CRAB: Advanced

J Term III
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CMS/Fermilab

Audience

- Assume you are already familiar with using CRAB
  - Lots of developments in the last year
  - Online tutorial for first time users
    - https://twiki.cern.ch/twiki/bin/view/Main/EricVaanderingCRABPreTutorialJTerm
- Give you an overview of things you can do with CRAB, some new, some never really explained
  - Using CRABServer & LPC CAF
  - Staging out and publishing data
  - Multiple datasets, RAW data
- CRAB Coming Attractions

Goals

- This talk won't explain in detail how to do anything but the most trivial things
- Instead, a quick overview and a pointer to more information
  - Usually a Workbook page or other Wiki page
- Following the talk (and break) we'll have a hands-on session
  - Encourage you to pick something new from the list I show and try it
  - PAT/SK starts at 11:00

CRABServer

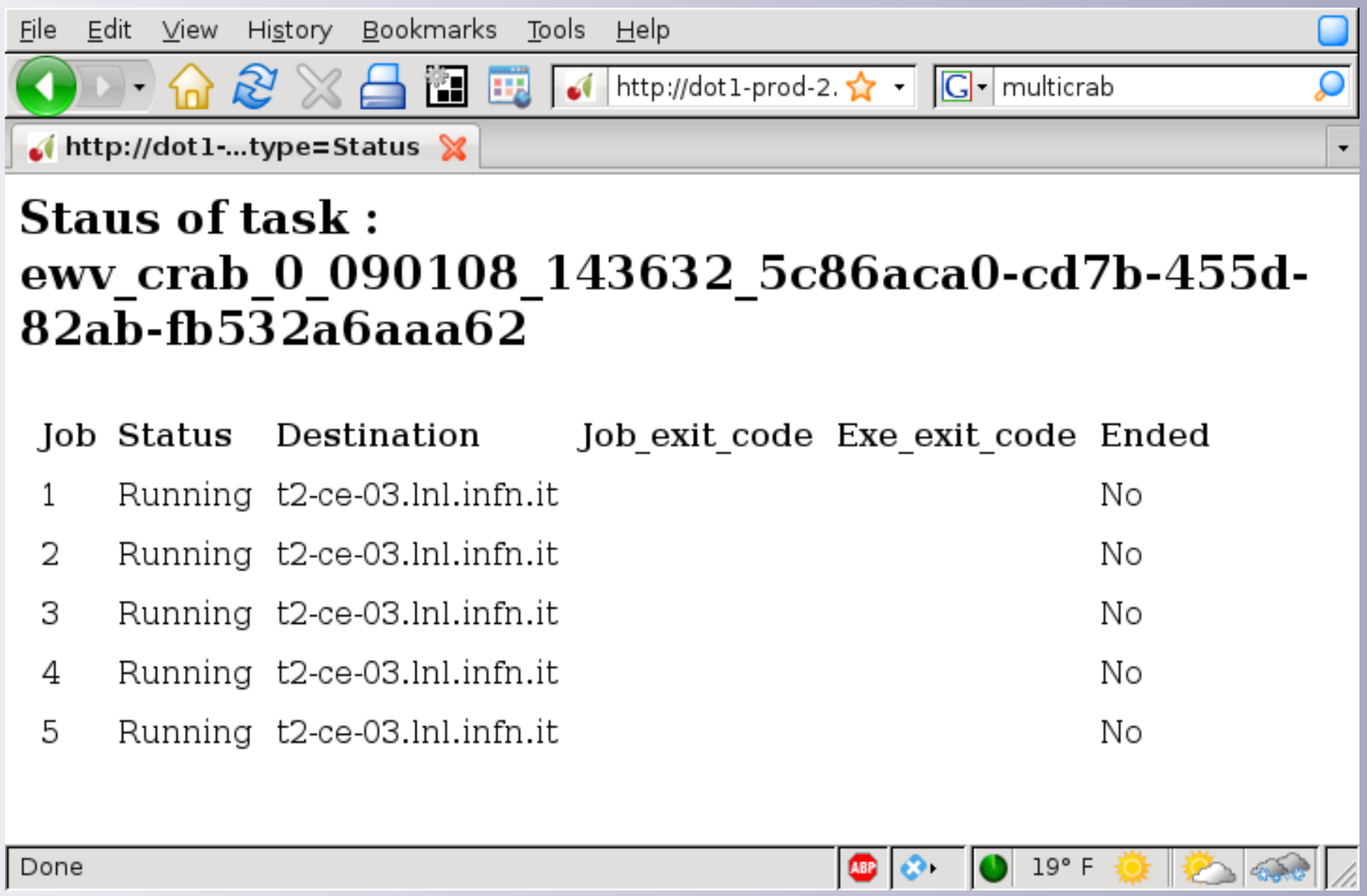
- What is the CRAB Server?
  - A central server (just a few in CMS)
  - Submits jobs, watches, re-submits
  - Collects output for easy retrieval
  - Best for large numbers of jobs (~20 or more)
  - Does a lot of the work of the user
  - Can notify you when your jobs are done

CRABServer Usage

- To first order very simple
  - Add `server_name = bari` to [CRAB] section of cfg
  - https://twiki.cern.ch/twiki/bin/view/CMS/CrabServer#Server_available_for_users keeps a list of servers you can use
- All commands (-create, -submit, -status, -getouput, -kill) work as usual
  - CS checks status itself every few minutes, so you are getting cached information
- Can be notified when your jobs finish
  - eMail = user@fnal.gov
  - thresholdLevel=100

CRABServer Monitoring

- In addition to the usual crab -status, you can directly check on your jobs with the server
  - crab -printId gives you the task name and URL to use



Tier1 Restrictions

- CRAB will no longer submit jobs to CMS Tier1 sites
  - Tier0 blocked some time ago
  - Tier1 resources are committed to central processing for CMS
  - Nothing left over for chaotic user analysis
  - If your favorite dataset is not at a Tier2, then you have to request it be copied to one
    - Tier2's are associated with Analysis Groups
      http://indico.cern.ch/materialDisplay.py?contribId=28&sessionId=22&materialId=slides&confId=41026
- Not quite an absolute ban, as we'll see later

FNAL LPC CAF Usage

- One way around the block on Tier1 sites
- From cmslpcXX you can submit to the local condor queue
  - No need to write your own job splitting
  - Provides the same interface you are used to
  - Data must be at FNAL, but LPC CAF has access to all the same data as the FNAL Tier1
- Just change to “scheduler = condor” in your crab.cfg
- One time setup with ~/.profile, for details see https://twiki.cern.ch/twiki/bin/view/Main/CRABonLPCCAF

Staging Out Data

- Every user will have access to /store/user space at a Tier2
- CRAB has a nice interface to this
  - Don't need to know details of directory hierarchy at a remote site
  - [USER]
    copy_data = 1
    storage_element = T1_US_FNAL_Buffer
    user_remote_dir = myTopAnalysis
- Will look up your HN username from SiteDB
- You can get storage space at your “local” Tier2
  - http://www.uscms.org/uscms_at_work/software_computing/tier2/store_user.shtml

Staging Out Data - 2

- The previous way of staging out to dCache resilient is still supported
- Not put onto tape (unlike /store/user at FNAL)
- crab.cfg settings have changed

```
[USER]
copy_data = 1
storage_element = cmssrm.fnal.gov
storage_path = /srm/managerv2?SFN=/resilient/USERNAME/OPTDIR/
user_remote_dir = SUBDIRECTORY
```

- For more options, see
  https://twiki.cern.ch/twiki/bin/view/CMS/SWGuideCrabHowTo#Store_output_with_CRAB_2_4_serie

Publishing Data

- You have to publish into a local DBS, not Global Production DBS
- Before submitting jobs, you have to prepare your crab.cfg config file to eventually publish
  - [USER]

```
copy_data = 1
storage_element = CMS_site_name
   (i.e T2_IT_legnaro)
publish_data=1
publish_data_name = data_name_to_publish
   (i.e  myprocessingCMSSW_1_6_8)
dbs_url_for_publication = your_local_dbs_url
   (i.e https://cmsdbsprod.cern.ch:8443/cms_dbs_prod_local_09_writer/servlet/DBSServlet)
```

- crab -publish when your output is retrieved
- More info:
  https://twiki.cern.ch/twiki/bin/view/CMS/SWGuideCrabForPublication

Using the Parent Dataset

- CMSSW supports running a job on two groups of files simultaneously
  - 2nd dataset must be parent of the dataset
  - Used to access event products discarded in later processing
    - e.g. RECO+RAW it was produced from
- CRAB supports this too
  - Both datasets must be at the same site
  - Set use_parent = True in the [CMSSW] section of crab.cfg

MultiCRAB

- Run CRAB multiple times on different datasets (other use cases too)

- Typical config file:

```
[MULTICRAB]
cfg=crab.cfg
[COMMON]
CMSSW.total_number_of_events=-1
[Wmunu]
CMSSW.datasetpath=/Wmunu/CSA08_CSA08_S156_v1/GEN-SIM-RECO
CMSSW.events_per_job=1000
[Zmunu]
CMSSW.datasetpath=/Zmunu/CSA08_CSA08_S156_v1/GEN-SIM-RECO
CMSSW.events_per_job=5000
```

- Creates a crab job in Wmunu/Zmunu directories

- Same commands as crab (-create, submit, etc.)

- More info:
  `https://twiki.cern.ch/twiki/bin/view/CMS/SWGuideMultiCrab`

CRAB Hints

- -extend: submit jobs on new data in a dataset (open datasets)
- -copyData: retrieve data from SE to working directory
- -match: shows if resources are available for your job (after white/blacklisting)
- -postMortem: why did your job abort?
- $CRABDIR/python/full_crab.cfg shows a config file with ALL available options

Coming Developments

- CondorG + CRABServer: quick, reliable access to US resources
- scheduler=glidein: pilot jobs pull your job to a site where CPU available and releases verified
- CRABServer+glidein
- Submission to CRABServer without LCG middleware (easily installed on your laptop)
- CRABServer for access to Tier1 data
- Support for Analysis Datasets
  - List of good run/lumis or run/events with a dataset