Workflows with HTCondor's DAGMan

OSG School 2025

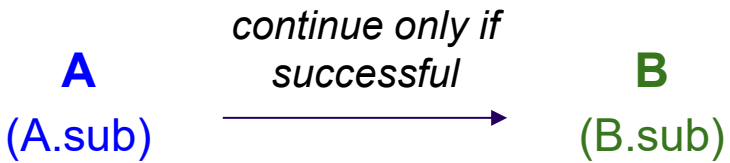
Andrew Owen

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 successfully



A is the parent
B is the child

How?

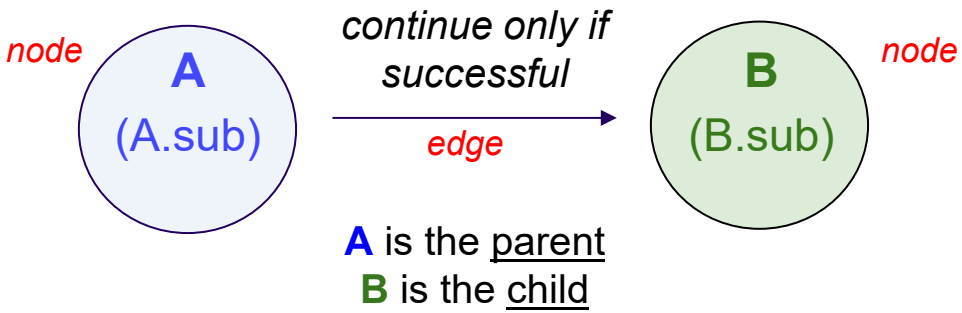
HTCondor offers you the services of the

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>

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In a file, you need to

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

my-first.dag

Syntax

JOB <node_name> <submit_file_name>

If any job fails in this submit file, the whole job (node) fails!

Create the DAG input file

In a file, you need to

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

A is the parent
B is the child

```
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?

- Default behavior: if the job exits with code 0 → successful

```
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?

- For more complex checks, you can use a script

```
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?

- For more complex checks, you can use a script

```
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*

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

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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

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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:

```
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-- 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", so DAGMan has only submitted 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
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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
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 returned exit code 0 → continue
4. B.sub executes → completes
5. DAG node scheduler job completes

Overview of process

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

PARENT A CHILD B
```

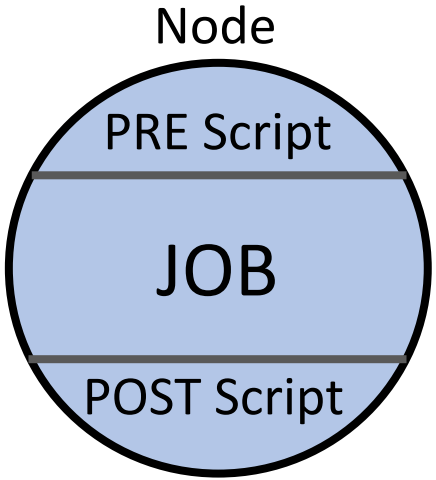
my-first.dag

`condor_submit_dag`

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

PRE/POST scripts

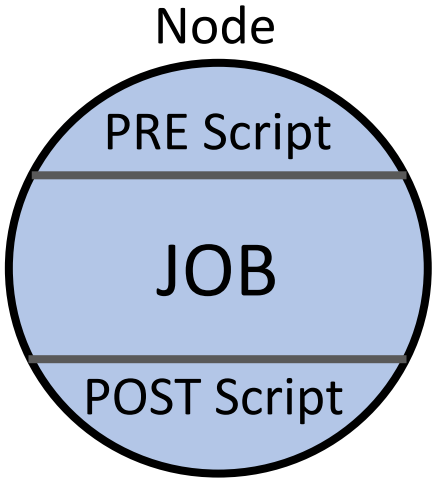
- All DAGMan PRE/POST scripts run on the Access Point and not on an Execution Point Slot.
- Scripts provide a way to perform tasks at key points in a node's lifetime.
  - *E.g., checking if files exist, creating directories, consolidating files*
- Should be lightweight (low computational) programs/tasks



DAGMan Node Scripts Documentation

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.log      my-first.dag.rescue001
(other job files)
```

Rescue DAGs Documentation

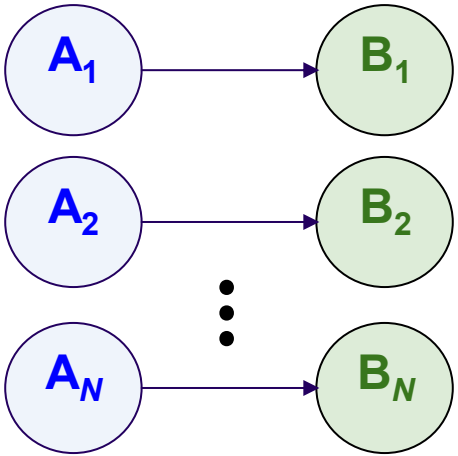
Dealing with a Failed DAG

- 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

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
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
JOB B B.sub

PARENT A CHILD B
```

my-first.dag

python
bash
…

```
JOB A1 A1.sub
JOB B1 B1.sub
PARENT A1 CHILD B1

JOB A2 A2.sub
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
JOB B1 B1.sub
PARENT A1 CHILD B1

JOB A2 A2.sub
JOB B2 B2.sub
PARENT A2 CHILD B2
        ⋮
```

my-big.dag

One Big DAG – Reuse Files

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

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

```
JOB A1 A.sub
JOB B1 B1.sub
PARENT A1 CHILD B1

JOB A2 A.sub
JOB B2 B2.sub
PARENT A2 CHILD B2
        ⋮
```

my-big.dag

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

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

DAG Description File Syntax
VARS <node_name> <variable>=<value>
Submit File Syntax
arguments = $(<variable>)

```
JOB A1 A.sub
VARS A1 number=1
JOB B1 B1.sub
PARENT A1 CHILD B1

JOB A2 A.sub
VARS A2 number=2
JOB B2 B2.sub
PARENT A2 CHILD B2
        ⋮
```

my-big.dag

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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**

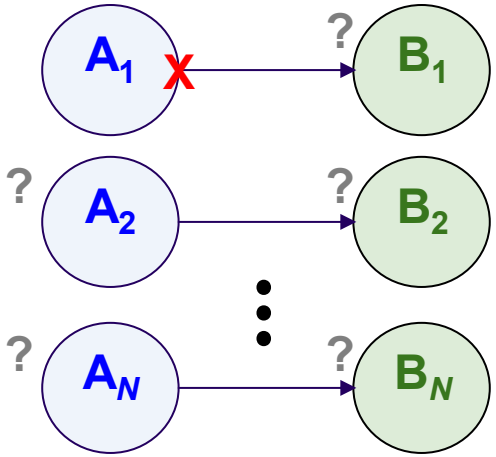
```
JOB A1 A.sub
VARS A1 number=1
JOB B1 B.sub
VARS B1 number=1
PARENT A1 CHILD B1

JOB A2 A.sub
VARS A2 number=2
JOB B2 B.sub
VARS B1 number=2
PARENT A2 CHILD B2
        ⋮
```

my-big.dag

One Big DAG - What If It Fails?

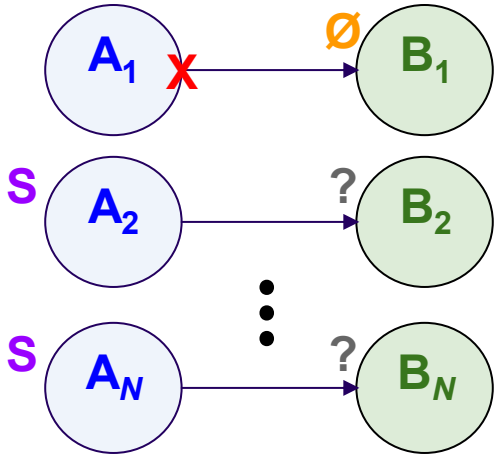
Let's say that A_1 job finishes and A-check.sh finds that the output of A_1 is incorrect, and that A_1 has failed. What happens?



One Big DAG - What If It Fails?

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.

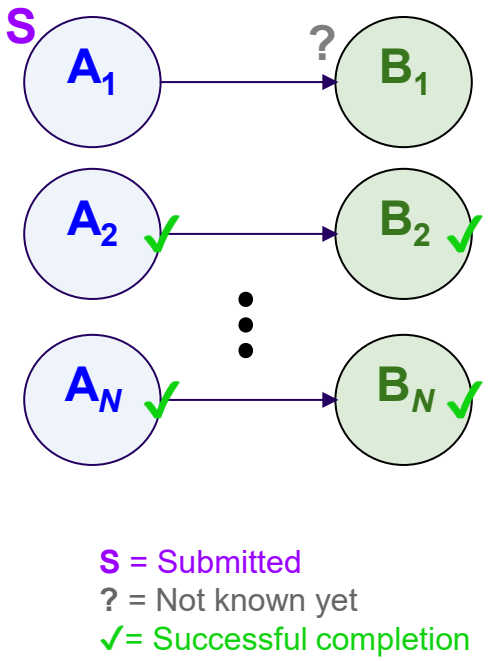


S = Submitted
X = Failed
Ø = Will not be submitted
? = Not known yet

One Big DAG - What If It Fails

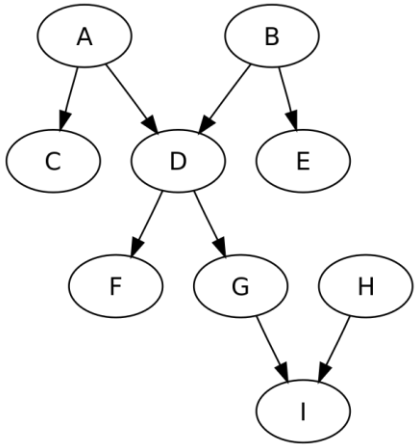
Let's say that A_1 job finishes and A-check.sh finds that the output of A_1 is incorrect, and that A_1 has failed. What happens?

- **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.

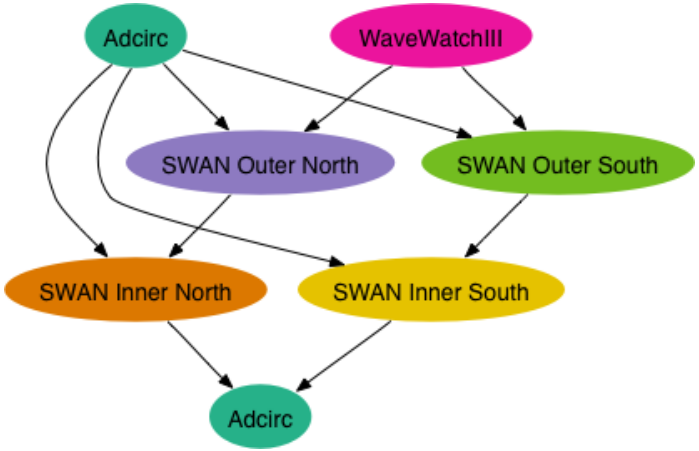


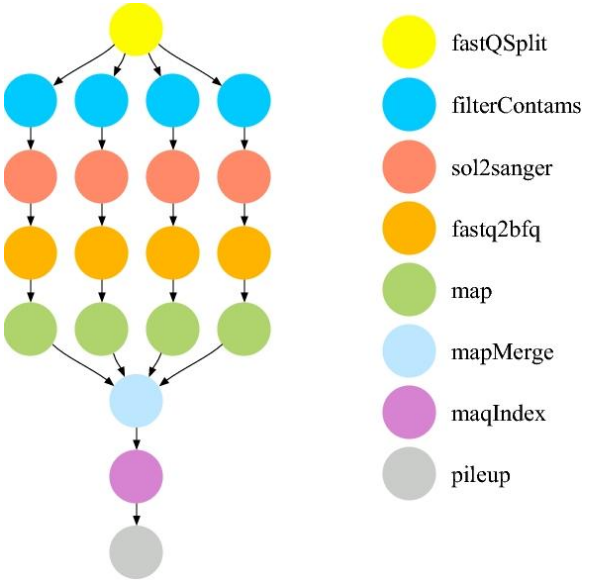
Endless Workflow Possibilities

Shared ancestor workflows



Wikimedia Commons



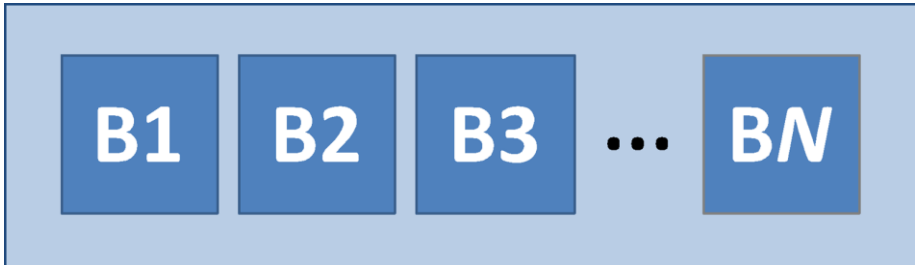


https://confluence.pegasus.isi.edu/display/pegasus/WorkflowGenerator

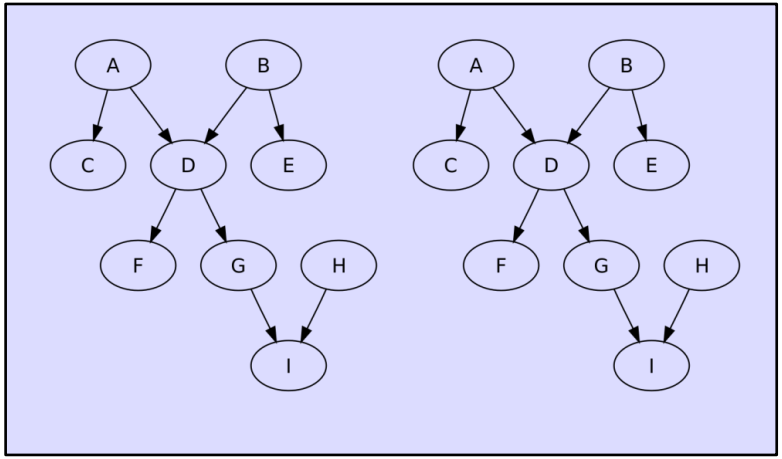
Endless Workflow Possibilities

Different ancestor workflows

A "Bag" of Jobs



Disjoined Workflows



Learn More

- 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?

Submit File Templates via *VARS*

- **VARS** line defines node-specific values that are passed into submit file variables

  VARS node_name var1="value" [var2="value"]

- Allows a single submit file shared by all B jobs, rather than one submit file for each JOB.

my.dag

```
JOB B1 B.sub
VARS B1 data="B1" opt="10"
JOB B2 B.sub
VARS B2 data="B2" opt="12"
JOB B3 B.sub
VARS B3 data="B3" opt="14"
```

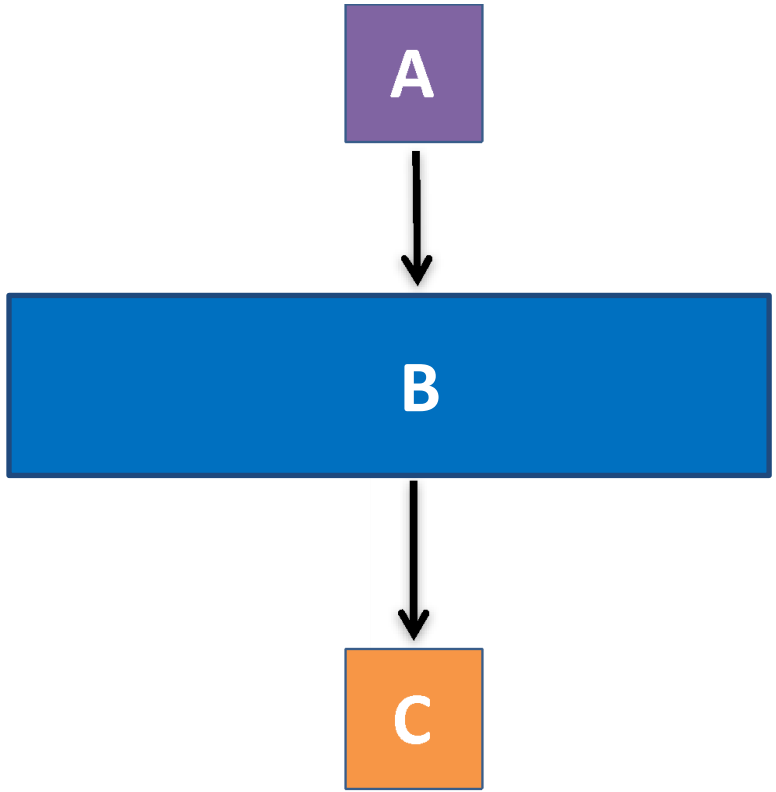
B.sub

```
…
InitialDir = $(data)
arguments = $(data).csv $(opt)
…
queue
```

A DAG within a DAG = "SUBDAG"

my.dag

```
JOB A A.sub
SCRIPT POST A generate_B.sh
SUBDAG EXTERNAL B B.dag
JOB C C.sub
PARENT A CHILD B
PARENT B CHILD C
```



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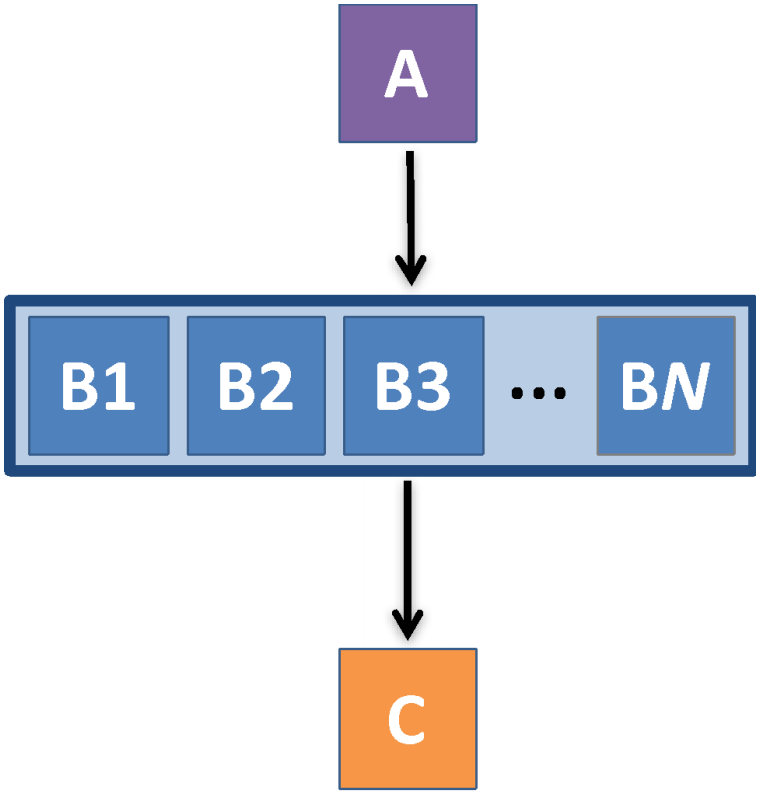
my.dag

```
JOB A A.sub
SCRIPT POST A generate_B.sh
SUBDAG EXTERNAL B B.dag
JOB C C.sub
PARENT A CHILD B
PARENT B CHILD C
```

B.dag

```
JOB B1 B1.sub
JOB B2 B2.sub
…
JOB BN BN.sub
```



A DAG within a DAG = "SUBDAG"

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SUBDAG EXTERNAL B B.dag
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PARENT A CHILD B
PARENT B CHILD C
```
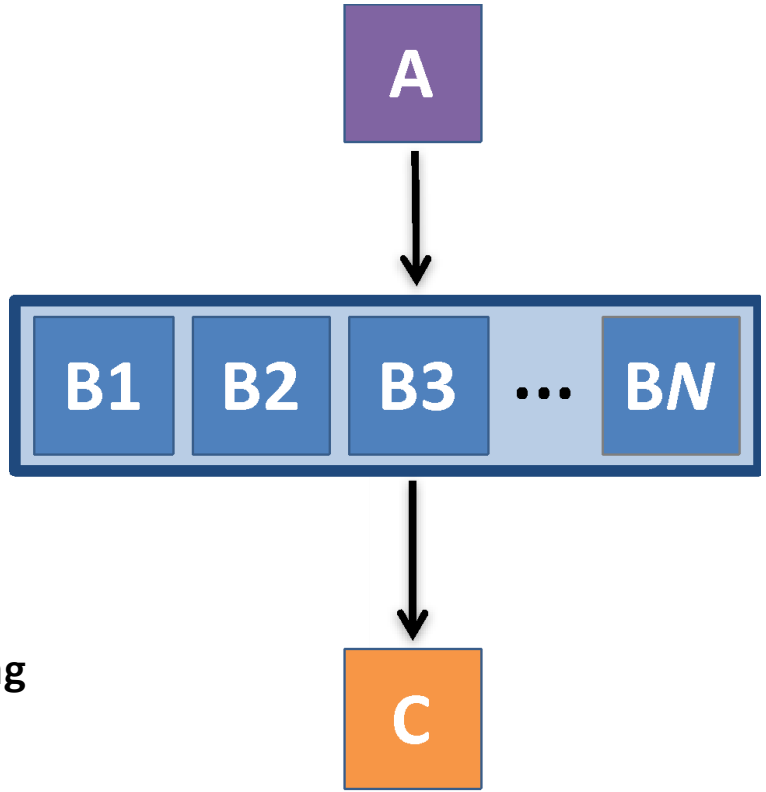
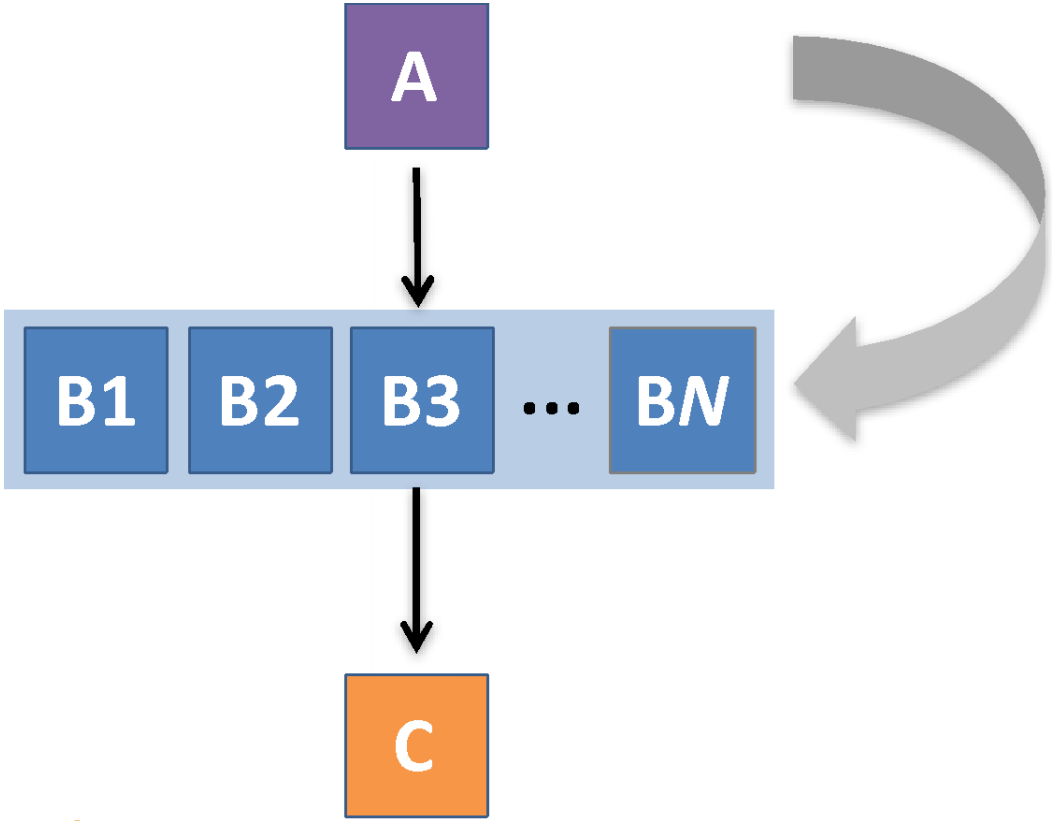



JOB → condor_submit
SUBDAG EXTERNAL → condor_submit_dag

A DAG within a DAG = "SUBDAG"



A can write the input files for subdag **B**!