

Information Visualization in the Open Microscopy Environment (OME)

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The Open Microscopy Environment (OME)

- Microscopy for functional genomics assays
- Data store, data model for digital microscopy image acquisition
- High-throughput automated analysis of 5D images
 - Computer vision for object identification, image classification...
- Open source community development (LGPL)

<http://www.openmicroscopy.org>

NIH MIT Dundee U-W Madison DKFZ

Modular Image Analysis

- Analysis Engine execute workflows
 - DAGs composed of modules implementing components of process
- "Semantic Types" (structs) as parameters
- Extend data model by importing modules, chain, and STs (defined in XML schema)
- All intermediate results stored in database
 - Complete data history

Visualization Issues

- Navigation of experimental structure

- experiments, image sets, etc.

- Analysis Visualization

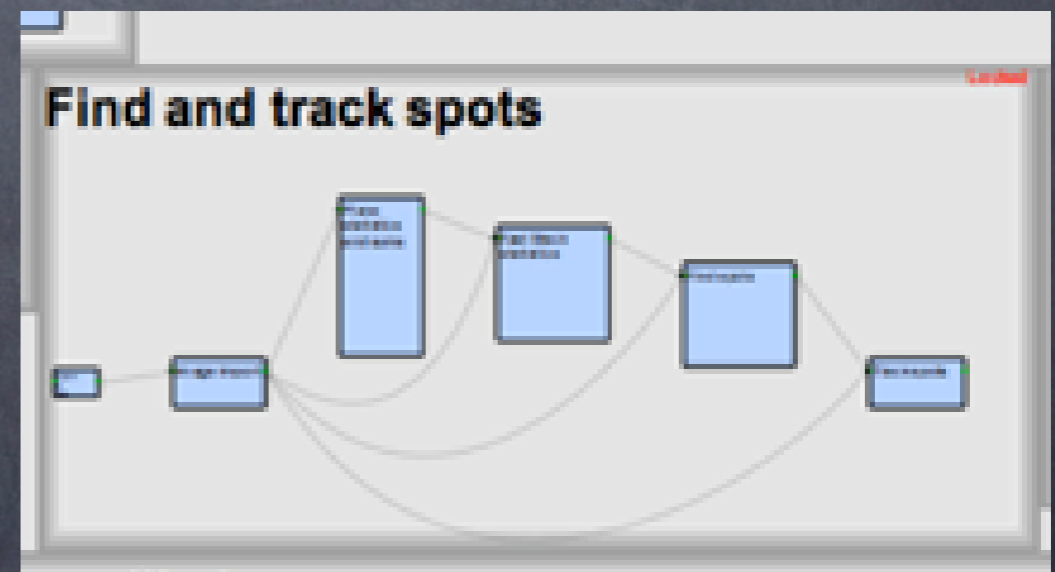
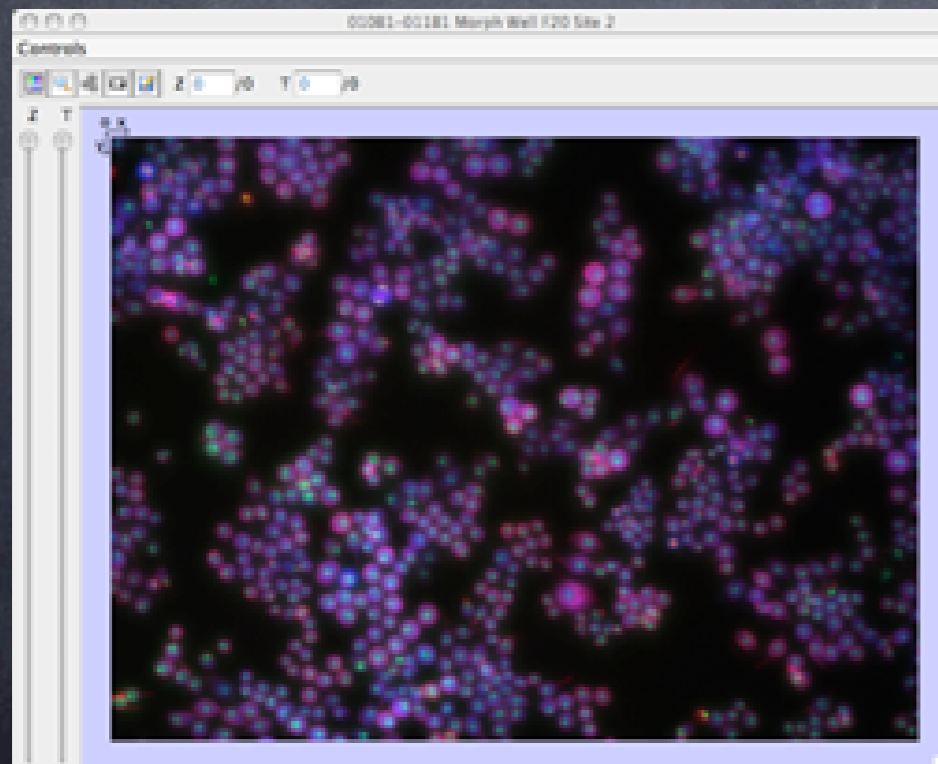
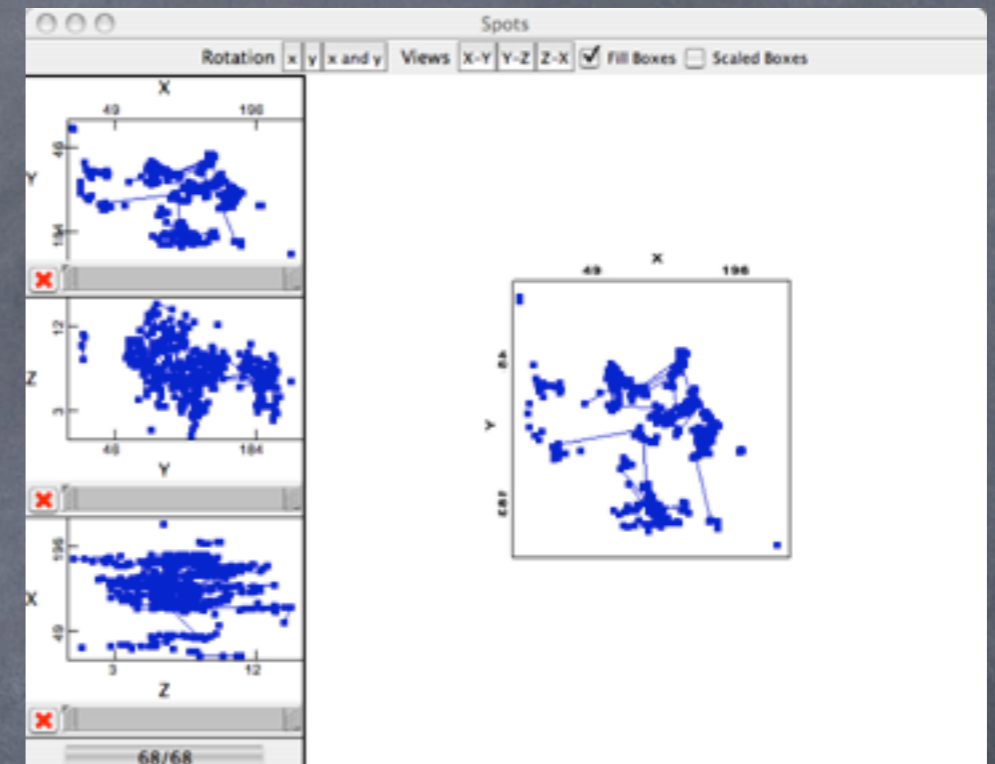
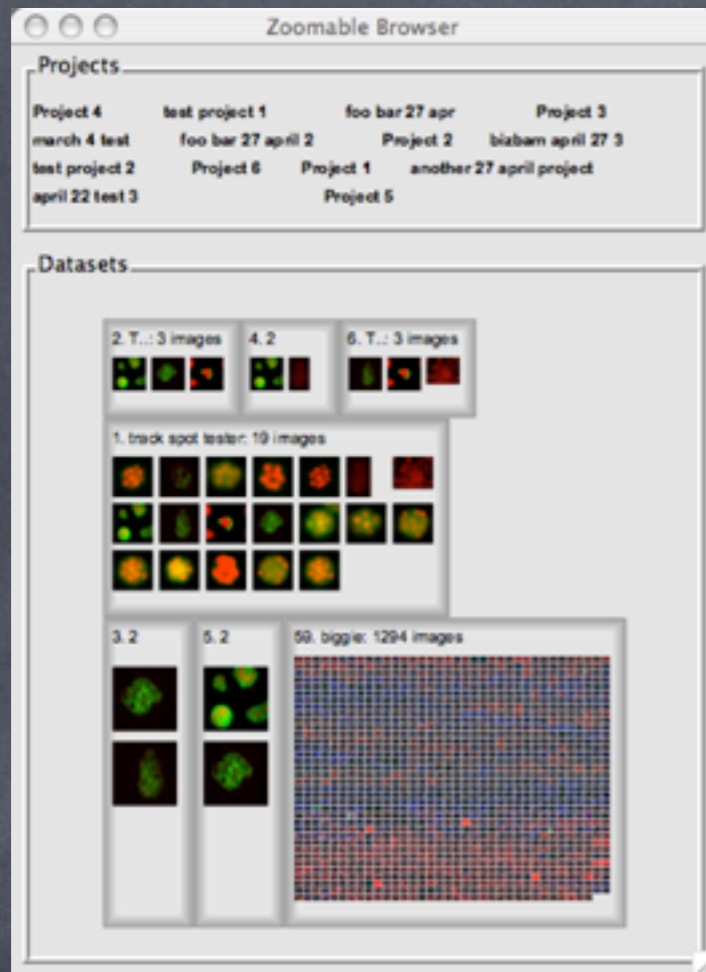
- As data: Find analyses of interest

- As data history: trace derivations

- Results

(of course, all visualizations linked, coordinated, etc.)

Screenshots



Data Management Strategies

- Data is (essentially) relational
- Can we provide ways to bridge the gap between client-server systems and info vis?
 - what to load and when?
 - RDBMS, CORBA, EJB, etc. Any help that we can provide might ease adoption and use of our tools/toolkits
- Inclusion might help adoption of infrastructure

Configurable Extension of Visualization Platforms

- OME: Extensible analysis: new computational modules, workflows, with new data types
- How to visualize new data types?
- Can we define an infrastructure that supports reuse of existing visualizations?
- Use explicit descriptions of visualization capability and data types to specify linkages
- InfoVis Description Language?

OME – www.openmicroscopy.org

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