Hands-on 3: Local and Distributed Execution

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Goals

- Create an actor to run BLAST in different environments
 - Local execution (blastall)
 - (Part 2) Distributed execution (mpiblast) on a cluster
- Configure ExecutionChoice to run BLAST
 - Inputs, Outputs, Parameters
 - Local and MPI choices

Running BLAST Locally

Example command line:

blastall -i query -d ref -p blastn -m 8 -e 1E-5 > align

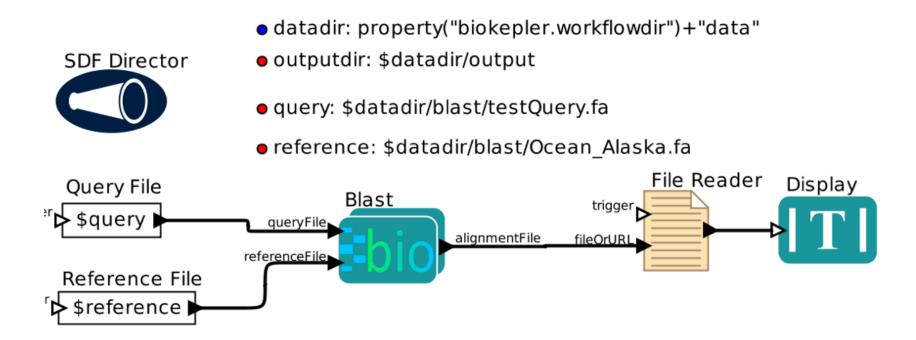
Running BLAST Locally

Example command line:

```
blastall -i query -d ref -p blastn -m 8 -e 1E-5 > align
Inputs Parameters Output
```

Step 1: Open Blast workflow

Workflow is /home/biokepler/Blast.kar



Step 2: Set Parameter Values

program:	blastall
Input File Parameters	
queryFile (-i):	
referenceFile (-d):	
Output File Parameters	
check Output Time stamp:	✓
alignmentFile (>):	\$HOME/alignment.txt
Parameters	
additionalOptions:	-e 1E-5 -p bastn -m 8

Step 3: Run Finished Workflow

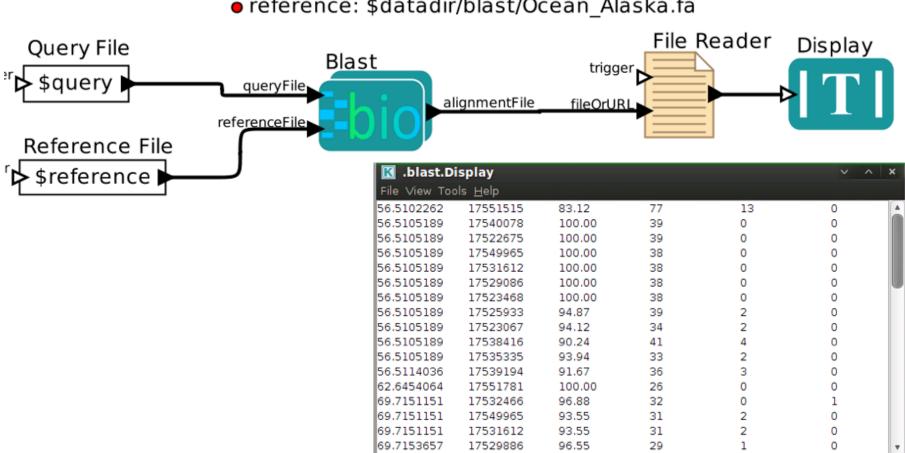
datadir: property("biokepler.workflowdir")+"data"

outputdir: \$datadir/output

SDF Director

query: \$datadir/blast/testQuery.fa

reference: \$datadir/blast/Ocean_Alaska.fa



mpiBLAST

- mpiBLAST is open source MPI based implementation of database segmentation for parallel BLAST search
- Super-linear performance gain with database segmenting technique
- Ideal database fragment is largest fragment that can sit in the memory
- Making fragments smaller than available memory adds to the overhead

mpiBLAST Algorithm

mpiBLAST algorithm consists of three steps:

- Segmenting and Distributing the database
- Running mpiBLAST queries on each node
- Merging the results from each node in a single output file

mpiBlast commands

 Formatting and Segmenting the database mpiformatdb –n NP -i ref.fa

Querying the database and merging the results

mpirun –n **NP** mpiblast -p blastp –d ref.fa -i query.fas –o blast_results.txt

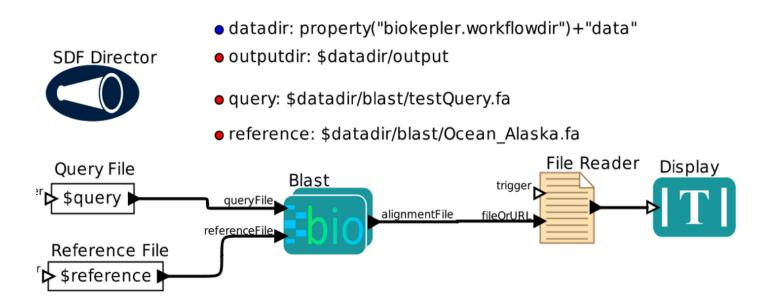
Goal: To run mpiBlast on HPC Cluster remotely through Kepler workflow: SDSC Gordon Supercomputer

```
mpirun –n NP mpiblast -p blastp -i query -d ref -m 8 -e 1E-5 > align Inputs
Parameters Output
```

NP – multiple parallel processes

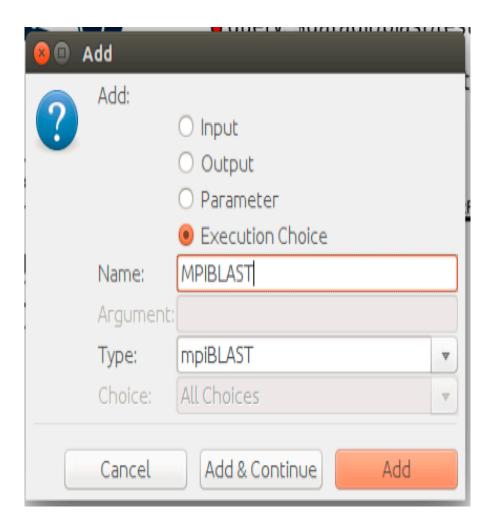
Step 1: Open blast workflow

- Go to Step 2, if Blast.kar is already open
- Else the workflow: /home/biokepler/Blast.kar



Step 2: Add new execution choice for MPIBLAST

- Double-click on the Blast actor and click on Add.
- Change radio button to Execution Choice.
- Select Type: mpiBLAST.
- Set Name to MPIBLAST.
- Click Add to close the dialog



Step 3:Configure the New Execution Choice

- Double-click on Blast actor
- Change to MPIBLAST tab
- Configure MPIBLAST tab:

Please use Gordon username assigned to you in place of LOGIN.

First parameter: TargetHost

Edit "TargetHost" parameter and set its value to be LOGIN@gordon.sdsc.edu

Second parameter: cmdFile

- If already set move next parameter
- Else set its value to be \$HOME/mpiBLAST/blastp_gordon.sh

Third parameter: commandLine

• Keep as it is. Move to next parameter.

Fourth parameter: outputFile

- If already set move next parameter
- Else set its value to be \$alignmentFile

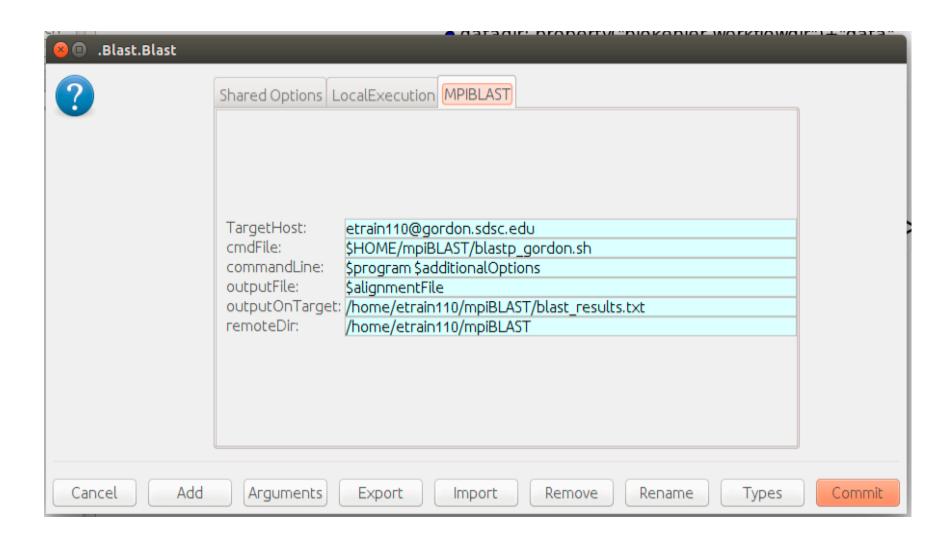
Fifth parameter: outputOnTarget

Set its value to be /home/LOGIN/mpiBLAST/blast_results.txt

Sixth parameter: remoteDir

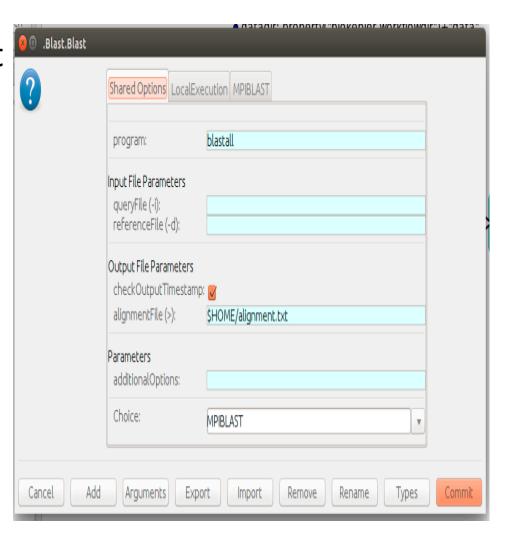
Set its value to be /home/LOGIN/mpiBLAST

Step 3: Configure the New Execution Choice



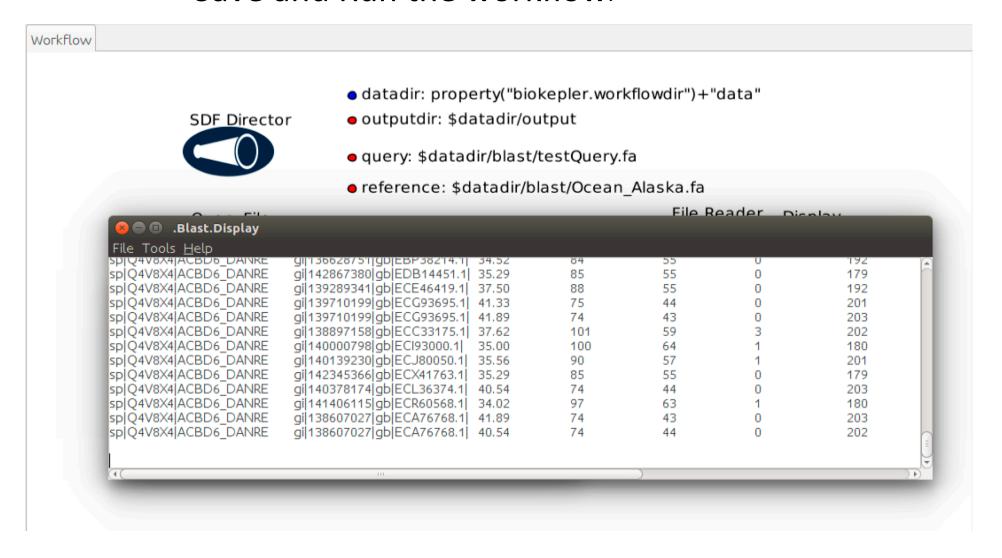
Step 4: Set the Execution Choice to MPIBLAST

- Double-click on the Blast actor and click on Add.
- Go to "Shared Options"tab
- Set Choice to MPIBLAST.
- Click on commit to save the changes and close the configuration box.



Step 5: Run Finished Workflow

Save and Run the workflow.



mpiBLAST Performance

#Nodes	Run Time (sec)	Speed-Up
1	80775	1.00
4	8752	9.23
8	4548	17.76
16	2437	33.15
32	1350	59.83
64	851	94.92
128	474	170.41

Parallel Computing: Software Technology, Algorithms, Architectures & Applications

Gerhard Joubert, Wolfgang Nagel, Frans Peters, Wolfgang Walter Elsevier, Sep 23, 2004