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@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. How do I add members to my HPC research group?
    - 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?

Software

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

Data Transfer and Storage

- Q. Do you allow users to NFS mount their own storage onto the compute nodes?
- Q. I can't transfer my data to HPC. I have an active account but I keep getting errors. What's wrong?
- Q. I accidentally deleted files, can I get them back?

Interactive Sessions

- Q. Why shouldn't I use Windfall with OnDemand?
- Q. My interactive session has been disconnected, can I return to it?
- Q. How do I access custom python packages from an OOD Jupyter session?

Errors

- Q. What does this error mean - pcmem (32gb != 6gb,42gb)
- Q. What does this error mean - "Not Running: PBS Error: Not enough time remaining to run your job"
- Q. I try to run a job and get: "Bad UID for job execution"
- Q. What does this error mean - Insufficient amount of resource: ...

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@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. How do I add members to my HPC research group?
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.
A. 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.

It should be noted that jobs using Standard hours are given higher priority than those submitted to Windfall. Windfall jobs have the additional disadvantage of being subject to preemption by higher-priority jobs and may be repeatedly suspended and queued depending on HPC usage. If you have a high-priority job, we recommend using your available Standard hours.

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 `vz`. 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 some troublesome packages documented in our Using and Customizing R Packages section. Check to see if your package is listed. If so, follow the steps listed.

If your package is not listed, there are a few reasons why you may be having difficulties. We cover in detail common issues people run into in the link above. For quick troubleshooting:

1. Do you have Anaconda installed? If so, follow the instructions under Resolving Anaconda Issues in the link above.
2. Make sure all of your R packages were installed with the same version of R.
3. Make sure all of your R packages were installed on the same cluster.
4. If your package relies on 3rd party software, make sure R has access to that software either through a local installation or by loading the correct module. We recommend installing packages that rely on other modules on the command line and not in an OOD RStudio session.
5. Try installing the package into a fresh library (see the linked section for instructions).
6. Check that your account doesn't have any of the following file types: saved R sessions, gnu compiles, windows files. These can corrupt your environment and lead to trouble.

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.

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!

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 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:
$ va

or through our web portal: 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, debug. 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](Running Jobs)

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.