





SAM4Users Tutorial

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What is SAM For Users?

- Utilities to assist individual users to make use of the SAM catalogue for their own data
- Advantages of using SAM for Users toolkit:
 - users' own data will be just like production data,
 - submitting grid jobs using SAM project;
 - making use of existing tools and monitoring for SAM jobs;
 - moving files between different storage locations are made simple.



List of available tools in SAM for Users toolkit

- Dataset commands:
 - sam_add_dataset
 - sam_revert_names
 - sam_modify_dataset_metadata
 - sam_validate_dataset
- Dataset copy and move:
 - sam_clone_dataset
 - sam move dataset
 - sam_move2archive_dataset
 - sam_copy2scratch_dataset
 - sam_move2persistent_dataset

- Delete datasets:
 - sam_unclone_dataset
 - sam_remove_location_dataset
 - sam_retire_dataset
- Miscellaneous commands:
 - sam_archive_dataset
 - sam_archive_directory_image
 - sam_restore_directory_image
 - sam_prestage_dataset
 - sam_audit_dataset
 - sam_condense_dataset
 - sam_pin_dataset

* Examples can be found in this tutorial



Hands-on session

- Required setups;
- Access files in scratch dCache:
 - Write, read and delete files;
- Using sam4users tool to:
 - Declare a dataset with files in scratch area;
 - Store files to persistent or tape-backed area;
 - Remove replicas of the dataset in the scratch area;
 - Validate dataset and what to do when a file is missing;
 - Retire a dataset.
- Commands in this session can be found at:
- http://home.fnal.gov/~dingpf/sam4users_tutorial_commands.txt



Setups

```
# On GPVM (e.g. dunegpvm01.fnal.gov)
# setup UPS etc.
source /cvmfs/dune.opensciencegrid.org/products/dune/setup_dune.sh
# Getting a valid certificate and VOMS proxy
kx509
voms-proxy-init -noregen -rfc -voms dune:/dune/Role=Analysis
# Setup fife utils, current version is v3 1 0
setup fife utils
# set experiment name
export EXPERIMENT=dune
```



Access file in dCache (I) – copy files to scratch

```
# Create a directory in scratch area for this tutorial
export SCRATCH DIR=/pnfs/dune/scratch/users/${USER}/tutorial
ifdh mkdir p ${SCRATCH DIR}
# Write files to scratch dCache (best to have files written in local
# disk or BlueArc first and then copy to the scratch area with ifdh
# or xrootd)
# create four 5MB dummy files, these files will be used for
# demonstration of data handling. You do not need to create the dummy
# files. You can use files of your own.
for i in `seq 0 3`; do \
head -c 5242880 /dev/urandom > \sim/dummy \{USER\} \{i\}.bin; \
done
# copy files into scratch dCache with "ifdh cp".
ifdh cp -D ~/dummy ${USER} [0-3].bin ${SCRATCH DIR}
# To explore other options available with "ifdh cp", just type "ifdh".
```

Access file in dCache (II) – delete files in scratch

```
# delete files with "ifdh rm"
ifdh rm ${SCRATCH DIR}/dummy ${USER} 0.bin
for i in seq `1 3`; do\
ifdh rm ${SCRATCH DIR}/dummy ${USER} ${i}.bin;\
done
# Copy files to scratch dCache using xrootd
xrdcp ~/dummy ${USER} [0-3].bin ${SCRATCH DIR}
# or
xrdcp ~/dummy ${USER} *.bin \
root://fndca1.fnal.gov:1094//pnfs/fnal.gov/usr/dune\
/scratch/users/${USER}/tutorial
# note that one should convert the path to scratch dCache to URI
 recognized by xrootd:
# e.g. from: /pnfs/dune/scratch/users/${USER}/dummy ${USER} 1.bin
#
         to: root://fndca1.fnal.gov:1094//pnfs/fnal.gov/usr/dune
          /scratch/users/${USER}/dummy ${USER} 1.bin
```

Store files to persistent/tape-backed area (I) - declare a SAM dataset with files in scratch area

```
# choose a dataset name, better to be user, purpose and time specific
export TUTORIAL DATASET=${USER} tutorial `date +%y%m%d%H%M` 01
# Add a SAM dataset for files in dCache scratch area
sam add dataset -n ${TUTORIAL DATASET} -d ${SCRATCH DIR}
# Instead of the "-d" option, it can take "-f" option followed by a
# text file containing a list of paths to files
# NOTE: sam add dataset will change the filename with UUID prefix.
ls ${SCRATCH DIR}
# List files in the dataset
samweb list-definition-files ${TUTORIAL DATASET}
```

Store files to persistent/tape-backed area (II) - clone the dataset to persistent/tape-backed area

```
# If the files under scratch area worth being kept for longer time,
# they can be added to SAM first with sam add dataset, followed by
# copying to the persistent or tape-backed area.
# create a destination directory in the persistent area first
export PERSISTENT_DIR=/pnfs/dune/persistent/users/${USER}/tutorial
mkdir -p ${PERSISTENT DIR}
# Copy the dataset to persistent area with sam clone dataset
sam_clone_dataset -n ${TUTORIAL_DATASET} -d ${PERSISTENT_DIR}
# Advanced tips for cloning large dataset:
# "sam clone dataset" has "--njobs" option to launch multiple jobs to do
# the cloning. "launch clone jobs" can lauch grid jobs to do the cloning.
```

Store files to persistent/tape-backed area (III) - remove replicas in the scratch area

check file locations, you will see two locations.

```
DUMMY_01=`samweb list-definition-files ${TUTORIAL_DATASET}|head -n 1`
samweb locate-file ${DUMMY_01}

# Remove replicas of the dataset files in the scratch area
sam_unclone_dataset -n ${TUTORIAL_DATASET} -d ${SCRATCH_DIR}

# List ${SCRATCH_DIR} to check if files are still there.
ls ${SCRATCH_DIR}

# check the file locations again, you will see only one location left
samweb locate-file ${DUMMY_01}
```

Store files to persistent/tape-backed area (IV) - validate dataset and dealing with missing files

```
# Validate dataset, that is to check if each files in a dataset exists
# in the storage volume
sam validate dataset -n ${TUTORIAL DATASET}
# Let's move one file in the dataset and run "sam validate dataset"
FPATH=`samweb locate-file ${DUMMY_01}|cut -d ':' -f 2`
ifdh mv ${FPATH}/${DUMMY 01} \
sam validate dataset -n ${TUTORIAL DATASET}
# When there is a file missing, one can either replace the file with
# a backup copy; or use "--prune" option to remove the file from the
# dataset; otherwise there will be errors when using SAM record for
# file access.
sam validate dataset -n ${TUTORIAL DATASET} --prune
# Let's list the files in the dataset again
samweb list-definition-files ${TUTORIAL DATASET}
```

Store files to persistent/tape-backed area (V) - retire dataset

```
# This will delete the dataset definition in SAM, retire all files
# contained in the dataset and delete them from disk. To be safe, use
# this command with "-j" ("--just say") option first to see what will
# be done before letting it take real action.
sam retire dataset -n ${TUTORIAL DATASET} -j
# You can use "--keep files" option if you don't want to delete the
# files.
sam retire dataset -n ${TUTORIAL DATASET} --keep files
# Once the dataset being retired, you can revert the file names for the
# last copy of files with sam revert names
sam revert names -d ${PERSISTENT DIR}
```

Summary (I)

- We have just gone through a full lifecycle of dataset files in the hands-on session;
- Please follow these practices in your own data management tasks, and keep the following things in mind:
 - Avoid using BlueArc area for grid jobs;
 - Avoid using "rsync" on any dCache volumes;
 - Store files into dCache scratch area first;
 - Always have files under persistent or tape-backed area bookkept by SAM;
 - Access files in dCache volumes via NFS is not as reliable as using "ifdh" or "xrootd".



Summary (II)

- With SAM for Users toolkit, one can:
 - Add own files to SAM
 - Copy/move dataset files between different storage locations
 - No accidents of deleting files
 - Most importantly: various tools for using production data are now available to users' own data.
- Additional links
 - Understanding storage volumes
 https://cdcvs.fnal.gov/redmine/projects/fife/wiki/Understanding_storage_volumes
 - SAM4Users wiki

https://cdcvs.fnal.gov/redmine/projects/sam/wiki/SAMLite_Guide

SAM wiki

https://cdcvs.fnal.gov/redmine/projects/sam/wiki/User_Guide_for_SAM



Backup



Modify file metadata (I)

- File metadata:
 - samweb get-metadata 43ccc572-d856-4413-8f41-535fd66755bf-neardet_r00011382_s15_nuexsec.root

```
File Name: 43ccc572-d856-4413-8f41-535fd66755bf-neardet_r00011382_s15_nuexsec.root
    File Id: 212505656
Create Date: 2016-06-21T16:12:22+00:00
    User: dingpf
    File Type: unknown
    File Format: unknown
    File Size: 6082761
    Checksum: (none)
Content Status: good
    Dataset.Tag: dingpf_test_20160621
```

Suggestion for experiments' SAM admins:

- add metadata parameters for users' own data;
- ask users to only modify metadata for those parameters.

novagpvm11: ~ \$ samweb add-parameter Users.AnalysisGroup string



Modify file metadata (II)

- Modify file metadata for a single file:
 - samweb modify-metadata \${FILE_NAME} \${METADATA_JSON_FILE}

```
novagpvm11: ~ $ cat ~/file.json
{
   "Users.AnalysisGroup": "NDXsec",
   "file_format": "root"
}
novagpvm11: ~ $
```

```
novagpvm11: ~ $ samweb get-metadata 3f2346bb-a886-415a-9515-74fd3b463c57-neardet_r00011361_s08_nuexsec.root
    File Name: 3f2346bb-a886-415a-9515-74fd3b463c57-neardet_r00011361_s08_nuexsec.root
    File Id: 212503465
    Create Date: 2016-06-21T16:12:23+00:00
        User: dingpf
    Update Date: 2016-06-21T16:33:18+00:00
    Update User: dingpf
    File Type: unknown
    File Format: root
    File Size: 6424415
        Checksum: (none)
    Content Status: good
    Dataset.Tag: dingpf_test_20160621

Users.AnalysisGroup: NDXsec
```

Modify file metadata (II)

- Modify file metadata for all files in a dataset:
 - sam_modify_dataset_metadata -n {DATASET_NAME} -m
 \${META_DATA_STRING_JSON}
- Or use SAM python API

```
import samweb_client as swc
sam = swc.SAMWebClient("nova")
mfmetadata = {"Users.AnalysisGroup": "NDXsec"}
f="3f2346bb-a886-415a-9515-74fd3b463c57-neardet_r00011361_s08_nuexsec.root"
sam.modifyFileMetadata(f,mfmetadata)
```

```
novagpvm11: ~ $ samweb list-files "Users.AnalysisGroup NDXsec" 3f2346bb-a886-415a-9515-74fd3b463c57-neardet_r00011361_s08_nuexsec.root
```

