

Intermediate Condor Monday morning, 11:30am

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Before we begin...

 Any questions on the lectures or exercises up to this point?





HTC: Reliability

- Two quotes from the first lecture:
 - "We don't care about operations per second, we care about operations per year"
 - "HTC focuses on reliability"
- How should we provide reliability?



First: why do jobs fail?

- The computer running the job fails
 - Or the network, or the disk, or the OS, or...
- Your job might be preempted:
 - Condor decides your job is less important than another, so your job is stopped and another started.
 - Not a "failure" per se, but it may feel like it to you.



Reliability example #1

- When a job fails or is preempted:
 - It stays in the queue (on the schedd)
 - A note is written to the job log file
 - It reverts to "idle" state
 - It is eligible to be matched again
- Relax! Condor will run your job again
 - "It's like money in the bank"



Reliability example #2: Checkpointing

- When Condor re-runs your job, it starts over from the beginning.
- Unless you use the standard universe
 - Huh? What's a "universe"?



Condor's Universes

- Condor can support various combinations of features/environments in different "universes"
- Different Universes provide different functionality for your job:
 - Vanilla: Run any serial job (your first job this morn')
 - Standard: Support for checkpointing & remote I/O
 - Java: Special support for Java
 - Parallel: Support for parallel jobs (such as MPI)

- ... and others



Process Checkpointing

- Condor's process checkpointing mechanism saves the entire state of a process into a checkpoint file
 - Memory, CPU, I/O, etc.
- The process can then be restarted from right where it left off
- Typically no changes to your job's source code needed—however, your job must be relinked with Condor's Standard Universe support library

To do this, just place "condor_compile" in front of the command you normally use to link your job:

```
% condor_compile gcc -o myjob myjob.c
-OR -
% condor_compile f77 -o myjob filea.f
fileb.f
```



Limitations of the Standard Universe

- Condor's checkpointing is not at the kernel level. Thus in the Standard Universe the job may not:
 - fork()
 - Use kernel threads
 - Use some forms of IPC, such as pipes and shared memory
- Many typical scientific jobs are OK
- Must be same gcc as Condor was built with



When will Condor checkpoint your job?

- Periodically, if desired (for fault tolerance)
- When your job is preempted by a higher priority job
- When your job is vacated because the execution machine becomes busy
- When you explicitly run:
 - condor_checkpoint
 - condor vacate
 - condor off
 - condor_restart



Access to data in Condor

- Option #1: Shared filesystem
 - Simple to use, but make sure your filesystem can handle the load
 - Not available for today's exercises
- Option #2: Condor's file transfer
 - Can automatically send back changed files
 - Atomic transfer of multiple files
 - Can be encrypted over the wire
 - This is what we'll do in the exercises
- Option #3: Remote I/O

Open Science Grid

Condor File Transfer

- ShouldTransferFiles = YES
 - Always transfer files to execution site
- ShouldTransferFiles = NO
 - Rely on a shared filesystem
- ShouldTransferFiles = IF_NEEDED
 - Will automatically transfer the files if needed

```
Universe = vanilla
Executable = my_job
Log = my_job.log
ShouldTransferFiles = YES
Transfer_input_files = dataset$(Process), common.data
Queue 600
```



Condor File Transfer with URLs

 Transfer_input_files can be a URL For example:

```
transfer input files = http://www.example.com/input.data
```

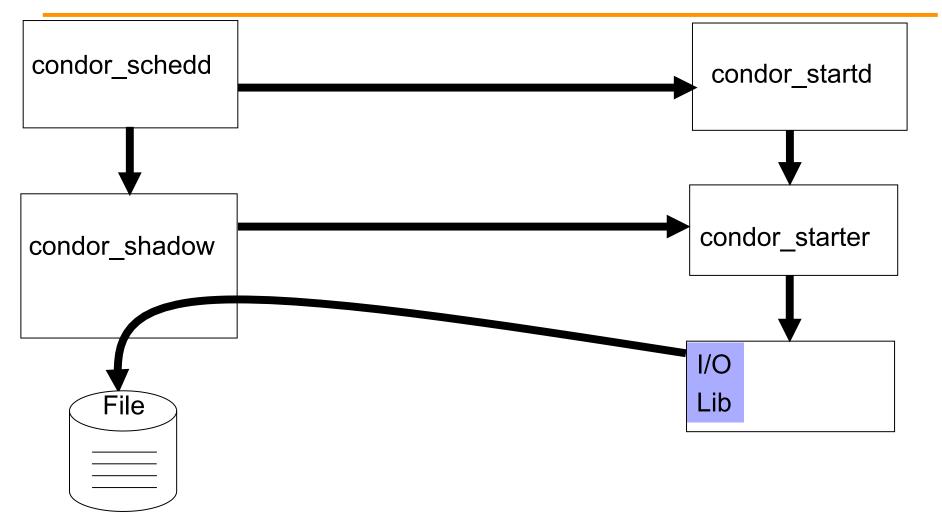


Standard Universe: Remote System Calls

- When your job accesses a file, we trap the access and do it on the submit computer
 - No file transfer needed
 - Can be faster if you don't access the whole file
- An essential part of checkpointing:
 - We know the state of the job, including the state of its files
 - We can re-run a job on a different machine without losing access to the files
- No source code changes required



Remote I/O





So Scot...

So far we've run one job at a time.
 Just one job.

ONE.

This doesn't seem very "high-throughput"



Open Science Grid

Clusters & Processes

- One submit file can describe lots of jobs
 - All the jobs in a submit file are a *cluster* of jobs
 - Yeah, same term as a cluster of computers
- Each cluster has a unique "cluster number"
- Each job in a cluster is called a "process"
- A Condor "job ID" is the cluster number, a period, and the process number ("20.1")
- A cluster is allowed to have one or more processes.
 - There is always a cluster for every job

Example Submit Description File for a Cluster Open Science Grid

```
# Example submit description file that defines a
# cluster of 2 jobs with separate working directories
Universe = vanilla
Executable = my_job
log = my_job.log
Arguments = -arg1 -arg2
Input = my_job.stdin
Output = my_job.stdout
Error = my_job.stderr
InitialDir = run_0
Queue Becomes job 2.0
InitialDir = run_1
Queue Becomes job 2.1
```

Submitting The Job



The \$(Process) macro

- The initial directory for each job can be specified as run_\$(Process), and instead of submitting a single job, we use "Queue 600" to submit 600 jobs at once
- The \$(Process) macro will be expanded to the process number for each job in the cluster (0 599), so we'll have "run_0", "run_1", ...
 "run_599" directories
- All the input/output files will be in different directories!



Example of \$(Process)



More \$(Process)

You can use \$(Process) anywhere:

```
Universe = vanilla
Executable = my_job
Log = my_job.$(Process).log
Arguments = -randomseed $(Process)
Input = my_job.stdin
Output = my_job.stdout
Error = my_job.stderr
InitialDir = run_$(Process)
Queue 600
```



Sharing a directory

- You don't have to use separate directories.
- \$(Cluster) will help distinguish runs

```
Universe
          = vanilla
Executable = my job
Arguments = -randomseed \$(Process)
     = my job.input.$(Process)
Input
Output = my job.stdout.$(Cluster).$(Process)
          = my job.stderr.$(Cluster).$(Process)
Error
Log = my job.$(Cluster).$(Process).log
```

Oueue 600



Complex sets of jobs

- What if you have a large set of jobs?
 - Different jobs have different purposes
 But all are needed for your science
 - Some jobs must run before others
- Hang tight, we'll talk about this after lunch



Job Priorities

- Are some of the jobs more interesting than others?
- condor prio lets you set the job priority
 - Priority relative to your jobs, not other peoples
 - Priority can be any integer
- Can be set in submit file:
 - -Priority = 14



Advanced Trickery

- Pretend: You submit several large sets of jobs
- These jobs are of two different types
 - e.g. analysis vs. simulation
- How can you look just the analysis jobs?



Advanced Trickery cont.

• In your job file:

```
+JobType = "analysis"
```

- You can see this in your job ClassAd condor q -1
- You can show jobs of a certain type:
 condor q -constraint 'JobType == "analysis"
- Try this during the exercises!
- Be careful with the quoting...



Time for more exercises!





Questions?

- Questions? Comments?
- Feel free to ask me questions later:
 Scot Kronenfeld <kronenfe@cs.wisc.edu>
- Upcoming sessions
 - Now 13:00
 - Hands-on exercises
 - -13:00 14:30
 - Lunch