

Part 1: Building Blocks & Tools

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Adaptive Execution

- Context: Distributed Comp. & Applications
- Goal driven, conditional executable <-> resource mapping and application decomposition based on (changing) application and resource properties
- Goals can be manifold: maximize throughput, optimize resource utilization, time-to-completion, resource or cost constraints, ...
- Sometimes referred to as *dynamic execution*, but that term is even more ambiguous

Application vs Executable

- Both terms are often used interchangeably...
- An *application* is software designed to perform a specific task. It consists of one or more *executables* or *executable instances* and possibly other things like files, databases, etc. That's why applications are usually *decomposable*!
- Executables realize a specific computational functionality of an application. They must be mapped to a computing resource

A Classification Attempt 1/3

- Based on where adaptive occurs:
 - A centralized adaptive execution 'component' controls all aspects of the optimization process, e.g., Condor's "match maker"
 - A set of *decentralized*, components contribute individually to the optimization process, e.g., based on agent-networks
 - Adaptive execution in *user-space* v.s. in *system-space* (or both?)

A Classification Attempt 2/3

- Based on how adaptivity is implemented:
 - Manually
 - Static Rules
 - Dynamic
 - Knowledge-based
 - Learning / AI based

A Classification Attempt 3/3

- Based on when adaptivity occurs:
 - A: pre-execution (one-time adaption):



• B: in-execution (continuous adaption):



Examples: Condor (A), Pegasus (A),
 Adaptive-Pegasus (B)

Analyze, Plan, Execute

Analyze

Plan

Execute

- APE: Building blocks for any class of adaptive execution system!
 - Analyze resource environment and application properties and requirements
 - Plan application decomposition, execution trajectory, resource mapping, ...
 - Execute the application according to plan ...

APE with SAGA?

- *E* is pretty obvious that's what the *SAGA Job API* is all about!
- A not so much. SAGA Service Discovery (SD) and Information Service (IS) APIs might help to analyze some resource aspects. Application analysis? No.
- P nope. No such thing in SAGA. Write your own planner application, tool, framework, ...

SAGA SD API

- saga.sd.Discoverer: knows and provides information about one or more services
- saga.sd.ServiceDescription: describes a service (name, type, access url, ...)
- saga.sd.ServiceData: exposes service properties. Dependent on type and backend, but Bliss tries to enforce the GLUE schema
- http://oweidner.github.com/bliss/apidoc/

SAGA SD Example

```
sdd = saga.sd.Discoverer("pbs+ssh://india.futuregrid.org")
services = sdd.list services()
for service in services:
   # for each service, get some key metrics via the
   # service data object
   data = service.get data()
   print " * Serivce: '%s', type: '%s', url: '%s'" \
     % (service.name, service.type, service.url)
   print " - Running Jobs
                                    : %s" \
     % (data.get attribute("GlueCEStateRunningJobs"))
   print " | - Waiting Jobs
                                    : %s" \
     % (data.get attribute("GlueCEStateWaitingJobs"))
   print " | - Total CPUs
                                    : %s" \
     % (data.get_attribute("GlueSubClusterPhysicalCPUs"))
   print " - Free CPUs
     % (data.get_attribute("GlueCEStateFreeCPUs"))
   print " '- CPUs per Node
                                    : %s" \
(data.get attribute("GlueHostArchitectureSMPSize"))
```

SAGA Job API

- saga.job.Description: describes the properties and requirements of an executable (job)
- saga.job.Service: represents a (remote) entity that can run jobs (e.g., a cluster)
- *saga.job.Job:* represent the executable itself and provides handles to control its execution (e.g., start, stop, ...)
- http://oweidner.github.com/bliss/apidoc/

A Simple Example 1/4

- Goals: Start application as soon as possible and use selected (HPC) resources as efficient as possible
- Resources: XSEDE, LONI and FutureGrid machines
- <u>Application</u>: DNA Short-read mapping against a reference genome (yes. *BFast*, of course)

A Simple Example 2/4

Analyze:

- Find out number of BFAST executable instances (defined by # read files)
- Find out which resource has how many nodes available (saga.sd)
- Find out the properties of the nodes, like memory, cpus, cores (saga.sd)
- https://github.com/oweidner/bliss/blob/master/examples/sd-api/

A Simple Example 3/4

- Plan: e.g., apply a simple, static rule
 - pick resource with the highest # of immediately available cores (nodes*cores).
 - If that's < # executable instances, add the resource with the 2nd highest # of immediately available cores ... and so on.
 - Map # cores BFast executable instances to each node

A Simple Example 4/4

• Execute:

- Create jobs for executable instances and run on the selected resources (saga.job)
 according to our plan
- https://github.com/oweidner/bliss/blob/master/examples/advanced/dynamic_execution_01.py
- DONE! We have just automated something using concepts of adaptive execution that many people still do by hand!

What's Next?

- Part 2: M as in monitoring
- Part 3: K as in Knowledge
- Part 4: MAPE-K Framework Design
- Part 5: System Survey
- Part 6: Experimental Results

Resources

- Contact: <u>ole.weidner@me.com</u>
- Bliss Discussion List:
 http://groups.google.com/group/saga-bliss
- Bliss Wiki & Documentation:
 https://github.com/oweidner/bliss/wiki
- These Slides: http://oweidner.github.com/bliss/docs/bliss_adex_101.1