

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 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 that:

- we impose quotas: limits on how much can be stored on each partition 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 even more disk space, ask to be allowed to 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), and for special cases it may be OK to use disk space local to the compute node.

[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 and 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 for 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.

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

	Maximum	Quotas per user		NetApp	
	disk	disk space	no. of files	snapshots	
Disk name	capacity	soft/hard	soft/hard	enabled?	Purpose
/home	10TB	50/100GB	1.8/2M	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.
/data/sao or /data/nasm	40TB*	1.9/2.0TB	4.75/5M	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.

/data/genomics	30TB*	0.45/0.5TB	1.19/1.25M	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.
/pool/sao or /pool/nasm	37TB	1.9/2.0TB	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	50TB	1.9/2.0TB	4.75/5M	no	For the bulk of your storage - your limit is high, and disk space is released right away, for non-SAO users.
/pool/biology	7TB	1.9/2.0TB	4.75/5M	no	For the bulk of your storage - your limit is high, and disk space is released right away, for non-SAO/NASM users.
/scratch	100TB	9.5/10.0TB	23.75/25M	no	For temporary storage, if you need more than what you can keep in /pool - SAO, NASM or non-SAO/NASM users should use /scratch/sao , /scratch/nasm or /scratch/genomics , respectively
Project specific disks					
/pool/kistlerl	21TB	20.0/21.0TB	49.9/52.5M	no	NMNH/Logan Kistler
/pool/kozakk	11TB	10.5/11.0TB	26.1/27.5M	no	STRI/Krzysztof Kozak
/pool/nmnh_ggi	21TB	15.0/15.8TB	37.4/39.4M	no	NMHN/GGI
/pool/sao_access	21TB	15.0/15.8TB	37.4/39.4M	no	SAO/ACCESS
/pool/sao_atmos	36TB	8.0/10TB	9/10M	no	SAO/ATMOS
/pool/sao_rtdc	10TB*	2.8/3.0TB	2.5/3.0M	no	SAO/RTDC
/pool/sao_cga	8TB	7.9/8TB	20/19M	no	SAO/CGA
/pool/sylvain	15TB	14/15TB	63/65M	no	SAO/Sylvain Korzennik
Extra					
/pool/admin	10TB*	5.7/6.0TB	14.3/15.0M	no	Sys Admin
/pool/galaxy	15TB,	10.7/11.3TB	26.7/28.1M	no	Galaxy
*: maximum size, disk size will increase up to that value if/when usage grows					

(as of May 1, 2018)

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 `tool/local` module)

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

You can compile the output of `du` into a more useful report with the `dus-report.pl` 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.pl /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.pl` with different options on the same intermediate file, like

```
% dus-report.pl -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.pl -help
```

to see how else you can use it.

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

```

% disk-usage.pl
Filesystem              Size      Used      Avail Capacity  Mounted on
NetApp.2:/vol_home      4.00T    1.72T    2.28T   43%/14%    /home
NetApp.2:/vol_data_genomics 18.00T   673.63G  17.34T    4%/1%    /data/genomics
NetApp.2:/vol_data/sao   27.00T    5.25T   21.75T   20%/14%    /data/sao
NetApp.2:/vol_data/nasm  27.00T    5.25T   21.75T   20%/14%    /data/nasm
NetApp.2:/vol_data/admin 27.00T    5.25T   21.75T   20%/14%    /data/admin
NetApp.2:/vol_biology    7.00T    8.64G    6.99T    1%/1%     /pool/biology
NetApp.2:/vol_genomics   50.00T   33.82T   16.18T   68%/11%    /pool/genomics
NetApp.2:/vol_sao        45.00T   14.15T   30.85T   32%/5%     /pool/sao
NetApp.2:/vol_sao/nasm   45.00T   14.15T   30.85T   32%/5%     /pool/nasm
Isilon.10:/ifs/nfs/hydra 60.00T   33.12T   26.88T   56%/89%    /pool/isilon
NetApp.2:/vol_scratch/genomics 100.00T  45.66T   54.34T   46%/38%    /scratch/genomics
NetApp.2:/vol_scratch/sao 100.00T  45.66T   54.34T   46%/38%    /scratch/sao
NetApp.2:/vol_scratch/nasm 100.00T  45.66T   54.34T   46%/38%    /scratch/nasm
NetApp.5:/vol/a2v1/genomics01 31.25T   4.62T   26.63T   15%/11%    /scratch/genomics01
NetApp.5:/vol/a2v1/sao01  31.25T   4.62T   26.63T   15%/11%    /scratch/sao01
NetApp.2:/vol_pool_nmnh_ggi 21.00T   4.35T   16.65T   21%/1%     /pool/nmnh_ggi
NetApp.2:/vol_pool_kistlerl 21.00T   1.98T   19.02T   10%/1%     /pool/kistlerl
NetApp.2:/vol_pool_kozakk  11.00T   7.06T   3.94T    65%/1%     /pool/kozakk
NetApp.2:/vol_sao_atmos  36.00T   15.30T   20.70T   43%/3%     /pool/sao_atmos
NetApp.2:/vol_sao_rtdc   2.00T   167.51G  1.84T    9%/1%     /pool/sao_rtdc
NetApp.2:/vol_pool_sao_access 21.00T  654.49G  20.36T    4%/1%     /pool/sao_access
NetApp.2:/vol_sylvain    30.00T   12.67T   17.33T   43%/23%    /pool/sylvain
NetApp.2:/vol_pool_admin  4.00T   912.88G  3.11T   23%/1%     /pool/admin
NetApp.2:/vol_pool_galaxy 10.00T    0.00G   10.00T    1%/1%     /pool/galaxy

```

Use

```
% disk-usage.pl -help
```

to see how else to use it.

You can, for instance, get the disk quotas and the max size with:

```
% disk-usage.pl -quotas
Filesystem      Size      Used      Avail Capacity  soft/hard   soft/hard   size Mounted on
NetApp.2:/vol_home      4.00T    1.72T    2.28T   43%/14%    50G/100G   1.80M/2.00M   10T /home
NetApp.2:/vol_data_genomics
/genomics      18.00T   673.63G   17.34T    4%/1%    486G/512G   1.19M/1.25M   30T /data
NetApp.2:/vol_data/*
nasm:admin      27.00T    5.25T    21.75T   20%/14%    1.9T/2.0T   4.75M/5.00M   40T /data/sao:
NetApp.2:/vol_biology
/biology      7.00T    8.64G    6.99T    1%/1%    1.9T/2.0T   4.75M/5.00M   n/a /pool
NetApp.2:/vol_genomics
/genomics      50.00T   33.79T   16.21T   68%/11%    1.9T/2.0T   4.75M/5.00M   n/a /pool
NetApp.2:/vol_sao
nasm      45.00T   14.33T   30.67T   32%/5%    1.9T/2.0T   4.75M/5.00M   n/a /pool/sao:
Isilon.10:/ifs/nfs/hydra
/isilon      60.00T   33.12T   26.88T   56%/89%    nyi/nyi     nyi/nyi     n/a /pool
NetApp.2:/vol_scratch/*
/genomics:sao:nasm
NetApp.5:/vol/a2v1/*
/genomics01:sao01
NetApp.2:/vol_pool_nmnh_ggi
/nmnh_ggi      21.00T    4.35T   16.65T   21%/1%    15.0T/15.8T  37.41M/39.38M n/a /pool
NetApp.2:/vol_pool_kistlerl
/kistlerl      21.00T    1.98T   19.02T   10%/1%    20.0T/21.0T  49.88M/52.50M n/a /pool
NetApp.2:/vol_pool_kozakk
/kozakk      11.00T    7.06T    3.94T   65%/1%    10.5T/11.0T  26.13M/27.50M n/a /pool
NetApp.2:/vol_sao_atmos
/sao_atmos      36.00T   15.30T   20.70T   43%/3%    25.7T/27.0T  64.13M/67.50M n/a /pool
NetApp.2:/vol_sao_rtdc
/sao_rtdc      2.00T   167.51G    1.84T    9%/1%    2.9T/3.0T    7.13M/7.50M   10T /pool
NetApp.2:/vol_pool_sao_access
/sao_access      21.00T   654.49G   20.36T    4%/1%    15.0T/15.8T  37.41M/39.38M n/a /pool
NetApp.2:/vol_sylvain
/sylvain      30.00T   12.67T   17.33T   43%/23%    28.5T/30.0T  71.25M/75.00M n/a /pool
NetApp.2:/vol_pool_admin
/admin      4.00T   912.88G    3.11T   23%/1%    5.7T/6.0T   14.25M/15.00M 10T /pool
NetApp.2:/vol_pool_galaxy
/galaxy      10.00T    0.00G   10.00T    1%/1%    10.7T/11.3T  26.72M/28.13M 15T /pool
```

Monitoring Quota Usage

The Linux command `quota` is working with the NetApp filers (old and new), although not the Isilon.

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](#))

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`, located in `/share/apps/adm/reports`.

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):

- [show-quotas.pl](#) - show quota values
- [parse-quota-report.pl](#) - parse quota report

Examples

[show-quotas.pl](#) - show quota values:

```
% show-quotas.pl -u sylvain
Limited to user=sylvain

----- quota -----
filesystem      type      name      space     #files
/data/sao:nasm:admin  user      sylvain   8.0TB    40.000M
/home            user      sylvain   100.0GB  2.000M
/pool/sao:nasm    user      sylvain   2.0TB    5.000M
/scratch/genomics:sao:nasm user      sylvain   10.0TB   25.000M
/pool/sylvain     user      sylvain   30.0TB   75.000M
```

Use

```
% show-quotas.pl -h
```

for the complete usage info.

[parse-quota-report.pl](#), will parse the quota report file and produce a more concise report:

```
% parse-quota-report.pl
Disk quota report: show usage above 75% of quota, (warning when quota > 95%), as of Wed Nov 22 09:00:04 2017.

disks=/data/admin or /data/nasm or /data/sao (volume=vol_data)
-- disk -- -- #files -- default quota: 2.00TB/5M
volume      usage  %quota  usage  %quota  name, affiliation - username (indiv. quota)
-----
vol_data    1.88TB 94.0%   0.01M  0.1%   Hotaka Shiokawa, SAO/RG - hshiokawa

disk=/pool/genomics (volume=vol_genomics)
-- disk -- -- #files -- default quota: 2.00TB/5M
volume      usage  %quota  usage  %quota  name, affiliation - username (indiv. quota)
-----
vol_genomics 1.84TB 92.0%   0.00M  0.1%   H.C. Lim, NMNH/IZ - limhc
vol_genomics 1.58TB 79.0%   0.15M  3.0%   Bastian Benthage, NMNH - benthageb
vol_genomics 707.4GB 34.5%   4.68M  93.5%  Molly M. McDonough, CCEG - mcdonoughm
vol_genomics 1.52TB 76.0%   0.00M  0.1%   Krzysztof Kozak, STRI - kozakk
vol_genomics 1.70TB 85.0%   0.04M  0.8%   Logan Kistler, NMNH/Anthropology - kistlerl
vol_genomics 2.00TB 100.0%  0.00M  0.0%   *** Xu Su, NMNH/Botany - sux

disk=/home (volume=vol_home)
-- disk -- -- #files -- default quota: 100.0GB/2M
volume      usage  %quota  usage  %quota  name, affiliation - username (indiv. quota)
-----
vol_home    80.3GB 80.3%   0.27M  13.5%  Tileman Birnstiel, SAO/RG - tbirnstiel
vol_home    77.4GB 77.4%   0.18M  9.1%   Rebecca Dikow, NMNH/NZP - dikowr
vol_home    88.3GB 88.3%   0.01M  0.7%   Gabriela Procópio Camacho, NMNH - procopiocamachog
vol_home    100.0GB 100.0%  0.02M  1.1%   *** Logan Kistler, NMNH/Anthropology - kistlerl

disks=/pool/nasm or /pool/sao (volume=vol_sao)
-- disk -- -- #files -- default quota: 2.00TB/5M
volume      usage  %quota  usage  %quota  name, affiliation - username (indiv. quota)
-----
vol_sao     3.63TB 181.5%  0.19M  3.8%   *** Guo-Xin Chen, SAO/SSP-AMP - gchen
vol_sao     1.54TB 77.0%   0.55M  11.0%  Anjali Tripathi, SAO/AST - atripathi
vol_sao     1.66TB 83.0%   0.20M  4.1%   Hotaka Shiokawa, SAO/RG - hshiokawa
vol_sao     2.00TB 100.0%  0.00M  0.1%   *** Chengcai Shen, SAO/SSP - chshen
```

reports disk usage where it is at 75% above quota.

Or you can check usage for a specific user (like yourself) with

```
% parse-quota-report.pl -u <username>
```

for example:

```
% parse-quota-report.pl -u hpc
Disk quota report: show usage (warning when quota > 95%),
for user 'hpc', as of Wed Nov 22 09:00:04 2017.

disks=/data/admin or /data/nasm or /data/sao (volume=vol_data)
-- disk -- -- #files -- default quota: 2.00TB/5M
volume      usage  %quota  usage  %quota  name, affiliation - username (indiv. quota)
-----
vol_data    43.2GB  2.1%    0.01M  0.1%    HPC admin - hpc

disk=/home (volume=vol_home)
-- disk -- -- #files -- default quota: 100.0GB/2M
volume      usage  %quota  usage  %quota  name, affiliation - username (indiv. quota)
-----
vol_home    4.9GB   4.9%    0.04M  2.0%    HPC admin - hpc

disk=/pool/admin (volume=vol_pool_admin)
-- disk -- -- #files -- default quota: 6.00TB/15M
volume      usage  %quota  usage  %quota  name, affiliation - username (indiv. quota)
-----
vol_pool_admin 907.8GB 14.8%   0.44M  2.9%    HPC admin - hpc

disks=/pool/nasm or /pool/sao (volume=vol_sao)
-- disk -- -- #files -- default quota: 2.00TB/5M
volume      usage  %quota  usage  %quota  name, affiliation - username (indiv. quota)
-----
vol_sao      0.0MB  0.0%    0.00M  0.1%    HPC admin - hpc

disks=/scratch/genomics or /scratch/nasm or /scratch/sao (volume=vol_scratch)
-- disk -- -- #files -- default quota: 10.00TB/25M
volume      usage  %quota  usage  %quota  name, affiliation - username (indiv. quota)
-----
vol_scratch  47.4GB  0.5%    0.00M  0.0%    HPC admin - hpc

disk= (volume=a2v1)
-- disk -- -- #files -- default quota: 15.00TB/12M
volume      usage  %quota  usage  %quota  name, affiliation - username (indiv. quota)
-----
a2v1        78.1MB  0.0%    0.00M  0.0%    HPC admin - hpc
```

Use

```
% parse-quota-report.pl -h
```

for the complete usage info.

Users whose quotas are above the 75% 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`).

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
 - non-SAO users: email the file(s) or the location of the files to SI-HPC@si.edu

8. SSD and Local Disk Space

We are in the process of making the local SSDs (solid state disks) available on a few nodes available, and for special cases it may be OK to use disk space local to the compute node.

You should [contact us](#) if your jobs can benefit from either SSDs or local disk space.

How to use the SSD is explained [here](#).

Last Updated 21 Dec 2018 SGK/PBF.