



Testing the use of OMERO as a bioimage informatics platform for HIV viral particle tracking

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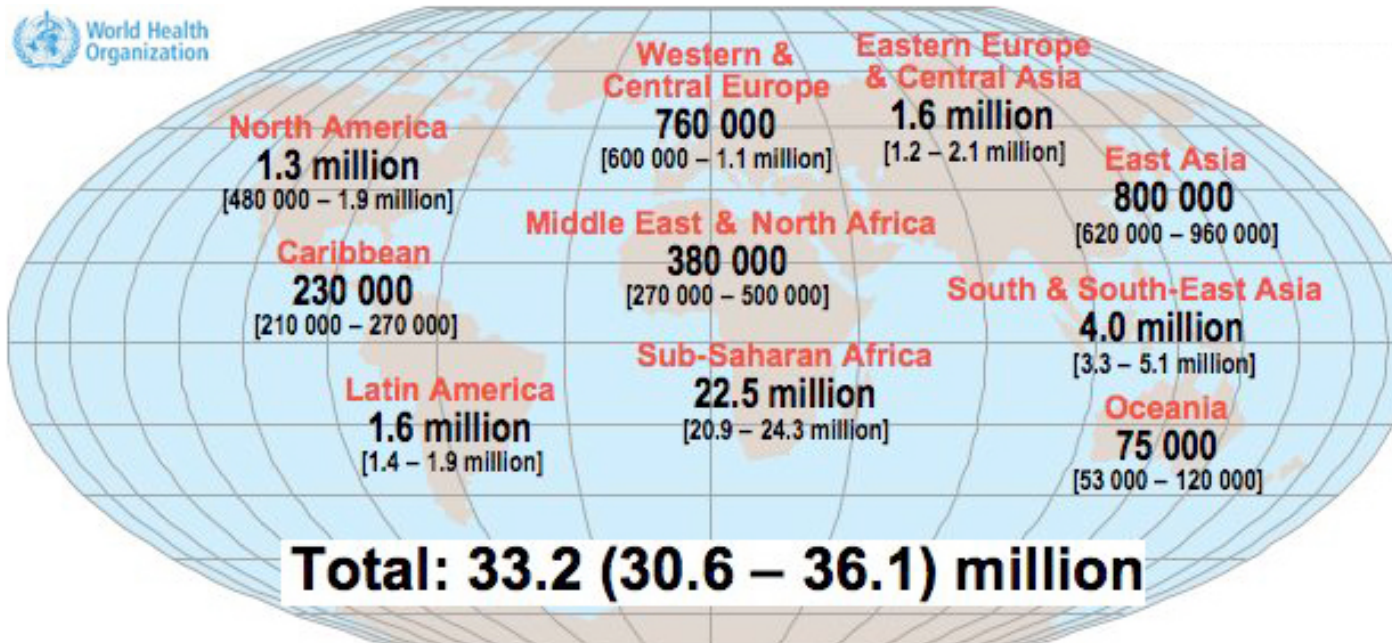
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What is our problem?

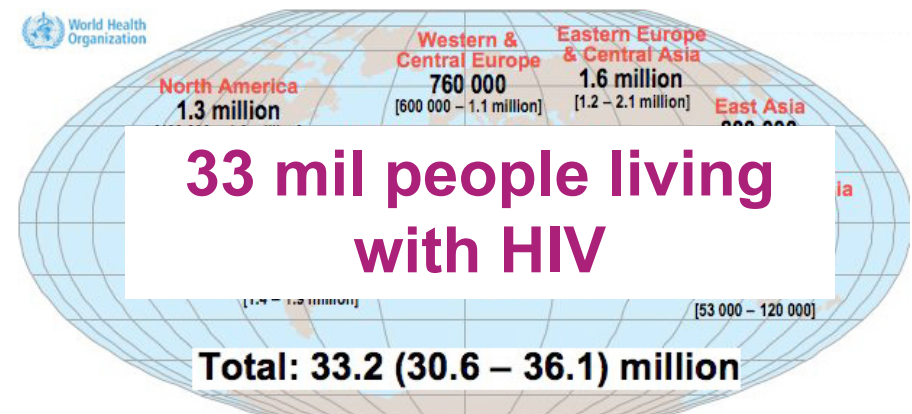
People living with HIV (2007)



25 years after the identification of the virus, we still know remarkably little about the cell biology of HIV-1!

What is our approach?

- **The question:**
How does the HIV-1 virus gain access to the cellular genome to ensure proviral DNA integration?
- **The obstacle:** the reductionist approach has reached its limit
- **The answer:** a systematic quantitative strategy requires a multidisciplinary team
 - Virology
 - Cell Biology
 - Bio-Image informatics = integration of **OME + analysis algorithms + integrated image analysis workflows**



Who are we?



Caterina Strambio
UniGe

Cell biology
bioimaging



Mario Valle
ETH-CSCS

Visualization
data analysis and
management



HIV-1
Virology

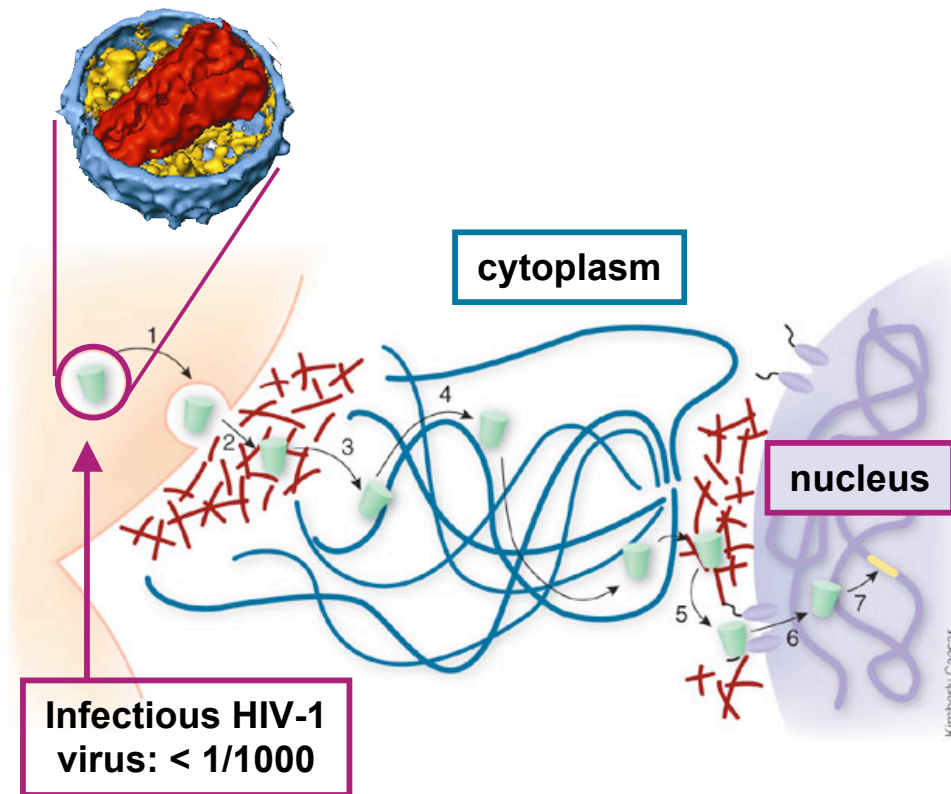


Jeremy Luban
UniGe



...and the team is growing!

The question: HIV-1 viral entry



- HIV-1 enters the cell and moves towards the nucleus
- Key virus-host interactions influence viral trajectory within the cell
- Biochemical and cell-fractionation studies have reached their limit
- Real-time tracking of viral particles and mathematical analysis of movement can provide key insights into the mechanism of infection



Huge challenge: What do we need to understand HIV-1 viral movement?

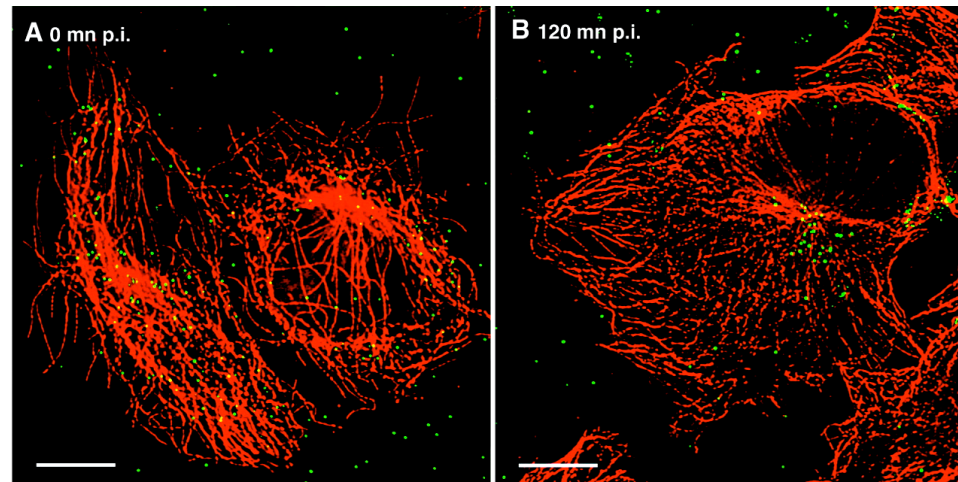
1. Infect primary human cells under strict bio-safety regimens
2. Visualize HIV-1 particles as they move within the cell with high spatial and temporal resolution
3. Keep track and manage multiple large datasets
4. Mathematical analysis of viral trajectories
5. Statistical analysis on multiple trajectories
6. Integrate with other kind of knowledge



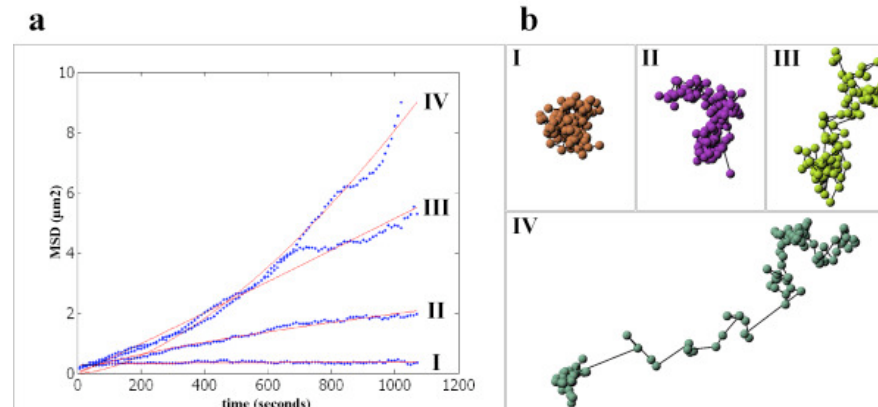
Essential to develop reproducible scientific workflows

The beginning of the answer: real-time 3D video microscopy of HIV-1

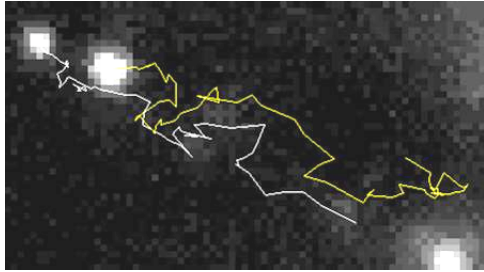
HIV-1 moves along the cytoskeleton



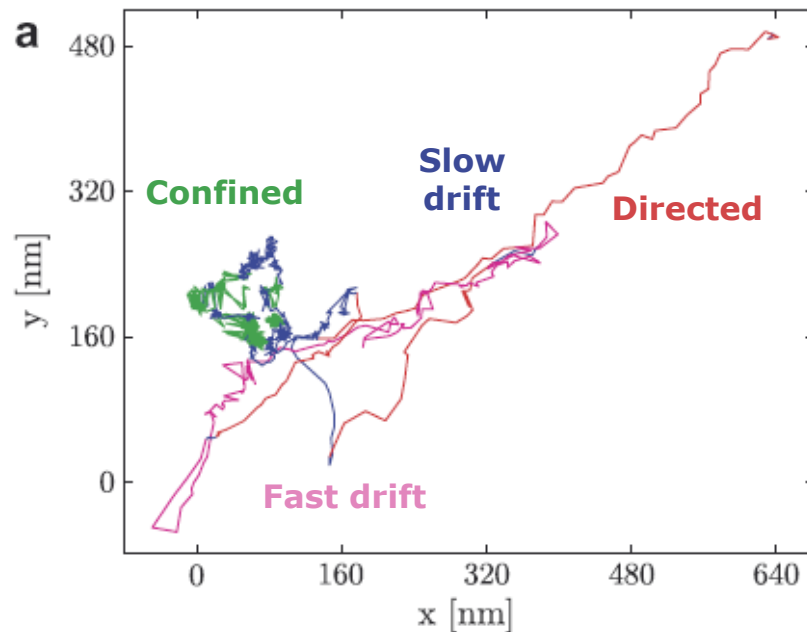
Mean Square Displacement analysis of trajectories



The workflow for real-time HIV tracking



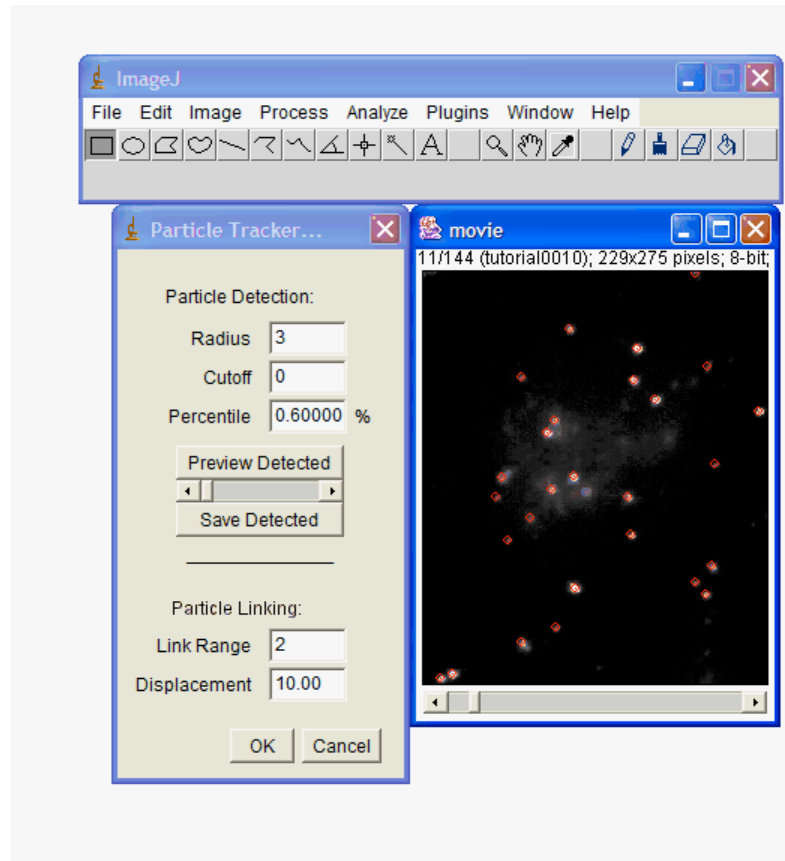
Sbalzarini and Koumoutsakos, J Struct Biol, 2005, 151:182



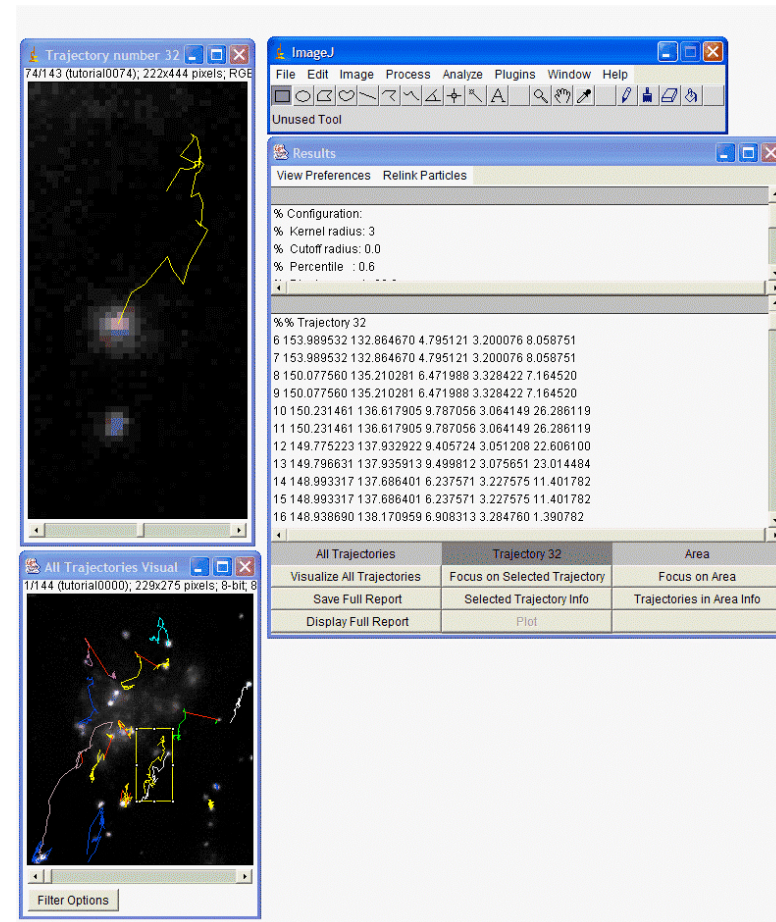
Helmuth et al. J Struct Biol, 2007, 159:347

- SPT: identification of viral trajectories in 3D image stacks over limited time
- Semi automated, supervised trajectory segmentation
- Manual statistical analysis of numerical trajectory data

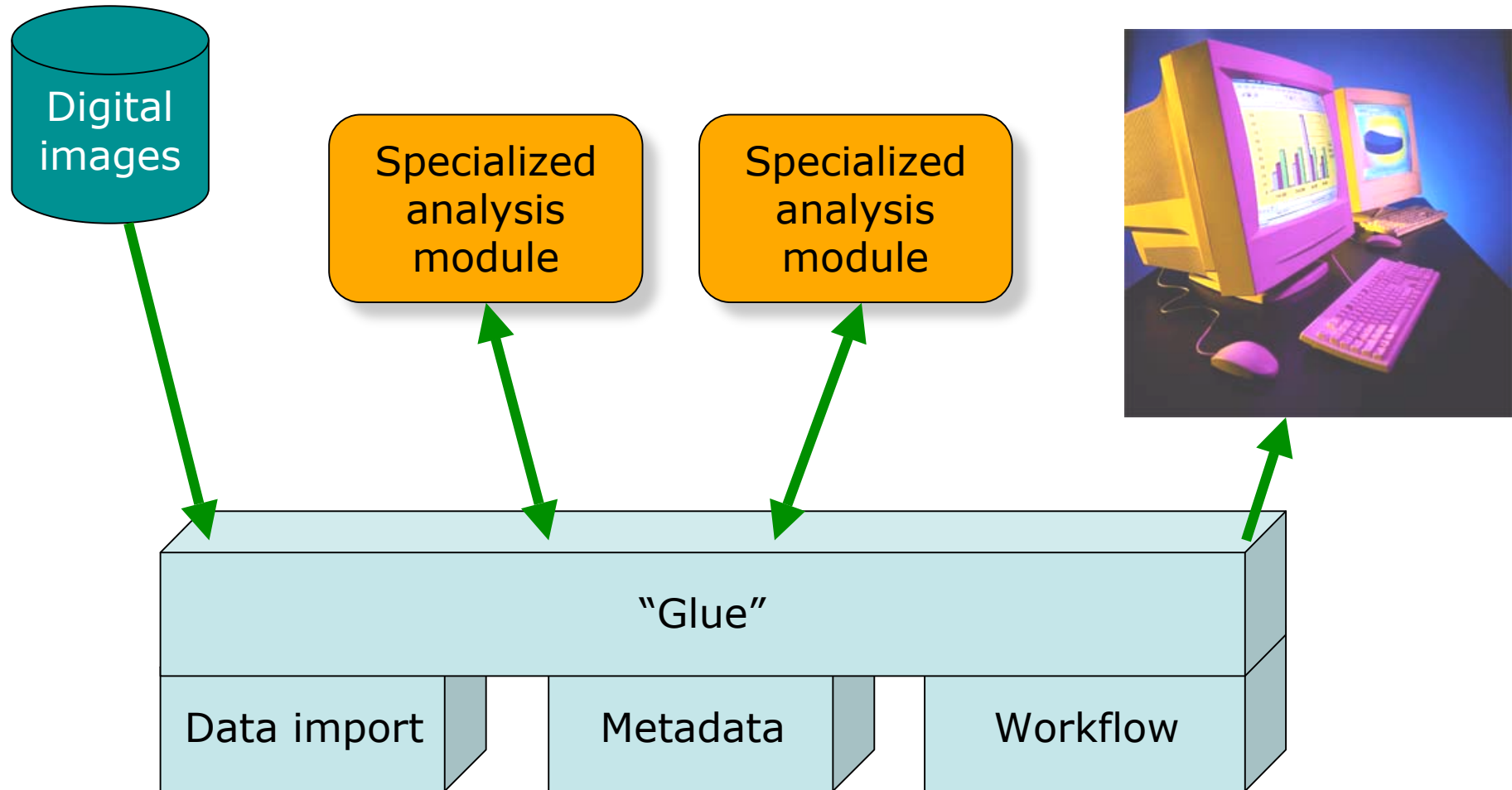
Stand alone software is being developed...



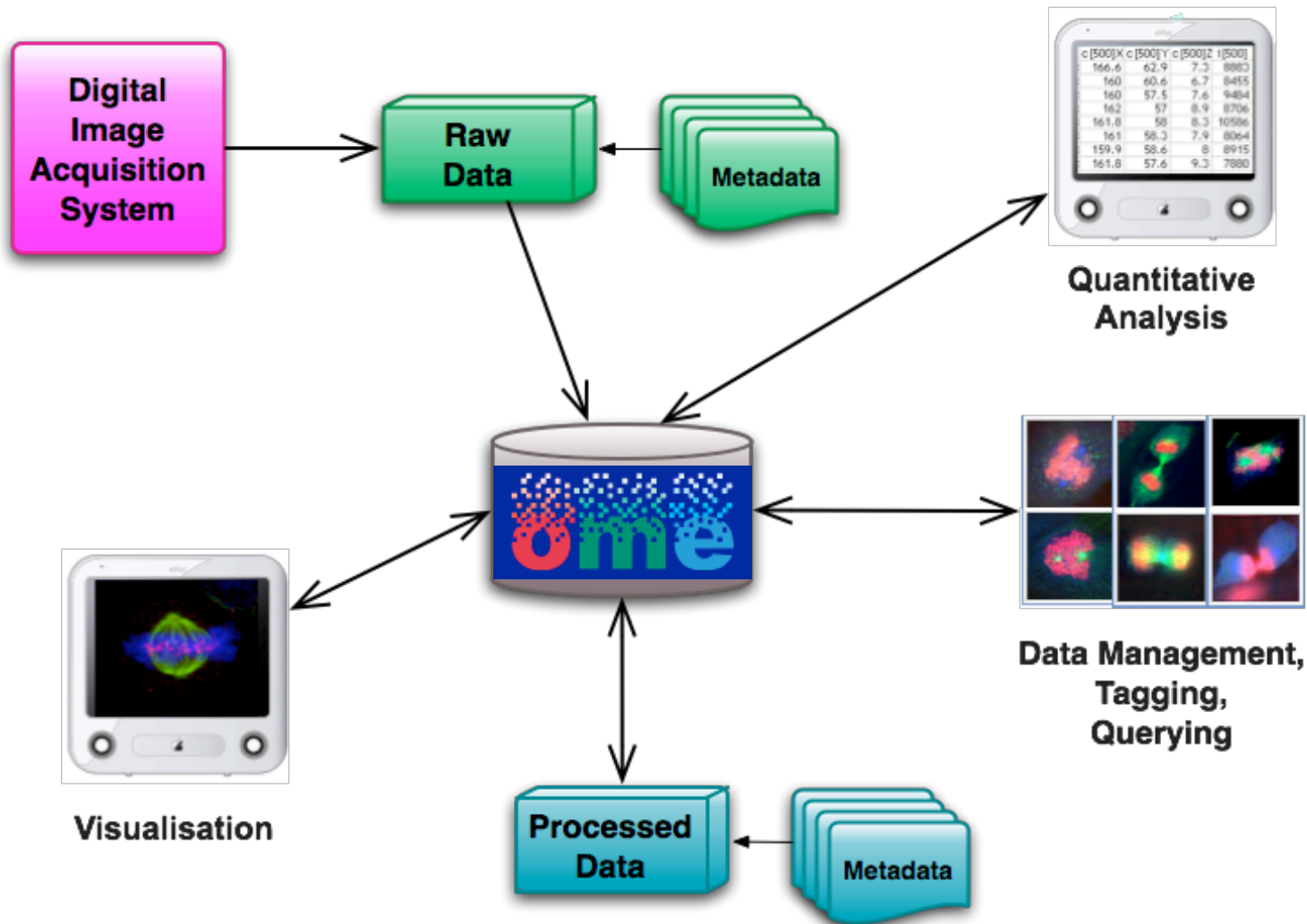
Sbalzarini and Koumoutsakos, J Struct Biol, 2005, 151:182



...but for systematic use it has to be integrated



Can OMERO provides the glue?





What do we need from OMERO?

- ✓ Image data management
- ✓ Image data visualization
- ✓ Metadata (both acquisition and custom) integration

→ Image analysis:

- Modular image analysis
- Keeping track of analysis outputs
- Managing complex workflows: Reproducibility across users, time and space

→ Facilitate integration of different data types and information source: semantic web



What we have done so far: OMERO testing on two fronts

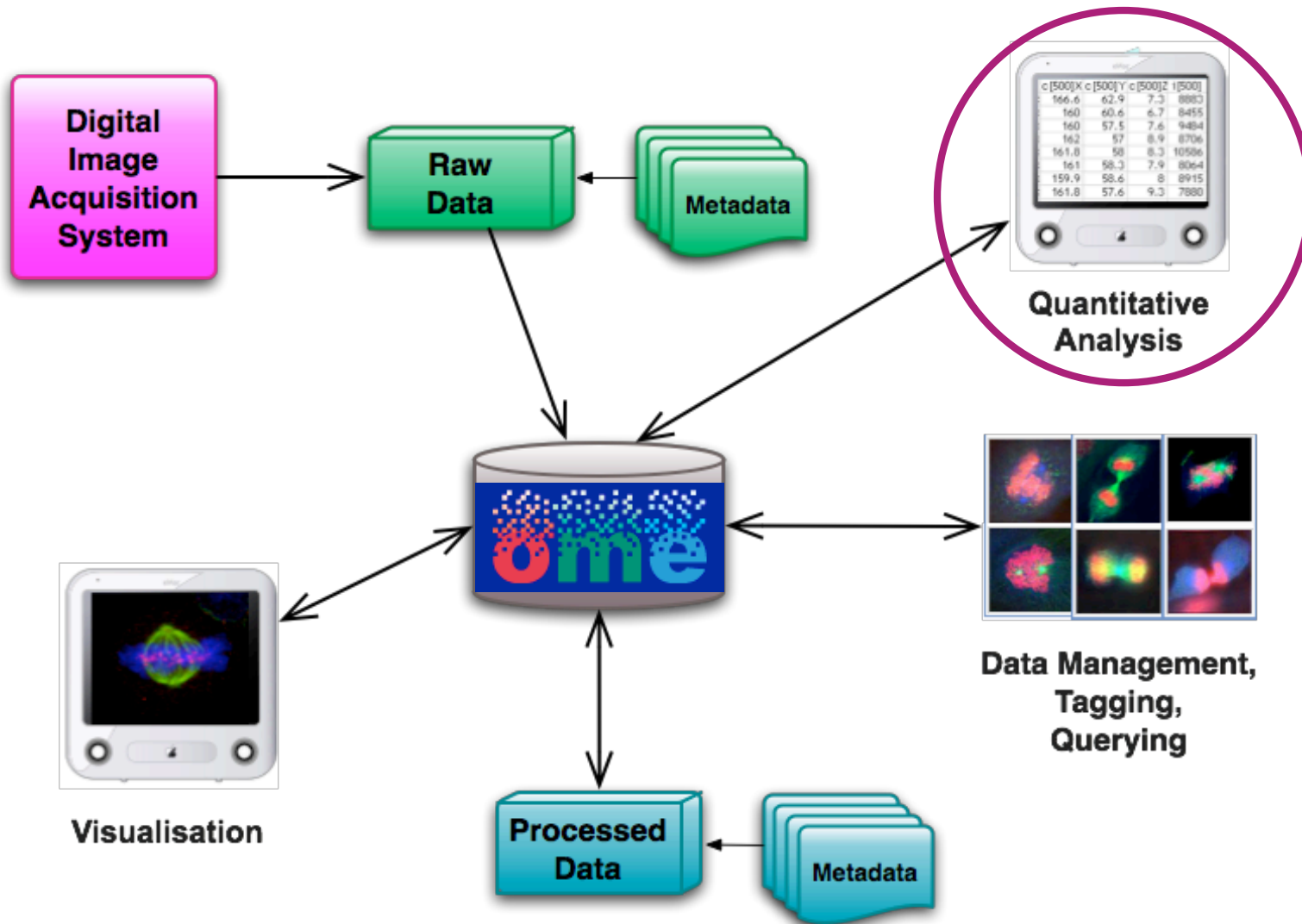
- **End user**

- Provide feed back on various aspects of OMERO usability and relevance
 - Data model
 - Data integrity and security issues
 - Metadata editability
 - OMERO.editor

- **Developer**

- Test feasibility of a local OMERO analysis paradigm
- Build a small custom C++ client that would serve as the interface between images stored in OMERO and the stand-alone SPT software

OMERO.analysis: local client model



OMERO.cpp: building a small custom client

- **Goals**

- Understand Client API writing a small C++ client
- Why C++?
 - Because the SPT algorithm is in C++
 - Because I know it.
 - Because ICE make languages interchangeable.

- **Results**

- Limited success...
- Connect, list user data, list user projects, list datasets for one project, list images for one dataset, access the image data, access the pixels

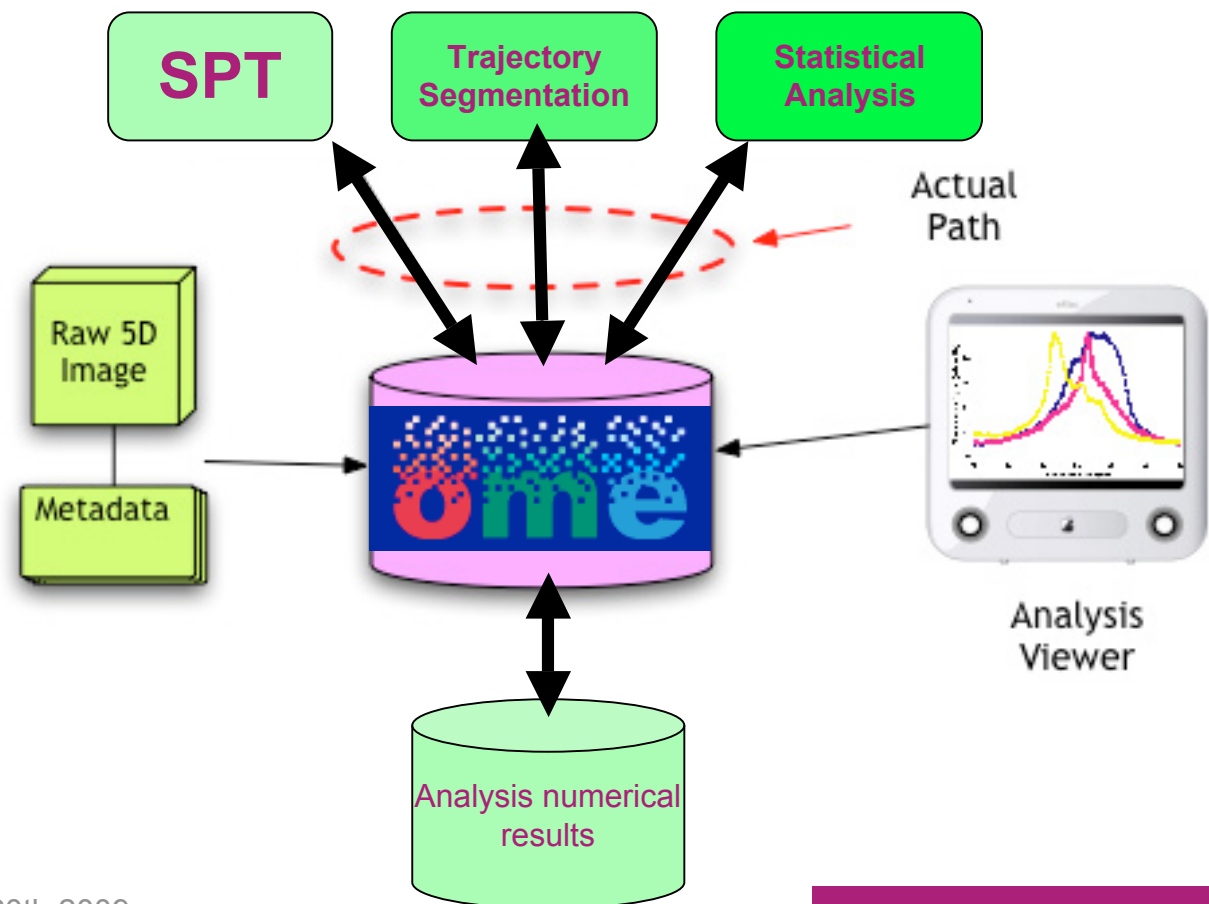
OMERO.cpp: building a small custom client

- **On the positive side**
 - It works, and compiles too!
 - New API simplifies common tasks
- **On the negative side**
 - Documentation is not available or at least not usable (not only about C++ API in general, but also about individual functions)
 - Javadoc pages are not up to date (OME vs OMERO not well documented in Javadoc...)
 - Code examples: would be useful to be able to share and re-use code the community develops.
 - Searchable list-serve archives (along the same lines) and/or community wiki would reduce workload from OME team

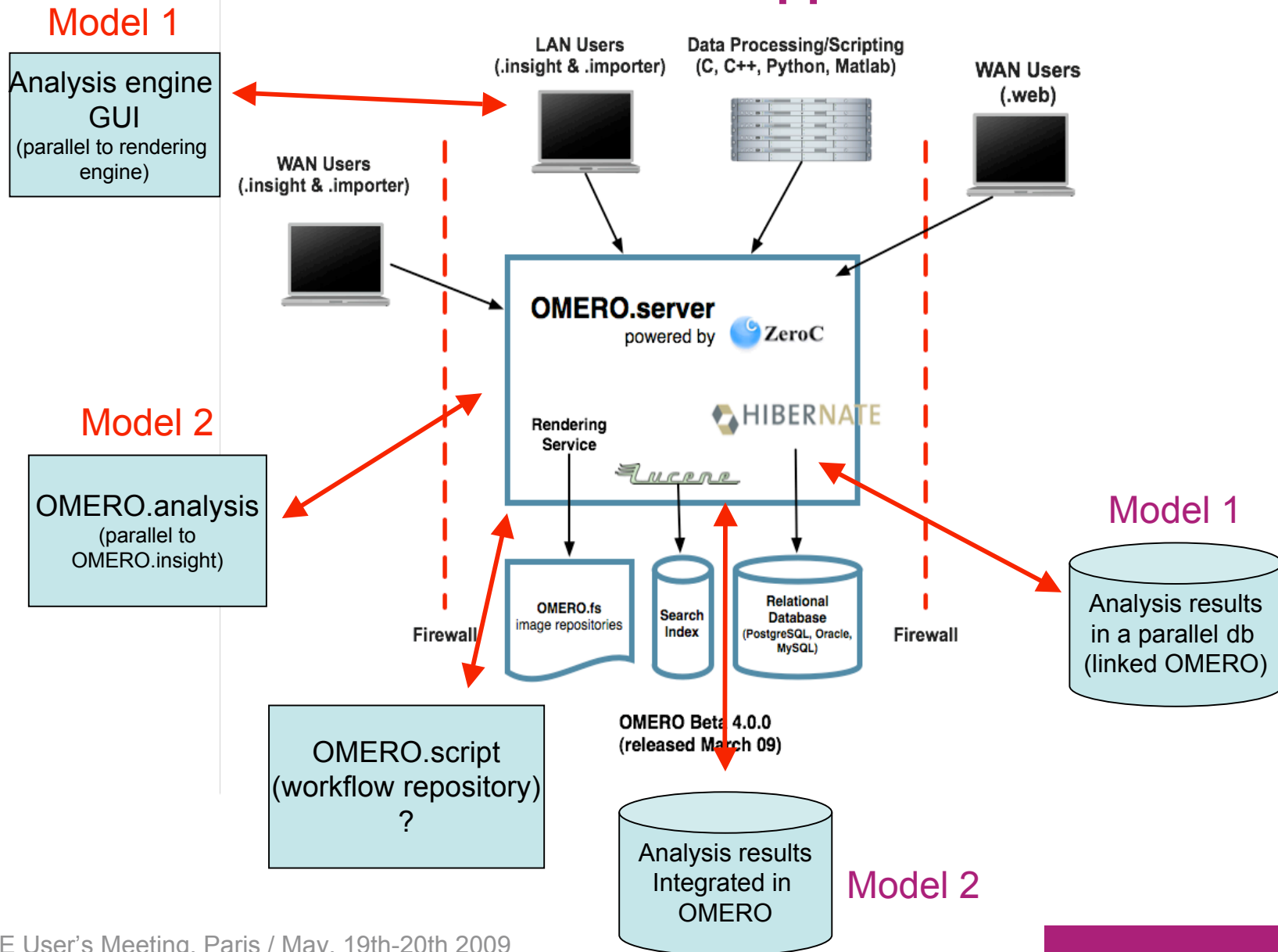


OMERO.analysis: modular analysis paradigm

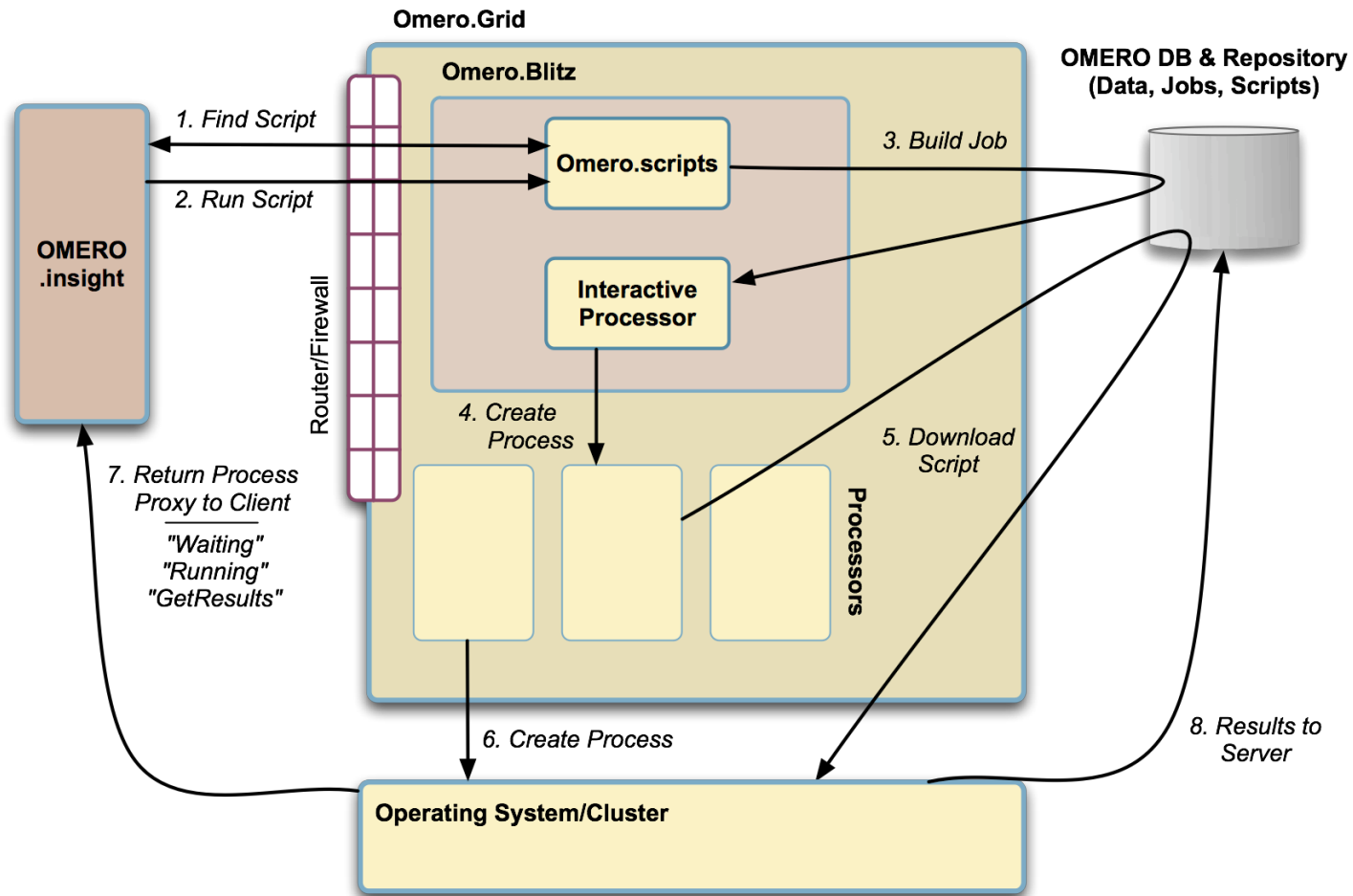
- What we need to allow specialized analysis modules full integration in the image database?
 - integrating analysis modules in the server
 - analysis modules repository for sharing
 - quantitative results stored in the database
 - repository for sharing and reusing workflows




What architecture for analysis will be supported?



OMERO.scripts and .grid: what is their future?





Scientific workflows for bio-image informatics: what do we need...

- Will OMERO support distributed modular analysis architectures?
- OMERO vs BISQUE?
- OMERO.workflow integrating OMERO with software such as TAVERNA to develop standardized bioimage informatics workflows



Thank you!

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