



Gestion du cycle de vie des images en microscopie pour la biologie:

Extraction de connaissances à partir d'une base de données images

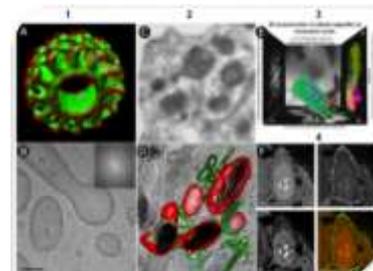
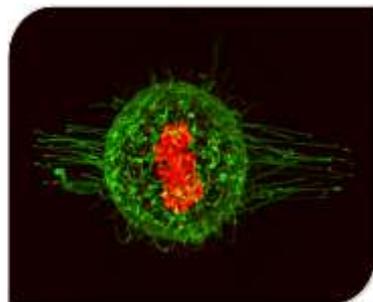


Problématique de la gestion de données image en microscopie pour la biologie

- **Définition des besoins et contexte.**
- **Formats et outils de gestion de données disponibles, base de données images ouvertes.**
- **Création du data center Curie, choix d'une collaboration avec une compagnie.**
- **Exemple d'utilisation et de partage dans le cadre de projet, et dans le cadre de données rendues publiques.**
- **Exploitation de la base de données**
- **Questions ouvertes**

Une plateforme de données hétérogènes: 200 To par an):

Cell & Tissue Imaging Facility PICT Institut Curie



Photonic

16 confocal laser scanning or spinning disk microscopes (3 equipped with femtosecond pulsed laser for multiphoton excitation, + laser photoperturbation modules),

- 8 video-microscopes,
- 3 3D deconvolution microscopes,
- 2 TIRF systems (with FRAP or PALM techniques),
- 2 FLIM systems (TCSPC and phase modulation),
- 2 high-resolution structured illumination microscopes (OMX and Nikon HR-SIM),
- 2 optical sectioning Zeiss Apotome systems
- new in 2015: 2 SPIM, une salle d'imagerie intravitale petit animal (multiphoton)
- several standard widefield microscopes for routine observation or histology.

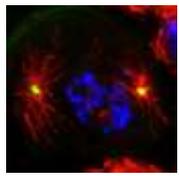
Electronic

4 electron microscopes (Cryo electron microscopy Cryotomography Cellular tomography, Transmission electron microscopy)

Ion spectroscopy

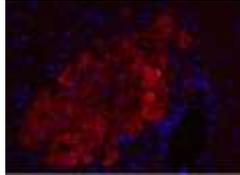
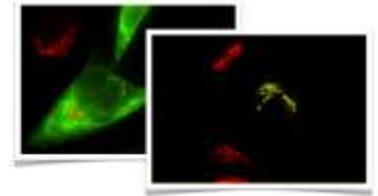
HCS: 2 InCell systems + Compound Libraries

Dans un contexte de questions scientifiques hétérogènes: ex: UMR144



Biology of centrosomes and Cilia BASTO

Dynamics of Intra-Cellular Organization PEREZ



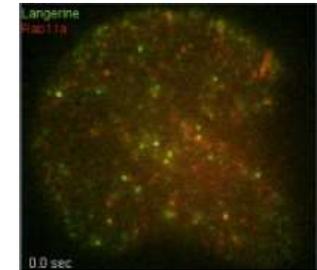
Morphogenesis and intracellular signalling LOUVARD

Biologie cellulaire systémique de la polarité et de la division PIEL



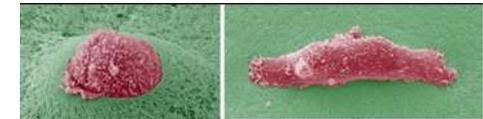
Biophysical and molecular basis of cell adhesion and migration DUFOUR

Space-time imaging of cellular dynamics of organelles and endomembranes SALAMERO



Cytoskeletal Architecture and Cellular Morphogenesis TRAN

Membrane and cytoskeleton dynamics CHAVRIER



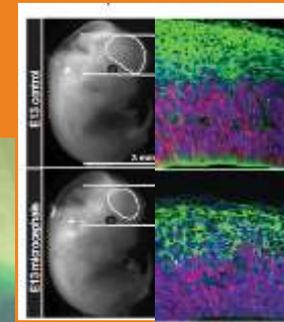
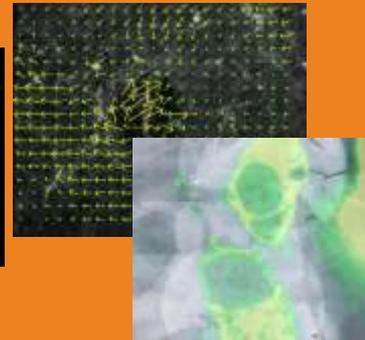
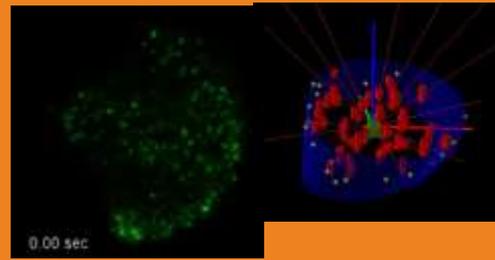
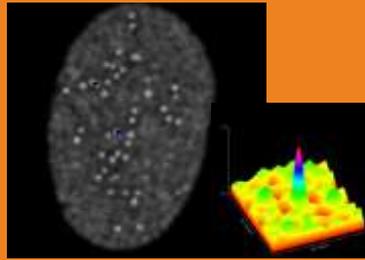
Traffic, Signaling and Delivery JOHANNES

Structure and Membrane Compartments RAPOSO



...

Example of Methods using bio image informatics for cell biology from microscopy



**Molecular dynamics/
Functional Imaging**

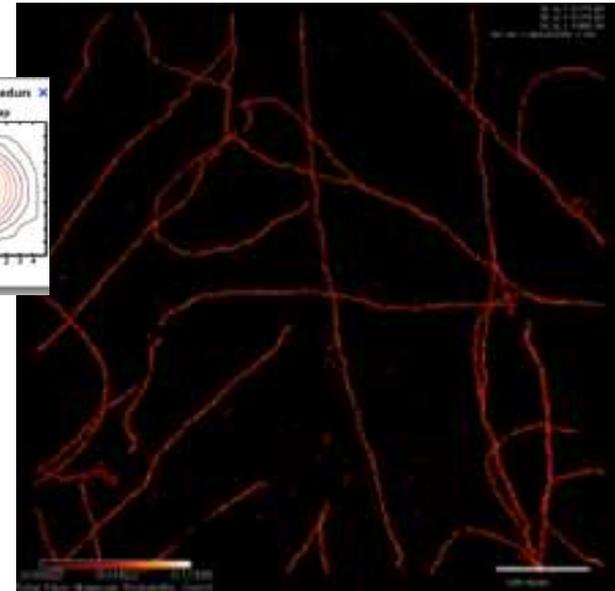
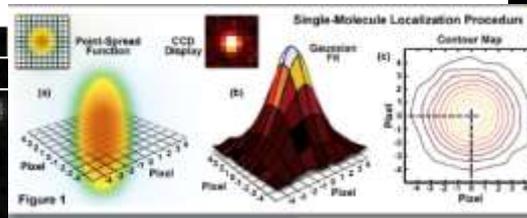
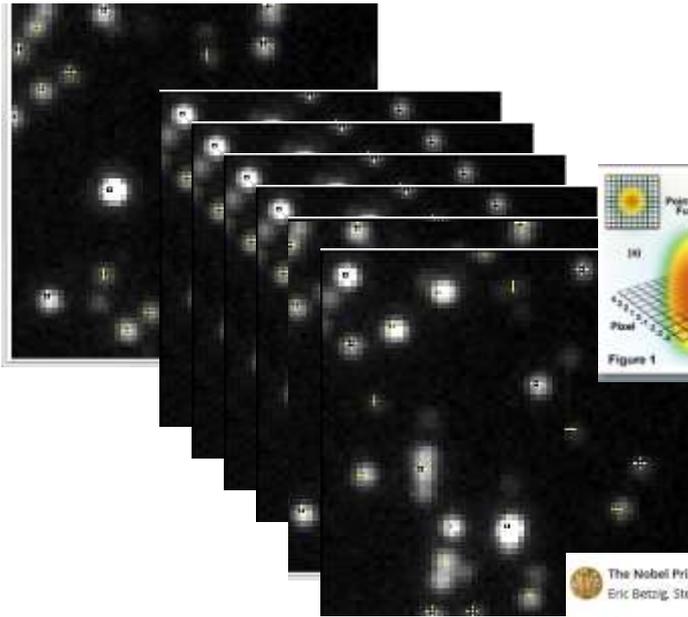
**Single cells studies:
never single -> cell
normalisation**

**Deformation
quantification and
registration
(Correlative
Microscopy)**

**Computational model
of embryonic brain
development.**

Exemple of imaging modalities: HR microscopy

Experimental sequence of 27 529 frames
(128x128 pixels) 16 bits for 1 final image : 1
GO



The Nobel Prize In Chemistry 2014
Eric Betzig, Stefan W. Hell, William E. Moerner

Share this:

The Nobel Prize in Chemistry 2014



Photo: Matt Steingard/HMML
Eric Betzig
Prize share: 1/3



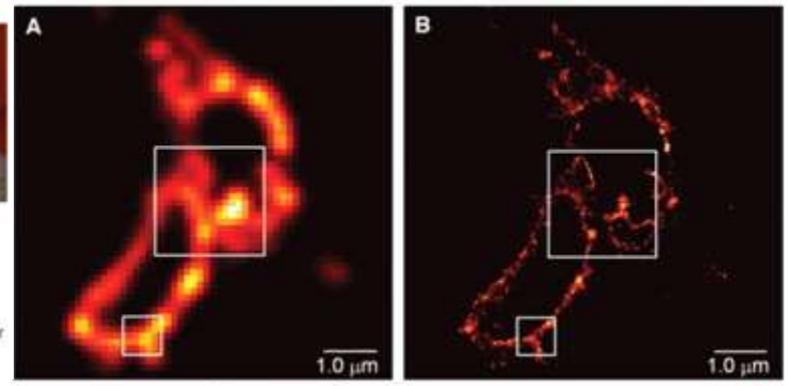
© Bernd Schulze, Max-Planck-Institut
Stefan W. Hell
Prize share: 1/3



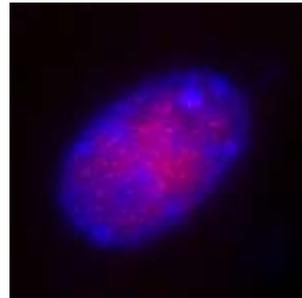
Photo: E. Lueder via Wikimedia Commons, CC-BY-SA-3.0
William E. Moerner
Prize share: 1/3

The Nobel Prize in Chemistry 2014 was awarded jointly to Eric Betzig, Stefan W. Hell and William E. Moerner "for the development of super-resolved fluorescence microscopy".

PALM etc.. Based on,
Blinking fluorescent
proteins

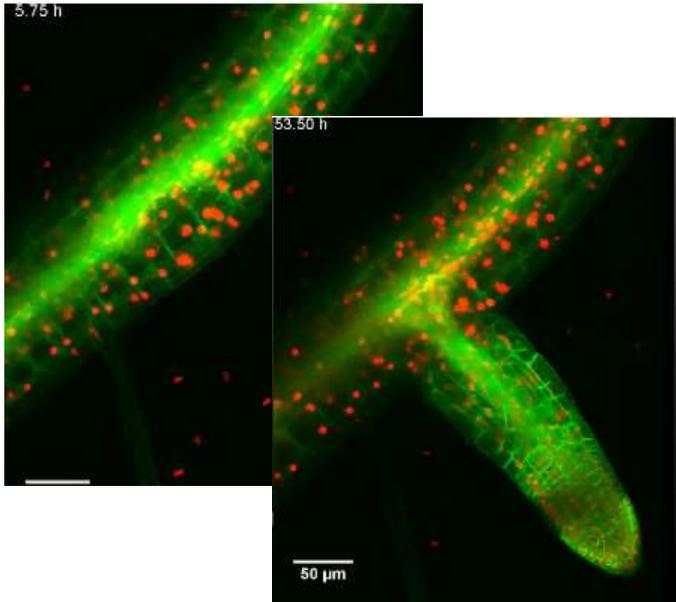
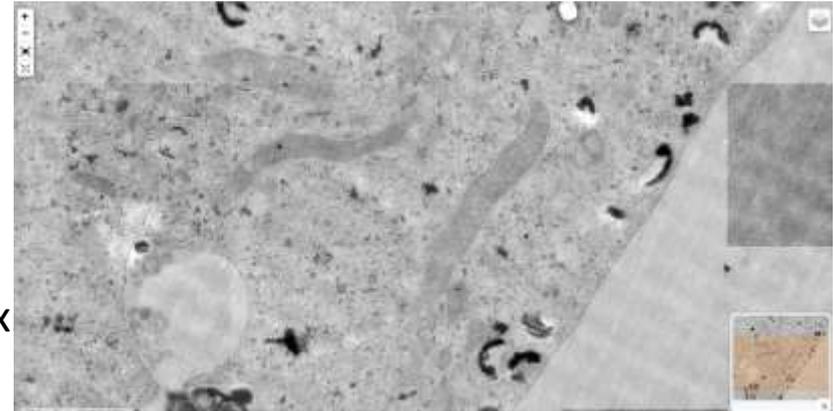


Nd-Images

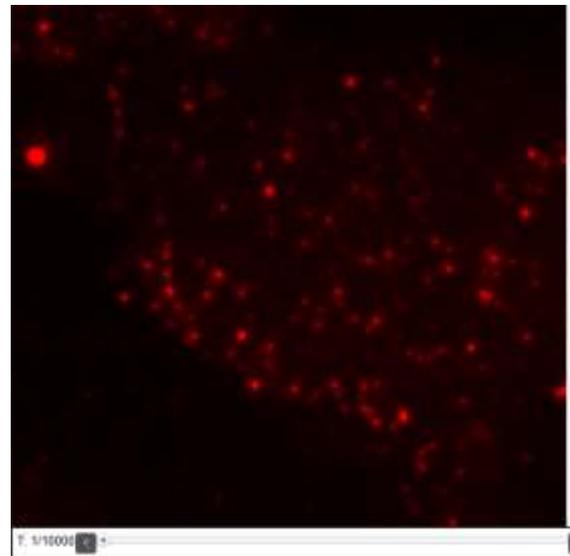


WF 384x384x50x
colorsx2 bytes
=29.5 MB

10000x10000x1 byte =100 MB



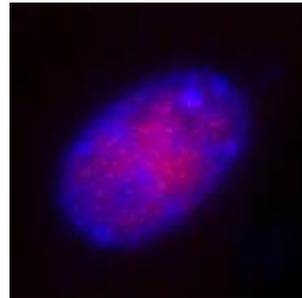
1040x1288x20x300x2
colorsx2 bytes =3.214GB
CIL:40982



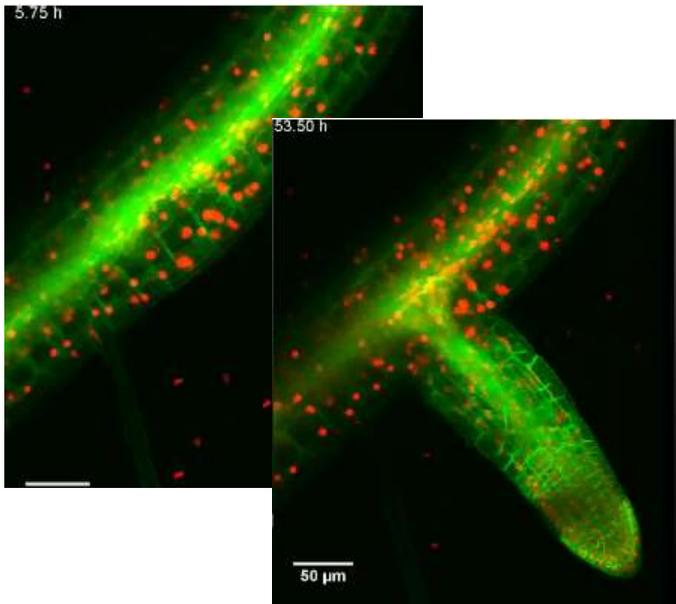
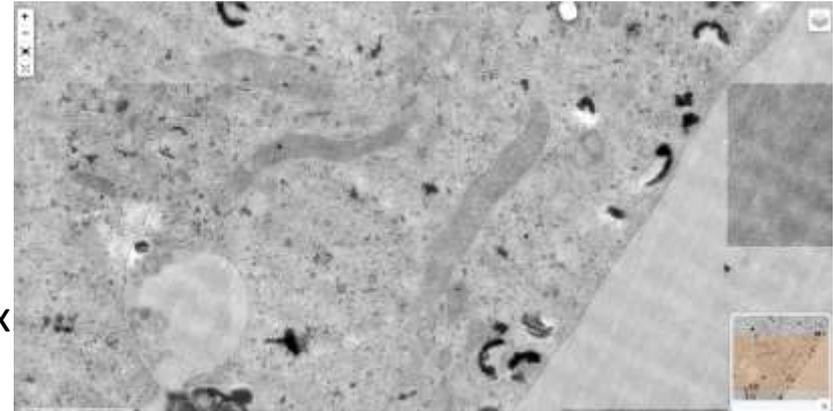
Palm Data
197*188*10000*2
bytes= 740MB

Nd-Images And co.

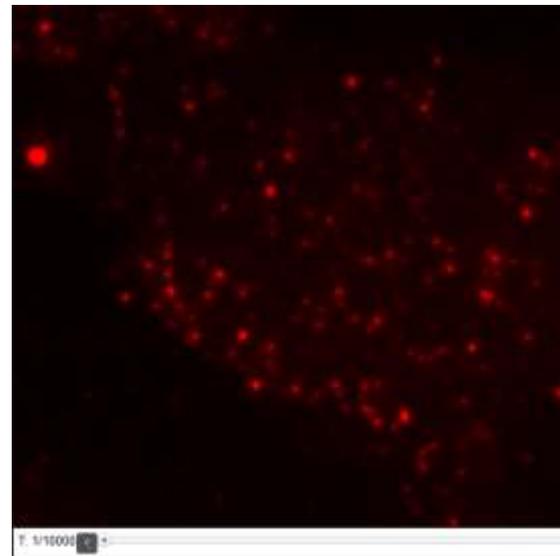
10000x10000x1 byte =100 MB + **3D reconstruction+ mosaick**



WF 384x384x50x
colorsx2 bytes
=29.5 MB + **3D deconvolution**

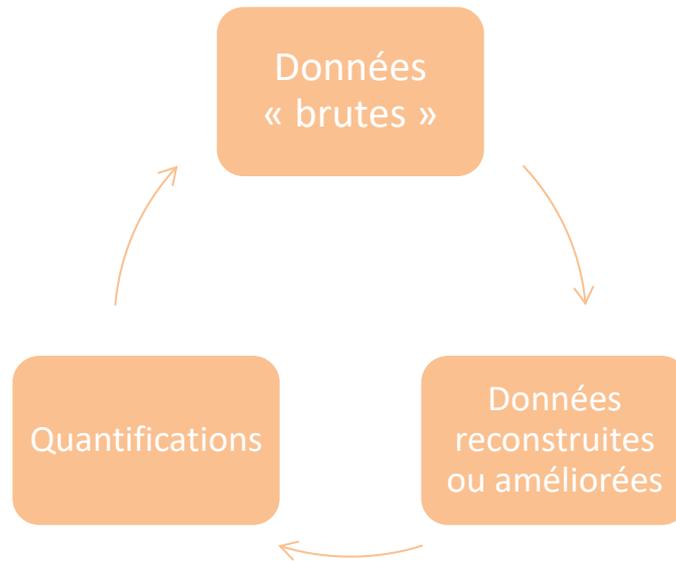


1040x1288x20x300x2
colorsx2 bytes =3.214GB
+ **Reconstructed Spim Data**



Palm Data
197*188*10000*2
bytes= 740MB
+ **reconstructed image+ intermediate detection**

-> Un traitement des données indissociables des données brutes.



-> **Données mieux résolues, diminution de la phototoxicité, imagerie multimodale (corrélative)**

Passage à l'unité de mesure d'archivage au Peta Octet

-> **Garantir l'accès aux données 5 ans après publication (responsabilité de l'utilisateur mais aussi de la plateforme?)**

2 types de besoins

Donner un accès publique mais sécurisé (cf. Recommandations BioMedBridges)

Gérer la production et l'analyse de données « de travail » produites sur une plateforme

The Bio-Formats Library

Bio-Formats, the solution for reading proprietary microscopy image data and metadata.



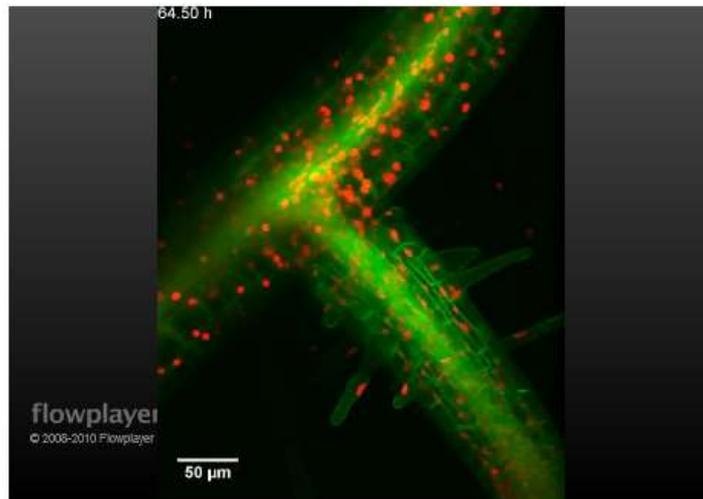
Bio-Formats is a software tool for reading and writing image data using standardized, open formats. Bio-Formats is a community driven project with a standardized application interface that supports open source analysis programs like [ImageJ](#), [CellProfiler](#) and [Icy](#), informatics solutions like [OMERO](#) and the [JCB DataViewer](#), and commercial programs like [Matlab](#).

Bio-Formats is developed by the Open Microscopy Environment consortium, including development teams at [LOCI at the University of Wisconsin-Madison](#), [University of Dundee](#) and [Glencoe Software](#). Licensing and citing information is on the [OME licensing page](#).

Bio-Formats currently reads and converts more than 120 [file formats](#) to the [OME-TIFF](#) data standard.



Available resources for biological images



Video Data Download Options...

Licensing



Attribution Non-Commercial; No Derivatives: This image is licensed under a Creative Commons Attribution, Non-Commercial, No Derivatives License. [View License Deed](#) | [View Legal Code](#)



Comments:

Add to Photobox

CIL:40982*

Description

A video of *Arabidopsis thaliana* showing a lateral root growing out of the primary root. *Arabidopsis thaliana* is widely used as a model organism in plant biology. This movie is created from image stacks recorded every 15 minutes over a period of 75 hours using digital scanned light-sheet microscopy. Second Prize, 2011 Olympus BioScapes Digital Imaging Competition®.

Technical Details



Biological Sources

NCBI Organism Classification

· *Arabidopsis thaliana* 
(thale cress)

Cellular Component

· plant-type cell wall
· male germ cell nucleus

Biological Context

Biological Process

· lateral root formation
· root development

Attribution

Imaging

Image Type

· recorded image

Imaging Mode

· scanned sheet microscopy
· fluorescence microscopy

Parameters Imaged

· fluorescence emission

Source of Contrast

· distribution of a specific protein

Processing History

· z-stack reconstruction

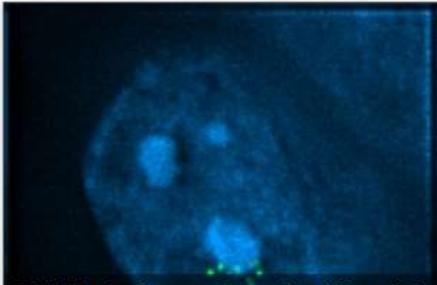
Sample Preparation

Available resources for biological images

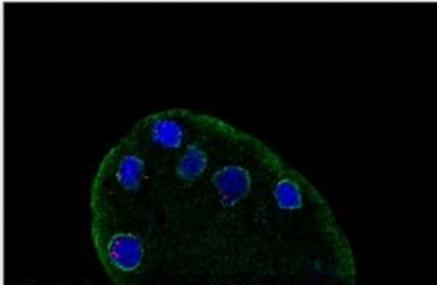
JCB Data Viewer [Home](#) [About](#) [Contact](#) **JCB** | [log in](#)

Welcome to the JCB DataViewer! The JCB DataViewer facilitates viewing, analysis, and sharing of multi-dimensional image data associated with articles published in *The Journal of Cell Biology*.

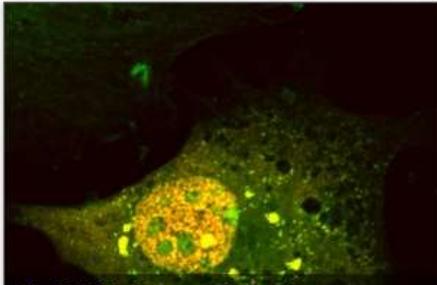
View



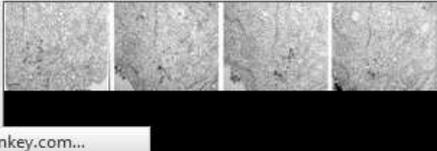
β -Globin cis-elements determine differential nuclear targeting through epigenetic modifications
Qian Bian, Nimish Khanna, Jurgis Alvikas, Andrew S. Belmont
jcb. 2013. 203:767-783 DOI: 10.1083/jcb.201305027.

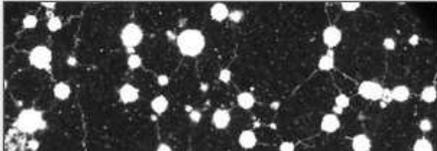


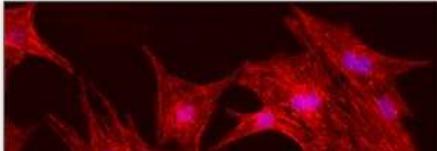
The shelterin protein POT-1 anchors Caenorhabditis elegans telomeres through SUN-1 at the nuclear periphery
Helder C. Ferreira, Benjamin D. Towbin, Thibaud Jegou, Susan M. Gasser
jcb. 2013. 203:727-735 DOI: 10.1083/jcb.201307181.



The RNA-binding protein Fus directs translation of localized mRNAs in APC-RNP granules
Kyota Yasuda, (...), Stavroula Mili
jcb. 2013. 203:737-746 DOI: 10.1083/jcb.201306058.







ente de www.surveymonkey.com...

Why do computer scientist needs access to sample annotated images

material to work/test/assess (CHALLENGES)

ACCESS to what other used (also processing)

BIII.info

+ taggathon

biii info: Bioimage Information Index
biii info/ • Traduire cette page
BIII is a website for organizing bioimage analysis resources. We manually edit following pages, for you to search tools, workflows and functions for bioimage ...
Vous avez consulté cette page de nombreuses fois. Date de la dernière visite: 15/12/14

- Workflows**
Home / Workflows: Workflows
Recent Edits: Bio-Image ...
- Languages**
Languages used for bio image informatics (click for details) ...
- RoadMap**
A tentative roadmap of BIII: Phase 0 (done), Tagging using the ...
- EuBIAS**
EuBIAS Manifesto: Date: June 19, 2013, Authors: Kota Mitura ...
- Components**
... new account - Request new password - Home / Components ...
- Forum**
Ported to Drupal by Drupalizing a Project of More than (just ...
- tissue**
Plot the centroid tracks and area evolution of the cells of a tissue ...
- About**
What BIII can do for you, what you can do for BIII. Existing software ...
- Feed aggregator**
Ported to Drupal by Drupalizing a Project of More than (just ...
- Software**
NeuronStudio, Susan L. Wearna Principal Investigator Patrick R ...

[Autres résultats sur biii info »](#)

Création d'une base d'outils et workflow logiciels , avec des données tests associées (vers du benchmarking?)

Available resources for biological images

Broad Bioimage Benchmark Collection

Annotated biological image sets for testing and validation



Introduction

Image sets

Benchmarking

Contribute

LEGEND: ABBRS OF IMAGE TYPES

- Counts
- Foreground/background
- Outlines of objects
- Biological labels

Image sets

Identification and segmentation

Accession	Description	Mode	Fields	Ground truth
BBBC001	Human HT29 colon-cancer cells	Fluorescent	8	
BBBC002	Drosophila Kc167 cells	Fluorescent	50	
BBBC003	Mouse embryos	DIC	15	
BBBC004	Synthetic cells	Fluorescent	100	
BBBC005	Synthetic cells	Fluorescent	19,200	
BBBC006	Human U2OS cells (out of focus)	Fluorescent	52,204	
BBBC007	Drosophila Kc167 cells	Fluorescent	16	
BBBC008	Human HT29 colon-cancer cells	Fluorescent	12	
BBBC009	Human red blood cells	DIC	5	
BBBC010	C. elegans live/dead assay (uneven illumination)	Bright field and fluorescence	384	

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Data

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[University](#)
[Labs](#)
[Center for Computational Biology](#)
[Center for Biomedical Informatics](#)
[Department of Biological Sciences](#)
[Department of Chemical and Biomolecular Engineering](#)

Most important

[2D HeLa](#)
[3D HeLa](#)
[2D 3T3 RT Set1](#)
[2D 3T3 RT Set2](#)
[3D 3T3](#)

Other Datasets

Raw and processed image collections
[2D CHO](#)
[2D 3T3 RT Set1](#)
[2D 3T3 RT Set2](#)
[3D UCE](#)
 Hand-labeled image collections
[2D 3T3 and U2OS segmented nuclei](#)
 Other collections
[UCSF yeast GFP images](#)

Supplementary Data

[BBBC 2006 SimEC2](#)
[ISMB 2007 Yeast Image Classification](#)
[Cytometry 2007 Generative Models](#)

[2D images of 3T3 and U2OS cells hand-segmented to show nuclear boundaries](#)

L.P. Coelho, A. Sharif and R. F. Murphy (2009). Nuclear segmentation in microscope cell images: A hand-segmented dataset and comparison of algorithms. Proceedings of the 2009 IEEE International Symposium on Biomedical Imaging (ISBI 2009), p. 518-521.

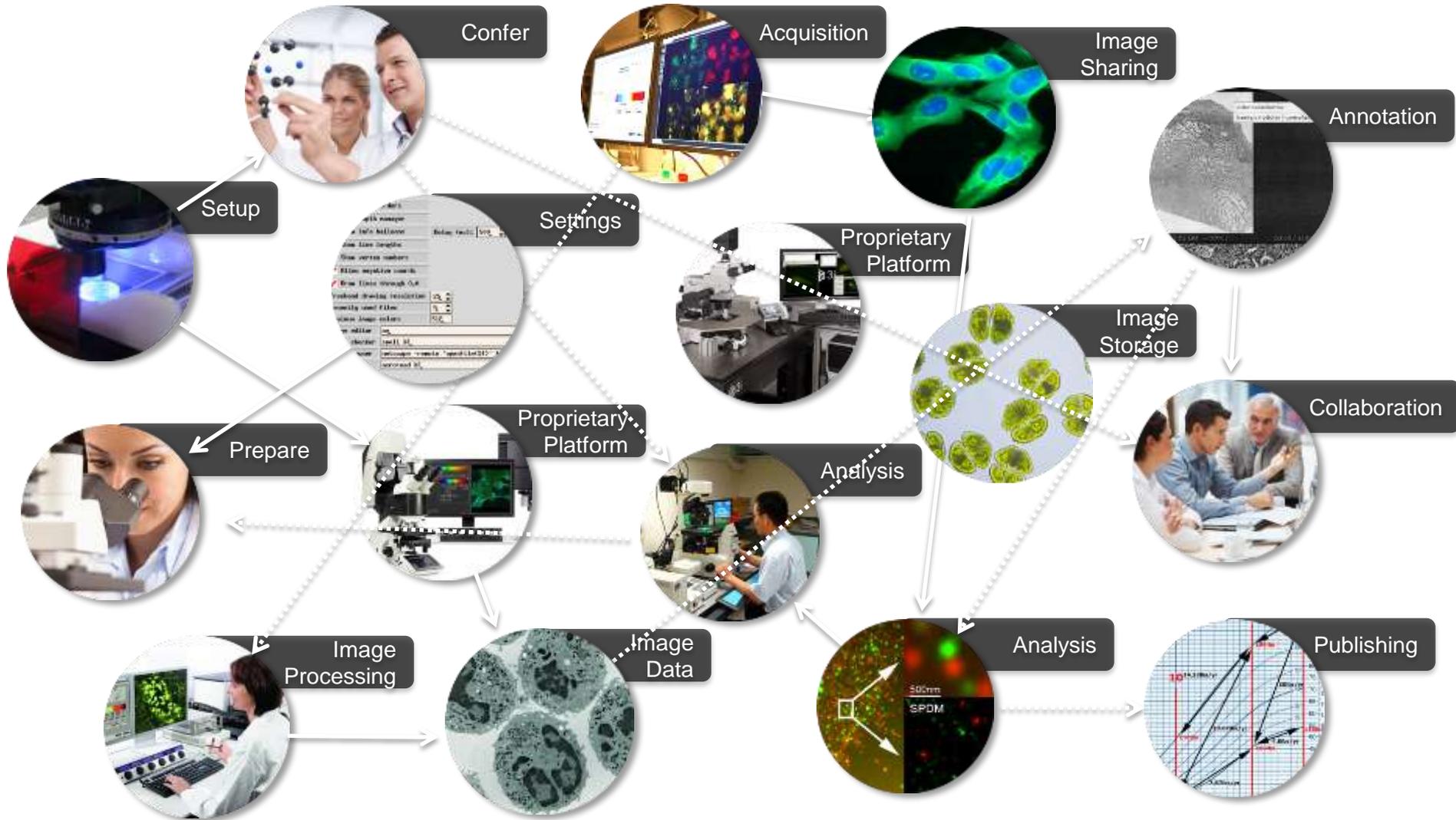
[Supplementary Data for Cytometry generative models paper](#)

T. Zhao and R.F. Murphy (2007). Automated learning of generative models for subcellular location. Building Blocks for system biology. Cytometry 71A:978-990.

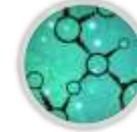
[Supplementary Data for ISMB/ECCB 2007 Yeast Image Classification paper](#)



Researchers deal with huge data and complex analysis workflows



Requirements for Image data base software



FRANCE-BIOIMAGING

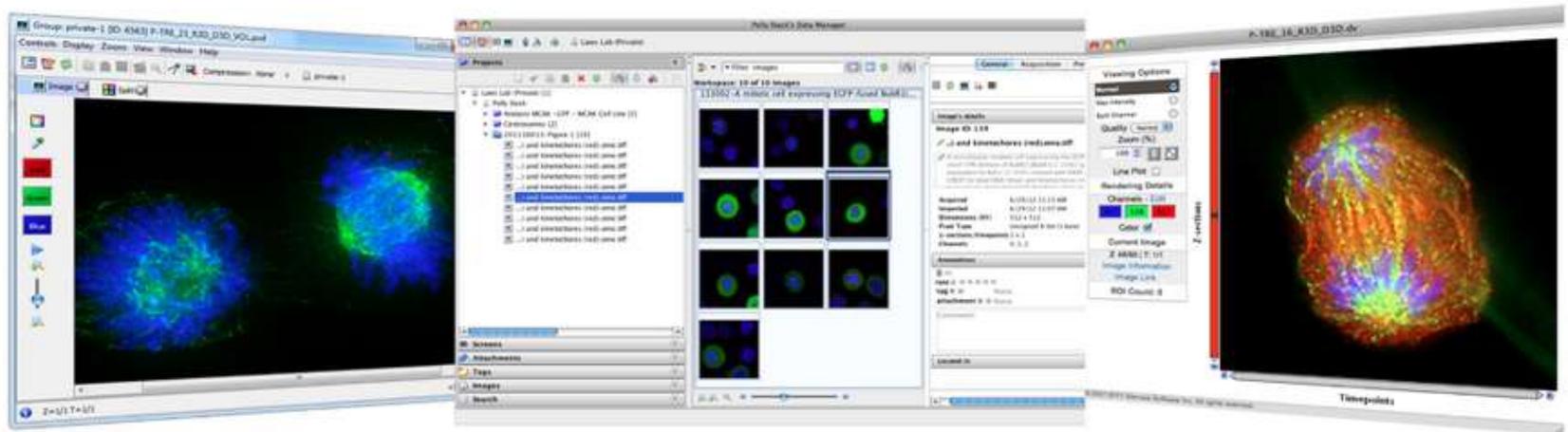
	Montpellier RIO Imaging WIDE	Institut Curie	Institut Interdisciplinaire des Neurosciences, Bordeaux Imaging Center, Bordeaux	IJM	Plateforme Bioemergences	synthèse minimale
Structure Plateforme						
Nombre d'utilisateurs (2011)	environ 600 actifs distribués sur différents sites (12 sites) 10 % venant du secteur privé	400 dont environ 10% externes	environ 100, dont un 20aine en SPT (Gros utilisateurs)	250	20	entre 100 et 1000 dont utilisateurs temporaires
Production annuelle (2011)	> 10 To (devrait augmenter)	>100 To (y compris données traitées)	>50 To (beaucoup de SPT, grosse bande passante : 20Go/h/poste)	>15 To/an pour 10 microscopes (devrais augmenter)	5 To	au minimum 100 to
Production à archiver archivage=archivage à long terme		Seulement un % de la production annuelle: données publiées et Gold standards. Durée de conservation: 4 ans après publication pour données publiées, sûrement plus pour Gold Standard/			100%	Cycle de vie des données: actives, archivées, supprimées.
remarques particulières	Plusieurs sites sur Montpellier	Multi site (Orsay et Paris)			Multi site	Fluidité entre les différents sites. Transparence des sites / projets. Une seule interface pour tous les projets quelque soit le site d'acquisition d'origine. Les données ne sont pas dupliquées et sont au plus près de l'utilisateur (projet) ou des traitements.

OMERO/ OMERO via Glencoe

About OMERO

What is OMERO?

From the microscope to publication, OMERO handles all your images in a secure central repository. You can view, organize, analyze and share your data from anywhere you have internet access. Work with your images from a desktop app (Windows, Mac or Linux), from the web or from 3rd party software.



Import

Over 100 file formats supported, including all major microscope formats.

Organize

Organize by 'Project', 'Tags' or acquisition date. Annotate with attachments, comments, ratings.

View

Move through multiple dimensions, copy and apply rendering settings, zoom and pan 'Big' images.

Analyze

Draw and measure regions of interest, write Python scripts in OMERO or connect to OMERO from your favorite analysis software.

Export

Export your images for analysis or publication. Save images as 'figures' ready for presentations.

BISQUE

Image Repository [Upload] [Download] [Analyze] [Browse] Find resources using tags [Sign in] [?]

Download Share Delete Visibility: **published** [Add images] [Remove selected] dataset: **Experiment3**

Preview for "Experiment3" [Add] [Reset] [Select a tag...]

Showing 1-6 of total 23

Annotate and modify [Annotations] [Analysis] [Operations] [Map] [Add] [Delete] [Import] [Export]

Name	Value
------	-------

Neuron7DIV21.oib Neuron7DIV14.oib Neuron7DIV7.oib

Neuron6DIV14.oib Neuron6DIV21.oib Neuron5DIV21.oib



Wide

The screenshot displays the Wide File Manager web interface. The browser window title is "Wide File Manager" and the address bar shows the URL "filemanager.lammi.cnrs.fr/wide_file_manager/wide.html". The interface includes a navigation menu with "Edit", "Display", "Tools", "Download", "Plugins", and "Help". A sidebar on the left shows a file tree with folders like "granier", "Image", and "lantaud". The main area displays a grid of microscopy images with their respective filenames and sizes. A right-hand panel shows the "Summary" metadata for the selected image "Abrieu-Ballon-137.jpg".

Wide File Manager

Folder: Images

Image	Filename	Size
	3.indd	747 MB
	20130221_FISH_CEL_2013_05_27_732.MD	159.8 KB
	Abrieu-Ballon-137.jpg	659.4 KB
	Abrieu-Eavardca-Y27.pc	185.9 KB
	Abrieu-CancerCell-Lytrich.jpg	159.1 KB
	Abrieu-CancerCell-MG.jpg	161.7 KB
	Abrieu-bpaca-148.jpg	248.1 KB
	Abrieu-FlyngCell.jpg	155.1 KB
	Abrieu-rboulca-NSC.jpg	253.8 KB
	Abrieu-LeMauvaisDeil	448.0 KB
	Abrieu-Midraas-H1H.jpg	61.8 KB
	Abrieu-Nd-Arappaco-148.jpg	72.6 KB
	Abrieu-Nd-Metaphaco	113.3 KB
	Abrieu-Nd-rometaphaco	471.4 KB
	Abrieu-Fantasma.jpg	385.2 KB
	Abrieu Symbolice.jpg	154.5 KB
	Abrieu-Yeastcell.jpg	

Summary

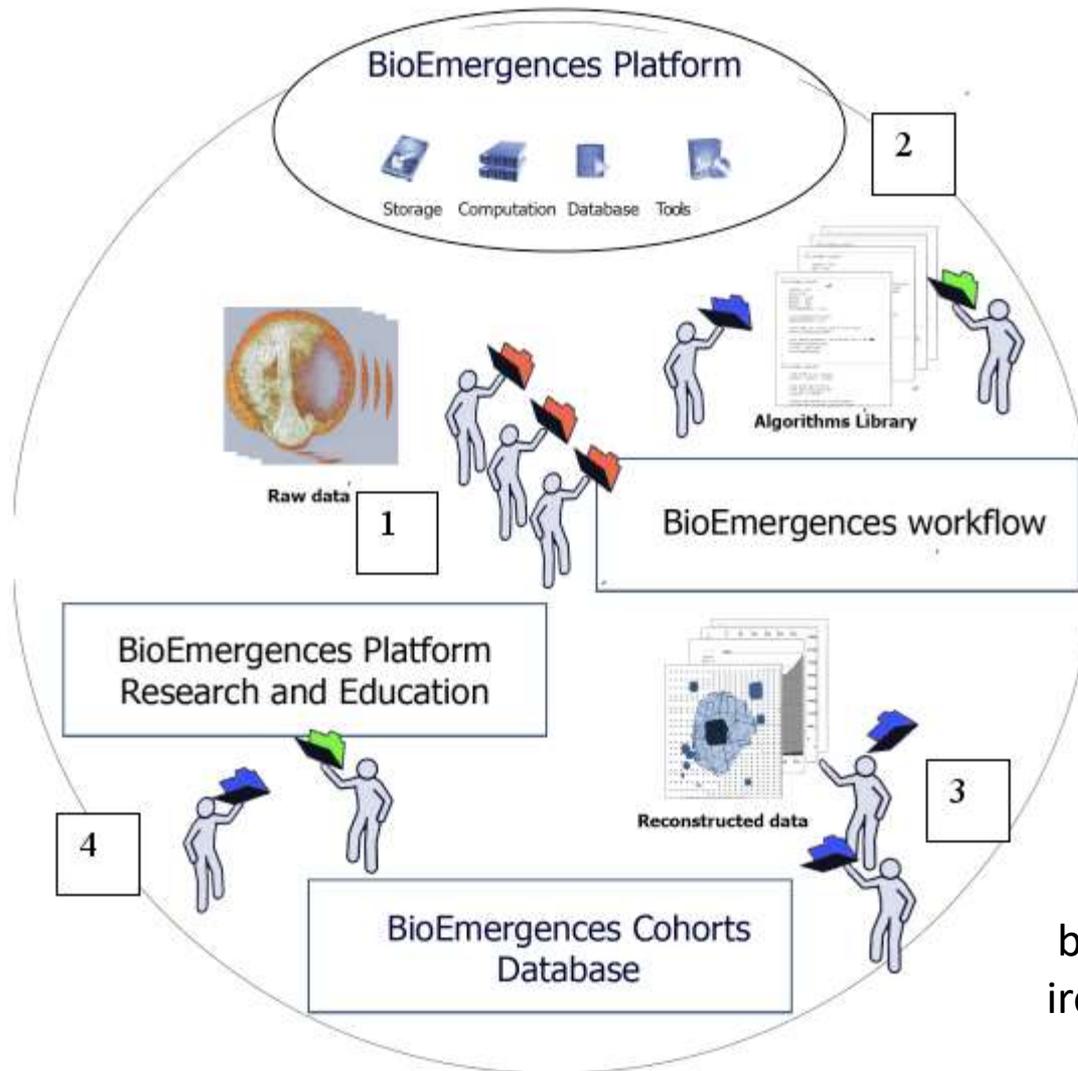
Abrieu-Ballon-137.jpg

Owner: granier
Dimension (XY): 524 x 764 px
Z-sections / time points: 1 x 1
Acquisition date: Jul 4, 2013

image: id: urn:sdm:cnrs:fr:image:25120
image name: 3035.jpg
Creation date: 2013-07-04T05:18:17
Description: No description
Dimension order: XYCZT

- Width: 524 px
- Height: 764 px
- Size Z: 1
- Size C: 3
- Size T: 1
- Physical size X: microns
- Physical size Y: microns
- Physical size Z: microns
- Time increment: 0.0 seconds
- Channels
 - Channel number: 0
 - Samples per pixel: 3

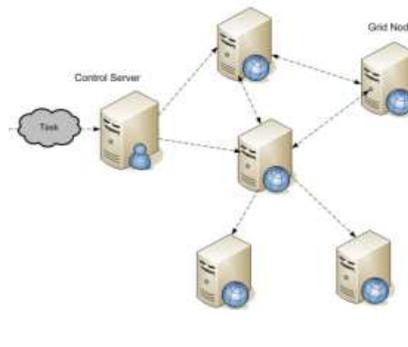
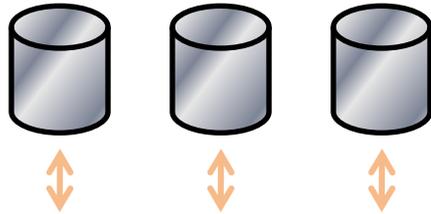
BioEmergences



based on
irods

Image data base

STORAGE



Processing batch of images on cluster (denoising, deconvolution, ...)

Images Server+ Metadata +annotations (manual or analysis results)/ attachments (publications,xls file..)

Acquisition Client



Web Client



Interface

Automatic analysis without full download, Data fusion, advanced visualisation EXEMPLE

Web admin for project managing

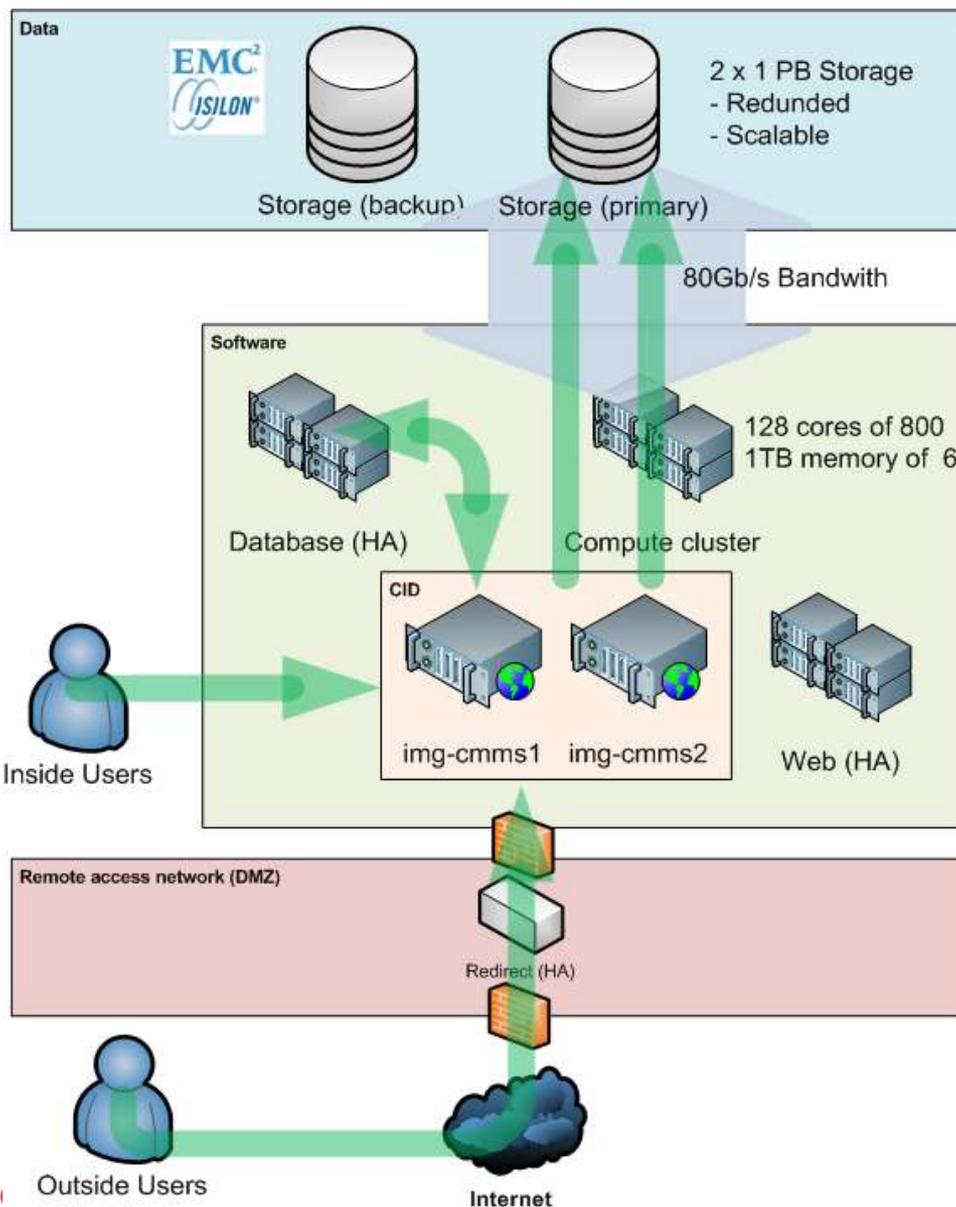


Dynamic Organisation, Visual search or advanced search functionalities

Metadata (pixel size, acquisition time,...) annotations, Parsing nD images Insuring reproducibility by storing all processing



CID now



True Collaborative tool :

- All users are accessing the same infrastructure with **hierarchical rights**.
- All images are stored on a **central secured place**, and are **indexed**

Security & Scalability :

We have an overall **High Availability infrastructure**, with many **parts shared between platforms** (NGS/ Bioinfo/Imaging/...):

- Network
- Storage
- Database
- Computing

What next ? :

Migrate CID on the Web shared infrastructure.
Take profit of « big data » processing.

Some key numbers :

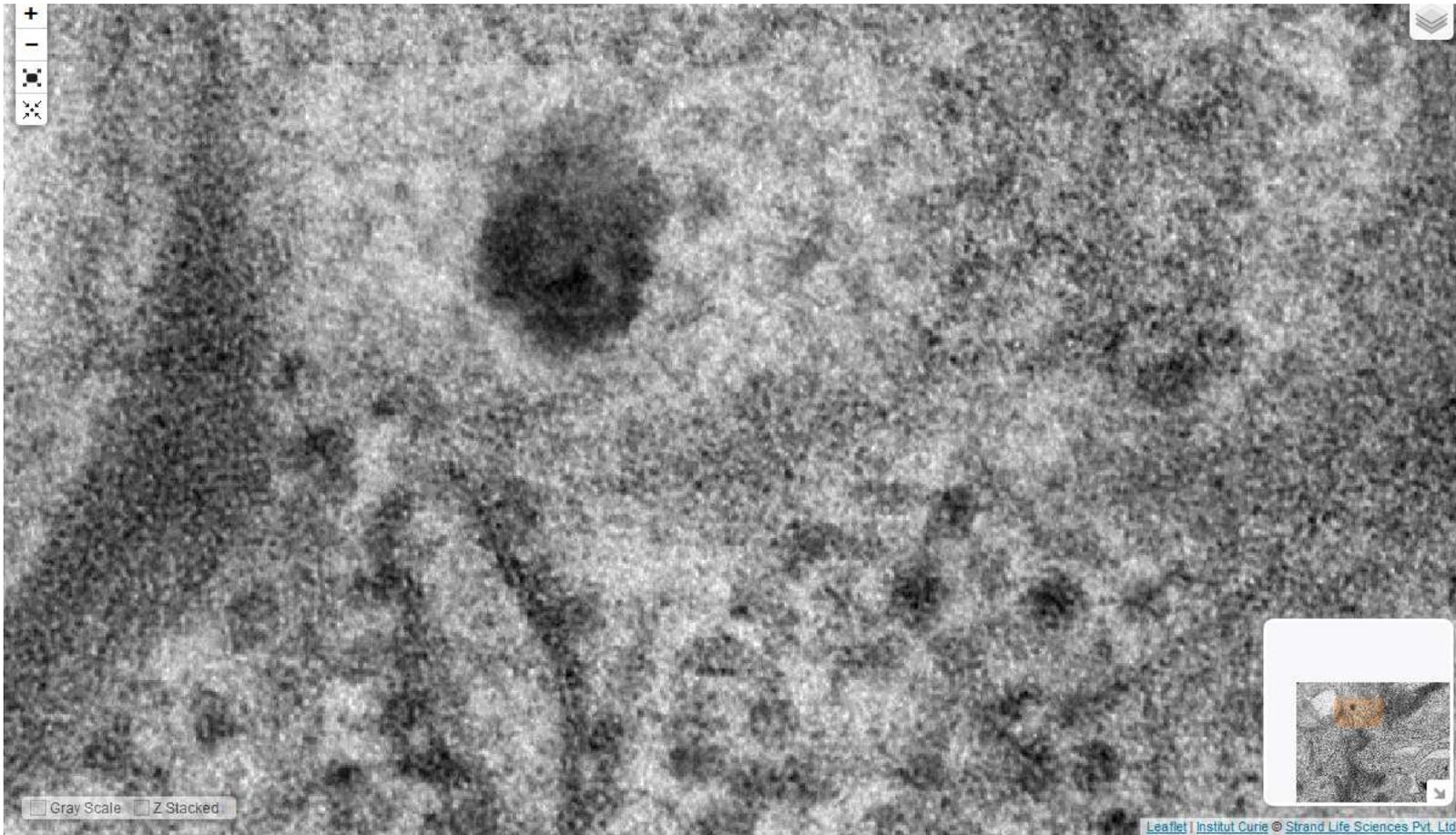
- 800 cores & 6TB compute Cluster
- 1 PB scalable & redundand storage
- High throughput network

Big Data processing ready ! ☺



Exemple of additional clients: Tile Viewer for big data through a url invocation

Search: **imageWidth:[5000 *]**



Example of additional clients: RUBIES: specific for HCS data (compound libraries management etc., hits...) (WebLab based)

The screenshot displays a software interface with a grid of microscopy images on the left and a metadata display portlet on the right. The grid consists of 15 columns and 15 rows of images, labeled A through I. The 10th column is highlighted in yellow. The metadata display portlet shows a list of files and their associated metadata, including file names, URIs, and wavelengths.

```
graph TD
    subgraph ComplexTypes
        direction TB
        PK[«ComplexType»  
PieceOfKnowledge  
data : anyType]
        An[«ComplexType»  
Annotation]
        LL[«ComplexType»  
LowLevelDescriptor  
data : anyType]
        CR[«ComplexType»  
ComposedResource]
        R[«ComplexType»  
Resource  
uri : anyURI]
    end
    PK --> R
    An -- "annotation [0..*]" --> R
    LL -- "desc [0..*]" --> R
    CR -- "resource [1..*]" --> R
```

Dmitri Voitsechovitch



FRANCE-BIOIMAGING

Organisation

Have access with different levels of rights

Users
(administrator/Facility Staff,
Team Leader, project
Manager, Team Member)

Active
Suspended
Deleted

Access to records are
defined by access to
projects

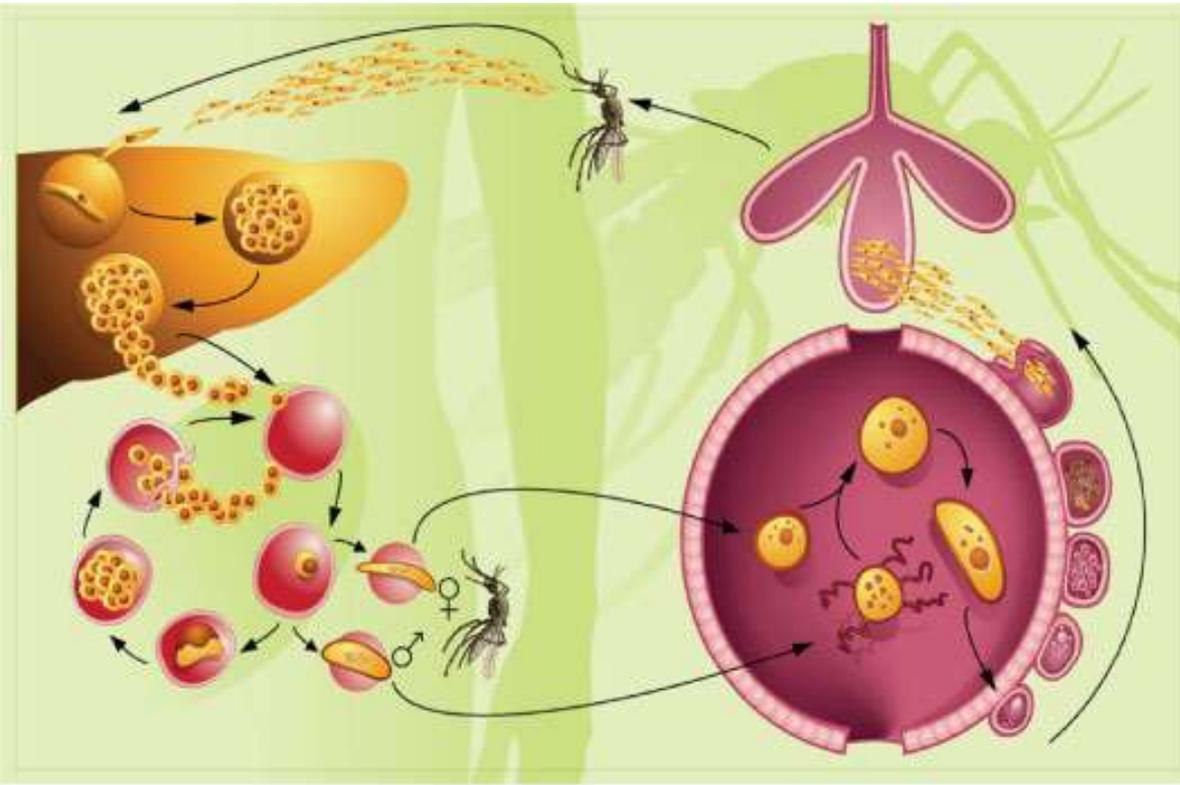
**Projects (=//
rdf graphe
nommé?)**

Active
Archived

Are part of one or several
projects (without
duplication)

**Records (=imagedata)
+Metadata, annotations,
attachments+ history and
links (SQL + noSql)**

Example of on-going project (under submission).



Malaria parasite invasion in the mosquito tissues

Gloria Volohonsky

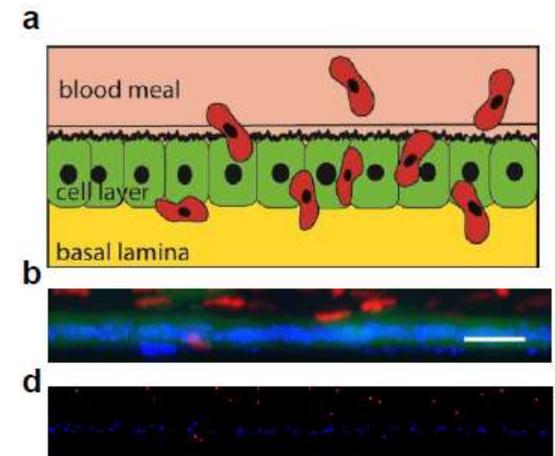
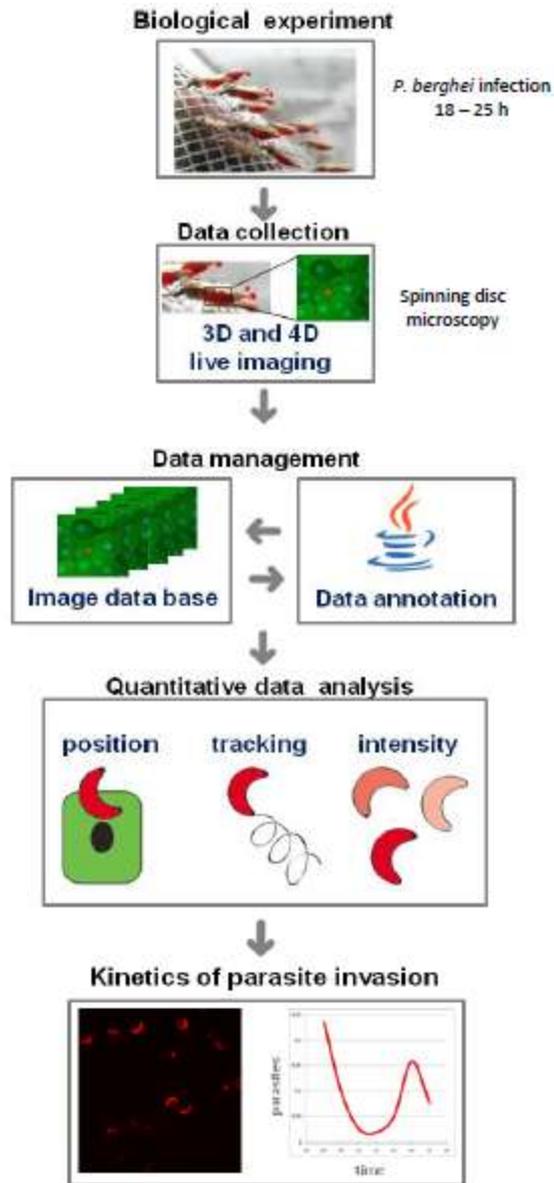
IBMC Anopheles group

Unistra

Elena Levashina

Max Planck Institute for
Infection Biology

malaria parasite invasion in the mosquito tissues



Data are annotated

Perinne Gilloteaux

Launch Acquisition Administrator Settings Help

Reset Zoom Set Thumbnail Screenshot Results Actions Enter Query

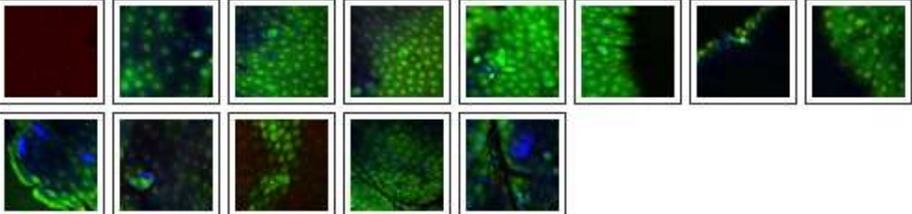
parasite invasion in the All Channels Full Resolution Attachments

Navigator

- ▼ Malaria parasite invasion in the mosquito tissues
 - ▶ mosquito (7B):36
 - ▼ mosquito (DSX):53
 - ▶ TPI (19):2
 - ▶ TPI (19.5):2
 - ▶ TPI (20):6
 - ▶ TPI (20.5):3
 - ▶ TPI (21):2
 - ▶ TPI (21.5):1
 - ▶ TPI (22):13
 - ▶ TPI (22.5):1
 - ▶ TPI (23):1
 - ▶ TPI (23.5):7
 - ▶ TPI (24-25):15
 - ▼ mosquito (G12):61
 - ▶ TPI (19):3
 - ▶ TPI (19.5):1
 - ▶ TPI (20):9
 - ▶ TPI (21):8

Apply Selection

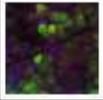
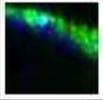
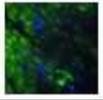
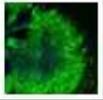
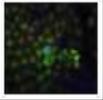
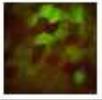
Thumbnail Fields



Data are annotated. Results of processing at the record level are uploaded by the processing algorithm

Navigator

- ▼ Malaria parasite invasion in the mosquito tissues
 - ▶ mosquito (7B):36
 - ▼ mosquito (DSX):53
 - ▶ NparasitesSemiManual (-8.70):22
 - ▶ NparasitesSemiManual (8.70-17.40):13
 - ▼ NparasitesSemiManual (17.40-26.10):8
 - ▶ Dextran (no):1
 - ▼ Dextran (yes):7
 - ▶ TPI (20):1
 - ▶ TPI (20.5):1
 - ▶ TPI (23.5):4
 - ▼ TPI (24.5):1
 - ▶ REVERSE ():1
 - ▶ NparasitesSemiManual (26.10-34.80):5
 - ▶ NparasitesSemiManual (34.80-43.50):2
 - ▶ NparasitesSemiManual (43.50-52.20):1
 - ▶ NparasitesSemiManual (60.90-69.60):1
 - ▼ NparasitesSemiManual (78.30-87.87):1
 - ▼ Dextran (yes):1

Thumbnail:  Fields:      

Apply Selection

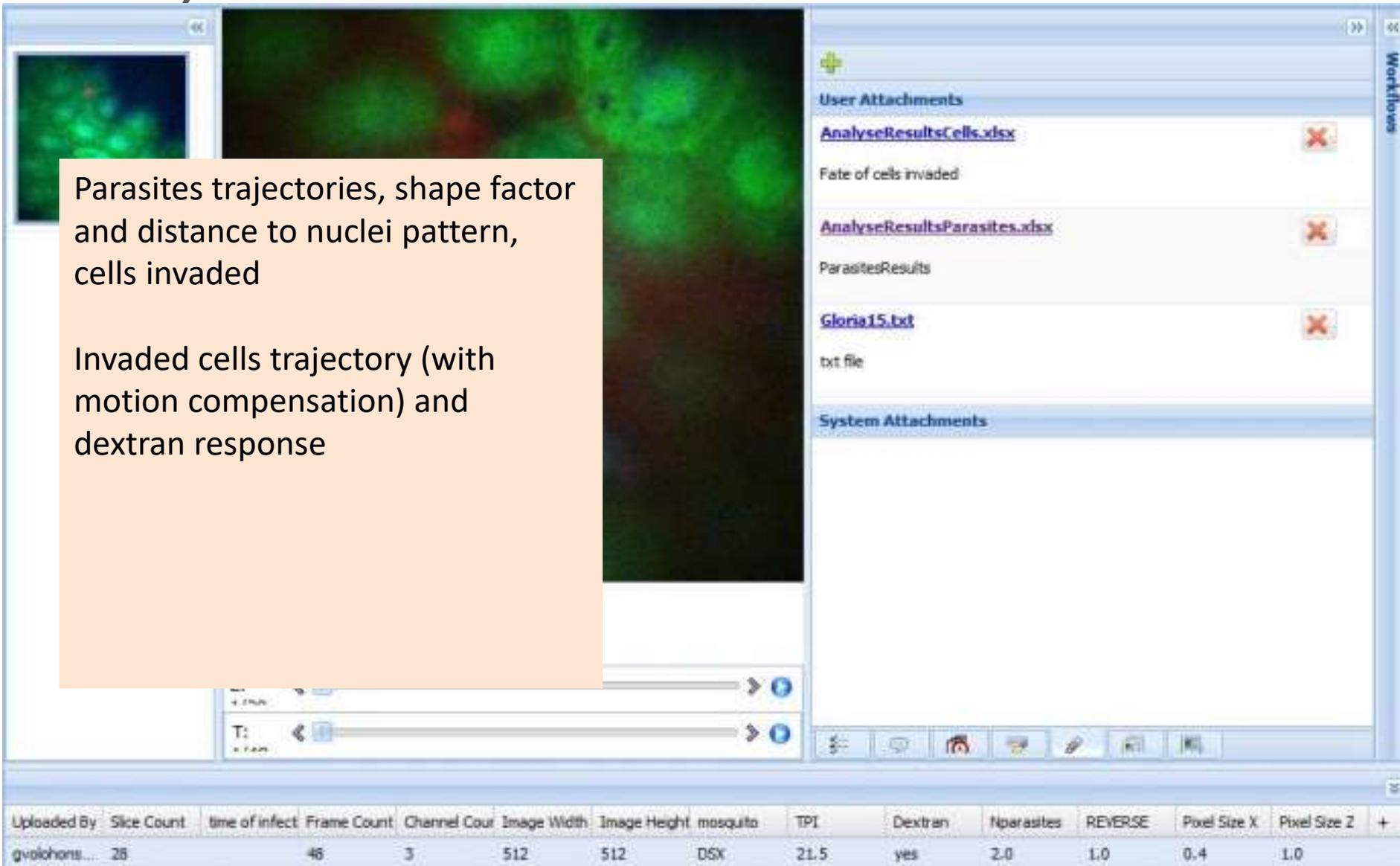
Annotation automatically created are also be visual.

The screenshot displays the Avadis iMANAGE software interface. The main window shows a multi-channel microscopy image of mosquito tissues with blue, green, and red channels. Several regions are highlighted with green boxes and numbered 1, 2, and 3, indicating automatic annotations. The interface includes a top navigation bar with options like 'Launch Acquisition', 'Settings', 'Help', and 'Logout'. A left sidebar contains a 'Navigator' with a grid of image thumbnails and a 'Channels' panel with checkboxes for 'All Channels', 'Full Resolution', 'Grey Scale', 'Legends', 'Scale Bar', and 'Z Projection'. Below the channels panel is a 'Select LUT for w0002' dropdown menu with various color maps. The bottom of the interface features a 'Pan and Zoom' section with 'Sites' and 'Channels' buttons, and a status bar showing 'Z: 19/47' and 'T: 10/120'. On the right side, there is a 'History' panel with a list of user annotations and task executions, including 'User Annotation Added by Gloria Volohonsky' and 'Task Executed by Facility Administrator'. The page number 'Page 49 of 4566' is also visible.

Information at the object level (here parasites and cells)

Parasites trajectories, shape factor and distance to nuclei pattern, cells invaded

Invaded cells trajectory (with motion compensation) and dextran response



The screenshot displays a software interface for analyzing microscopy data. The main window shows a large image of a biological sample with green and red fluorescence. A smaller thumbnail of the same image is visible in the top-left corner. On the right side, there is a 'Workflows' panel with a '+' icon at the top. Below this, the 'User Attachments' section lists three files: 'AnalyseResultsCells.xlsx', 'AnalyseResultsParasites.xlsx', and 'Gloria15.txt'. Each file has a red 'X' icon to its right. Below the user attachments is the 'System Attachments' section, which is currently empty. At the bottom of the interface, there is a table with the following data:

Uploaded By	Slice Count	time of infect	Frame Count	Channel Cour	Image Width	Image Height	mosquito	TPI	Dextran	Nparasites	REVERSE	Pixel Size X	Pixel Size Z	+
gvolohons...	28		48	3	512	512	DSX	21.5	yes	2.0	1.0	0.4	1.0	

Example of analysis: proportion of parasites crossing the cell layer against time post infection

Script in Matlab: surface fitting by a global 3rd degree polynomial in x and Y of the nuclei position to re expressed all parasites coordinates relatively to the cell layer

```
ispace.login(true,Server,443,AppID, password); CONNECTION
```

```
projectList = ispace.getActiveProjects(); SEARCH DATA
```

```
is=ImageSpaceObject.getImageSpace();
```

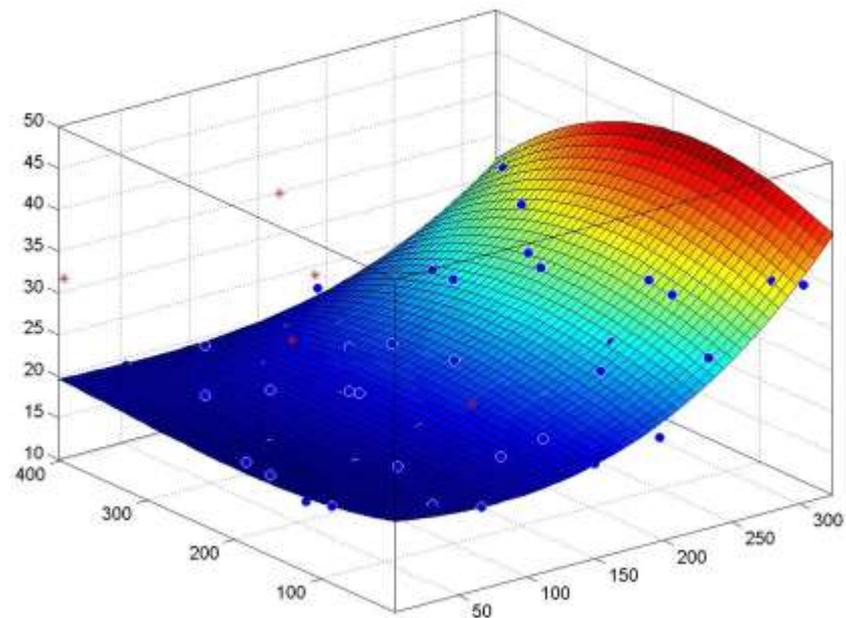
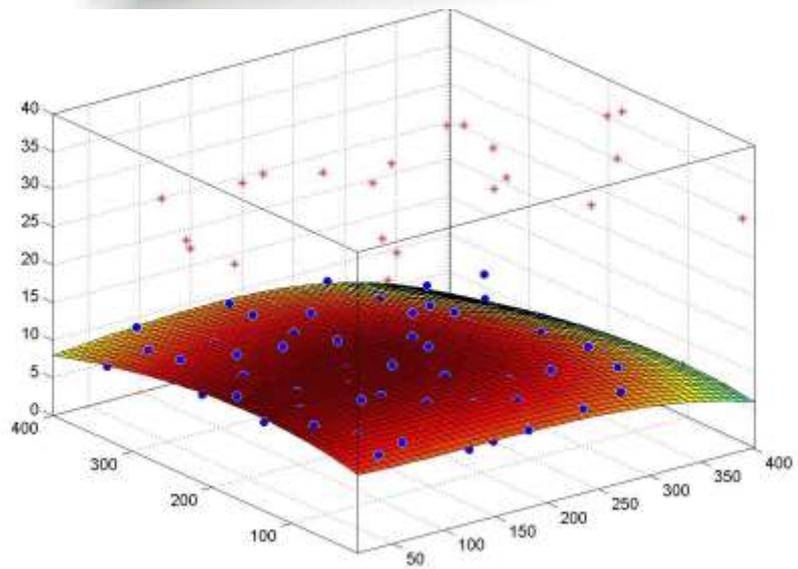
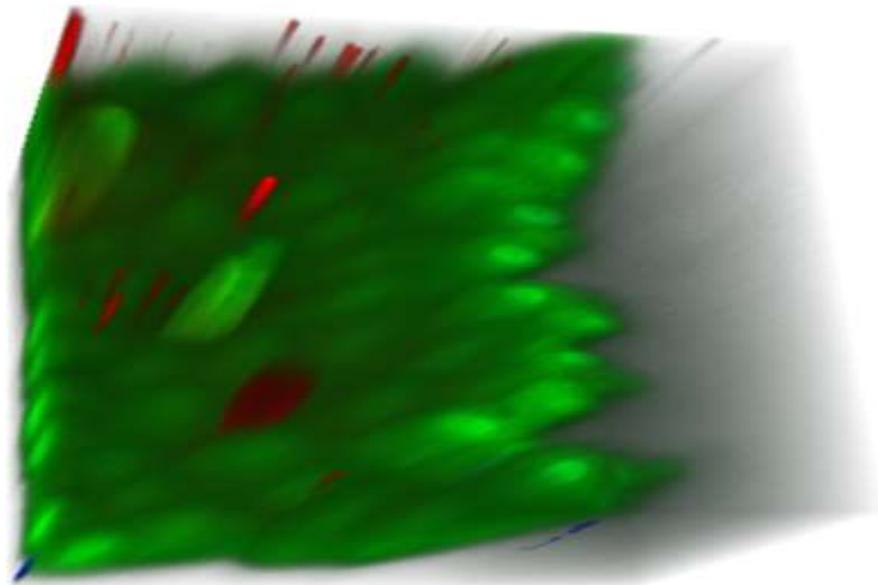
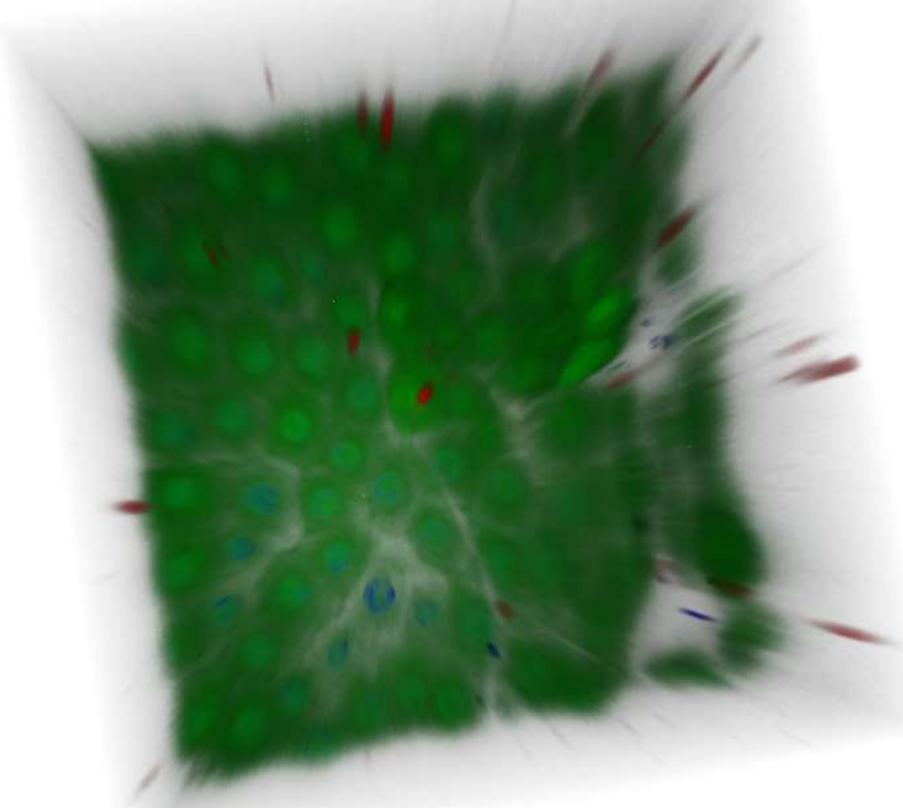
```
projectSpecGuids=is.search('DSX', 'Malaria parasite invasion  
in the mosquito tissues', conditions, 100);
```

```
for i=1:length(projectSpecGuids) GET DATA AND PROCESS DATA
```

```
test=rec.getAttachments();
```

```
Upload Results and fill History
```

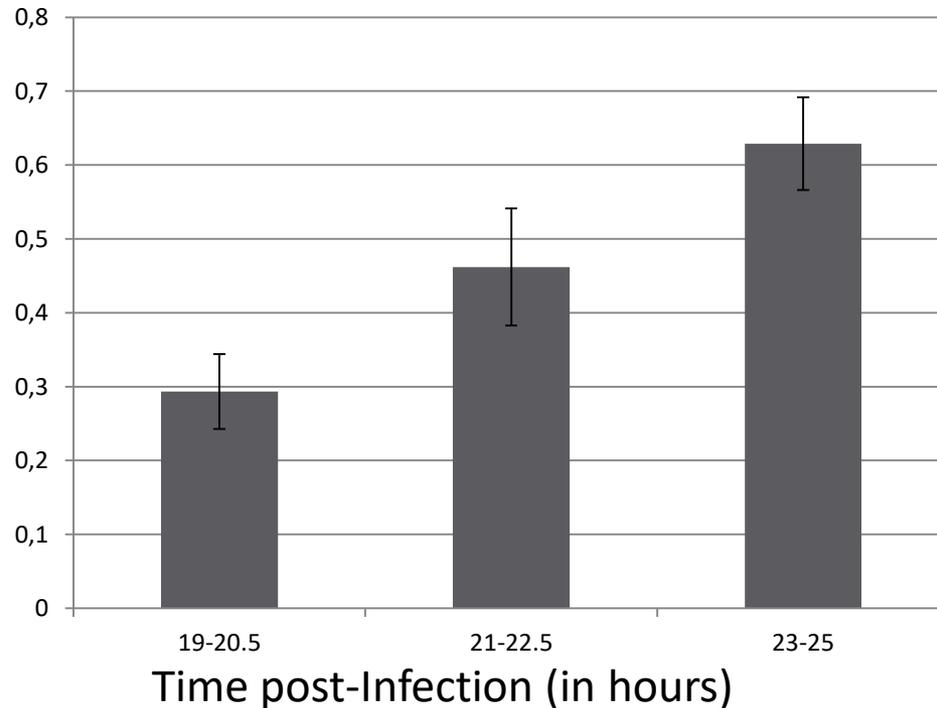
```
end
```



Example of request done from Matlab to the database: for Anopheles Gambiae (DSX)

Probability that the parasites can NOT cross the midgut epithelial tissue

computed as the ratio of parasites not having crossed (inside or under the cell layer) against total number of parasites)



Once ready for publication: Making the dataset public or creating an account for reviewer:

Administration ✕

Projects ✕

Projects | Memberships | **Team-Project Association** | User Annotations

Choose Project:

Members

| | | |

User	Project	Role
gvolohonsky	Malaria parasite invasion in the mosquito tissues	Manager

Add Member

User:

Role:

Autre exemple d'exploitation de données interprojets:

(Projet en cours nœud IPDM FBI (Ferreol Soulez, Cedric Matthews, Fabrice de Chaumont, Perrine Paul-Gilloteaux):

Génération d'un outil de métrologie automatique:

Utiliser la base de données imageset metadata d'intérêt (microscopes, datas, microscopes settings...) avec une tâche de déconvolution aveugle lancée automatiquement sur toutes les images par microscopes:

Les psf générées sont uploadées et liées aux images avec les annotations nécessaires , avec également les PSF réelles (possibilités de mise en place d'un système d'alerte en fonction de la date par rapport à la dernière PSF réel ou une derive de qualité de psf calculée)

Questions ouvertes

-L'interopérabilité plutôt que la centralisation

Interopérabilité déjà possible (standardisation de la définition des ROI, API commune (proposition faites de webservices 'de traduction', web sémantique pour inférer les demandes: ex requete: image reponse image et api dispos) inférence de type?.

- Intégration de données hétérogènes:

Un seul serveur ou des bases liées par API?
client tiers de liage (Exemple projet Shiva KDI Bioinfo Curie)

- Réduction des volumes: Données à conserver?
Nouveaux formats éparses? Nouveaux format de compression?

Acknowledgments

Conception et spécifications :CID iManage PICT IBISA Curie, Curie IT department, Strand Life sciences

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Funding: France Bioimaging, Cancéropole Ile de France.

Réseaux: France BioImaging (Bio Image Informatics Node (ex IPDM)), EUBIAS/ BIAS, RtMFM/MIFOBIO, GDR2588, EuroBioimaging/EuLife, Réseau RBDD

Need (1/2)

No image data conversions, no duplication

- Uploads data to a secure server in the original format
- Unique id for data (check sum like)

Supports sharing and collaboration with access control

- Allows users to upload, view, update or download data based on their access privileges

Supports multiple ways of attaching meta-information

- Annotations, comments and file attachments
- Analysis results as query-able visual objects

-Supports Archiving (data moving to another long-term storage but still searchable)

Need (2/2)

Facilitates custom visualization and analysis

- Access data from preferred analysis and visualization tools
- Access relevant bits of data to build efficient web and mobile Applications

Facilitate quota of storage and facility administration

Facilitate easy access to analysis and visualization applications hosted on other servers

- Run analysis on dedicated compute clusters
- Access applications hosted and published by other users

Highly Scalable

- Supports on-the-fly addition of server nodes to scale concurrent usage

Architecture

- Tomcat (clustering)

- 2 mysql databases (project independant tables (such as microscopes tables , users, teams, quota, etc...)+ project-specific tables (records storage location and metadata, membership, etc..)

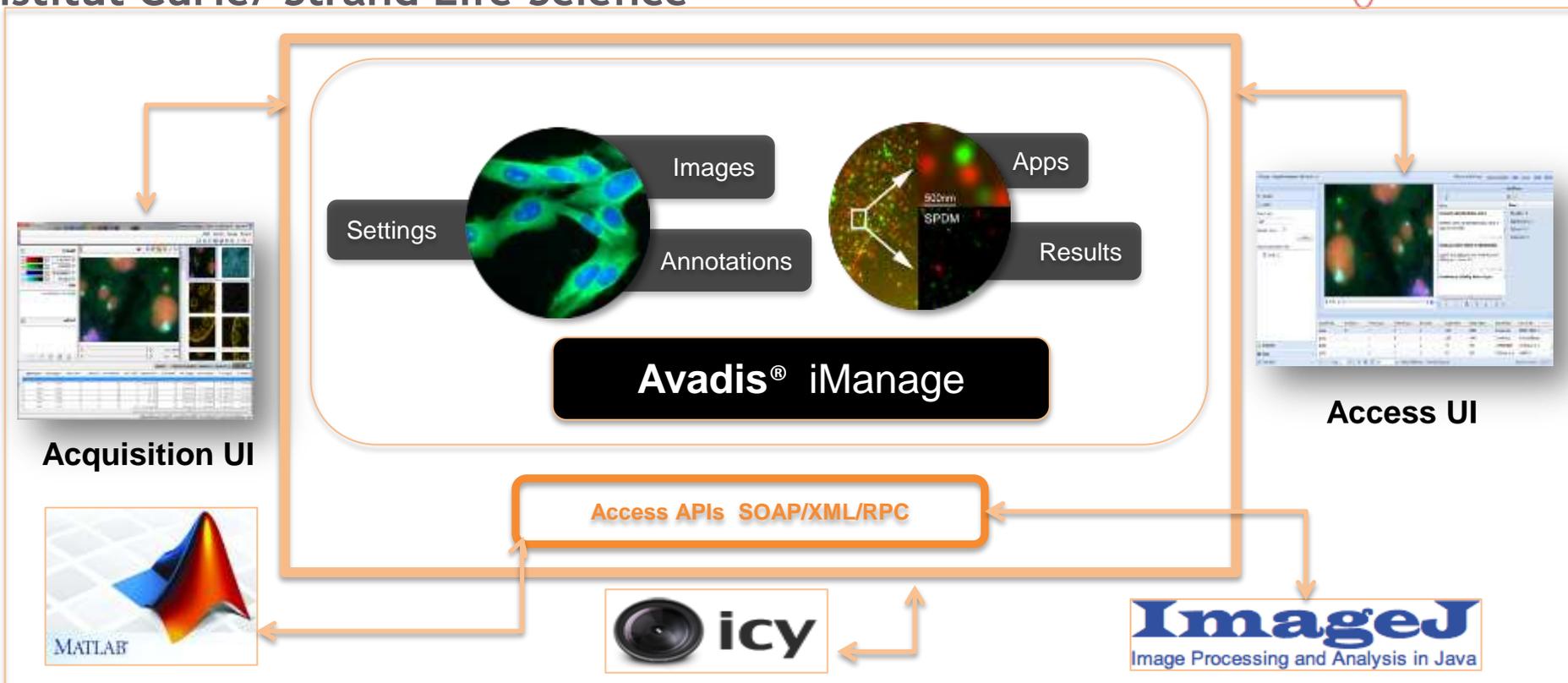
- + NoSQL key-value database(MemCached)

queries

Possibilities of query:

The screenshot shows a search interface with the following elements:

- Search text:** A text input field containing "Hela".
- Advance Query:** A checkbox that is checked, with a link to "Advance Query Syntax Help".
- Submit:** A button to execute the search.
- Results:** A list of 65 records for "Hela". The records are categorized into folders:
 - Henri's Project (34)
 - Microscopes Checks (4) - This folder is selected and highlighted.
 - Record Metadata (4) - Subfolder of Microscopes Checks.
 - Open Image Data Base (24)
 - History (24) - Subfolder of Open Image Data Base.
 - Misc (24) - Subfolder of Open Image Data Base.
 - PreClem (1)
 - Strand Test (1)
- Apply Selection:** A button at the bottom to apply the selected filters.
- Image Thumbnails:** Four small image thumbnails are displayed at the top right of the search results area, showing green and red fluorescence patterns.



Avadis® iMANAGE is an enterprise-wide image and analysis management software platform for Bio-Imaging researchers.



Avadis® iMANAGE provides shared, secure, uniform and open access to image life cycle data and algorithms. It facilitates effective management of heterogeneous images and complex analysis workflows.

IMANAGE ACCESS



A browser based application to access, annotate and analyze image data sets hosted on a central server

IMANAGE ADMIN



A browser based application to facilitate user management, resource management and access control

IMANAGE ACQUISITION



A desktop application for viewing and annotating data locally before uploading to the iMANAGE server.

IMANAGE MOBILE



A browser based application for quick browsing and visualization of image data sets on mobile devices.

IMANAGE APIs



APIs that provide secure access to all the image data sets and associated information stored in the iMANAGE server.

www.strandis.com/products/Imanage



Avadis® iMANAGE Highlights:

No image data conversions

- Uploads data to a secure server in the original format

Supports sharing and collaboration with access control

- Allows users to upload, view, update or download data based on their access privileges

Supports multiple ways of attaching meta-information

- Annotations, comments and file attachments
- Analyzes results as query-able visual objects

Facilitates custom visualization and analysis

- Access data from preferred analysis and visualization tools
- Access relevant bits of data to build efficient web and mobile applications

Facilitate easy access to analysis and visualization applications hosted on other servers

- Run analysis on dedicated compute clusters
- Access applications hosted and published by other users

Support applications on mobile devices

- Seamless portability

Highly Scalable

- Supports on-the-fly addition of server nodes to scale concurrent usage

How does Avadis iMANAGE help users at your lab?

Imaging Facility

- Simplifies data management for heterogeneous images acquired using different microscopes
- Set-up projects with a storage quota
- Set project specific access rights to upload, read, modify, download or delete data for each user
- No loss of data in storage. Original data can be retrieved and migrate later
- Set-up quality processes by publishing quality control workflows

Biologist

- Upload data to a project and share with users in other projects without duplicating
- Create dynamic folder hierarchies based on meta-data for easy browsing
- Batch process data with live progress monitors and store both analysis parameters and results
- Share data with external users by creating "download links" to download data
- Annotate, Comment, Attach Publication, Share with all to collaborate within a team
- Search and explore cross-lab acquired data to get insights as well as to enrich them with newer information
- Integrate and access image data from other biological databases like genomics databases, clinical databases etc.

Image Analyst

- An intelligent proxy metadata writer to access only the relevant bits of images
- Access to data from third party applications like Matlab, ImageJ, Icy etc. seamlessly using secure and uniform APIs
- Publish analysis workflows for researchers on cloud compute resources

IT

- Provide Secure and Scalable access to the Storage and Compute resources
- Manage users and provide access control using the preferred authentication scheme
- Provides multiple device to track and monitor usage of resources
- Supports a single click installation on preferred IT infrastructure

Example of additional clients: RUBIES: specific for HCS data (compound libraries management etc., hits...) (WebLab based)

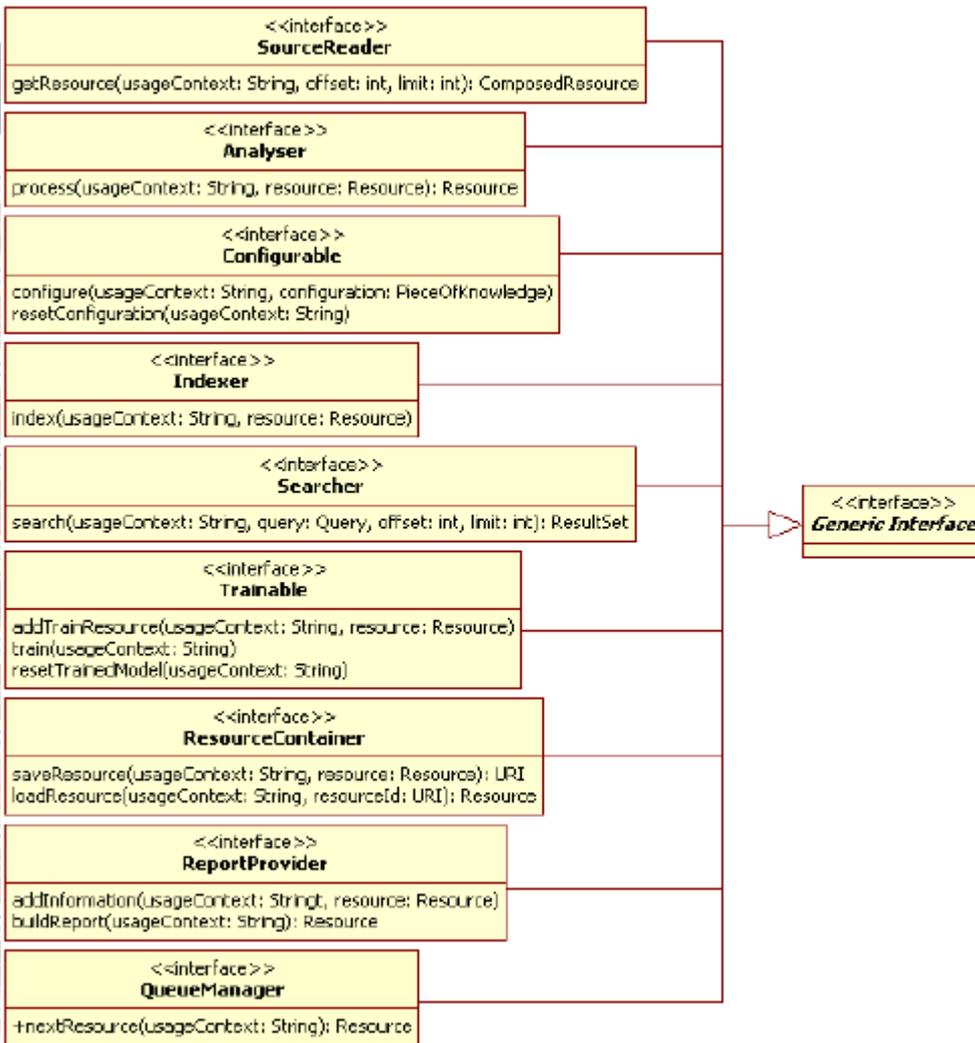
Dmitri Veitchevitch

```

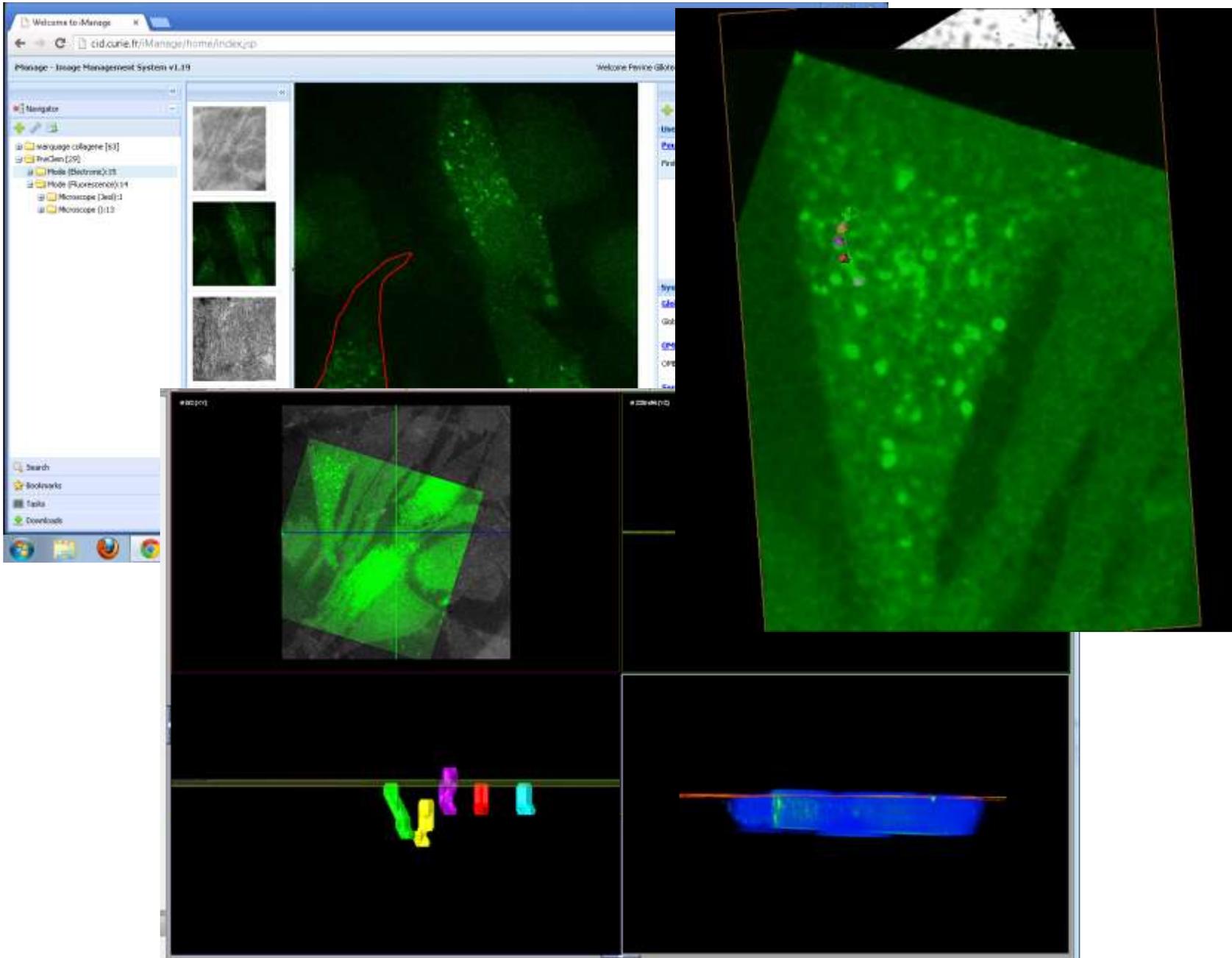
Successfully downloaded well F4
Successfully downloaded well N13
Successfully downloaded well B11
Successfully downloaded well I6
Successfully downloaded well C24
    
```

```

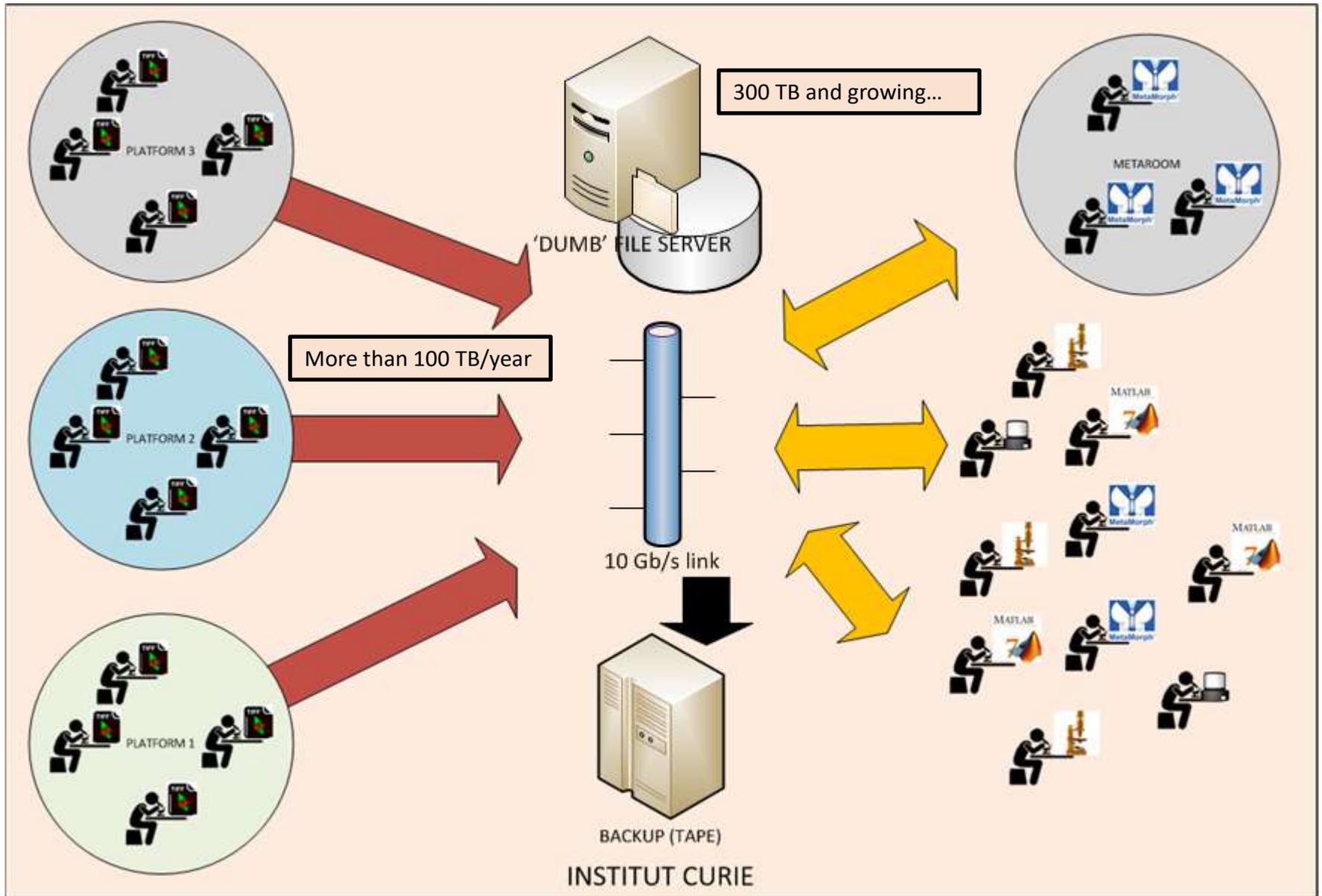
classDiagram
    class PieceOfKnowledge {
        data : anyType
    }
    class Annotation {
    }
    class LowLevelDescriptor {
        data : anyType
    }
    class Resource {
        uri : anyURI
    }
    class ComposedResource {
    }
    PieceOfKnowledge --> Annotation : annotation [0..*]
    Annotation --> LowLevelDescriptor : desc [0..*]
    Annotation --> Resource
    LowLevelDescriptor --> Resource
    ComposedResource --> Resource : resource [1..*]
    
```



Correlative microscopy



Before (Legacy "workflows")



Malaria parasite invasion in the mosquito tissues

- Proteins attacking the parasite in mosquito LRIM, APL1, TEP 1 (hemocyte)
- Species of mosquito:
 - G12 (india)
 - DSX and HYPER (African)
- Marker of damaged cells: Sugar Dextran, or hyper protein becoming fluorescent when binded to H2O2 or whith OPH changed.
- Different time of infection, different times post infection.

Questions to answer:

→ Parasite going out the gut wall: rate and proportion against different time?

→ Is there any shape factor of the mosquito as an additional parameter?

→ Inside the midgut: which are the mode of displacement of the parasite among cells?

(assumption: the defense of cells attempting to eject the parasite would actually trigger the displacement)