



Directed Acyclic Graph Scheduling with User Defined Validation and Assimilation

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BOINC Workshop
27 Sept 2012

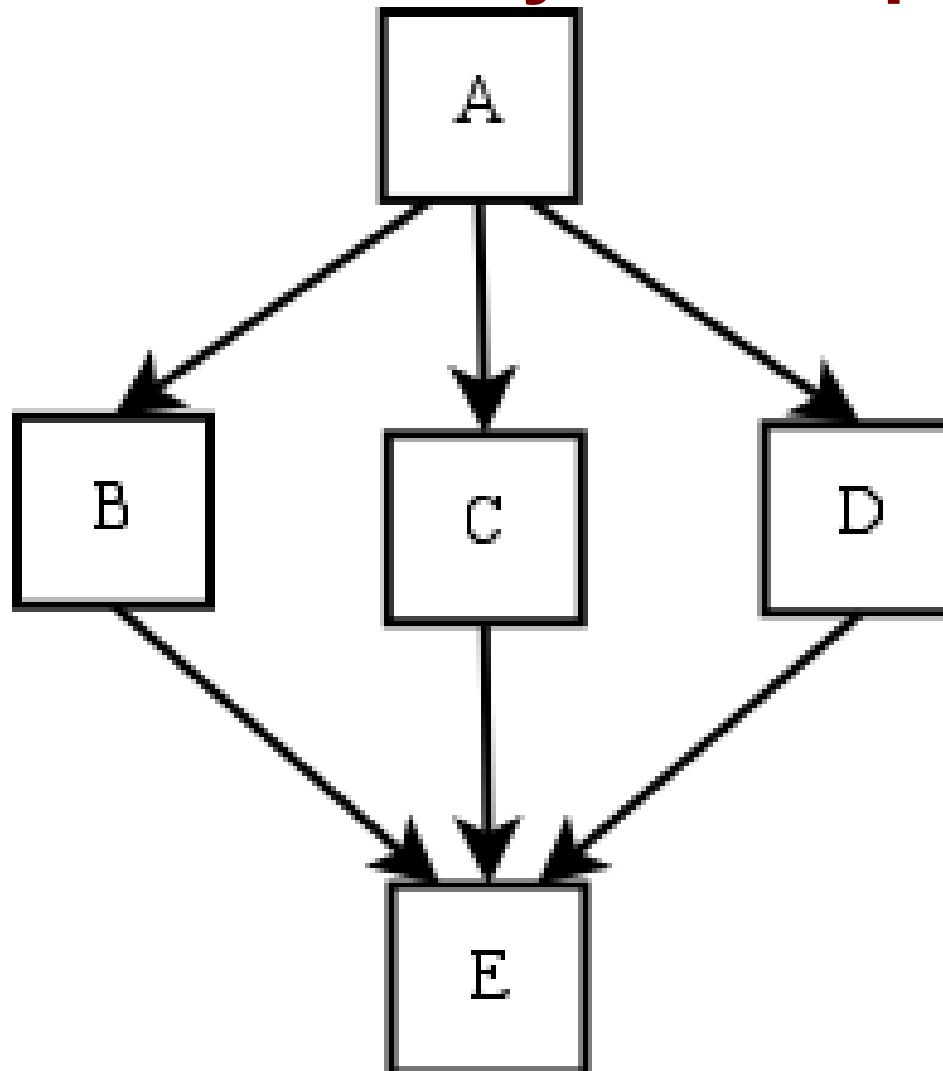


Outline

- Goals and Definitions
- Functionality
- Use Case
- To do



Directed Acyclic Graph





Goals

- Reusable method of parallelization
- Provide dynamic validation and assimilation
- Add Server-Side Job Functionality
- Provide Fault Tolerance/Error Handling



Goals

- Reusable method of parallelization
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gsub

- Commands to be run written like shell script
- *gsub* parses script
- Commands are mapped to user-defined routines in Parser Dictionary
 - Parser routines create list of Process Objects
- *gsub* creates graph (DAG) of interdependent processes
- Jobs are started (create_work)



gsub

- Run as user
 - DAG creation code is completely user customizable
- Calls `create_work`
 - Requires no BOINC code to follow during development
- Parsing functions are defined in `~/.boincdag`



Validator

- Adds layer to BOINC API
 - `init_result`, `compare_results` and `clean_result` are embedded python functions to setup and run user defined routines based on Command → Routine Map
 - Adds `BoincResult` Python class



Assimilator

- `assimilate_handler`
 - Embedded python function calls corresponding user defined code for application
 - Loads DAG object and starts child work units

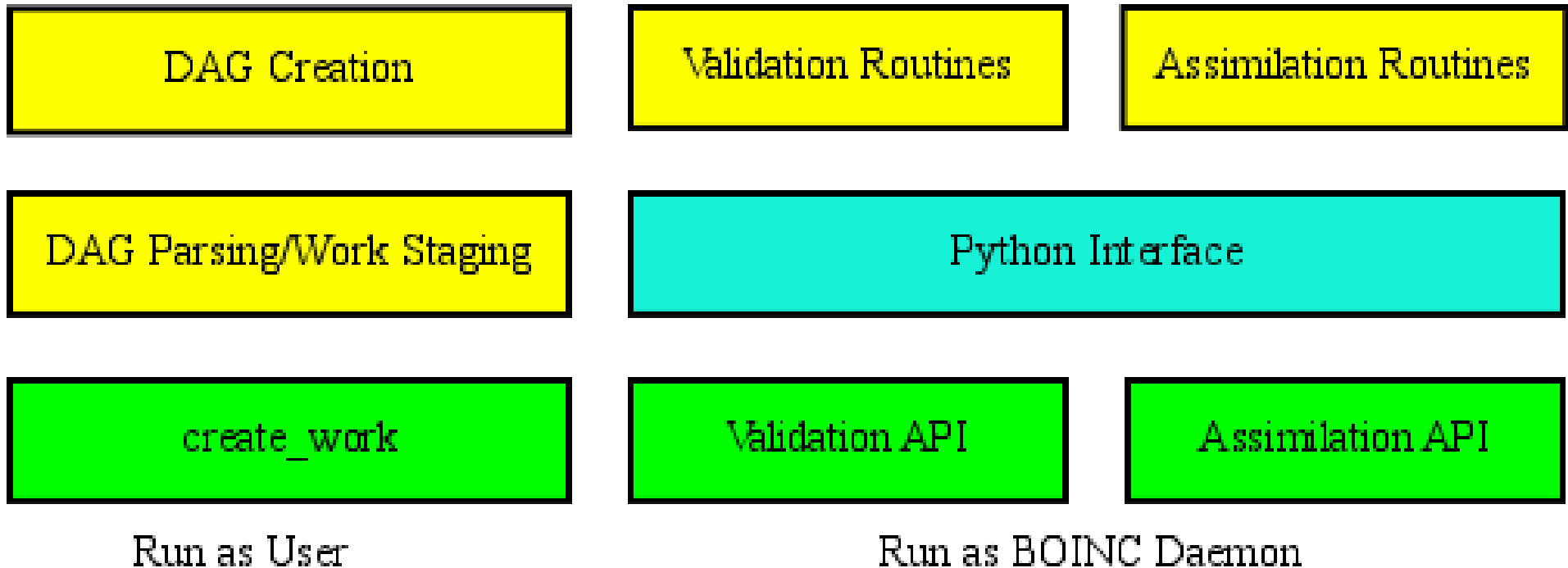


Design

- Written in a combination of Pure and Embedded Python
 - ✓ Allows changes to validation routines without need to restart daemon
 - ✓ Adds flexibility in user-defined routines
 - ✓ Easier for users with less programming experience to create custom validation code



Design



Legend



Python



Embedded Python



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Finding cures. Saving children.



Use Case

Microna – DNA Binding Prediction

- Embarrassingly parallel
- Operates on segments of DNA
- Results of Segments are recombined
- End Result is Reformated for Database



Example

```
[dcoss@stjudeathome2 Y]$ cat job.sub  
trident hsa_all_mirna-1.fasta chrY.fasta -brief -out chrY_mirna-1.out  
trident hsa_all_mirna-2.fasta chrY.fasta -brief -out chrY_mirna-2.out
```



Example

```
[dcoss@stjudeathome2 Y]$ cat ~/.boincdag  
parsers['trident'] = 'trident_segmenter.parse'  
import trident_segmenter
```



Example

```
[dcoss@stjudeathome2 Y]$ python -m gsub --setup_only job.sub
```

Running `trident_segmenter.parse(parser_args)`

Running trident with miRNA `hsa_all_mirna-1.fasta` and DNA `chrY.fasta`
with flags `-brief -out chrY_mirna-1.out`

Created 566 dna files

Running `trident_segmenter.parse(parser_args)`

Running trident with miRNA `hsa_all_mirna-2.fasta` and DNA `chrY.fasta`
with flags `-brief -out chrY_mirna-2.out`

Created 566 dna files

Saved DAG as `jobs.dag`



Example

```
[dcoss@stjudeathome2 Y]$ python -m update_dag list|head  
trident-113812189: trident  
trident-542977945: trident  
trident-471964252: trident  
trident-542491246: trident  
trident-134625408: trident  
trident-209129499: trident  
trident-436703746: trident  
trident-048747455: trident  
trident-414265868: trident  
trident-853879748: trident
```




Example

```
[dcoss@stjudeathome2 depend_tests]$ python -m update_dag print
```

```
trident
```

```
State: RUNNING(2)
```

```
Input: hsa_all_mirna-1.fasta, chrMT.fasta, chrMT.fasta_hsa_all_mirna-1.fasta-job.xml (job.xml)
```

```
Output: step1.out
```

```
Workunit Name: trident-569267845
```

```
Workunit Template: tmppEvgIY
```

```
Result Template: tmpLRDvpT
```

```
args: -brief -out step1.out
```

```
Children:
```

```
trident-736471555(trident)
```



Example

trident

State: CREATED(0)

Input: hsa_all_mirna-2.fasta, step1.out, step1.out_hsa_all_mirna-2.fasta-job.xml (job.xml)

Output: chrMT_150000-1_mirna-2.out

Workunit Name: trident-736471555

Workunit Template: tmpAo0Leb

Result Template: tmpXhYdAf

args: -brief -out chrMT_150000-1_mirna-2.out

Children:

Depends on: trident

Unfinished Dependencies

Process: trident-569267845

File: step1.out

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TODO

- Server-Side Mechanism
 - Indicate that process is Python code or server program
- Explicit dependency
 - Currently only file based dependency
- Conditional Branches



Acknowledgments & Thanks

- Work supported financially by American Lebanese Syrian Associated Charities
- Use case is part of a project with Steve Paugh of St Jude