

# SciCat at DESY

## Grouping SciCat Scan datasets in Measurement datasets

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Beamline PC

DESY IT

Sardana

Ingestor

SciCat

1. perform a scan
2. append the scan name to a scan-list file

inotify event

3. read metadata from NXS or FIO
4. rearrange metadata
5. ingest to scicat

REST API request

6. store in mongodb

The scan-list file may also contain start/stop measurement tags, i.e. `__command__`

# Scan-list file example

myscan\_00012

myscan\_00013

\_\_command\_\_ start my\_measurement

myscan\_00014

myscan\_00015

myscan\_00016

\_\_command\_\_ stop

my\_measurement: 1704367280.9590826

myscan\_00017

\_\_command\_\_ start my\_measurement

myscan\_00017: 1704367282.023423

\_\_command\_\_ stop

my\_measurement: 1704367286.3453534

# Scan-list file example

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# Rearranging scientific Metadata with copy-map

The `scientificMetadata` can be changed i.e. copied or removed, by `copy-map {target: source}`

- a file containing the `copy-map` is defined by **`metadata_copy_map_file`** (*str*), default: `None`  
`/home/p08user/.config/DESY/scingestor-metadata-copy-map.lst`
- the `copy-map` file contain `'json'`, `'yaml'` or `'text'` file with a dictionary or two column array
- the `copy-map` can be also defined in a NeXus field:  
`/:NXentry/nxsfileinfo_parameters:NXparameters  
/copymap`
- the above NeXus field `copy-map` would be provided by a NeXus component  
so different `copy-maps` could be used in various measurement groups

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so **different copy-maps** could be used in **various measurement groups**

# ScientificMetadata with copy-map in text

- a (black) source from the second column is copied to the corresponding (blue) target
- when a (black) source is missing the (blue) target is removed

```
scientificMetadata.instrument_name scientificMetadata.instrument.name.value
scientificMetadata.sample_name scientificMetadata.sample.name.value
scientificMetadata.instrument
scientificMetadata.sample
scientificMetadata.data
scientificMetadata.experiment_description
scientificMetadata.experiment_identifier
scientificMetadata.end_time scientificMetadata.end_time.value
scientificMetadata.start_time scientificMetadata.start_time.value
scientificMetadata.title scientificMetadata.title.value
scientificMetadata.program_name
```

# Grouping scientificMetadata with group-map

The scan `scientificMetadata` can be grouped in measurement `scientificMetadata` by `group-map`

- a file containing the `group-map` is defined by **`metadata_group_map_file`** (*str*) , default: None  
`/home/p08user/.config/DESY/scingestor-metadata-group-map.lst`
- the `group-map` file contain `'text'` file with two or three column array,  
i.e. `<target> <source> [<target type>]`
- `target type` is not mandatory, and it can be:  
`Min, Max, MinMax, Range, List, UniqueList, Dict, First, Last, FirstLast, Endpoints`
- if the `target type` is missing for the numerical source values we store: `average, min, max, std, counts`
- if the `target type` is missing for the string source values unique string is stored

# Group-map file structure

the (black) source from the second column is grouped to the corresponding (blue) target with use of the (green) target type

```
scientificMetadata.ScanCommand scientificMetadata.ScanCommand List
scientificMetadata.source_energy scientificMetadata.instrument.source.energy Dict
scientificMetadata.source_current scientificMetadata.instrument.source.current Range
scientificMetadata.sample_chemical_formula scientificMetadata.sample.chemical_formula.value
scientificMetadata.sample_temperature scientificMetadata.sample.temperature.value
scientificMetadata.sample_name scientificMetadata.sample.name.value
scientificMetadata.HKLmatrix scientificMetadata.user_data.flathklmatrix UniqueList
```

# Measurement in Raw/Derived Datasets

The group measurement `Datasets` are stored in

- `DerivedDatasets`  
in case we store both scan `Datasets` and grouped (measurement) `Datasets`
- `RawDatasets`  
in case we **don't store scan `Datasets`** but only grouped (measurement) `Datasets`

The choice is made in the `scingestor` configuration by setting, e.g.

```
skip_scan_dataset_ingestion: True  
raw_metadata_callback: True
```

# Start Sardana scan: metadata only from NeXus

To start **Sardana scan** on `haspp081isa2.desy.de` (P08 beamline)

- select **NeXus configuration components** e.g. in

```
nxselector
```

- run

```
spock
```

- in **the spock command-line interface** execute

```
scdd/door/hasvmscdd01.01 [1]:  senv NXSApendSciCatDataset True
scdd/door/hasvmscdd01.01 [1]:  senv SciCatDatasetListFileLocal True
scdd/door/hasvmscdd01.01 [1]:  qscan 0.0 0.0 0.0 0.0 0.068 0.135 14 1.0
```

Also `ScanFile`, `ScanDir` and `ScanID` need to be defined

# Support for FIO files and general hooks

- support for **fetching Metadata** from NeXus and FIO files
- **default order** of **searching** for master metadata file:  
**"nxs", "h5", "ndf", "nx", "fio"**

```
from sardana.macros.server.macro import Macro
from nxstools.pyeval import scdataset
```

```
class gh_post_scan(Macro):
```

```
    def run(self):
        scdataset.append_scicat_dataset(self)
```

# Start Sardana scan: metadata from NeXus, FIO

To start **Sardana scan** on `haspp081isa2.desy.de` (P08 beamline)

- select **NeXus configuration components** e.g. in

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- run

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```

Also `ScanFile`, `ScanDir` and `ScanID` need to be defined

# Measurement sardana macros

The `measurement` can be started/stopped with `sardana macros` manually

- `start_measurement <dataset_name>`  
starts a new measurement with the given name
- `make_measurement <dataset_name>`  
starts a new measurement with the given name and adds to the measurement the last scan
- `stop_measurement`  
updates the current measurement dataset in the SciCat database and stops the measurement
- `update_measurement`  
updates the current measurement dataset in the SciCat database
- `show_current_measurement`  
shows the current measurement name

# AutoGrouping measurement mode

We can switch on the **AutoGrouping** mode by

```
scdd/door/hasvmscdd01.01 [1]:  setenv SciCatAutoGrouping True
```

In this mode

- scan metadata is grouped automatically in the measurement dataset
- the measurement dataset updated after each scan
- the name of measurement is taken from the base scanname after removing ScanID,  
e.g. for `<scanname> = "mycalib2_00012"`  
the measurement name is "mycalib2"

# Datasets in the SciCat frontend

[Help](#)[About](#)

Datasets / TestJK01/water\_meas

[Details](#)[Datafiles](#)[Related Datasets](#)[Reduce](#)[Logbook](#)[Attachments](#)[Lifecycle](#)[Admin](#)[Jupyter Hub](#)

## General Information

**Name** water\_meas  
**Description** Water test  
**PID** testjk01/water\_meas   
**Type** derived  
**Creation Time** 2024-01-14 17:58  
**Keywords** measurement water\_meas

[Edit](#)

## Creator Information

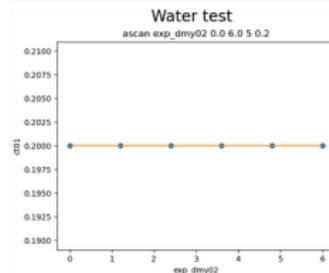
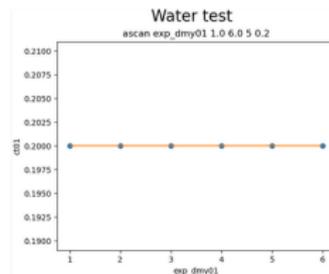
**Owner** Smithson  
**Investigator** appuser@fake.com  
**Contact Email** appuser@fake.com  
**Owner Group** testjk01-dmgt  
**Access Groups** testjk01-dmgt,testjk01-cbl,testjk01-part,p00dmgt,p00stalf

## File Information

**Source Folder** /asap3/petra3/gfs/p00/2022/data/testjk01/raw  
**Size** 4 MB

## Related Documents

**Input Datasets** testjk01/mywscan\_00008,  
testjk01/mywscan\_00009

 Public

# Questions ?

# Thank You !