

# Disk Space and Disk Usage

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## 1. What Disks to Use

All the useful disk space available on the cluster is mounted off a dedicated device (aka appliance or server), a NetApp filer.

The available disk space is divided in several area (aka volumes, filesets or partitions):

- a small partition for basic configuration files and small storage, the `/home` partition ,
- a set of medium size partitions, one for SAO users, one for non-SAO users, the `/data` partitions,
- a set of large partitions, one for SAO users, one for non-SAO users, the `/pool` partitions,
- a second set of large partitions for temporary storage, the `/scratch` partitions.

### Note

- we impose quotas: limits on how much can be stored on each disk (partition/volume/fileset) by each user, and
- we monitor disk usage;
- `/home` should not be used to keep large files, use `/pool` instead;
- `/pool` is for active temporary storage (i.e., while a job is running).
- If you need more disk space or your job(s) use(s) a lot of I/Os, use `/scratch`.
  - Both partitions (`/pool` and `/scratch`) are **scrubbed (see below)**: old stuff is deleted to make sure there is space for active users.
- None of the disks on the cluster are for long term storage:
  - please copy your results back to your "home" computer and
  - delete what you don't need any longer.
- While the disk system on Hydra is highly reliable, none of the disks on the cluster are backed up.
- Once you reach your quota you won't be able to write anything on that partition until you delete stuff.
- A few nodes have local SSDs (solid state disks), [contact us](#) if your jobs can benefit from more disk space, SSDs or local disk space.

## 2. How to Copy Files to/from Hydra

⚠ When copying to Hydra, especially large files, be sure to do it to the appropriate disk (and not `/home` or `/tmp`).

### 2a. To/From Another Linux Machine

- You can copy files to/from `hydra` using `scp`, `sftp` or `rsync`:
  - to Hydra you can only copy from *trusted* hosts (computers on SI or SAO/CfA trusted network, or VPN'ed),
  - from Hydra to any host that allows external `ssh` connections (if you can `ssh` from Hydra to it, you can `scp`, `sftp` and `rsync` to it).
- For large transfers (over 70GB, sustained), we ask users to use `rsync`, and limit the bandwidth to 20 MB/s (70 GB/h), with the "`--bwlimit=`" option:
  - `rsync --bwlimit=20000 ...`  
If this pose a problem, contact us (Sylvain or Paul).
  - Baseline transfer rate from SAO to HDC (Herndon data center) is around 300 Mbps, single thread, or ~36 MB/s or ~126 GB/h (as of Aug. 2016)  
The link saturates near 500 Mbps (50% of Gbps) or 62 MB/s or 220 GB/h
- Remember that `rm`, `mv` and `cp` can also create high I/O load, so consider to
  - limit your concurrent I/Os: do not start a slew of I/Os at the same time, and
  - serialize your I/Os as much as possible: run one *after* the other.

### NOTE for SAO Users:

🔑 Access from the "outside" to SAO/CfA hosts (computers) is limited to the *border control hosts* ([login.cfa.harvard.edu](http://login.cfa.harvard.edu) and [pogoN.cfa.harvard.edu](http://pogoN.cfa.harvard.edu)), instructions for tunneling via these hosts is explained on

- the CF's [SSH Remote Access](#) page, or
- the HEAD Systems Group's [SSH FAQ](#) page.

## 2b. From a Computer Running MacOS

A trusted or VPN'd computer running MacOS can use `scp`, `sftp` or `rsync`:

- Open the Terminal application by going to /Applications/Utilities and finding Terminal.
- At the prompt, use `scp`, `sftp` or `rsync`, after `cd`'ing to the right place.
- For large transfers limit the bandwidth and use "`rsync --bwlimit=4000`".



Alternatively you can use a GUI based `ssh/scp` compatible tool like [FileZilla](#). Note, Cyberduck is not recommended because it uses a lot of CPU cycles on Hydra.

You will still most likely need to run VPN.

## 2c. From a Computer Running Windows

You can use `scp`, `sftp` or `rsync` if you install [Cygwin](#) - Note that Cygwin includes a X11 server.

Alternatively you can use a GUI based `ssh/scp` compatible tool like [FileZilla](#) or [WinSCP](#). Note, Cyberduck is not recommended because it uses a lot of CPU cycles on Hydra.

You will still most likely need to run VPN.

## ~~2d. Using Globus~~

~~(instructions missing)~~

## 2e. Using Dropbox

Files can be exchanged with Dropbox using the script [Dropbox-Uploader](#), which can be loaded using the `tools/dropbox_uploader` module and running the `dropbox` or `dropbox_uploader.sh` script. Running this script for the first time will give instructions on how to configure your Dropbox account and create a `~/dropbox_uploader` config file with authentication information.

Using this method will not sync your Dropbox, but will allow you to upload/download specific files.

## 2f. Using Firefox Send

- [Firefox Send](#) is a free online file-sending service (or a file exchange mechanism).
- Using this system along with the command `ffsend` available on Hydra (module `load bioinformatics/ffsend`), you can transfer files to/from Hydra *without needing VPN*.
- Firefox Send is a two-step process,
  1. you first upload a file (or a set of files packed in an archive) to the Firefox Send server which will generate a unique URL for the upload, and
  2. you download the file using that URL and recover the file's original name.

You can upload up to 1GB at a time, and if you sign up for a Firefox account, that limit increases to 2.5GB.

### Example 1: Sending to Hydra

#### a. Uploading files from your local machine (workstation/laptop) using the [Firefox Send website](#):

1. Open the [Firefox Send website](#) (`send.firefox.com`) from any browser.
2. Choose a file to upload, and optionally:
  - a. use `tar`, `zip` etc. to upload an archive of several files.
  - b. modify the expiration of the file (number of downloads or number of days), the default is to allow only one download and it expires within one day.
  - c. add a password that's needed to download the file.
3. Copy the URL generated for your upload.

⚠ You need to save that unique URL to get that file later. Unlike Dropbox or Google Drive, Firefox Send will not show you what you uploaded.

#### b. Downloading on Hydra from Firefox Send using `ffsend`

## on Hydra

```
$ module load bioinformatics/ffsend
$ ffsend download https://send.firefox.com/download/7800f8272ba5ef7b/#cNSwgMaNqmdsdwG6RxM71A
Download complete
```

## Example 2: Sending *from* Hydra

### a. Uploading from Hydra using ffsend

## on Hydra

```
$ module load bioinformatics/ffsend
$ ffsend upload test.tar.gz
Upload
complete

https://send.firefox.com/download/0324d02485dc9a02/#cxER28yNyf2dcwzwlIla6g
```

**b. Downloading to your local machine (workstation/laptop)** Optional: `ffsend` has options for setting a password and expiration. See `ffsend help` for more information.

Open the URL created on Hydra in a web browser to download the file to your local machine.

## 3. Disk Quotas

To prevent the disks from filling up and hose the cluster, there is a limit (aka quota) on

- how much disk space and
- how many files (in fact "inodes": the sum of number of files and number of directories) each user can keep.

Each quota type has a soft limit (warning) and a hard limit (error) and is specific to each partition. In other words exceeding the soft limit produces warnings; while exceeding the hard limit is not allowed, and results in errors.

## 4. Disk Configuration

[ Updated 20 Dec 2019 ]

	Maximum	Quotas per user			
	disk	disk space	no. of files	Snapshots	
Disk name	capacity	soft/hard	soft/hard	enabled?	Purpose
<a href="#">/home</a>	20T*	100/200G	3.6/4M	yes: 4 weeks	For your basic configuration files, scripts and job files - your limit is low but you can recover old stuff up to 4 weeks.
<a href="#">/data/sao</a> or <a href="#">/data/nasm</a>	45T	1.9/2.0T	4.8/5M	yes: 2 weeks	For important but relatively small files like final results, etc. - your limit is medium, you can recover old stuff, but disk space is not released right away. For SAO or NASM users.
<a href="#">/data/genomics</a>	45T	0.8/1.0T	2.4/2.5M	yes: 2 weeks	For important but relatively small files like final results, etc. - your limit is medium, you can recover old stuff, but disk space is not released right away. For non-SAO/NASM users.
<a href="#">/pool/sao</a> or <a href="#">/pool/nasm</a>	80T	1.9/2.0T	4/5M	no	For the bulk of your storage - your limit is high, and disk space is released right away, for SAO or NASM users.

/pool/genomics	80T	1.9/2.0T	4.8/5M	no	For the bulk of your storage - your limit is high, and disk space is released right away, for non-SAO users.
/pool/biology	200G	100/200G	0.45/0.5M	no	For the bulk of your storage - your limit is high, and disk space is released right away, for non-SAO/NASM users.
/scratch/genomics	350T	9/10T	25/26M	no	For temporary storage, if you need more than what you can keep in /pool for non-SAO/NASM users
/scratch/sao <del>/scratch/nasm</del>	350T	9/10T	25/26M	no	For temporary storage, if you need more than what you can keep in /pool for SAO, <del>NASM</del> users
					<b>Project specific disks (/pool)</b>
/pool/kistlerl	21T	20.0/21.0T	49.9/52.5M	no	NMNH/Logan Kistler
/pool/kozakk	11T	10.5/11.0T	26.1/27.5M	no	STRI/Krzysztof Kozak
/pool/nmnh_ggi	21T	15.0/15.8T	37.4/39.4M	no	NMNH/GGI
/pool/sao_access	21T	15.0/15.8T	37.4/39.4M	no	SAO/ACCESS
/pool/sao_rtdc	10T*	2.8/3.0T	2.5/3.0M	no	SAO/RTDC
/pool/sylvain	30T	29/30T	71/75M	no	SAO/Sylvain Korzennik
					<b>Project specific disks (/scratch)</b>
/scratch/bradys	25T	-	-	no	NMNH/Seán Brady/BRADY_LAB
/scratch/usda_sel	25T	24/25T	52M/62M	no	NMNH/Christopher Owen/USDA_SEL
/scratch/nzp_ccg	25T	24/25T	52M/62M	no	NZP/Michael Campana/CCG
/scratch/kistlerl	50T	-	-	no	NMNH/Logan Kistler
/scratch/meyerc	25T	24/25T	52M/62M	no	NMNH/Christopher Meyer
/scratch/nmnh_ggi	25T	24/25T	52M/62M	no	NMNH/GGI
/scratch/nmnh_lab	25T	4/5T	10M/12M	no	NMNH/LAB
/scratch/stri_ap	25T	4/5T	10M/12M	no	STRI/W. Owen McMillan/STRI_AP
/scratch/sao_atmos	186T	98/100T	252M/261M	no	SAO/ATMOS
/scratch/sao_cga	25T	7/8T	18M/20M	no	SAO/CGA
/scratch/sao_tess	50T	36/40T	94M/210M	no	SAO/TESS
/scratch/sylvain	50T	48/50T	115M/128M	no	SAO/Sylvain Korzennik
/scratch/schultzt	25T	-	-	no	NMNH/Ted Schultz/SCHULTZ_LAB
/scratch/wrbu	40T	38/40T	99M/100M	no	WRBU
					<b>Extra</b>
/pool/admin	10T*	5.7/6.0T	14.3/15.0M	no	Sys Admin
/pool/galaxy	15T*	10.7/11.3T	26.7/28.1M	no	Galaxy
					<b>Near line (/store)</b>
/store/public	270T	5/5T	n/a	yes: 8 weeks	Public, available upon request
/store/admin	20T	-	n/a	yes: 8 weeks	Sys Admin
/store/bradys	40T	-	n/a	yes: 8 weeks	NMNH/Seán Brady/BRADY_LAB
/store/nmnh_ggi	40T	-	n/a	yes: 8 weeks	NMNH/GGI
/store/sao_atmos	300TB	-	n/a	yes: 8 weeks	SAO/ATMOS
/store/sylvain	100TB	-	n/a	yes: 8 weeks	SAO/Sylvain Korzennik
/store/schultzt	40TB	-	n/a	yes: 8 weeks	NMNH/Ted Schultz/SCHULTZ_LAB
/store/wrbu	40TB	-	n/a	yes: 8 weeks	WRBU
	*: maximum size, disk size will increase up to that value if/when usage grows				

(as of Nov 2019)

## Notes

- The notation
  - 1.8/2.0TB means that the soft limit is 1.8TB and the hard limit is 2.0TB of disk space, while
  - 4/5M means that the soft limit is 4 million `inodes` and the hard limit is 5 million.
- It is inefficient to store a slew of small files and if you do you may reach your `inodes` quota before your space quota (too many small files).
  - Some of the disk monitoring tools show the `inode` usage.
  - If your `%(inode)>%(space)` your disk usage is inefficient, consider archiving your files into `zip` or `tar-compressed` sets.
- While some of the tool(s) you use may force you to be inefficient while jobs are running, you should remember to
  - remove useless files when jobs have completed,
  - compress files that can benefit from compression (with `gzip`, `bzip2` or `compress`), and
  - archive a slew of files into a `zip` or a `tar-compressed` set, as follows:

```
% zip archive.zip dir/
```

or

```
% tar -czf archive.tgz dir/
```

both examples archive the content of the directory `dir/` into a single `zip` or a `tgz` file. You can then delete the content of `dir/` with

```
% rm -rf dir/
```
- You can unpack each type of archive with

```
% unzip archive.zip
```

or

```
% tar xf archive.tgz
```
- The sizes of some of the partitions (aka the various disks) on the NetApp will "*auto-grow*" until they reach the listed maximum capacity, so the size shown by the traditional Un\*x command, like `df` does not necessarily reflect the maximum size.

We have implemented a FIFO (first in first out) model, where old files are deleted to make space, aka scrubbed.

- There is an age limit, meaning that only files older than 180 days (or 90 days) get deleted.
- Older files get deleted before the newer ones (FIFO),
- We run a [scrubber](#) on a regular interval.
- In any case, we ask you to remove from `/pool` and `/scratch` files that you do not need for active jobs.
- For projects that want dedicated disk space, such space can be secured with project's specific funds when we expand the disk farm ([contact us](#)).

## 5. Disk Monitoring

The following tools can be used to monitor your disk usage.

- You can use the following Un\*x commands:

<code>du</code>	show disk use
<code>df</code>	show disk free

or

- you can use Hydra-specific home-grown tools, (these require that you load the `tools/local` or `tools/local+` modules)

<code>dus-report</code>	run <code>du</code> and parse its output in a more user friendly format
<code>disk-usage</code>	run <code>df</code> and parse its output in a more user friendly format

- You can also view the disk status at the cluster status web pages, either
  - [here](#) (at `cfa.harvard.edu`)
  - or
  - [here](#) (at `si.edu`).

Each site shows the disk usage and a quota report, under the "Disk & Quota" tab, compiled 4x a day respectively, and has links to plots of disk usage vs time.

### Disk usage

The output of `du` can be very long and confusing. It is best used with the option "`-hs`" to show the sum ("`-s`") and to print it in a human readable format ("`-h`").

⚠ If there is a lot of files/directory, `du` can take a while to complete.

📄 For example:

```
% du -sh dir/
136M  dir/
```

The output of `df` can be very long and confusing.

👉 You can use it to query a specific partition and get the output in a human readable format ("`-h`"), for example:

```
% df -h /pool/sao
Filesystem      Size  Used Avail Use% Mounted on
10.61.10.1:/vol_sao  20T   15T   5.1T   75% /pool/sao
```

or try

```
% df -h --output=source,fstype,size,used,avail,pcent,file /scratch/genomics
Filesystem      Type  Size  Used Avail Use% File
gpfs01          gpfs  400T   95T  306T   24% /scratch/genomics
```

You can compile the output of `du` into a more useful report with the `dus-report` tool. This tool will run `du` for you (can take a while) and parse its output to produce a more concise/useful report.

For example, to see the directories that hold the most stuff in `/pool/sao/hpc`:

```
% dus-report /pool/sao/hpc
612.372 GB /pool/sao/hpc
capac. 20.000 TB (75% full), avail. 5.088 TB
447.026 GB 73.00 % /pool/sao/hpc/rtdc
308.076 GB 50.31 % /pool/sao/hpc/rtdc/v4.4.0
138.950 GB 22.69 % /pool/sao/hpc/rtdc/vX
137.051 GB 22.38 % /pool/sao/hpc/rtdc/vX/M100-test-oob-2
120.198 GB 19.63 % /pool/sao/hpc/rtdc/v4.4.0/test2
120.198 GB 19.63 % /pool/sao/hpc/rtdc/v4.4.0/test2-2-9
83.229 GB 13.59 % /pool/sao/hpc/c7
83.229 GB 13.59 % /pool/sao/hpc/c7/hpc
65.280 GB 10.66 % /pool/sao/hpc/sw
64.235 GB 10.49 % /pool/sao/hpc/rtdc/v4.4.0/test1
49.594 GB 8.10 % /pool/sao/hpc/sw/intel-cluster-studio
46.851 GB 7.65 % /pool/sao/hpc/rtdc/vX/M100-test-oob-2/X54.ms
46.851 GB 7.65 % /pool/sao/hpc/rtdc/vX/M100-test-oob-2/X54.ms/SUBMSS
43.047 GB 7.03 % /pool/sao/hpc/rtdc/vX/M100-test-oob-2/X220.ms
43.047 GB 7.03 % /pool/sao/hpc/rtdc/vX/M100-test-oob-2/X220.ms/SUBMSS
42.261 GB 6.90 % /pool/sao/hpc/c7/hpc/sw
36.409 GB 5.95 % /pool/sao/hpc/c7/hpc/tests
30.965 GB 5.06 % /pool/sao/hpc/c7/hpc/sw/intel-cluster-studio
23.576 GB 3.85 % /pool/sao/hpc/rtdc/v4.4.0/test2/X54.ms
23.576 GB 3.85 % /pool/sao/hpc/rtdc/v4.4.0/test2-2-9/X54.ms
23.576 GB 3.85 % /pool/sao/hpc/rtdc/v4.4.0/test2/X54.ms/SUBMSS
23.576 GB 3.85 % /pool/sao/hpc/rtdc/v4.4.0/test2-2-9/X54.ms/SUBMSS
22.931 GB 3.74 % /pool/sao/hpc/rtdc/v4.4.0/test2/X220.ms
22.931 GB 3.74 % /pool/sao/hpc/rtdc/v4.4.0/test2-2-9/X220.ms
report in /tmp/dus.pool.sao.hpc.hpc
```

You can rerun `dus-report` with different options on the same intermediate file, like

```
% dus-report -n 999 -pc 1 /tmp/dus.pool.sao.hpc.hpc
```

to get a different report, to see the list down to 1%. Use

```
% dus-report -help
```

to see how else you can use it.

The tool `disk-usage` runs `df` and presents its output in a more friendly format:

```

% disk-usage -d all+
Filesystem              Size      Used      Avail Capacity  Mounted on
netapp-n1:/vol_home    6.40T    3.05T    3.35T   48%/38%    /home
netapp-n2:/vol_data_genomics 36.00T   4.83T   31.17T   14%/2%    /data/genomics
netapp-n2:/vol_data/sao 27.00T   8.65T   18.35T   33%/19%    /data/sao
netapp-n2:/vol_data/nasm 27.00T   8.65T   18.35T   33%/19%    /data/nasm
netapp-n2:/vol_data/admin 27.00T   8.65T   18.35T   33%/19%    /data/admin
netapp-n1:/vol_pool_bio 200.00G  30.25G  169.75G   16%/1%    /pool/biology
netapp-n2:/vol_pool_genomics 55.00T  37.98T  17.02T   70%/15%    /pool/genomics
netapp-n1:/vol_pool_sao 37.00T   7.68T  29.32T   21%/1%    /pool/sao
netapp-n1:/vol_pool_sao/nasm 37.00T   7.68T  29.32T   21%/1%    /pool/nasm
emc-isilon:/ifs/nfs/hydra 60.00T  39.82T  20.18T   67%/1%    /pool/isilon
gpfs01:genomics       400.00T  94.60T  305.40T   24%/9%    /scratch/genomics
gpfs01:sao            400.00T   5.04T  394.96T    2%/1%    /scratch/sao
netapp-n1:/vol_pool_kistler1 21.00T  18.50T   2.50T   89%/1%    /pool/kistler1
netapp-n2:/vol_pool_kozakk 11.00T   7.82T   3.18T   72%/1%    /pool/kozakk
netapp-n1:/vol_pool_nmnh_ggi 21.00T  14.79T   6.21T   71%/8%    /pool/nmnh_ggi
netapp-n1:/vol_pool_sao_access 21.00T   2.37T  18.63T   12%/2%    /pool/sao_access
netapp-n2:/vol_pool_sao_rtdc  2.00T   62.13G   1.94T    4%/1%    /pool/sao_rtdc
netapp-n1:/vol_pool_sylvain 30.00T  24.83T   5.17T   83%/36%    /pool/sylvain
gpfs01:nmnh_bradys   25.00T  58.71G  24.94T   1%/1%    /scratch/bradys
gpfs01:usda_sel      25.00T  651.81G  24.36T    3%/4%    /scratch/usda_sel
gpfs01:nzp_ccg       25.00T  924.33G  24.10T    4%/1%    /scratch/nzp_ccg
gpfs01:nmnh_kistler1 50.00T  11.93T  38.07T   24%/1%    /scratch/kistler1
gpfs01:nmnh_meyerc   25.00T   0.00G  25.00T    0%/1%    /scratch/meyerc
gpfs01:nmnh_ggi      25.00T   4.85T  20.15T   20%/1%    /scratch/nmnh_ggi
gpfs01:nmnh_lab      25.00T   0.00G  25.00T    0%/1%    /scratch/nmnh_lab
gpfs01:stri_ap       25.00T   0.00G  25.00T    0%/1%    /scratch/stri_ap
gpfs01:sao_atmos     186.00T  51.15T  134.85T   28%/6%    /scratch/sao_atmos
gpfs01:sao_cga       25.00T   8.14T  16.86T   33%/4%    /scratch/sao_cga
gpfs01:sao_tess      50.00T   3.29T  46.71T    7%/4%    /scratch/sao_tess
gpfs01:sao_sylvain   50.00T   6.63T  43.37T   14%/2%    /scratch/sylvain
gpfs01:nmnh_schultzt 25.00T  376.87G  24.63T    2%/3%    /scratch/schultzt
gpfs01:wrbu          40.00T   3.00T  37.00T    8%/1%    /scratch/wrbu
netapp-n1:/vol_pool_admin  3.92T   2.71T   1.21T   70%/5%    /pool/admin
netapp-n1:/vol_pool_galaxy 400.00G  194.15G  205.85G   49%/1%    /pool/galaxy
gpfs01:admin         20.00T   1.96T  18.04T   10%/21%    /scratch/admin
gpfs01:bioinformatics_dbs 10.00T  868.14G   9.15T    9%/1%    /scratch/dbs
nas:/mnt/pool_01/admin 20.00T   1.67T  18.33T    9%/1%    /store/admin
nas:/mnt/pool_02/nmnh_bradys 40.00T  306.52G  39.70T    1%/1%    /store/bradys
nas:/mnt/pool_02/nmnh_ggi 40.00T  22.09T  17.91T   56%/1%    /store/nmnh_ggi
nas:/mnt/pool_03/public 270.00T  22.55T  247.45T    9%/1%    /store/public
nas:/mnt/pool_01/sao_atmos 299.97T  68.73T  231.24T   23%/1%    /store/sao_atmos
nas:/mnt/pool_01/sao_sylvain 100.00T   8.39T  91.61T    9%/1%    /store/sylvain
nas:/mnt/pool_02/nmnh_schultzt 40.00T   2.49T  37.51T    7%/1%    /store/schultzt
nas:/mnt/pool_02/wrbu  40.00T  618.24G  39.40T    2%/1%    /store/wrbu

```

## Use

```
% disk-usage -help
```

to see how else to use it.

You can, for instance, get the disk quotas and the max size, for all the disks, including `/store`, with:





## Monitoring Quota Usage

The Linux command `quota` is working with the NetApp (`/home`, `/data` & `/pool`), but not on the GPFS (`/scratch`) or the NAS (`/store`).

For example:

```
% quota -s
Disk quotas for user hpc (uid 7235):
  Filesystem  blocks    quota  limit  grace  files  quota  limit  grace
10.61.10.1:/vol_home
    2203M  51200M   100G
    46433  1800k  2000k
10.61.10.1:/vol_sao
    1499G  1946G  2048G
    1420k  4000k  5000k
10.61.10.1:/vol_scratch/genomics
    48501M  2048G  4096G
    1263  9000k  10000k
10.61.200.5:/vol/a2v1/genomics01
    108M  14336G  15360G
    613  10000k  12000k
10.61.10.1:/vol_home/hydra-2/dingdj
    2203M  51200M   100G
    46433  1800k  2000k
```

reports your quotas. The `-s` stands for `--human-readable`, hence the 'k' and 'G'. While

```
% quota -q
```

will print only information on filesystems where your usage is over the quota. ([man quota](#))

🔧 The command `quota+` (need to load `tools/local`) return disk quota for all the disks (see the [quota+](#) section in [Additional Tool](#)).

## Other Tools

- We compile a quota report 4x/day and provide tools to parse the quota report.
  - The daily quota report is written around 3:00, 9:00, 15:00, and 21:00
    - in a file called `quota_report_YYDDMM_HH.txt`, located in `/data/sao/hpc/quota-reports/unified/`.
  - The string `YYDDMM_HH` corresponds to the date & hour of the report: "160120\_09" for Jan 20 2016 9am report.
  - The format of this file is not very user friendly and users are listed by their user ID.

The Hydra-specific tools, (i.e., requires that you load the `tools/local` module):

- `quota+` - show quota values
- `parse-disk-quota-reports` - parse quota reports

## Examples

- `quota+` - show quota values:

```
% quota+
Disk quotas for user sylvain (uid 10541):
Mounted on          Used    Quota  Limit  Grace  Files  Quota  Limit  Grace
-----
/home                11.00G  50.00G  100.0G  0      73.13k  2.00M  2.00M  0
/data/sao            1.92T   7.60T   8.00T   0      37.53M  78.00M  80.00M  0
/pool/sylvain        8.79T  12.50T  14.00T  0      57.93M  71.00M  75.00M  0
/scratch/sao         10.00G  11.00T  12.00T  0         2  25.17M  26.21M  0
/scratch/sylvain     6.63T  50.00T  50.00T  0      1.89M  99.61M  104.9M  0
/store/admin         1.00G   none    none    0
/store/sylvain       8.39T   none    none    0
```

Use `quota+ -h`, or read the man page ([man quota+](#)), for the complete usage info.

- `parse-disk-quota-reports` will parse the disk quota report file and produce a more concise report:

```
% parse-disk-quota-reports
Disk quota report: show usage above 85% of quota, (warning when quota > 95%), as of Wed Nov 20 21:00:05 2019.
```

```
Volume=NetApp:vol_data_genomics, mounted as /data/genomics
-- disk -- -- #files -- default quota: 512.0GB/1.25M
Disk usage %quota usage %quota name, affiliation - username (indiv. quota)
-----
/data/genomics 512.0GB 100.0% 0.17M 13.4% *** Paul Frandsen, OCIO - frandsenp
```

```
Volume=NetApp:vol_data_sao, mounted as /data/admin or /data/nasm or /data/sao
-- disk -- -- #files -- default quota: 2.00TB/5M
Disk usage %quota usage %quota name, affiliation - username (indiv. quota)
-----
/data/admin:nasm:sao 1.88TB 94.0% 0.01M 0.1% uid=11599
```

```
Volume=NetApp:vol_home, mounted as /home
-- disk -- -- #files -- default quota: 100.0GB/2M
Disk usage %quota usage %quota name, affiliation - username (indiv. quota)
-----
/home 96.5GB 96.5% 0.41M 20.4% *** Roman Kochanov, SAO/AMP - rkochanov
/home 96.3GB 96.3% 0.12M 6.2% *** Sofia Moschou, SAO/HEA - smoschou
/home 95.2GB 95.2% 0.11M 5.6% *** Cheryl Lewis Ames, NMNH/IZ - amesc
/home 95.2GB 95.2% 0.26M 12.8% *** Yanjun (George) Zhou, SAO/SSP - yjzhou
/home 92.2GB 92.2% 0.80M 40.1% Taylor Hains, NMNH/VZ - hainst
```

```
Volume=NetApp:vol_pool_genomics, mounted as /pool/genomics
-- disk -- -- #files -- default quota: 2.00TB/5M
Disk usage %quota usage %quota name, affiliation - username (indiv. quota)
-----
/pool/genomics 1.71TB 85.5% 1.23M 24.6% Vanessa Gonzalez, NMNH/LAB - gonzalezv
/pool/genomics 1.70TB 85.0% 1.89M 37.8% Ying Meng, NMNH - mengy
/pool/genomics 1.45TB 72.5% 4.56M 91.3% Brett Gonzalez, NMNH - gonzalezb
/pool/genomics 133.9GB 6.5% 4.56M 91.2% Sarah Lemer, NMNH - lemers
```

```
Volume=NetApp:vol_pool_kistler1, mounted as /pool/kistler1
-- disk -- -- #files -- default quota: 21.00TB/52M
Disk usage %quota usage %quota name, affiliation - username (indiv. quota)
-----
/pool/kistler1 18.35TB 87.4% 0.88M 1.7% Logan Kistler, NMNH/Anthropology - kistler1
```

```
Volume=NetApp:vol_pool_nmnh_ggi, mounted as /pool/nmnh_ggi
-- disk -- -- #files -- default quota: 15.75TB/39M
Disk usage %quota usage %quota name, affiliation - username (indiv. quota)
-----
/pool/nmnh_ggi 14.78TB 93.8% 8.31M 21.3% Vanessa Gonzalez, NMNH/LAB - gonzalezv
```

```
Volume=NetApp:vol_pool_sao, mounted as /pool/nasm or /pool/sao
-- disk -- -- #files -- default quota: 2.00TB/5M
Disk usage %quota usage %quota name, affiliation - username (indiv. quota)
-----
/pool/nasm:sao 1.78TB 89.0% 0.16M 3.2% Guo-Xin Chen, SAO/SSP-AMP - gchen
```

reports disk usage when it is above 85% of the quota.

Use `parse-disk-quota-reports -h`, or read the man page (`man parse-disk-quota-reports`). for the complete usage info.

## Note

- Users whose quotas are above the 85% threshold will receive a warning email one a week (issued on Monday mornings).
  - This is a warning, as long as you are below 100% you are OK.
  - Users won't be able to write on disks on which they have exceeded their hard limits.

## 6. NetApp Snapshots: How to Recover Old or Deleted Files.

Some of the disks on the NetApp filer have the so called "snapshot mechanism" enabled:

- This allow users to recover deleted files or access an older version of a file.
- Indeed, the NetApp filer makes a "snapshot" copy of the file system (the content of the disk) every so often and keeps these snapshots up to a given age.
- So if we enable hourly snapshot and set a two weeks retention, you can recover a file as it was hours ago, days ago or weeks ago, but only up to two weeks ago.
- The drawback of the snapshot is that when files are deleted, the disk space is not freed until the deleted files age-out, like 2 or 4 weeks later.

### How to Use the NetApp Snapshots:

To recover an old version or a deleted file, `foo.dat`, that was (for example) in `/data/genomics/frandsen/important/results/`:

- If the file was deleted:

```
% cd /data/genomics/.snapshot/XXXX/frandsen/important/results
% cp -pi foo.dat /data/genomics/frandsen/important/results/foo.dat
```

- If you want to recover an old version:

```
% cd /data/genomics/.snapshot/XXXX/frandsen/important/results
% cp -pi foo.dat /data/genomics/frandsen/important/results/old-foo.dat
```

- The "-p" will preserve the file creation date and the "-i" will prevent overwriting an existing file.
- The "XXXX" is to be replaced by either:
  - `hourly.YYYY-MM-DD_HHMM`
  - `daily.YYYY-MM-DD_0010`
  - `weekly.YYYY-MM-DD_0015`where `YYY-MM-DD` is a date specification (i.e., `2015-11-01`)
- The files under `.snapshot` are read-only:
  - they be recovered using `cp`, `tar` or `rsync`; but
  - they cannot be moved (`mv`) or deleted (`rm`).

## How to Use the NAS/ZFS Snapshots:

- The snapshots on the `/store` disks are:
  - located under `/store/XXX/.zfs/snapshot` (where `XXX` is, for example, `public`) and
  - in sub-directories named `auto-YYMMDD.0230-8w` where `YYMMDD` represent the date of the snapshot.
- Content of NAS/ZFS snapshots can be recovered as described above.

## 7. Public Disks Scrubber

In order to maintain free disk space on the public disks, we are about to implement disk scrubbing: removing old files and old empty directories.

### What is Scrubbing?

We remove old files and old empty directories from a set of disks on a weekly basis.

Old empty directories will be deleted, old files will be, at first, moved away in a staging location, then deleted.



#### Please Note

Since the scrubber moves old files away at first, and delete them later,

- there is a grace period between the scrubbing (move) and the *permanent* deletion to allow users to request for some scrubbed files to be restored;
- reasonable requests to restore scrubbed files must be sent no later than the Friday following the scrubbing, by 5pm;
- scrubbed files still "count" against the user quota until they are *permanently* deleted.

Requests to restore scrubbed file should be

- rare,
- reasonable (*i.e.* no blanket request), and,
- can only be granted while the scrubbed files are not yet *permanently* deleted.

Past the grace period, the files are no longer available, hence users who want their scrubbed files restore have to act *promptly*.

The following instructions explain

- What disks will be scrubbed.
- What to do to access the scrubber's tools.
- How to
  - look at the scrubber's report;
  - find out which old empty directories were scrubbed;
  - find out which old files were scrubbed;
  - create a recovery request.

### What disks will be scrubbed?

The disks that will be scrubbed are:

- `/pool/biology` - 180 days
- `/pool/genomics` - 180 days
- `/pool/sao` - 180 days

- /scratch/genomics - 90 days
- /scratch/genomics01 - 90 days
- /scratch/sao - 90 days
- /scratch/sao01 - 90 days

## How to access the scrubber's tools

- load the module:

```
module load tools/scrubber
```

- to get the list of tools, use:

```
module help tools/scrubber
```

- to get the man page, accessible after loading the module, use:

```
man <tool-name>
```

## How to check what will be scrubbed

- To check what files will be scrubbed, use:

```
find-scrub [-in <dir>] [-age <age>]
```

this will look for files older than <age> days in <dir>, by default dir=current working directory, and age=173 or 83 days.

- This search taxes the file system (aka disk server), especially if you have a lot of files, so use as needed only.

## How to look at the scrubber's results

- To look at the report for what was scrubbed on Jul 21 2016 under /pool/genomics/frandsenp:

```
show-scrubber-report /pool/genomics/frandsenp 160721
```

- To find out which old empty directories were scrubbed:

```
list-scrubbed-dirs [-long|-all] /pool/genomics/frandsenp 160721 [<RE>|-n]
```

where the <RE> is an optional regular-expression to limit the printout, w/o an RE you get the complete list, unless you specify -n and you get the number of scrubbed directories.

The -long or -all option allows you to get more info (like age, size and owner)

- To find out which old files were scrubbed:

```
list-scrubbed-files [-long|-all] /pool/genomics/frandsenp 160721 [<RE>|-n]
```

where again the <RE> is an optional regular-expression to limit the printout, w/o an RE you get the complete list, unless you specify -n and you get the number of scrubbed files;

the -long option will produce a list that includes the files' age and size, -all will list age, size and owner.

- 📄 The <RE> (regular expressions) are PERL-style RE:
  - . means any char,
  - .\* means any set of chars,
  - [a-z] means any single character between a and z,
  - ^ means start of match,
  - \$ means end of match, etc ([see gory details here](#)).
- for example:

```
'^/pool/genomics/blah/project/.*\.log$'
```

means all the files that end in '.log' under '/pool/genomics/blah/project/'

## How to produce a list of files to restore

- To produce the list of files to restore as some of the files scrubbed under /pool/genomics/frandsenp/big-project, you can:

1. create a list with

```
list-scrubbed-files /pool/genomics/frandsenp 160721 /pool/genomics/frandsenp/big-project > restore.list
```

this will list all the scrubbed files under 'big-project/' and save the list in restore.list

⚠ Note that `/pool/genomics/frandsenp/big-project` means `/pool/genomics/frandsenp/big-project*`, if you want to restrict to `/pool/genomics/frandsenp/big-project`, add a `'/'`, i.e.: use `/pool/genomics/frandsenp/big-project/`

2. edit the file 'restore.list' to trim it, with any text editor (if needed),
3. verify with:  
`verify-restore-list /pool/genomics/frandsenp 160721 restore.list`  
or use  
`verify-restore-list -d /pool/genomics/frandsenp 160721 restore.list`  
if the verification produced an error.
4. Only then, and if the verification produced no error, submit your scrubbed file restoration request as follow:
  - SAO users: email the file(s) or the location of the files to Sylvain at [hpc@cfa.harvard.edu](mailto:hpc@cfa.harvard.edu)
  - non-SAO users: email the file(s) or the location of the files to [SI-HPC@si.edu](mailto:SI-HPC@si.edu)

## 8. SSD Local Disk Space

- Local SSDs (solid state disks) are available on a few nodes available.
- You should [contact us](#) if your jobs can benefit from accessing local SSD.
- How to use the SSD is explained [here](#).