A Framework for Distributed Data-Parallel Execution in the Kepler Scientific Workflow System



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http://biokepler.org/

Background

Scientific data

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- Enormous growth in the amount of scientific data
- Applications need to process large-scale data sets

Data-intensive computing

- Distributed data-parallel (DDP) patterns, e.g., PACT and MapReduce, facilitate data-intensive applications
- Increasing number of execution engines available for these patterns, such as Hadoop and Stratosphere







Challenges

- Applications or workflows built using these DDP patterns are usually tightlycoupled with the underlying DDP execution engine
- None of existing applications/systems support workflow execution on more than one DDP execution engine



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The bioKepler Approach

- Use Distributed Data-Parallel (DDP) frameworks, e.g., MapReduce, to execute bioinformatics tools
- Create configurable and reusable DDP components in Scientific Workflow System
- Support different execution engines
 and computational environments

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Conceptual Framework



bioKepler Architecture





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Distributed Data-Parallel bioActors

- Set of steps to execute a bioinformatics tool in DDP environment
- Can either be:
 - as sub-workflows (composite)
 - in Java code (atomic)
- Includes:

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- Data-parallel patterns, e.g., Map, Reduce, All-Pairs, etc. to specify data grouping
- I/O to interface with storage
- Data format specifying how to split and join





Distributed Data-Parallel Directors

- Directors implement a Model of Computation
 - Specify when actors execute

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- How data transferred between actors
- DDP Directors run bioActors on DDP execution engines
 - Hadoop director converts workflow into MapReduce, runs on Hadoop
 - Stratosphere director converts workflow into PACT program, executes on Nephele
 - Generic DDP director automatically detect available DDP engines and select the best





DDP BLAST Workflow



DDP bioActor Usage Model





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DDP BLAST Workflow Experiments



Summary

- The bioKepler approach
 - Facilitates using data-parallel patterns for distributed execution of bioinformatics tools
 - Interfaces with different execution engines to use various computational resources
- Future Work

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- Which patterns for which tools?
- New patterns needed?





Questions?

More Information

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