

SRB in the BioEmergences project

Dominique de Waleffe
dominique.dewaleffe@denali.be

Denali SA

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- 1 The project
- 2 The architecture
- 3 SRB usage
- 4 iRODS?



Partners

- Framework Program 6 project
- Consortium:
 - CNRS – Centre De Recherche en Epistémologie Appliquée (CREA) (FRANCE)
 - Institut Curie (France)
 - Slovenska Technicka Univerzita V Bratislave (Slovakia)
 - Universidad de Málaga (Spain)
 - Denali Consulting S.A. (Belgium)
 - European Molecular Biology Laboratory (Germany)
 - University of Bologna (Italy)
 - CNRS – CC-IN2P3 (France)
- Project fact sheet on CORDIS:<http://tinyurl.com/5yc42k>



Project goals

What?

With the BioEMERGENCES project, we aim at providing an **experimental platform** to observe **in vivo** emergent patterns at various scales and **measure their variability between different individuals** of the same species. This is a strategy towards the measurement of the individual susceptibility to genetic diseases or response to treatments.

...

The main result expected from BioEMERGENCES is the **specification of a European platform to achieve high throughput measurement** of individual differences and screening of drugs combinations such as bi or tri-therapies.

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Industrialize

- Platform for high throughput execution of the processes



Some details

Gather observations

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- Repeated for many individuals under different conditions



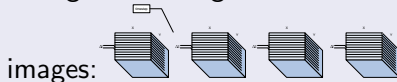
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- Repeated for many individuals under different conditions

Output

- A large set of large files containing raw



- A set of metadata describing the experiment



Some details

Reconstruct cell lineage tree

- Invent different algorithms to:
 - filter images (remove noise)
 - detect centers of cell nuclei ((x, y, z) position)
 - determine membrane contours (set of 3-D polygons)
 - determine nucleus contours (set of 3-D polygons)
 - identify mitosis (cell divisions)
 - track individual cell from step T_i to step T_{i+1} and build lineage tree
 - compare lineage trees , infer new results



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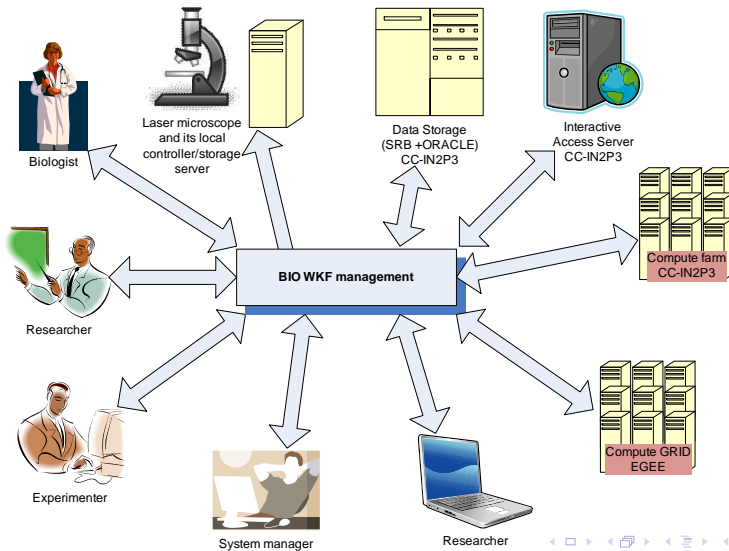
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 - compare lineage trees , infer new results
- visualize reconstructions
- correct and annotate datasets



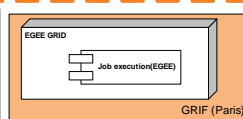
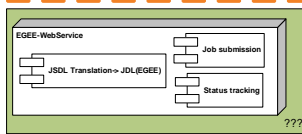
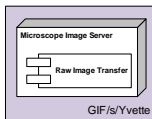
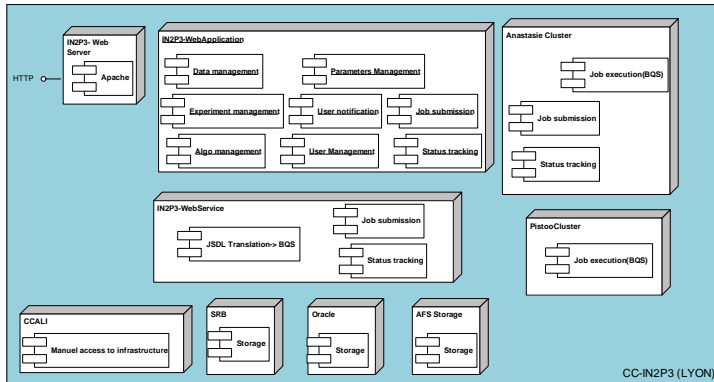
Some figures

- Image sizes:** $512 * 512 * 8$ to $1024 * 1024 * 8$ pixels,
 $0.5\mu < \delta x, \delta y < 1.5\mu$, but soon: $2048 * 2048 * 24$,
- Number of images in stack:** between 50 and 200,
- Number of time steps:** ΔT typically between 1 and 10 minutes, a few tens to a few hundreds of time intervals captured.
- Raw data volumes:** 50 to 60 *Gigabytes* of raw image files per experiment (size: 512) but will soon be $1/2$ *Terabytes* with new microscope.
- Number of cells:** lineage trees contains several million cells.
- Current storage used (SRB):** in excess of 8 TB.

Context diagram



Deployment viewpoint



Application: experiment list

| EXPERIMENT LIST | | | | | | | | | | | | | |
|----------------------------------|-----------------|-------------|-----------------------|-------------------|------------|--------|----------------|------------------------|--------|---|-----------------------------------|--|------------------|
| Search for: <input type="text"/> | | | | | | | | | | Status: <input type="text" value="- All -"/> | | Page <input type="text" value="1"/> of 6 | |
| | | | | | | | | | | Display <input type="text" value="25"/> of 108 refs | <input type="checkbox"/> Show all | | |
| All | Name | Date | Species | Scheme | Treatment | Nuclei | Voxel | Volume | Zsteps | Timestep | ΔT | Status | Operator |
| <input type="checkbox"/> | 071019esserie02 | 19 Oct 2007 | paracentrotus lividus | | RNAinj | 0 | 0.48x0.48x0.96 | 122.88x122.88x73.92 | 78 | 1 | 1'00" | New | Duloquin Louise |
| <input type="checkbox"/> | 071019esserie01 | 19 Oct 2007 | paracentrotus lividus | | RNAinj | 0 | 0.48x0.48x0.48 | 122.88x122.88x73.92 | 155 | 1 | 3'26" | New | Duloquin Louise |
| <input type="checkbox"/> | 071019esserie00 | 19 Oct 2007 | paracentrotus lividus | | RNAinj | 0 | 0.48x0.48x0.48 | 245.76x245.76x73.92 | 155 | 2 | 3'23" | New | Duloquin Louise |
| <input type="checkbox"/> | 071019esserie03 | 19 Oct 2007 | paracentrotus lividus | | RNAinj | 0 | 0.48x0.48x0.96 | 245.76x245.76x73.92 | 78 | 2 | 1'00" | New | Duloquin Louise |
| <input type="checkbox"/> | 070429a | 29 Apr 2007 | danio rerio | VP6 | transg | 0 | 1.37x1.37x1.37 | 1399.81x1399.81x175.36 | 129 | 23 | 5'13" | New | Peyrieras Nadine |
| <input type="checkbox"/> | 070411d | 11 Apr 2007 | danio rerio | AP5 | RNAinj | 0 | 0.8x0.8x0.8 | 409.6x409.6x149.6 | 188 | 23 | | Sent | Peyrieras Nadine |
| <input type="checkbox"/> | 070411b | 11 Apr 2007 | danio rerio | AP5 | RNAinj | 0 | 0.8x0.8x0.8 | 409.6x409.6x132.8 | 167 | 23 | 1'02" | New | Peyrieras Nadine |
| <input type="checkbox"/> | 070411c | 11 Apr 2007 | danio rerio | AP5 | RNAinj | 0 | 1.37x1.37x1.37 | 699.9x699.9x138.37 | 102 | 29 | 1'05" | Sent | Peyrieras Nadine |
| <input type="checkbox"/> | 080318aF | 18 Mar 2008 | paracentrotus lividus | 6 (19hpf-24hpf) | RNAinj | 0 | 0.6x0.6x1.2 | 307.2x307.2x152.4 | 128 | 31 | 2'56" | New | Duloquin Louise |
| <input type="checkbox"/> | 080312aF | 12 Mar 2008 | paracentrotus lividus | 6 (19hpf-24hpf) | RNAinj | 0 | 0.6x0.6x1.2 | 307.2x307.2x152.4 | 128 | 31 | 2'56" | Sent | Duloquin Louise |
| <input type="checkbox"/> | 071223a | 23 Dec 2007 | danio rerio | VP8 | RNAinj | 0 | 1.37x1.37x1.37 | 699.9x699.9x162.67 | 120 | 33 | 2'36" | Sent | Peyrieras Nadine |
| <input type="checkbox"/> | 070719a | 19 Jul 2007 | paracentrotus lividus | 1 (3h15pf-7h30pf) | RNAinj | 0 | 0.48x0.48x0.96 | 246.02x246.02x91.19 | 96 | 41 | 6'00" | New | Duloquin Louise |
| <input type="checkbox"/> | 060303 | 03 Mar 2006 | danio rerio | AP4 | RNAinj | 0 | 0.58x0.58x1.2 | 296.96x296.96x30.16 | 30 | 49 | | New | Peyrieras Nadine |
| <input type="checkbox"/> | 070118b | 18 Jan 2007 | danio rerio | AP0 | D bait 32H | 1 | 0.68x0.68x2.05 | 696.32x696.32x190.65 | 94 | 55 | 3'15" | Sent | Maury Benoit |
| <input type="checkbox"/> | 071227dF | 27 Dec 2007 | danio rerio | AP0 | trans+inj | 0 | 1.51x1.51x1.51 | 773.12x773.12x314.08 | 209 | 57 | 4'41" | Sent | Peyrieras Nadine |
| <input type="checkbox"/> | 080123aF | 23 Jan 2008 | danio rerio | AP0 | D bait 32H | 1 | 1.32x1.32x1.32 | 673.79x673.79x317.16 | 242 | 64 | 6'13" | Sent | Iemesse vincent |
| <input type="checkbox"/> | 070221 | 21 Feb 2007 | danio rerio | AP4 | RNAinj | 0 | 0.68x0.68x2.05 | 696.32x696.32x178.25 | 88 | 66 | 3'47" | Sent | Peyrieras Nadine |
| <input type="checkbox"/> | 070117a | 17 Jan 2007 | danio rerio | AP0 | D bait 32H | 1 | 1.36x1.36x2.32 | 696.32x696.32x225.04 | 98 | 71 | 4'26" | Sent | Maury Benoit |
| <input type="checkbox"/> | 070205a | 05 Feb 2007 | danio rerio | AP0 | untreated | 1 | 0.68x0.68x2.05 | 696.32x696.32x166.05 | 82 | 72 | 3'05" | Sent | Maury Benoit |
| <input type="checkbox"/> | 080101aF | 01 Jan 2008 | danio rerio | AP4 | RNAinj | 0 | 1.21x1.21x1.21 | 619.52x619.52x257.73 | 214 | 72 | 4'47" | Sent | Peyrieras Nadine |



Application: processing pipelines

Details button: brings view below:

The screenshot shows a web-based interface for managing pipelines. At the top, there is a search bar and a 'Display 25 of 14 refs' indicator. Below this is a table of pipeline instances. A 'Details' button is highlighted for one instance, which opens a detailed view. This view includes a flowchart diagram of the pipeline, a table of its components, and a pie chart showing the status of the pipeline's tasks.

| Label | Algorithm | Infra | Status | Actions |
|---|-------------------------|-------|---------|-------------------|
| p-drugTreatment_ZB-e-081014aF-a-GMCF-K5-ITS-NUC-328 | GMCF-K5-ITS-NUC | EGEE | Waiting | [Refresh] [Close] |
| p-drugTreatment_ZB-e-081014aF-a-GMCF-K2-ITS-NUC-328 | GMCF-K2-ITS-NUC | EGEE | Waiting | [Refresh] [Close] |
| p-drugTreatment_ZB-e-081014aF-a-CenterDetect-OP-13-328 | CenterDetect-OP-13 | EGEE | New | [Refresh] [Close] |
| p-drugTreatment_ZB-e-081014aF-a-NucleusSegmentation-328 | NucleusSegmentation-328 | EGEE | New | [Refresh] [Close] |

| Label | Algorithm | Infra | Status | Actions |
|-------------------------------------|-----------|----------------------|---------|-------------------------|
| drugTreatment_ZB on 081014aF id 328 | 081014aF | 19 Jan 2009 12:14:51 | RUNNING | EGEE [Details] [Graph] |
| drugTreatment_ZB on 081014a id 327 | 081014a | 19 Jan 2009 12:14:11 | RUNNING | IN2P3 [Details] [Graph] |
| drugTreatment_ZB on 080923aF id 329 | 080923aF | 19 Jan 2009 12:11:53 | RUNNING | IN2P3 [Details] [Graph] |
| drugTreatment_ZB on 081015aF id 325 | 081015aF | 19 Jan 2009 11:49:02 | RUNNING | EGEE [Details] [Graph] |
| drugTreatment_ZB on 080916aF id 324 | 080916aF | 19 Jan 2009 11:42:44 | RUNNING | EGEE [Details] [Graph] |
| drugTreatment_ZB on 080916a id 322 | 080916a | 19 Jan 2009 11:42:07 | RUNNING | EGEE [Details] [Graph] |
| drugTreatment_ZB on 081015a id 303 | 081015a | 17 Jan 2009 07:31:56 | DONE | IN2P3 [Details] [Graph] |

Details for Pipeline drugTreatment_ZB on 081014aF id 328

Treatment_ZB-e-081014aF-a-GMCF-K2-ITS-NUC-328

Done (161) | Queued (17) | Error (3)

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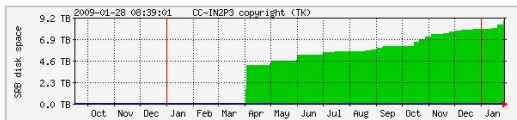
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- Stores algorithms (scripts, sources, builds procedures, executables)



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Yearly Graph (1 Day Average)



| | Max | Average | Current |
|-------------|-----------|-----------|-----------|
| space used: | 9059.0 GB | 3747.0 GB | 9059.0 GB |



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- deleted stuff is not always fully deleted



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- sources available.



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 - rule syntax (one liners, readability, choices of operators, comments?)

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myRule|foo==1|action1(...);action2(...);...|action3(...);action4(...);...
```



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  do {  
    /* watch that this action has side-effects */  
    action1 (...);  
    action2 (...);...  
  }  
  on failure {  
    action3 (...);  
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- can I define new microServices as complex jobs (e.g submit job(s) to farm) without going to C programming?



Conclusion

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- BioEmergences has complex distributed data/processing needs
- Could make use of iRODS if risks are shown to be a non issue



Questions?

