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- how to locate CMS data
- how to analyse CMS data on the grid (using CRAB)
- how to store your job output on the grid
- how to access this job output
  - by copying it to a local machine
  - interactively from the naf
  - with batch jobs on the naf
  - with grid jobs
- how to monitor your grid jobs

### **Outline**

- Locating Data
  - The Data Bookkeeping System
  - DBS Web Interface
  - DBS Query Language
- The CMS Remote Analysis Builder (CRAB)
  - Introduction
  - Configuration
  - Running CRAB
  - CRAB Server
  - Storing the Output
  - Publishing the Output
  - CRAB on the NAF
- Troubleshooting
  - Common Problems
- Monitoring Grid Jobs
- Dashboard



Dashboard

## Locating Data

The Data Bookkeeping System (DBS) is the authoritative source for information about stored data in CMS

- Information about produced data like location, file names, size, creation date, run number, ...
- Information is stored in MySQL and Oracle data base backends
- Several instances for production, analysis, etc. Most important one: global DBS
- APIs allow communication with DBS used e.g. by Monte Carlo production tools
- A Query Language (QL) has been developed to support complex DBS queries. Those can be done via:
  - Web interface: Data Discovery Service
  - Command Line Interface

### **DBS Web Interface**

### Webinterface for DBS searches:

http://cmsweb.cern.ch/dbs\_discovery/



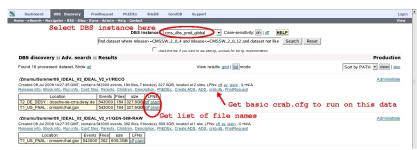
- Menu driven search
- Query Language Search
- Links to help and examples
- Different instances selectable (in 'Production' view only)



## **DBS Web Interface**

The search result gives access to information related to the dataset:

- Info about software releases, run numbers, lumi sections, related datasets, . . .
- Can obtain a basic configuration file to analyze this data with CRAB
- Can get a list of filenames (LFNs)



Click around to find any information you need.



## **DBS Query Language**

The DBS query language is SQL syntax oriented and is rather human friendly:

- QL Syntax: find <key1>, <key2.attribute> where <key> <op> <value> and/or ...
- Keywords: dataset, block, file, site, release, run, lumi, primds, procds, tier
- Operators: <=, <, >=, >, =, not like, like, in, between
- Some Attributes:
  - dataset: .name
  - block: .name, .size
  - file: .name,.numevents, .size
  - run: .number, numevents, .starttime, .endtime

### Some documentation can be found on

https://twiki.cern.ch/twiki/bin/view/CMS/QL

### and

https://twiki.cern.ch/twiki/bin/view/CMS/DataDiscoveryInterface



## DBS Query Language: Examples

#### Examples for the Data Discovery search

- find dataset where dataset like \*
  → look-up all datasets in DBS
- find dataset where dataset like \*Online\* and site like T2\_DE\*
   → look-up datasets with dataset path matching pattern \*Online\* and located at a T2\_DE site
- find dataset where run between 34850 and 36000 or run in (34850,34890)
   → look-up dataset with runs within given run ranges.
- find file where release>CMSSW\_1\_6\_7 and site=T2\_UK

   → find files located on T2\_UK sites which were processed with release CMSSW\_1\_6\_7 and above.
- find file,run where dataset=/Commissioning2008Ecal-A/Online/RAW
   → look-up files and runs for given dataset name
- find sum(file.size),run where dataset=/Commissioning2008Ecal-A/Online/RAW
   → look-up total size of files and list runs for given dataset name

A lot of examples can be found on: https://twiki.cern.ch/twiki/bin/view/CMS/QL

The CMS Remote Analysis Builder (CRAB) is a command line tool for analysis of CMS data on the grid Its purpose is

- to allow data analysis while hiding the complexities of the grid:
  - Find the distributed data
  - Take care of the runtime environment on the grid worker nodes
  - Execute the code the user developed locally
- to automate the workflow (status tracking, resubmissions,...) (CRAB server)

Need to tell CRAB about the desired CMSSW version, the dataset and the CMSSW configuration file to use.

## CRAB Workflow

- Create task
  - Prepare jobs for remote environment
  - Split input data according to your request and its distribution among sites
- Submit the jobs
- Monitor job progress (CRAB server)
- Move job output to a storage element (or return it to the user)
- Resubmit failed jobs
- Notify about progress via email
- Publish the output (make it available for grid/CRAB jobs)

## **CRAB Configuration**

CRAB is steered with a single configuration file (crab.cfg):

- Parameters are set as key = value pairs
- Parameters are grouped in macro sections like [CRAB],
   [CMSSW], [USER], ...

Templates with a minimal/full parameterset are distributed with the CRAB release (\$CRABDIR/python/(full\_)crab.cfg)

## **CRAB Configuration Example**

### A minimal crab.cfg file looks like this:

```
[CRAB]
jobtype = cmssw
scheduler = glite
[CMSSW]
### The data you want to access (to be found on DBS)
datasetpath=/RelValTTbar/CMSSW 3 1 0-MC 31X V1-v1/GEN-SIM-RECO
### The ParameterSet you want to use
pset=PhysicsTools/PatAlgos/test/patLayer1 fromAOD full cfg.py
### Splitting parameters
total number of events=-1
number of jobs = 15
### The output files (comma separated list)
output file = PATLayer1 Output.fromAOD full.root
[USER]
### OUTPUT files Management
return data = 1
## RB/WMS management:
rb = CNAF
group = dcms
```

Will introduce more parameters later ...



# First we need to set up the environment for gLite, CMSSW and CRAB:

- Set up the grid user interface: ini glite
- In your CMSSW src-directory: cmsenv
- Set up the local CRAB installation: ini crab

### If you want to use the DESY WMS:

• edit your crab.cfg file:

```
[GRID]
rb = DESY
```

copy its config in your working directory:

```
cp $GLITE_LOCATION/etc/cms/glite_wms.conf
glite_wms_DESY.conf
```

### After preparing the crab.cfg file you can start:

- Create jobs: crab -create
  - The project is created in a directory like crab 0 080903 142652
- Submit jobs: crab -submit [<all | number | range>] [-c <crab\_dir>] If -c is omitted the latest project in the current directory is taken.
- Get status of jobs: crab -status [-c <crab dir>]
- Get output of finished jobs:

```
crab -getoutput [<all | job number | range>] [-c
<crab dir>1
```

The output is by default stored in crab\_dir/res/ and for each job i consists of CMSSW\_i.stdout, CMSSW\_i.stderr, crab\_fjr\_i.xml (and output files).

## CRAB: Basic commands II

- Ocancel jobs:
   crab -kill < job number/range> [-c < crab\_dir>]
- Resubmit failed/cancelled jobs: crab -resubmit <number | range> [-c <crab\_dir>]
- Cleanup the directory crab -clean [-c <crab dir>]

A descriptions of all available options can be obtained with crab -h We will introduce a few more later .

## **CRAB Server**

### The CRAB server

- monitores the progress of user jobs
- resubmits failed jobs
- notifies via email when a certain fraction has finished

### The necessary configuration parameters are:

```
[CRAB]
server name=bari
[USER]
eMail=your@email.address
## Fraction of finished jobs before email notification:
thresholdLevel=100
```

Instead of retrieving your job output to the UI it is recommended to copy it on to storage element. In the crab.cfg this can be enabled with:

```
[USER]
return_data=0
copy_data=1
## Storage element at your home site or site name
storage_element= T2_DE_DESY
## subdirectory in your /store/user/<hypernews_name>
directory user remote dir = mySubDir
```

## Manipulating files on the SE

If you need to handle your files on a storage element

- dCache storage at DESY is mounted under /pnfs/desy.de/cms/ and can be still explored using 1s
- For managing your files on a storage element however you need to use grid tools
- You must setup the gLite UI and create a grid proxy before you can use them

```
Copy file from local disk to SE:
srmcp -2 "file:///path/file
srm://dcache-se-cms.desv.de:8443/srm/managerv2?SFN=
/pnfs/desy.de/cms/tier2/store/user/yourname/file"
Copy file from SE to local disk:
srmcp -2 -streams num=1
"srm://dcache-se-cms.desy.de:8443/srm/managerv2?SFN=
/pnfs/desy.de/cms/tier2/store/user/yourname/file file:///path/file"
List directory:
srmls "srm://dcache-se-cms.desy.de:8443/srm/managerv2?SFN=
/pnfs/desy.de/cms/tier2/store/user/yourname/"
```

#### Move/rename file:

```
srmmv "srm://dcache-se-cms.desy.de:8443/srm/managerv2?SFN=
/pnfs/desy.de/cms/tier2/store/user/yourname/oldfile
srm://dcache-se-cms.desy.de:8443/srm/managerv2?SFN=
/pnfs/desy.de/cms/tier2/store/user/yourname/newfile"
```

#### Remove file:

srmrm "srm://dcache-se-cms.desy.de:8443/srm/managerv2?SFN=
/pnfs/desy.de/cms/tier2/store/user/yourname/file"

#### If you want to remove all files from a directory:

```
for i in `ls /pnfs/desy.de/cms/tier2/store/user/user_name/directory`; do srmrm "srm://dcache-se-cms.desy.de:8443/srm/managerv2?SFN= /pnfs/desy.de/cms/tier2/store/user/user_name/directory/\$i"; done
```

#### Make directory:

```
srmmkdir "srm://dcache-se-cms.desy.de:8443/srm/managerv2?SFN=
/pnfs/desy.de/cms/tier2/store/user/yourname/newdir"
```

#### Remove (empty) directory:

```
srmrmdir "srm://dcache-se-cms.desy.de:8443/srm/managerv2?SFN=
/pnfs/desy.de/cms/tier2/store/user/yourname/dir"
```

## Publishing your files in DBS I

Output files which you want to analyse further with CRAB jobs (e.g. a private MC production) have to be published in DBS.

```
[USER]
return data=0
copy data=1
storage element = T2 DE DESY
publish_data=1
publish data name=aNameForYourDataSet
# There are several instances, ask the expert in your institute which one
to use
dbs_url_for_publication=
https://cmsdbsprod.cern.ch:8443/cms dbs ph analysis 02 writer/servlet/DBSServlet
publish_with_import_all_parents=0
```

### The files will appear at:

SE+/store/user/<hypernewsname>/<PDName>/aNameForYourDataSet/<hash>

## Publishing your files in DBS II

Run CRAB as usual and retrieve the output. If all jobs have been successful qo.

crab -publish

You can check the results on the command line:

InspectDBS2.py -DBSURL=<dbs url> -datasetPath=<name of your dataset> or on the DBS web interface selecting the right instance in the production view

In order to run CRAB jobs on your own dataset you need to set:

#### [CMSSW]

dbs url=

http://cmsdbsprod.cern.ch/cms dbs ph analysis 02/servlet/DBSServlet datasetpath=/OriginalDataSet/aNameForYourDataSet/USER

For details consult https://twiki.cern.ch/twiki/bin/view/CMS/ SWGuideCrabForPublication

You can delete your dataset from DBS with:

python DBSDeleteData.py -DBSURL=<dbs\_url\_for\_adminstrator> -datasetPath=<name of vour dataset>



### CRAB is documented on several webpages:

```
https:
```

//twiki.cern.ch/twiki/bin/view/CMS/WorkBookRunningGrid https:

//twiki.cern.ch/twiki/bin/view/CMS/SWGuideCrabHowTo https://twiki.cern.ch/twiki/bin/view/CMS/SWGuideCrabFaq

### Hypernews list for CRAB suppport:

hn-cms-crabFeedback@cern.ch

Most problems are very frequent, so seach the forum before writing

### CRAB can be used to submit jobs to the NAF batch system.

```
[CRAB]
scheduler=sge
[GRID]
# From the NAF you can only access data located at DESY
se_whitelist=desy.de
[SGE]
# parameters for SGE job submission
resource = -V -1 h_vmem=2G -1 site=hh -1 h_cpu=0:60:00 -1 os='1s4|s15'
```

Important: When using the local batch system you **cannot**:

run on data located at other sites

## **Common Problems**

### Troubleshooting:

- Strange python errors or commands not found: Environment not set up correctly. Set up gLite, CMSSW and CRAB in this order
- Failed jobs: After crab -getoutput do a crab -status to see the exit codes. Check the wiki for their meaning: https://twiki.cern.ch/twiki//bin/view/CMS/JobExitCodes
- Many failures are related to the job output:
  - 60302: output file not found → check file name to be identical in crab.cfg your CMSSW config file
  - $\bullet$  60303: file already exists in SE  $\rightarrow$  Delete it or change the storage path
  - 70000: output too big → The size of the output sandbox is limited, use the copy\_data option
- No compatible site found: Check your job requirements, availability of data and CMSSW version
- Get more information from the WMS about failed/aborted jobs: crab
   -postMortem



One can manage CRAB jobs using the gLite tools:

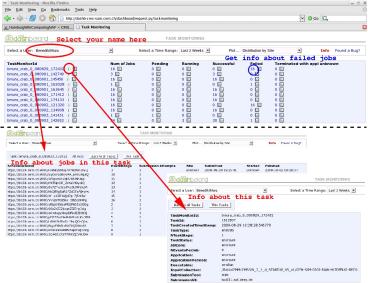
- Get the job IDs for your crab jobs / the job collection
  - by crab -printId
  - by searching in crab\_dir/log/crab.log for the Collection ID, e.g.:

```
https://lb106.cern.ch:9000/s22aPplJptmt6dsm2B9LWg
```

- Use the glite commands to manage these jobs
  - glite-wms-job-status <jobID>
  - glite-wms-job-logging-info <jobID> (equivalent to -postMortem option)
  - glite-wms-job-output <jobID>
  - glite-wms-job-cancel <jobID>
- inspect JDL with crab -createJdl 1

## **Monitoring Grid Jobs**

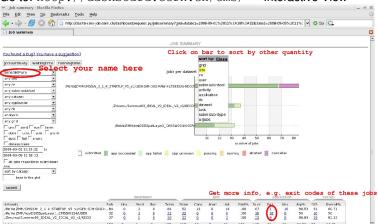
Go to:  $\texttt{http://dashboard.cern.ch/cms/} \to \textbf{Task monitoring for the analysis users}$ 





## **Monitoring Grid Jobs**

### Go to: http://dashboard.cern.ch/cms/ $\rightarrow$ Interactive View



## Monitoring Grid Jobs

- There is a delay for your jobs to show up
- Info on dashboard may differ from CRAB/glite job info. The later is more reliable, because reporting to the dashboard might fail.
- If many of your jobs fail check if this is a site problem:
  - Check if they all ran at the same site and if other user get the same errors at that site
  - Check the 'Site status board' link on the dashboard: check the 'Analysis' column
  - If you have problems at a particular site try to use another one hosting that dataset (black/white list in crab.cfg)
  - If the problem persists inform site admins/open a GGUS ticket