

EMBL-EBI wellcome trust Sanger institute

How to eHive

Leo Gordon
EnsEMBL/Compara
EMBL-EBI
Wellcome Trust Genome Campus
Hinxton CB10 1SD, UK



eHive: definitions

- eHive: a database-centric system for setting up and running software pipelines on a multithreaded compute resource
- software pipeline: a system of inter-linked data processing steps where the input of one step is the output of another
- Runnable/code: a PERL module to be run
- job: an individual data processing step (completely defined by Runnable+parameters)
- input & output: job parameters in the form of PERL hash







Flat parameter space vs. analysis abstraction

Flat parameter space:

```
{ 'species' => 'Human', 'chr' => 1}
{ 'species' => 'Human', 'chr' => 2}
...
{ 'species' => 'Human', 'chr' => 'X'}

{ 'species' => 'Mouse', 'chr' => 1}
{ 'species' => 'Mouse', 'chr' => 2}
...
{ 'species' => 'Mouse', 'chr' => X}
```

Analysis abstraction level:

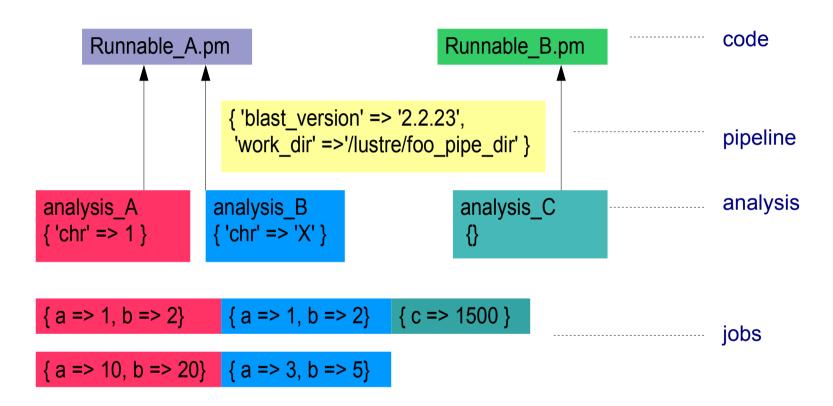
```
Analysis_A: { 'species' => 'Human'}
     \{ 'chr' => 1 \}
     \{ 'chr' => 2 \}
     { 'chr' => 'X'}
Analysis_B: { 'species' => 'Mouse'}
     { 'chr' => 1}
     \{ 'chr' => 2 \}
     { 'chr' => 'X'}
```







parameters (code, pipeline, analysis, job)









Static vs. dynamic job creation

Database: blackboard with jobs to do. Why not write on it?

Static:

(EnsEMBL pipeline RuleManager.pl)

- 1. Create <u>all</u> the jobs first
- Create "blocking" rules that define the order of execution
- 3. Run jobs that happen to be unblocked
- 4. Refresh blocked status by reapplying rules
- 5. Repeat from 3.

<u>Dynamic:</u>

(eHive's beekeeper + Workers)

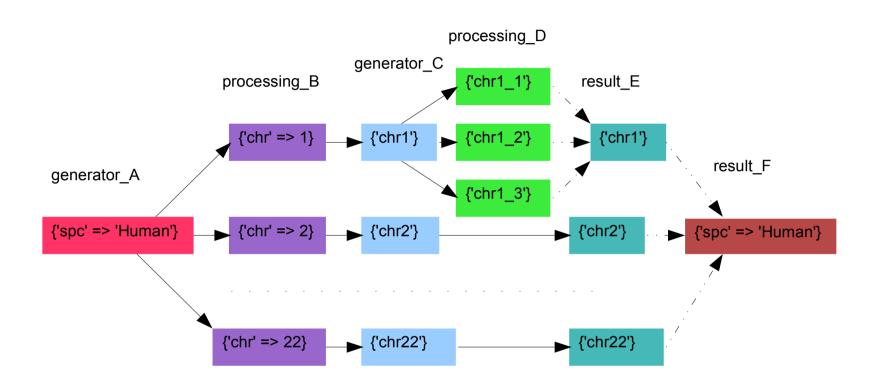
- 1. Create some jobs
- 2. Create rules of job creation (s.-c. dataflow)
- 3. Create blocking/waiting rules
- 4. Run jobs that happen to be unblocked
- 5. Refresh blocked status by reapplying rules
- 6. Repeat from 3.







typical eHive dataflow diagram

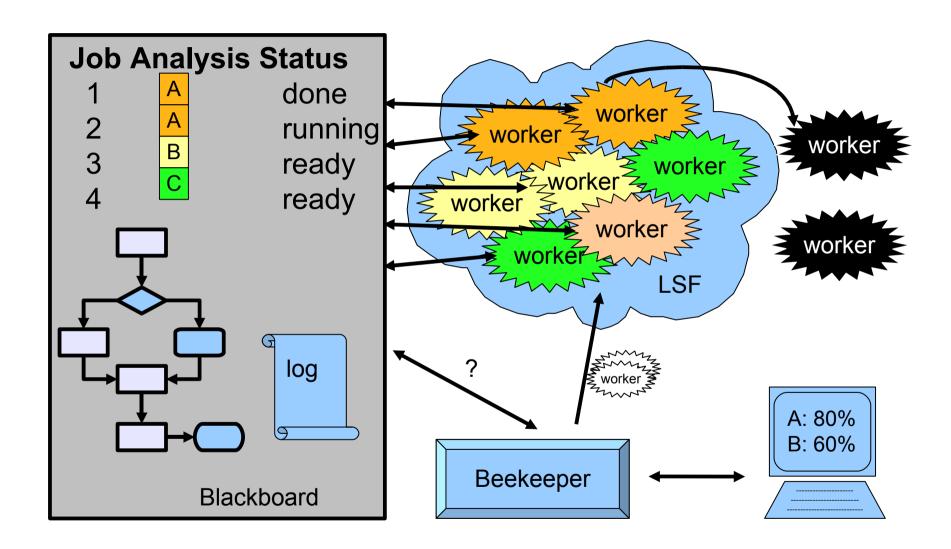








eHive: Workers as autonomous agents









Long multiplication example

```
9650156169
        \times 327358788
        77201249352
       77201249352
      67551093183
     77201249352
    48250780845
+
   28950468507
  67551093183
 19300312338
28950468507
3159063427494563172
```

```
Intermediate results:
```

```
9650156169 x 2 = 19300312338

9650156169 x 3 = 28950468507

9650156169 x 5 = 48250780845

9650156169 x 7 = 67551093183

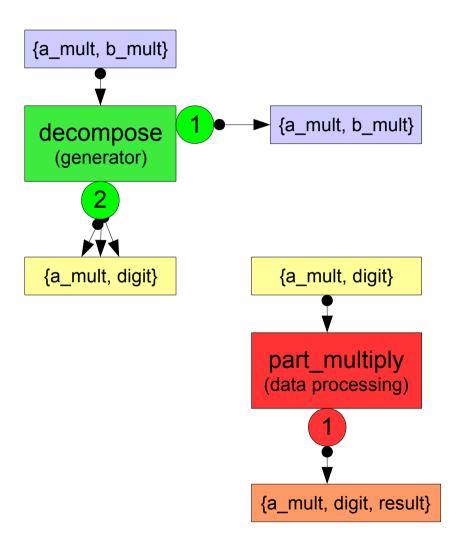
9650156169 x 8 = 77201249352
```

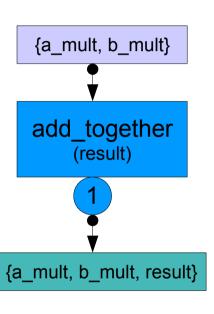






Long multiplication pipeline building blocks and interfaces



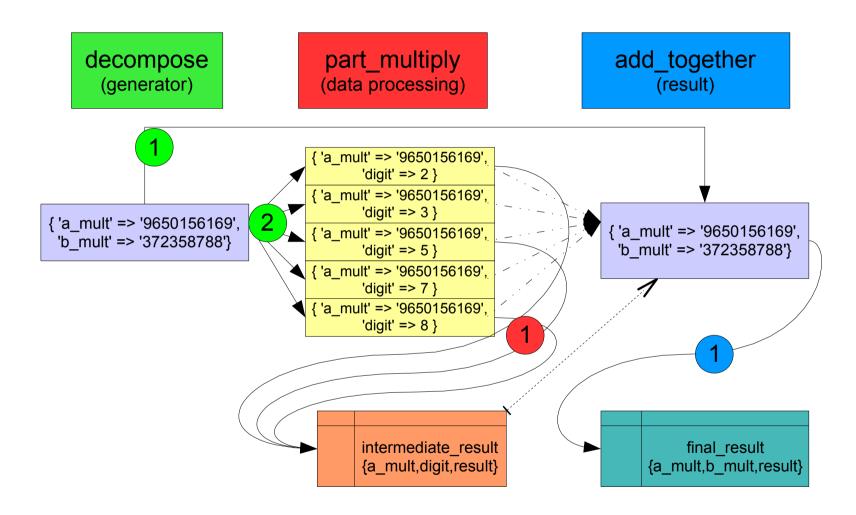








Long multiplication pipeline dataflow diagram









Parameter substitution & Universal building blocks (1)

```
compressor [ SystemCmd.pm ]
{ 'cmd' => 'gzip #filename#' }
```

- Expessive power of Unix shell + parallel execution of the farm
- Job tracking, retry, throttling, tricky dependencies, etc







Parameter substitution & Universal building blocks (2)

```
myisamiser [ SqlCmd.pm ]
{ 'sql' =>
  'ALTER TABLE #table#' engine=MyISAM' }
```

```
{ 'table' => 'protein_tree_node' }

{ 'pattern' => 'protein\\_tree\\_%'}

{ 'table' => 'protein_tree_member' }

{ 'table' => 'protein_tree_stable_id' }

{ 'table' => 'protein_tree_tag' }
```

- JobFactory.pm turns anything into a list of jobs (files, shell, sql, lists). Parser.
- SystemCmd.pm executes any shell command
- SqlCmd.pm executes an SQL session, returns insert_ids







References & acknowledgements

- BioMed Central Bioinformatics (11 May 2010):
- "eHive: An Artificial Intelligence workflow system for genomic analysis"
- Jessica Severin^{1,2}, Kathryn Beal¹, Albert J Vilella¹, Stephen Fitzgerald¹, Michael Schuster¹, Leo Gordon¹, Abel Ureta-Vidal^{1,3}, Paul Flicek¹ and Javier Herrero¹
- Compara:
 - Kathryn Beal
 - Stephen Fitzgerald
 - Albert Vilella
 - Javier Herrero
- original developers:
 - Jessica Severin
 - Abel Ureta-Vidal
 - Michael Schuster

- Everyone in EnsEMBL, esp
 - Bronwen Aken
 - Paul Flicek
 - Pablo Marin-Garcia
- ehive-users mailing list members
- ISG & farm support





