FAQ

• Account Access
  • Q. How do I create an account?
  • A. A step-by-step guide is available on our Account Creation page.
  • Q. Why can't I log in?
  • A. You haven't created an account yet.
  • A. Your account isn't sponsored yet.
  • A. You aren't using two-factor authentication (NetID+).
  • A. You need to wait 15 minutes. If you just created your account, it takes time before you can log in.
  • A. You're trying to connect using ssh NetID@login.hpc.arizona.edu. This will not work. Instead, use: ssh NetID@hpc.arizona.edu.
  • A. You're using NetID@hpc.arizona.edu or NetID@email.arizona.edu as your username in PuTTY. Instead, use only your NetID.
  • Q. I've forgotten my password, how can I reset it?
  • A. HPC uses the same NetID login credentials as all UA services. If you need to reset your NetID password you can do so using the NetID portal: https://netid-portal.iam.arizona.edu
  • Q. How do I add members to my HPC research group?

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  • Q. Why do my jobs keep getting interrupted?
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  • Q. How do I access custom python packages from an OOD Jupyter session?

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  • Q. How do I run a job and get: "Bad UID for job execution"
  • Q. What does this error mean - Insufficient amount of resource: ...
  • Q. My OOD Desktop session failed with "Could not connect to session bus: failed to connect to socket /tmp/dbus-
  • Q. Why does my job exit with "/bin/bash^M: bad interpreter: No such file or directory"?
  • Q. Why am I getting "command: module not found" on Puma?
A. Faculty Members (PIs) may add members by following the step-by-step instructions available on the Account Creation page under Sponsoring HPC Accounts.

Q. I'm leaving the university/not affiliated with the university, can I maintain/receive access to HPC?

A. Yes, if you are a former university affiliate or campus collaborator participating in research, you may register as a Designated Campus Colleague (DCC). Once your DCC status has been approved, you will receive a NetID+ which you may use to create an HPC Account. If you already have an HPC Account, no further action is required.

General Computing

Q. Why isn't my job running?

A. There are a few reasons your job may not be running:

1. Due to the number of HPC users, it may not always be possible to run a submitted job immediately. If there are insufficient resources available, your job will be queued and it may take up to a few hours for it to begin executing.
2. Make sure you haven't included -l place=pack:shared when submitting a multi-node PBS job.

Q Why do my jobs keep getting interrupted?

A. If your jobs keep stopping and restarting, it's likely because you are using Windfall which is considered lower priority and is subject to preemption. Before submitting a job to Windfall, consider using your group's allotted monthly hours first. Jobs using Standard hours will queue for a shorter period of time and will not be interrupted. You can check your group's remaining hours using the command va. To see more information on your allotted hours and the different job queues, see: Allocation and Limits.

Q. Can I run programs on the login nodes?

A. Well yes. But only for testing your code and not for more than an hour. Jobs running on the head node are subject to being terminated if we think they are affecting other users of the login nodes.

Q. Can I get root access to my compute nodes?

A. That is not possible. The compute nodes get their image from the head node and have to remain the same. If you need to install software that needs root access, for example, you can install the software to your home directories. See this example.

Q. I accidentally deleted files, can I get them back?

A. Unfortunately, backups are not made on HPC. To avoid data loss:

- Make frequent backups, ideally in three places and two formats. Information helpful to making backups can be found in our page on Transferring Files.
- Use rm and rm -r with caution as these commands cannot be undone! Consider using rm -i when removing files/directories. The -i flag will prompt you to manually confirm file removals to make sure they can be deleted.

Software

Q. How do I install this R package/Why can't I install this R package?

A. R installations can sometimes be frustrating. We have instructions for how to set up a usable R environment, how to diagnose and troubleshoot problems, and steps to help with known troublesome packages documented in in our Using and Customizing R Packages section.

Q. I have been using an older version of Singularity and now it is not available.
The current version of Singularity on Ocelote and Elgato is 3.6.0. Prior versions have been removed. Only the latest one is considered secure. Notify the consultants if you need help with transition to the current version. In general you should "module load singularity" without reference to the version number.

Q. What is the name of the executable for the module?

Load the module, find the path to the executable, then list the contents. For example:

```
module load lammps
echo $PATH
ls /opt/ohpc/pub/apps/lammps/3Mar20/bin
lmp_mpi
```

General Data Transfer and Storage

Q. Do you allow users to NFS mount their own storage onto the compute nodes?

A. No. We NFS mount storage across all compute nodes so that data is available independent of which compute nodes are used. See this section for how to transfer data.

Q. I can't transfer my data to HPC. I have an active account but I keep getting errors. What's wrong?

A. After creating your HPC Account, your home directory will not be created until you log in for the first time. Without your home directory, you will not be able to transfer your data to HPC. If you are struggling and receiving errors, sign into your account either using the CLI through the bastion or logging into OnDemand and then try again.

If you are using WinSCP and are receiving errors, make sure your hostname is set to filexfer.hpc.arizona.edu (not hpc.arizona.edu).

Q. I accidentally deleted files, can I retrieve them?

A. Unfortunately, no. Backups are not made and anything deleted is permanently erased. It is impossible for us to recover it. We recommend data be backed up elsewhere, preferably in three places and two formats. We also recommend including the -i flag when executing the rm command:

```
rm -i <filename> # for single-file deletions
# or
rm -i -R <directory> # for deleting full directories
```

When run, this forces you to manually confirm the deletion of each file. It may be cumbersome, but it can prevent massive headaches in the future!

Q. What do these Globus errors mean?

A. Endpoint too busy: This is most commonly seen when users are transferring directories to Google Drive. This is because Google has user limits restricting the number of files that can be transferred per unit time. When many files are being transferred at once, that limit may be exceeded. Globus will automatically hold the transfer until the limit is reset at which point it will continue. One way to avoid this is to archive your work prior to the transfer (e.g. in .tar.gz form). Additionally, archiving will also speed up your transfers considerably, sometimes by orders of magnitude.

A. Fatal FTP Response, PATH_EXISTS: Globus is finicky about the destination endpoint. If you get this error, check to see whether duplicate files/directories exist at the destination. This can happen frequently with Google Drive as multiple files/directories can exist in the same location with the same name. If duplicates exist, try moving, removing, or renaming them and reinitiate the transfer.

xdisk
Q. Why am I getting xdisk emails?
A. xdisk is a temporary storage space available to your research group. When it's close to its expiration date, notifications will be sent to all members of your group. For detailed information on xdisk allocations, see: Storage

Q. Why am I getting "/xdisk allocations can only be authorized by principal investigators”?
A. xdisks are managed by your group's PI by default. This means if you want to request an xdisk or modify an existing allocation (e.g., extending the time limit or increasing the storage quota), you will need to consult your PI. Your PI may either perform these actions directly or, if they want to delegate xdisk management to a group member, they may do so by following the instructions under Delegating xdisk Management Rights.

Q. What happens when our xdisk allocation expires?
A. Once an xdisk expires, all the associated data in that allocation are deleted. Once this happens, they are non-retrievable as HPC is not backed up. It’s advised to keep frequent backups of your data on different platforms, for example a local hard drive or a cloud-based service like Google Drive, or (even better) both!

Q. How can we modify our xdisk allocation?
To modify your allocation's time limit or storage quota, your PI can either do so through the Web Portal under the Storage tab, or via the command line. If your PI has delegated or would like to delegate management rights to a group member, follow the instructions under Delegating xdisk Management Rights.

Q. Can we keep our xdisk allocation for more than 300 days?
A. No, once an xdisk has reached its time limit it will expire. It's a good idea to start preparing for this early by making frequent backups and paying attention to xdisk expiration emails.

Q. Once our xdisk expires, can we request a new one?
Yes, a new xdisk may be requested immediately after the old partition expires. Data, however, may not be transferred directly from the old partition to the new one.

Interactive Sessions

Q. Why shouldn't I use Windfall with OnDemand?
A. Windfall jobs can be preempted by a higher priority queue. Each session creates an interactive job on a node. It is unsatisfactory to be dumped in the middle of that session. A desktop session would have the same unpleasant result. Windfall can be used if you do not have enough standard time left. Consider though that a one hour session using one compute core only takes up 1 cpu hour out of your group’s 36,000 hours.

Q. My interactive session has been disconnected, can I return to it?
A. No, unfortunately when an interactive job ends it is no longer accessible. This applies to both OOD sessions and those accessed via the command line.

Q. How do I access custom python packages from an OOD Jupyter session?
A. Instructions on accessing custom packages are under Accessing Custom Packages from a Jupyter Session in our documentation on Using and Installing Python.

Errors
Q. What does "Post job file processing error" mean?

A. While a job runs, PBS stores the associated temporary files (such as .o and .e files) before delivering them to your account. Sometimes PBS fails to deliver those files after the job is finished. Those files also count against your /home allocation.

To find undelivered files on Ocelote, use the following commands:

```bash
$ module load unsupported
$ module load ferng/find-pbs-files
$ pbs-files NetID
```

where NetID is your NetID (name of your HPC account).

The output of the pbs-files command will contain the full path to all the undelivered files. You can then use the full path to move or delete the files.

Q. What does this error mean - pcmem (32gb != 6gb,42gb)

A. pcmem is per core memory. Each node has a fixed amount of memory and number of cores. All of the standard nodes have 168GB memory allocated to PBS and 28 cores. $168 / 28 = 6$. The high memory node has a ratio of 42GB. So those are the only valid options.

Q. What does this error mean - "Not Running: PBS Error: Not enough time remaining to run your job"

A. Make sure you have standard hours available to run your jobs. To check your hours allocations, you may do so either on the command line:

```bash
$ va
```

or through our web portal: [https://portal.hpc.arizona.edu/](https://portal.hpc.arizona.edu/)

Q. I try to run a job and get: "Bad UID for job execution"

A. This happens most frequently for new users. It takes a while to propagate new accounts to all the right places. Come back after a coffee break.

Q. What does this error mean - Insufficient amount of resource: ...

A. qlist: Your job is waiting for a node/nodes to open up that will accept your job. Some nodes only take a specific subset of queues, queues being: standard, windfall, high_priority, and qualified. Note: The qualified queue is only available to users with a special project. Once a node/nodes become available that will accept your queue, the job will run.

A. np100s: Your job is waiting for the an np100 node to become available. If you are requesting two np100s on a single node, there is only one of these available and the wait time may be long. To speed up the process, you may consider requesting np100s=1 if your work allows it.

A. ncpus: Double-check the resources you're requesting. This error can pop up when the system is being asked for an impossible configuration. For example, requesting 40 cores on a single node. Because no node exists with 40 cores, you will receive this message and your job will never run.

Another possibility is you've requested multiple nodes and have used the place=pack:shared option. The system will attempt to find a single node with all of the cores requested for the job. When asking for multiple nodes, use place=free instead. For more information, see: Running Jobs with PBS (Ocelote and El Gato)

If the requested configuration is valid on the system, then there are currently not enough free cores. Your job will remain queued until the relevant resources become available.

Q. My OOD Desktop session failed with "Could not connect to session bus: failed to connect to socket /tmp/dbus-"

A. This is most commonly seen with users who have Anaconda or Miniconda installed in their accounts. To resolve this issue, open the file ~/.bashrc (a hidden file in your home directory) and comment out everything between:
Additionally, if you have any lines that look like:

```
export PATH=/path/to/anaconda/or/miniconda/bin:$PATH
```

comment these out as well. Then try starting your Desktop session again. You may uncomment these lines when needed.

**Q. Why does my job exit with "/bin/bash\^M: bad interpreter: No such file or directory"?**

A. Scripts created in a Windows environment and transferred to HPC retain hidden carriage returns (^M) that PBS cannot interpret. You can convert your Windows file to Unix format with:

```
$ dos2unix <filename>
```

**Q. Why am I getting "command: module not found" on Puma?**

A. There are two possible reasons:

1. You are not in an interactive session. Unlike ElGato and Ocelote, modules are not available on the Puma login nodes. You may request an interactive session by using the command `interactive`.

2. You have modified or deleted your ~/.bashrc. If this is the case, open (if the file exists) or create and open (if the file is missing) the file .bashrc in your home directory and add the lines:

```
if [ -f /etc/bashrc ]; then
    . /etc/bashrc
fi
```