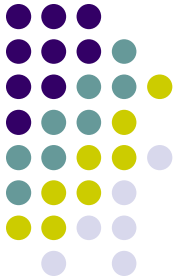
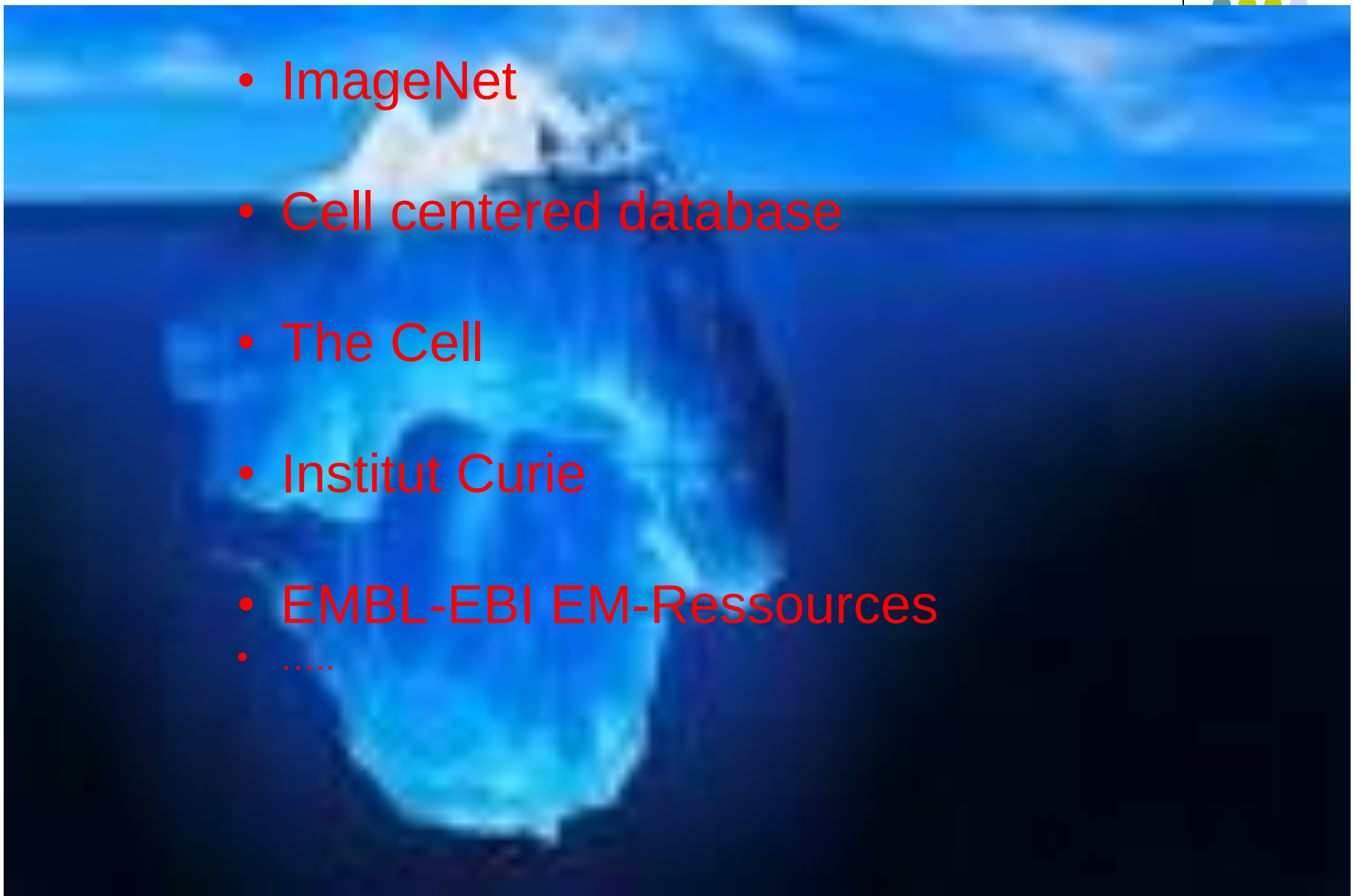
Images & Open Science en bref

A. Trubuil
INRA/MaIAGE, Jouy en Josas

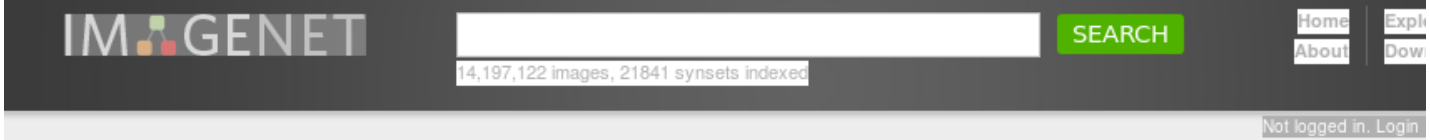


1. Ressources ouvertes
   - Données
   - Logiciels
   - Connaissances
2. Besoins
   - Données
   - Logiciels
   - Connaissances
   - Défis
3. Exemple

1. Ressources ouvertes : données



- ImageNet
- Cell centered database
- The Cell
- Institut Curie
- EMBL-EBI EM-Ressources
- …..



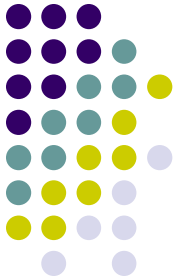
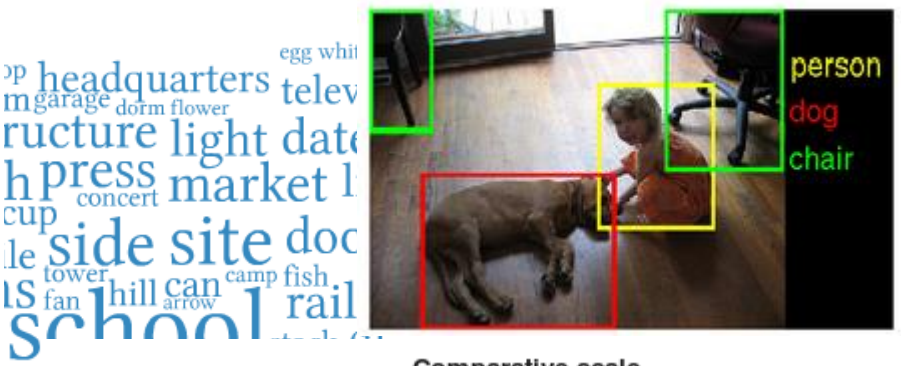


Image classification

Year	Codename	Error (percent)	99.9% Conf Int
2014	**GoogLeNet**	**6.66**	**6.40 - 6.92**
2014	VGG	7.32	7.05 - 7.60
2014	MSRA	8.06	7.78 - 8.34
2014	AHoward	8.11	7.83 - 8.39
2014	DeepcrVision	9.51	9.21 - 9.82
2013	Clarifai†	11.20	10.87 - 11.53
2014	CASIAWS†	11.36	11.03 - 11.69
2014	Trimps†	11.46	11.13 - 11.80
2014	Adobe†	11.58	11.25 - 11.91
2013	**Clarifai**	**11.74**	**11.41 - 12.08**
2013	NUS	12.95	12.60 - 13.30
2013	ZF	13.51	13.14 - 13.87
2013	AHoward	13.55	13.20 - 13.91
2013	OverFeat	14.18	13.83 - 14.54
2014	Orange†	14.80	14.43 - 15.17
2012	SuperVision†	15.32	14.94 - 15.69
2012	**SuperVision**	**16.42**	**16.04 - 16.80**
2012	ISI	26.17	25.71 - 26.65
2012	VGG	26.98	26.53 - 27.43
2012	XRCE	27.06	26.60 - 27.52
2012	UvA	29.58	29.09 - 30.04

Single-object localization

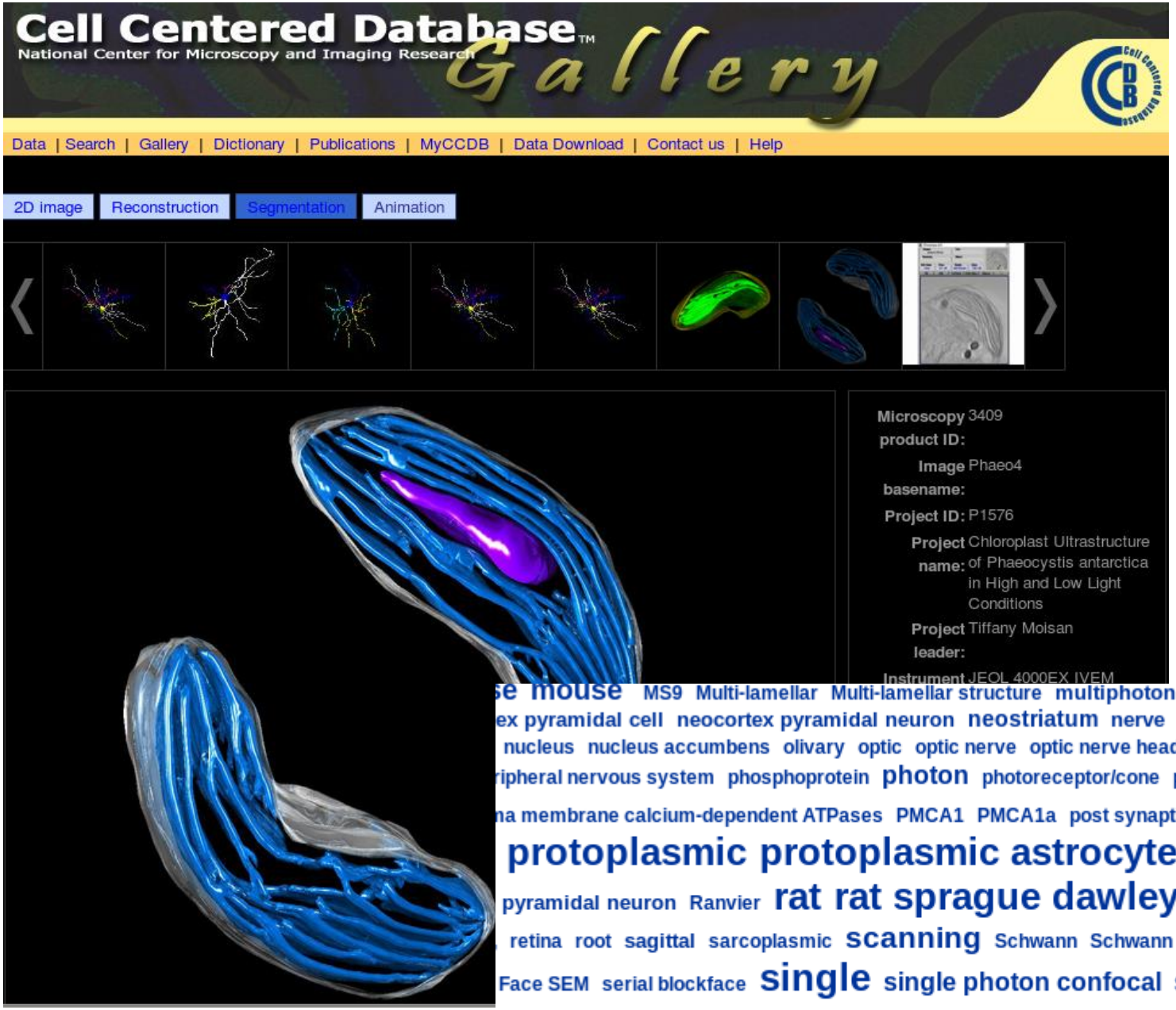
Year	Codename	Error (percent)	99.9% Conf Int
2014	**VGG**	**25.32**	**24.87 - 25.78**
2014	GoogLeNet	26.44	25.98 - 26.92
2013	**OverFeat**	**29.88**	**29.38 - 30.35**

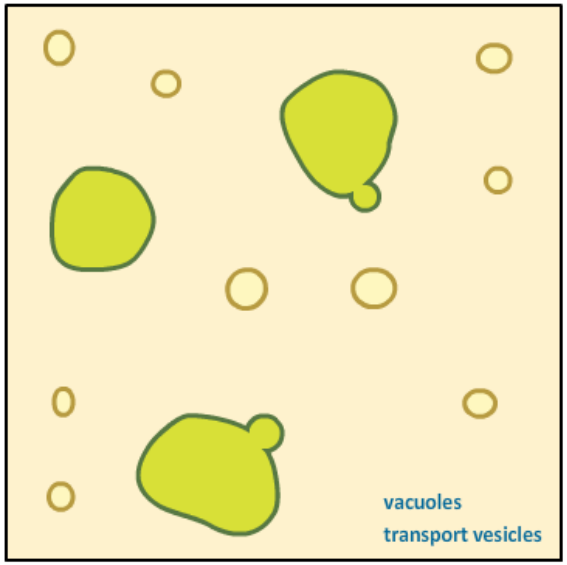


Comparative scale

		PASCAL VOC 2012	ILSVRC 2014
Number of object classes		20	**200**
Training	Num images	5717	456567
	Num objects	13609	478807
Validation	Num images	5823	20121
	Num objects	13841	55502
Testing	Num images	10991	40152
	Num objects	---	---

Olga Russakovsky et al. ImageNet Large Scale Visual Recognition Challenge, 2014.


Cell Centered Database™
National Center for Microscopy and Imaging Research
Gallery
Data | Search | Gallery | Dictionary | Publications | MyCCDB | Data Download | Contact us | Help
2D image
Reconstruction
Segmentation
Animation
Microscopy product ID: 3409
Image basename: Phaeo4
Project ID: P1576
Project name: Chloroplast Ultrastructure of Phaeocystis antarctica in High and Low Light Conditions
Project leader: Tiffany Moisan
Instrument JEOL 4000EX IVEM
se mouse MS9 Multi-lamellar Multi-lamellar structure multiphoton myocardium m
ex pyramidal cell neocortex pyramidal neuron neostriatum nerve Nerve cell layer
nucleus nucleus accumbens olivary optic optic nerve optic nerve head Pannexin1 Par
ripheral nervous system phosphoprotein photon photoreceptor/cone plasma plasma
na membrane calcium-dependent ATPases PMCA1 PMCA1a post synaptic density Ppp1r
protoplasmic protoplasmic astrocyte pump Purkinje
pyramidal neuron Ranvier rat rat sprague dawley receptor regu
retina root sagittal sarcoplasmic scanning Schwann Schwann cell sciatic scia
Face SEM serial blockface single single photon confocal Slc18a2 slice
piny spiny dendrite spiny dendrite, synaptic vesicles sprague striatum structu
plex synapse synaptic synuclein TEM test tissue thin tissue transmitted tra
HVEM ventricle VeroE6 vesicles vesicular vesicular monoamine transporter 2 virologic



Vacuole

Forming membrane-bound cytoplasmic compartments in many eukaryotic cells, vacuoles vary widely in size, number and function. Plant cells contain large vacuoles that can store water and help maintain hydrostatic pressure.the quick recovery of a wilted plant when watered is due to the filling of water vacuoles in the cells. Fungal cells and some bacteria also have vacuoles, which can function in storage of a wide range of ions as well as water balance. Cells with vacuoles have relatively less cytoplasm, and the presence of a large central vacuole can push organelles towards the periphery of the cell. In those animal cells that have vacuoles they are used for water, food and waste storage. Vacuoles are formed by the fusion of smaller vesicles.

Related Molecular Functions

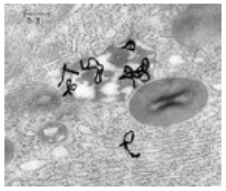
- Alpha-1,2-mannosyltransferase activity
- Calcium ion binding
- Water transmembrane transporter activity
- Proton motive force dependent protein
- 1-phosphatidylinositol 4-kinase activity

Related Biological Processes

- Contractile vacuole organization
- Digestive system process
- Cytoplasm organisation
- Autophagy
- Cortical microtubule cytoskeleton

Images of : Vacuole

Still Images ☐ Video/Animation ☐ Z-Stack ☐ Time Series ☐ Refresh



CIL:37119
NCBI Organism Classification
- *Cavia porcellus* (Guinea-pig)

Biological Process
- protein secretion

Cellular Component
- vacuole

Electron microscope autoradiograph showing the high concentration of radioactivity over

CIL:40415
NCBI Organism Classification
- *Saccharomyces cerevisiae* (Baker's Yeast, Brewer's Yeast)

Biological Process
- organelle organization

Cellular Component
- vacuole

Transmission electron micrograph of a representative sertraline-treated chc1

CENTER FOR BIO-IMAGE INFORMATICS

Engineering, Biology and Computer Science, working together.

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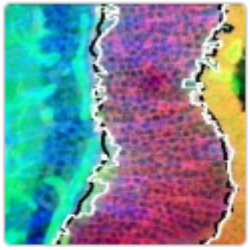
- Video Demos
- Active Users

Bisque Database

Bisque (Bio-Image Semantic Query User Environment) : Store, visualize, organize and analyze images in the cloud. Bisque was developed for the exchange and exploration of biological images. The Bisque system supports several areas useful for imaging researchers from image capture to image analsysis and querying. The bisque system is centered around a database of images and metadata. Search and comparison of datasets by image data and content is supported. Novel semantic analyses are integrated into the system allowing high level semantic queries and comparison of image content.

FEATURES

- Bisque is free and open-source
- Flexible textual and graphical annotations
- Cloud scalability: PBs of images, millions of annotations
- Distributed storage: local, iRODS, S3
- Integrated image analysis, high-throughput with Condor
- Analysis in MATLAB, Python, Java+ImageJ
- 100+ biological image formats
- Very large 5D images (100+ GB)



Bio-Segmentation

The UCSB Bio-Segmentation Benchmark that can be used for evaluating the perform segmentation, classification, and tracking.

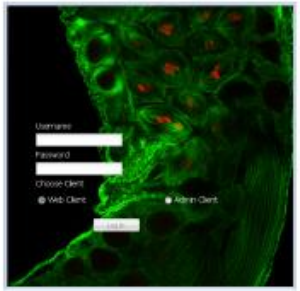
qPLANT

With the emergence of smart phones and identification from geo-tagged images. The information about plant taxonomy and habi structure, and flower attributes, where app returns a list of plant species that are close

CellECT (Cell Evolution Capturing Tool)

IMAGE DATABASE ON MICROSCOPY FACILITY

Managing images is a bottleneck in modern biology, in particular on a microscopy facility, due to the huge size and different formats of acquired images. For example, the volume of images produced on our facility at the Institut Curie can reach around 200 Terrabytes a year, with different format produced by around 40 microscopes. Images obtained in other places in case of remote collaboration can be added to these numbers. These images are further processed using off-site or on-site processing facilities. In consequence, it is important to develop software tools to store data and track the history of their changes. Multiple users need to access these images between acquisition and analysis to generate meaningful results. These are some of the challenges that led us to the development and deployment of a new image database for our facility.



CID login interface

The Curie image database was developed in collaboration with the Strand Scientific Intelligence (San Francisco, USA) company. It is based on client-server architecture, with a heavy client for the import of image from microscopes and a web client for the management and processing of images. It allows the dynamic organization of data by projects, as well as their annotations, either manual or automatic, extracted from the acquisition itself [1] or from the result of an analysis. It also allows other applications to access images from the data base using well defined web services.

A particular focus has been given to the speed of access, the security of the data, and the management of storage quota. All these points are taken into account in a multiple user and highly collaborative environment. The image database will also allow users to integrate and apply processing workflows on calculation cluster.

Microscopy image database is not expected to be only a storage and a management tool. It should also be a research tool which is flexible and supports multiple use cases. Several examples of ongoing projects that are using the image database will be presented.

Next steps will include the integration of this image database with other, such as genome database, or clinical and anatomy-pathological data related to clinical projects. Ensuring the quality of data uploaded is also one goal for the next release.

References

[1] M.Linkert et al. Journal of Cell Biology, 189:5777-782, 2010

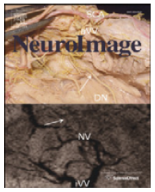
Démarche en plein essor dans certains domaines

NeuroImage 82 (2013) 645–646

Contents lists available at ScienceDirect

NeuroImage

journal homepage: www.elsevier.com/locate/ynimg



Editorial

Introduction to the special issue: Toward a new era of databasing and data sharing for neuroimaging

Brain imaging informatics as a new growing discipline

Neuroimaging is slowly undertaking a revolution that parallels the increasing availability of high-performance and cloud-based computing resources. In recent years, the computational aspects of neuroimaging (which we refer to as "neuroinformatics") have become increasingly important within the brain imaging community activity. This extends to nearly every aspect of neuroimaging: Handling and storing the data themselves, their processing and analysis, and the specification of precise meta data. Neuroinformatics has become a small but rapidly expanding field, with available tools for storing, documenting, retrieving and sharing data steadily growing in numbers. This special issue is

Fourth, brain imaging is now an established field that is attracting new research communities. Notably, the field of high-performance computing and the nascent field of "data science" may offer new solutions for optimizing the handling and processing of data, and will certainly play an increasing role in the field as datasets start to outstrip the ability of existing processing models. In the future, we envision that the brain imaging researcher will need to have the skills to handle this new type of work, similar to the growing need for bioinformatics expertise amongst researchers in domains of molecular biology and genomics.

The challenges: Why are we not yet there?

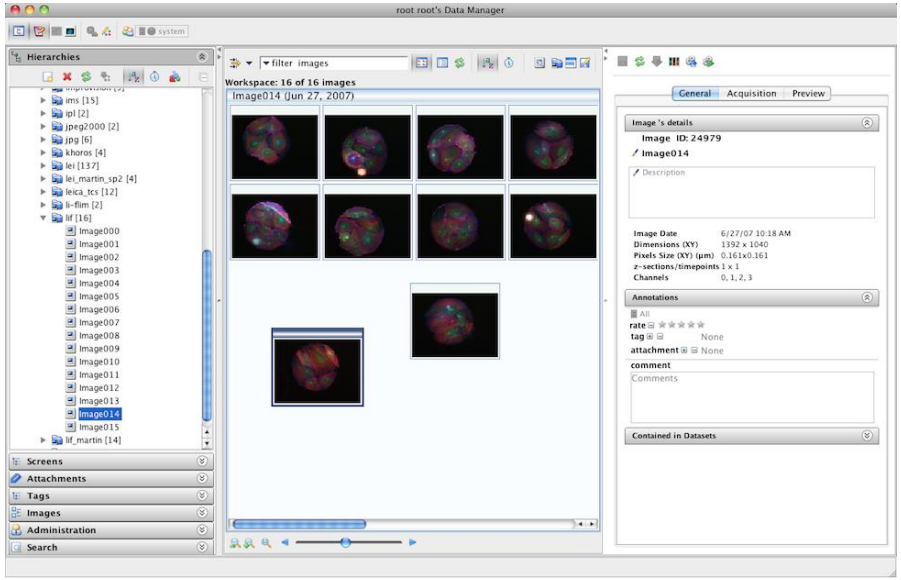
Ressources ouvertes : logiciels

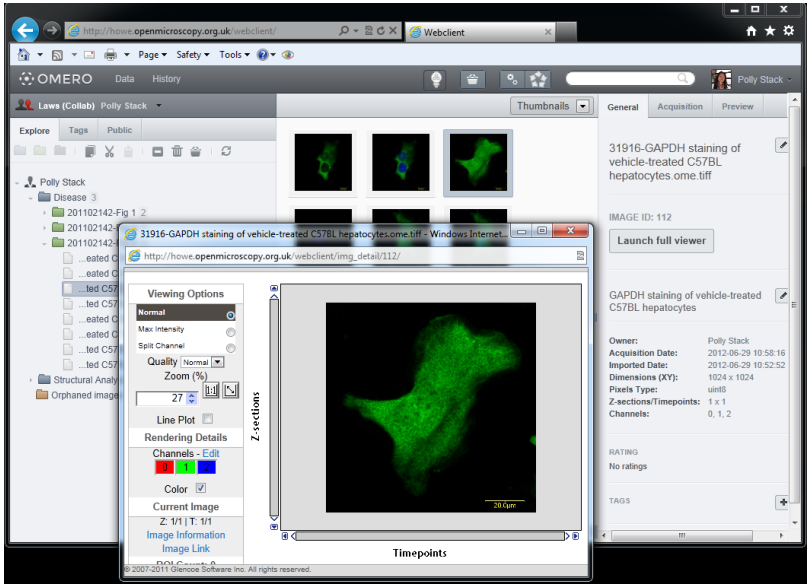
Questions :

- Comment **organiser / classer** des images selon un ensemble de critères ?
  - Recherche par le contenu
- Comment **explorer** des données images
  - Visualisation données >3D, multi-sujets…
- Comment **extraire** les infos d'une image ?
  - Segmentation automatisée
- Comment **intégrer / fusionner** les informations sur plusieurs images ?
  - Atlas, modélisation statistique

Organiser un ensemble d'images

- Open-Microscopy environement
  - Système intégré de gestion de base de données d'images
  - http://www.openmicroscopy.org/site/products/omero

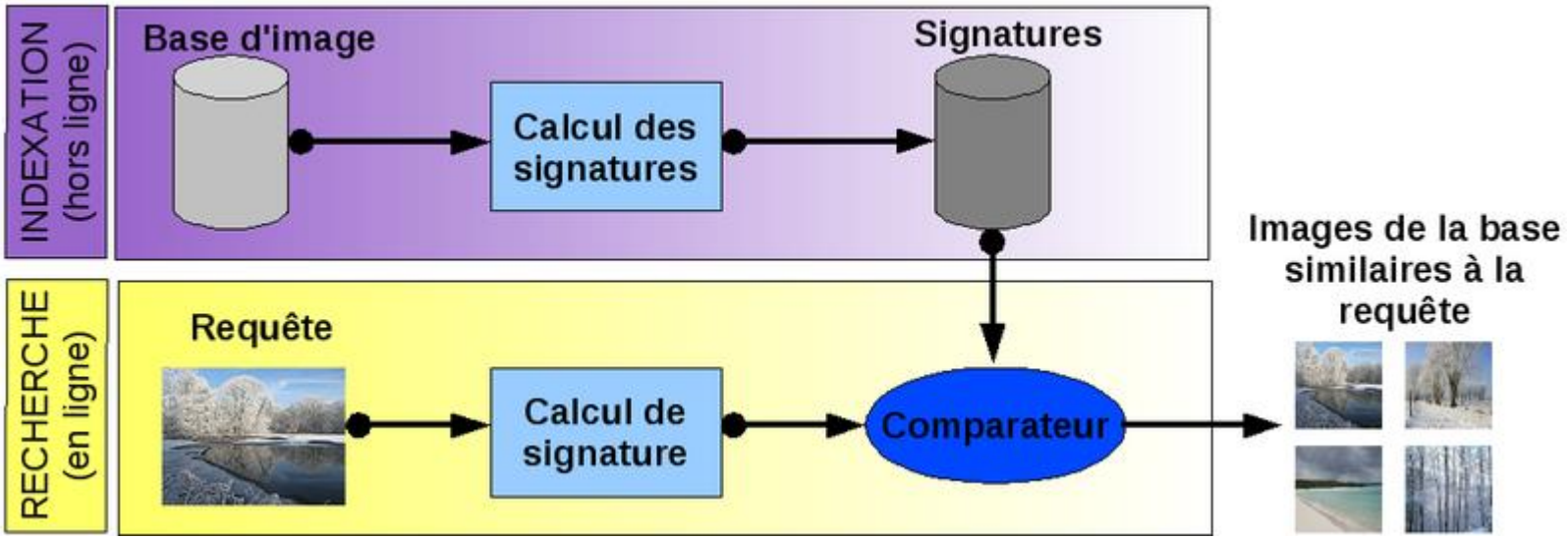




Dantas, et al., JCB, DOI: 10.1083/jcb.201012093

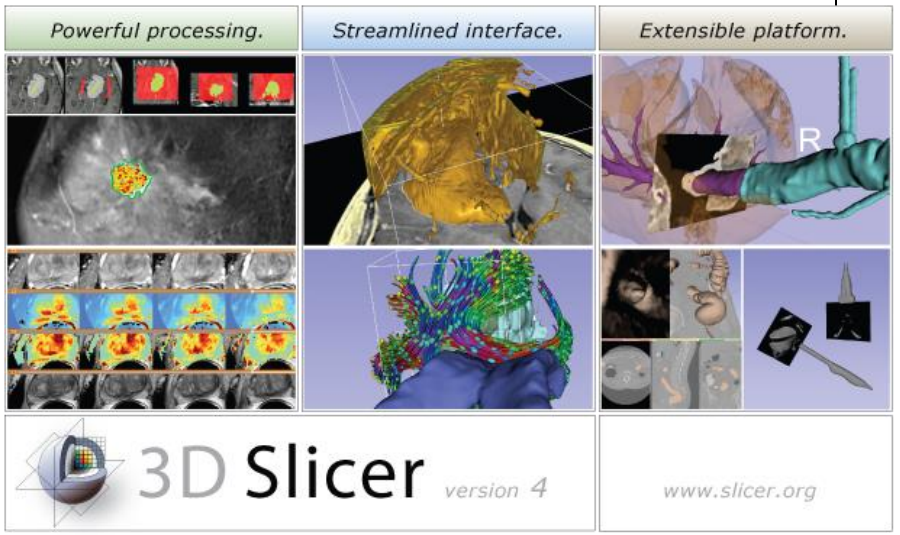
Recherche d'images par le contenu

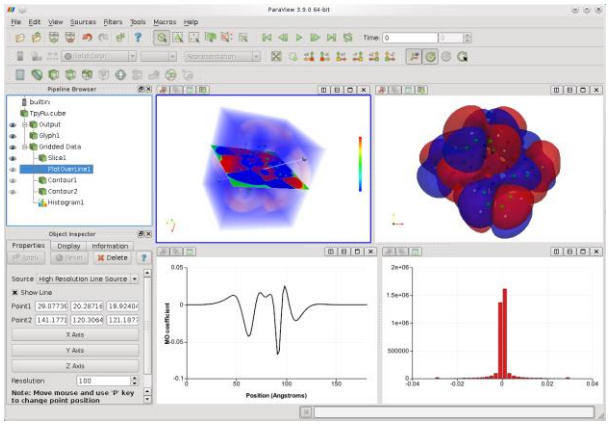
- Idée :
  - Une image est décrite par un ensemble de paramètres
  - On recherche les images les plus proches dans l'espace des paramètres

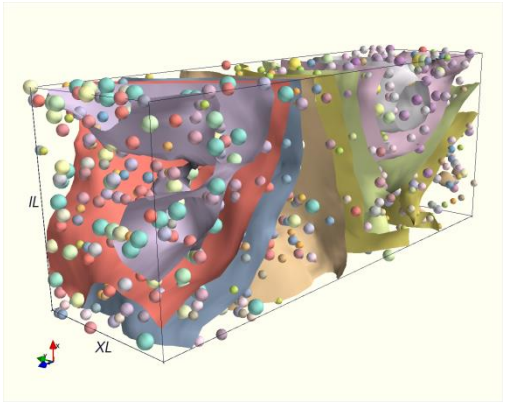


Logiciels de visualisation 3D+

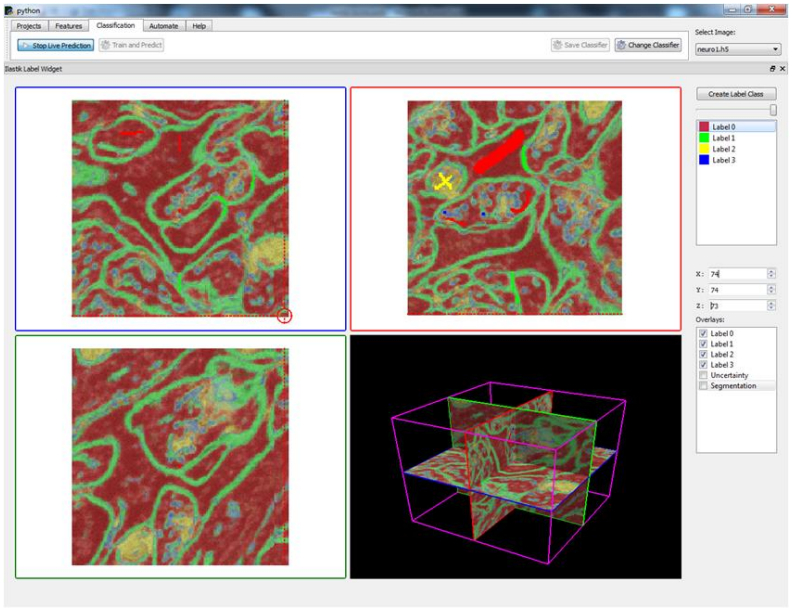
- Libres
  - 3DSlicer
  - Mayavi
  - VisIt
  - Paraview
- Commerciaux
  - Avizo
  - Matlab
- Représentent données + modèles

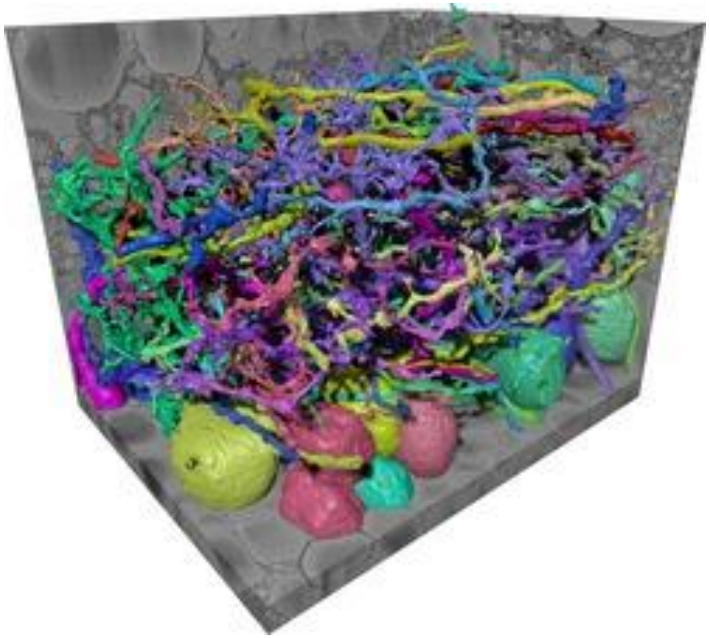




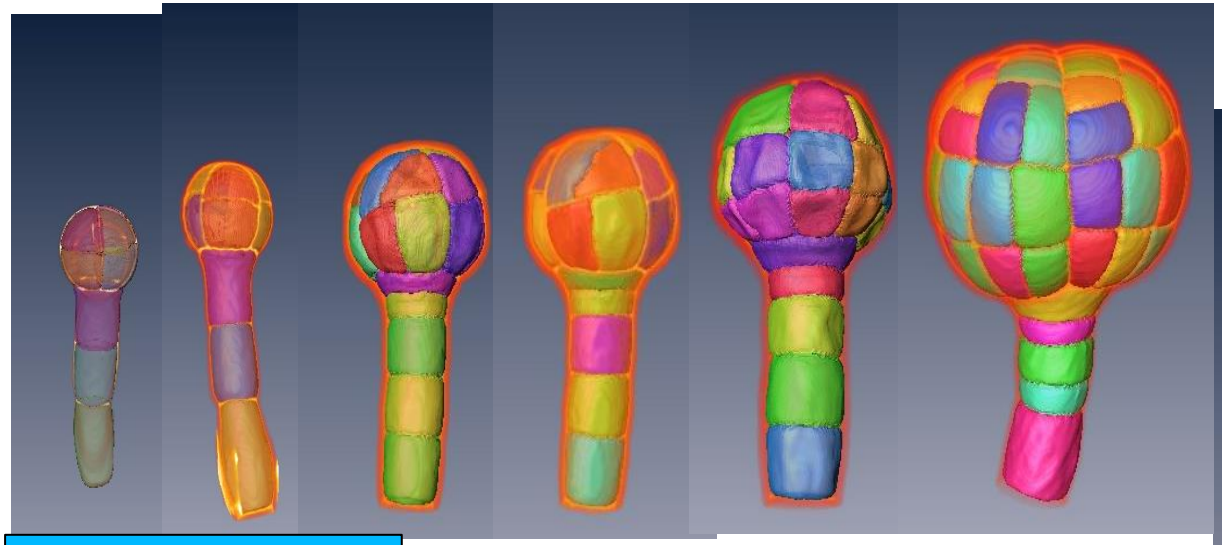


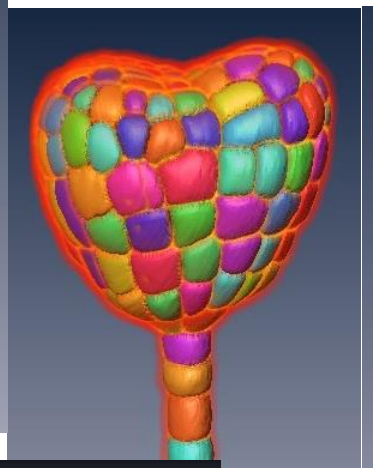
Extraire les infos d'une image

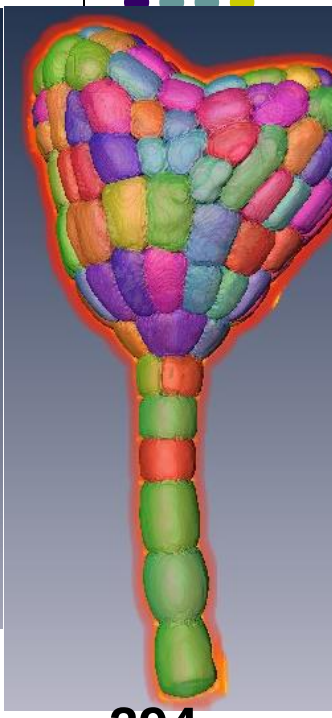




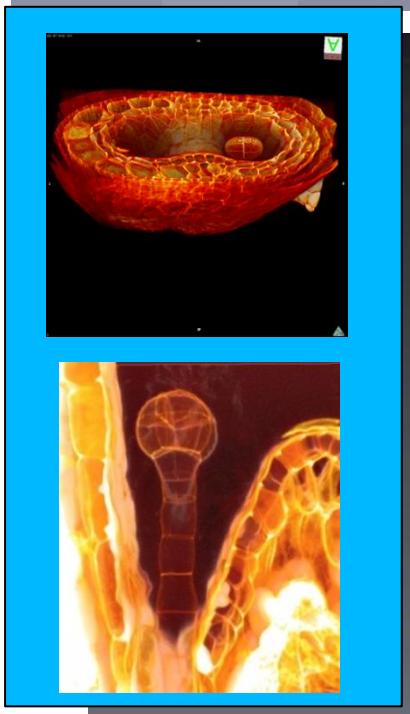
- Segmentation supervisée d'images :
  - Extraction de paramètres
  - Sélection de régions d'intérêt
  - Apprentissage supervisé des classes







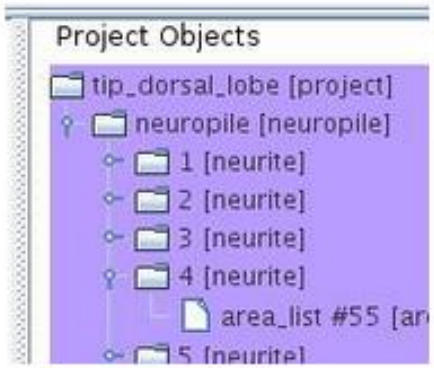
294
cells

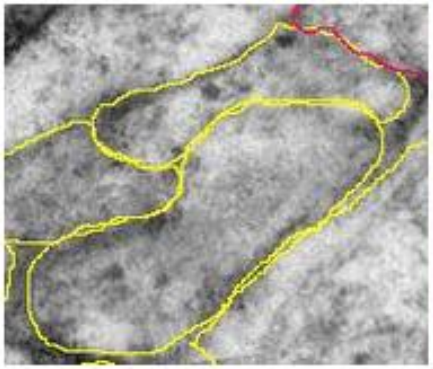


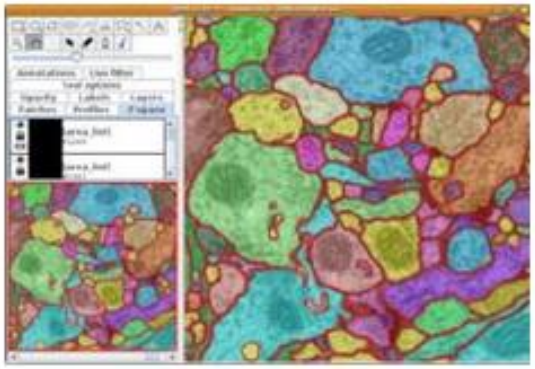
ImageJ +plugins, Fiji, ICY

TrakEM2 Snapshots

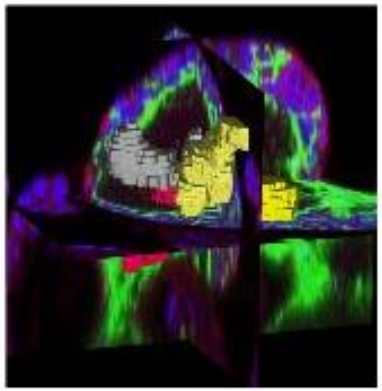
- The semantic segmentation editor: specify what you want, and then assign segmentation profiles such as area lists in an orderly manner:

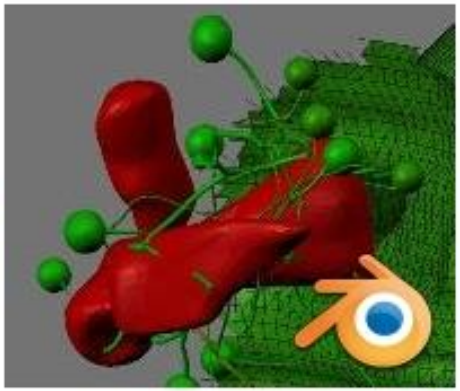


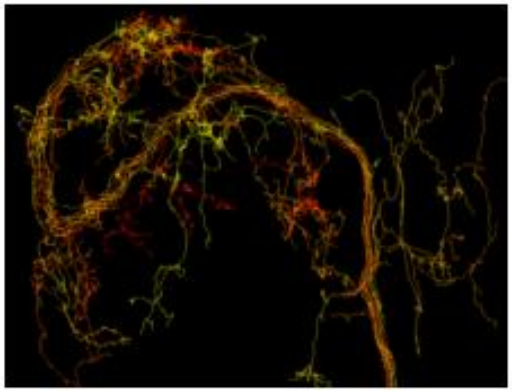




- TrakEM2 interacts directly with the ImageJ 3D Viewer, and exports to WaveFront and DXF for further mesh processing in CAD programs such as Blender. Meshes, pixel volumes and orthoslices are all supported.







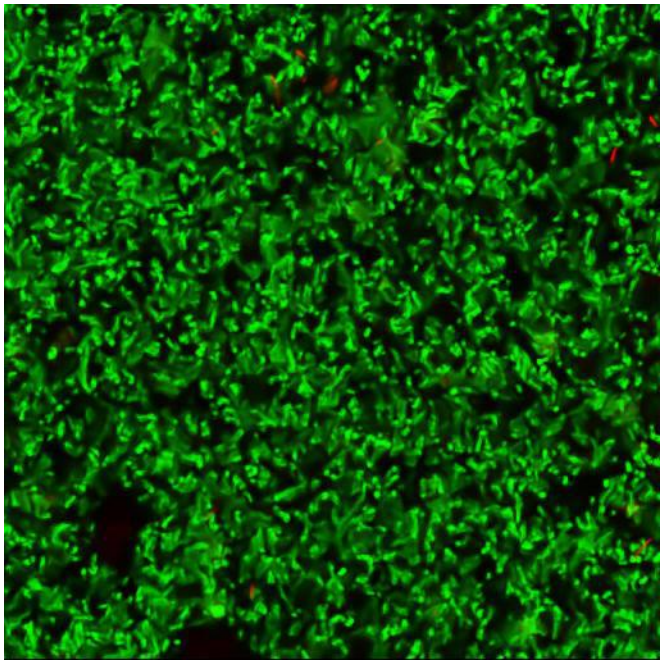
Albert Cardona, et al. 2012. TrakEM2 Software for Neural Circuit Reconstruction. PLoS ONE 7(6): e38011.

Extraction et Analyse de dynamiques

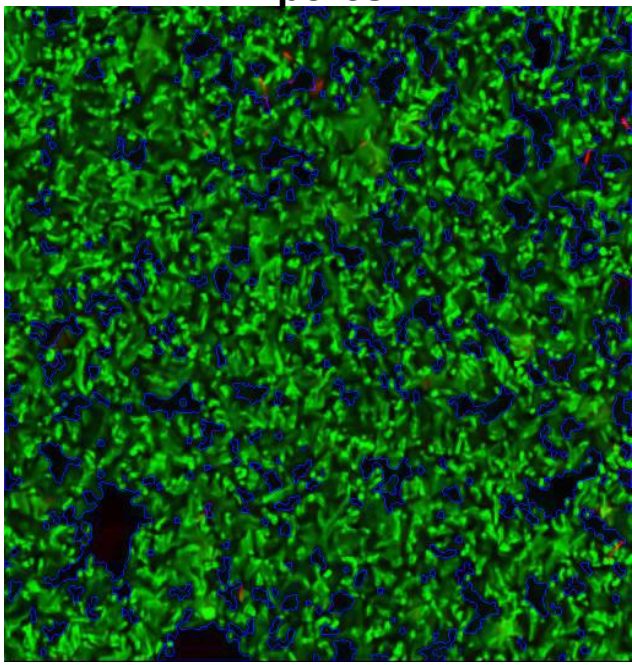
- Extraction : U-Track [Jaqaman], pyTrack,
- Challenge ISBI

projections maximales

trajectoires

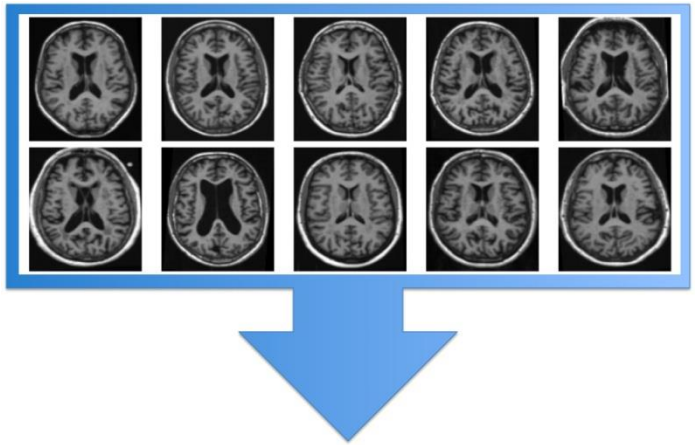


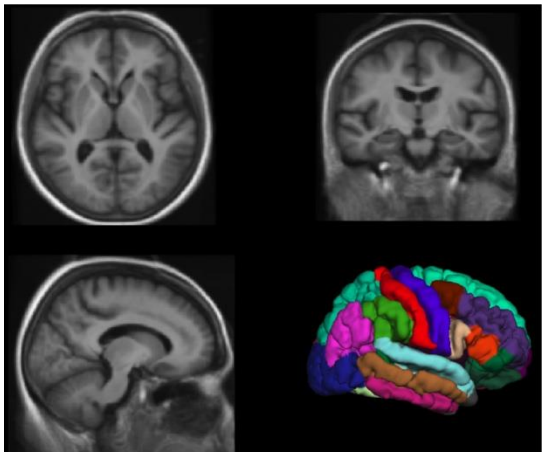
pores



Fusion de plusieurs images

- Création d'atlas
  - N images observées
  - Une image « moyenne »
  - Différences entre images





⟹ FreeD

Mobyle@SERPICO

(guest)
set email | sign-in | activate | sign-out
refresh workspace

SERPICO team (INRIA Rennes - Bretagne Atlantique) is partner of France-BioImaging

Search

Programs

- Backwarping
- CRFMovingSpotDetection
- HotSpotDetection
- Hullkground
- KLTracker
- Motion2D
- MS-Detect
- NDSafir
- OpticalFlow
- OpticalFlowStack

Tutorials

- registration

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Welcome to Mobyle, a portal for bioinformatics analyses

Space timE RePresentation, Imaging and cellular dynamics of molecular COmplexes

SERPICO

Programs available

- **Backwarping:** *Warp sequence with parametric motion model*
- **CRFMovingSpotDetection:** *Detecting moving spots/vesicles using Conditional Random Fields*
- **HotSpotDetection:** *Robust detection of fluorescence accumulation over time in video-microscopy*
- **HullkGround:** *Separation of moving and non moving part in a sequence*
- **KLTracker:** *Track vesicle and POI in image sequences*
- **Motion2D:** *Estimate 2D parametric motion model*
- **MS-Detect:** *Detecting moving objects in image sequences by background subtraction*
- **ND-SAFIR:** *Denoise N-Dimensional images*
- **Optical-flow:** *Compute Optical Flow between 2 images*
- **OpticalFlowStack:** *Compute Optical Flow between each pair of images in a TIFF stack*

Credits

Mobyle is a platform developed jointly by the Institut Pasteur Biology IT Center and the Ressource Parisienne en Bioinformatique Structurale.
More information about this project can be found here.

FRANCE-BIOIMAGING

Connaissances du domaine

Welcome

This website is intended to be a useful source of information for people interested or working in the various fields of imaging. It collects links to relevant websites on image formation, image reconstruction, image processing, image analysis, computer vision, pattern recognition, and visualization. We invite you to contribute to this website by informing us of other useful websites that we could add here.

Organizations

ASPRS (Imaging and Geospatial Information)
EMS (European Microscopy Society)
ESR (European Society of Radiology)
IAPR (Association for Pattern Recognition)
IEEE (Electrical and Electronics Engineers)
IS&T (Imaging Science and Technology)
ISMRM (Magnetic Resonance in Medicine)
MSA (Microscopy Society of America)
OBIA (Open Bio Image Alliance)
RSNA (Radiological Society of North-America)
SMPTE (Motion Picture and Television Engineers)
SPIE (Photo-Optical Instrumentation Engineers)
WMIS (World Molecular Imaging Society)

Conferences

Main Conferences

BII (Bioimage Informatics)
CVPR (Computer Vision and Pattern Recognition)
ECCV (European Computer Vision)
ECR (European Radiology)
ELMI (European Light Microscopy)
EMIM (European Molecular Imaging)
FOM (Microscopy Imaging)
ICCV (Computer Vision)
ICIP (Image Processing)
ICPR (Pattern Recognition)

News

Computer Vision Central
ImageWorld Mailing List
MedImaging Daily Radiology News
Microscopy News
Molecular Imaging News
ScienceDaily Medical Imaging News

Journals

Biomedical Imaging

Computerized Medical Imaging and Graphics
IEEE Transactions on Medical Imaging
Imaging Systems and Technology
International Journal of Biomedical Imaging
Journal of Digital Imaging
Medical Image Analysis

Computer Vision

Computer Vision and Image Understanding
Image and Vision Computing
International Journal of Computer Vision
Journal of Mathematical Imaging and Vision

Cardiovascular Imaging

CardioVascular and Interventional Radiology
Circulation: Cardiovascular Imaging
International Journal of Cardiovascular Imaging
Journal of Vascular and Interventional Radiology

Image and Video Processing

EURASIP Journal on Image and Video Processing
IEEE Transactions on Image Processing
Journal of Electronic Imaging
Journal of Real-Time Image Processing
Signal, Image and Video Processing
Visual Communication and Image Representation

Imaging Science

Imaging Science Journal
JOSA A: Optics, Image Science, and Vision

Software

Image Analysis

Bio7
BioImage Suite
BioImageXD
CATMAID
CellProfiler
Crystal Image
CVIPTools
DIPimage & DIPlib
Endrov
Fiji
GeoS
GIMP
Icy
Ilastik
ImageJ
ImageJDev
IMAL
KNIME
NIH Image
PhenoRipper

Image Management

BISQUE
OMERO
µManager

Visualization

3DSlicer
AMIDE
BioImageXD
OsiriX
Vaa3D
VisBio
VisIt

Toolkits

Bio-Formats (Image Reading and Writing)
FARSIGHT (Microscopy Image Analysis)

IPOL is a research journal of image processing and image analysis. Each article contains a text describing an algorithm and source code, with an online demonstration facility and an archive of online experiments. The text and source code are peer-reviewed and the demonstration is controlled. IPOL is an Open Science and Reproducible Research journal.

Editorial Policy Editorial Board Submit an Article

Index · Articles 2013 2012 2011 2010 · Preprints

Latest Articles

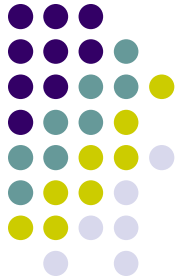
follow IPOL

- **Robust Optical Flow Estimation**
  2013-10-28 · Javier Sánchez Pérez, Nelson Monzón López, Agustín Salgado de la Nuez
- **Recovering the Subpixel PSF from Two Photographs at Different Distances**
  2013-10-23 · Mauricio Delbracio, Andrés Almansa, Pablo Musé
- **Exemplar-based Texture Synthesis: the Efros-Leung Algorithm**
  2013-10-23 · Cecilia Aguerrebere, Yann Gousseau, Guillaume Tartavel
- **Selective Contrast Adjustment by Poisson Equation**
  2013-09-26 · Ana-Belen Petro, Catalina Sbert
- **Analysis and Extension of the Ponomarenko et al. Method, Estimating a Noise Curve from a Single Image**
  2013-07-23 · Miguel Colom, Antoni Buades
- **Horn-Schunck Optical Flow with a Multi-Scale Strategy**
  2013-07-19 · Enric Meinhardt-Llopis, Javier Sánchez Pérez, Daniel Kondermann

Topics

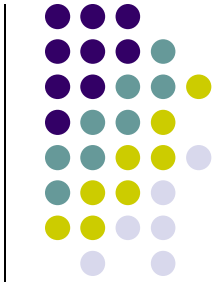
- 3D
- Blur
- Calibration
- Color and Contrast
- Computational Photography
- Demosaicking
- Denoising
- Infrared
- Inpainting
- Interpolation
- Image Comparison
- Optical Flow
- PDE
- Segmentation and Edges
- Stereovision
- Texture
- Vision Through Turbulence
- Other Topics

2. Besoins



- Données
  - biologie: plusieurs échelles, plusieurs espèces moléculaires, dynamique
    - Complémentarité des données
    - Réutilisation des données
  - environnement :
  - procédés
  - Astronomie: ex mission Corot

- Logiciels



- The grand challenges chosen for ISBI 2015 are the following:
- 1. White Matter Modeling
- 2. Cell Tracking Challenge
- 3. Segmentation of Overlapping Cervical Cells from Multi-layer Cytology Preparation Volumes
- 4. Grand Challenges in Dental X-ray Image Analysis
- 5. Longitudinal Multiple Sclerosis Lesion Segmentation
- 6. MR Brain Image Segmentation in Neonates versus Adults (NEATBrainS15)
- 7. Automatic Polyp Detection Challenge in Colonoscopy Videos
- 8. VISCERAL Anatomy for Grand Challenge

Conclusions

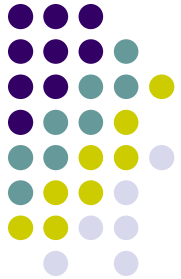
- Multiplicité d'entrepôts, de logiciels
- Communautés autour de logiciels
- Efforts de fédérations, clarifications
- Organiser des challenges
- Créer une communauté

Sachant cela :

Poser une question, répondre, ne pas réinventer,

Image Processing & Data Management (IPDM) [Node of France BioImaging]

http://france-bioimaging.org/network/image-processing-data-management-ipdm



- exhaustive analysis of bioimaging data sets;
  - deciphering of key steps of biological mechanisms at organ, tissular, cellular and molecular levels through the systematic use of time-lapse+3D microscopy and image processing methods;
  - storage and indexing of extracted and associated data and metadata through an intelligent data management system

The major goals are to develop:

- an integrated and cutting-edge image processing software platform to harbor next generation algorithms for image processing;
- an integrated workflow for launching algorithmic pipelines on the FranceBioImaging computation grid or local computer clusters for high throughput processing of image data sets;
- the development of standard methods in statistics and machine learning for multi-scale analysis and categorization of biological features;
- the development of standardized evaluation metrics for assessing the quality, precision and accuracy of a processing workflow;
- a data management solution to accommodate the storage, query and annotation of large amounts of image data and metadata.; and
- a resource management system to allow remote reservation, payment and image management from internal or distant sites by all the users of the FranceBioImaging infrastructures.

Conclusions

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OMERO, scikit-image, scikit-learn, icy,…

Conclusions

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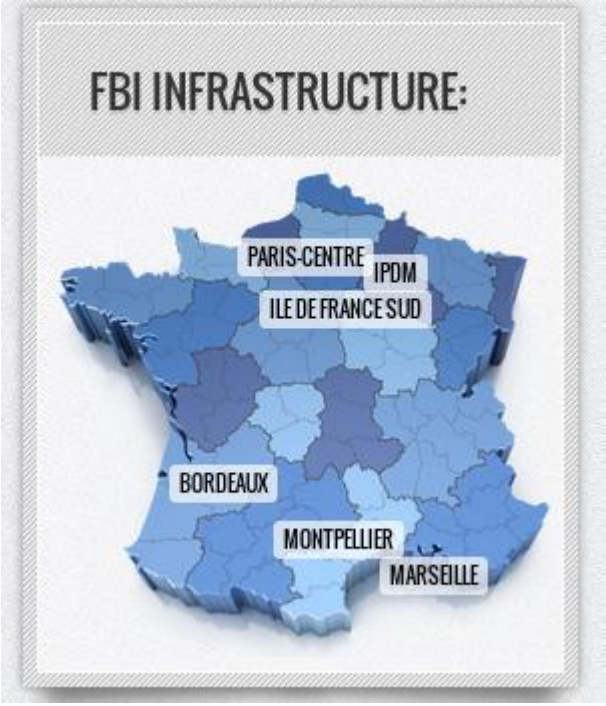
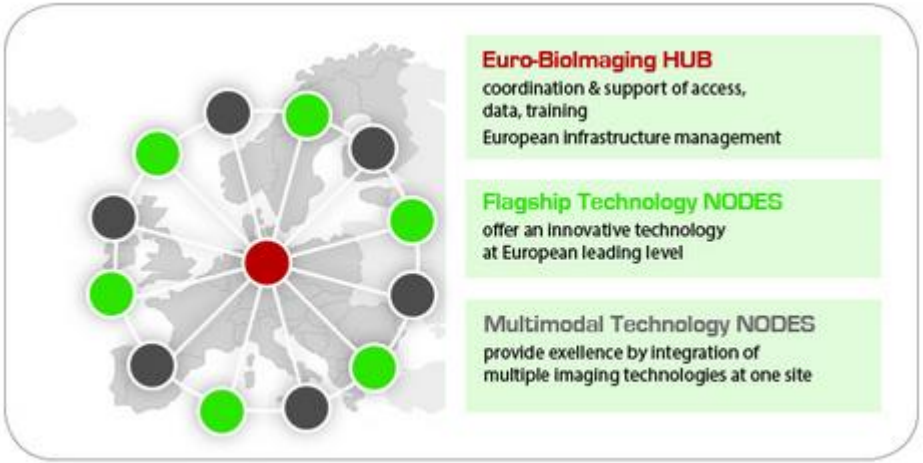
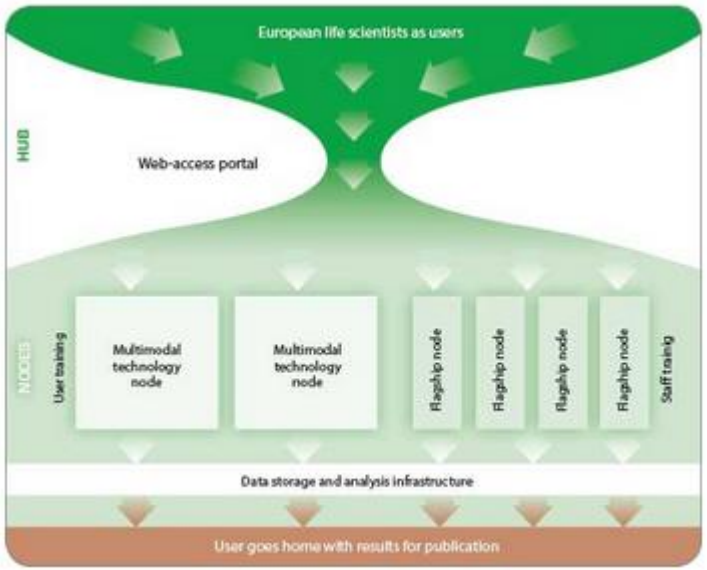

FBI INFRASTRUCTURE:
PARIS-CENTRE
IPDM
ILE DE FRANCE SUD
BORDEAUX
MONTPELLIER
MARSEILLE


Euro-BioImaging HUB
coordination & support of access, data, training
European infrastructure management
Flagship Technology NODES
offer an innovative technology at European leading level
Multimodal Technology NODES
provide exellence by integration of multiple imaging technologies at one site


European life scientists as users
HUB
Web-access portal
NODES
User training
Multimodal technology node
Multimodal technology node
Flagship node
Flagship node
Flagship node
Flagship node
Staff training
Data storage and analysis infrastructure
User goes home with results for publication

Conclusions

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IDEX DataSciences (Saclay)

centré sur l'exploration de données de tous types (tableaux, images, texte) et toutes provenances (biologie, physique,…

Exemple: Le frigidaire

« Une Webcam dans le frigidaire »

- Détection de mouvement (actions: bouger, retirer, ajouter)
- Identification des objets (forme, modèle 3D)

Farnstrom et al, ‘Computer Vision for Determination of Fridge Contents’,

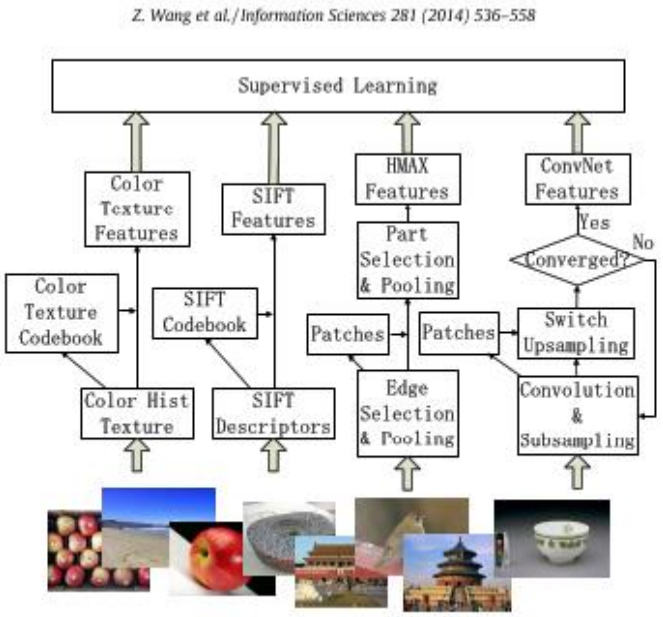

Fig. 1. A framework of image classification including four pathways.

Figure 12: The training images for two objects are shown on the left. These can be recognized in a cluttered image with extensive occlusion, shown in the middle. The results of recognition are shown on the right. A parallelogram is drawn around each recognized object showing the boundaries of the original training image under the affine transformation solved for during recognition. Smaller squares indicate the keypoints that were used for recognition.

A. Vedaldi and B. Fulkerson, VLFeat: An Open and Portable Libraryof Computer Vision Algorithms , 2008
K. Simonyan and A. Zisserman Very Deep Convolutional Networks for Large-Scale Image Recognition, arXiv 2014