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## Overview

This page contains a few instructions on how to use the data from the grid

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## Download a single file

Before submitting to the grid, it is useful to test your scripts locally. To do it, one should locate and download a single test file. Here are the instructions on how to do it:

### With xrdcp command:

```
xrdcp root://cms-xrd-global.cern.ch//store/path/to/file /some/local/path
```

from US, use `root://cmsxrootd.fnal.gov//store/path/to/file`. If global redirector is not working try `xrootd-cms.infn.it`

## Another ways of getting a file

### download from specific site

Locate the file in DAS [↗](#) by searching for `file dataset=DATASET`

example [▢](#) close example [▢](#)

```
file dataset=/SingleMuon/Run2017H-17Nov2017-v2/MINIAOD
```

Choose one site (in this example `t2_us_mit`), and get file PFN by executing the following commands (replace the site and file name by one you need):

```
site=T2_US_MIT
lfn=/store/data/Run2017H/SingleMuon/MINIAOD/17Nov2017-v2/90000/FA9FA831-8B34-E811-BA1D-008CFAC93C
pfl=`curl -ks "https://cmsweb.cern.ch/phedex/datasvc/perl/prod/lfn2pfn?node=${site}&lfn=${lfn}&pr
```

then I create a user proxy:

```
voms-proxy-init -voms cms
```

Set your UID from created proxy in `/tmp/x509up_u{UID}` ., and then set the correct `X509_USER_PROXY` and copy the file:

```
UID=58751
env -i X509_USER_PROXY=/tmp/x509up_u$UID gfal-copy -n 1 $pfl "file:///`pwd`/miniAOD.root"
```

## Locating a PFN (physical file name)

OR you can locate it physical file name

```
edmFileUtil -d /store/relval/CMSSW_10_6_4/RelValZMM_13/MINIAODSIM/PUpmx25ns_106X_upgrade2018_real
```

## Submit jobs using crab

### Crab operations

After submitting a job via the CRAB3ConfigurationFile, a folder PROJECTFOLDER will appear. You can see your submission process and do some operation using the crab commands. The full list of crab commands can be found here: CRAB3Commands

Here is the list of the most common commands:

- Inspect how the submission process proceeds: `crab status -d PROJECTFOLDER`
  - ◆ In case of errors, use `crab status --verboseErrors` for details
  - ◆ To resubmit failed jobs with extra options: `crab resubmit -d PROJECTFOLDER --maxmemory=4000 --maxjobruntime=360 --numcores=1 --jobids=1,2`
  - ◆ To kill a project: `crab kill -d PROJECTFOLDER`
- The results will appear in `cat PROJECTFOLDER | grep config.Data.outLFNDirBase | awk '{print $3}' | sed -e 's/"\\//\\eos\\/cms\\//g' | sed -e 's\\/group\\/g' | sed -e 's/"\\/g'`

### View jobs

To view running jobs goto <https://monit-grafana.cern.ch/>, click on JOBS CMS Task Monitoring - Task View

### Debug failed jobs

If some of the jobs have errors, you can rerun the job locally using the following commands:

- Inspect job ID with `crab status --long -d PROJECTFOLDER`. If all jobs have errors, then look at the first few jobs. Here we rerun for `--jobid=0`
- To see the job log, run `crab getlog --short -d PROJECTFOLDER --jobid=0` and inspect the PROJECTFOLDER/crab.log file

To resubmit the job locally:

- run `crab preparelocal -d PROJECTFOLDER`.
- from PROJECTFOLDER/local execute `run_job.sh 1` to run the first job, the job will be executed locally after unpacking CMSSW setup.
- kill the process with `Ctrl+C`
- run `cmsRun -j FrameworkJobReport.xml PSet.py` to inspect the output.

To inspect memory usage (you are limited to 2GB by default), execute `ps aux` in a different shell.

```
cd JOBNAME/inputs
cmsRun PSet.py
```

### Crabcache

Before executing these lines, run `export X509_USER_PROXY=/tmp/x509up_u58751`

- To get all the files uploaded by a user to the crabcache and the amount of quota (in bytes) he's using:

```
curl -X GET 'https://cmsweb.cern.ch/crabcache/info?subresource=userinfo&username=mpitt' --key $X509
```

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- To get more information about one specific file (the file must be owned by the user who makes the query):

```
curl -X GET 'https://cmsweb.cern.ch/crabcache/info?subresource=fileinfo&hashkey=697a932e19bd29127'
```

- To remove a specific file (currently you can only remove your files. In the future power users should be able to remove everything):

```
curl -X GET 'https://cmsweb.cern.ch/crabcache/info?subresource=fileremove&hashkey=697a932e19bd291'
```

- To get the quota each user has in MegaBytes:

```
curl -X GET 'https://cmsweb.cern.ch/crabcache/info?subresource=basicquota' --key $X509_USER_PROXY
```

## Restoring task folders:

To get full task list execute: `crab tasks`

- To restore lost folder: `crab remake --task=XXX`
- To clean the cache of killed job `crab purge FOLDER`

## Obtaining Luminosity per dataset

From `crab report`, the location of JSON-formatted report file is listed. Copy this file to `lplus`: `cp PROJECTFOLDER/results/processedLumis.json .`

```
#setup BRIL (for the first time run pip install)
export PATH=$HOME/.local/bin:/cvmfs/cms-bril.cern.ch/brilconda/bin:$PATH
# pip install --install-option="--prefix=$HOME/.local" brilws
# get lumi from the crab submission:
brilcalc lumi -b "STABLE BEAMS" -i processedLumis.json -c /cvmfs/cms.cern.ch/SITECONF/T0_CH_CERN/
```

## Using DAS

Several option exists to retrieve info about a dataset, here is an example for finding AOD parent file of miniAOD file:

```
for f in `dasgoclient --query="parent file=/store/data/Run2017D/SingleElectron/MINIAOD/09Aug2019_
dasgoclient --query="child file=$f" | grep AOD/09Aug2019_UL
done
```

❌ The additional option `--normtag`

`/afs/cern.ch/user/l/lumipro/public/Normtags/normtag_DATACERT.json` is not working for me...

## Accessing grid files in condor [↗](#):

To use local condor batch to analyze files located at remote sites add `use_x509userproxy = true` in condor jdl file and setup proxy in your run file (recommended to set the proxy path first):

```
export X509_USER_PROXY=${HOME}/private/.x509up_${UID}
echo YOURPASSWORD | voms-proxy-init -voms cms -rfc -out ${HOME}/private/.x509up_${UID} -valid 192
```

### debug condor jobs

Full list of jobs `condor_q -nobatch`

To connect to a running job: `condor_ssh_to_job JobId`

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If jobs on hold: `condor_q -hold -af HoldReason`

-- MichaelPitt - 2019-12-08

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