Parallelization techniques: Applying Map, Reduce and Cross concepts using bioActors



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What is Parallelization?





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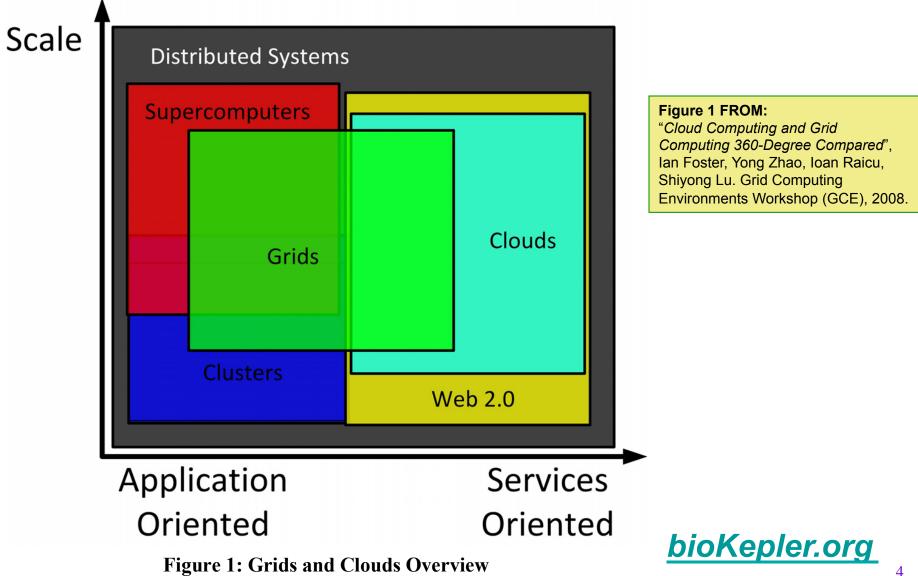
What is Parallelization?





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Distributed Computing Environments



Parallelization Solutions in Distributed Environments

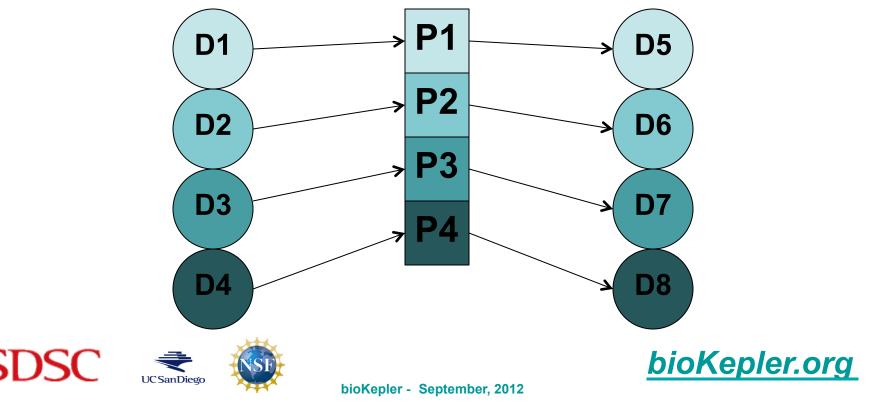
- Traditional parallel programming interfaces
 - Examples: MPI and OpenMP
 - Hard to implement
 - Original sequential tools cannot be reused
- Parallel job execution
 - Examples: SGE and Condor
 - Original sequential tools can be reused
 - Create small jobs by splitting data or tasks
 - Hard to achieve data locality for each job
- Data parallel job execution
 - Examples: Hadoop and Stratosphere
 - Original sequential tools can be reused
 - Support customized and automatic data partition and distribution
 - Support data locality for each job through special distributed file system, HDFS





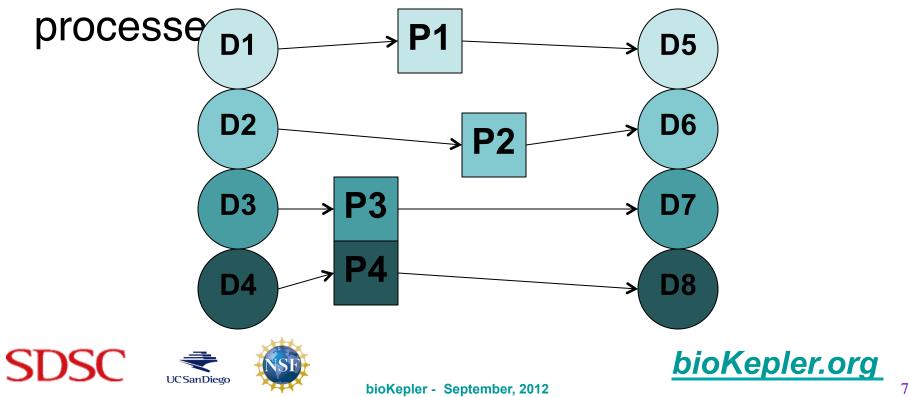
Data Parallel Task Execution

- Static executables run as processes
- Independent data items are assigned to processes



Distributed Data Parallel (DDP)Task Execution

- Static executables run as processes on distributed environments
- Independent data items are assigned to



MapReduce:

A Typical DDP Execution Pattern

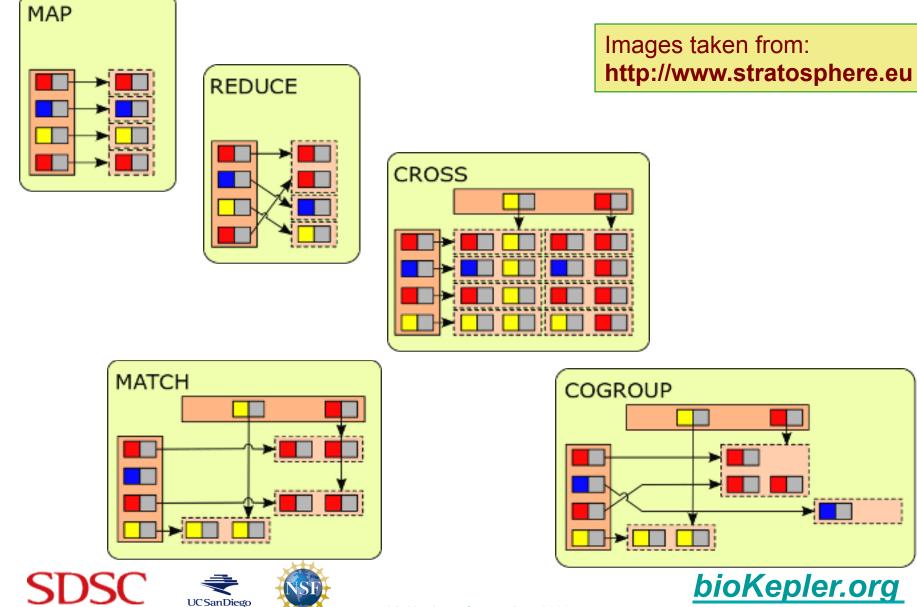
- <u>Chop the data based on *a feature of interest* (value)
 (key)
 </u>
- Iterate a function on each value
- Order the intermediate data products' (intermediate value)
- <u>Stitch</u> the intermediate values
 - Can execute using a specialized engine Examples: Hadoop and Nephele





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Many Other DDP Patterns



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Distributed Data-Parallel bioActors

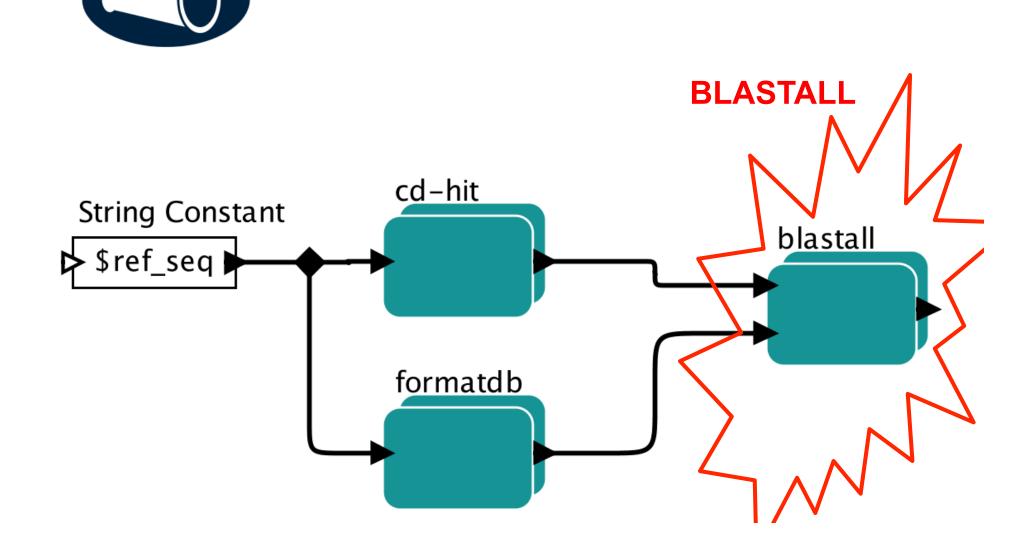
- Set of steps to execute a bioinformatics tool in DDP environment
- Customized from the ExecutionChoice actor
- Includes:
 - Data-parallel patterns, e.g., Map, Reduce, Cross, All-Pairs, etc., to specify data grouping
 - I/O to interface with storage
 - Data format specifying how to split and join



A Workflow with Three bioActors

• ref_seq: small.faa

SDF Director



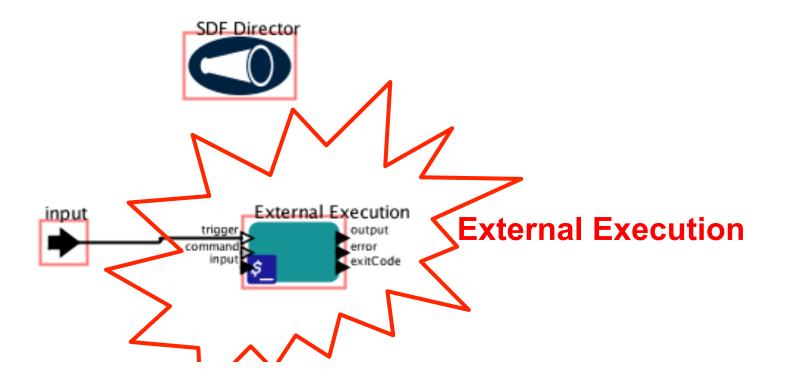
Configuring the BLASTALL bioActor

	blastall	
	program: programOptions:	blastall
		-p blastn -d \$ref_seq -i \$input -b1 -v1 -m8 -e \$max_evalue
	Inputs	
	input:	/Users/jianwu/Projects/bioinfo/testQueryFile/testQuery.fa
	Outputs	
	outputOption: output:	-0
		\$output_dir/test.out
	Execution Choice	CrossReduce

SDS

Inside the LocalExecution Tab

		V	Vorkflow		
(Local Execution	Sun Grid Engine	MapOnly	MapReduce	CrossReduce



Inside the MapReduce Tab Workflow Local Execution Sun Grid Engine MapOnly MapReduce CrossReduce ReferenceFile: \$DataDir/Ocean_Alaska.fa LocalRefFile: \$DataDir/Ocean_Alaska.fa DBFormatCmd: formatdb DataDir: /Users/jianwu/Projects/bioinfo/testQueryFile/ • DBFormatOptions: -p F -o F BLASTDir: /Users/jianwu/Projects/CAMERA/cvs/workflows/ca DBPath: /tmp/ StratosphereConfPath: ParallelNumber: 2 BLASTCmd: blastall BLASTOptions: -p blastn -i stdin -m 8 -e 1e-5 RefSeqLength: 3311966 QueryFile: \$DataDir/testQuery.fa AlignmentLimit: 250 OutputFile: \$DataDir/blast-map-reduce.out SDF Director Stratosphere Blast ReferenceFile2 input Stratosphere Blast ReferenceFile OutputFile2 \$OutputFile trigger.

Inside the MapReduce Tab Workflow Local Execution Sun Grid Engine MapOnly MapReduce CrossReduce ReferenceFile: \$DataDir/Ocean_Alaska.fa LocalRefFile: \$DataDir/Ocean_Alaska.fa DBFormatCmd: formatdb DataDir: /Users/jianwu/Projects/bioinfo/testQueryFile/ • DBFormatOptions: -p F -o F BLASTDir: /Users/jianwu/Projects/CAMERA/cvs/workflows/ca DBPath: /tmp/ StratosphereConfPath: ParallelNumber: 2 BLASTCmd: blastall BLASTOptions: -p blastn -i stdin -m 8 -e 1e-5 RefSeqLength: 3311966 QueryFile: \$DataDir/testQuery.fa AlignmentLimit: 250 OutputFile: \$DataDir/blast-map-reduce.out SDF Director Stratosphere Blast input ReferenceFile2 SReferenceFile OutputFile2 trigger \$OutputFile

BLASTALL with MapReduce

pler	Local Execution MapReduce				
DBFo	rmatCmd:	\$BLASTDir/formatdb	Configure		
BLAS	FCmd:	\$BLASTDir/blastall	Configure		
BLAST	TOptions:	-p blastn -i stdin -m 8 -e 1e-5	Configure		
Query	/File:	/usr/local/bioinf/sampledata/blast/testQuery.fa	Configure		
RefSe	qLength:	3311966	Configure		
DBFo	rmatOptions:	-p F -o F	Configure		
DBPat	th:	/tmp/	Configure		
Align	mentLimit:	250	Configure		
Parall	elNumber:	2	Configure		
Strate	osphereConfPath:		Configure		
Local	RefFile:	/usr/local/bioinf/sampledata/ocean_alaska_seqs/Ocean_Ala	Configure		
BLAS	TDir:	/usr/bin	Configure		
Refer	enceFile:	/usr/local/bioinf/sampledata/ocean_alaska_seqs/Ocean_Ala	Configure		
Outp	utFile:	property("user.home")+ "/blast-map-reduce.out"	Configure		

SD

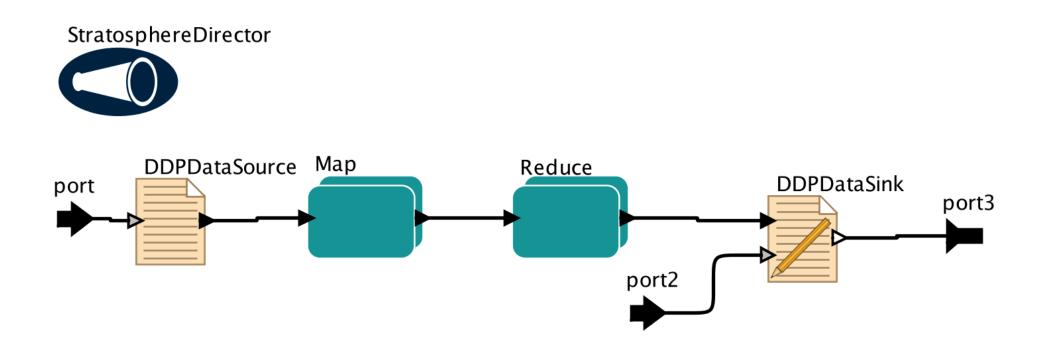
G

OK

Cancel

Add

Inside the Stratopshere Blast

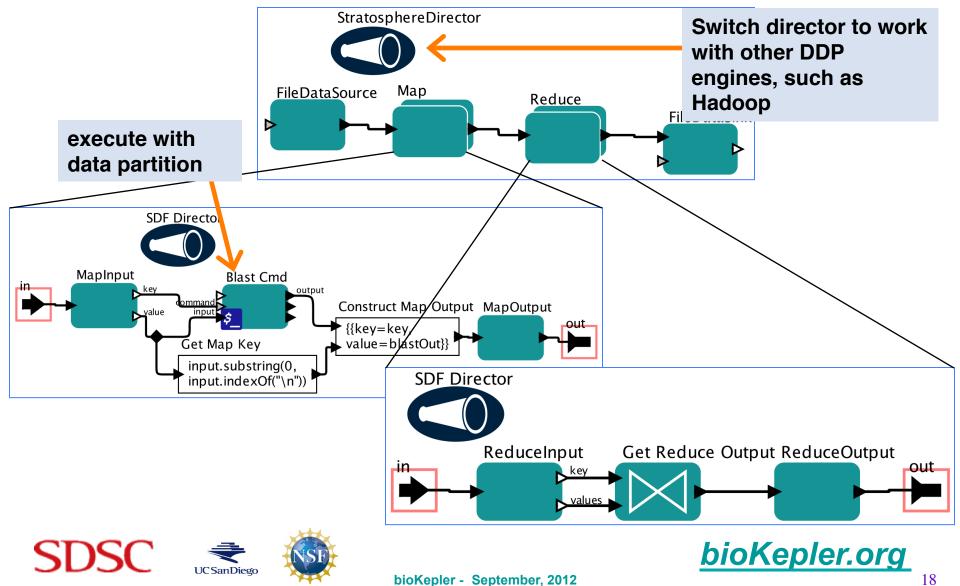






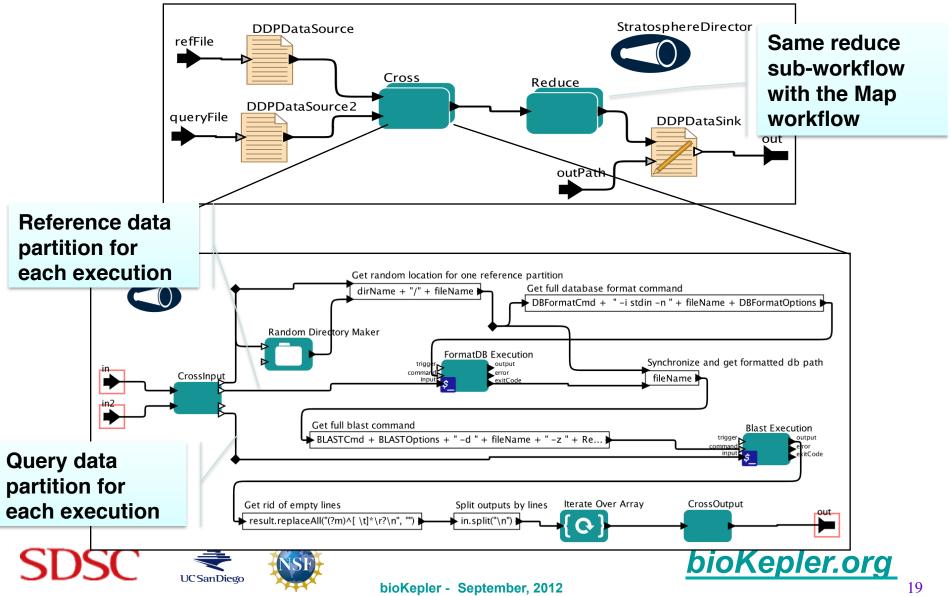
DDP BLAST Workflow via Splitting Query

Sequences

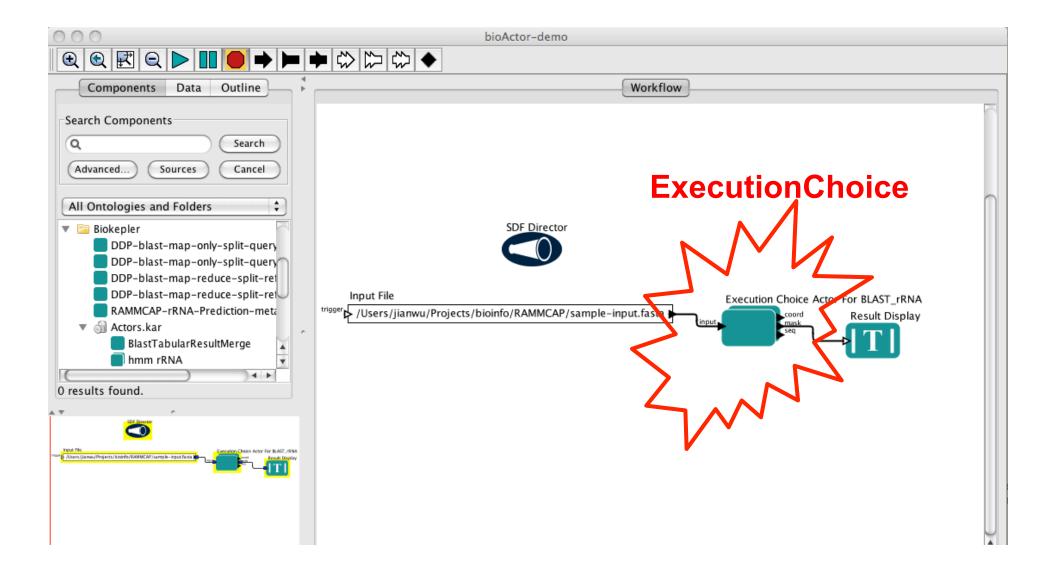


DDP BLAST Workflow using Cross and

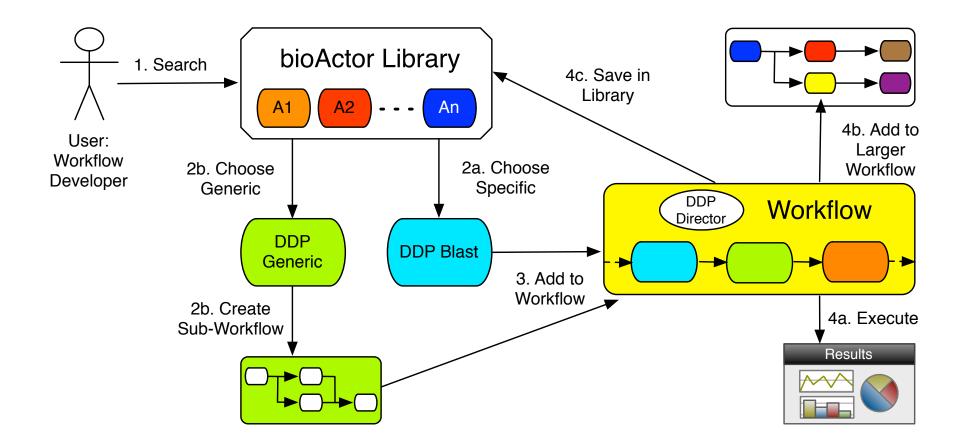
Reduce



What if the bioActor I need is not available?



DDP bioActor Usage Model







NEXT: Kepler Interface and Introductory Examples on Using Kepler

Daniel Crawl

1st Workshop on bioKepler Tools and Its Applications





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