

# BISQUE and BISQUIK

Kristian Kvilekval

- [Bioimage.ucsb.edu](http://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 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

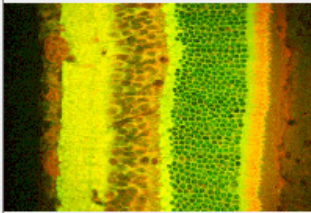
# Screenshots (Digital Notebook)

Digital Notebook

Image Name:

Path:

Name	Modified
<input type="checkbox"/> NCXSY01_equalize.TIF	2004-02-12 12:04:06
<input type="checkbox"/> NCXSY01_normalize.TIF	2004-02-12 11:25:04
<input type="checkbox"/> NCXSY02_equalize.TIF	2004-02-12 12:02:30
<input type="checkbox"/> NCXSY02_normalize.TIF	2004-02-12 11:23:36
<input type="checkbox"/> NCXSY04_equalize.TIF	2004-02-12 12:02:30
<input type="checkbox"/> NCXSY04_normalize.TIF	2004-02-12 11:23:36
<input checked="" type="checkbox"/> NCXSY05_equalize.TIF	2004-02-12 12:04:08
<input type="checkbox"/> NCXSY05_normalize.TIF	2004-02-12 11:25:06
<input type="checkbox"/> NCXSY06_equalize.TIF	2004-02-12 12:02:24
<input type="checkbox"/> NCXSY06_normalize.TIF	2004-02-12 11:23:30
<input type="checkbox"/> NCXSY07_equalize.TIF	2004-02-12 12:02:24
<input type="checkbox"/> NCXSY07_normalize.TIF	2004-02-12 11:23:30
<input type="checkbox"/> NCXSY14_equalize.TIF	2004-02-12 12:03:40
<input type="checkbox"/> NCXSY14_normalize.TIF	2004-02-12 11:24:38
<input type="checkbox"/> NCXSY50_equalize.TIF	2004-02-12 12:04:16
<input type="checkbox"/> NCXSY50_normalize.TIF	2004-02-12 11:25:12
<input type="checkbox"/> NCXSY51_equalize.TIF	2004-02-12 12:03:34
<input type="checkbox"/> NCXSY51_normalize.TIF	2004-02-12 11:24:34
<input type="checkbox"/> NCXSY53_equalize.TIF	2004-02-12 12:02:08
<input type="checkbox"/> NCXSY53_normalize.TIF	2004-02-12 11:23:14
<input type="checkbox"/> NCXSY54_equalize.TIF	2004-02-12 12:02:10



[Internal Metadata]

[Document Name]  
D:\VTR\Cat\redgreen\section\normal\NCXSY05\_equalize.TIF

[Software]  
ImageMagick 5.4.9 09/01/02 Q16  
<http://www.imagemagick.org>

[Date Time]  
11-24-1992

[Artist]  
1992 ACCUSOFT INC, ALL RIGHTS RESERVED

Species

Animal ID

Experimental Condition

Imaging date

Image Source ID

Image ID

File Name

View

Location

Magnification

Antibody Channel 1 (red)

Cell Type Antibody Channel 1 (red)

Antibody Channel 2 (green)

Cell Type Antibody Channel 2 (green)

Antibody Channel 3 (blue)

Cell Type Antibody Channel 3 (blue)

notes

# Graphical Ground truth

The screenshot shows a software window titled "D:/dima\_data/images/\_BIO/STK/c13.stk". The interface is divided into several panels:

- Mode:** A dropdown menu set to "Tracking mode".
- Load/Save tracks:** A table with a "track ID" header and three entries: "track1" (red), "track2" (blue), and "track3" (green). Below the table are "+" and "-" buttons.
- Configuration:** A section with three checked options: "Display prev points", "Auto page advance", and "Page skip" (set to 1). Below these are sliders for "Line thickness" (set to 2) and "Page skip" (set to 1).
- Channels:** A panel with three color selection dropdowns: "Red: ch 1 (Luminance)", "Green: ch 1 (Luminance)", and "Blue: ch 1 (Luminance)".
- Live enhancement:** A panel with an "Enhancement" dropdown set to "Stretch with tolerance" and a "Scale" dropdown set to "[2:1]".
- Image View:** A large central window showing a grayscale image of a biological structure with three colored tracks overlaid: a red track at the bottom, a blue track in the middle, and a green track at the top. Small colored circles mark points on the tracks.
- Image Controls:** A panel with a zoomed-in view of the image, zoom in/out buttons (-), a "1:1" button, and a zoom in button (+).
- Page 10/30:** A panel with an "Initial" button, left and right navigation arrows, and a scroll bar.
- Metadata:** A panel displaying the following information: "[MetaMorph Stack (STK) Fields]", "Name: Time Series", "AutoScale: 1", "MinScale: 1564", "MaxScale: 16383", "SpatialCalibration: 1", "XCalibration: 1/1", "YCalibration: 1/1", "CalibrationUnits:", "ThreshState: 0", "ThreshStateRed: 0", and "ThreshStateGreen: 0".
- Buttons:** "Apply", "OK", and "Cancel" buttons at the bottom right.

At the bottom left of the window, the status bar shows "[600x512] chan: 1/16bit" and "[0x0] Done in 29ms".

# 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

# Screenshots (browsing)

UCSB Center for BioImage Informatics - Mozilla Firefox

File Edit View Go Bookmarks Tools Help

http://biodev.ece.ucsb.edu/bisque/#

ITR BioImage Retina OME ITR Database

University of California, Santa Barbara You are now logged in as kris kvilekval.

## Center for BioImage Informatics

Select: [Create](#) | [Search](#) | [Options](#) | Help Mode: **Dual**

Search: [Project](#) | [Dataset](#) | [Image](#) | [Retina Image](#) | [Microtubule Image](#)

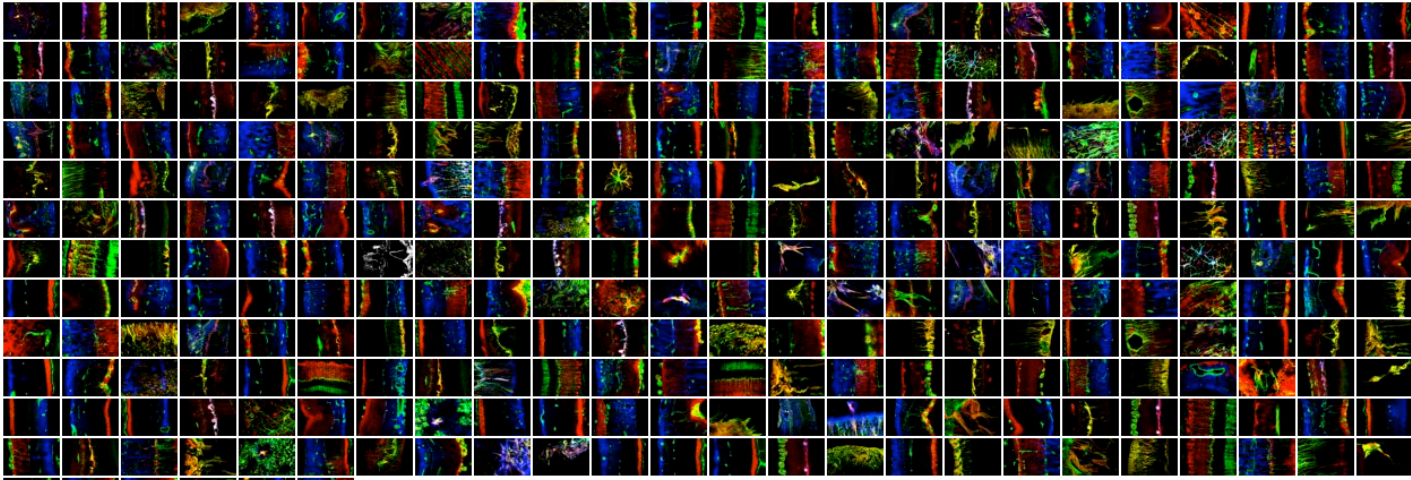
Dataset Search Close

owner	group	name
All	All	
kris kvilekval	OME	description
swaroop	6193_searchat	
august	6193_downloa	

Search: in [left](#) | [right](#) pane [results as XML](#)

**Dataset: Retina multichannel** (294 images)

Group: OME  
Owner: kris kvilekval  
Description: These images were imported using the OME command-line tool on Mon Mar 6 19:43:02 2006. This description was auto-generated. Use the -D command-line parameter to specify your own descriptions during image import.



Transferring data from biodev.ece.ucsb.edu...

start C:\Documents and Se... C:\Documents and Se... Microsoft PowerPoint ... UCSB Center for BioI... 10:36 AM



# Screenshots (search)

UCSB Center for BioImage Informatics - Mozilla Firefox

http://biodev.ece.ucsb.edu/bisque/#

University of California, Santa Barbara You are now logged in as kris kvilekval.

## Center for BioImage Informatics

Select: [Create](#) | [Search](#) | [Options](#) | [Help](#) Mode: [single](#)

Search: [Project](#) | [Dataset](#) | [Image](#) | [Retina Image](#) | [Microtubule Image](#)

Searching: RedCy3=rod\_opsin

441 Result(s), Page 1 of 37  
 << [1](#) [2](#) [3](#) [4](#) [5](#) [6](#) [7](#) [8](#) [9](#) [10](#) >>

	<p><b>Image:</b> D5-29  <b>Retinal Condition:</b> 3days+28days(r)  <b>View:</b> section  <b>Red Cell:</b> microglia  <b>Green Cell:</b> rod  <b>Blue Cell:</b> muller  <b>Red:</b> rod_opsin  <b>Green:</b> IsolectinB4  <b>Blue:</b> GFAP  <b>Species:</b>  <b>Animal Id:</b> QBD5  <b>Location:</b> REST  <b>Magnification:</b> 0.206239  <b>Tissue:</b>  <b>CD Number:</b> 113  <b>Notes:</b> 206 D5P29.TIF 3days+28days(r) section rod_opsin isolectinB4 GFAP 0.2062388 3 microglia rod muller 1-21-03 113 QBD5 REST RetinalImage</p>
	<p><b>Image:</b> 28D-41  <b>Retinal Condition:</b> 28days  <b>View:</b> section  <b>Red Cell:</b> microglia  <b>Green Cell:</b> rod  <b>Blue Cell:</b> muller  <b>Red:</b> rod_opsin  <b>Green:</b> IsolectinB4  <b>Blue:</b> GFAP  <b>Species:</b>  <b>Animal Id:</b> 765  <b>Location:</b> REIT  <b>Magnification:</b> 0.309358  <b>Tissue:</b>  <b>CD Number:</b> 116  <b>Notes:</b> 64 28DP41.TIF 28days section rod_opsin isolectinB4 GFAP 0.309358 3 microglia rod muller 2-11-03</p>

Searching: GreenCy2=vimentin

64 Result(s), Page 1 of 6  
 << [1](#) [2](#) [3](#) [4](#) [5](#) >>

	<p><b>Image:</b> 41VR-5  <b>Retinal Condition:</b> 7days(1+6days_O2)  <b>View:</b> section  <b>Red Cell:</b> muller  <b>Green Cell:</b> redgreen  <b>Blue Cell:</b>  <b>Red:</b> red_green_cone_opsin  <b>Green:</b> vimentin  <b>Blue:</b>  <b>Species:</b>  <b>Animal Id:</b> 141  <b>Location:</b> REST  <b>Magnification:</b> 0.220148  <b>Tissue:</b>  <b>CD Number:</b> 77  <b>Notes:</b> 496 41VRP5.TIF 7days(1+6days_O2) section red_green_cone_opsin vimentin none 0.2201479 2 muller redgreen 9-27-01 77 141 REST RetinalImage</p>
	<p><b>Image:</b> 41VR-3  <b>Retinal Condition:</b> 7days(1+6days_O2)  <b>View:</b> section  <b>Red Cell:</b> muller  <b>Green Cell:</b> redgreen  <b>Blue Cell:</b>  <b>Red:</b> red_green_cone_opsin  <b>Green:</b> vimentin  <b>Blue:</b>  <b>Species:</b>  <b>Animal Id:</b> 141  <b>Location:</b> REST  <b>Magnification:</b> 0.236659  <b>Tissue:</b>  <b>CD Number:</b> 77  <b>Notes:</b> 522 41VRP3.TIF 7days(1+6days_O2) section red_green_cone_opsin vimentin none 0.236659 2 muller</p>

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Start | C:\Documents and Se... | C:\Documents and Se... | Microsoft PowerPoint... | UCSB Center for BioI... | 10:40 AM

# Screenshots (search)

UCSB Center for BiImage Informatics - Mozilla Firefox

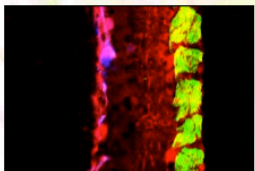
File Edit View Go Bookmarks Tools Help

http://biodev.ece.ucsb.edu/bisque/#

ITR Bioimage Retina OME ITR Database

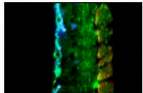
( Included in dataset(s): **Mon Mar 6 19:36:04 2006 Import Dataset , Retina multichannel** )

581 Result(s), Page 1 of 49  
 << 1 2 3 4 5 6 7 8 9 10 >>

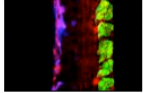


**ID:** 1  
**Group:** OME  
**Owner:** kris kvilekval  
**Size X,Y,Z,T,C:** (768, 512, 1, 1, 3)  
**Original Files:** NCCNP1\_normalize.TIF  
[\[image\]](#) [\[download\]](#)  
 NCCNP1\_equalize.TIF  
[\[image\]](#) [\[download\]](#)  
 NCCNP1.TIF  
[\[image\]](#) [\[download\]](#)

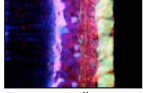
**Other Pixels**



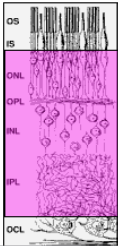
**Tag:** zseries  
**X,Y,Z,T,C:** (768, 512, 7, 1, 3)



**Tag:** normalize  
**X,Y,Z,T,C:** (770, 513, 1, 1, 3)



**Tag:** equalize  
**X,Y,Z,T,C:** (770, 513, 1, 1, 3)



**Retinal Image Meta Data**

**Retinal Condition:** normal  
**View:** section  
**Red Cell:** horizontal  
**Green Cell:** ganglion  
**Blue Cell:** amacrine  
**Red:** calretinin  
**Green:** neurofilament  
**Blue:** calbindin  
**Species:**  
**Animal Id:** 097b  
**Location:** LEST  
**Magnification:** 0.228656  
**Tissue:**  
**CD Number:** 133  
**Notes:** 852 NCCNP1.TIF normal section calretinin neurofilament calbindin 0.2286561 3 horizontal ganglion amacrine 7-21-03 133 097b LEST RetinalImage

---

**Image:** D5-29  
**Retinal Condition:** 3days+28days(r)  
**View:** section  
**Red Cell:** microglia  
**Green Cell:** rod  
**Blue Cell:** muller  
**Red:** rod\_opsin  
**Green:** isolectinB4  
**Blue:** Glial Fibrillary Acid Protein  
**Species:**  
**Animal Id:** QBD5  
**Location:** REST  
**Magnification:** 0.206239  
**Tissue:**  
**CD Number:** 113  
**Notes:** 206 D5P29.TIF 3days+28days(r) section rod\_opsin isolectinB4 GFAP 0.2062388 3 microglia rod muller 1-21-03 113 QBD5 REST RetinalImage

---

**Image:** 28D-41  
**Retinal Condition:** 28days  
**View:** section  
**Red Cell:** microglia  
**Green Cell:** rod  
**Blue Cell:** muller  
**Red:** rod\_opsin  
**Green:** isolectinB4  
**Blue:** Glial Fibrillary Acid Protein  
**Species:**  
**Animal Id:** 765  
**Location:** REIT  
**Magnification:** 0.309358  
**Tissue:**  
**CD Number:** 116  
**Notes:** 64 28DP41.TIF 28days section rod\_opsin isolectinB4 GFAP 0.3093582 3 microglia rod muller 2-11-03 116 765 REIT RetinalImage

---

**Image:** 7DMI-2  
**Retinal Condition:** 7days  
**View:** section  
**Red Cell:** microglia  
**Green Cell:** rod  
**Blue Cell:** muller  
**Red:** rod\_opsin

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Center for  
Bioimaging  
Informatics

# Screenshots (search similar)

UCSB Center for BioImage Informatics - Mozilla Firefox

http://biodev.ece.ucsb.edu/bisque/index.html#

ITR Bioimage Retina OME ITR Database

OME

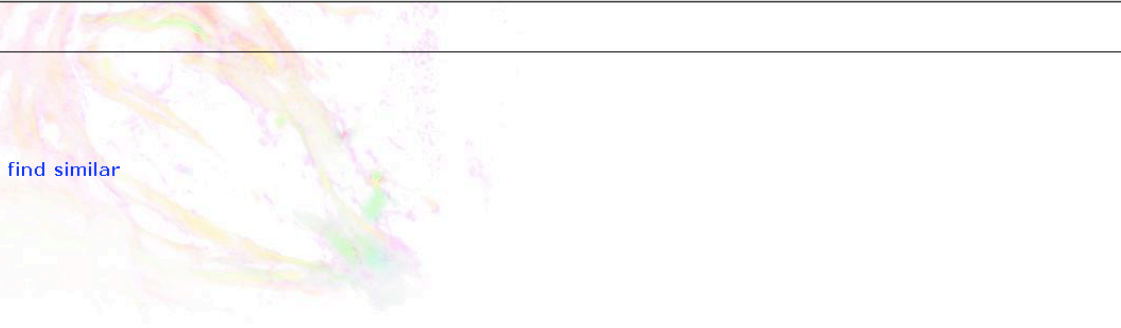
UCSB Center for BioImage Informatics Welcome

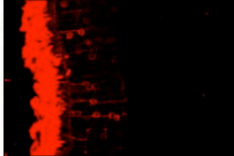
**RetinaImage Search** Close

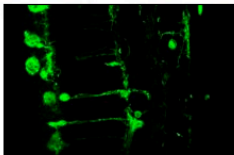
Retinal Condition	Red Cell	Red Cy3	Species	Location	Magnification
Any	Any	rod_opsin	Any		
View	Green Cell	Green Cy2	Image Num	Notes	Tissue
Any	Any	Any			
	Blue Cell	Blue Cy5	Animal Id	CD Number	
	Any	Any			

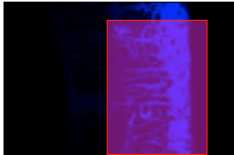
Search: in left | right pane results as XML

**Image: 28D-41**



 [find similar](#)

 [find similar](#)

 [find similar](#)

ID: 3  
Group: OME  
Owner: kris kvilekval

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start C:\Documents and Se... C:\Documents and Se... Microsoft PowerPoint... UCSB Center for BioI... BisqueViewer v.0.1 - ... 10:56 AM

May 2007

# Screenshots (search similar)

UCSB Center for BioImage Informatics - Mozilla Firefox

File Edit View Go Bookmarks Tools Help

http://biodev.ece.ucsb.edu/bisque/index.html#

ITR Bioimage Retina OME ITR Database


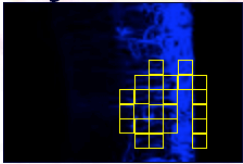
OME

UCSB Center for BioImage Informatics Welcome

Any	Any	Any		
Blue Cell	Blue Cy5	Animal Id	CD Number	
Any	Any			

Search: in left | right pane results as XML

**Image: 28D-41**

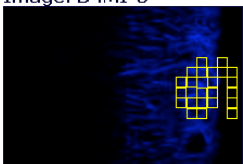


ID: 3  
Group: OME  
Owner: kris kvilekval  
Retinal Condition: 28days  
View: section  
Red Cell: microglia  
Green Cell: rod  
Blue Cell: muller  
Red: rod\_opsin  
Green: isolectinB4  
Blue: GFAP

Number of results searched: 3

[Render Rectangles](#)

**Image: D4MI-3**



ID: 161  
Group: OME  
Owner: kris kvilekval

http://biodev.ece.ucsb.edu/bisque/index.html#

start C:\Documents and Se... C:\Documents and Se... Microsoft PowerPoint ... UCSB Center for Bio... BisqueViewer v.0.1 - ... 10:59 AM

UCSB Center for BioImage Informatics - Mozilla Firefox

http://biodev.ece.ucsb.edu/bisque/#

ITR Bioimage Retina OME ITR Database

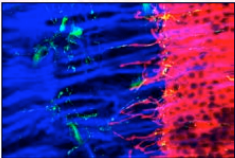
University of California, Santa Barbara You are now logged in as kris kvilekval.

## Center for BioImage Informatics

Select: [Create](#) | [Search](#) | [Options](#) | Help Mode: [single](#)

Search: [Project](#) | [Dataset](#) | [Image](#) | [Retina Image](#) | [Microtubule Image](#)

Edit Image, ID=2



You are not the owner of this image, editing will be prohibited

Name:

Description:

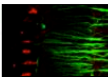
Permissions:  Private  
 Search enabled for:  All  Group  
 Download enabled for:  All  Group

[Submit](#) | [Cancel](#)

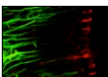
Searching: GreenCy2=vimentin

64 Result(s), Page 1 of 6  
 << [1](#) [2](#) [3](#) [4](#) [5](#) >>

---

 **Image:** 41VR-5  
**Retinal Condition:** 7days(1+6days\_O2)  
**View:** section  
**Red Cell:** muller  
**Green Cell:** redgreen  
**Blue Cell:**  
**Red:** red\_green\_cone\_opsin  
**Green:** vimentin  
**Blue:**  
**Species:**  
**Animal Id:** 141  
**Location:** REST  
**Magnification:** 0.220148  
**Tissue:**  
**CD Number:** 77  
**Notes:** 496 41VRP5.TIF 7days(1+6days\_O2) section red\_green\_cone\_opsin vimentin none 0.2201479 2 muller redgreen 9-27-01 77 141 REST RetinalImage

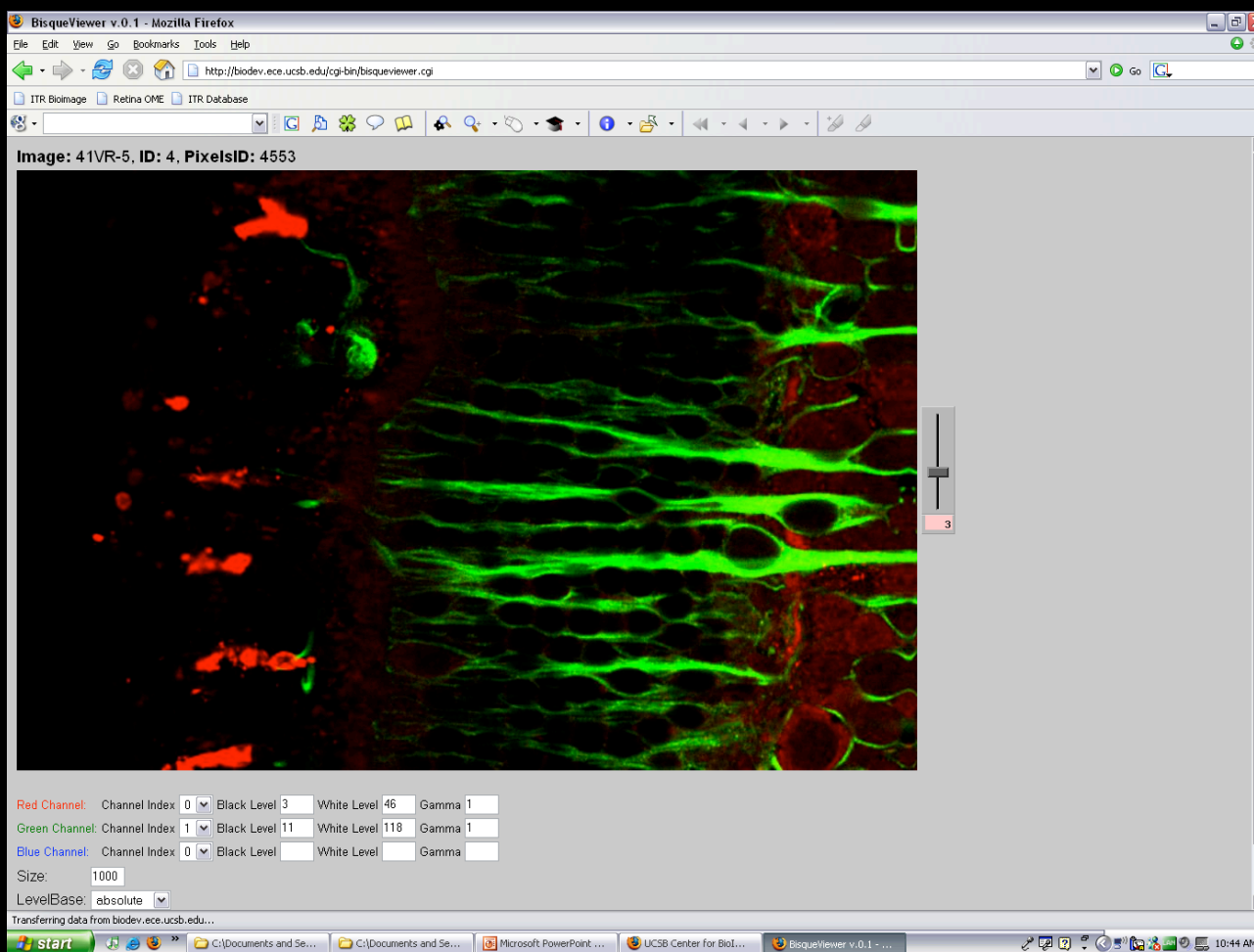
---

 **Image:** 41VR-3  
**Retinal Condition:** 7days(1+6days\_O2)  
**View:** section  
**Red Cell:** muller  
**Green Cell:** redgreen  
**Blue Cell:**  
**Red:** red\_green\_cone\_opsin  
**Green:** vimentin  
**Blue:**  
**Species:**  
**Animal Id:** 141  
**Location:** REST  
**Magnification:** 0.236659  
**Tissue:**  
**CD Number:** 77  
**Notes:** 522 41VRP3.TIF 7days(1+6days\_O2) section red\_green\_cone\_opsin vimentin none 0.236659 2 muller

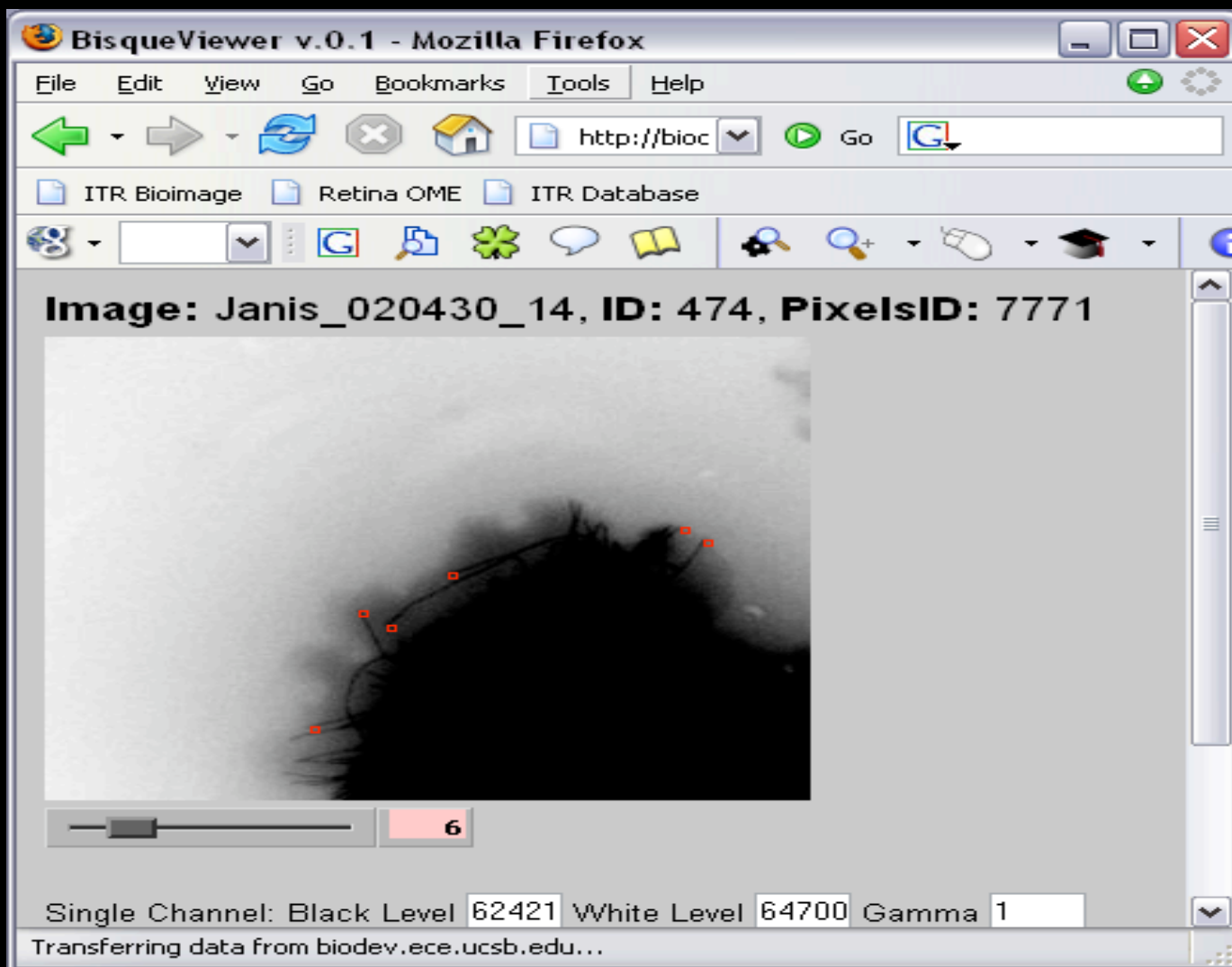
Transferring data from biodev.ece.ucsb.edu...

start C:\Documents and Se... C:\Documents and Se... Microsoft PowerPoint... UCSB Center for BioI... 10:42 AM

# Screenshots (5D Viewer)



# Screenshot (5D with tracks)



May 2007


UCSB Center for Bioimage Informatics - Mozilla Firefox

File Edit View History Bookmarks Tools Help

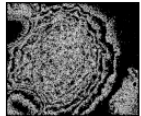
http://biodev.ece.ucsb.edu/cgi-bin/serve.pl

Local

Google Search PageRank ABC Check AutoLink AutoFill Subscribe Options



Other Pixels



Tag: Binarized  
X,Y,Z,T,C: (600, 512, 1, 31, 1)

Parameters are as following:  
 PkgName: Default  
 Growth Rate: 2  
 Shortening Rate: 2  
 G\_length: 1  
 S\_length: 0.5  
 A\_length: 15  
 Save\_flag: Off

Microtubule Track Analysis

1 microtubules are being tracked

475A282A0=509A215A4.2=509A216A8.2=506A218A12.2=509A214A16.2=510A214A20.2=509A215A24.2=509A213A28.2=509A213A32.2=  
 mt\_ID:100569

Event	Begin	End
U	4.2	44.2
D	44.2	68.2
U	68.2	100.2
A	100.2	112.2

Growth			Shortening			ATTEN/Undef			CAT RESCUE 1 1
Rate	DUR	LENGTH	Rate	DUR	LENGTH	Rate	DUR	LENGTH	
19.313	0.40	7.725	0.280	0.67	0.187	4.564	0.53	2.434	
			0.660	0.20	0.132				

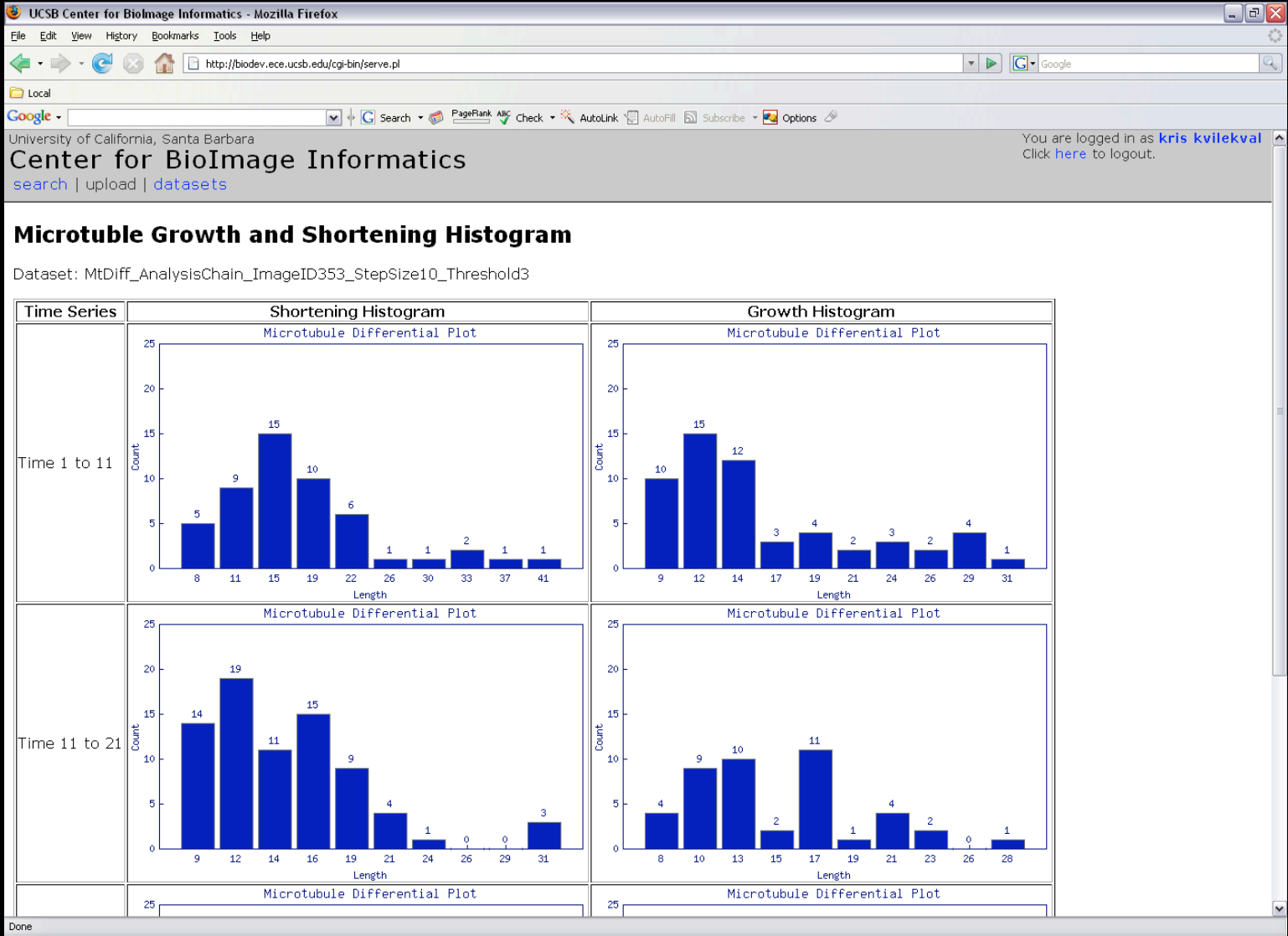
Microtubule Life Plot

Done





# MT Global Dynamics



- 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 1<sup>st</sup> 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

# 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

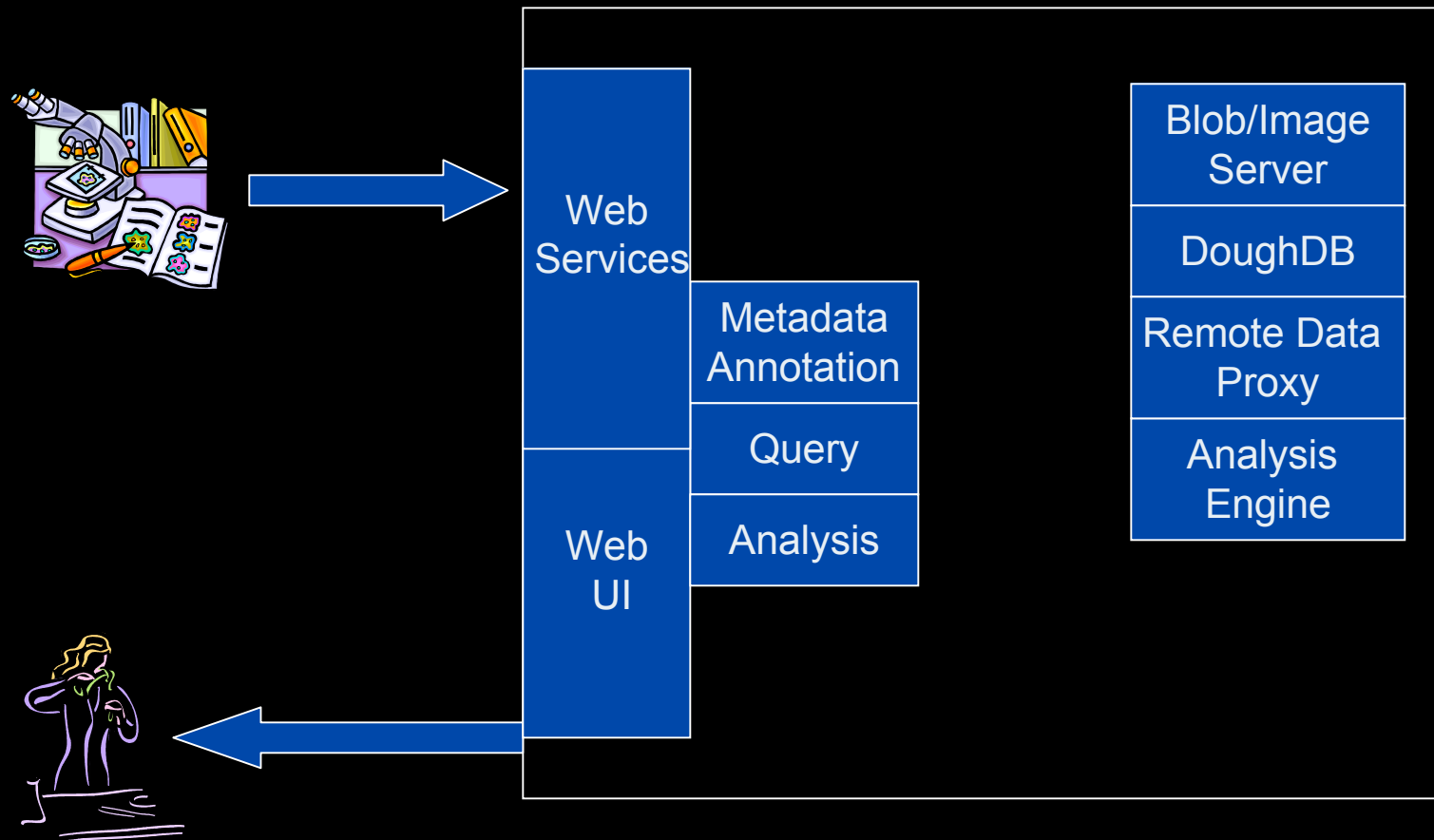
- Allow researchers to add data sets with minimal help of engineers
  - Metadata is often a (changing) list of experimental parameters
- Give analysis writers easy access to data
- Integrate data and analysis access to other systems:
  - OME
  - PSLID
- Build on previous system (BISQUE/OME)



# 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

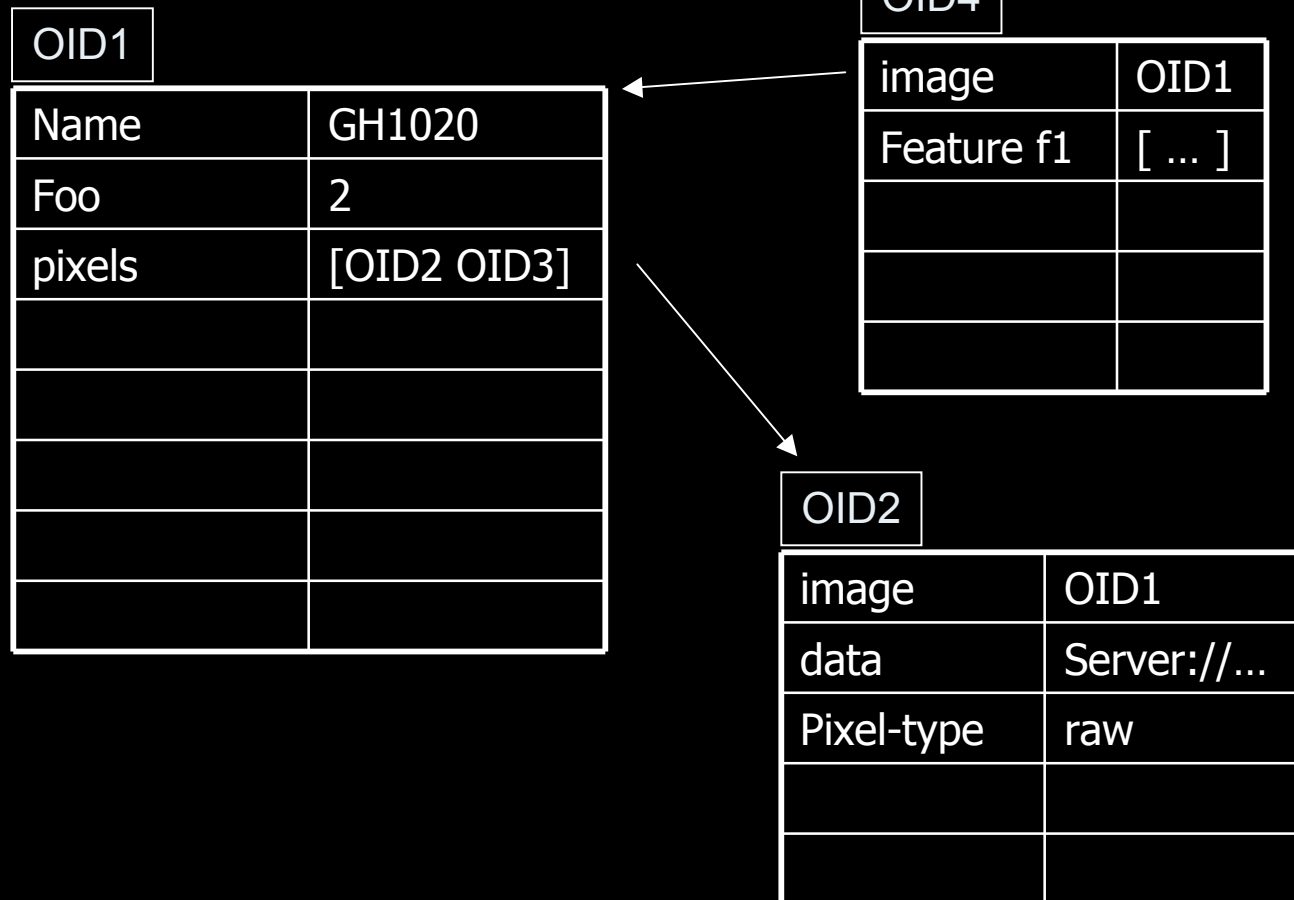
# Components



# 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

# Bisquik: DoughDB



# 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  $I_2(r.f1, r1[ \dots ]) < 10$

# 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

# Simple annotation

UCSB Center for BiImage Informatics - Mozilla Firefox

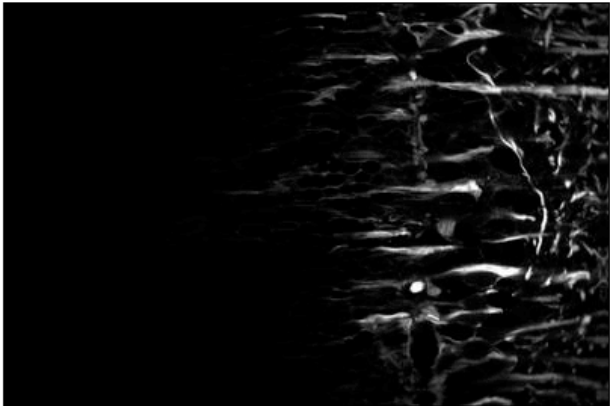
File Edit View History Bookmarks Tools Help

http://arno.ece.ucsb.edu:8080/bisquik/image?resource=/images/13

Local BISQUE Bisquik Development

Google Search PageRank Check AutoLink AutoFill Subscribe Options

+ - edit



0

name	AAA	^vX
GObject	/gobjects/26	^vX
description	retinal	^vX
type	aaa	^vX
condition	3 day	^vX

add tag/value pair add from template

Save Cancel Delete

Done

# Region annotation

The screenshot shows a web browser window titled "Bisque - Iceweasel" with the URL `http://oib.ece.ucsb.edu/bisquik/`. The browser's address bar and menu bar are visible. The page content includes the University of California, Santa Barbara logo and the text "Center for BioImage Informatics". A user is logged in as "kris kvilekval" with a last login date of "Monday, February 5, 2007". A "search | upload | login" menu is present. The main content area displays a microscopy image with a region of interest highlighted in yellow. A dialog box is open over the image, containing a "Comment" field with the text "anoth", a "Save" button, and a "Cancel" button. The dialog also includes a "Comment" label, a "Interesting comment" label, and a "add tag/value pair" button. Below the dialog, a red message states "No tags for this, click to add one." The footer of the page contains the text "University of California at Santa Barbara, Santa Barbara, CA 93106. Based on Bisque/OME. For problems or questions regarding this web application contact august((at))develop\_dot\_ment\_dot\_org".

May 2007

# Search (metadata)

UCSB Center for BioImage Informatics - Mozilla Firefox

File Edit View History Bookmarks Tools Help

http://arno.ece.ucsb.edu:8080/bisque/search

Local BISQUE Bisquik Development

Google Search PageRank Check AutoLink AutoFill Subscribe Options

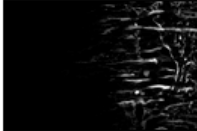
University of California, Santa Barbara Please [login](#)

## Center for BioImage Informatics

Click [here](#) to logout.

name: AA\* search upload

---

 **name:** AAA **1**  
**description:** A  
**GObject:** /gobjects/26  
**type:** aaa

---

University of California at Santa Barbara, Santa Barbara, CA 93106.  
Based on [Bisque/OME](#). For problems or questions regarding this  
web application, contact [bisque-dev@biodev.ece.ucsb.edu](mailto:bisque-dev@biodev.ece.ucsb.edu).

Done

# Segmentation Analysis

UCSB Center for BioImage Informatics - Mozilla Firefox

File Edit View History Bookmarks Tools Help

http://asimo.ece.ucsb.edu:8080/bisque/image?resource=/images/79

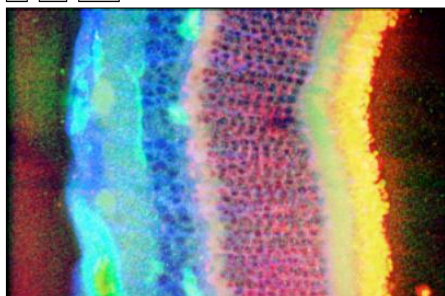
Local

Google Search PageFlink ABC Check AutoLink AutoFill Subscribe Options

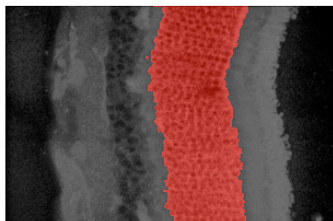
University of California, Santa Barbara Please [login](#)

Center for BioImage Informatics Click [here](#) to logout.

search [upload](#)



mask: /images/92  
name:  
description:  
reference: /images/22



- ONL
- IS
- OS
- ML

University of California at Santa Barbara, Santa Barbara, CA 93106.  
Based on [Bisque/OME](#). For problems or questions regarding this  
web application, contact [bisque-dev\(\(at\)\)biodev.ece.ucsb.edu](mailto:bisque-dev((at))biodev.ece.ucsb.edu).

Done



UCSB Center for BioImage Informatics - Mozilla Firefox

File Edit View History Bookmarks Tools Help

http://asimo.ece.ucsb.edu:8080/bisque/search?query=&tg\_paginate\_limit=10&tg\_paginate\_no=3

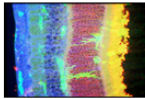
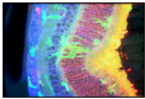


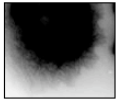
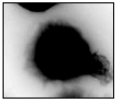
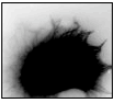
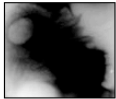
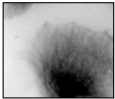
Local

Google Search PageRank ABC Check AutoLink AutoFill Subscribe Options

University of California, Santa Barbara Please [login](#)

## Center for BioImage Informatics

[upload](#) Click [here](#) to logout.

	<b>name:</b> <b>description:</b> <b>reference:</b> /images/22 <b>mask:</b> /images/130		<b>name:</b> <b>description:</b> <b>reference:</b> /images/22			1 2 3 4
					<b>microtubule:</b> /microtubule/1058 <b>microtubule:</b> /microtubule/1100 <b>microtubule:</b> /microtubule/1131	
	<b>microtubule:</b> /microtubule/1146					

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Based on [Bisque/OME](#). For problems or questions regarding this web application, contact [bisque-dev@biodev.ece.ucsb.edu](mailto:bisque-dev@biodev.ece.ucsb.edu).

Done

# 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

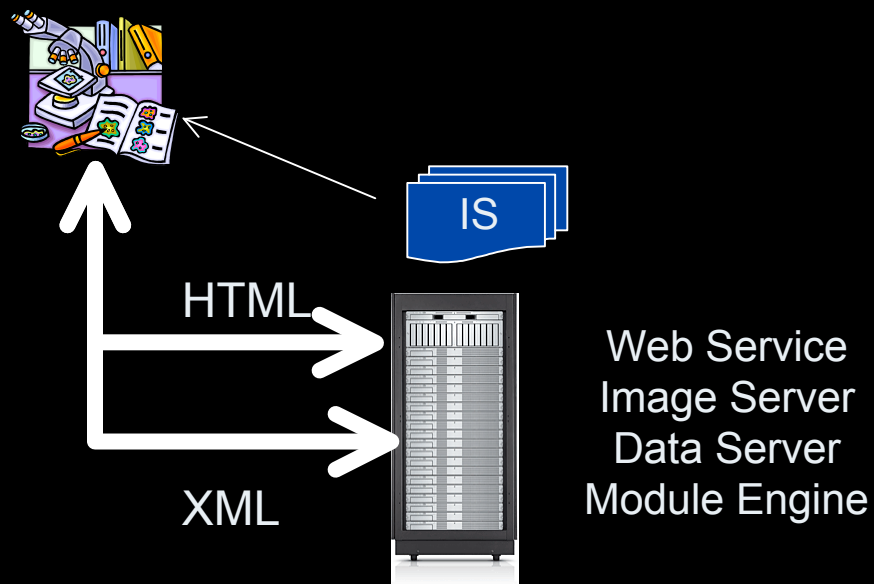
# Blob+Image server

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

- 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

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

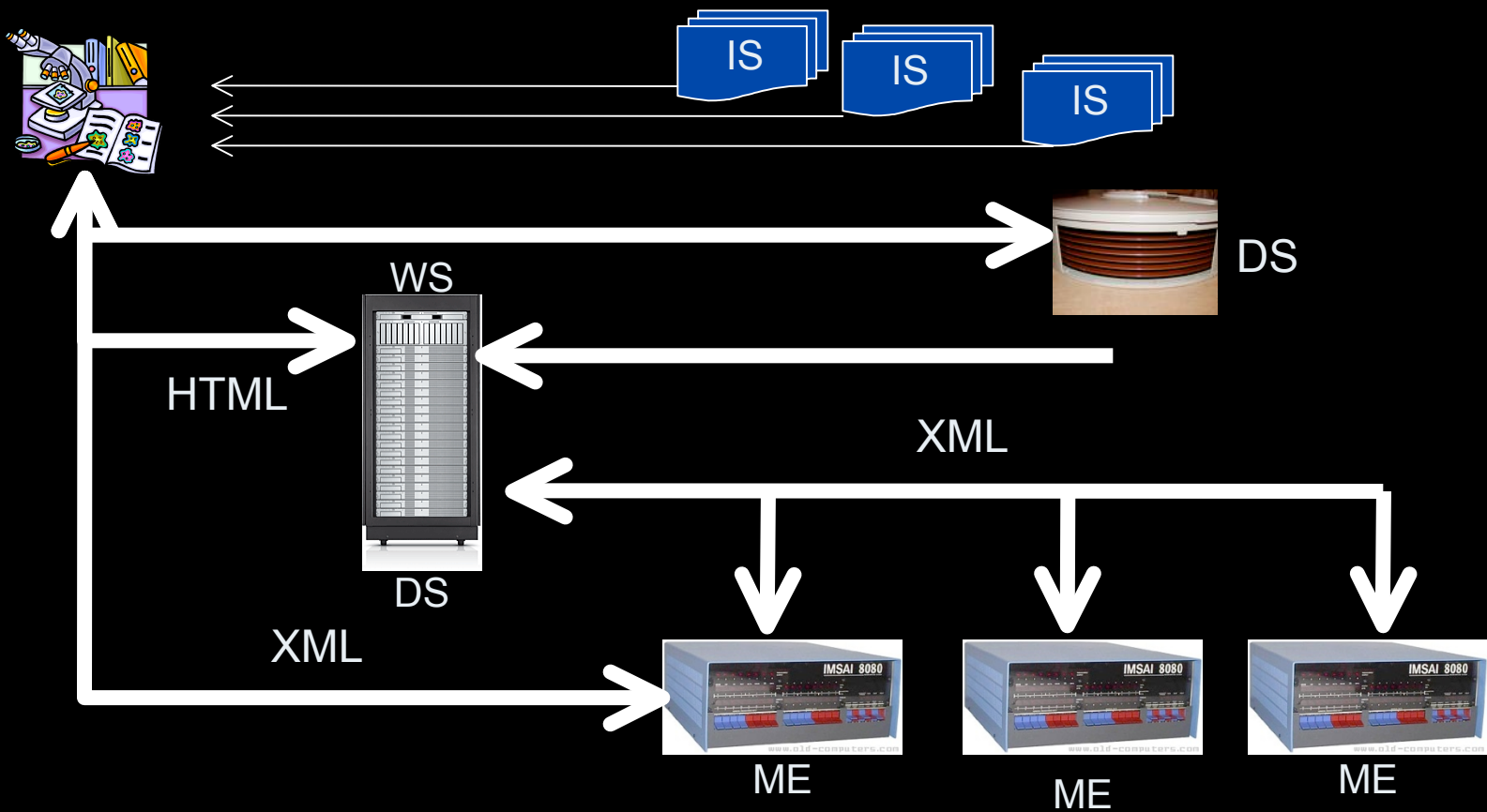
# Simple deployment



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

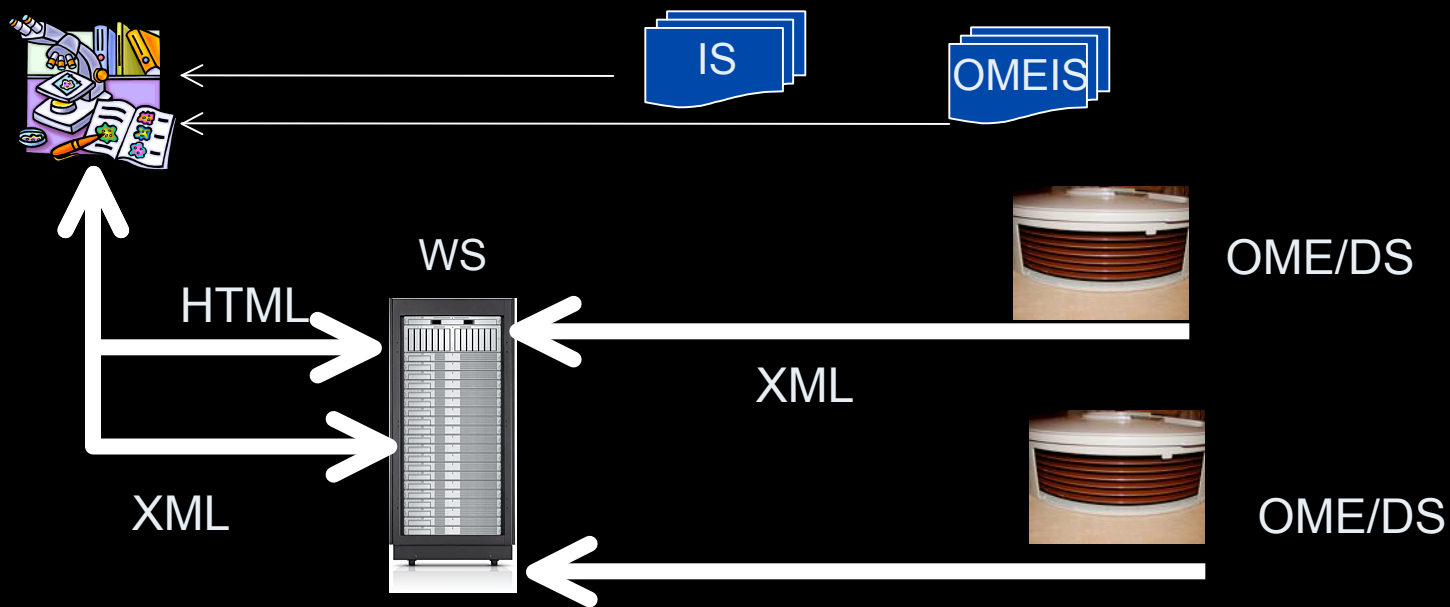
RC – Rich Client    WS-web server    IS - Image Server    DS – Data Server  
MS - Module Scheduler    ME – Module Engine

# Scalable services



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

# 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](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)

- 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

- 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 Rittenberg