Workflows

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Some Slides Contributed by the University of Wisconsin HTCondor Team, Scot Kronenfeld and Kyle Gross

Before we begin…

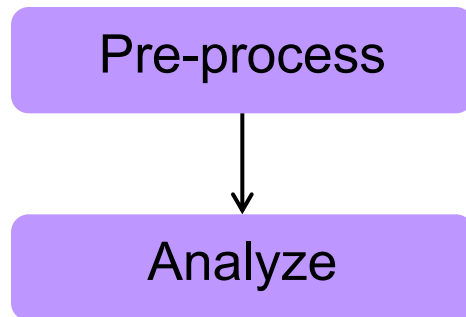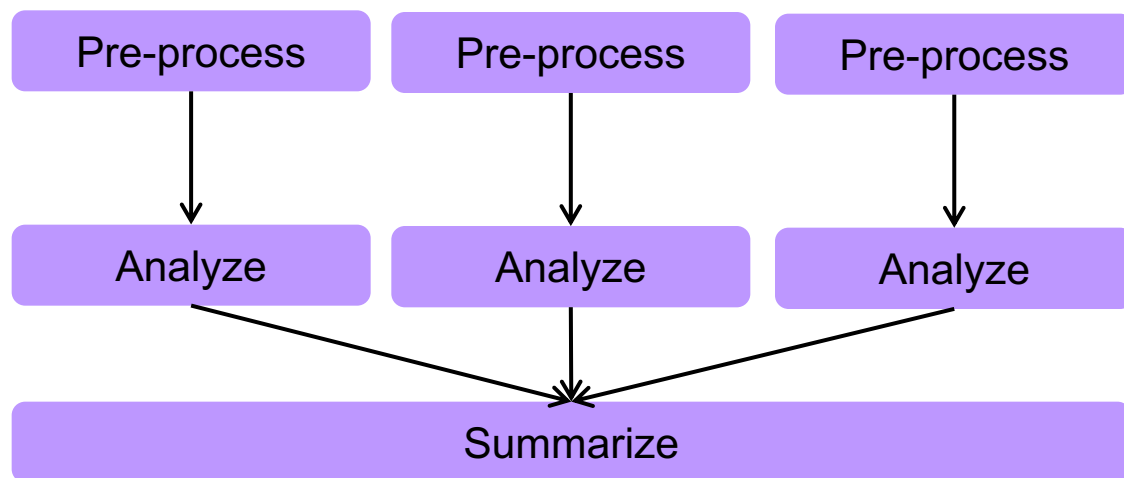- Any questions on the lectures or exercises up to this point?

Workflows

- What if you have a complex set of programs to run for your science?

- For example:
  - You want to analyze a set of images
  - Each image needs to be pre-processed
  - Each image needs to be analyzed
  - You need to summarize the results of all the analyses
  - Each of these is done with a separate application

Workflows

One Image:

```
┌─────────────────┐
│   Pre-process   │
└─────────────────┘
         │
         ▼
┌─────────────────┐
│     Analyze     │
└─────────────────┘
```

Three Images:

```
┌──────────────┐   ┌──────────────┐   ┌──────────────┐
│ Pre-process  │   │ Pre-process  │   │ Pre-process  │
└──────────────┘   └──────────────┘   └──────────────┘
       │                  │                  │
       ▼                  ▼                  ▼
┌──────────────┐   ┌──────────────┐   ┌──────────────┐
│   Analyze    │   │   Analyze    │   │   Analyze    │
└──────────────┘   └──────────────┘   └──────────────┘
         \                │                /
          \               │               /
           ▼              ▼              ▼
┌────────────────────────────────────────────────────┐
│                    Summarize                        │
└────────────────────────────────────────────────────┘
```
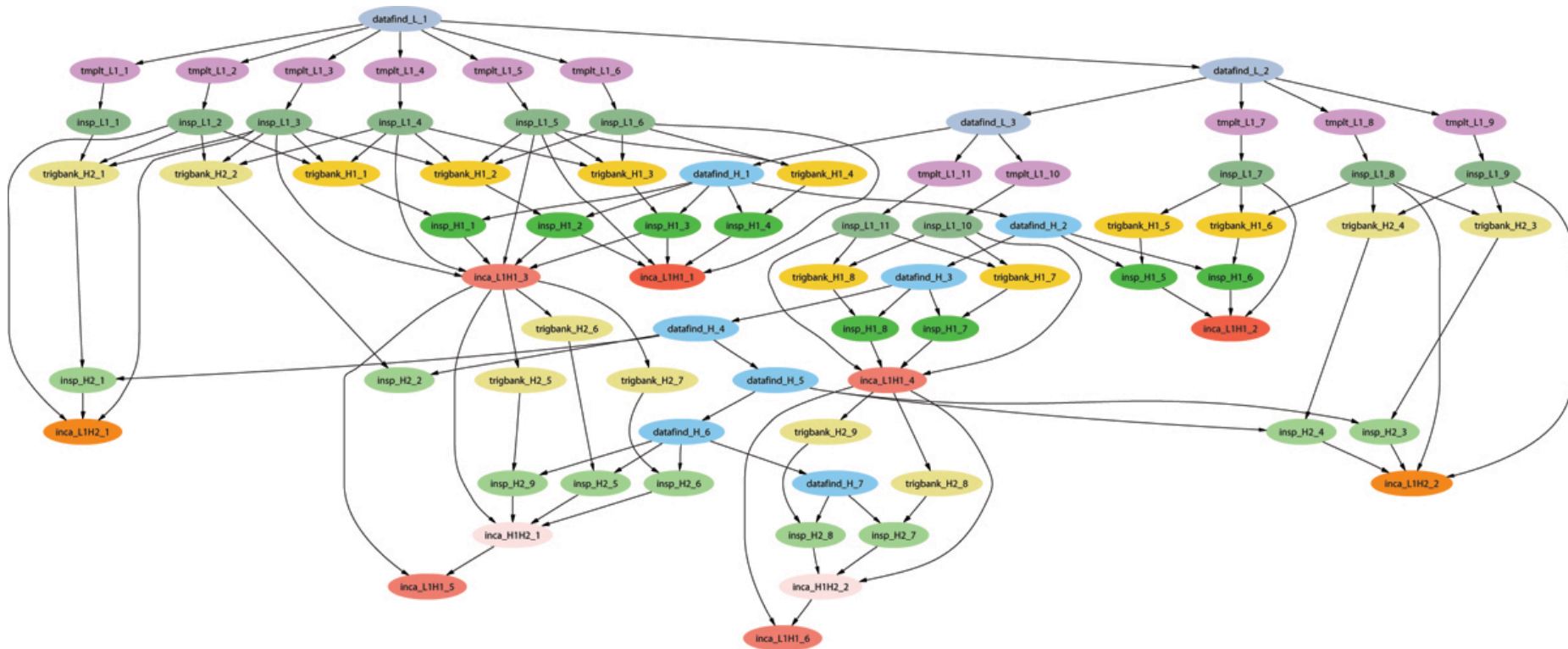
Workflows: definition

Definition 1:
A set of steps to complete a complex task

Definition 2:
A graph of jobs to run: some jobs need to run before others while other jobs can run in parallel

Example of a LIGO Inspiral DAG

• Condor handles 10's of millions of jobs per year running on the LDG, and up to 500k jobs per DAG.

• Condor standard universe check pointing widely used, saving us from having to manage this.

• At Caltech, 30 million jobs processed using 22.8 million CPU hrs. on 1324 CPUs in last 30 months.

• For example, to search 1 yr. of data for GWs from the inspiral of binary neutron star and black hole systems takes ~2 million jobs, and months to run on several thousand ~2.6 GHz nodes.
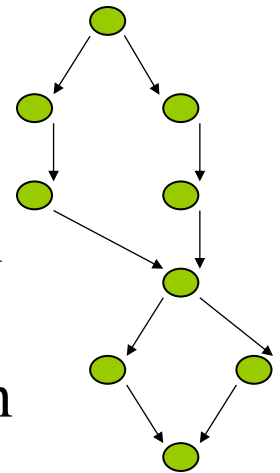
(Statement from 2010—"last 30 months" isn't from now. Also, I think they do up to 1 million jobs per DAG now.)

Example workflow: Bioinformatics
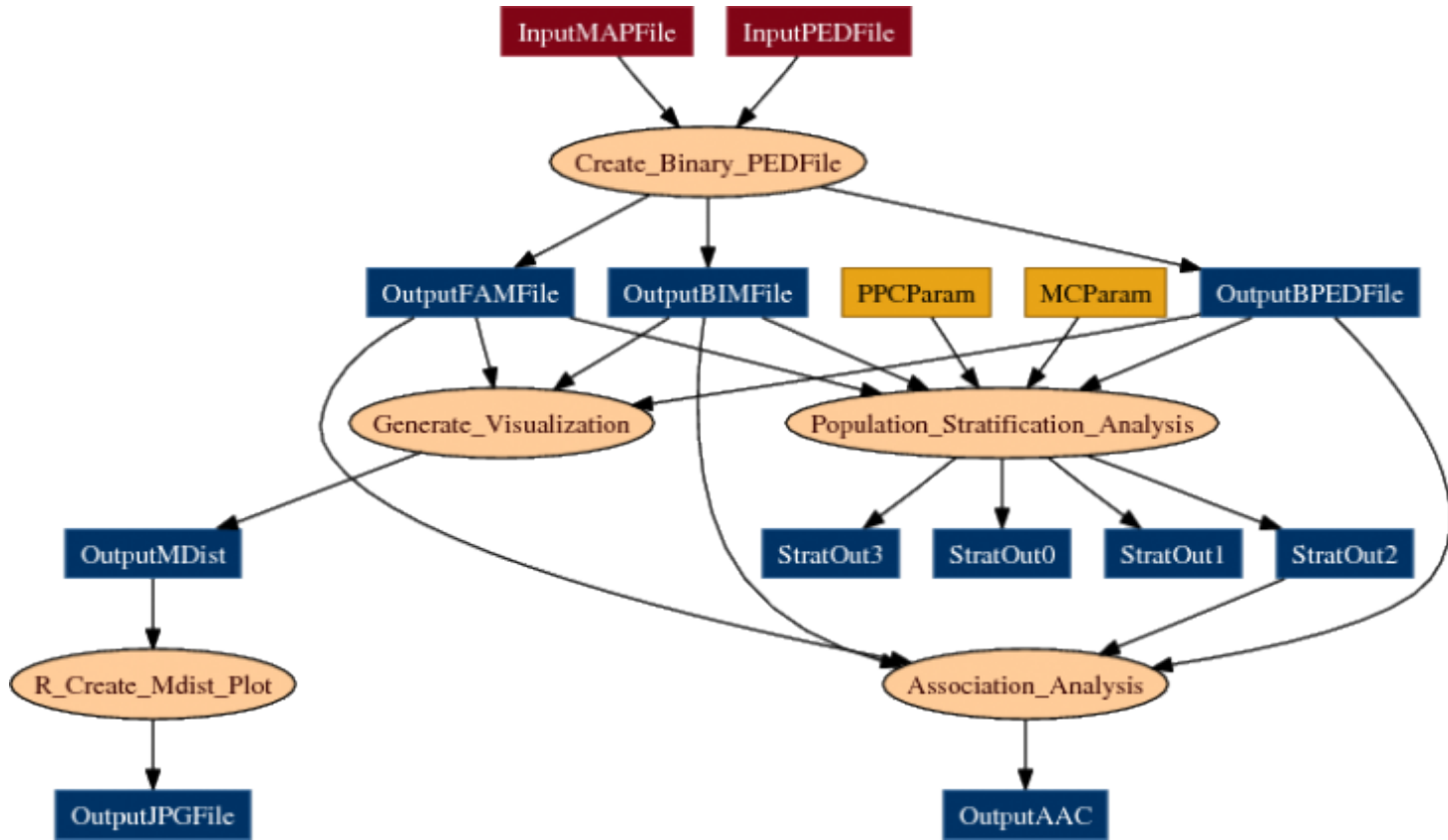
From Mason, Sanders, State (Yale)

http://pegasus.isi.edu/applications/association_test

DAGMan

- DAGMan:

    Directed Acyclic Graph (DAG)

    Manager (Man)

- Allows you to specify the dependencies between your jobs

- Manages the jobs and their dependencies

- That is, it manages a workflow of jobs

What is a DAG?

- A DAG is the structure used by DAGMan to represent these dependencies.

- Each job is a node in the DAG.

- Each node can have any number of "parent" or "children" nodes – as long as there are no loops!
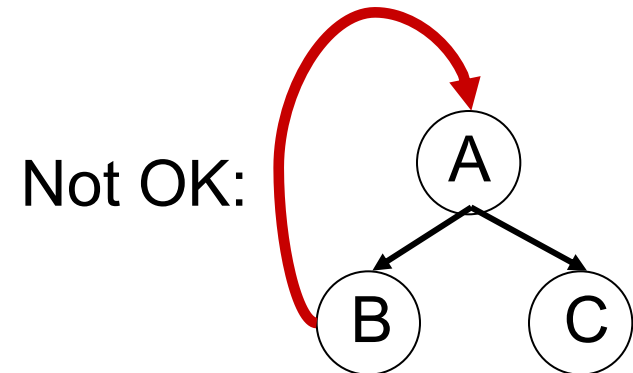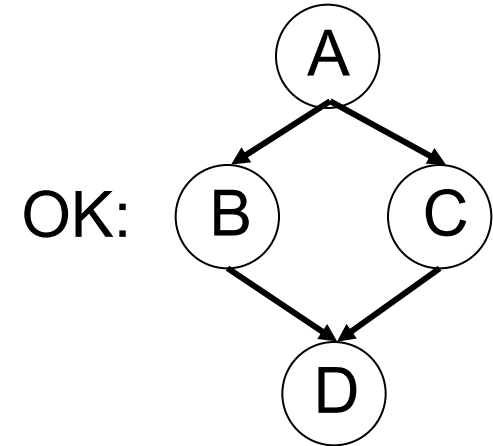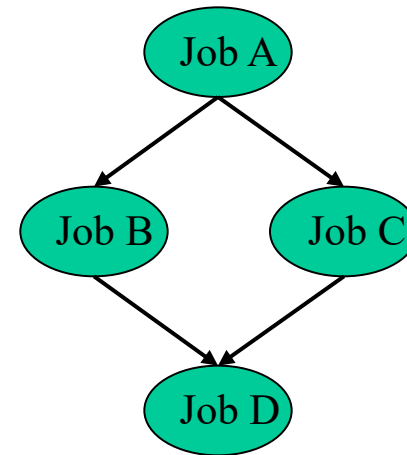
Defining a DAG

- A DAG is defined by a *.dag file*, listing each of its nodes and their dependencies. For example:

```
Job A a.sub
Job B b.sub
Job C c.sub
Job D d.sub

Parent A Child B C
Parent B C Child D
```

DAG Files....

- **This complete DAG has five files**

One DAG File:

Four Submit Files:

```
Job A a.sub
Job B b.sub
Job C c.sub
Job D d.sub


Parent A Child B C
Parent B C Child D
```

```
Universe = Vanilla
Executable = analysis…
```

```
Universe = …
```

Submitting a DAG

- To start your DAG, just run **`condor_submit_dag`** with your .dag file, and Condor will start a DAGMan process to manage your jobs:
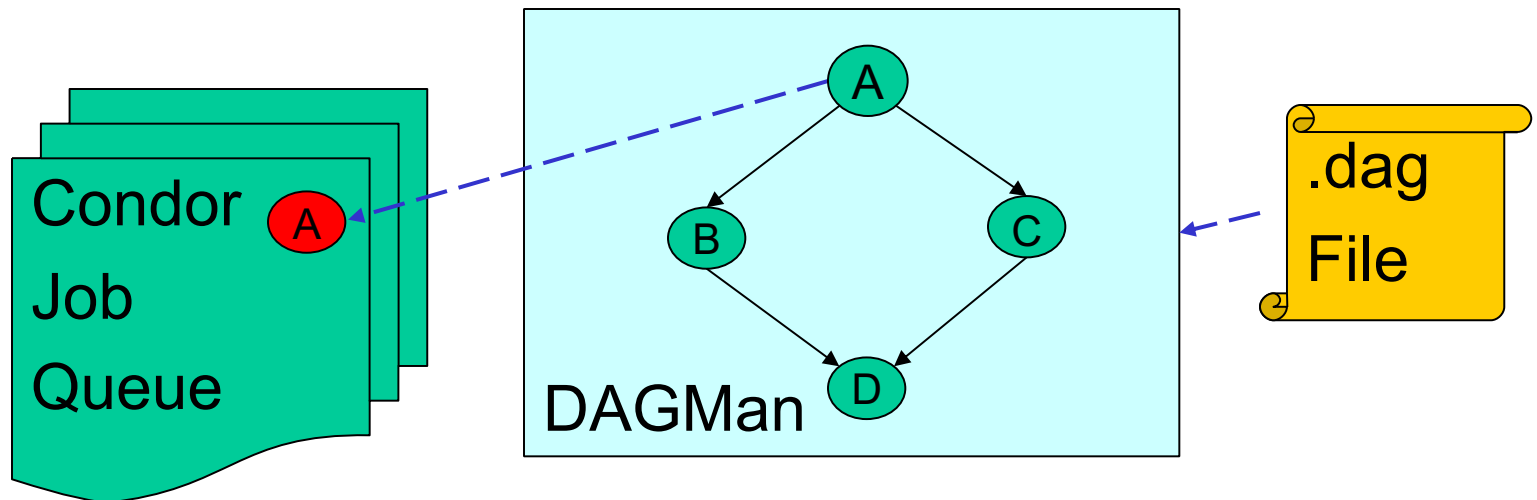
```
% condor_submit_dag diamond.dag
```

- condor_submit_dag submits a Scheduler Universe job with DAGMan as the executable

- Thus the DAGMan daemon itself runs as a Condor job, so you don't have to baby-sit it
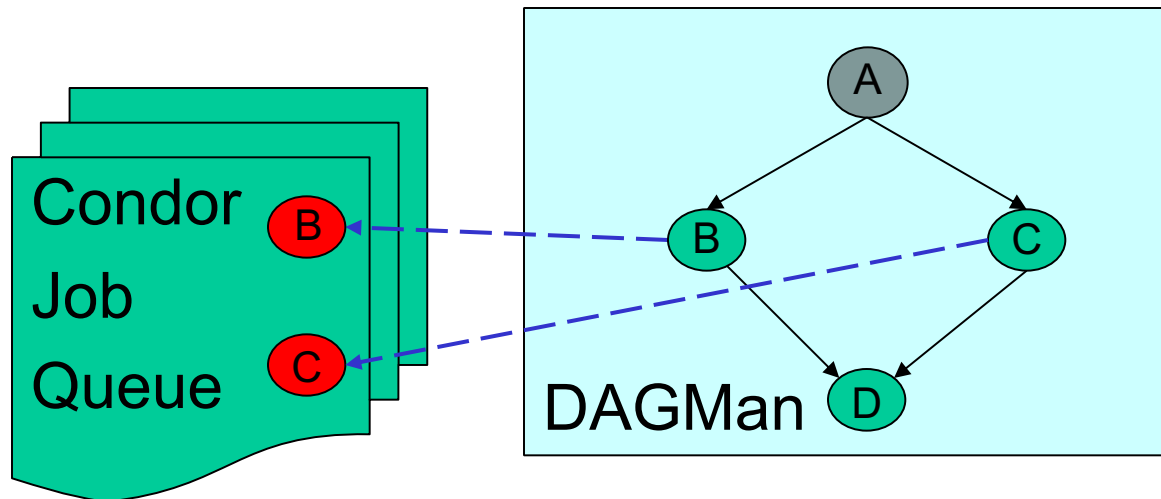
- DAGMan acts as a scheduler, managing the submission of your jobs to Condor based on the DAG dependencies

- DAGMan submits jobs to Condor at the appropriate times
- For example, after A finishes, it submits B & C

Running a DAG (cont'd)

- A job *fails* if it exits with a non-zero exit code
- In case of a job failure, DAGMan runs other jobs until it can no longer make progress, and then creates a *"rescue" file* with the current state of the DAG
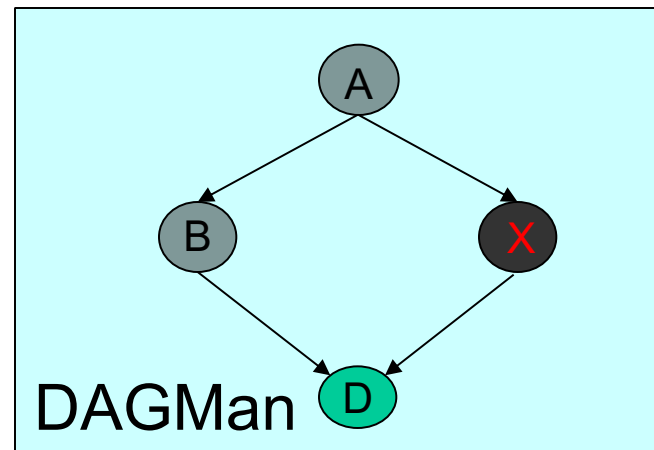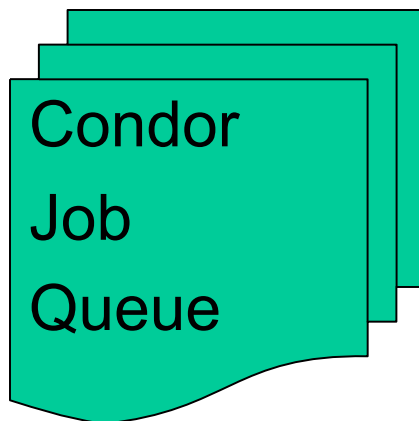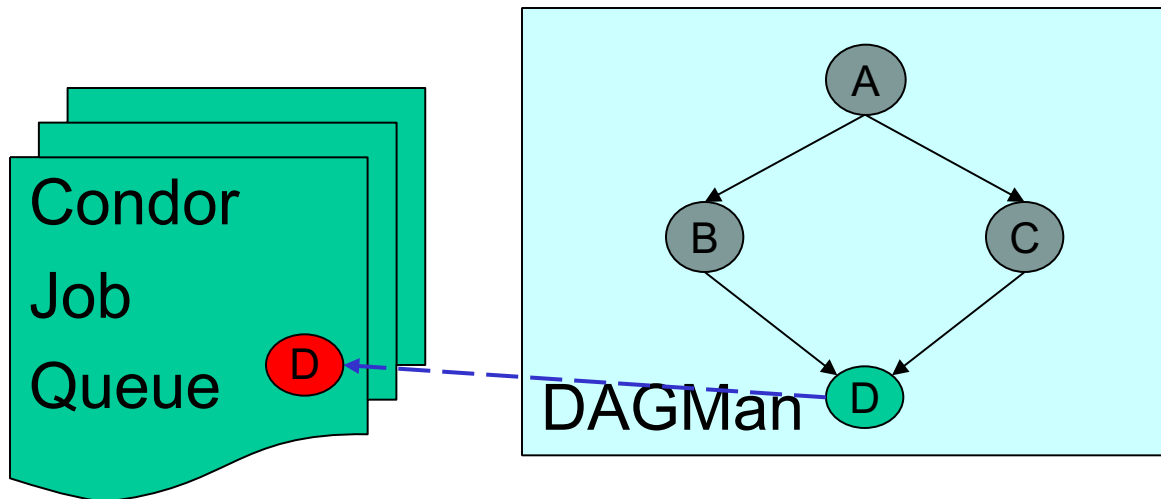
Recovering a DAG

- Once the failed job is ready to be re-run, the rescue file can be used to restore the prior state of the DAG
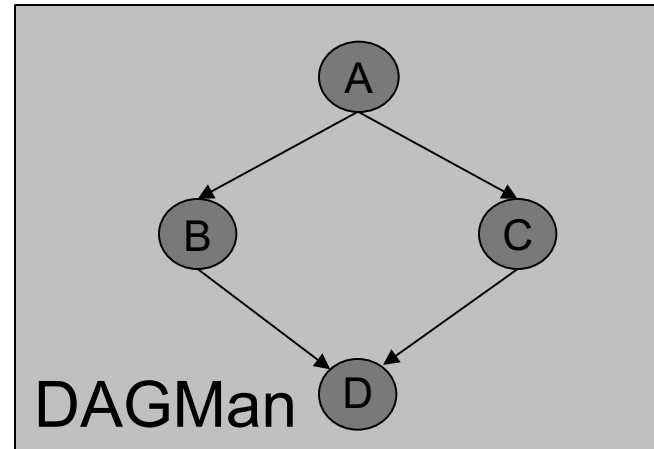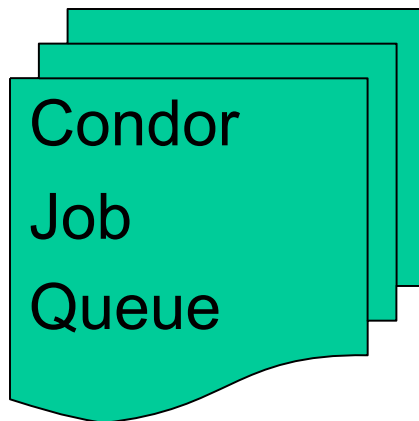 - Another example of reliability for HTC!
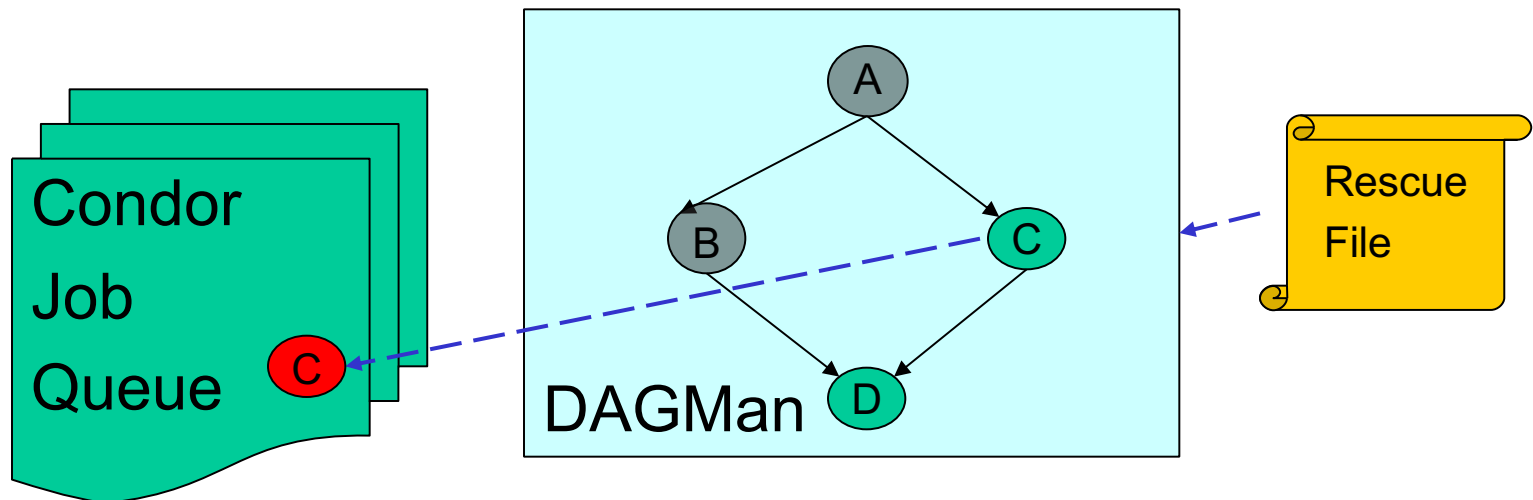
- Once that job completes, DAGMan will continue the DAG as if the failure never happened

- Once the DAG is complete, the DAGMan job itself is finished, and exits

Condor
Job
Queue

DAGMan

DAGMan & Fancy Features

- DAGMan doesn't have a lot of "fancy features"
  - No loops
  - Not much assistance in writing very large DAGs (script it yourself)
- Focus is on solid core
  - Add the features people need in order to run large DAGs well
  - People build systems on top of DAGMan

Related Software

Pegasus: http://pegasus.isi.edu/
- Writes DAGs based on abstract description
- Runs DAG on appropriate resource (Condor, OSG, EC2…)
- Locates data, coordinates execution
- Uses DAGMan, works with large workflows

Makeflow: http://nd.edu/~ccl/software/makeflow/
- User writes *make* file, not DAG
- Works with Condor, SGE, Work Queue…
- Handles data transfers to remote systems
- Does not use DAGMan

DAGMan: Reliability

- For each job, Condor generates a log file
- DAGMan reads this log to see what has happened
- If DAGMan dies (crash, power failure, etc…)
  - Condor will restart DAGMan
  - DAGMan re-reads log file
  - DAGMan knows everything it needs to know
  - Principle: DAGMan can recover state from files and without relying on a service (Condor queue, database…)
- Recall: HTC requires reliability!

Advanced DAGMan Tricks

- Throttles
- DAGs without dependencies
- Sub-DAGs
- Pre and Post scripts: editing your DAG

- Failed nodes can be automatically retried a configurable number of times
  - Helps recover from jobs that crash some percentage of the time
- Throttles to control job submissions
  - Max jobs submitted
  - Max scripts running
  - These are important when working with large DAGs

DAGs without dependencies

- ## Submit DAG with:
  - 200,000 nodes $\quad$ A_1 $\quad$ A_2 $\quad$ A_3 $\quad$ ...
  - No dependencies

- ## Use DAGMan to throttle the job submissions:
  - Condor is scalable, but it will have problems if you submit 200,000 jobs simultaneously
  - DAGMan can help you with scalability even if you don't have dependencies
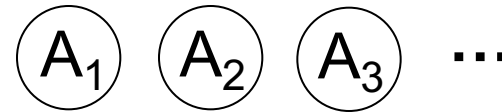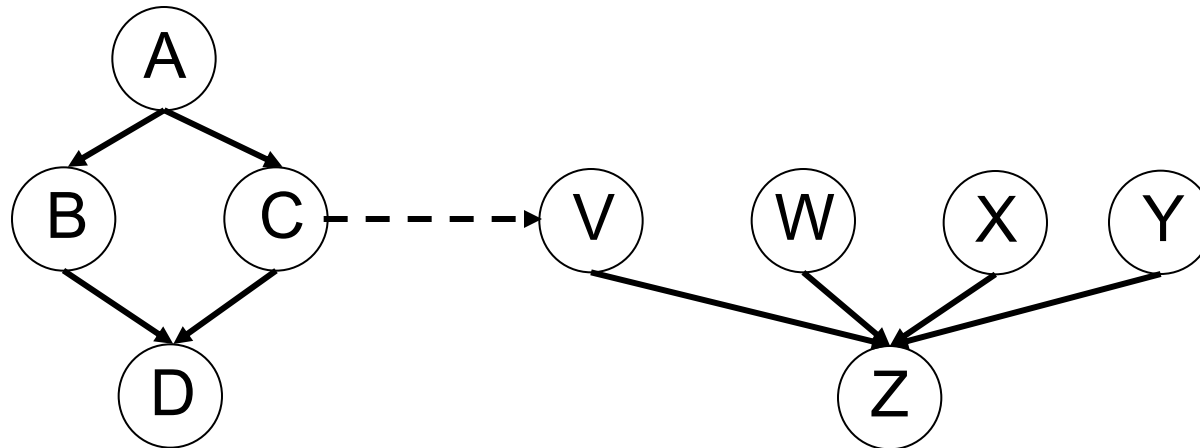
Sub-DAG

- Idea: any given DAG node can be another DAG

  – SUBDAG External Name DAG-file

- DAG node will not complete until sub-dag finishes

- Interesting idea: A previous node could *generate* this DAG node

- Why?

  – Simpler DAG structure

  – Implement a fixed-length loop

  – Modify behavior on the fly

Sub-DAG

DAGMan scripts

- DAGMan allows pre & post scripts
  - Run before (pre) or after (post) job
  - Run on the same computer you submitted from
  - Don't have to be scripts: any executable
- Syntax:

```
JOB A a.sub
SCRIPT PRE A before-script $JOB
SCRIPT POST A after-script $JOB $RETURN
```

So What?

- Pre script can make decisions
  - Where should my job run? (Particularly useful to make job run in same place as last job.)
  - What should my job do?
  - Generate Sub-DAG

- Post script can change return value
  - DAGMan decides job failed in non-zero return value
  - Post-script can look at {error code, output files, etc} and return zero or non-zero based on deeper knowledge.
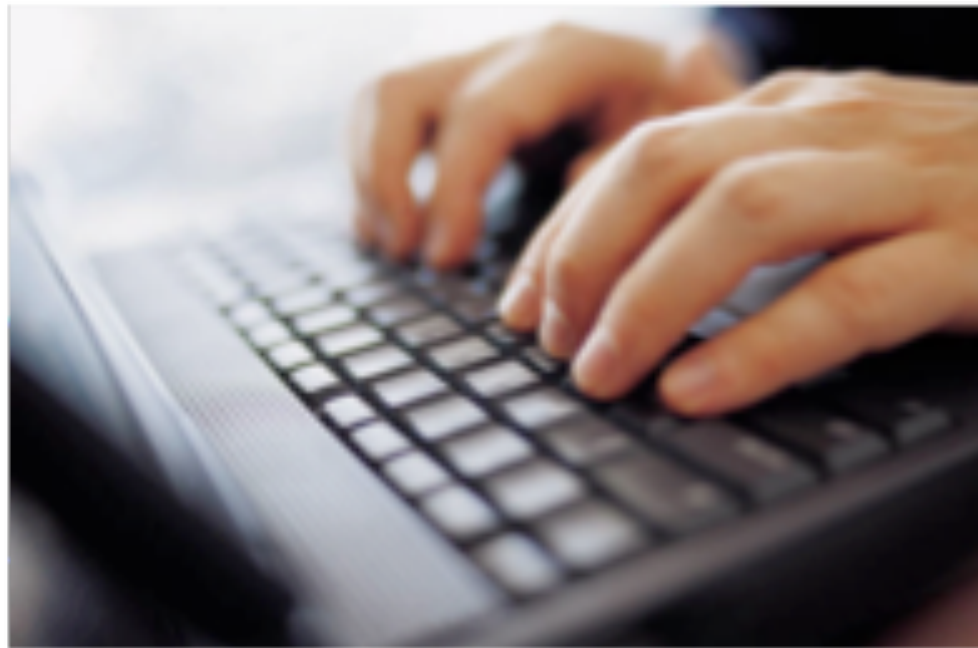
- `$`
- `nano, vi, emacs, cat >, etc.`
- `module, `**`scp`**`, cp, `**`watch,`**` cat, ls, rm`

Let's try it out!

- Exercises with DAGMan.

Questions?

- Questions? Comments?

- Feel free to ask me questions now or later:

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