### SWIF and hdswif

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### SWIF

- Scientific Workflow Indefatigable Factotum
- Developed by Chris Larrieu in SciComp group <a href="mailto:larrieu@jlab.org">larrieu@jlab.org</a>
- <a href="https://scicomp.jlab.org/docs/swif">https://scicomp.jlab.org/docs/swif</a>
- Advantages:
  - Better control
    - Auger does not relate tape retrieval and jobs efficiently
    - Auger submission is slow
       (Java parsing XML)
    - Control over jobs in phases

- ► Info on jobs
  - Success/problems
  - Resource usage



### Using SWIF Directly

create workflow swif create my\_workflow

```
swif command
                                                                                           swif options
 swif add-job -workflow my_workflow -project gluex -track reconstruction -cores 6 -disk 40g
ram 5g -time 8h -os centos65
-input hd rawdata 002333 000.evio mss:/mss/halld/RunPeriod-2014-10/rawdata/Run002333/
hd rawdata 002333 000.evio
-stdout /home/gxproj1/logfiles/stdout
-stderr /home/gxproj1/logfiles/stderr
-name my_job
home/gxproj1/script.sh TAGH_online 002333 000 6
```

script to execute with options

register job

```
swif run my_workflow
                               run jobs: SWIF will dispatch jobs as it deems fit
swif status my_workflow
                               check status
swif status my_workflow -runs
                               check status for individual jobs
swif cancel my_workflow -delete
                               cancel jobs, option -delete removes workflow
```

### hdswif

- For most part just a wrapper around swif, but also
  - use config file to set up jobs more easily
  - organize SWIF output to check job status
- Check out from svn: <a href="https://halldsvn.jlab.org/repos/trunk/scripts/monitoring/hdswif">https://halldsvn.jlab.org/repos/trunk/scripts/monitoring/hdswif</a>
- Written in python, uses PyROOT (officially ROOT supported Python extention) for ROOT functionality (histograms, graphics, etc.)
- Offline monitoring code developed by Sean was heavily referenced for development, config file similar to Nathan's Julia scripts



### How swif works

- Can run by typing swif in ifarm terminal
- Jobs are grouped into workflows, most natural to have separate workflows for different kinds of jobs
- Can get info with

```
> swif help
> swif help [command]
```

- List all workflows:
- > swif list
- Show workflow status:
- > swif status [workflow]



## Setting Up hdswif

- Check out source code: <a href="https://halldsvn.jlab.org/repos/trunk/scripts/monitoring/hdswif">https://halldsvn.jlab.org/repos/trunk/scripts/monitoring/hdswif</a>
- Provide valid \$ROOTSYS compiled with PyROOT enabled, have
   \$ROOTSYS/bin in PATH, \$ROOTSYS/lib in LD\_LIBRARY\_PATH
- hdswif will set PYTHONPATH to contain \$ROOTSYS/bin internally
- The officially supported ROOT builds on the JLab ifarm CentOS6.5

/group/halld/Software/builds/Linux\_CentOS6-x86\_64-gcc4.4.7/root/prod

has PyROOT enabled



## Wrappers in hdswif

• All of the following are equivalent:

swif command	hdswif command	what it does
swif list	hdswif.py list	Lists all workflows for user
swif create [workflow]	hdswif.py create [workflow]	Create new workflow
swif status [workflow]	hdswif.py status [workflow]	Show status of workflow
swif run [workflow]	hdswif.py run [workflow]	Start submitting jobs
swif cancel [workflow]	hdswif.py cancel [workflow]	Cancel running jobs

Commands wrapped for convenience, but calling swif directly is faster



# Additions in hdswif.py

hdswif.py command	result	
hdswif.py fullstatus [workflow] [format]	Show status of all runs, equivalent to swif status [workflow] -runs -summary -display [format] [format] is one of simple, xml, json	
hdswif.py run [workflow] [njobs]	Run only [njobs], equivalent to swif run [workflow] -joblimit	
hdswif.py delete [workflow]	Stop all running jobs and delete workflow. Equivalent to swif cancel [workflow] -delete	
hdswif.py summary [workflow]	Create XML file for all jobs, and summary webpage of results based on this XML file	



## Adding Jobs

#### • In swif:

swif command

swif options

```
> swif add-job -workflow my_workflow -project gluex -track reconstruction -cores 6 -disk 40g
-ram 5g -time 8h -os centos65
-input hd_rawdata_002333_000.evio mss:/mss/halld/RunPeriod-2014-10/rawdata/Run002333/
hd_rawdata_002333_000.evio
-stdout /home/gxproj1/logfiles/stdout
-stderr /home/gxproj1/logfiles/stderr
-name my_job
/home/gxproj1/script.sh TAGH_online 002333 000 6
```

script to execute with options

#### • In hdswif:

```
> hdswif.py add my_workflow -c myconfig.txt
```

all options handled with config file



# Config File Example

• Included example input.config:

```
PROJECT
                               gluex
TRACK
                               reconstruction
OS
                               centos65
NCORES
                               40
DISK
RAM
TIMELIMIT
                               myjobs
JOBNAMEBASE
                               2015-03
RUNPERIOD
                                                Example of other variables included in variable.
                               99
VERSION
OUTPUT TOPDIR
                               /volatile/halld/test/RunPeriod-[RUNPERIOD]/ver[VERSION]
                               /home/gxproj5/halld/hdswif/script.sh
SCRIPTFILE
                               /home/gxproj5/halld/hdswif/setup jlab-2015-03.csh
ENVFILE
```

Must specify full path

These will overwrite defaults - safer to specify them in config file



## Config File Variables

- Variables should be obvious for the most part
- RUNPERIOD is used to look for file in /mss/halld/RunPeriod-[RUNPERIOD]/rawdata/ for evio data files
- VERSION is a variable for offline monitoring do not need to use
- Config variables can depend on each other:

```
OUTPUT_TOPDIR /volatile/halld/test/RunPeriod-[RUNPERIOD]/ver[VERSION]
```

• Replacements will be made (do not put in cyclic dependencies)



## User Tags

- To easily access information about jobs, SWIF allows user-defined tags
- Specify with -tag [tag name] [tag value] when using SWIF
- hdswif gives each job tags user\_run and user\_file for the run and file specified for parsing output



# Specifying Runs/Files

- Specify runs, files with -r [RUN] and -f [FILE]
- If option -r is not specified, will run over ALL runs in RUNPERIOD
- Same for files
- Can use UNIX-style wildcards

```
> hdswif.py add my_workflow
> hdswif.py add my_workflow -r 3185
> hdswif.py add my_workflow -r 3185 -f 1
> hdswif.py add my_workflow -r '318[05]' -f '01[0-9]'
```

Run over all runs, files in RUNPERIOD

Run over all files in run 003185

Run over file 001 in run 003185

Run over files 010-019 in run 003180, 003185



## Re-Submitting Jobs

• In swif:

```
swif command modification problem type

> swif modify-jobs -workflow my_workflow -ram add 2gb -problems AUGER-OVER_RLIMIT
```

• In hdswif:

Currently only supports AUGER-OVER\_RLIMIT, can add more resolutions to different types of problems as they show up



## Job Summary

• In hdswif:

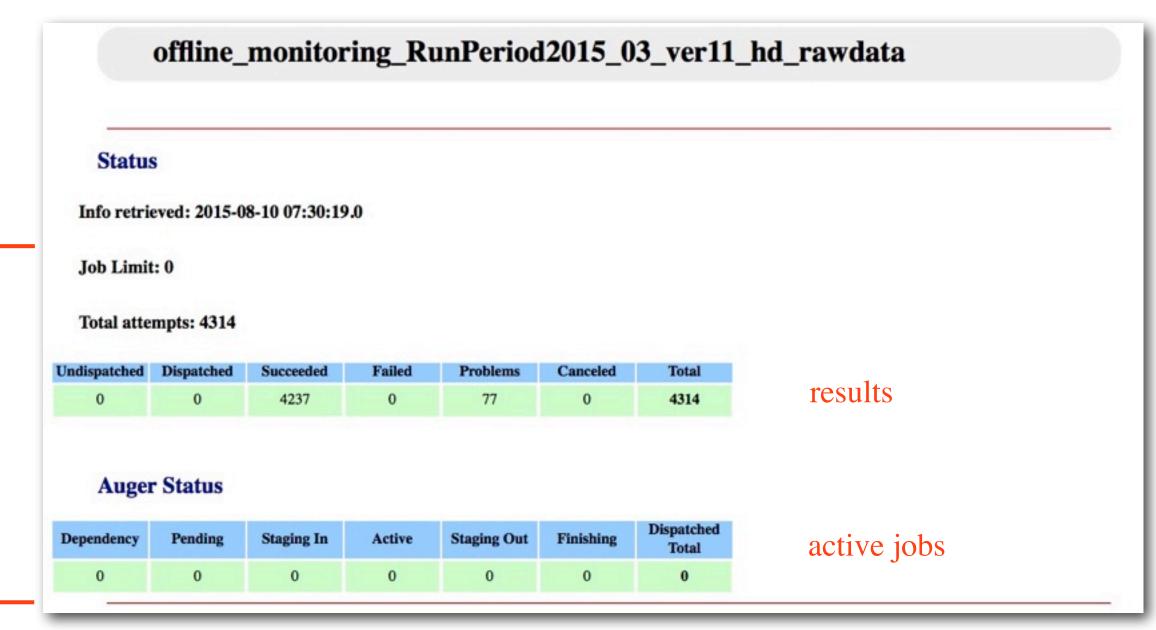
> hdswif.py summary my\_workflow

Creates html page summary\_swif\_output\_[workflow].html

Note:

Need CSS file mystyle.css for html formatting, included in svn

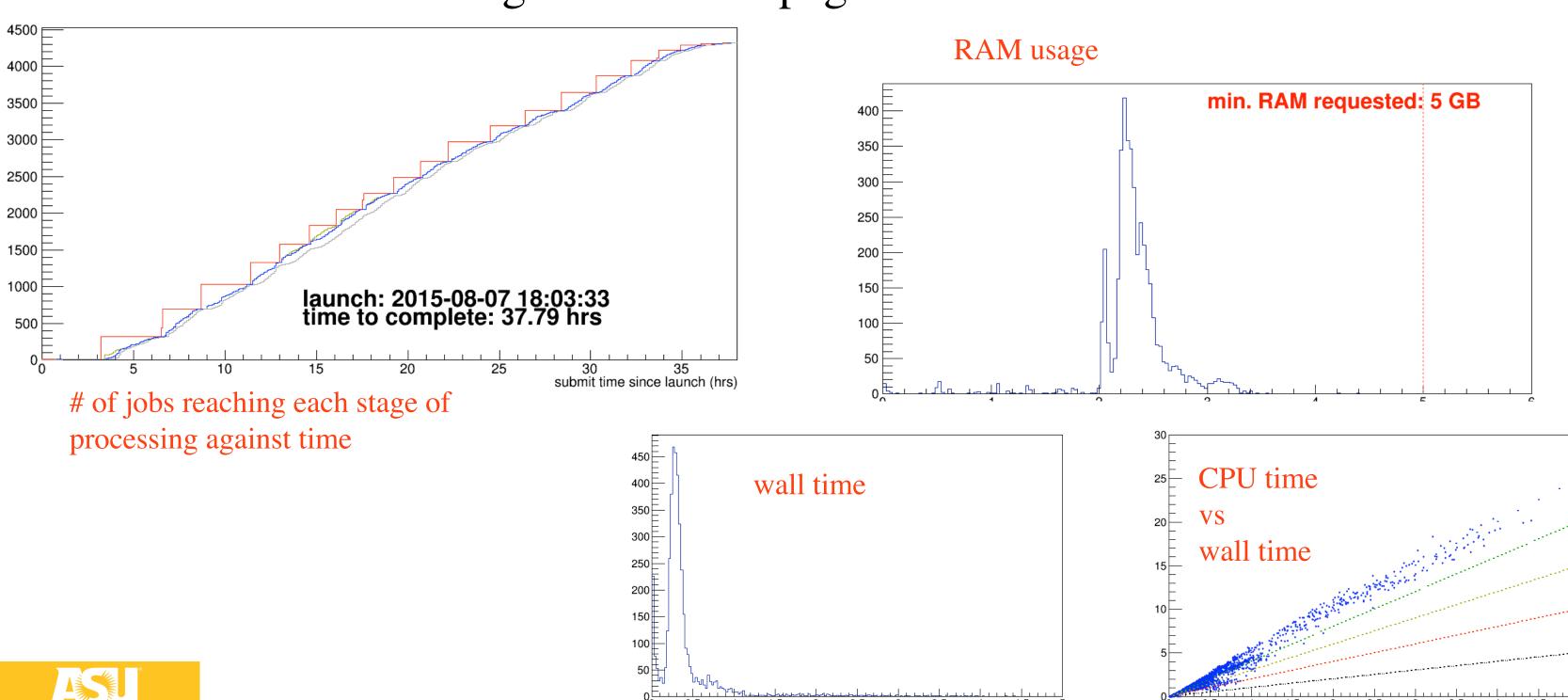
summary of jobs





# Job Summary Figures

• All included in same generated webpage



### hdswif Cheatsheet

hdswif command	what it does
hdswif.py create [workflow]	Create workflow
hdswif.py status [workflow] (format)	Check status
hdswif.py add [workflow] -c (config file) -r (runs) -f (files)	Add jobs to workflow
hdswif.py run [workflow]	Run workflow
hdswif.py run [workflow] (n)	Only run n jobs
hdswif.py resubmit [workflow] (n)	Resubmit jobs with nGB of additional RAM
hdswif.py cancel [workflow]	Cancel all dispatched jobs
hdswif.py delete [workflow]	Delete workflow



### TO DO

- Working with Chris on quicker batch submission
- Better control of resubmitting failed jobs
- Freeze option to stop modifications to workflow

• Questions, comments, requests are very welcome

