Schedule

12:30	**Lunch**
13:00	**Part I** ● [15 min] Placing lists of jobs ● [20 min] What happened to my job? ● [15 min] Data placement ● [30 min] Troubleshooting strategies ● [20 min] GPU jobs
14:40	**Break**
14:50	**Part II** ● [40 min] Principles of DAGMan ● [40 min] Hands-on: DAGMan ● [20 min] Python bindings ● [20 min] Hands-on Python bindings ● [10 min] Computing at Nikhef ● [25 min] Philosophy & architecture
17:25	**Social**

Principles of DAGMan

Scenario

You have two jobs to run: job **A** and job **B**.

You have two corresponding template submit files: **A.sub** and **B.sub**

You want job B to run only after job A has completed <u>successfully</u>

- To determine success, need to check the output of job **A**

$$\begin{tikzcd}
\begin{matrix}\mathbf{A}\\ \text{(A.sub)}\end{matrix} \arrow[r, "\textit{continue only if successful}"] & \begin{matrix}\mathbf{B}\\ \text{(B.sub)}\end{matrix}
\end{tikzcd}$$

B
is dependent on
A

How?

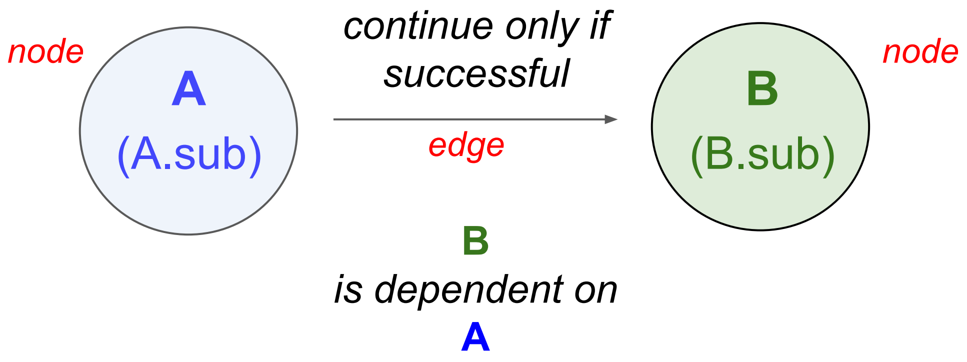
HTCondor offers you the services of the

Directed Acyclic Graph Manager → **DAGMan**

to automate the submission of jobs (with dependencies)

How?

The Directed Acyclic Graph Manager (DAGMan) manages the placement of lists of jobs represented by “nodes” that are connected by “edges”



Create the DAG input file

In a file, you need to

(1) declare the job submissions and (2) declare the dependencies.

my-first.dag

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```
JOB A A.sub
JOB B B.sub
```

my-first.dag

Syntax

JOB <node_name> <submit_file_name>

Create the DAG input file

In a file, you need to

(1) declare the job submissions and (2) declare the dependencies.

```
JOB A A.sub
JOB B B.sub
```

my-first.dag

Syntax

JOB <node_name> <submit_file_name>

A single template submit file can queue a ***list of jobs****

*if 1 job fails, then the whole list is removed from the queue

Create the DAG input file

In a file, you need to

(1) declare the job submissions and (2) declare the dependencies.

```
JOB A A.sub
JOB B B.sub

PARENT A CHILD B
```

my-first.dag

Syntax

PARENT <node_name> CHILD <node_name>

depends on

Create the DAG input file

In a file, you need to

(1) declare the job submissions and (2) declare the dependencies.

```
JOB A A.sub
JOB B B.sub

PARENT A CHILD B
```

my-first.dag

Create the DAG input file

How can we tell if job **A** completed successfully?

- To determine success, need to check the output of job **A** using **A-check.sh**

```
JOB A A.sub
JOB B B.sub

PARENT A CHILD B
```

my-first.dag

Create the DAG input file

How can we tell if job **A** completed successfully?

- To determine success, need to check the output of job **A** using **A-check.sh**

```
JOB A A.sub
SCRIPT POST A A-check.sh
JOB B B.sub

PARENT A CHILD B
```

my-first.dag

Syntax

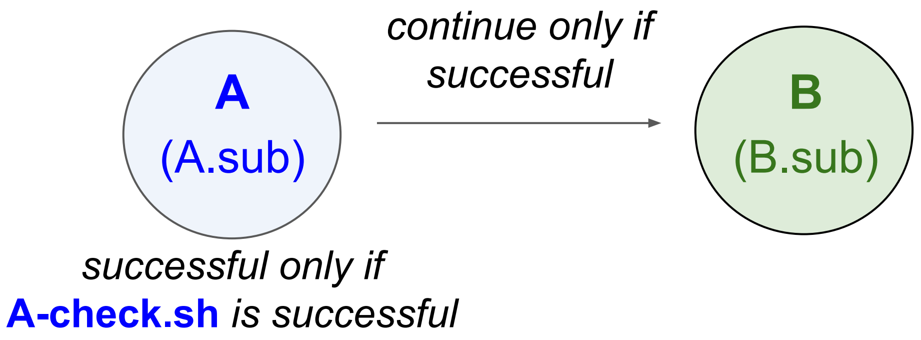
SCRIPT POST <node_name> <script_name>

**order of lines does not actually matter*

Create the DAG input file

How can we tell if job **A** completed successfully?

- To determine success, need to check the output of job **A** using **A-check.sh**



Submitting and Monitoring the DAG

Submit the DAG

By default, DAGMan expects the submit files `A.sub` and `B.sub` are in the same directory as `my-first.dag`, along with `A-check.sh`, on an HTCondor Access Point

Basic Working Directory

```
DAG_simple/
     |-- my-first.dag
     |-- A.sub
     |-- A-check.sh
     |-- B.sub
```

Submit the DAG

By default, DAGMan expects the submit files `A.sub` and `B.sub` are in the same directory as `my-first.dag`, along with `A-check.sh`, on an HTCondor Access Point

Basic Working Directory

```
DAG_simple/
     |-- my-first.dag
     |-- A.sub
     |-- A-check.sh
     |-- B.sub
```

It is possible to create other directory structures, but for now we will use this simple, flat organization.

Submit the DAG

Command to submit, or place, the DAGMan job:

```
condor_submit_dag <dag_description_file>
condor_submit_dag my-first.dag
```

This then starts the DAG **node scheduler** job, which we can see in the queue:

```
[user@ap40 DAG_simple]$ condor_q

-- Schedd: ap40.uw.osg-htc.org : <128.105.68.92:9618?... @ 09/01/24 11:26:51
OWNER    BATCH_NAME            SUBMITTED     DONE   RUN   IDLE  TOTAL JOB_IDS
user     my-first.dag+562265   09/01 11:26    _      _     1      2   562279.0
```

Monitor the DAG

This then starts the DAG **node scheduler** job, which we can see in the queue:

```
[user@ap40 DAG_simple]$ condor_q

-- Schedd: ap40.uw.osg-htc.org : <128.105.68.92:9618?... @ 09/01/24 11:26:51
OWNER    BATCH_NAME            SUBMITTED     DONE   RUN   IDLE   TOTAL JOB_IDS
user     my-first.dag+562265   09/01 11:26     _      _      1       2  562279.0
```

BATCH_NAME for the DAGMan job is the name of the input description file, `my-first.dag`, plus the Job ID of the scheduler job (562265)

Monitor the DAG

This then starts the DAG **node scheduler** job, which we can see in the queue:

```
[user@ap40 DAG_simple]$ condor_q

-- Schedd: ap40.uw.osg-htc.org : <128.105.68.92:9618?... @ 09/01/24 11:26:51
OWNER    BATCH_NAME            SUBMITTED     DONE   RUN    IDLE   TOTAL JOB_IDS
user     my-first.dag+562265   09/01 11:26    _      _      1      2   562279.0
```

The total number of jobs for `my-first.dag+562265` corresponds to the total number of nodes in the DAG (2)

Monitor the DAG

This then starts the DAG **node scheduler** job, which we can see in the queue:

```
[user@ap40 DAG_simple]$ condor_q

-- Schedd: ap40.uw.osg-htc.org : <128.105.68.92:9618?... @ 09/01/24 11:26:51
OWNER    BATCH_NAME            SUBMITTED      DONE   RUN   IDLE   TOTAL JOB_IDS
user     my-first.dag+562265   09/01 11:26     _      _      1       2  562279.0
```

Only 1 node is listed as "Idle", meaning that DAGMan has only materialized 1 job so far. This is consistent with the fact that node **A** has to complete before DAGMan can submit the job for node **B**.

Monitor the DAG

For more detailed monitoring:

```
[user@ap40 DAG_simple]$ condor_q -dag -nob

-- Schedd: ap40.uw.osg-htc.org : <128.105.68.92:9618?... @ 12/14/23 11:27:03
 ID          OWNER/NODENAME          SUBMITTED      RUN_TIME ST PRI SIZE CMD
562265.0    user                    09/01 11:26    0+00:00:37 R  0    0.5 condor_dagman
562279.0     |-A                    09/01 11:26    0+00:00:00 I  0    0.0 A.sh
```

First entry: **dag node scheduler job** created upon submission

Monitor the DAG

For more detailed monitoring:

```
[user@ap40 DAG_simple]$ condor_q -dag -nob

-- Schedd: ap40.uw.osg-htc.org : <128.105.68.92:9618?... @ 12/14/23 11:27:03
 ID          OWNER/NODENAME      SUBMITTED     RUN_TIME ST PRI SIZE CMD
562265.0    user                09/01 11:26   0+00:00:37 R  0    0.5 condor_dagman
562279.0     |-A                09/01 11:26   0+00:00:00 I  0    0.0 A.sh
```

Additional entries: correspond to **nodes** whose jobs are **currently** in the queue.

- *Reminder: Nodes that have not yet been submitted by DAGMan or that have completed and thus left the queue will not show up in `condor_q` output.*

Additional Tools to Monitor your Workflow

DAGMan will produce helpful files to learn about and troubleshoot your workflow.

```
[user@ap40 DAG_simple]$ condor_submit_dag my-first.dag

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

Submitting job(s).
1 job(s) submitted to cluster 562265.
-----------------------------------------------------------------------
```

Overview of process

```
JOB A A.sub
SCRIPT POST A A-check.sh
JOB B B.sub

PARENT A CHILD B
```

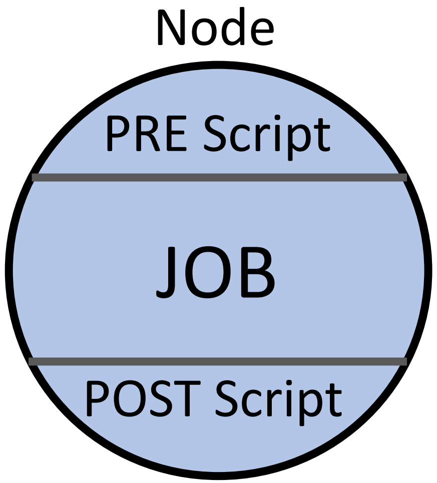
my-first.dag

`condor_submit_dag`

1. DAG node scheduler job starts
2. A.sub executes → completes
3. A-check.sh execute → completes
4. B.sub executes → completes
5. DAG node scheduler job completes

PRE/POST scripts

- All DAGMan PRE/POST scripts run on the Access Point and not on an Execution Point Slot.
- Scripts provide a way to perform tasks at key points in a node's lifetime.
  - *E.g., checking if files exist, creating directories, consolidating files*
- Should be lightweight (low computational) programs/tasks



DAGMan Node Scripts Documentation

Overview of process

```
JOB A A.sub
SCRIPT POST A A-check.sh
JOB B B.sub

PARENT A CHILD B
```

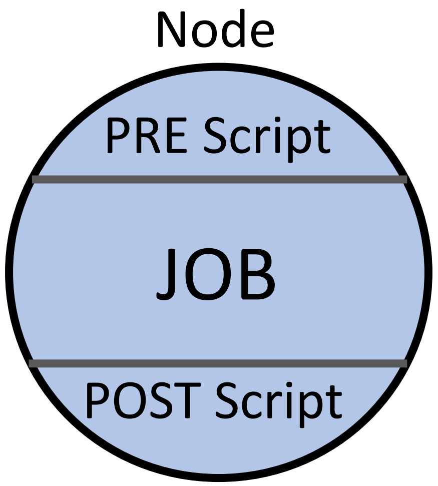
my-first.dag

1. `condor_submit_dag`
2. DAG node scheduler job starts
3. A.sub executes → completes
4. check-A.sh execute → completes
5. B.sub executes → completes
6. DAG node scheduler job completes

Throughout this workflow, DAGMan is monitoring for failures/successes

What is Considered a Failure

- A **non-zero exit code** in the PRE script, JOB, or POST script is considered a failure
- DAGMan will continue running work until can no longer progress



Overall

DAGMan will do *as much work as it can* until completion (“success”) or failure

A Failed DAG

- Once a node has failed and no more progress in the DAG can be made, DAGMan will produce a rescue file and exit.
  - Rescue file is named **`<dag_description_file>.rescue001`**
    - “001” increments for each new rescue file
  - Records which NODEs have completed successfully
    - does not contain the actual DAG structure

`DAG_simple/`

```
A.sub                        B.sub                    check-A.sh
my-first.dag              my.-first.dag.condor.sub   my.dag.dagman.log
my-first.dag.dagman.out     my-first.dag.lib.err        my-first.dag.lib.out
my-first.dag.metrics      my-first.dag.nodes.logmy-first.dag.rescue001
(other job files)
```

Rescue DAGs Documentation

Dealing with a Failed DAG

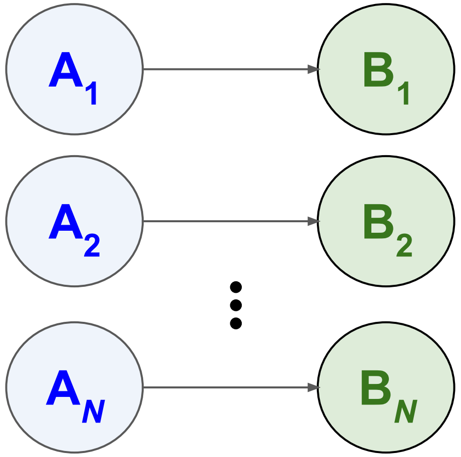
- Search for issue in `<dag filename>.dagman.out` and job standard error/output files
- Once issue is fixed, resubmit with `condor_submit_dag`
    - Rescue file will be automatically detected and progress will resume from the point it left off

Rescue DAGs Documentation

Many DAGs

Many DAGs

Scenario: Now you have to run the A→B workflow many times in parallel



How to accomplish?

Many DAGs … or One Big DAG

Write a script that generates your DAG description file* for you
(and the needed files)

```
JOB A A.sub
SCRIPT POST A A-check.sh
JOB B B.sub

PARENT A CHILD B
```

my-first.dag

*for now. We are working to develop better of ways of handling this scenario.

Many DAGs … or One Big DAG

Write a script that generates your DAG description file* for you

(and the needed files)

```
JOB A A.sub
SCRIPT POST A A-check.sh
JOB B B.sub

PARENT A CHILD B
```

my-first.dag

python
bash
…

```
JOB A1 A1.sub
SCRIPT POST A1 A1-check.sh
JOB B1 B1.sub
PARENT A1 CHILD B1

JOB A2 A2.sub
SCRIPT POST A2 A2-check.sh
JOB B2 B2.sub
PARENT A2 CHILD B2
        ⋮
```

my-big.dag

*for now. We are working to develop better of ways of handling this scenario.

One Big DAG

Once ready, do a single `condor_submit_dag` command

The DAG node scheduler job will manage all of the submissions while keeping track of the dependencies

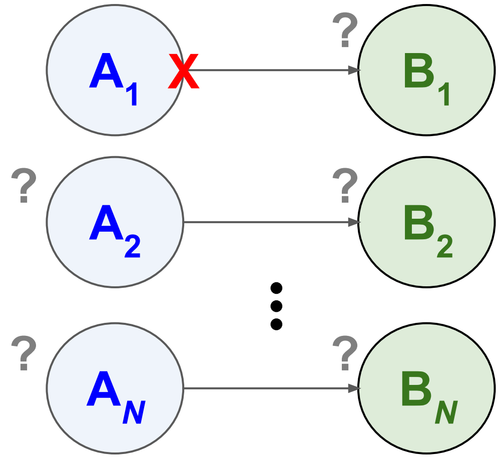
```
JOB A1 A1.sub
SCRIPT POST A1 A1-check.sh
JOB B1 B1.sub
PARENT A1 CHILD B1

JOB A2 A2.sub
SCRIPT POST A2 A2-check.sh
JOB B2 B2.sub
PARENT A2 CHILD B2
            ⋮
```

my-big.dag

One Big DAG - What If There Is a Failure?

Let's say that A_1 job finishes and A-check.sh finds that the output of A_1 is incorrect, and that A_1 has failed. What happens?

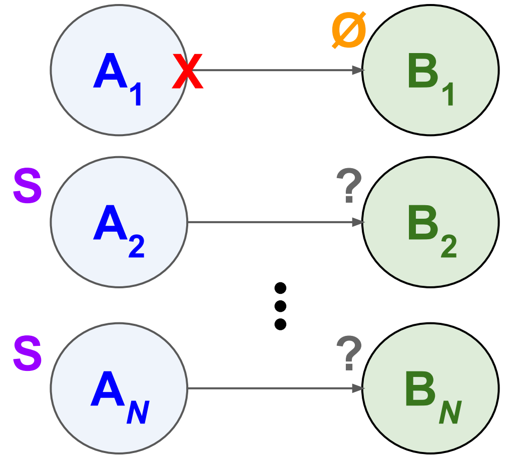


X = Failed
? = Not known yet

One Big DAG - What If There Is a Failure?

Let's say that A_1 job finishes and A-check.sh finds that the output of A_1 is incorrect, and that A_1 has failed. What happens?

- **DAGMan does as much work as it can, then creates a Rescue DAG.**
- While B_1 won't be started, the DAG node scheduler will keep submitting and managing the other A_N & B_N jobs until there is no more work.

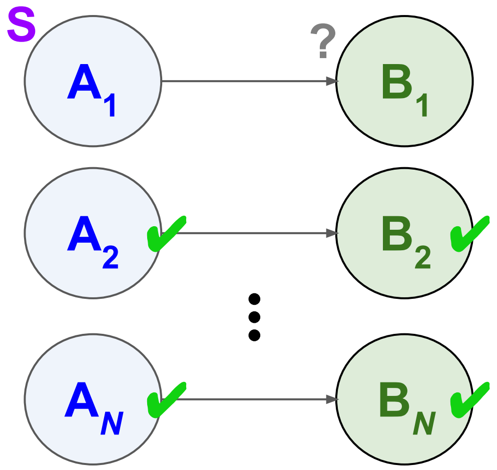


S = Submitted
X = Failed
Ø = Will not be submitted
? = Not known yet

One Big DAG - What If There Is a Failure?

Let's say that A_1 job finishes and A-check.sh finds that the output of A_1 is incorrect, and that A_1 has failed. What happens?

- **The Rescue DAG is used automatically the next time you run `condor_submit_dag`, and the DAG node scheduler job will only submit the unsuccessful nodes.**
    - If all but $A_1 \rightarrow B_1$ completed successfully, then when the Rescue DAG is submitted, only the $A_1 \rightarrow B_1$ will be attempted.



S = Submitted
? = Not known yet
✓= Successful completion

An Aside: Reuse files in your DAG

In the input description file with many DAGs, there were a lot of similar files:

A{x}.sub, **A{x}-check.sh**, **B{x}.sub**

```
JOB A1 A1.sub
SCRIPT POST A1 A1-check.sh
JOB B1 B1.sub
PARENT A1 CHILD B1

JOB A2 A2.sub
SCRIPT POST A2 A2-check.sh
JOB B2 B2.sub
PARENT A2 CHILD B2
                  ⋮
```

my-big.dag

An Aside: Reuse files in your DAG

In the big DAG, there were a lot of similar files: **A{x}.sub**, **A{x}-check.sh**, **B{x}.sub**

Instead of **A1.sub**, **A2.sub**, … **AN.sub**, can use **A.sub**

```
JOB A1 A.sub
SCRIPT POST A1 A1-check.sh
JOB B1 B1.sub
PARENT A1 CHILD B1

JOB A2 A.sub
SCRIPT POST A2 A2-check.sh
JOB B2 B2.sub
PARENT A2 CHILD B2
          ⋮
```

my-big.dag

An Aside: Reuse files in your DAG

In the big DAG, there were a lot of similar files: **A{x}.sub**, **A{x}-check.sh**, **B{x}.sub**

Instead of **A1.sub**, **A2.sub**, … **AN.sub**, can use **A.sub**

Then pass the number to the submit file with the **VARS** command

```
JOB A1 A.sub
VARS A1 number=1
SCRIPT POST A1 A1-check.sh
JOB B1 B1.sub
PARENT A1 CHILD B1

JOB A2 A.sub
VARS A2 number=2
SCRIPT POST A2 A2-check.sh
JOB B2 B2.sub
PARENT A2 CHILD B2
            ⋮
```

my-big.dag

An Aside: Reuse files in your DAG

In the big DAG, there were a lot of similar files: **A{x}.sub**, **A{x}-check.sh**, **B{x}.sub**

Instead of **A1.sub**, **A2.sub**, … **AN.sub**, can use **A.sub**

Then pass the number to the submit file with the **VARS** command

<u>DAG Description File Syntax</u>

```
VARS <node_name> <variable>=<value>
```

<u>Submit File Syntax</u>

```
arguments = $(<variable>)
```

```
JOB A1 A.sub
VARS A1 number=1
SCRIPT POST A1 A1-check.sh
JOB B1 B1.sub
PARENT A1 CHILD B1

JOB A2 A.sub
VARS A2 number=2
SCRIPT POST A2 A2-check.sh
JOB B2 B2.sub
PARENT A2 CHILD B2
        ⋮
```

my-big.dag

An Aside: Reuse files in your DAG

In the big DAG, there were a lot of similar files: **A{x}.sub**, **A{x}-check.sh**, **B{x}.sub**

Instead of **A1.sub**, **A2.sub**, … **AN.sub**, can use **A.sub**

Then pass the number to the submit file with the **VARS** command

Can repeat for **B.sub**

*can achieve similar outcome for **A-check.sh** (not using VARS though)

```
JOB A1 A.sub
VARS A1 number=1
SCRIPT POST A1 A1-check.sh
JOB B1 B.sub
VARS B1 number=1
PARENT A1 CHILD B1

JOB A2 A.sub
VARS A2 number=2
SCRIPT POST A2 A2-check.sh
JOB B2 B.sub
VARS B1 number=2
PARENT A2 CHILD B2
                ⋮
```

my-big.dag

Learn More

DAGMan Resources

- Beginner DAGMan Resources:
  - https://www.youtube.com/watch?v=OuIBf6x24r0&pp=ygUGZGFnbWFu
  - https://portal.osg-htc.org/documentation/htc_workloads/automated_workflows/dagman-workflows/
  - https://portal.osg-htc.org/documentation/htc_workloads/automated_workflows/dagman-simple-example/
- Intermediate DAGMan Resources:
  - https://portal.osg-htc.org/documentation/support_and_training/training/osgusertraining/
  - https://github.com/OSGConnect/tutorial-dagman-intermediate
- DAGMan Core Documentation
  - https://htcondor.readthedocs.io/en/latest/automated-workflows/index.html

HTCondor Software Suite

Questions?

Schedule

12:30	**Lunch**
13:00	**Part I** ● [15 min] Placing lists of jobs ● [20 min] What happened to my job? ● [15 min] Data placement ● [30 min] Troubleshooting strategies ● [20 min] GPU jobs
14:40	**Break**
14:50	**Part II** ● [40 min] Principles of DAGMan ● [40 min] Hands-on: DAGMan ● [20 min] Python bindings ● [20 min] Hands-on Python bindings ● [10 min] Computing at Nikhef ● [25 min] Philosophy & architecture
17:25	**Social**