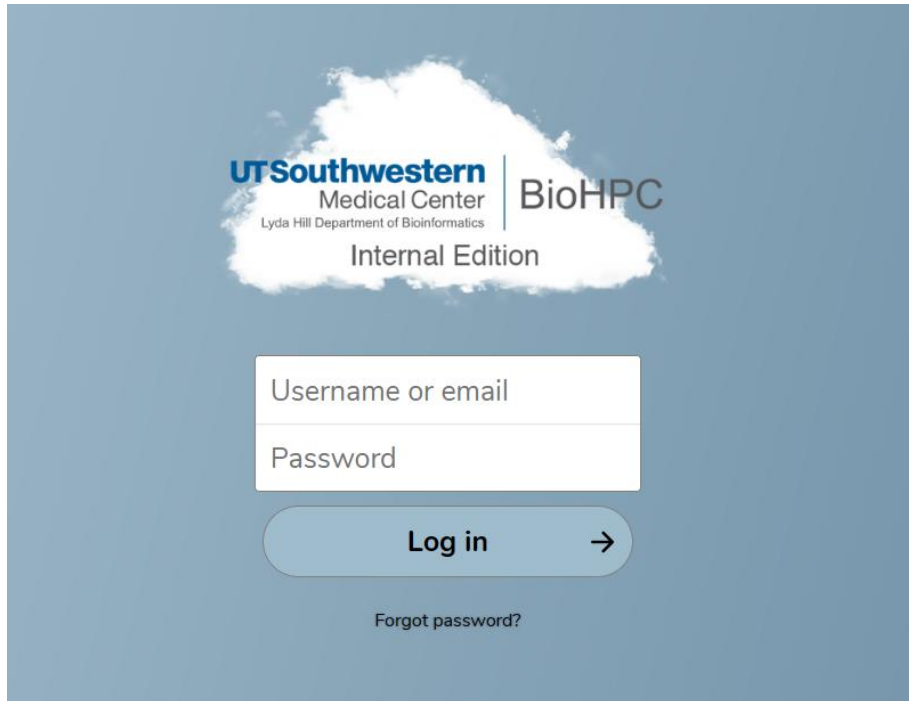
/archive storage -- Single namespace

- upgrade in next two days
- No downtime
- multi-tiers ready
- Waiting for the legal review





Lamella upgrade



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Internal Edition

Username or email

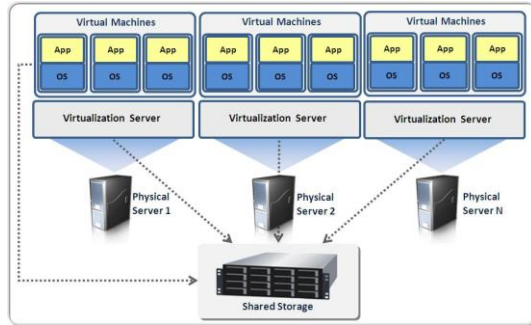
Password

Log in →

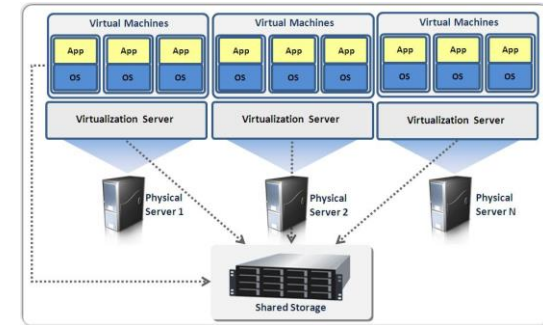
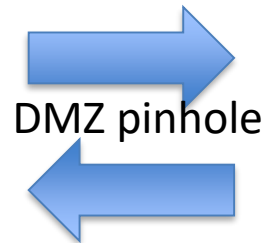
[Forgot password?](#)

- System upgraded
- Security upgraded
- Web interface will upgrade in next two weeks

Virtualizing machine farm upgrade



Campus



DMZ

- Improving service reliability, frequency of updates, shortening downtimes
- Virtual GPUs, other passthrough hardware available

Astrocyte 2.0

BioHPC is UT Southwestern's high performance computing (HPC) group, providing access to HPC systems, support and training to contributing departments. BioHPC maintains a 112 node compute cluster, Nucleus, and large-scale storage systems to support the wide range of computational research at the institution.

A significant focus of BioHPC is providing easy-to-use web based access to our resources, tailored to the needs and experience of a wide range of users. Astrocyte is our in-house workflow platform that allows bioinformaticians to easily deploy their workflows to the web, making use of the nucleus cluster to run them while presenting a simple interface to end users.

BioHPC provides example astrocyte workflows here, as well as working closely with other groups to bring their workflows to astrocyte.

Read more about BioHPC on our [web portal](#).

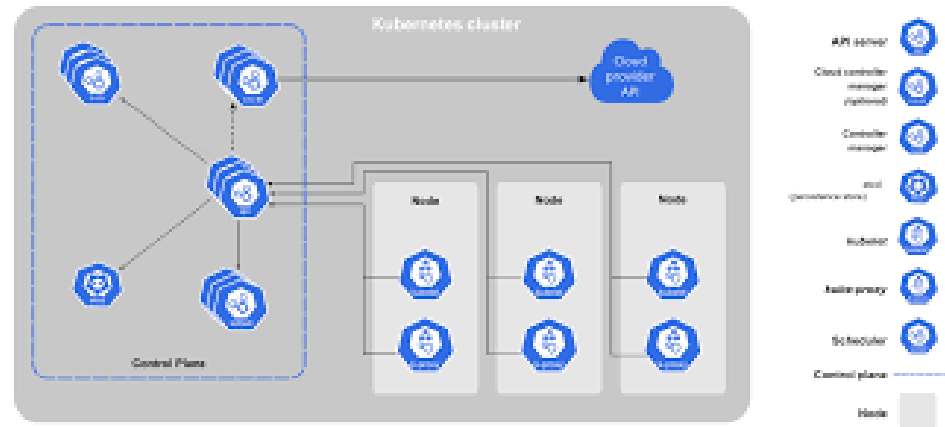
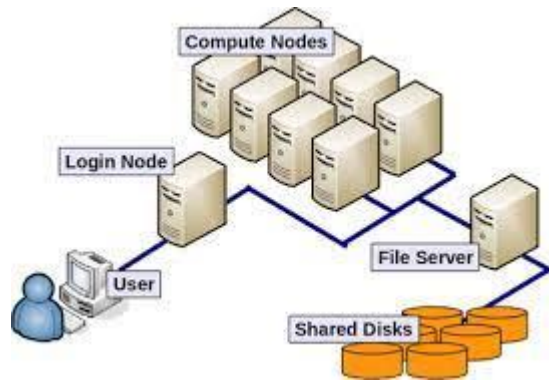
Please email biohpc-help@utsouthwestern.edu with questions or comments about these workflows.

Astrocyte Autodock Workflow Run molecular docking with Autodock and/or Autodock Vina.	Current Version: astrocyte_autodock - 1.2.1 Author: Peng Lian Contact: biohpc-help@utsouthwestern.edu	▶ Run Workflow 📄 Documentation ☰ View Versions
Astrocyte CHARMM-GUI MD Workflow Run MD simulations based on the input files from CHARMM-GUI at https://charmm-gui.org . Build trajectory.vmd for visualizing results.	Current Version: astrocyte_charmmgui_md - 1.2.0 Author: Peng Lian Contact: biohpc-help@utsouthwestern.edu	▶ Run Workflow 📄 Documentation ☰ View Versions
Astrocyte AlphaFold Workflow This workflow is based on AlphaFold 2.1.1 that supports multimer	Current Version: astrocyte_alphafold - 0.0.3 Author: Peng Lian, Xiaochu Lou, Yingfei Chen Contact: biohpc-help@utsouthwestern.edu	▶ Run Workflow 📄 Documentation ☰ View Versions

- Summer to DMZ



Hybrid HPC—rootless podman ready



podman

- Rolling update this/next Month
- No downtime
- Rootless podman

Thank you

