Open Science Grid

Intermediate Condor

Tuesday morning, 10:45am

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Before we begin...

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

How can my jobs access their data?

Access to Data in Condor

- Use shared filesystem if available
  -
- No shared filesystem?
  -
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  -
  -

Condor File Transfer

- ShouldTransferFiles = YES
  –
- ShouldTransferFiles = NO
  –
- ShouldTransferFiles = IF_NEEDED
  –

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

Some of the machines in the Pool do not have enough memory or scratch disk space to run my job!

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Specify Requirements

- An expression (syntax similar to C or Java)
- Must evaluate to True for a match to be made

```
Universe     = vanilla
Executable   = my_job
Log          = my_job.log
InitialDir   = run_$(Process)
Requirements = Memory >= 256 && Disk > 10000
Queue 600
```

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Specify Rank

- All matches which meet the requirements can be sorted by preference with a Rank expression.
- Higher the Rank, the better the match

```
Universe    = vanilla
Executable = my_job
Log         = my_job.log
Arguments  = -arg1 -arg2
InitialDir = run_$(Process)
Requirements = Memory >= 256 && Disk > 10000
Rank = (KFLOPS*10000) + Memory
Queue 600
```

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My jobs run for 20 days...

- What happens when they get pre-empted?
- How can I add fault tolerance to my jobs?

Condor's Standard Universe to the rescue!

- Condor can support various combinations of features/environments in different "Universes"
- Different Universes provide different functionality for your job:
  -
  - Standard: Support for transparent process checkpoint and restart

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Process Checkpointing

- Condor’s process checkpointing mechanism saves the entire state of a process into a checkpoint file
  -
- 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

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Relinking Your Job for Standard Universe

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
```

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Limitations of the Standard Universe

- Condor's checkpointing is not at the kernel level. Thus in the Standard Universe the job may not:
  –
  –
  –
- Many typical scientific jobs are OK
- Must be same gcc as Condor was built with

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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:
  - –
  - –
  - –
  - –

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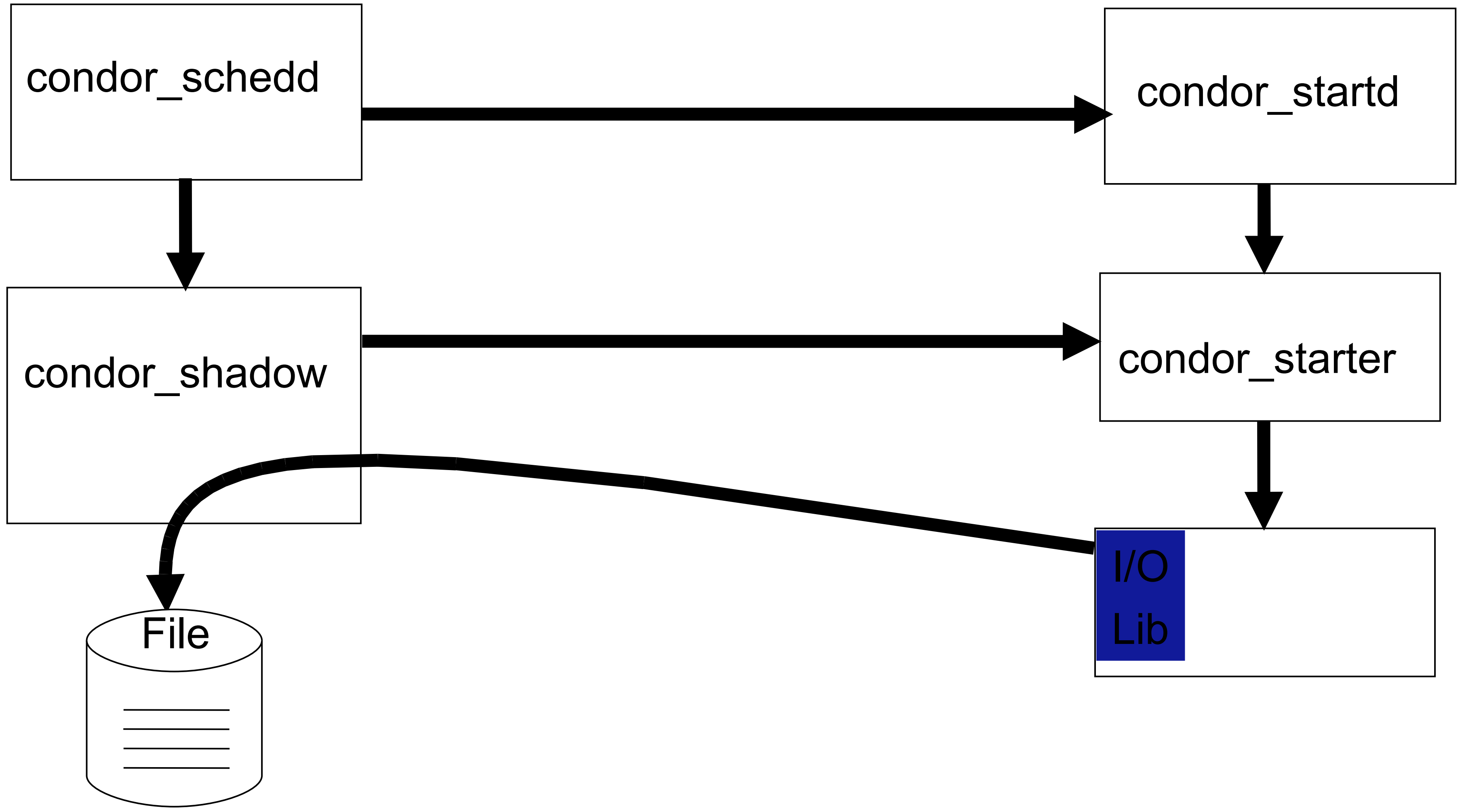
Remote System Calls

- I/O system calls are trapped and sent back to submit machine
- Allows transparent migration across administrative domains
  –
- No source code changes required
- Language independent
- Opportunities for application steering

Remote I/O


condor_schedd
condor_startd
condor_shadow
condor_starter
I/O
Lib
File

Clusters and Processes

- If your submit file describes multiple jobs, we call this a "cluster"
- 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.
  -

Example Submit Description File for a Cluster

```
# 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
InitialDir = run_1
Queue
```

Becomes job 2.0

Becomes job 2.1

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Submitting The Job

```
% condor_submit my_job.submit-file
Submitting job(s).
2 job(s) submitted to cluster 2.

% condor_q
-- Submitter: perdita.cs.wisc.edu : <128.105.165.34:1027> :
 ID      OWNER            SUBMITTED     RUN_TIME ST PRI SIZE CMD
  2.0    frieda          4/15 06:56   0+00:00:00 I  0   0.0  my_job
  2.1    frieda          4/15 06:56   0+00:00:00 I  0   0.0  my_job
2 jobs; 2 idle, 0 running, 0 held
```

Submit Description File for a BIG Cluster of Jobs

- 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!

Submit Description File for a *BIG* Cluster of Jobs

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```
# Example condor_submit input file that defines
# a cluster of 600 jobs with different 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_$(Process)
Queue 600
```

- run_0 … run_599
- Creates job 3.0 … 3.599

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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
```

·run_0 … run_599

·Creates job 3.0 … 3.599

Sharing a directory

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

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

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Job Priorities

- Are some of the jobs in your sweep more interesting than others?
- `condor_prio` lets you set the job priority
  -
  -
- Can be set in submit file:
  -

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What if you have LOTS of jobs?

- Set system limits to be high:
  - –
  - –
  - –
- Each condor_schedd limits max number of jobs running
  - –
  - –
- Consider multiple submit hosts
  - –
  - –
- We constantly strive to improve scalability

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Advanced Trickery

- You submit 10 parameter sweeps
- You have five classes of parameters sweeps
  -
- How can you look at the status of jobs that are part of Type B parameter sweeps?

Advanced Trickery cont.

- In your job file:

+SweepType = “B”

- You can see this in your job ClassAd

```
condor_q -l
```

- You can show jobs of a certain type:

```
condor_q -constraint ‘SweepType == “B”’
```

- Very useful when you have a complex variety of jobs
- Try this during the exercises!
- Be careful with the quoting…

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Time for more exercises!

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Questions?

- Questions? Comments?
- Feel free to ask me questions later:

Zach Miller <zmiller@cs.wisc.edu>

- Upcoming sessions
  -
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