DRAFT

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DRAFT How to run DQM code for DT Offline using CRAB at CAF

Pre-requirements: you need to be on lxplus and to be allowed to run at CAF

1. Set up CMSSW area

- Download and build the code the first time:

```
cd YOURDIR
scramv1 project CMSSW CMSSW_2_1_10
cd CMSSW_2_1_10/src
cvs co DQM/DTMonitorModule
cvs co DQM/DTMonitorClient
cvs co UserCode/DTDPGAnalysis
eval `scramv1 runtime -csh`
scramv1 b
```

- Set the enviornment:

```
cd YOURDIR/CMSSW_2_1_10/src
eval `scramv1 runtime -csh`
```

2. Set up CRAB environment

```
source /afs/cern.ch/cms/ccs/wm/scripts/Crab/crab.csh
```

3. Configure CRAB to run DQM DT Offline code

- Copy the crab template configuration file:

```
cp YOURDIR/CMSSW_2_1_10/src/UserCode/DTDPGAnalysis/test/crab_runDQM_template.cfg .
```

- Configure it changing:
  - ♦ the pset location, filling YOURDIR:

```
pset  = YOURDIR/CMSSW_2_1_10/src/UserCode/DTDPGAnalysis/python/test/runDQMOfflineDP
```

  - ♦ the area where to stage out the output filling CASTOR_AREA:

```
storage_path=/castor/cern.ch
lfn=/CASTOR_AREA/DQMDTRunINSERTRUN
## for example:
# lfn=/user/a/afanfani/DQMDTRunINSERTRUN
```

  - ♦ you might want to change the statistics to precess and the splitting into several jobs:

```
total_number_of_events  = 400000
number_of_jobs          = 20
```

- The replacement of the run (i.e. 66733) to use can be done simply with:

```
less  crab_runDQM_template.cfg | sed -e "s?INSERTRUN?66733?g"  >  crab_runDQM_66733.cfg
```

4. Submit the jobs to produce DQM root files

- Submit the jobs:

```
crab -create -submit -cfg crab_runDQM_66733.cfg
```

- Check the status with:

```
crab -status -c runDQM_66733
```

5. Produce DQM plots

Once the jobs above have finished they have produced several DQM root files that need to be read to produce DQM plots.

- Download the template python configuration file to produce those plots and an auxiliary script:

```
cp YOURDIR/CMSSW_2_1_10/src/UserCode/DTDPGAnalysis/python/test/runDQMOfflineDPGClients_cf
cp YOURDIR/CMSSW_2_1_10/src/UserCode/DTDPGAnalysis/test/configureDQMplotter.sh .
```

- Run the configureDQMPlotter.sh script providing the Run Number and the castore area where DQM root files where produced:

```
./configureDQMPlotter.sh <RunNumber> /castor/cern.ch/user/a/afanfani/DQMCRAFT/DQMDTRun<Run
```

- Run the cmsRun :

```
cmsRun runDQMOfflineDPGClients_cfg_<Run Number>.py
```

The output will be a directory Run with summary plots and plots split into the usual wheel's sub-directories.

DRAFT How to store output with CRAB 2_4_0

Warning: since CRAB_2_4_0 release the parameters for stageout configuration are changed, so your older crab.cfg can not be used.

CRAB allows you to copy your analysis outputs directly to a Tier2 or Tier3 Storage Element. You can decide to store them in a Storage Element of an "official CMS site" or in your local SE.

The various options are:

1. Stage out to an "official CMS site" *without* publication in DBS

you have to configure the crab.cfg with:

```
[USER]
copy_data = 1
storage_element = "The official CMS site name"
user_remote_dir = subdirectory where your output will be stored
```

- The official CMS site names are reported in the SiteDB list ☑. The mapping between the StorageElement name and CMS site names is reported here ☑. Note that there are two exceptions: you

have to use T1_FR_CCIN2P3_Buffer instead of T2_FR_CCIN2P3 and T2_RU_IHEP_Disk instead of T2_RU_IHEP.

- The area in which your output file will be written is:

```
site's endpoint +  /store/user/<yourHNusername>/<user_remote_dir>/<output-file-name
```

where the site's endpoint is discovered by CRAB and your HyperNews username is extracted form SiteDB.

Important Note: you need to be registered in SiteDB. The instructions to register in SiteDB are in: SiteDBForCRAB .

For example:

```
storage_element = T2_ES_CIEMAT
user_remote_dir = myTestDir
```

will write the output into:

```
srm://srm.ciemat.es:8443/srm/managerv2?SFN=/pnfs/ciemat.es/data/cms/store/user/<yourHNusername
```

2. Stage out to an "official CMS site" *with* publication in DBS

you have to configure the crab.cfg with:

```
[USER]
copy_data = 1
storage_element = "The official CMS site name"
publish_data=1
publish_data_name = "data name to publish"
dbs_url_for_publication = "your local dbs_url"
```

- The official CMS site names are reported in the SiteDB list . The mapping between the StorageElement name and CMS site names is reported here . Note that there are two exceptions: you have to use T1_FR_CCIN2P3_Buffer instead of T2_FR_CCIN2P3 and T2_RU_IHEP_Disk instead of T2_RU_IHEP.
- The directory and LFN of your output file are enforced to be:

```
site's endpoint +  /store/user/<yourHyperNewsusername>/<primarydataset>/<publish_data_name>
```

where the site's endpoint is discovered by CRAB and your HyperNews username is extracted form SiteDB. More information about publicataion are available in SWGuideCrabForPublication.

3. Stage out to a "not official CMS site" that means not included in the

you have to write in the crab.cfg:

```
[USER]
copy_data = 1
storage_element = the complete Storage Element name (i.e se.xxx.infn.it).
storage_path= the full path of the Storage Element writeable by all
lfn = the directory or tree of directories that !CRAB will create under the storage path of t
```

where *storage_path* is the mountpoint of the SE (i.e /srm/managerv2?SFN=/pnfs/se.xxx.infn.it/yyy/zzz/) and *lfn* is the directory or tree of directories that CRAB will create under the storage path of the SE.

1. Stage out to an "official CMS site" without publication in DBS   3

That *lfn* will be used as logical file name of your files in the case of publication in DBS. Publication in DBS make sense if the data are accessible via a Grid Computing Element.

4. Stage out in your own directory in CASTOR at CERN

You are encouraged to stage out your data at Tier2s you are associated with, however if you want to stage out in your area in CASTOR you have to configure the crab.cfg with:

```
[USER]
copy_data = 1
storage_element=srm-cms.cern.ch
storage_path=/srm/managerv2?SFN=/castor/cern.ch
lfn=/user/<yourinitial>/<username>/whatever
```

You should also make sure that your area need to have permissions to allow write access to the group:

```
rfchmod 775  /castor/cern.ch/user/.....
```

5. CAF Stage out

If you are running jobs at CAF then the stageout options are:

- Stage out into your own directory in CASTOR configuring crab.cfg with:

```
[USER]
  copy_data = 1
  storage_element=srm-cms.cern.ch
  storage_path=/castor/cern.ch
  lfn=/user/<yourinitial>/<username>/whatever
```

- Stage out into CAF /store/user area

```
[USER]
copy_data = 1
storage_element=T2_CH_CAF
```

T2_CH_CAF is the offical site name for CAF and the stageout configuration there is the same as described in Section 1. and Section 2. above.

END END END END CRAB part

-- AlessandraFanfani - 21 Jan 2007

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