

**SGCI Webinar:  
Empowering job  
management in Science  
Gateways with  
HTCondor**

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# University of Wisconsin Center for High Throughput Computing



# HTCondor

- › Open source distributed high throughput computing
- › Schedule, provision, manage compute resources, containers, jobs, and workflows
- › Primary objective: assist the scientific community with their high throughput computing needs
- › Mature technology...

# Mature... but actively developed

- › Regular releases, both a stable (bug fixes only) and new features series
- › Open source development model
- › Evolve to meet the needs of the science community in an ever-changing computing landscape

	All Time	12 Month	30 Day
Commits:	39067	2349	141
Contributors:	152	21	10
Files Modified:	11588	1665	169
Lines Added:	12352208	444401	29395
Lines Removed	6810332	187595	7835

Source: <https://www.openhub.net/p/condorproject>

# Why am I presenting?

- › Our goal is for folks who work on science gateways to focus on the interaction with the science and scientists, and not worry about provisioning, scheduling, and job/workflow management.
- › Job management work has been done, why reinvent?
- › Many organizations have built gateways on top of HTCondor:
  - LHC CMS, Pegasus, BMRB, NEOS, Leica, Dreamworks, Hubble Telescope Operations, NOAA, ..

**THREE THINGS YOU SHOULD  
KNOW ABOUT HTCONDOR**





**Take Away Item #1:  
HTCondor embodies principle  
*"Submit Local, Run Global"***

**What does this mean?**

# Well, HTCondor is different...

- › Unlike a typical scheduler, HTCondor does *not* require:
  - A shared file system (NFS, Gluster, ...) between submit and execute (worker) nodes
  - Scheduler services installed by root and running as root
  - Unified user logins between submit and execute nodes
  - Full network communication between nodes
  - Static and reliable set of compute servers
- › Result: Once a job is submitted into HTCondor, it can run almost anywhere

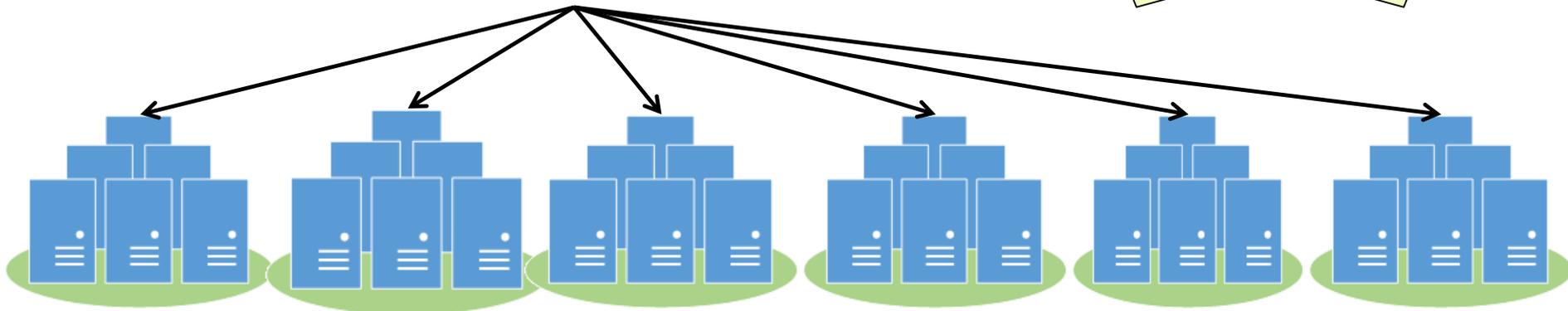


# Science Gateway

Submit jobs or workflows

"Submit local...  
and run global!"

## HTCCondor



Local  
HTCCondor  
cluster

Remote  
HTCCondor  
cluster

Backfill  
SLURM,  
PBS, SGE  
campus  
clusters

Open  
Science  
Grid  
(OSG)

EXCEDE

Amazon  
EC2

# Submitting Jobs

- › Submit a single batch or interactive job, a "bag" of jobs, or a workflow via
  - Command line tools or
  - Python module
- › Can specify resources required, files to transfer (if required) or stream, job priority, submitting user and group, retry policy, ...
- › Monitor progress of your remote job via
  - command-line tools
  - Python module
  - streaming stdout / stderr
  - job event log file (both human readable and machine readable)
  - condor\_ssh\_to\_job

# Example of a job submit

```
% condor_submit job.submit
```

```
job.submit
```

```
executable = analyze.exe  
arguments = file.in file.out  
transfer_input_files = file.in
```

```
log = job.log
```

```
queue 1
```

# Example of a bag of 500 jobs with InitialDir

(submit\_dir)/

job.submit	job0/	job1/	job2/
analyze.exe	file.in	file.in	file.in
	job.log	job.log	job.log
	job.err	job.err	job.err
	file.out	file.out	file.out

job.submit

```
executable = analyze.exe
initialdir = job$(ProcId)
arguments = file.in file.out
transfer_input_files = file.in

log = job.log
error = job.err

queue 500
```

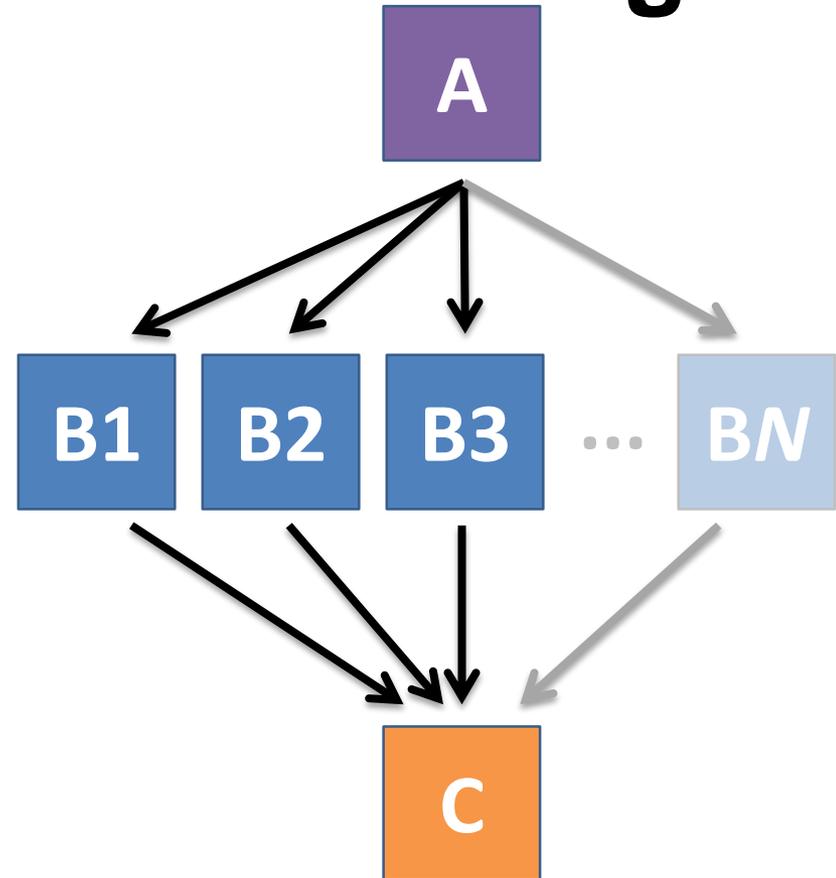
# Workflows with condor\_dagman

## Basic DAG input file:

### JOB nodes, PARENT-CHILD edges

my.dag

```
JOB A A.sub
JOB B1 B1.sub
JOB B2 B2.sub
JOB B3 B3.sub
JOB C C.sub
PARENT A CHILD B1 B2 B3
PARENT B1 B2 B3 CHILD C
```



# Submitting a DAG to the queue

- Submission command:

`condor_submit_dag dag_file`

```
$ condor_submit_dag my.dag
```

```
-----  
File for submitting this DAG to HTCondor           : mydag.dag.condor.sub  
Log of DAGMan debugging messages                  : mydag.dag.dagman.out  
Log of HTCondor library output                    : mydag.dag.lib.out  
Log of HTCondor library error messages            : mydag.dag.lib.err  
Log of the life of condor_dagman itself           : mydag.dag.dagman.log
```

```
Submitting job(s).
```

```
1 job(s) submitted to cluster 87274940.
```



**Take Away Item #2:  
Leverage the fact that HTCondor  
is a NoSQL database!**

**What does this mean?**

# Avoid challenges of synchronizing two databases

## Science Gateway (SG)



SG database

→ mmtmm<sup>2</sup>°Cmm in. □ mm kgm<sup>3</sup>.  
>> ↓ <% □ mm<sup>2</sup> gccmm<sup>2</sup> lmmmm<sup>2</sup>%  
↔ gmm<sup>2</sup>mm lmm<sup>3</sup> oz. mmtmm<sup>3</sup>kl  
□ mkm<sup>2</sup>mm<sup>2</sup>kmccm lmm<sup>2</sup>gm ↓ k



HTCondor database

□ mkm<sup>2</sup>mm<sup>2</sup>kmccm lmm<sup>2</sup>gm ↓ k  
□ °Fmm<sup>2</sup>mcctmm<sup>2</sup> ↓ kllkmmmm<sup>2</sup>  
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Submit jobs or workflows



# Avoid challenges of synchronizing two databases

## Science Gateway (SG)



SG database

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>> ↓ <% □ mm<sup>2</sup>gccmm<sup>2</sup> ℓ mmm<sup>2</sup>%  
↔ gmm<sup>2</sup>mm ℓ mm<sup>3</sup> oz. mmtmm<sup>3</sup>kl ℓ  
□ mkm<sup>2</sup>mm<sup>2</sup>kmccmℓmm<sup>2</sup>gm ↓ k



HTCondor database

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□ mkm<sup>2</sup>mm<sup>2</sup>kmccmℓmm<sup>2</sup>gm ↓ k  
□ °Fmm<sup>2</sup>mcctmm<sup>2</sup> ↓ kℓkmmm<sup>2</sup>  
«mgcc\$kgmmm<sup>2</sup>mm<sup>2</sup> [ °F°F°



Submit jobs or workflows



**HTCondor**

# Avoid challenges of synchronizing two databases

## Science Gateway (SG)



Submit  
jobs or  
workflows



**HTCondor**



HTCondor database

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□ °Fmm<sup>2</sup> mcctmm<sup>2</sup> ↓ kelkmm<sup>2</sup>  
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## Take Away Item #3:

We've already done the work to handle job management for you!

What does this mean?

# *For me? Yes, for you!*

- › HTCondor is open source, funded primarily by NSF, developed within a University computing center
  - Proven, mature, but actively evolving
  - Multiple options for support
  - If you give HTCondor your workflow, many ways we can schedule and monitor. Doesn't already do something you need? Lets talk!
- › **Helping the scientific community is our primary focus.**

**Thank You!**

**Questions?**