BISQUE and BISQUIK

Kristian Kvilekval

UCSB Bio-Imaging

- Bioimage.ucsb.edu
- 5 Year project UCSB, CMU, …
  - Manjunath: UCSB
  - Murphy: CMU
- Center for bio-image informatics
- UCSB: Ece, CS, Neuroscience institute
  - Retinal detachment : Fischer, Marc lab UT
  - MT Dynamics: Wilson & Fienstein

BISQUE

Bio-Image Semantic Query User Environment

- BISQUE functionality
  - Ground truth acquisition
  - Data management
  - Analysis
- Experimental Data sets (2d images)
  - Retinal detachment experiments 50k
  - Retinal EM (cell morphology) 23k
  - Microtubule >100K

Data management capabilities

- Digital notebook
  - Capture experimental/image parameters
  - Direct import process
  - Reconfigurable (confocal, 4 x microtubule, etc)
  - Offline and Online
- Web
  - Web access and browsing
  - Organize images and metadata
  - Data sharing environment
  - Search by metadata or content
  - Integrated analysis

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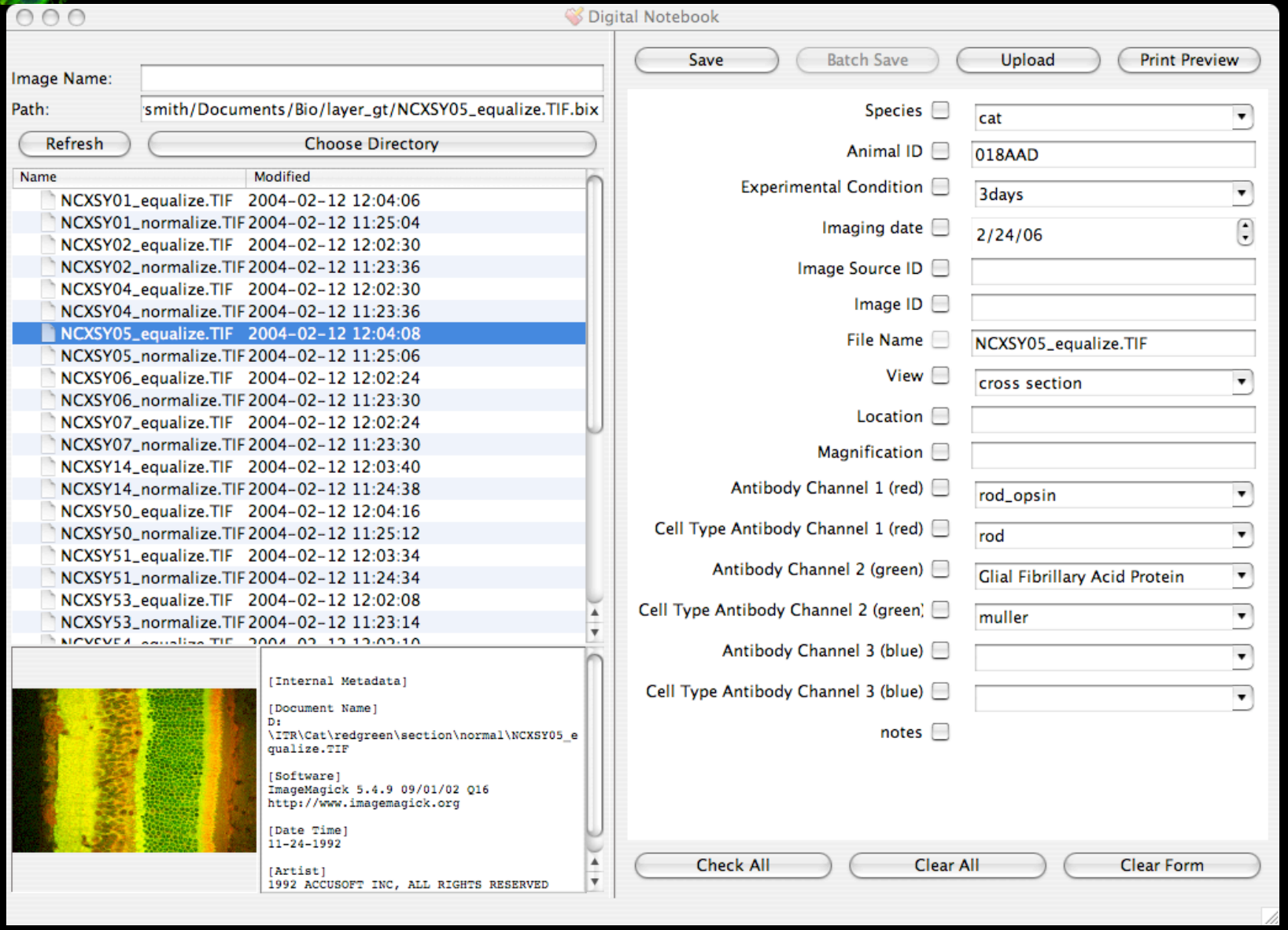
Screenshots (Digital Notebook)



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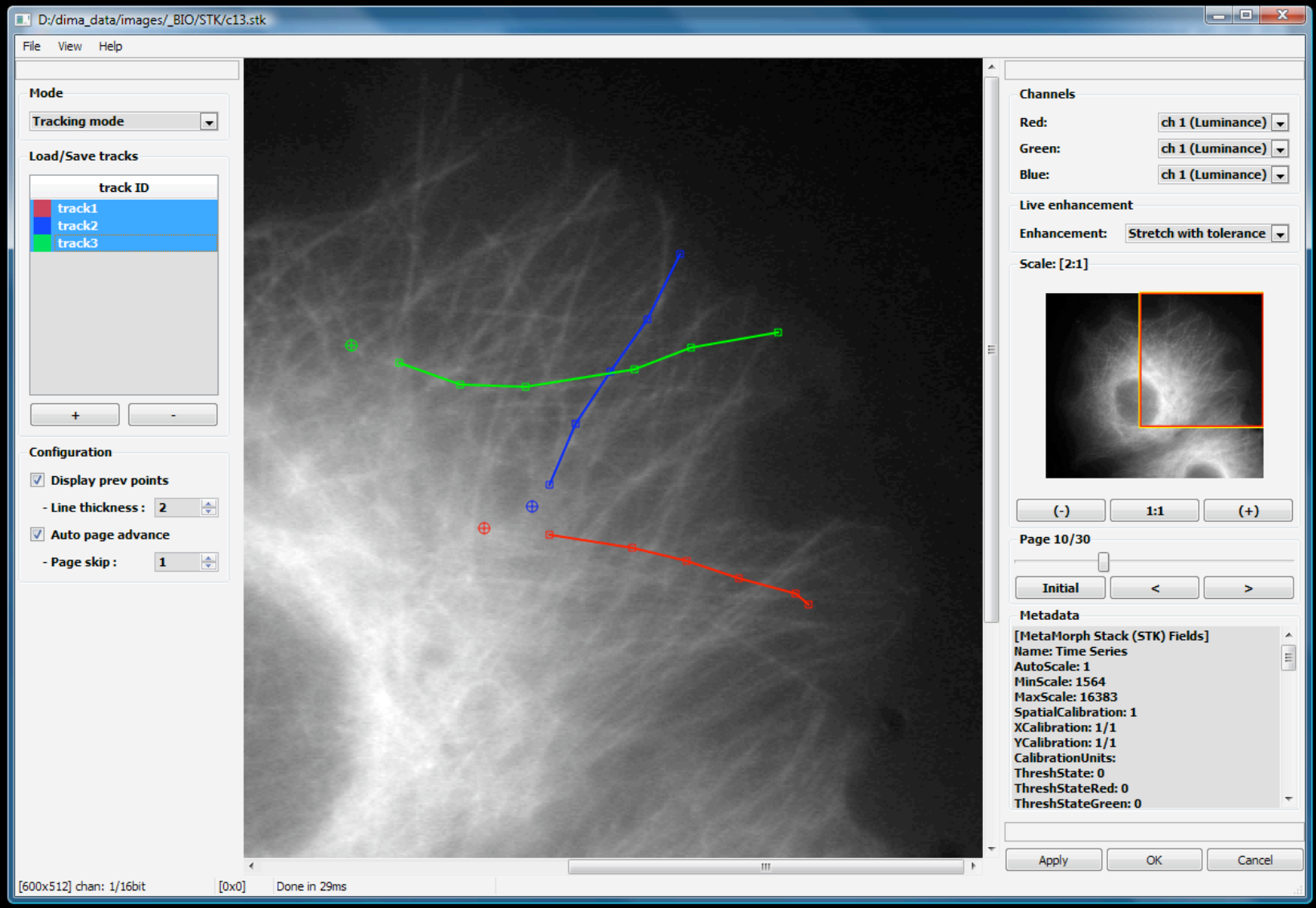
Graphical Ground truth



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Data management capabilities

- Web accessible features
  - Experimental image/data capture and upload
  - Image access and browsing
  - Organize images and metadata
  - Data sharing environment
  - Search by metadata or content
  - Integrated analysis

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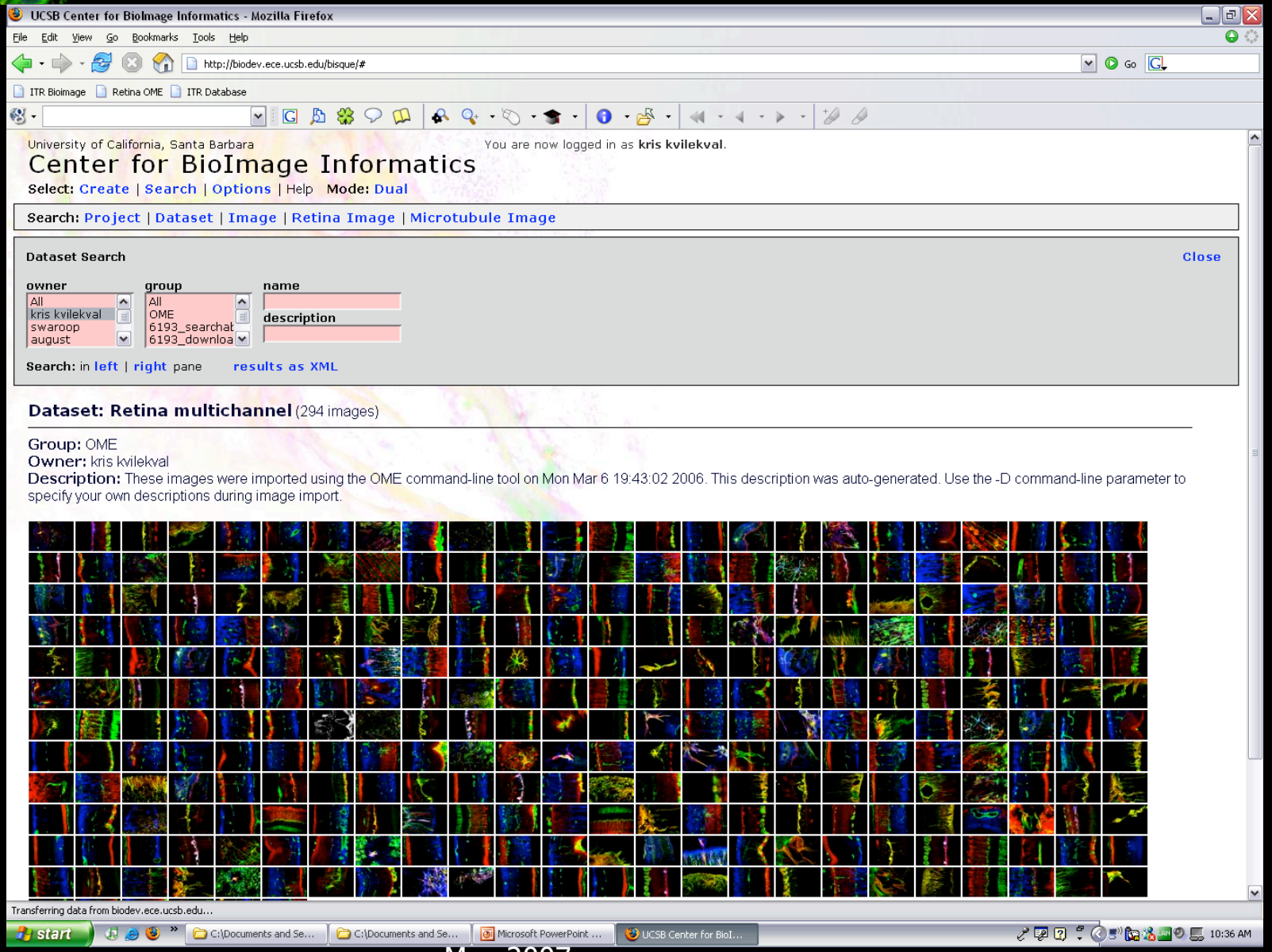
Screenshots (browsing)



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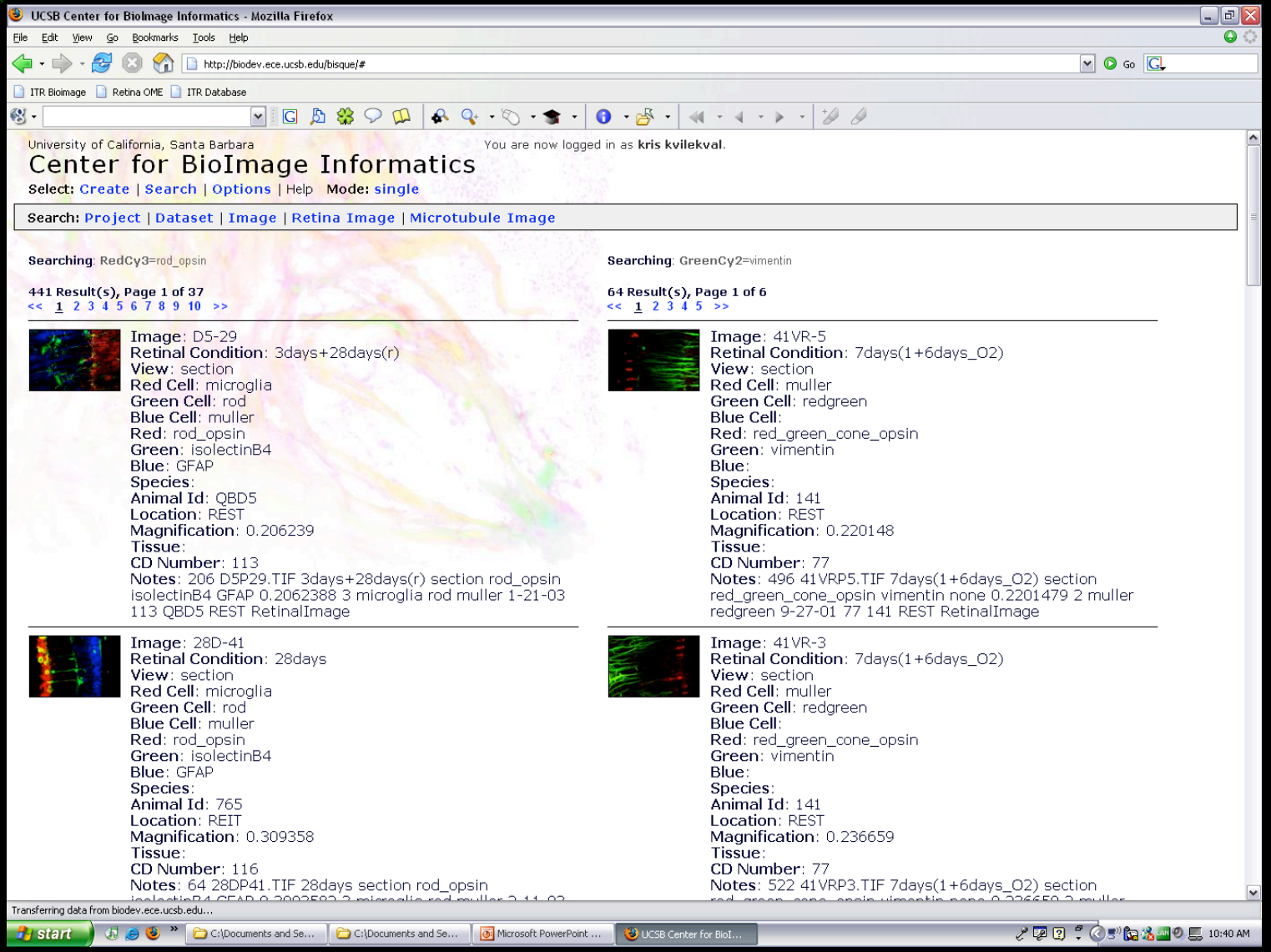
Screenshots (search)



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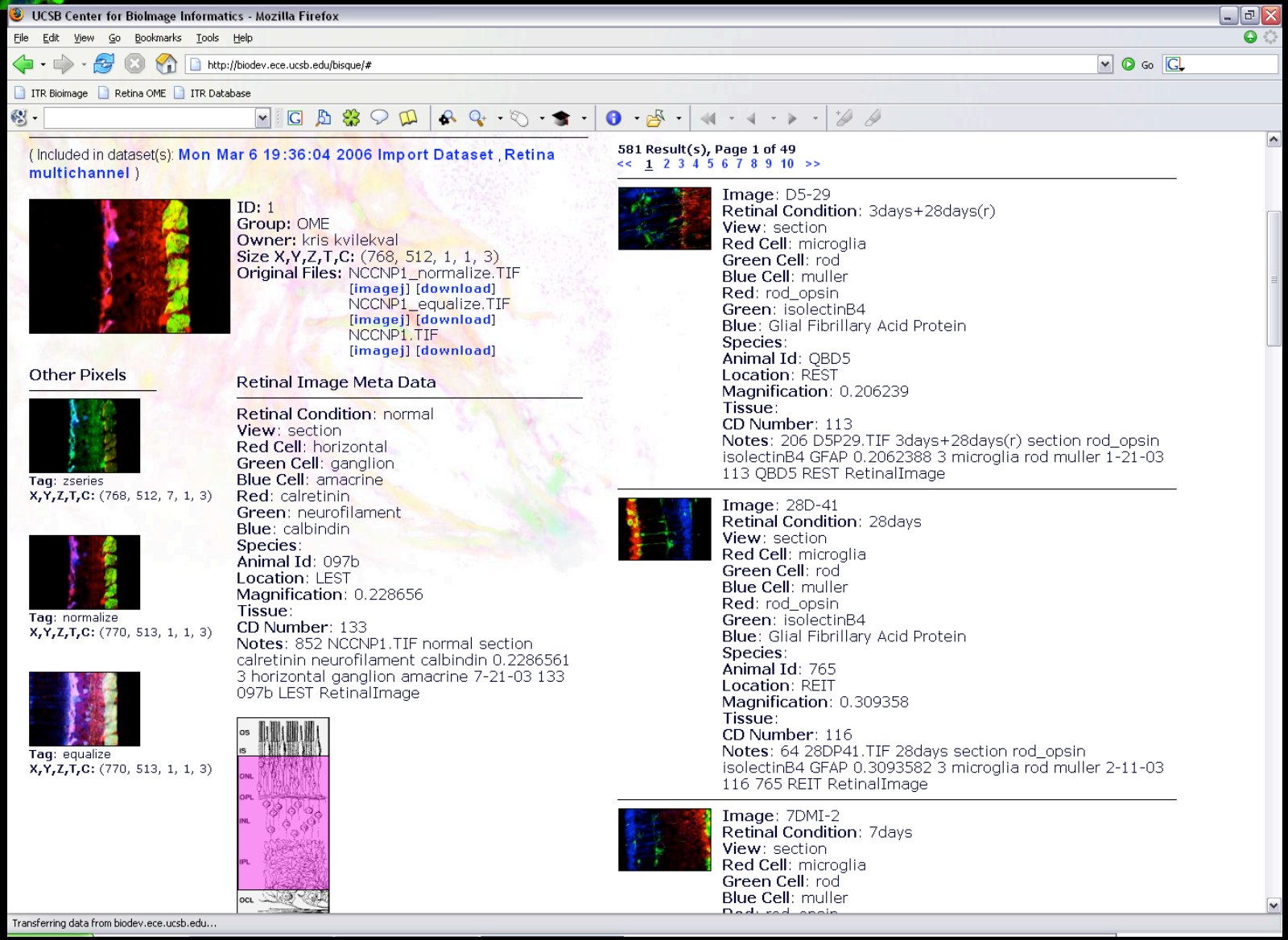
Screenshots (search)



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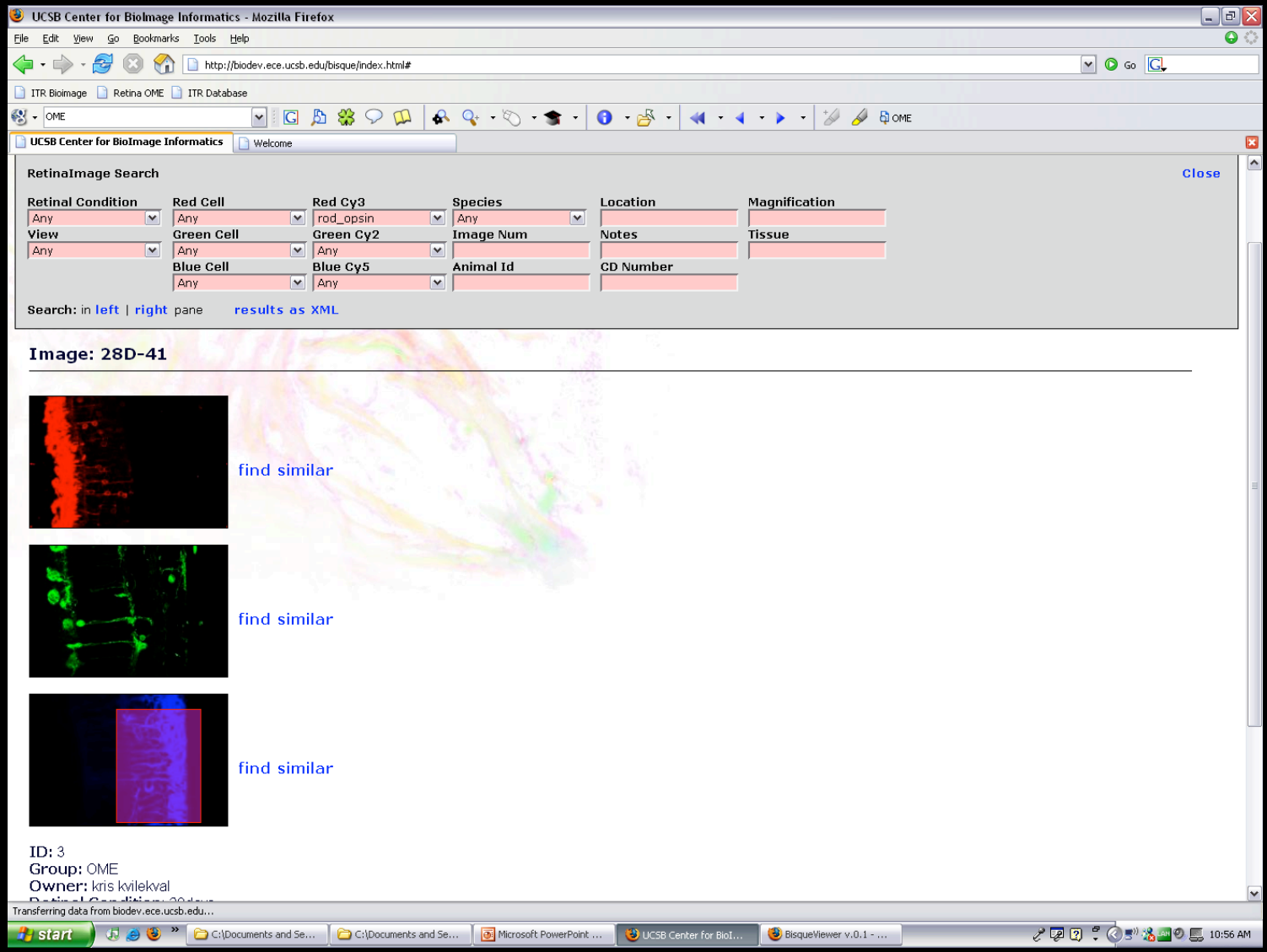
Screenshots (search similar)



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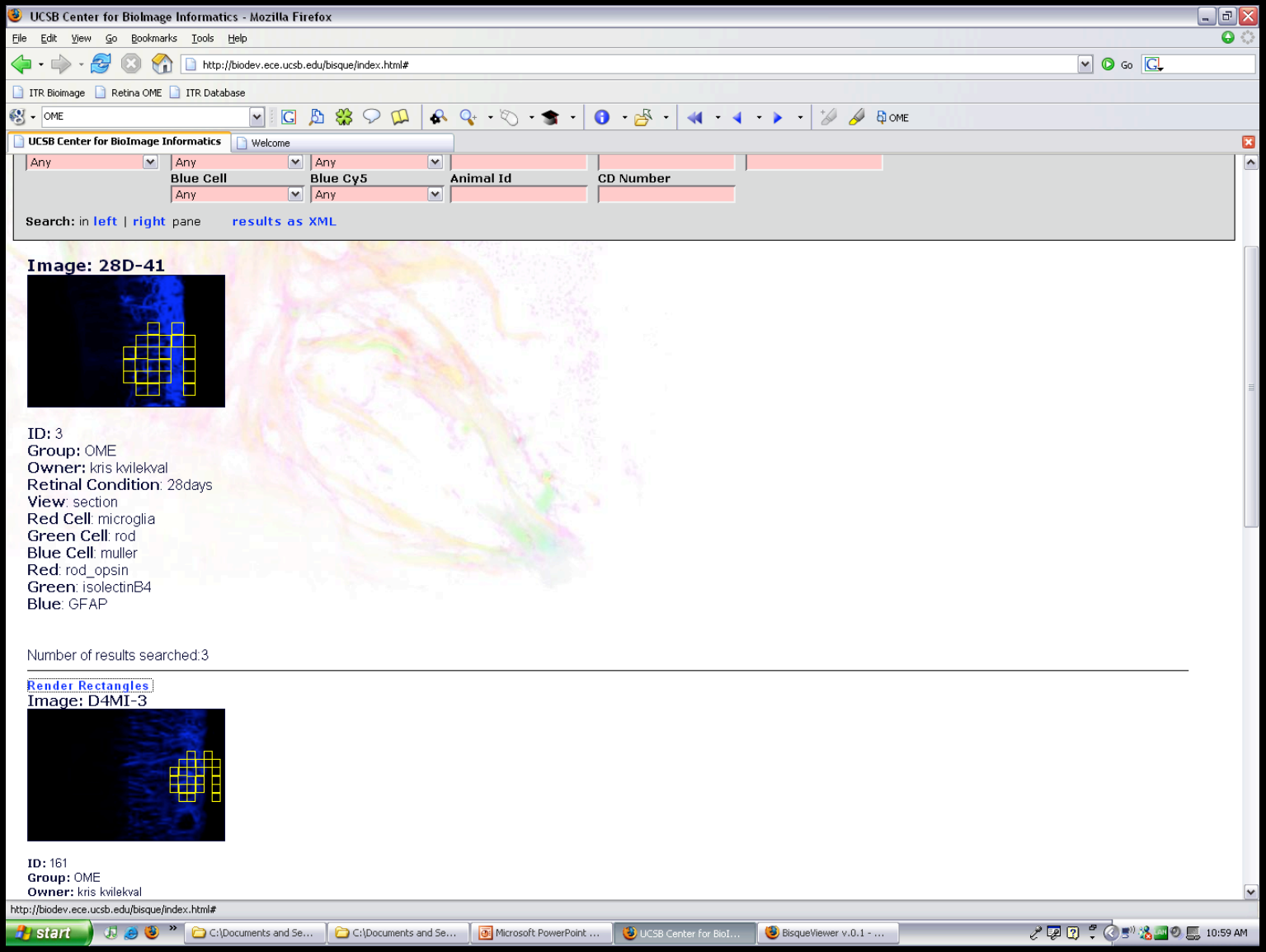
Screenshots (search similar)



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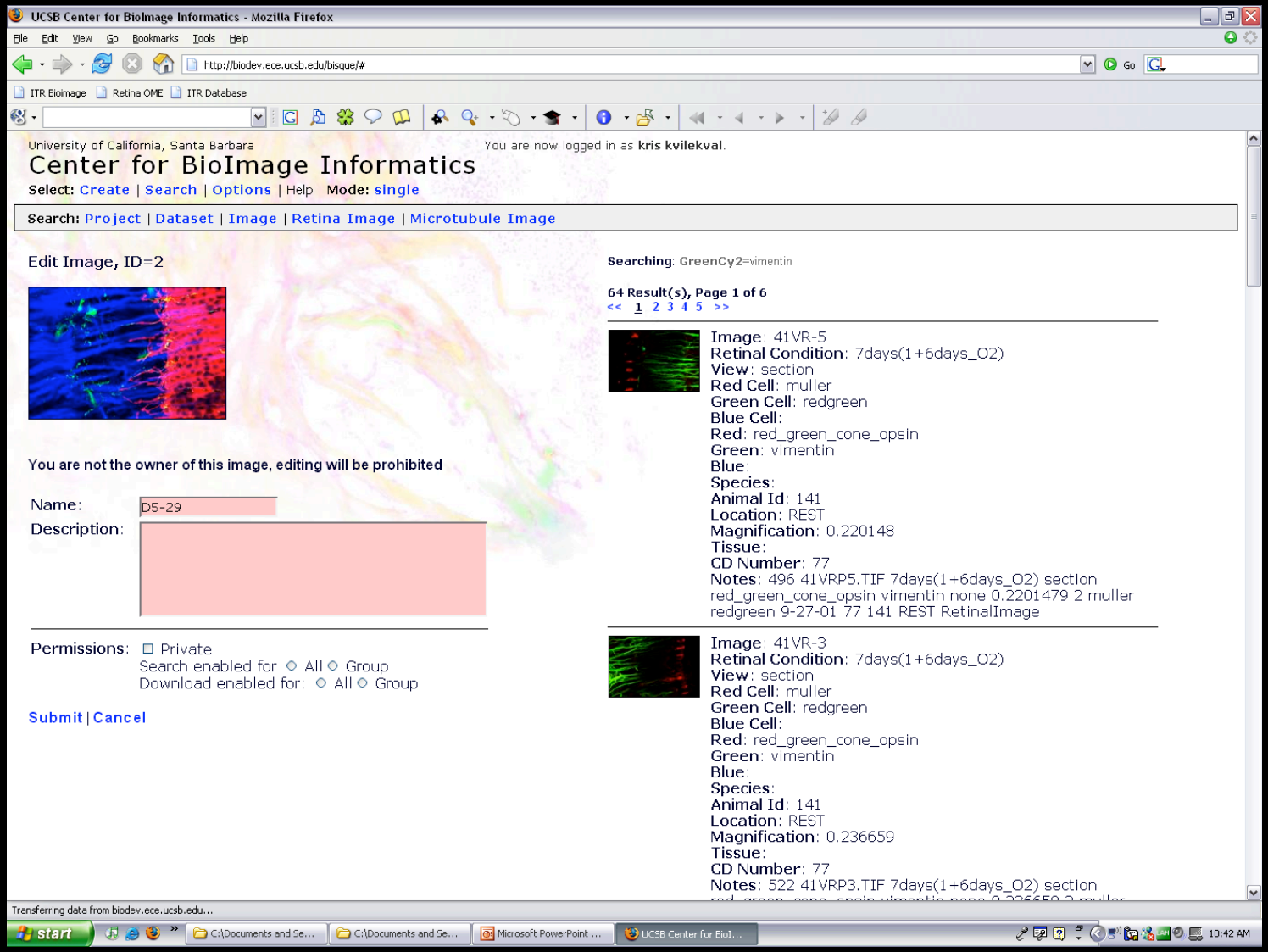
Screenshots (personal collection)



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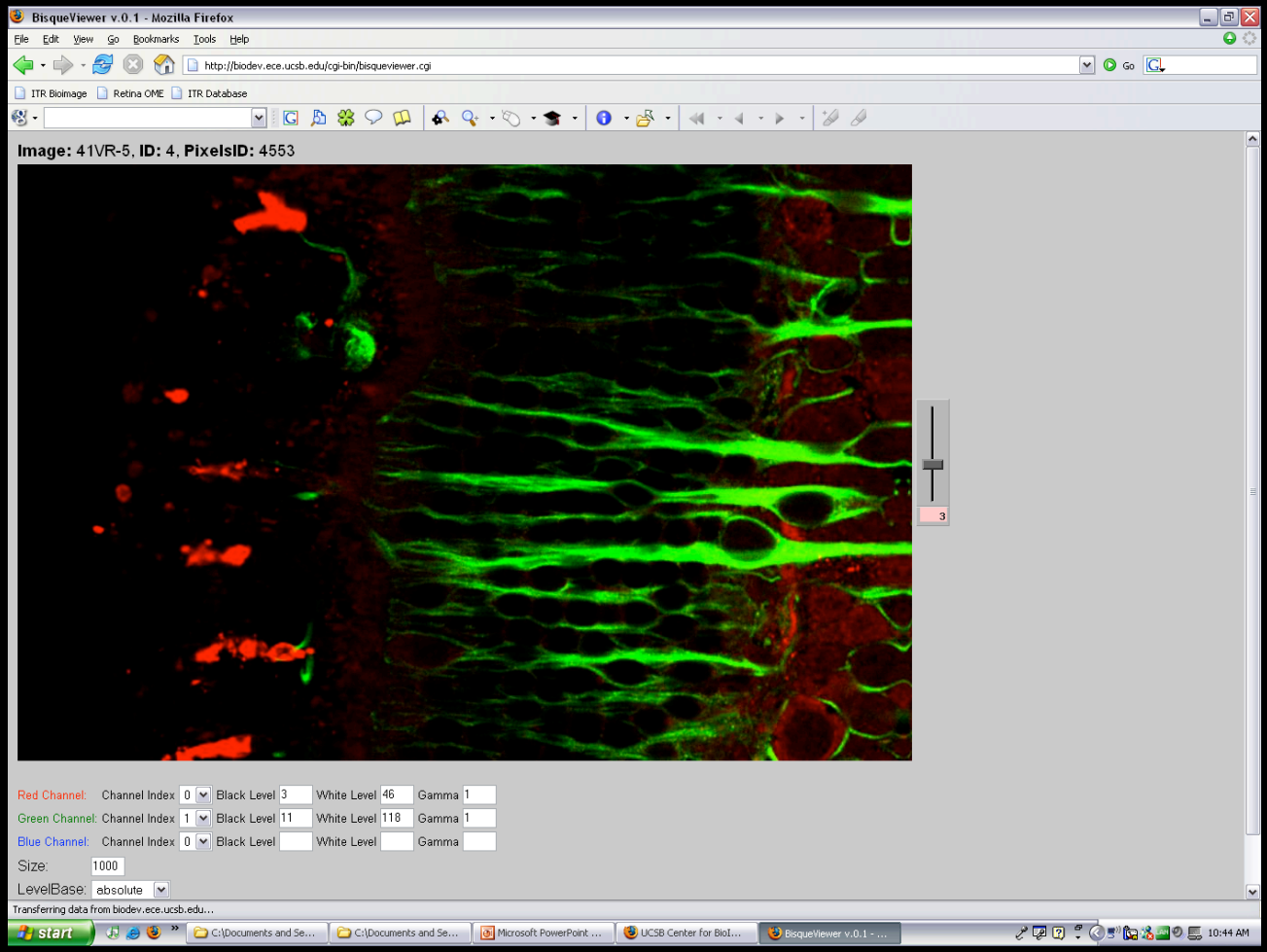
Screenshots (5D Viewer)



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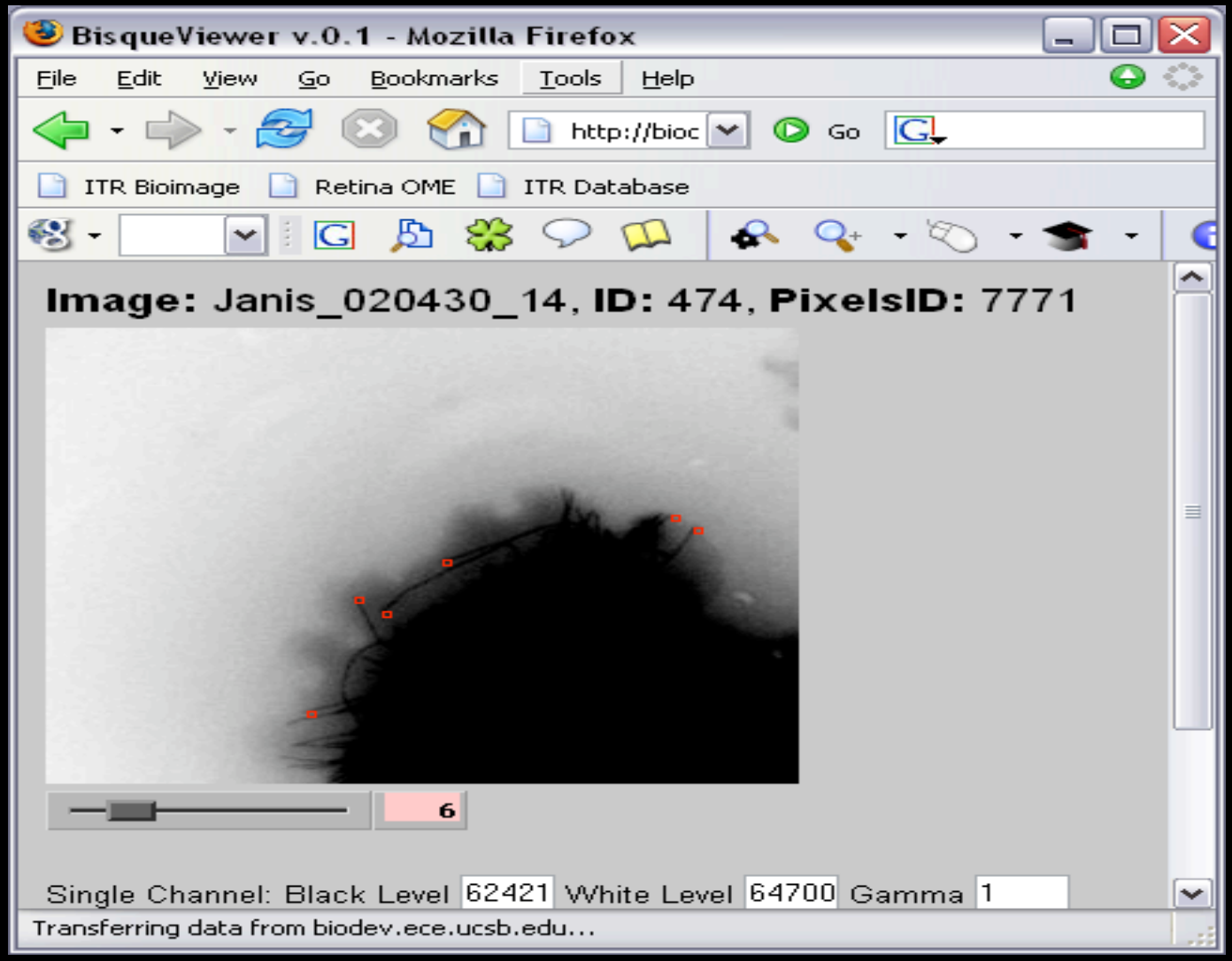
Screenshot (5D with tracks)



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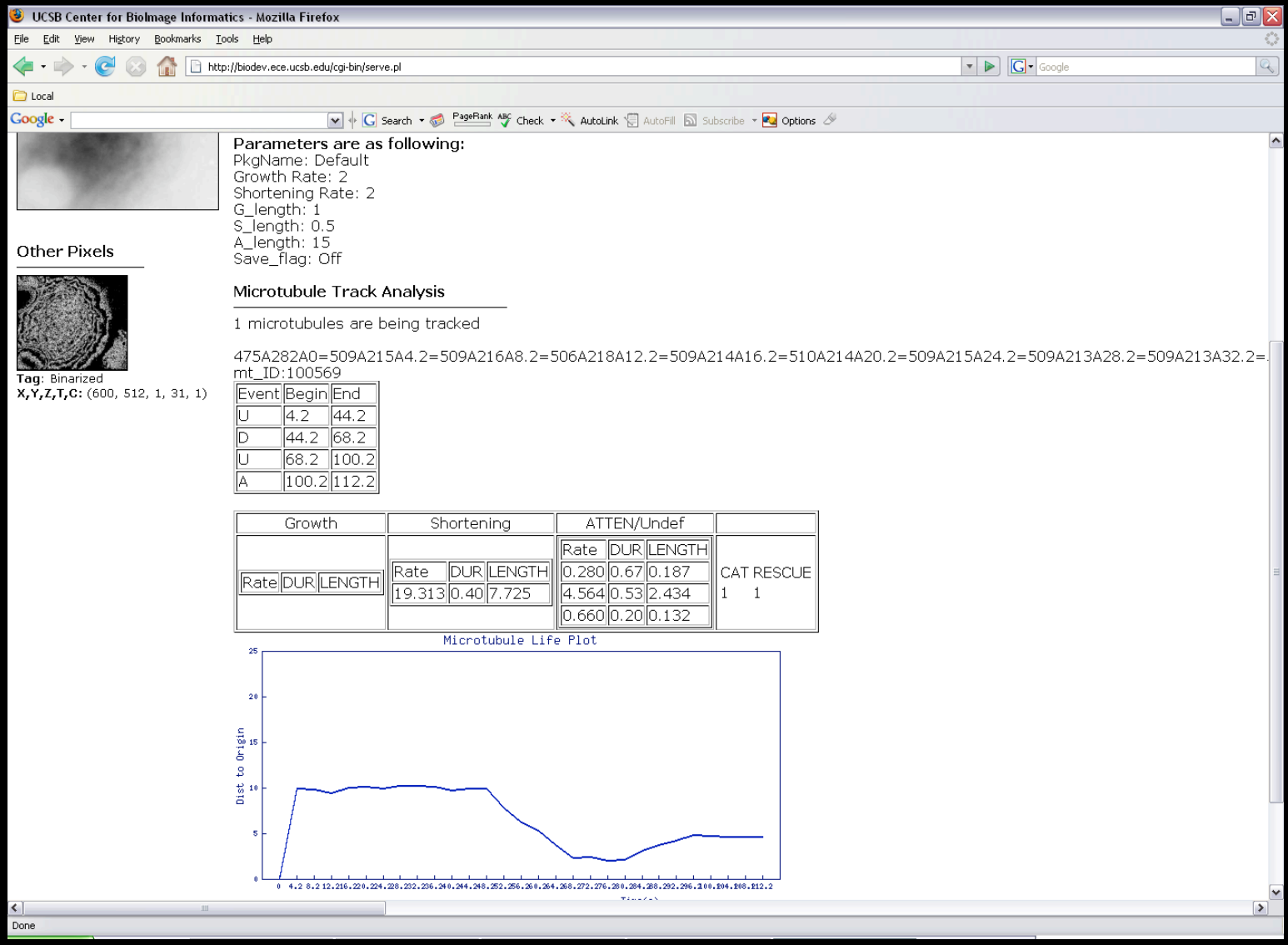
MT Life Dynamics



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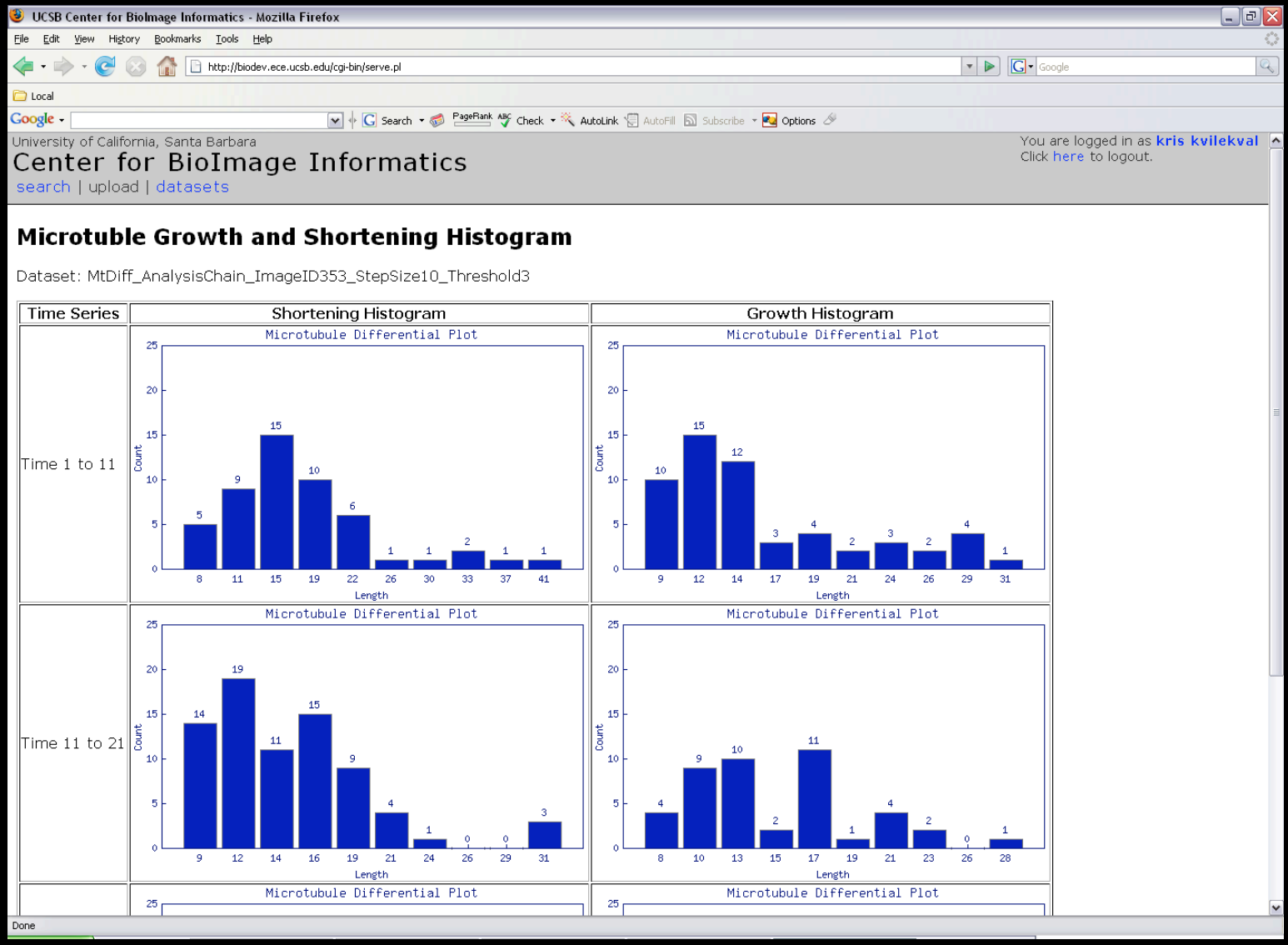
MT Global Dynamics



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BISQUE

Bio-Image Semantic Query User Environment

- Integrated Analysis
  - Cell counter (ImageJ)
  - MT Dynamics analysis
  - MT Global Differential
- Soon to be integrated
  - MT tip tracking
  - Standalone MT growth analysis (Aleem)
  - MT body tracking (alphan)

Bisque Conclusions

- Built on OME/Postgres environment
  - Extended schema
  - Rewrote UI
  - Integrated analysis
  - Built 1st generation in use at UCSB
  - Diverse datasets
    - >5000 5D images (> 100K 2D images)
  - Integrated several *useful* analyses

Bisque/OME lessons learned

- *New data sets take significant resources to incorporate.*
  - Schema, tool, and interface modifications
- *Changing experiments also require effort.*
  - Per experiment meta data may also require significant changes
- *Building analysis should be straight forward.*
  - Researchers balk at learning complex software
  - Simpler is better

Bisque/OME Challenges

- *Automatic and semi-automatic analysis are needed:*
  - Our problems are less about bulk processing
  - High value images may need intervention
- *Semi-automatic analysis requires rich set of user tools*
  - Google, flickr, etc have raised the bar

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Motivation:

- Current metadata model is inflexible
  - Adding new experimental images requires:
    - Changes to Digital notebook
    - Changes to Bisque interface
    - Changes to OME/postgres schema
- Shouldn't this be easier?
  - "Add my images with this experimental data"
  - "Find images tagged with rod-opsin and GFAP "
  - "Create a region and specify an object type there"
  - "Try my new segmentation algorithm given …"

New project: Bisquik

- Easily support new image collections and experimental data
- Support cross-server/lab collections/queries
- Integrate different labs metadata
- Support semi-automatic analysis
- Allow rapid prototyping of new analyses

Bisquik: Requirements

- Allow researchers to add data sets with minimal help of engineers
  - Metadata is often a (changing) list of experimental parameters
- Give analysis writers easy access to data
- Integrate data and analysis access to other systems:
  - OME
  - PSLID
- Build on previous system (BISQUE/OME)

Example analysis

- Segmentation -> automated nucleus count
  - Segment retinal layers and count
- MT Dynamics
  - Pick one more MT and measure dynamicity
- MT motility
  - Pick several MTs and measure velocity

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Components

Web Services

Web UI

Metadata Annotation

Query

Analysis

Blob/Image Server

DoughDB

Remote Data Proxy

Analysis Engine

Flexible Metadata

- Support rapid addition of new datasets including experimental metadata
- Support new experimental protocols
- Allow analysis to create new metadata structures without a lot of work
- Extendible list of tagged values seems to be simplest model

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Bisquik: DoughDB

OID1

Name	GH1020
Foo	2
pixels	[OID2 OID3]

OID4

image	OID1
Feature f1	[…]

OID2

image	OID1
data	Server://…
Pixel-type	raw

DoughDB requirements

- Add new tag/value pairs to any db object
  - (Foo,2)
  - (visible-cell, rod)
- Allow multiple tags with same value
  - (visible-cell, rod)
  - (visible-cell, muller)
- Support fine-grained tag permission/visibility
  - Tags have creators and access control
- Support update semantics & preserve history
  - Timestamp tags
  - No deletes (except under restricted conditions)

DoughDB queries

- Find objects (images) with tag “foo”
  - Select a.foo
- Find images with name “GV100”
  - Select a.name = “gv100”
- Find images with cellcount < 100
  - Select a.cellcount < 100
- Find images with a region similar to r1 based on feature f1
  - Select r.image = i and l2(r.f1, r1[…]) < 10

DoughDB key features

- Open ended data model
  - tag/value pairs
  - Templates for common sets
- Pair values have ts, owner, acl
- Preserves history of annotations
- SQL like query language
- Simple keyword queries
  - Antibody:rod-opsin AND antibody:gfap
  - Rod-opsin AND glial fibrillary acid protein

Bisquik ontology support

- "**ontology** is a data model that represents a domain and is used to reason about the objects in that domain and the relations between them"
- Unstructured tag/value
  - Great for taggers
  - Unhappy searchers
- Different labs use different terms for the same object.

Bisquik ontology support

- Dictionary of terms and relations
- Require (or strongly suggest) that tags and value are defined before use
- Drop into ontology editor when new values and tags are encountered.
- Integrated into search system
  - Permit (or offer) 'alias' 'part-of' 'related-to' searches

Programming Toolkit

- Goal: Allow vision researcher to easily test and incorporate new analysis
- Image/Object/Tag query/creation
- Implemented as web services
  - Resources exposed through web interfaces
  - Libraries provided for python, matlab access
- Support for data provenance
- Module execution from any environment

Module Scheduler/Engine

- Track free computational resources
- Execution engine
  - Schedule executions on module engines
  - Automatic component placement
- Permit development outside cluster environment
- Permit scalable deployment inside cluster environment

Bisquik interface

- Current Bisque functionality
  - Browse/Organize/Analyze
- Supports 5D images
- Flickr-like interface for image/region tagging
- Complex region definition and tagging

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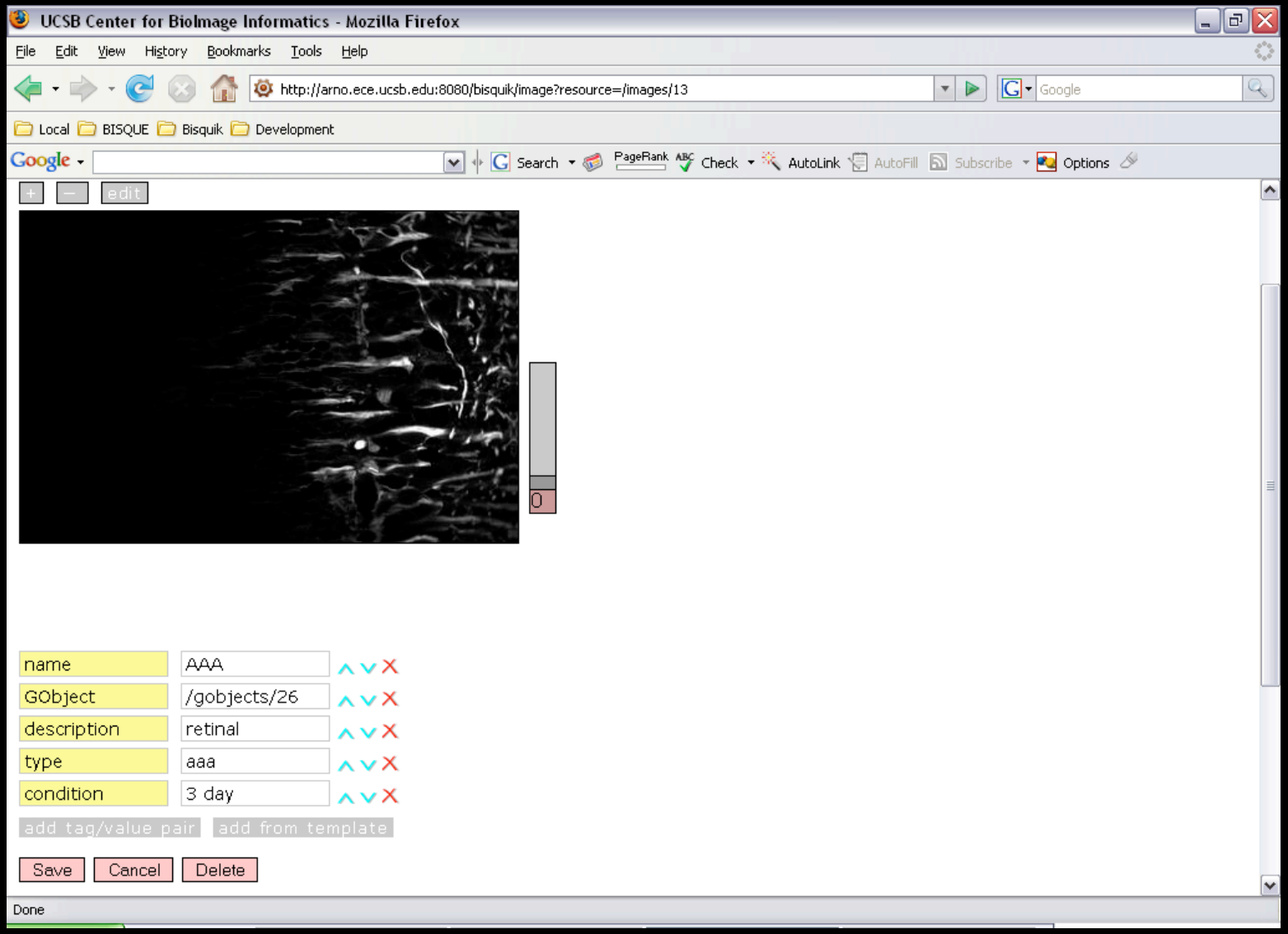
Simple annotation



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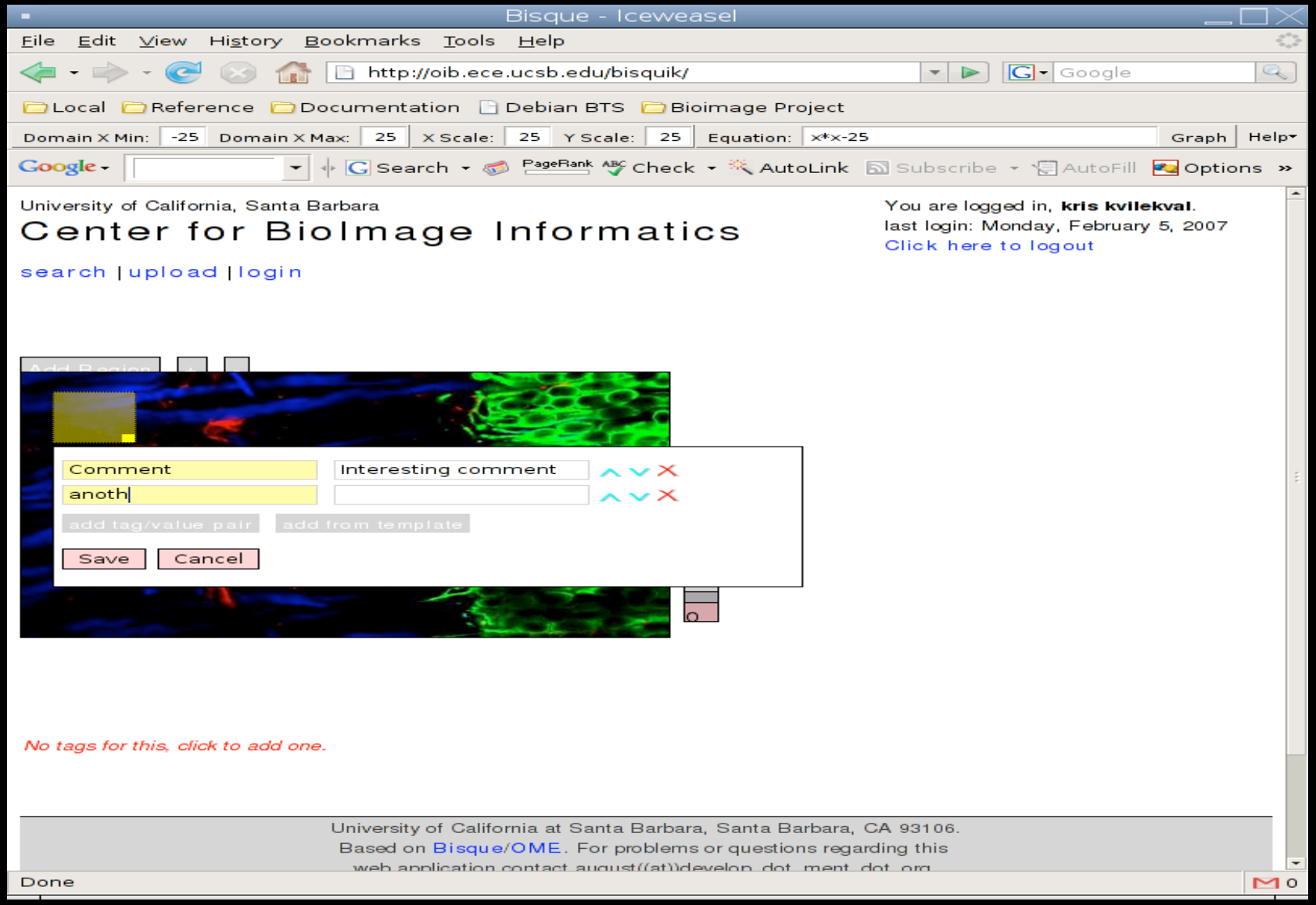
Region annotation



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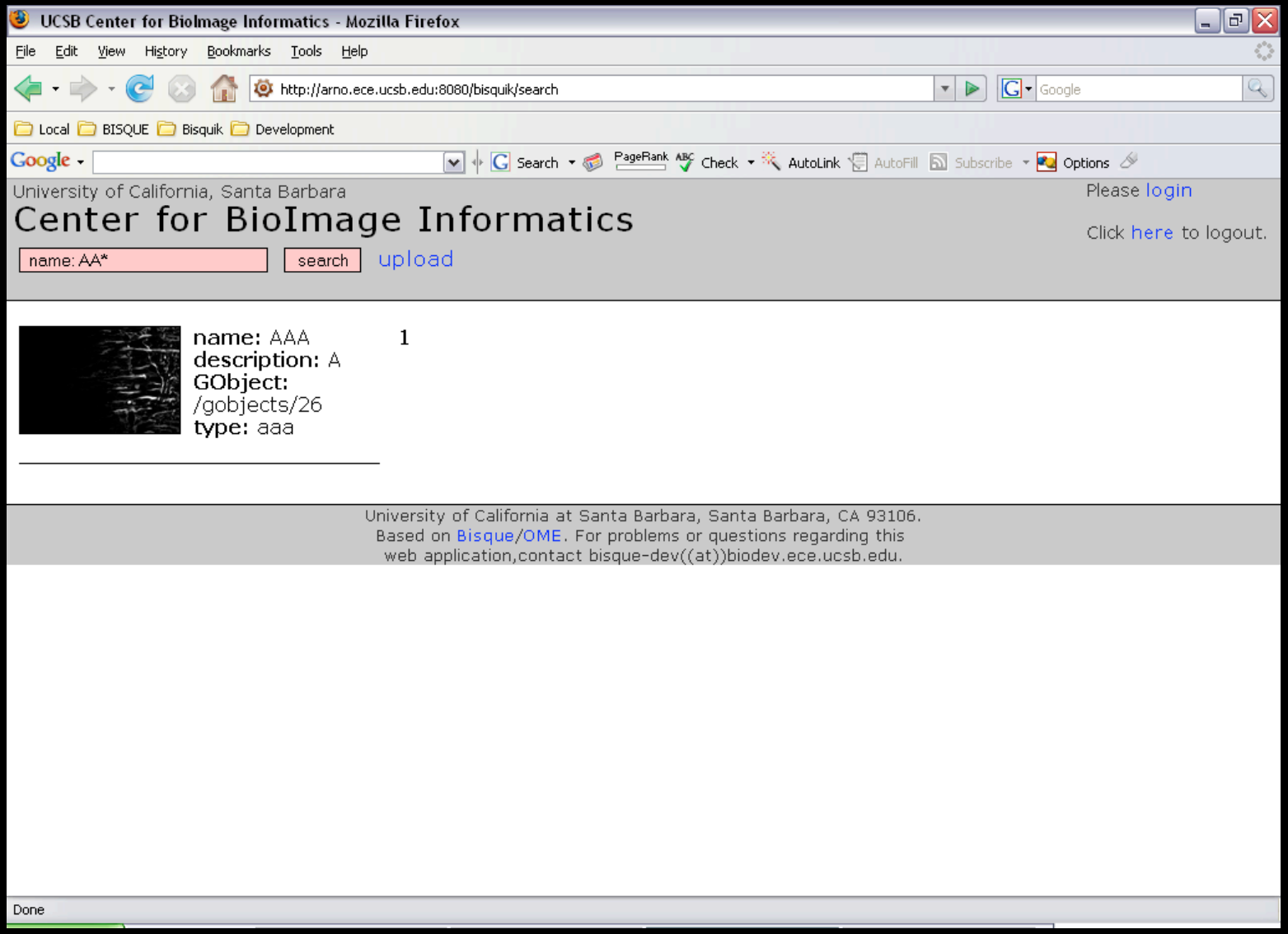
Search (metadata)



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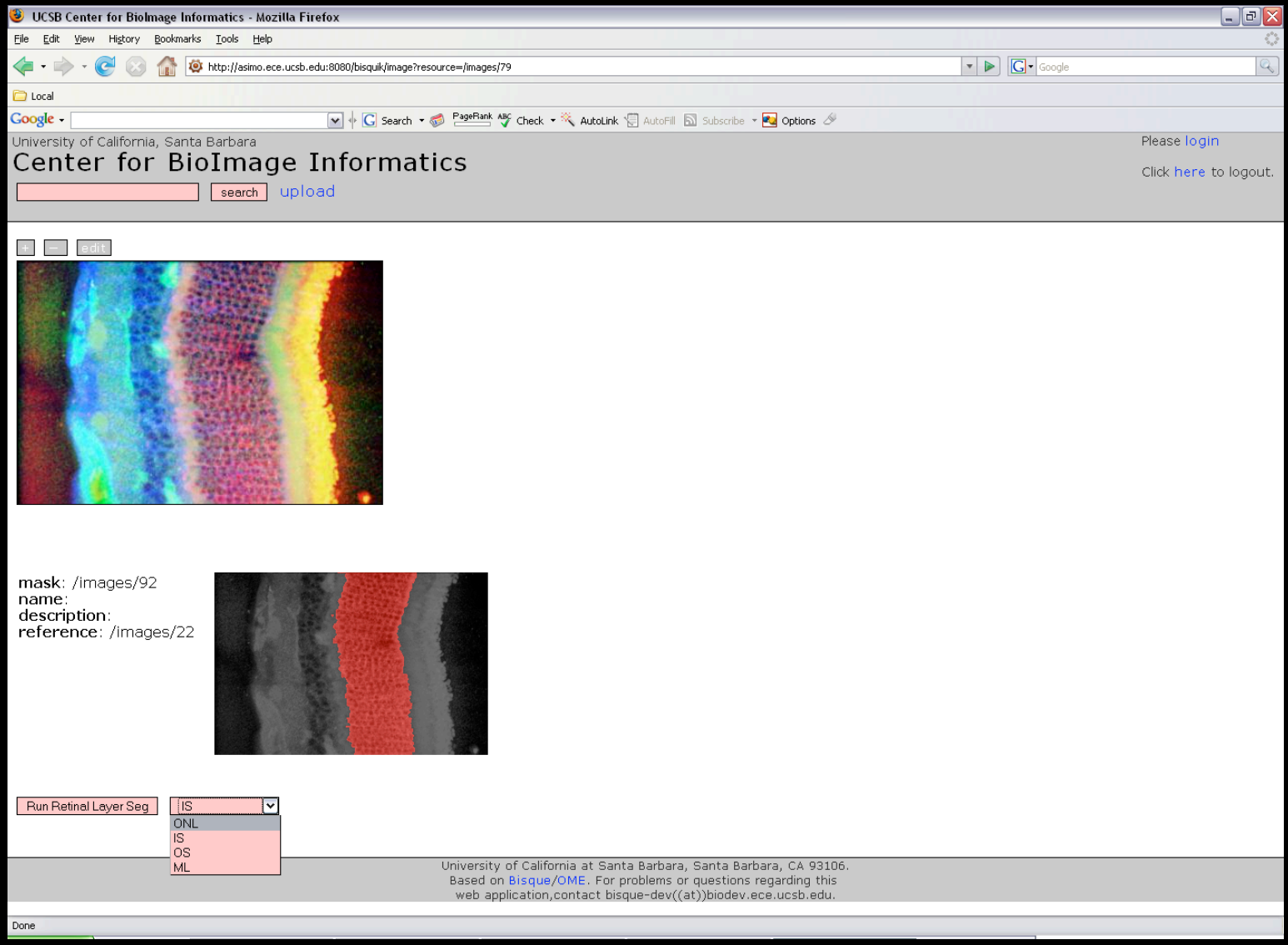
Segmentation Analysis



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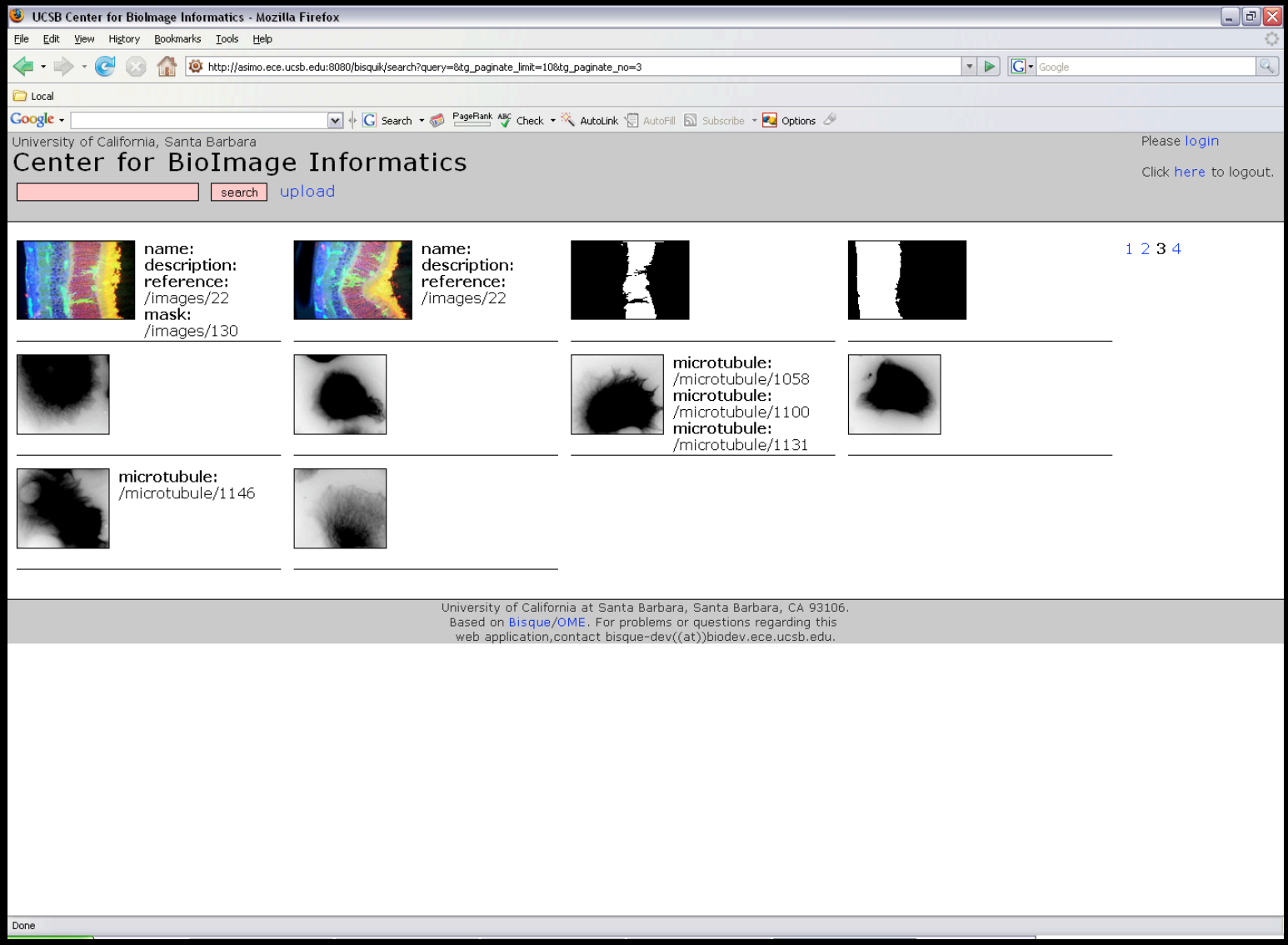
Local and remote access



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Bisquik Metadata Annotation

- Unified offline (Digital Notebook) and online manipulation.
- Easy to build annotation forms/templates
- Allow "schema" modification "in field"
- Permit annotation templates to be shared between DN and Bisquik
- Graphical geometry annotator

Blob+Image server

- Extensible server for read-only objects
  - Pixels
  - Features
- Pluggable transforms
  - Thumbnails, slices
  - pixel transforms (watermarks)
  - Graphical metadata renderers
- Feature server

Remote Access

- All basic services are web accessible:
  - RESTful (simple model, web caching)
  - DoughDB, Image server, Module engines
- Cluster Database support
  - Image collections are split across machines
  - Unified view
  - Query engine distributes and resolves
- Already supports access to 'foreign' data sources:
  - multiple BISQUE/PSLID/OME sources

Scalable/distributed deployment

- Components services
  - Image Server
    - Manipulations (slice, format, etc)
  - Data Service (query, storage)
  - Module Engine (Analysis Executions)
  - Web Service (browser, aggregation support)

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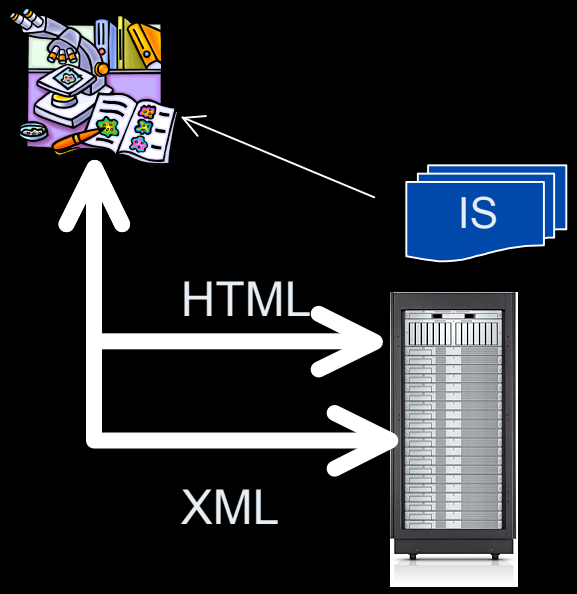
Simple deployment



Web Service
Image Server
Data Server
Module Engine

- Image Service
- (Meta) Data Service
- HTML Server
- Module Engine

RC – Rich Client WS-web server IS - Image Server DS – Data Server
MS - Module Scheduler ME – Module Engine

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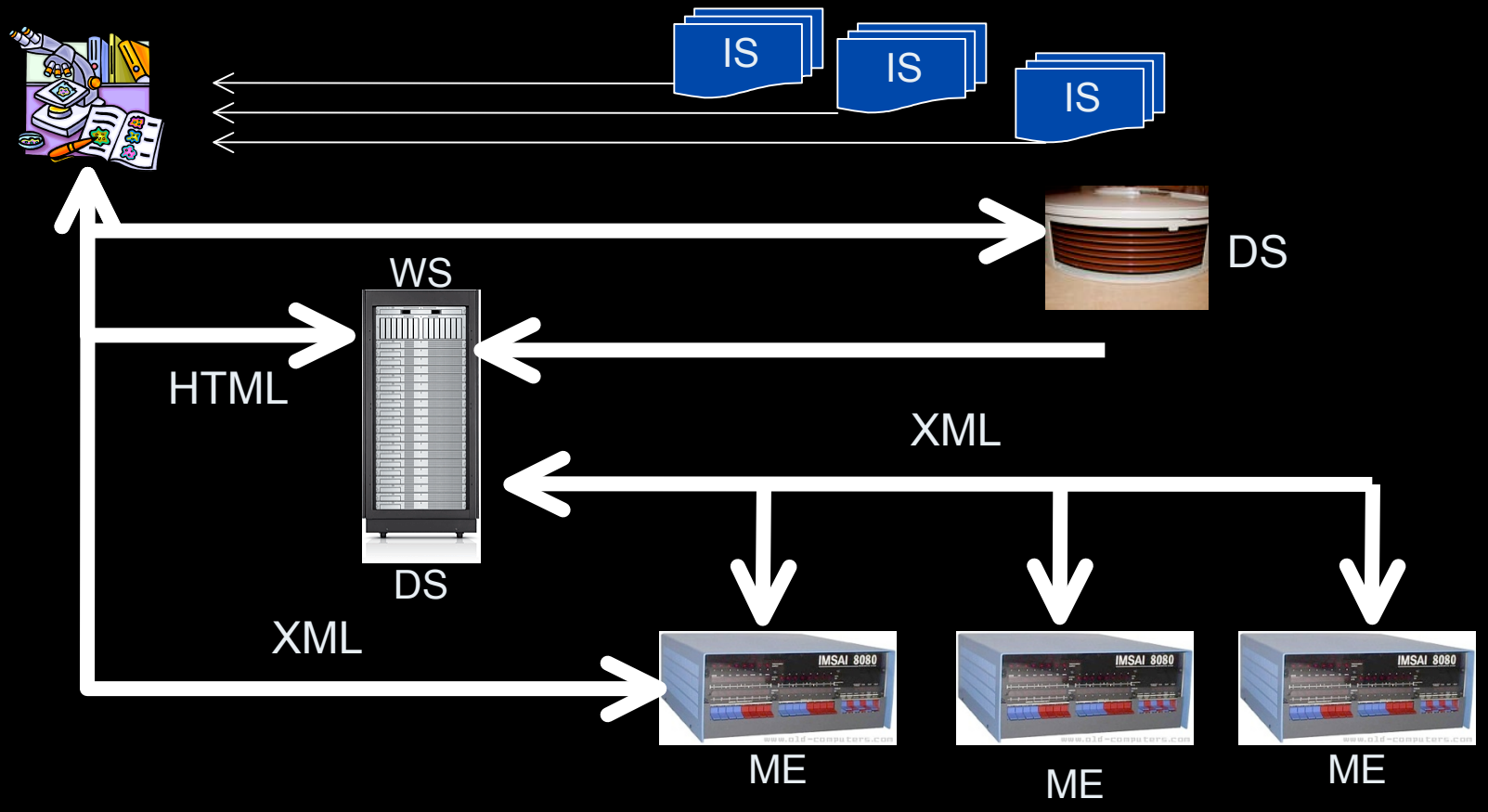
Scalable services



RC – Rich Client WS-web server IS - Image Server DS – Data Server
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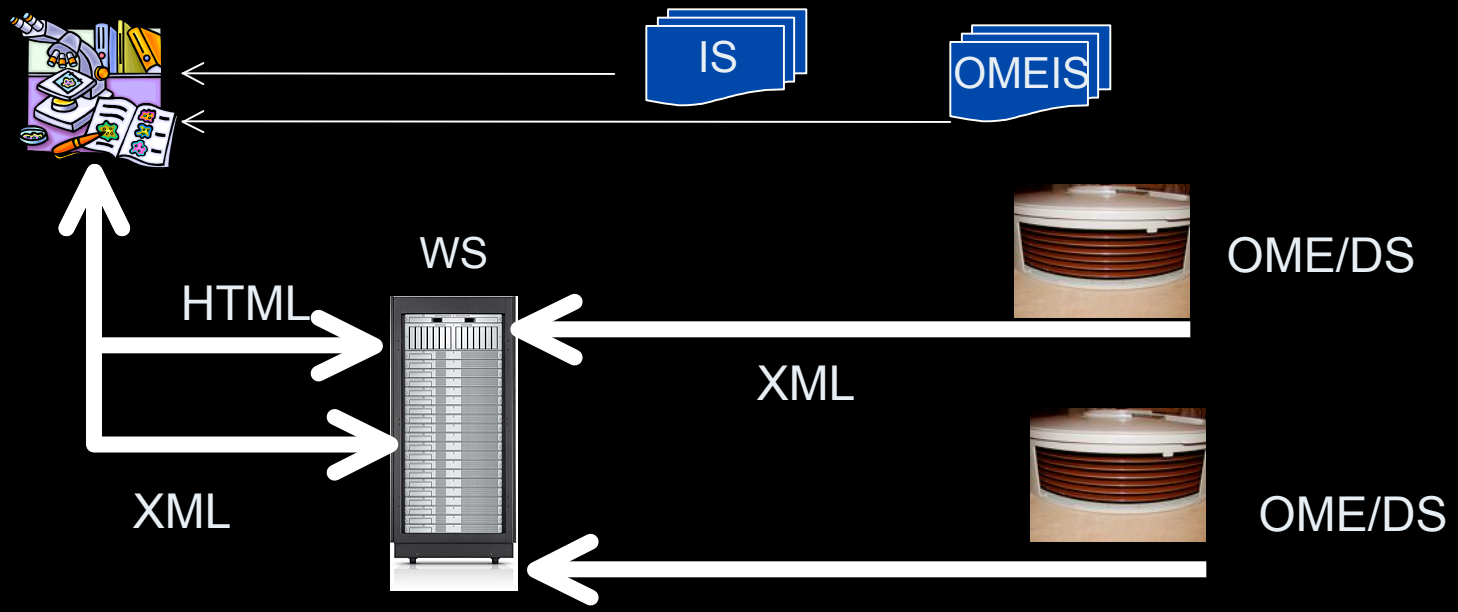
Remote services



RC – Rich Client WS-web server IS - Image Server DS – Data Server
MS - Module Scheduler ME – Module Engine

Service Examples

- http://host/images

```
<response>
 <image resource="/images/1/" imgurl="/imgsrv/2" />
 <image resource="/images/2/" imgurl="/imgsrv/3" />
</response>
```

- http://host/images/1?view=full

```
<response>
 <image resource="/images/1/" x="512 y="512"
     imgurl="/imgsrv/2">
    <tag resource="/tags/10"
         name="description" value="mt image" />
 </image>
</response>
```

Service Examples

- GET http://host/modules

```
<response>
 <image resource="/images/1/" imgurl="/imgsrv/2" />
 <image resource="/images/2/" imgurl="/imgsrv/3" />
</response>
```

- POST http://host/modules/1

```
<request>
  <tag name="p1" value="/images/1" />
  <tag name="count" value="0" />
</request>

<response>
 <image resource="/images/1/" />
 <microtubule resource="/microtubule/1" />
</response>
```

Bisquik Status:

- Web UI
  - Uploading, Tagging, simple searches
  - Demo at http://biodev.ece.ucsb.edu:8080/bisquik
- DoughDB
  - Prototype based on SQL/BerkelyDB
  - Multi node storage aggregation and queries
- Analysis
  - Layer segmentation
- In Development
  - Ontology support, advanced query/indexing

Bisquik: Initial impressions

- Focus : Ease of Use
  - For biologists: simple data model, easy searching
  - For analysis developers: develop in comfortable environment
- Web UI
  - Tools developed for semi-automatic analysis
- DoughDB
  - Performance needs to be tested on large sets
- Analysis ***
  - < 1 day for researcher to use tool kit
  - ~1 day for interface improvements
- Development
  - Rapid development tools
  - Agile language and methods (python)
  - Lots of progress in little time (march 15-Now)

Conclusion/Vision

- Prototype data model and analysis in Bisquik
- Use data and analysis from multiple sources
- Migrate to backend systems (OME/PSLID) as needed

Bisquik plan

- Release 0.1 : April 2007
  - Bisquik Tagging + DoughDB
  - Bisque/OME Bridge (image + metadata)
  - Simple queries (antibody:vimentin and 'cross section')
  - Blob server
- Release 0.2 : May 2007
  - Web + DN Metadata annotations (text,graphical)
  - Distributed queries
  - Several analyses (segmentation, MT motility)
- Release 0.3 : June 2007
  - Ontology support (DoughDB + UI + query support)
  - Access to 'foreign' analysis BISQUE/PSLID
  - Other analysis from local researchers
- Release 0.4 :
  - Analysis engine scheduling + performance tests

Info

- Open Source Code
  - http://biodev.ece.ucsb.edu/projects/bioimage
- Demo and UCSB collections
  - http://biodev.ece.ucsb.edu/bisque
  - http://biodev.ece.ucsb.edu:8080/bisquik

Development Team

August Black, Jae Choi, Dmitry Fedorov, Brian Ruttenberg