

Collaborative analysis of multimodal imaging data with cytomine web platform



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cytominE (short) story and ecosystem

- 2010-... : R&D project initiated at University of Liège  for cyto-histopathology image analysis (<https://uliege.cytomine.org>)
- 2016-.... : Open-source release (<https://github.com/cytomine/>) 
- 2017-... : *Cytomine not-for-profit cooperative company* (<https://cytomine.org>) for code maintenance, documentation, and open-source community management 
- 2021-... : *Cytomine corporation* is selling services on top of the open-source software (<https://cytomine.com>)
- Cytomine is distributed under a **permissive licence (Apache 2.0)**, and used by thousands of users in research/education settings

cytominé is widely known for histology

Numerous Cytomine server installations around the world



HELSE VEST IKT



LABORATORIO DE
PATOLOGÍA
DR. NOY



SAAB

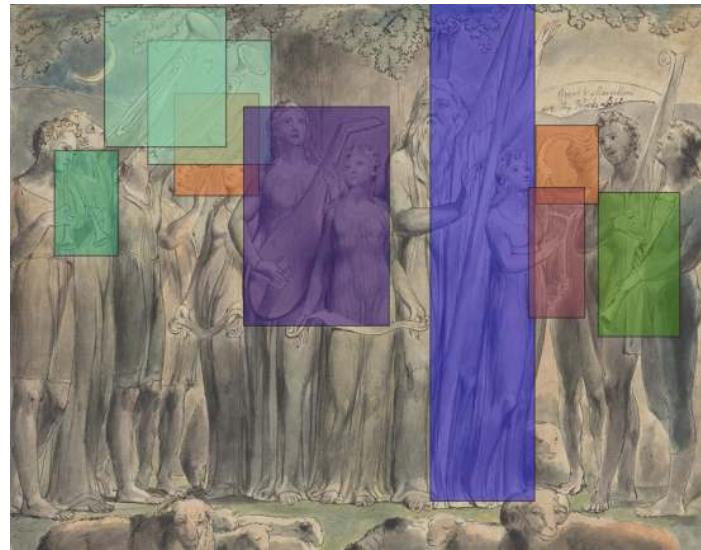


BIGPICTURE
European Digital Pathology Platform

(2021-2027-...) innovative medicines initiative



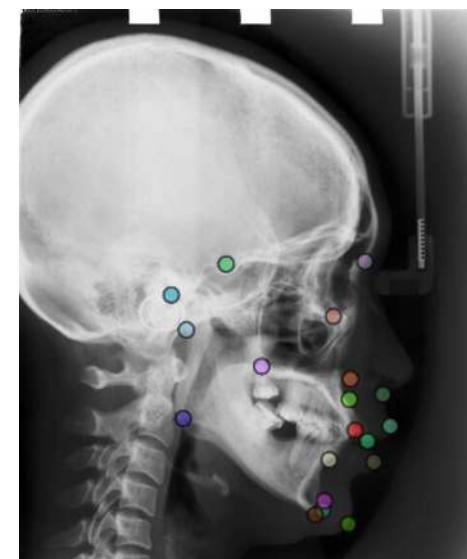
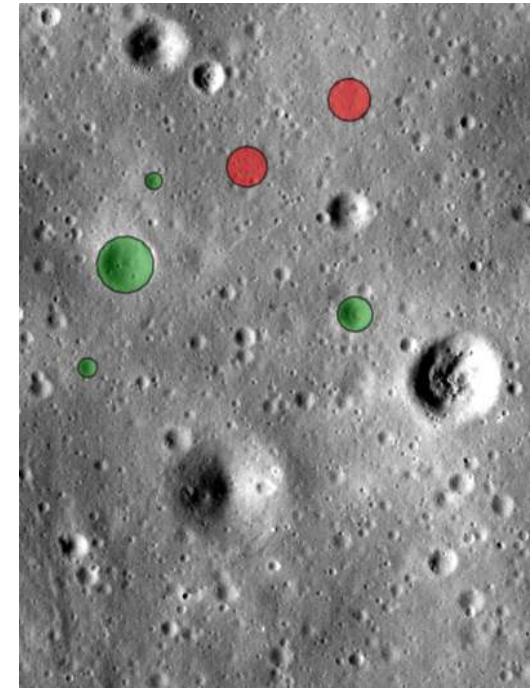
cytominne is not only meant for histology



(Sabatelli et al., DHQ 2021)



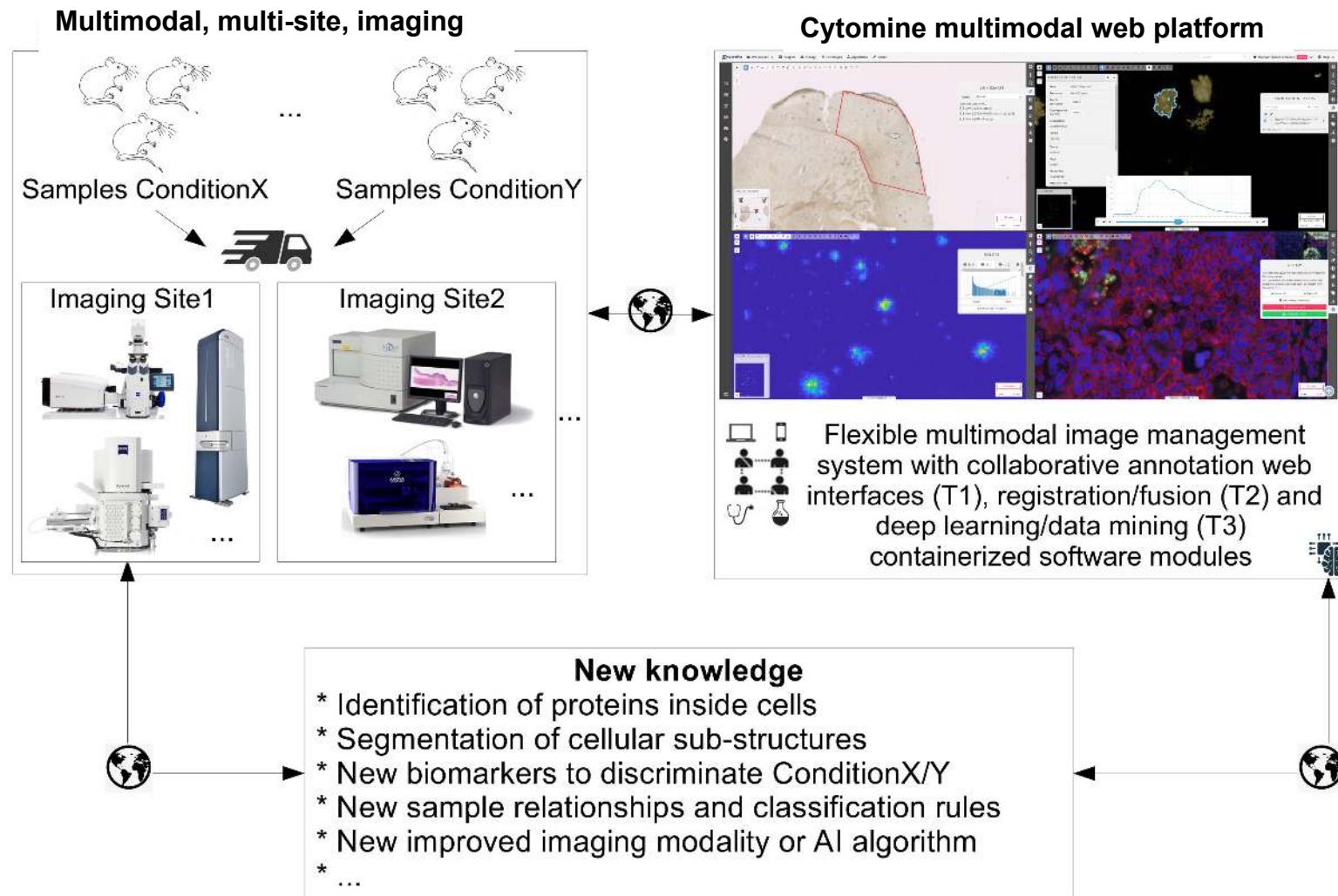
(Vandaele et al., 2018)



(Vandaele et al., 2018)

cytominer is not meant only for histology

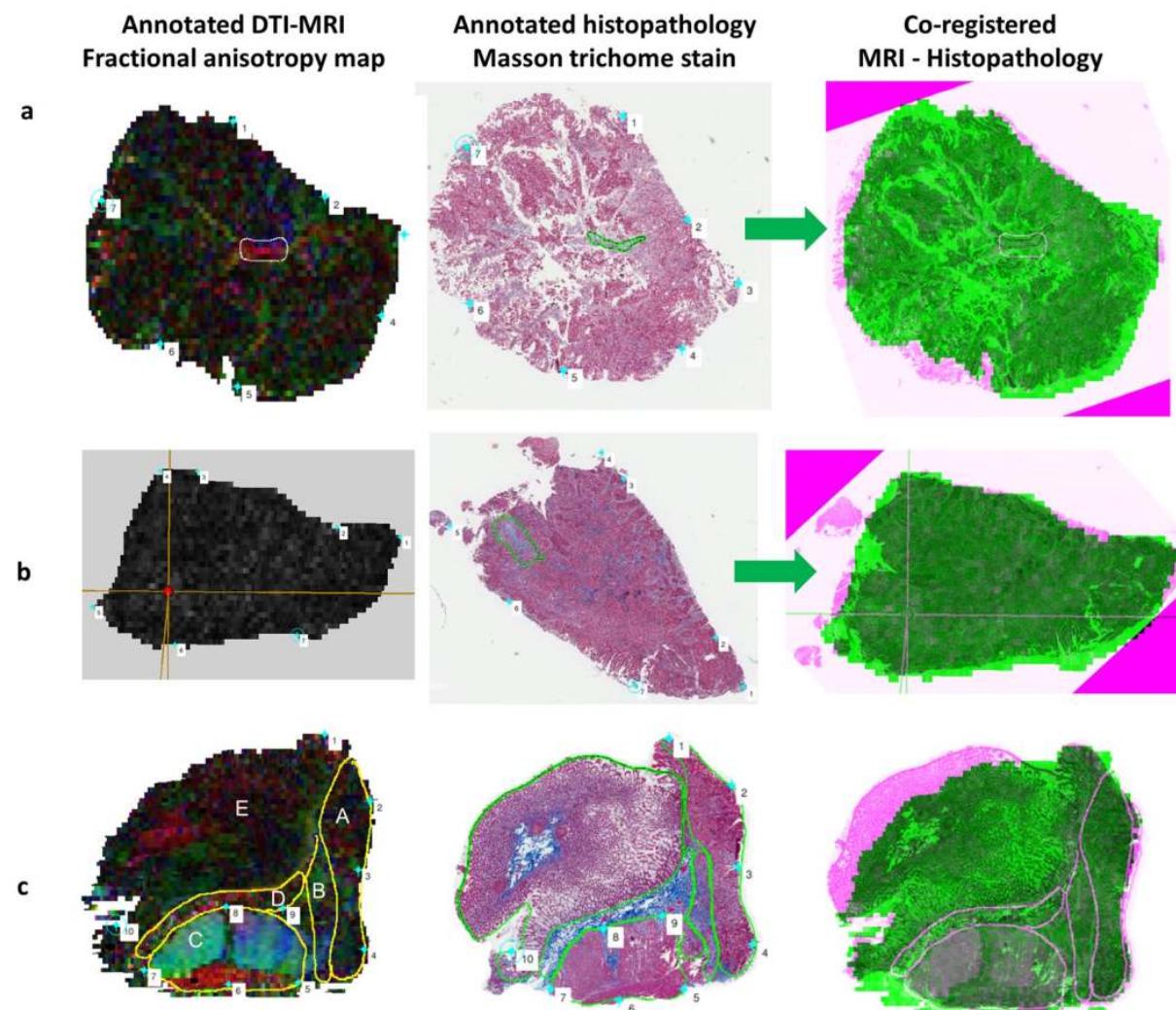
Ongoing and future developments / objectives :



Correlated Multimodal Imaging examples

Correlation of ultra-high field MRI with histopathology for evaluation of rectal cancer heterogeneity (Scientific Reports, 2019)

Trang T. Pham^{1,2,3}, Timothy Stait-Gardner⁴, Cheok Soon Lee^{2,3,5,6}, Michael Barton^{1,2,3},
Petra L. Graham^{1,2,3}, Gary Liney^{1,2,3}, Karen Wong^{1,2,3} & William S. Price^{1,4,5}



Correlated Multimodal Imaging examples

Correlative x-ray phase-contrast tomography and histology of human brain tissue affected by Alzheimer's disease

(NeuroImage 2020)

Mareike Töpperwien ^a, Franziska van der Meer ^c, Christine Stadelmann ^c, Tim Salditt ^{a,b,*}

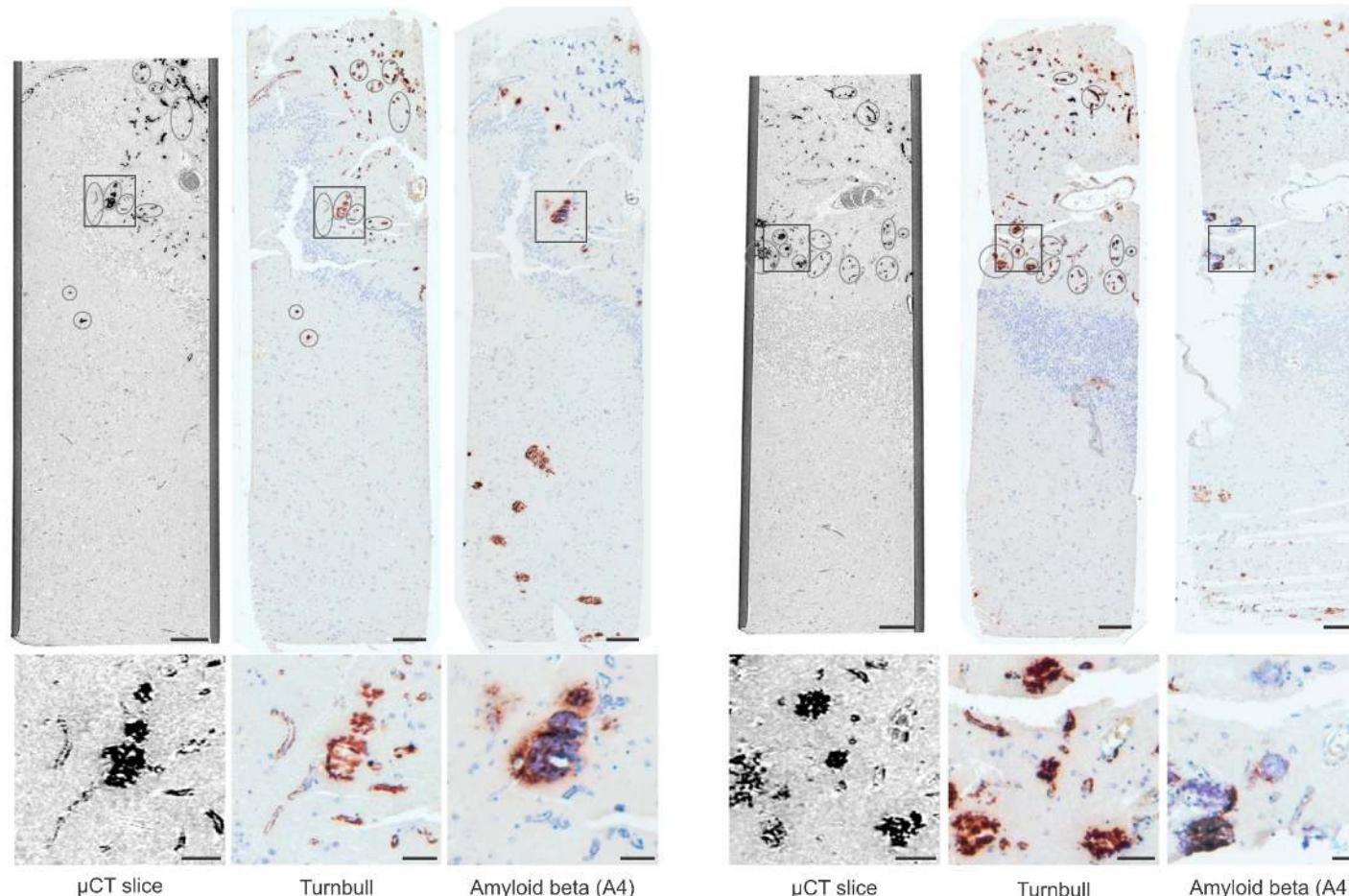
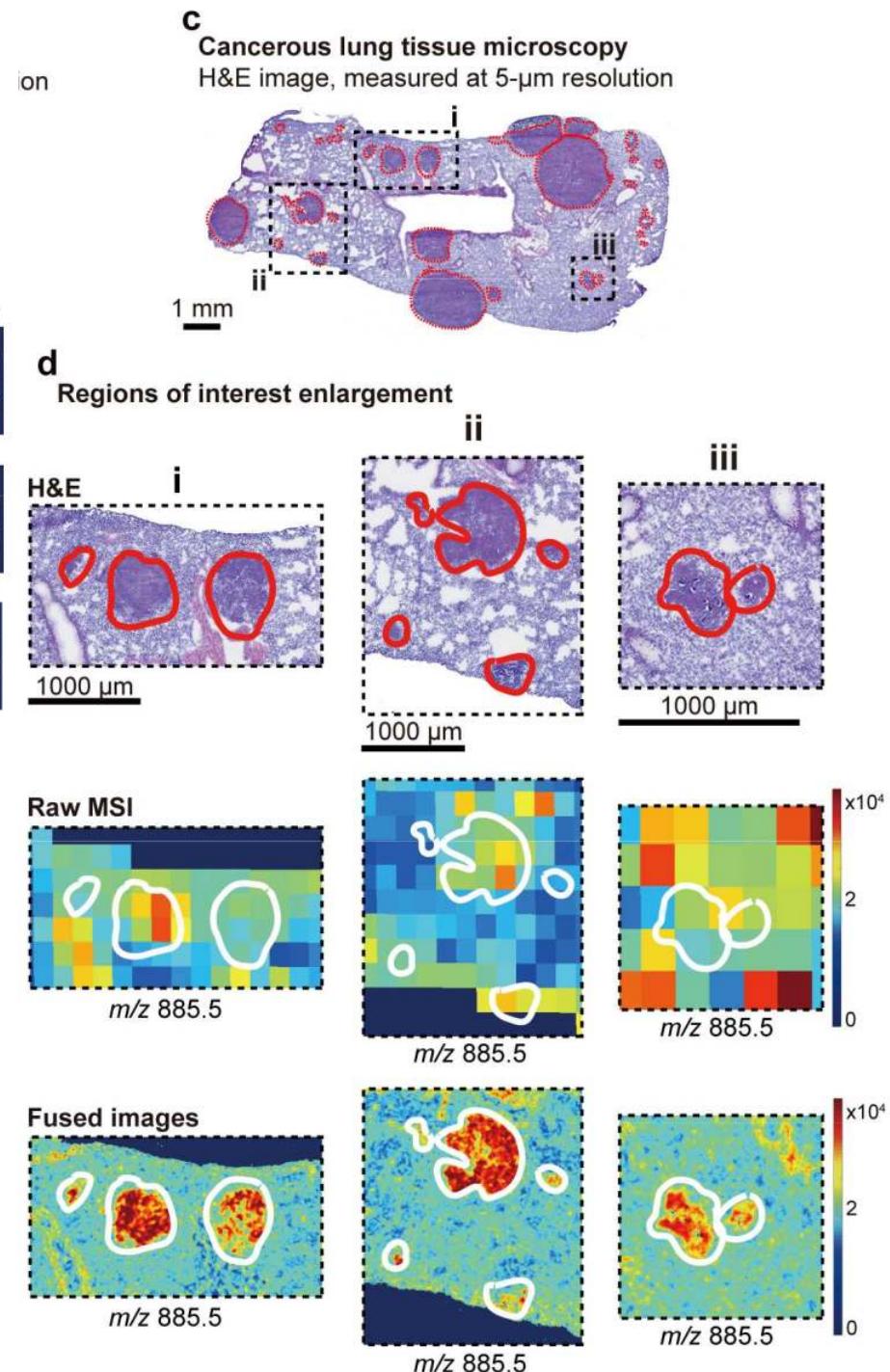
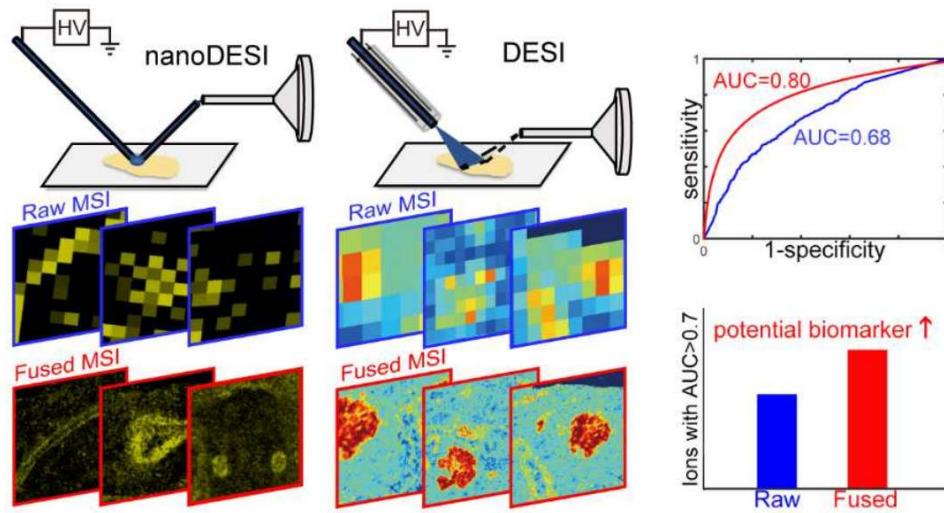
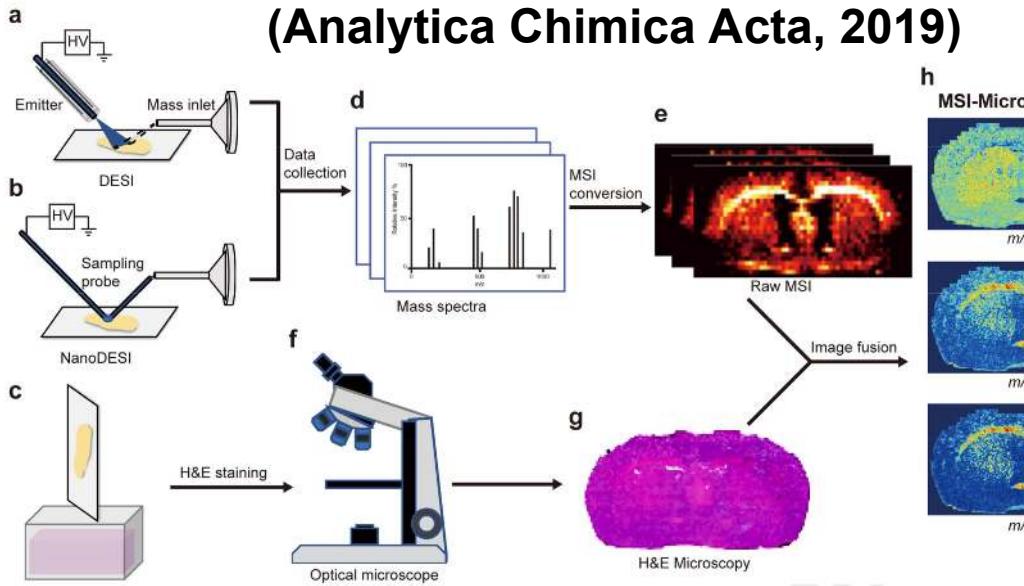


Fig. 6. Comparison between virtual slices through the laboratory μ CT results (left) and histological sections using a β -amyloid (A4) staining protocol (right). As in Figs. 4 and 5, the encircled features in the virtual slice and the histological sections show similarities which indicate that the positions of the virtual slices from the μ CT results and the histological sections approximately coincide. Also in this case, the electron-dense plaque-like structures correspond to features containing iron, as observed in the corresponding histological section stained according to the Turnbull protocol (center). The β -amyloid (A4) together with the hematoxylin stain additionally shows that they consist of calcified structures and β -amyloid, proving that they are indeed mineralized β -amyloid plaques. Note that the contrast in the microscope images of the histology sections has been adjusted to ensure maximum visibility of the features of interest. Scale bars: 200 μm (top) and 50 μm (bottom).

Correlated Multimodal Imaging examples

Precision Biomarker Discovery Powered by Microscopy Image Fusion-assisted High Spatial Resolution Ambient Ionization Mass Spectrometry Imaging

(*Analytica Chimica Acta*, 2019)



Correlated Multimodal Imaging examples

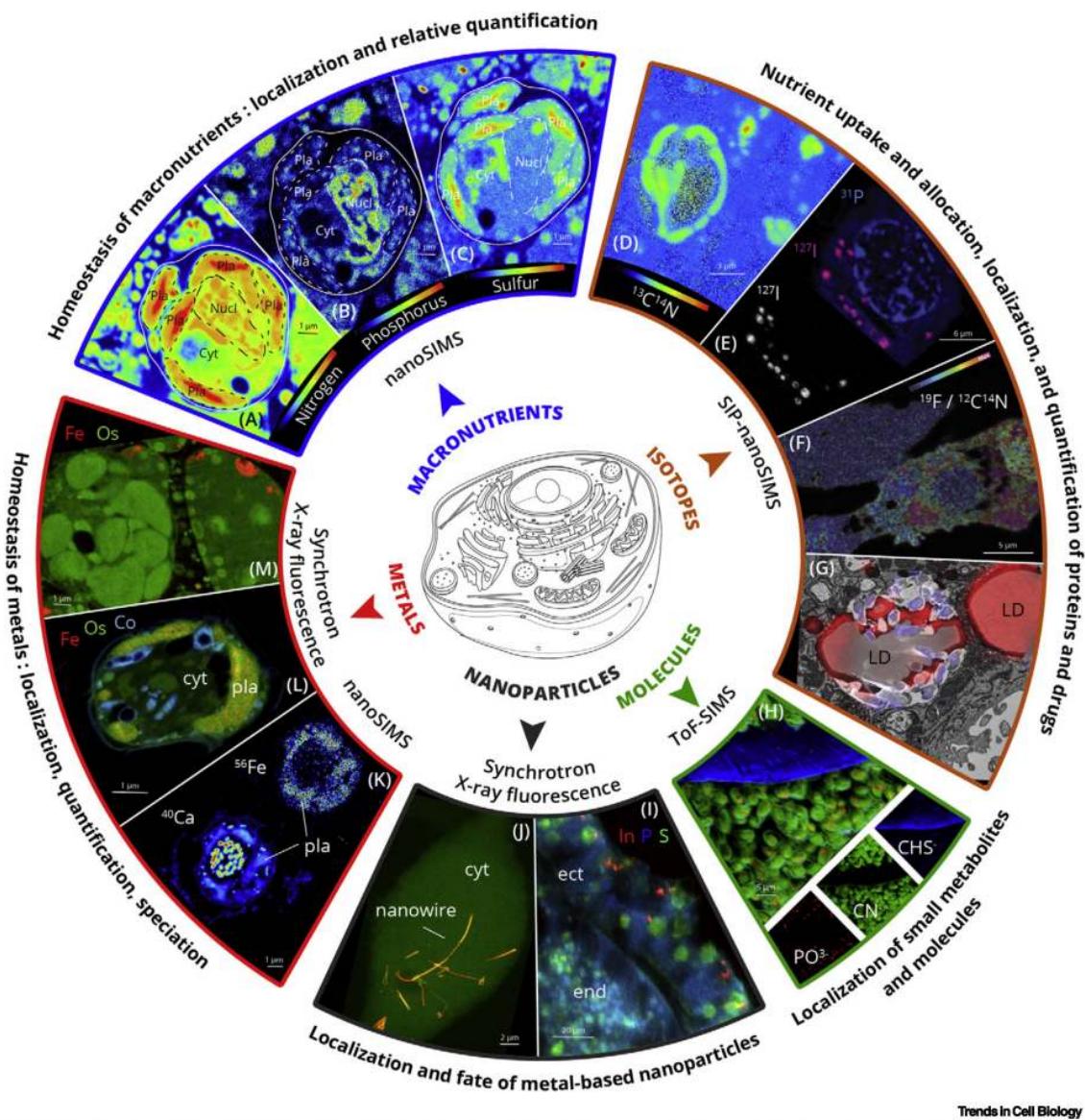


Figure 2. The Potential of Chemical Imaging to Unveil the Chemical Landscape of a Cell: Composition and Distribution of Elements, Isotopes, and Molecules at the Nanoscale. (A–C) Nano-secondary ion mass spectrometry (nanoSIMS) images showing the distribution of the macronutrients nitrogen [^14N], phosphorus [^31P], and sulfur [^32S] in a cell. (D–F) Correlation between electron microscopy (EM) and chemical imaging.

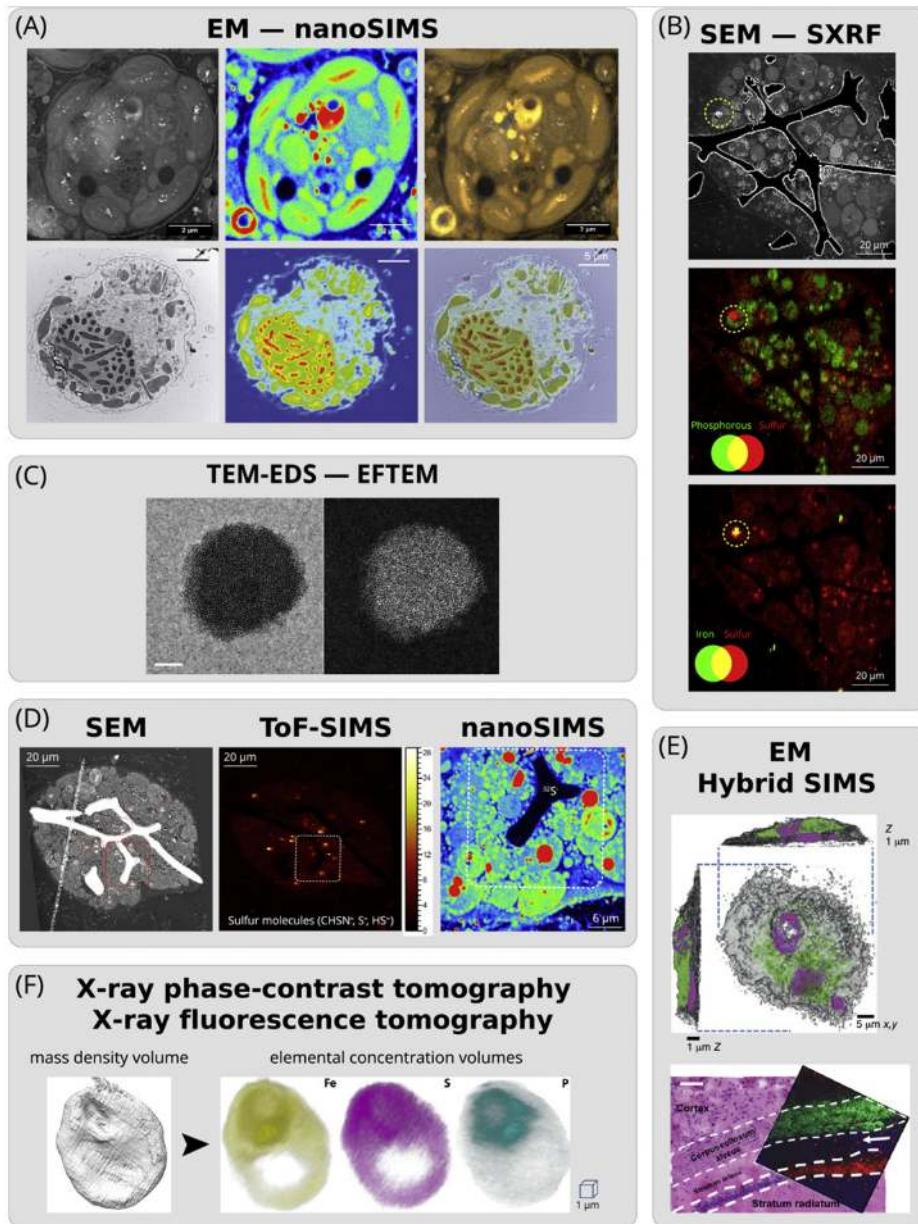
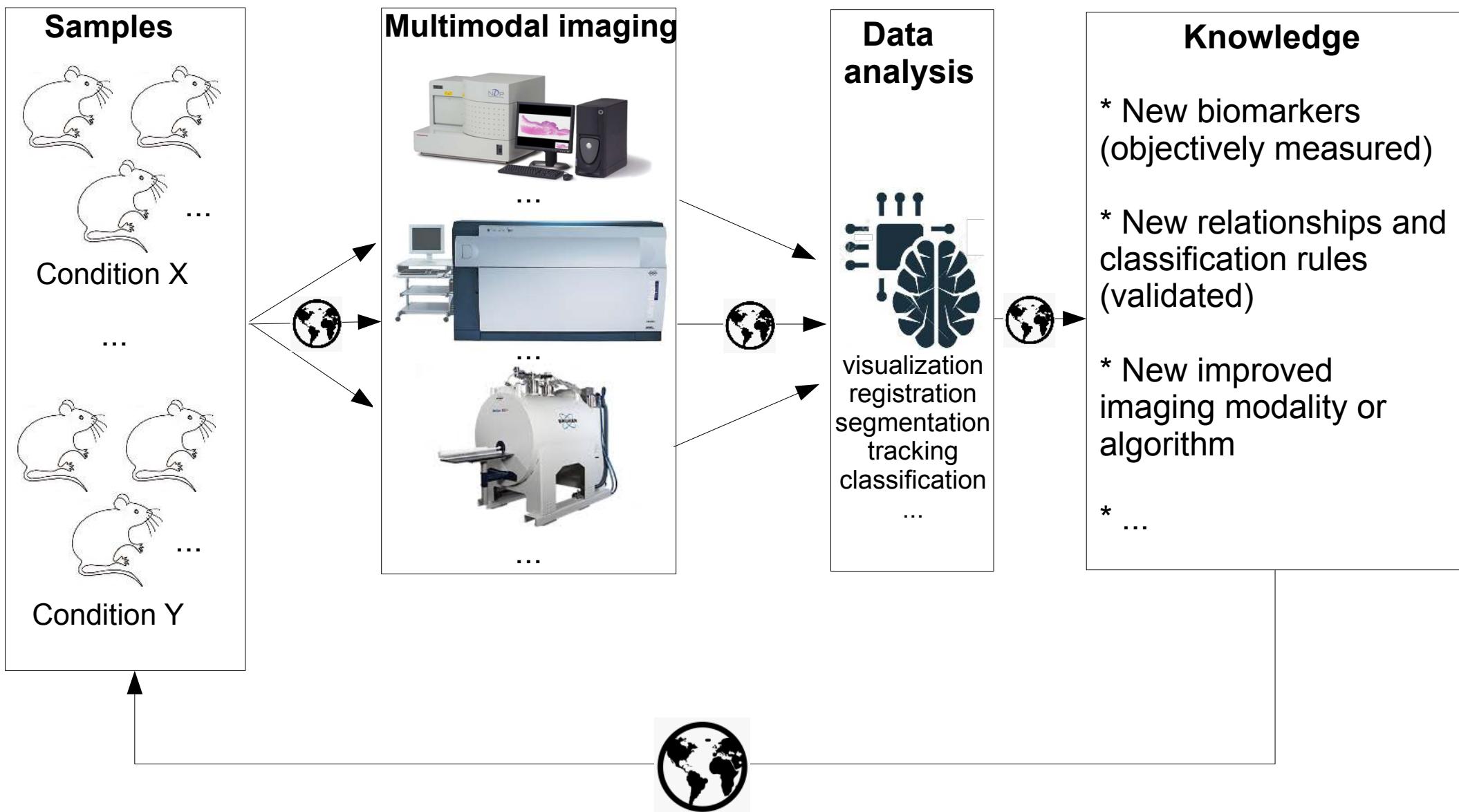


Figure 3. Examples of Correlated Electron Microscopy (EM) and Chemical Imaging. (A) Correlation between EM

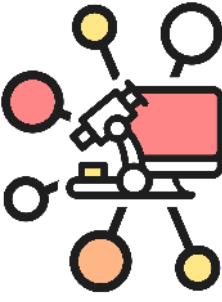
Decelle et al., Subcellular Chemical Imaging: New Avenues in Cell Biology (CellPress Reviews, 2020)

Ideal correlative/multimodal workflow

(Exploratory analysis / Biomarker discovery / Classification of samples)

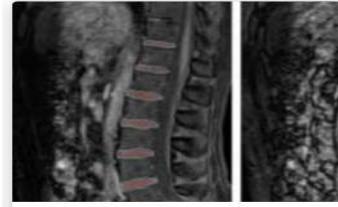


A plethora of image analysis tools



BiiI
BioImage
Informatics
Index

<https://biii.eu/>
(> 1331 « software »)



Medical Image Segmentation

57 benchmarks
113 papers with code

<https://paperswithcode.com/>
(> 11000 ML papers with code)

openneuroscience
<https://open-neuroscience.com>

 **Quantitative Plant**

<https://www.quantitative-plant.org/>

<http://spatialomics.net/>

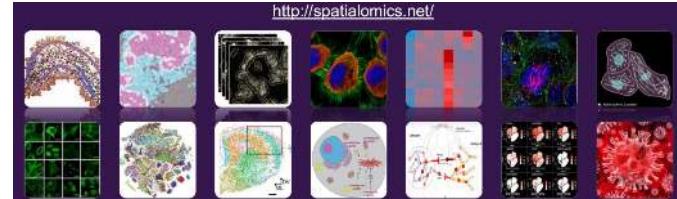


Image registration :

« *literally hundreds of different registration algorithms exist* »
(Borovec et al., IEEE TMI 2020)

Visual proteomics:

HistoCat (Schapiro 2017) ; Basis (Veselkov et al., 2018) ; OpenMSI & BASTet (Rübel et al., 2018) ; Starfish (Ganguli et al., 2018) ; ImaCyte (Somarakis 2019) ; Giotto (Dries et al., 2020) ; TissUUmaps (Solorzano 2020) ; SpaCell (Tan et al., 2020) ; BIRDS (Wang et al., 2021) ; QuPath (Bankhead et al., 2017) ; ec-CLEM (Paul-Gilloteaux, 2017) ; CloudReg (Chandrashekhar et al., 2021), Tangram (Biancalani et al., 2021), Vitessce (), SquidPy (Palla et al., 2022), ...

CMI data analysis is not ideal ... Why ?

Challenges for biologists:

« Not easy to reuse previous work on my data because ... »

... many nice biology papers do not come with a tool

... reproducibility is quite low because of complex workflows

... which algorithm/tool to choose in the zoo ? How can I trust it ?

... best algorithms might not be implemented in user-friendly software tool

... many algorithms are not interpretable (black box, proprietary)

... lack of multimodal software toolbox

... too much data, too few computer resources

... publish or perish ... (a lot of work is lost after publication e.g. data, image analysis results & tuned methods)...

Challenges for computer scientists :

« Not easy to design generic methodologies & tools because ... »

... so many imaging techniques & combinations

... few datasets available (and proprietary formats)

... even less annotated datasets (ground-truths) available

... meaningful results ?

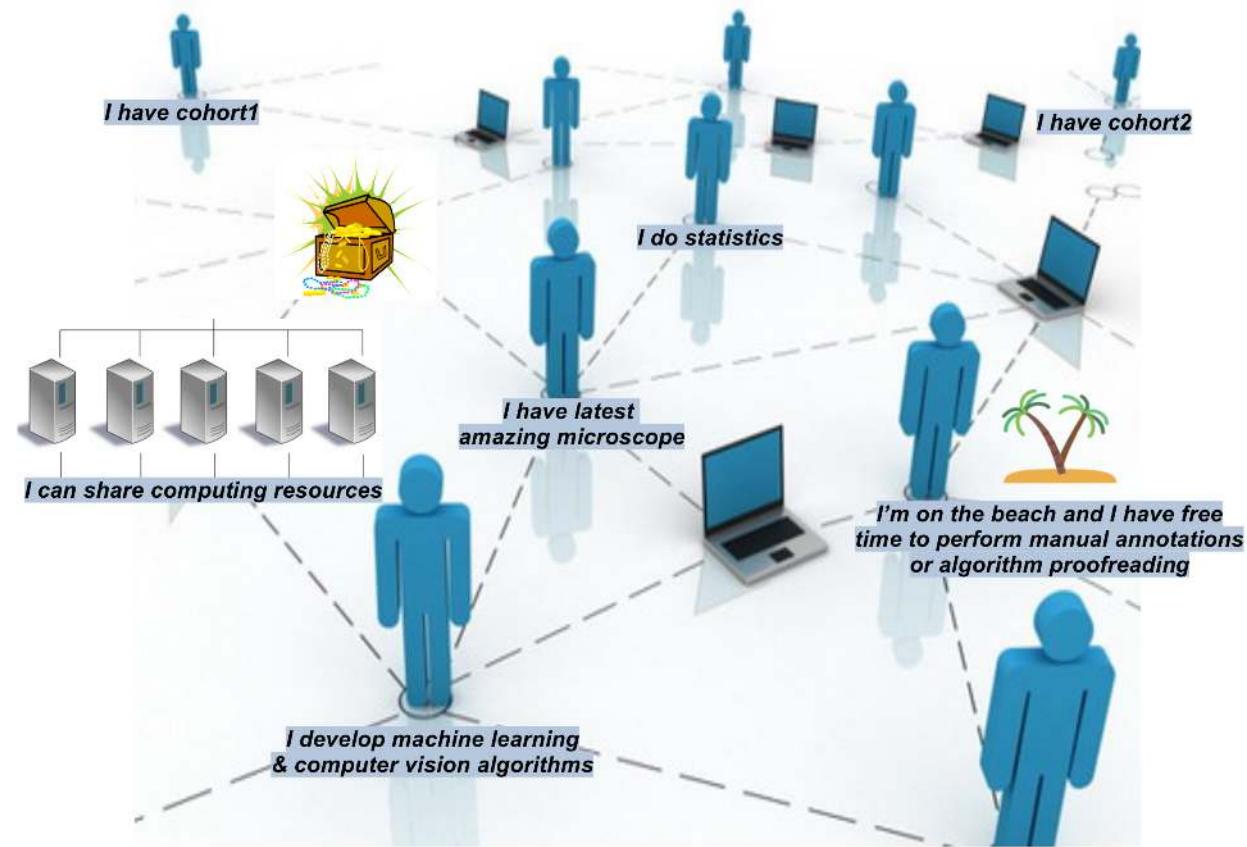
... publish & perish... validation only on 1-2 (small) dataset(s) : ad hoc

Can we solve this by tomorrow? No, but...

Let's try to **collaborate** more effectively towards **more generic** and **reproducible** correlative/multimodal image analysis workflows.

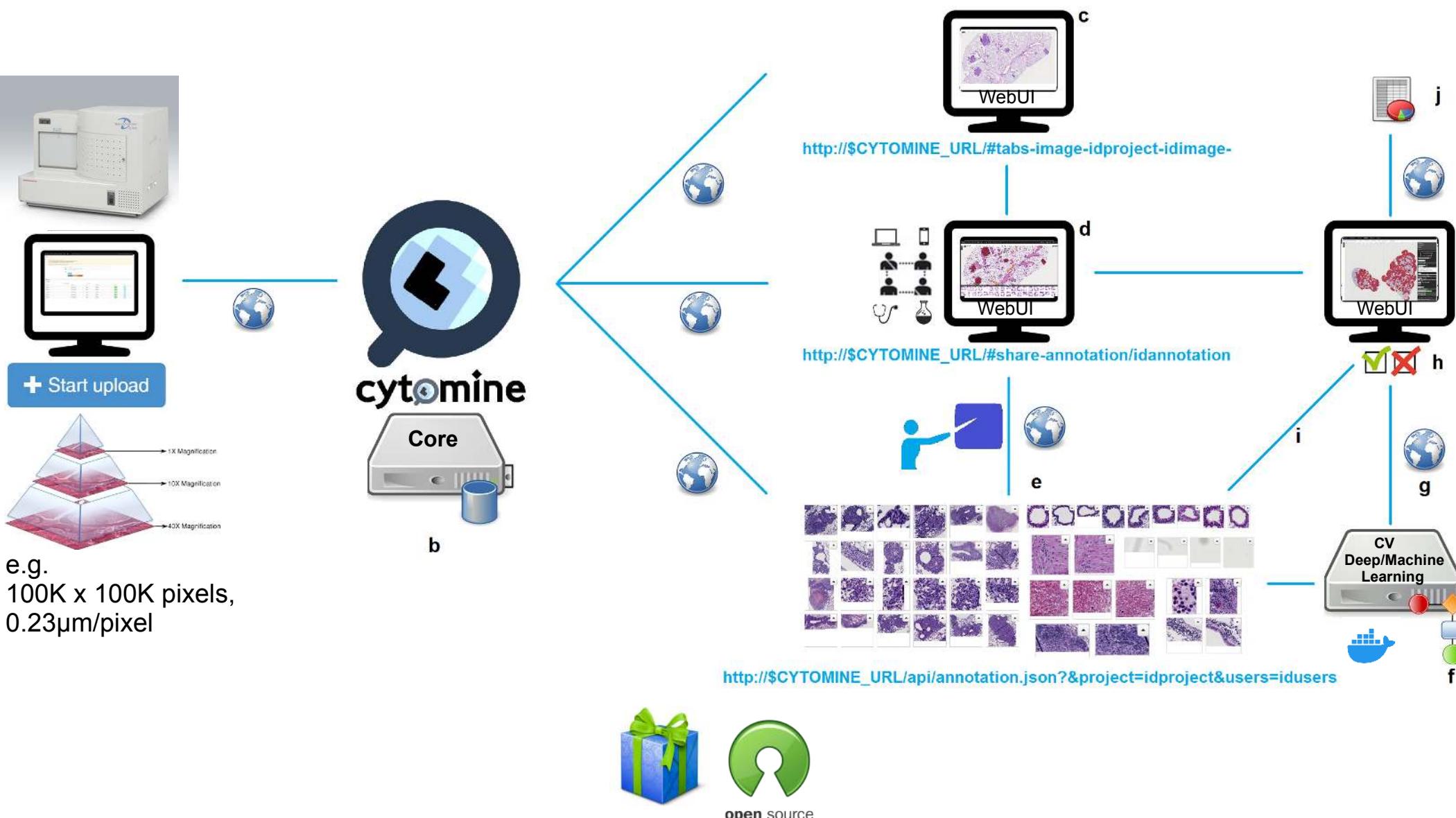
« *Sharing everything* »

- **Images (raw & metadata)**
- **Annotations**
(ground truths, atlases)
- **Source code**
(for reproducible analysis)
- **Quantitative results**



cytominne enables collaboration through the web (Sharing of images, annotations, algorithms, results)

(Marée et al., Bioinformatics 2016 ; Rubens et al., Proteomics Clin Appl. 2019 ; Rubens et al., Cell Patterns, 2020)

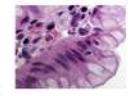
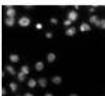
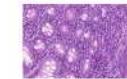
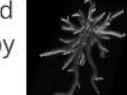
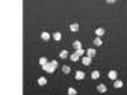


Note : Cytomine-Core can be installed on Linux-based servers or on a desktop/laptop (but then without collaborative features)

cytominE : organize your images on the web

Create and manage multiple **projects** :

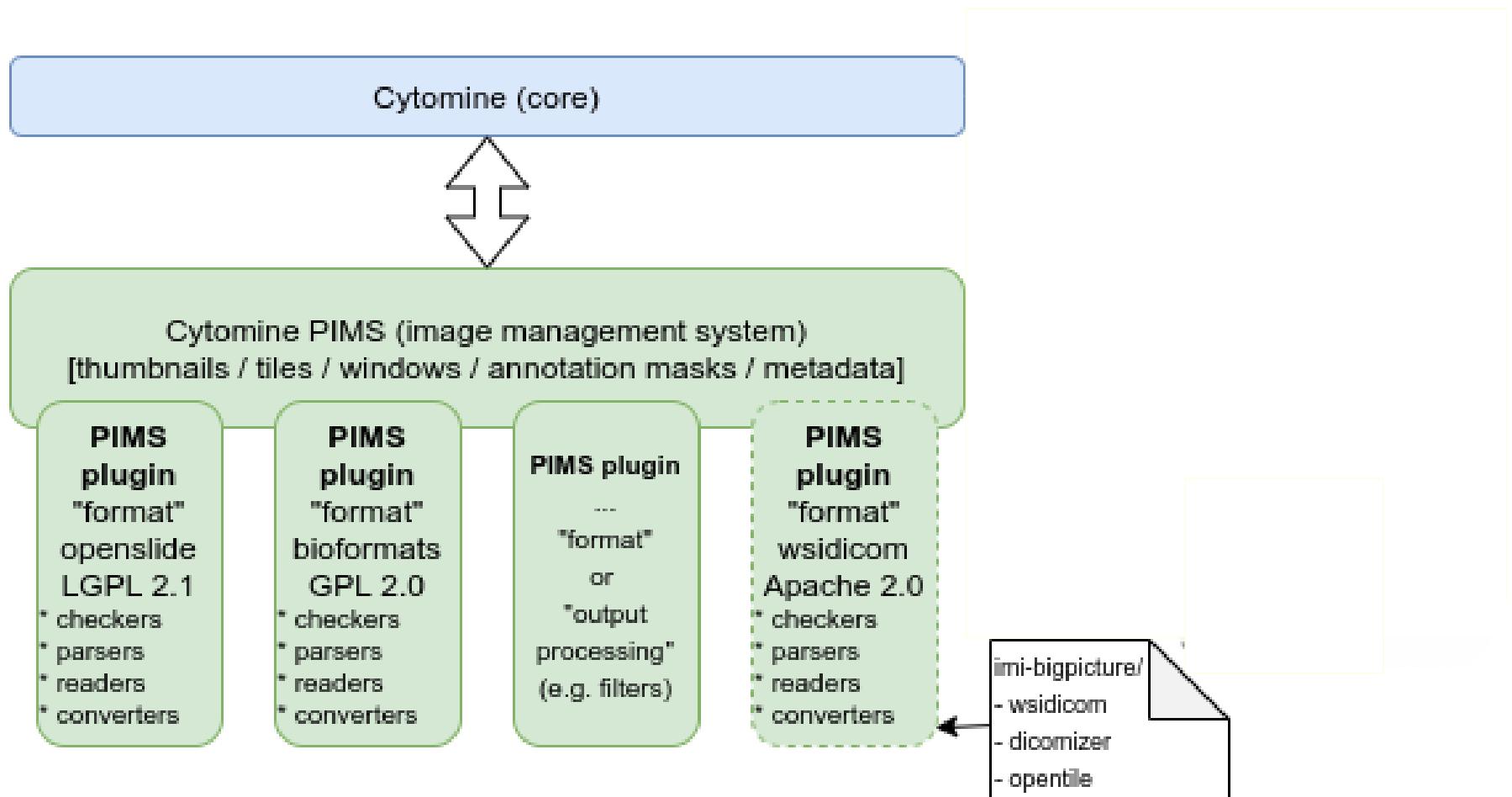
- Users with **authentification** (e.g. LDAP), **access rights**, and **roles**

Name ↑	Description	Members	Images
➤ DATA-SCIENCE-BOWL-2018	Heterogeneous collection of 2D images used to illustrate nuclei segmentation. Includes stage1_test image set from BBBC038v1 , available from the Broad Bioimage Benchmark Collection [Ljosa et al., <i>Nature Methods</i> , 2012].	 	5 130
➤ GLAND-SEGMENTATION-TEST	The aim of this problem is to classify pixels belonging to glands in histopathology images cropped out from images of 2015 MICCAI challenge of gland segmentation (GLaS 2015).		5 480
➤ GLAND-SEGMENTATION-TRAIN	The aim of this problem is to classify pixels belonging to glands in histopathology images cropped out from images of 2015 MICCAI challenge of gland segmentation (GLaS 2015). These images were used to train the machine learning classifiers available in GLAND-SEGMENTATION-TEST.		5 671
➤ LANDMARKS-DROSO	Landmark detection in Drosophila wings, data from UPMC (Vandaele et al., Nature Scientific Reports, 2018).		5 60
➤ NEURON-TRACING-3D	Neuron tracing from 3D images. The images are from the DIADEM challenge (olfactory bulb projection fibers labeled with GFP) and were acquired by confocal microscopy (40x, NA = 1.3).		5 4
➤ NEURON-TRACING-TREES-3D	Neuron tracing in 3D images. The ground truth trees were generated by TREES Toolbox as SWC files and transformed into binary masks by Vaa3d . The masks were then convolved by a synthetic PSF (Born & Wolf) generated by ImageJ PSF Generator and some noise was added with ImageJ Random .		5 2
➤ NUCLEI-SEGMENTATION	Nuclei segmentation from 2D images. The images were generated by SIMCEP , a widefield fluorescence microscopy biological images simulator.		5 30

cytominE : extensible image management system

Python Image Management System (PIMS : <https://github.com/Cytomine-ULiege/pims>):

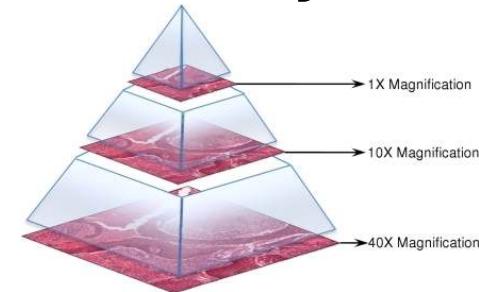
- Support **various digital pathology, microscopy & other image formats** (Pyramidal TIFF, WSI-DICOM, OME-TIFF, ...)
- **Flexible architecture** with plug-ins (using various libraries e.g. OpenSlide, BioFormats, Zarr, WSIDicom, ...)



cytominE : visualize large 2D images, remotely

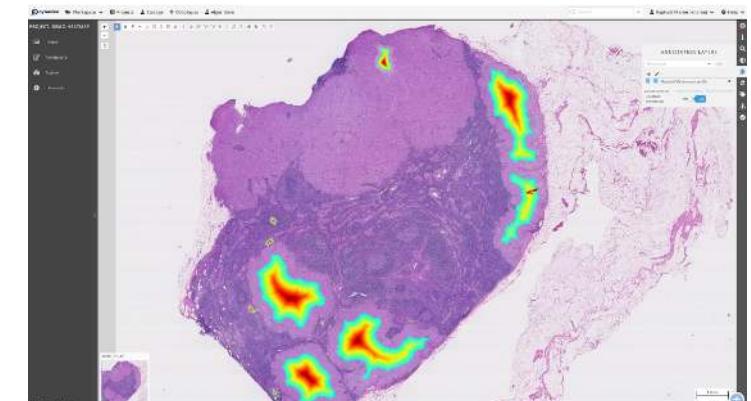
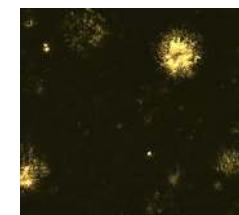
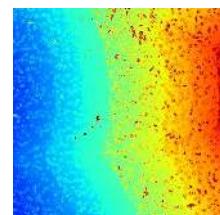
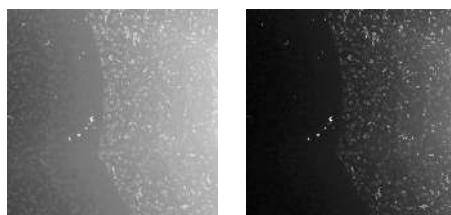
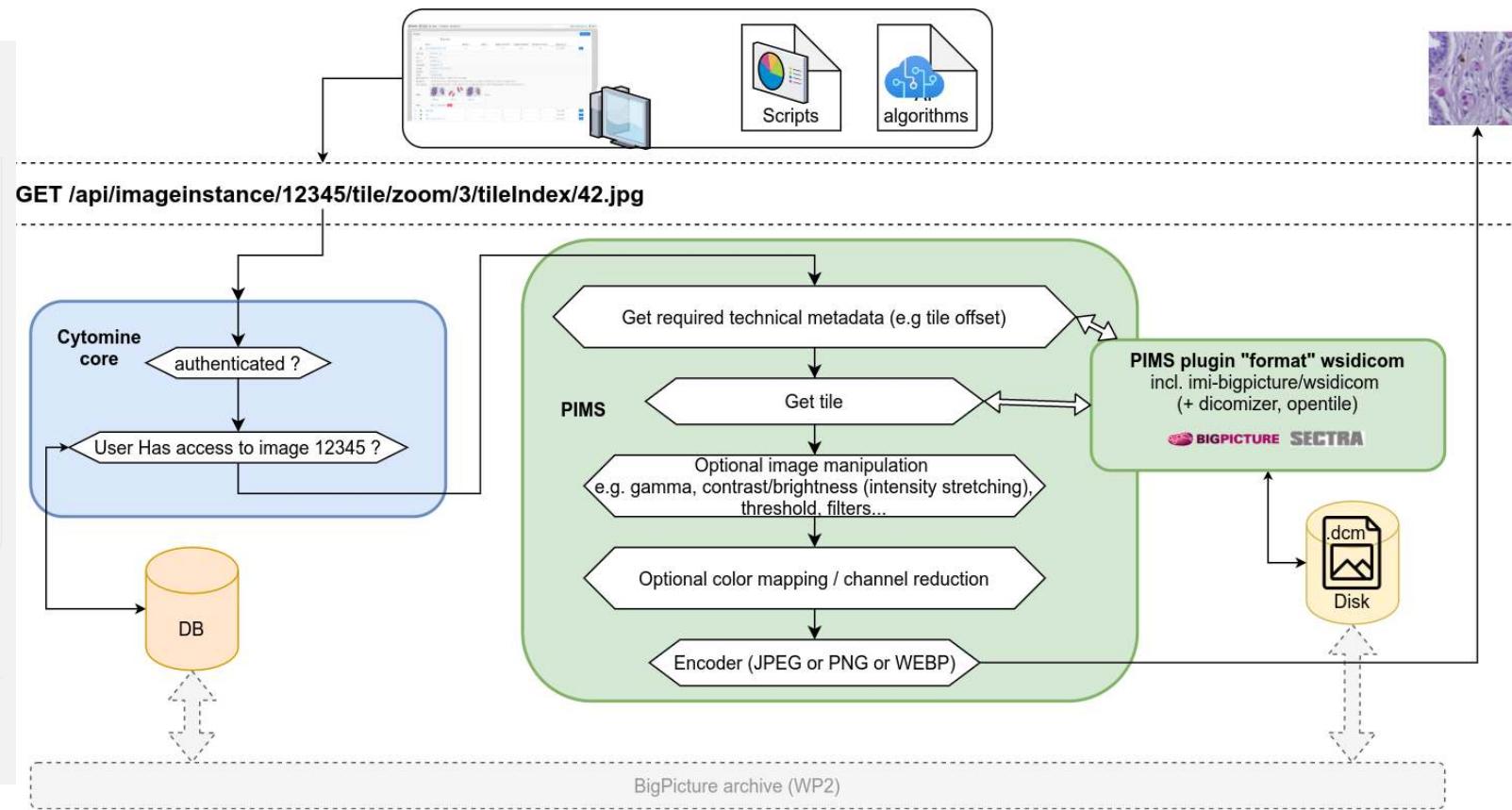
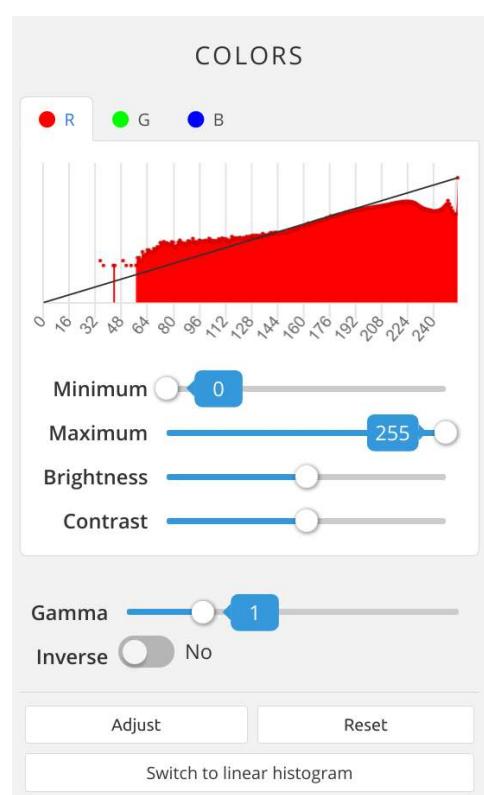
- Explore **large** (multi-gigapixel) images at multiple resolutions, **remotely**
- OpenStreetMaps browsing style (zoom in/out, pyramid tile-based)

e.g. one tissue slice = 40000 x 30000 pixels (0.23µm/pixel)



A screenshot of the cytominE software interface. The main window displays a large, detailed histological image of a tissue slice, likely stained with hematoxylin, showing various cellular structures and nuclei. Below this main image, there is a smaller, zoomed-in view of a specific area, showing more detail of the cellular morphology. The interface includes a toolbar on the left with various icons for image manipulation, a header bar with user information, and a navigation bar at the bottom.

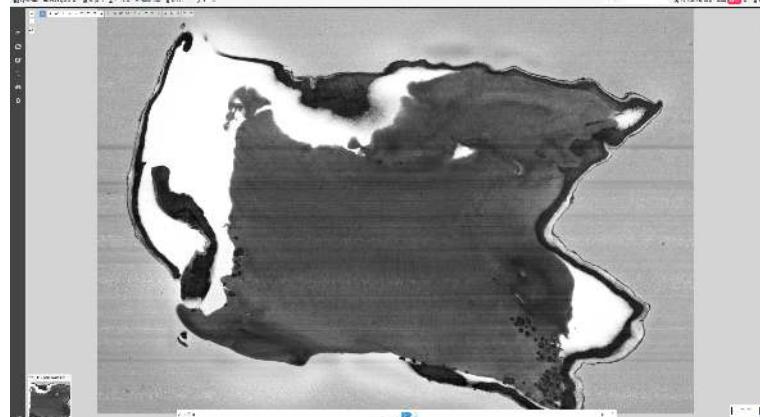
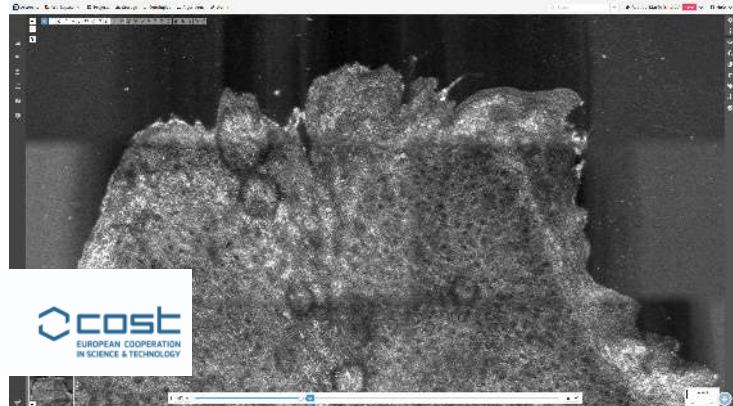
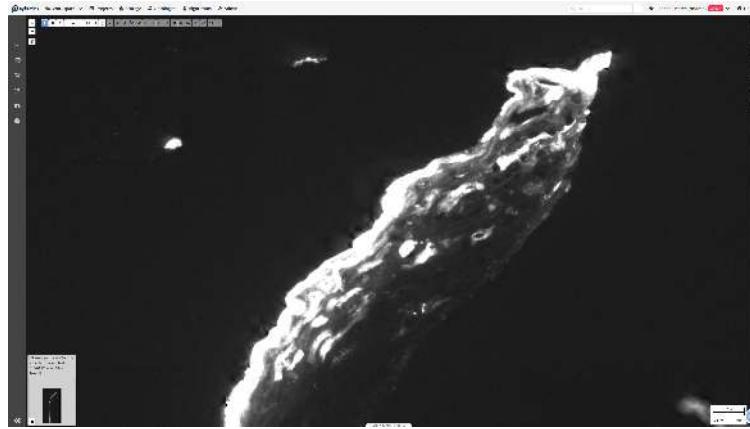
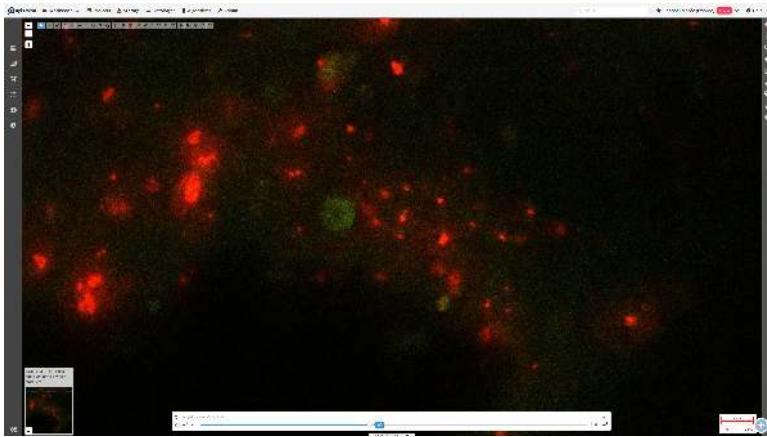
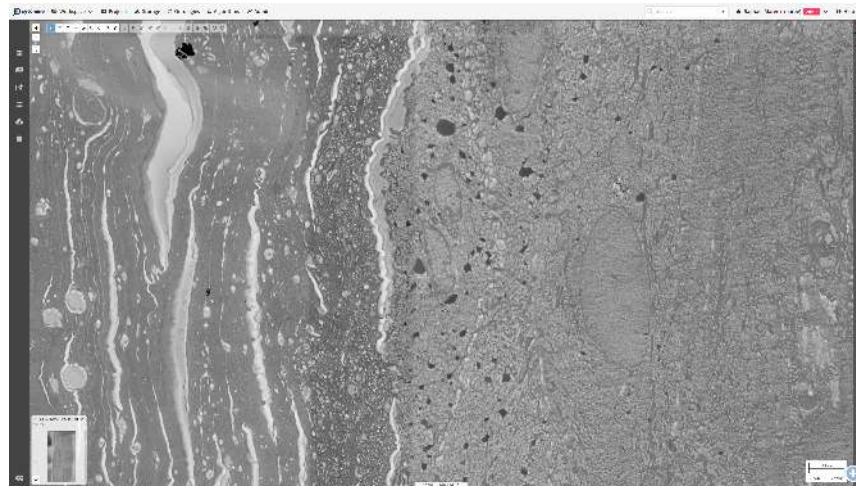
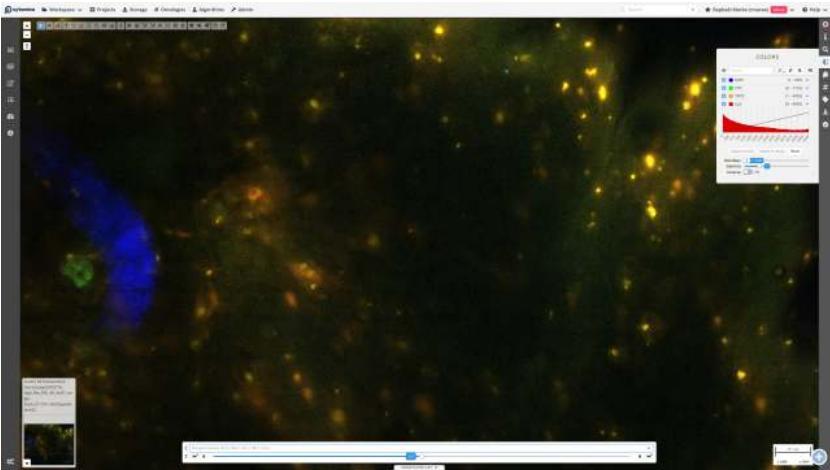
cytominE PIMS on-the-fly (tile) image operations



Gamma, min/max stretching, histograms, color mapping, merge channels, ...

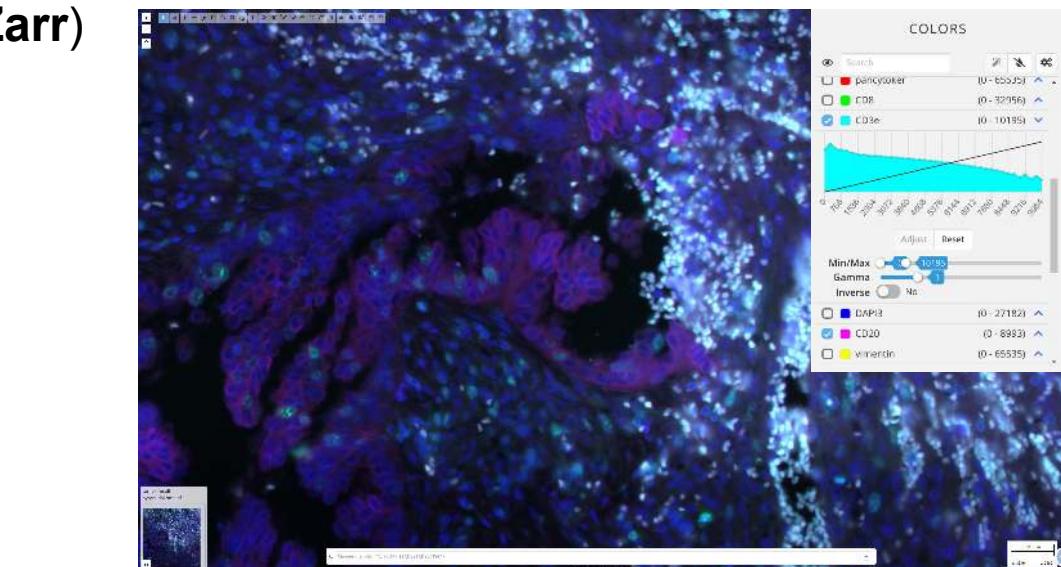
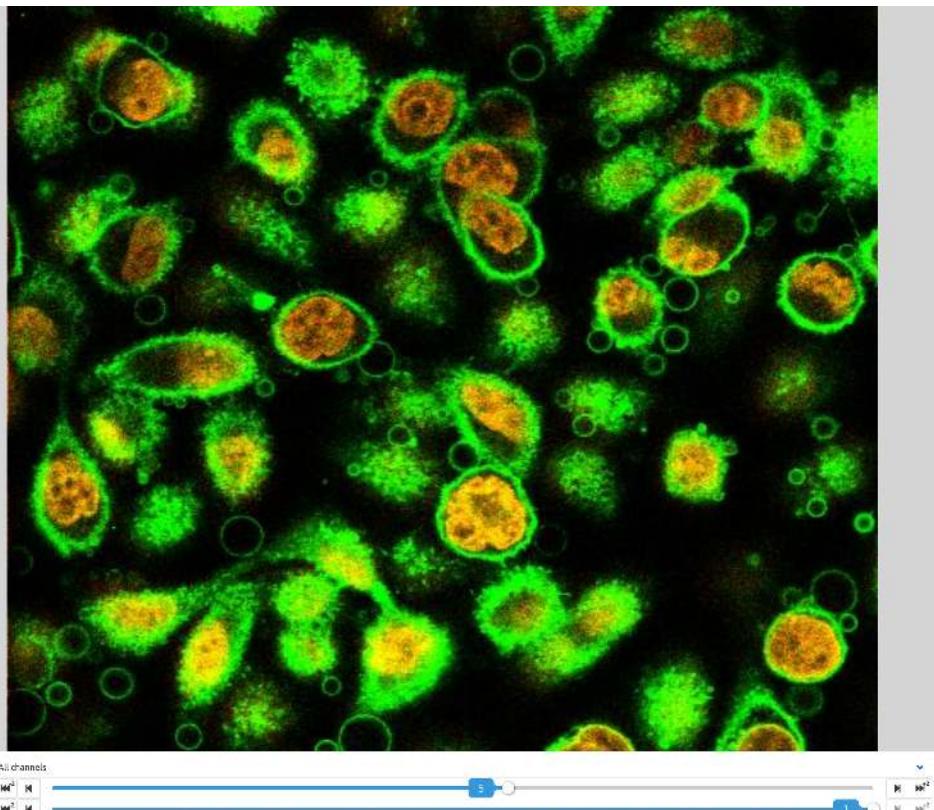
cytominE : Support of 2D+c+z+t image formats

- e.g. ND2, CZI, OME-tiff, DICOM, LIF, ...

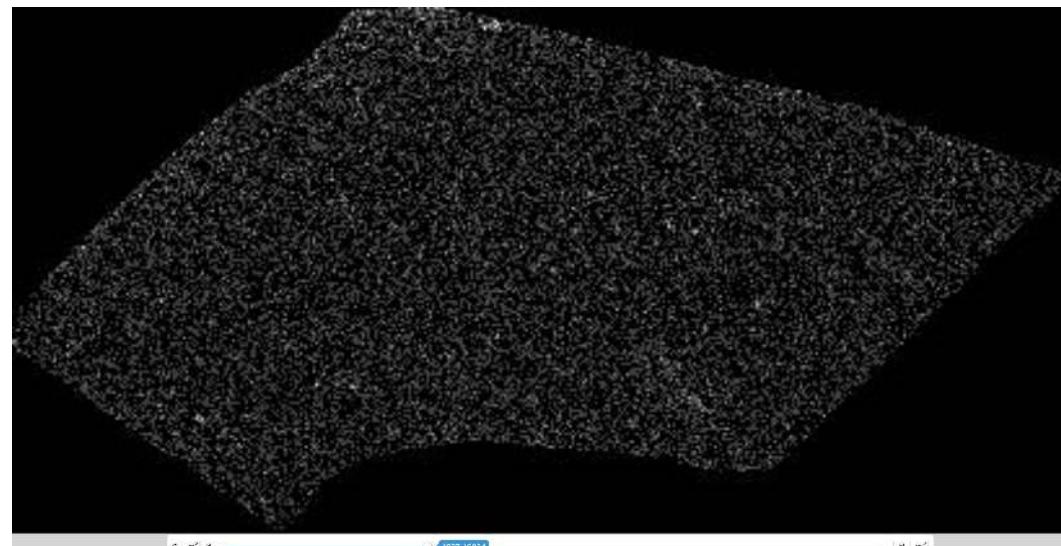


Ongoing developments : Benchmarking data structures for large spectral & temporal data e.g.

- Imaging mass spectrometry with thousands of spectral bands
(ibd+imzml converted into **Ome-Zarr**)
- Hyperspectral CZI
- Spatial *Omics
- ...



(data: VIB (top) ; CCIC Gothenburg University (bottom))

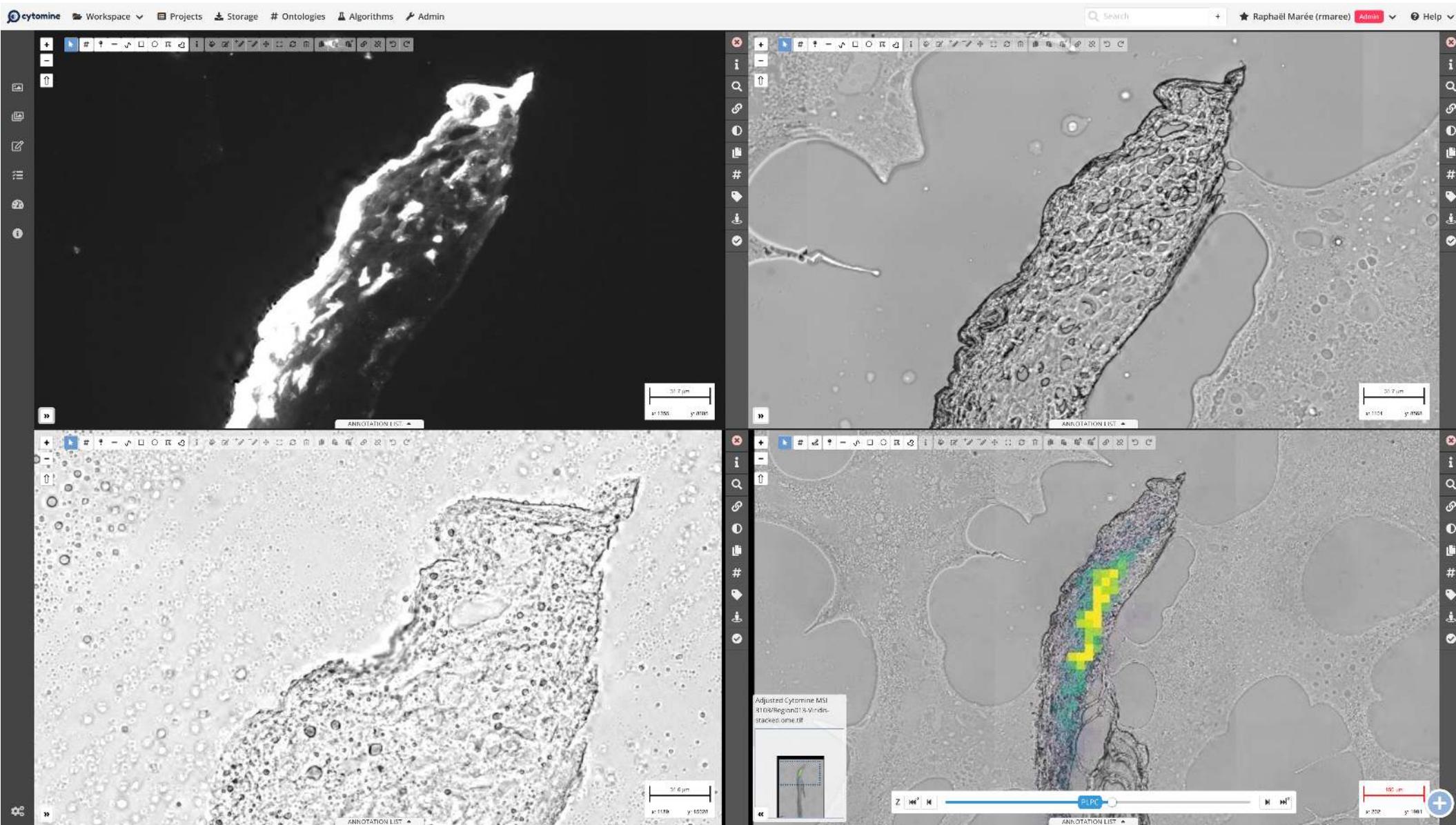


cytominE: joint visualization of multimodal datasets

- Side-by-side web viewer for multiple images with diverse X/Y/C/Z/T dimensions
- (No automatic registration, yet)

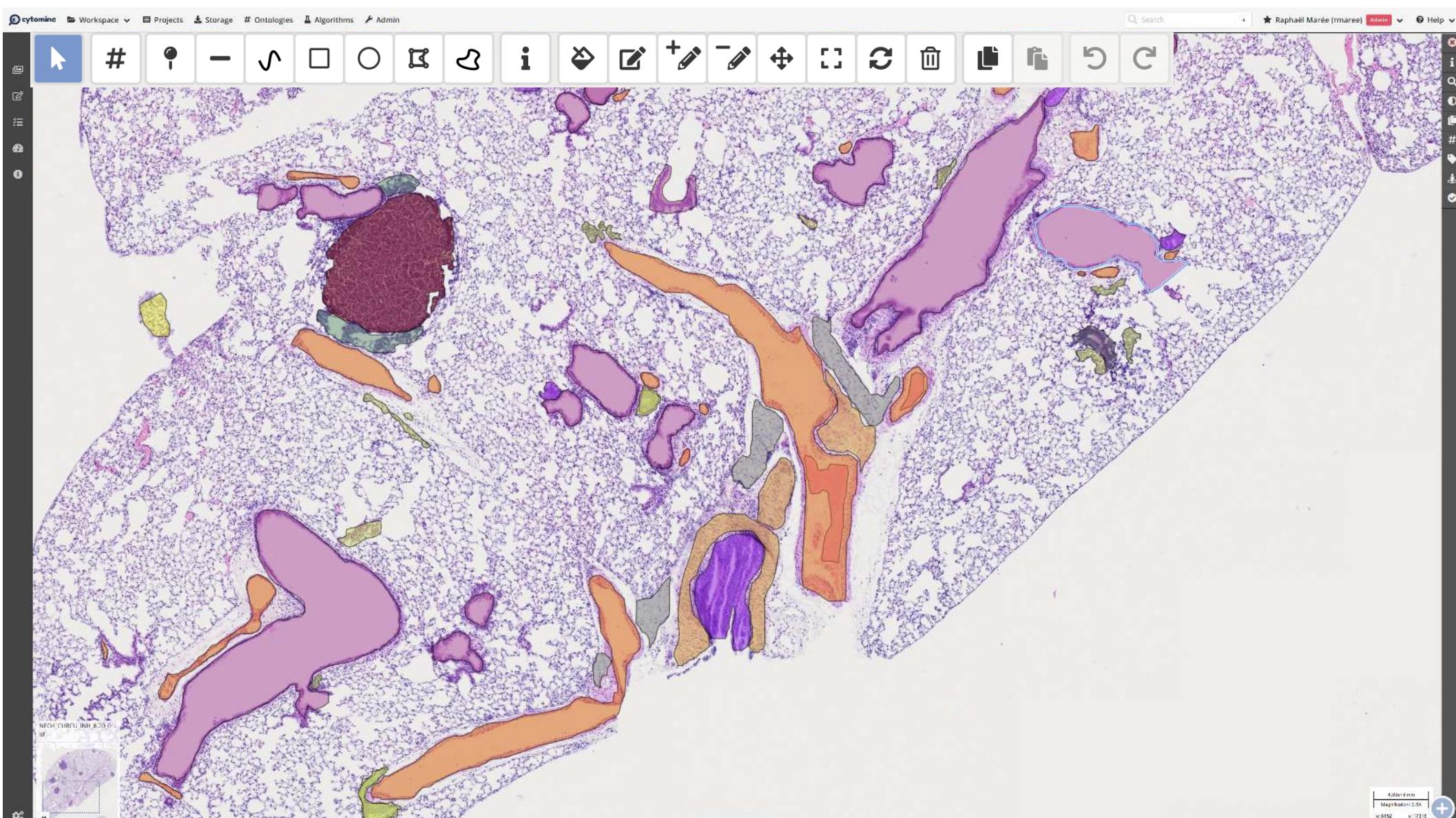


(data : COMULIS)



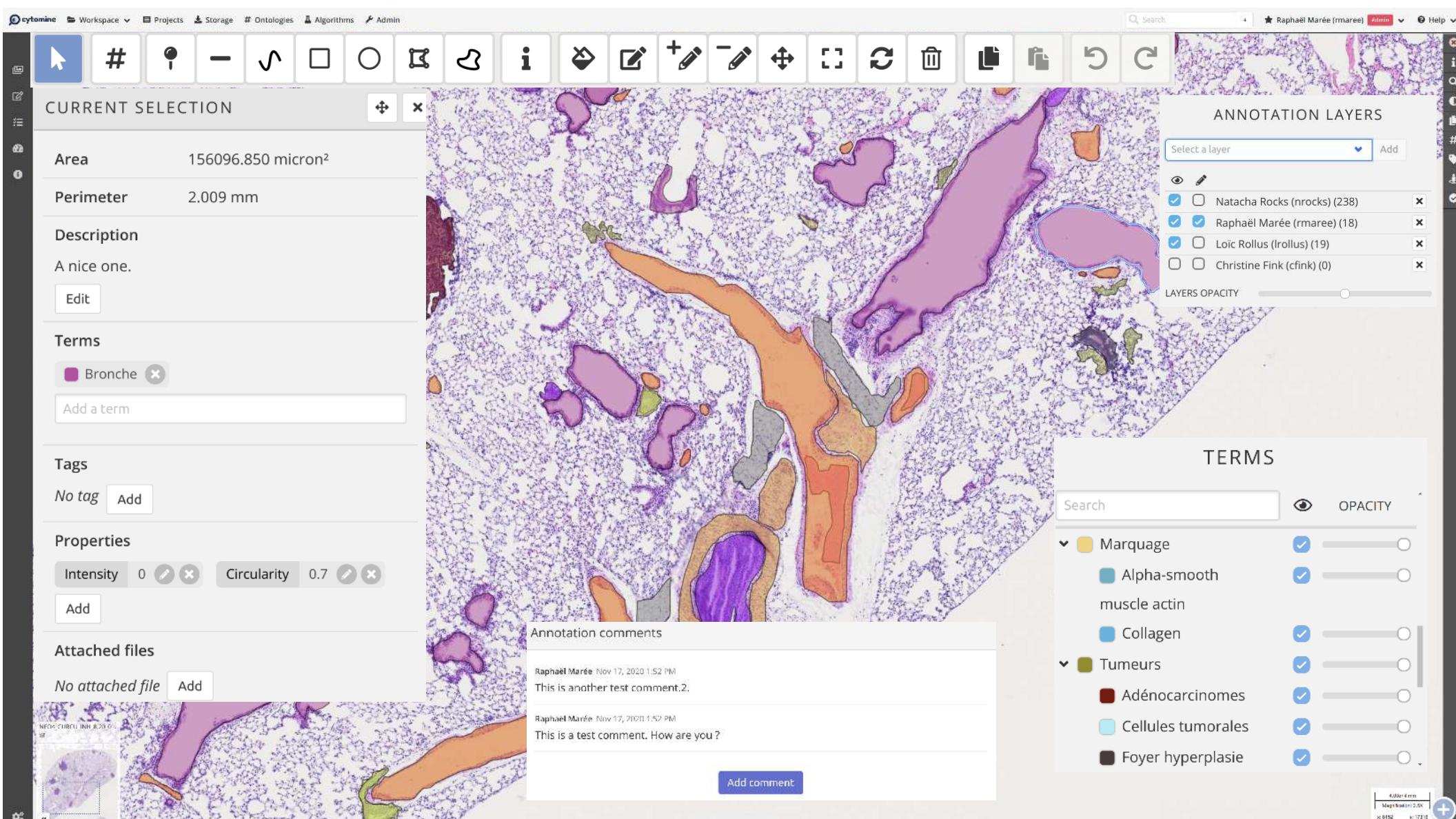
cytominE : annotate semantically, collaboratively

- Annotate images using various **drawing tools**, with **user-specific layers**
- Describe ROIs **semantically** with (user-defined) **ontology terms**
- Associate any **key-value properties, tags, file, or text description**



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cytominE : annotate multimodal datasets

– Centralize and standardize the way images are annotated in a multimodal project

1) Create « Image Groups » (e.g. multiple images describing the same sample)

(image data: COMULIS COST Action)

Image groups

Add image group

Region

Overview

Name ↑

Images

Created on Jan 26, 2022

Description No description Add

Tags No tag Add

Properties No property Add

Attached files No attached file Add

Actions Rename Add images Delete

Region 13

9 Open

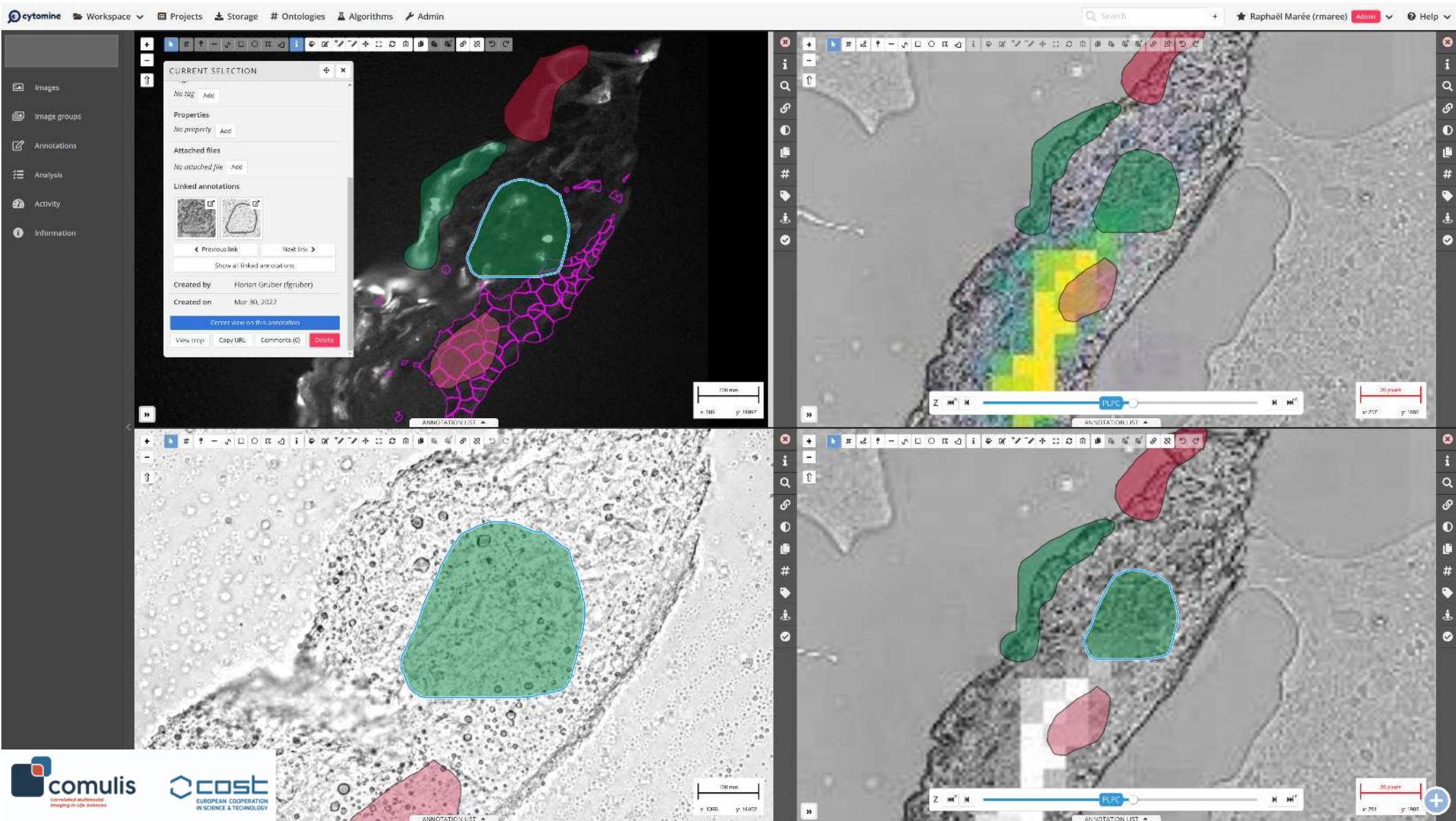
Images

Adjusted Cytomine MSI 3103/Laserspot-position-mask.jpg	Adjusted Cytomine MSI 3103/Mask-Exp-v2.png	Adjusted Cytomine MSI 3103/Mask-Exp-v2.png	Adjusted Cytomine MSI 3103/Mask-Exp-v2.png	Adjusted Cytomine MSI 3103/Region013-Grayscale-stacked.ome.tif	Microscope Images/Regions 013-015/2021-07-06-aS80CTa_S80CTa-Region-013-Texa.jpg	Microscope Images/Regions 013-015/2021-07-06-aS80CTa_S80CTa-Region-013-Texa.jpg	staining post MSI/Region 013 nuc+gH2AX-Tran.tif	staining post MSI/S80CTa #1-3 - Region 013 nuc+gH2AX-masks_TEXa.tif
Remove	Remove	Remove	Remove	Remove	Remove	Remove	Remove	Remove

cytominE : annotate multimodal datasets

– Centralize and standardize the way images are annotated in a multimodal project

- 1) Create « **Image Groups** » (e.g. multiple images describing the same sample)
- 2) « Smart » Copy/paste, **link annotations** across multiple images



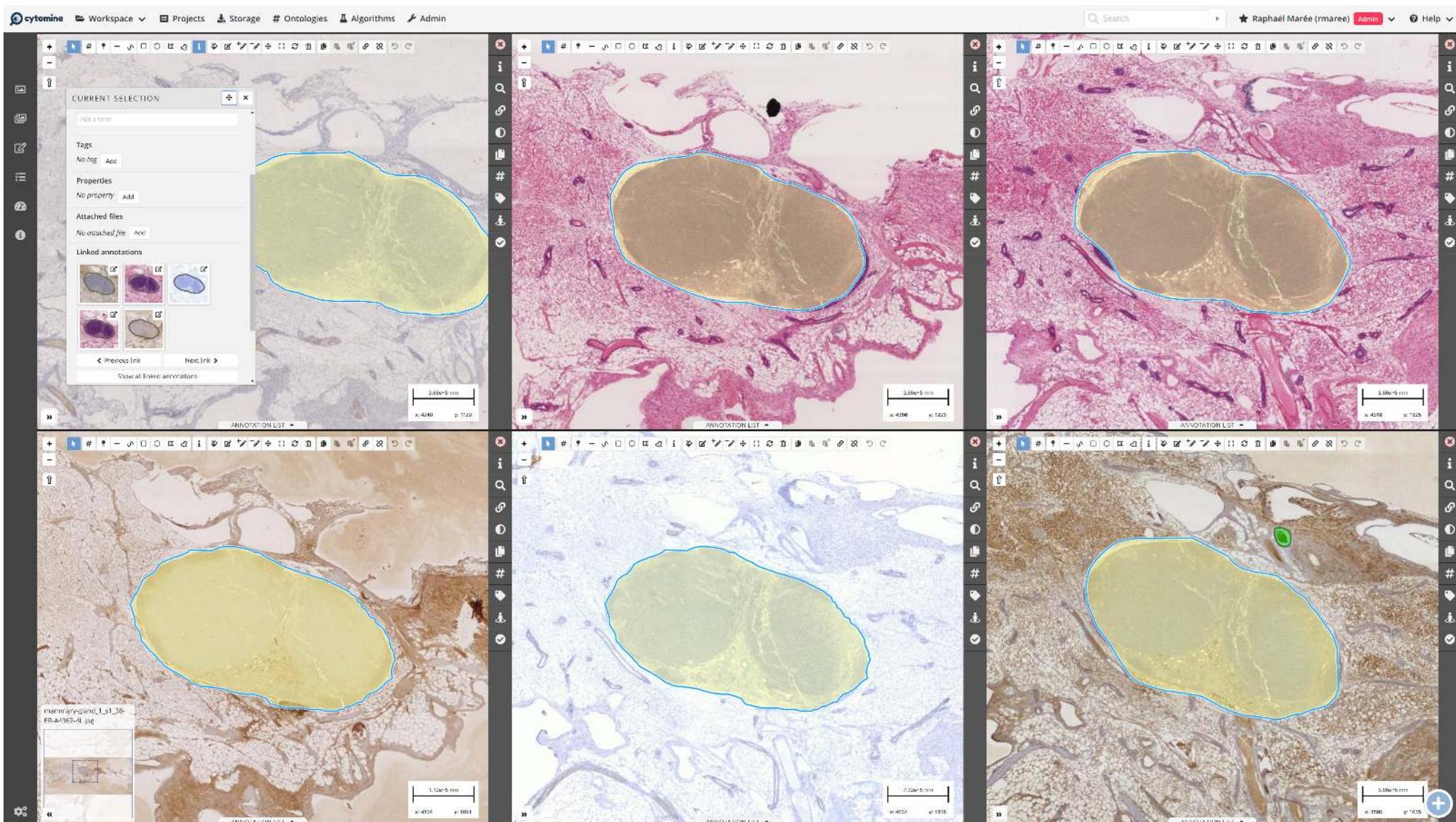
(image data: COMULIS COST Action)

cytominE : annotate multimodal datasets

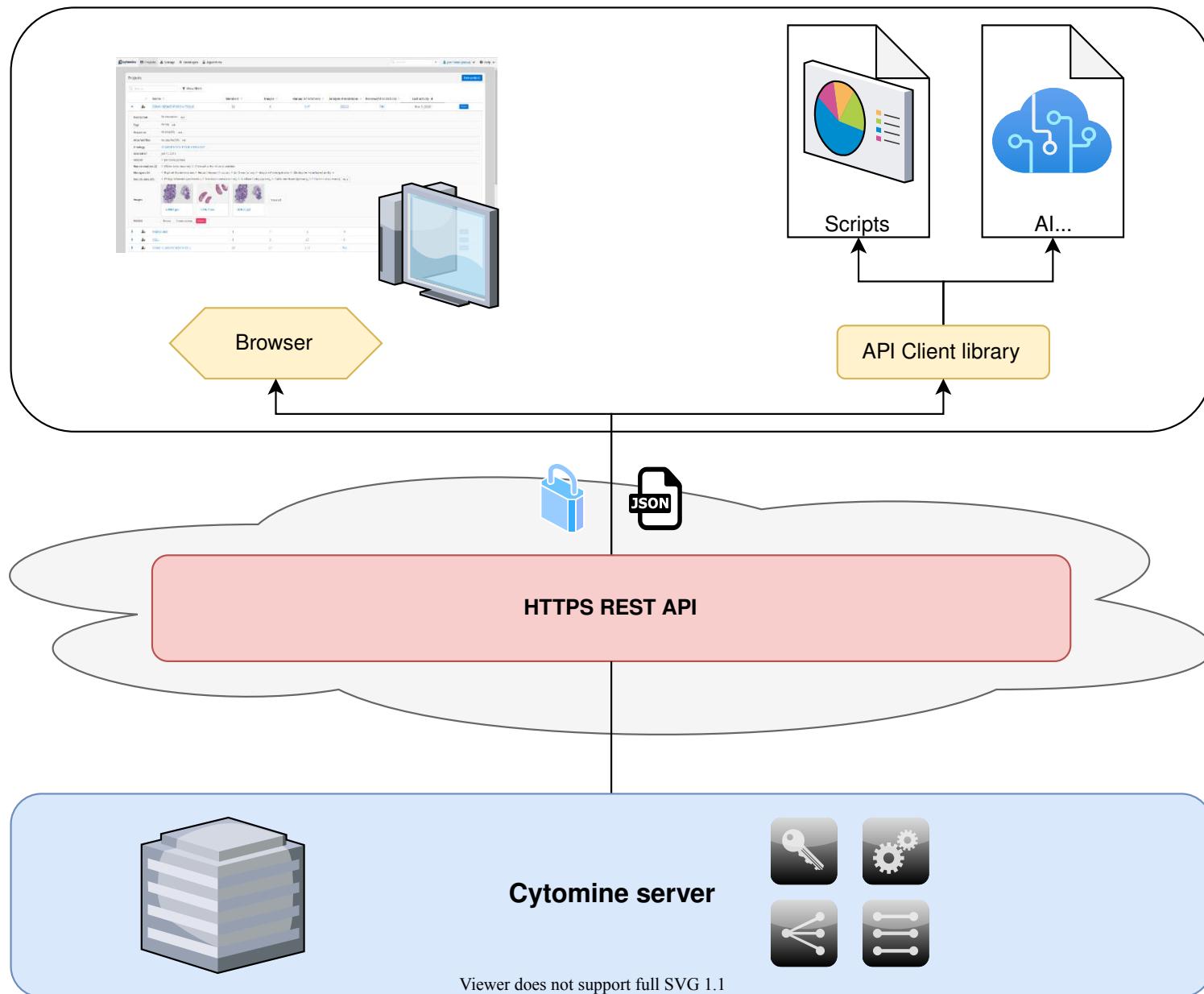
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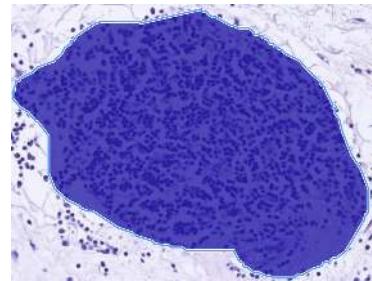
(image data: ANHIR challenge)



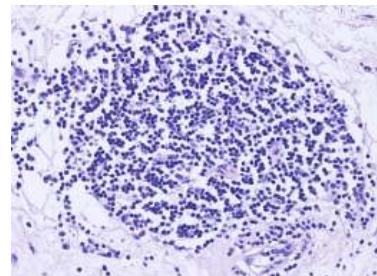
cytominE is highly interoperable : API (web services) to share/import/export all data



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RESTful API →



```
{"class": "be.cytomine.ontology.UserAnnotation", "id": 26675587, "created": "15888778", "updated": "null", "deleted": "null", "eLice": 146698793, "image": 24935900, "project": "24796414", "user": "24760144", "location": "POLYGON ((40164 22674, 40320 22710, 40320 22706, 40336 22702, 40336 22699, 40348 22699, 40356 22699, 40392 22670, 40416 22662, 40448 22662, 40452 22654, 40456 22648, 40476 22642, 40476 22638, 40488 22634, 40496 22622, 40504 22622, 40508 22614, 40516 22614, 40516 22610, 40528 22606, 40528 22602, 40544 22594, 40572 22578, 40588 22558, 40624 22526, 40624 22518, 40632 22514, 40651 22466, 40656 22458, 40668 22458, 40668 22446, 40672 22439, 40680 22398, 40794 22338, 40798 22382, 40798 22382, 40748 22250, 40748 22198, 40748 22186, 40749 22186, 40731 22179, 40688 22090, 40684 22074, 40656 22074, 40648 22066, 40632 22062, 40620 22054, 40604 22046, 40576 22030, 40564 22030, 40560 22026, 40508 22026, 40484 22030, 40464 22038, 40452 22038, 40436 22050, 40428 22050, 40424 22052, 40416 22066, 40400 22094, 40298 22094, 40268 22102, 40236 22106, 40208 22110, 40192 22118, 40152 22130, 40144 22138, 40108 22150, 40040 22194, 40078 22194, 40008 22202, 40088 22206, 39976 22222, 39944 22250, 39928 22290, 39928 22386, 39900 22422, 39896 22422, 39876 22446, 39850 22458, 39838 22482, 39838 22502, 39840 22502, 39844 22526, 39852 22526, 39856 22534, 39808 22550, 39098 22562, 39944 22578, 39944 22582, 39966 22594, 39968 22610, 39984 22622, 39984 22630, 39992 22630, 40008 22642, 40048 22674, 40064 22678, 40164 22678, 40164 22674))", "geometryCompression": "3..0", "centroid": {"x": 10315.73937190692, "y": 12371.35279565198}, "arcu": 0.1131.054189176363, "arcaUnit": "micron", "perimeter": 1.2823770183507887, "perimeterUnit": "mm", "term": "[25635608]", "nbComments": 18, "cropURL": "https://research.cytomine.be/api/userannotation/26675587/crop.png", "smallCropURL": "https://research.cytomine.be/api/userannotation/26675587/crop.png?maxSize=256", "url": "https://research.cytomine.be/api/userannotation/156138240/crop.png", "imageURL": "https://research.cytomine.be/#/project/24796414/image/24935900", "reviewed": false}
```

Get linked annotations in a given ImageGroup:

[https://research.cytomine.be/api/annotation.json?
project=526102245&showLink=true&showImageGroup=true&showMeta=true&group=526756968](https://research.cytomine.be/api/annotation.json?project=526102245&showLink=true&showImageGroup=true&showMeta=true&group=526756968)

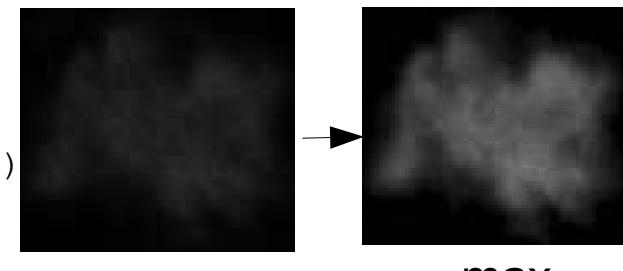


Get maximum projection of an annotation as an image:

<https://research.cytomine.be/#/project/146747628/image/153042325/annotation/156138240>
<https://research.cytomine.be/api/annotation/156138240/profile/max-projection.png>

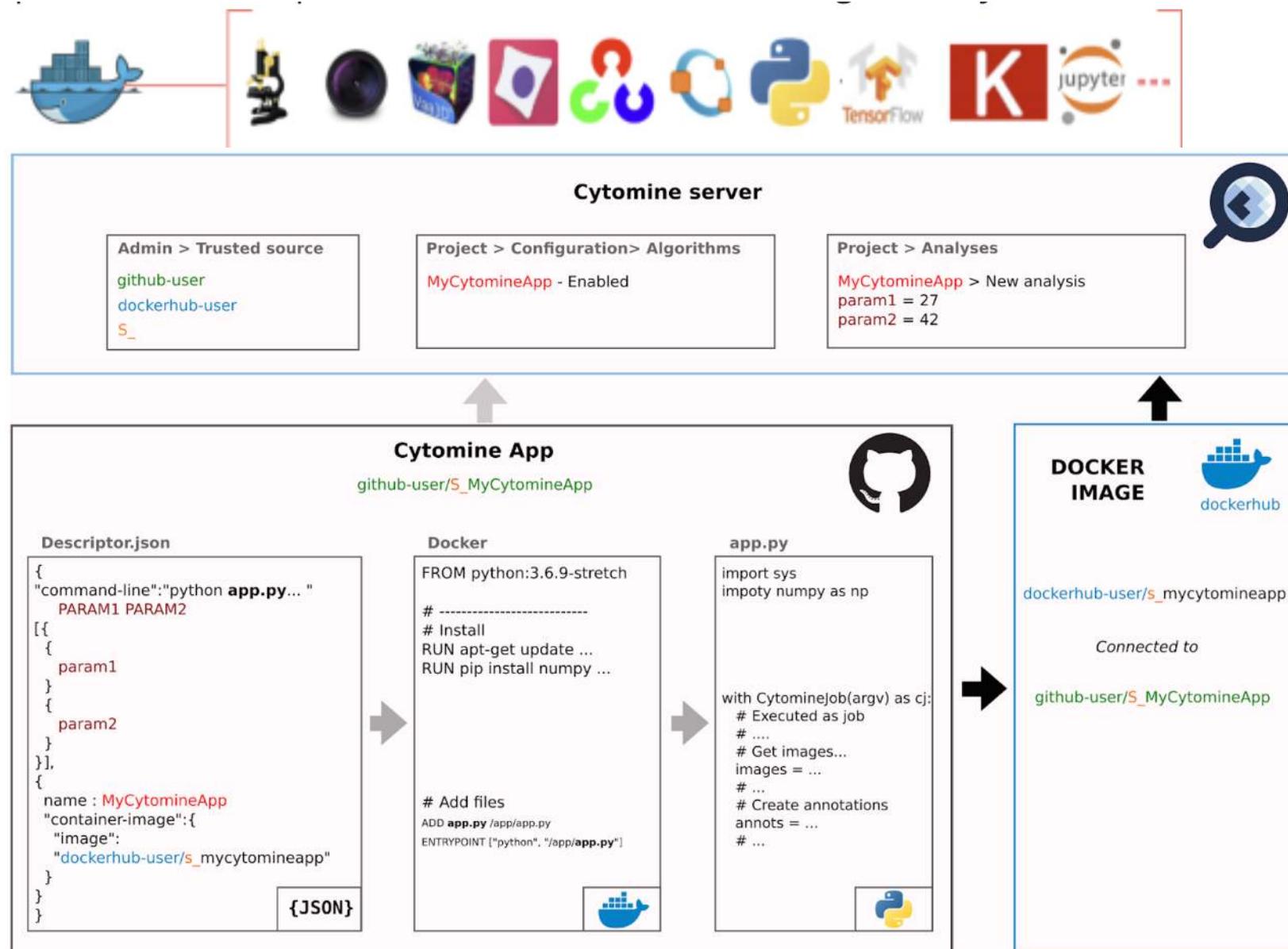
Python client:

```
a = Annotation().fetch(156138240)
a.profile_projection(projection='max', dest_pattern="myimage.png")
```



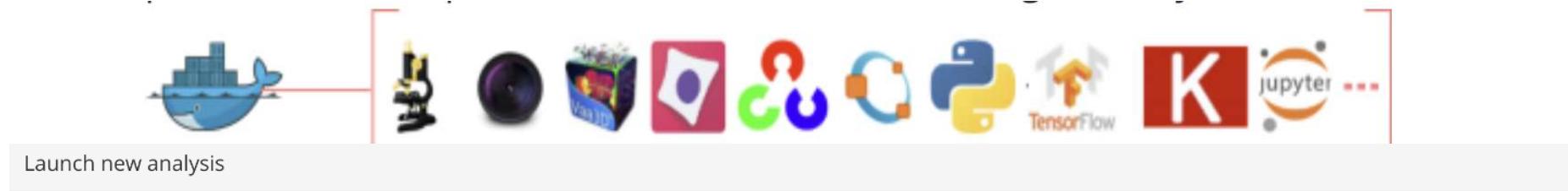
cytominE is highly extensible : « Apps »

- Integrate algorithms from any other tool (ImageJ, Fiji, Icy, CellProfiler, ilastik, Vaa3D, Python, Keras/Tensorflow, OpenCV, ...) using web API, Python/Java clients, JSON, and containers (Docker/Singularity) and make them available (CLI and web UI)
- Reproducibility : saving parameter values, versioned source code and libraries,...



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Algorithm Segment-CV-Object-Projection (v1.0)

Name	Value
Images to process	G1_7_top.czi
Optional parameters Hide	
Term to predict	ROI
Pre-filled parameters Hide	
Projection	max
Thresholding filter	otsu
Tile size	1024
Tile overlap	32
Minimum Object Area	100
Slices to use for annotations	median

(Rubens et al., Cell Patterns, 2020)

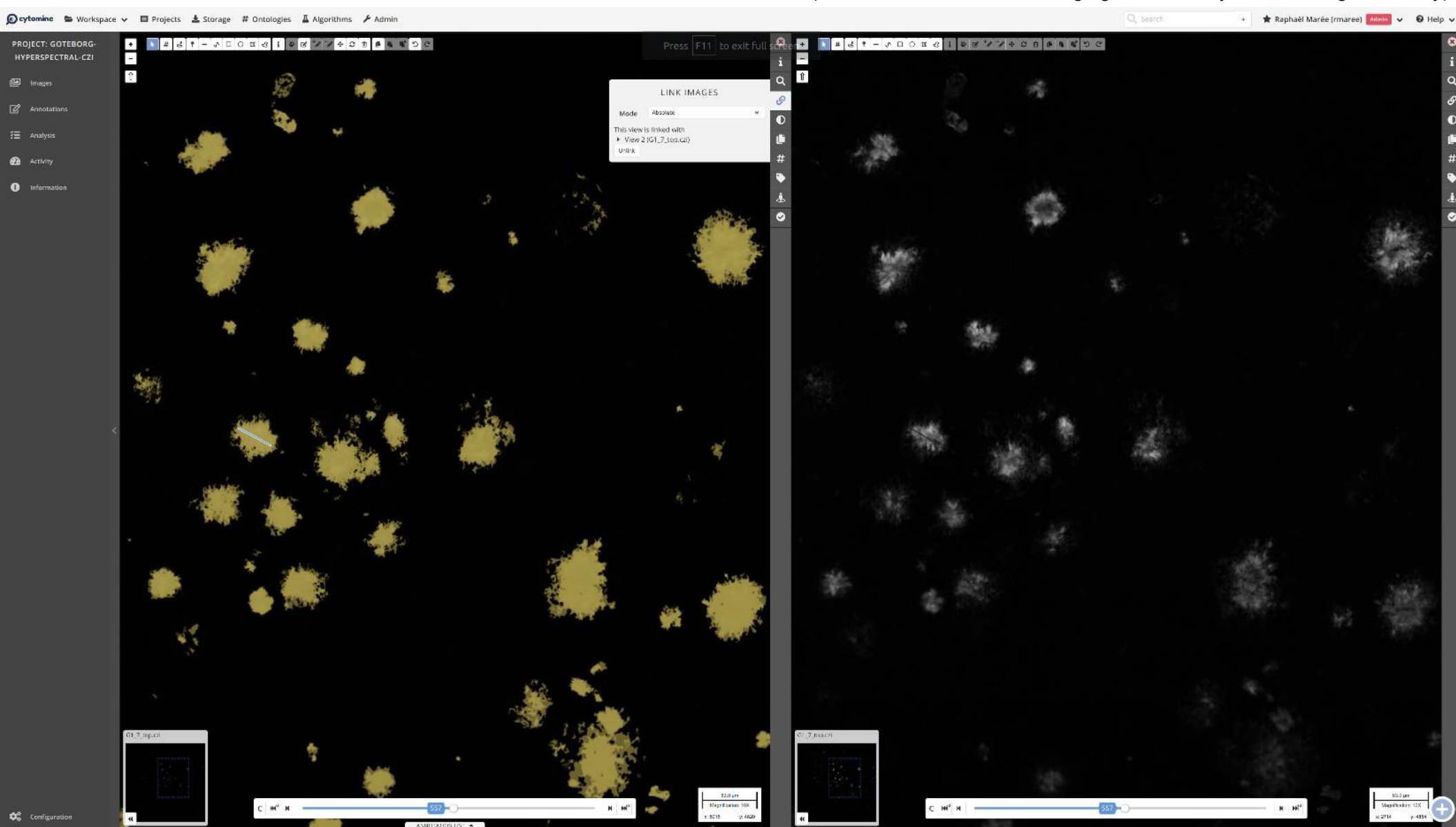
Cancel

Launch new analysis

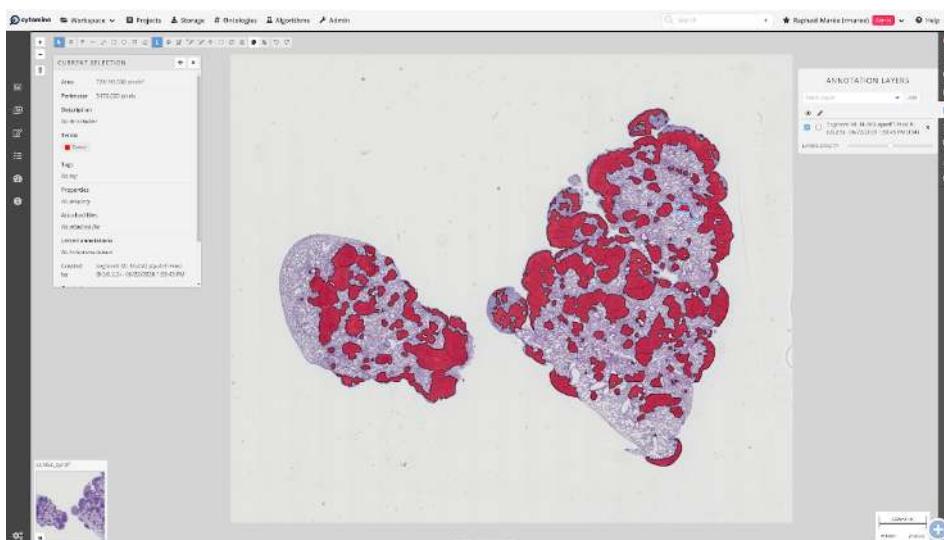
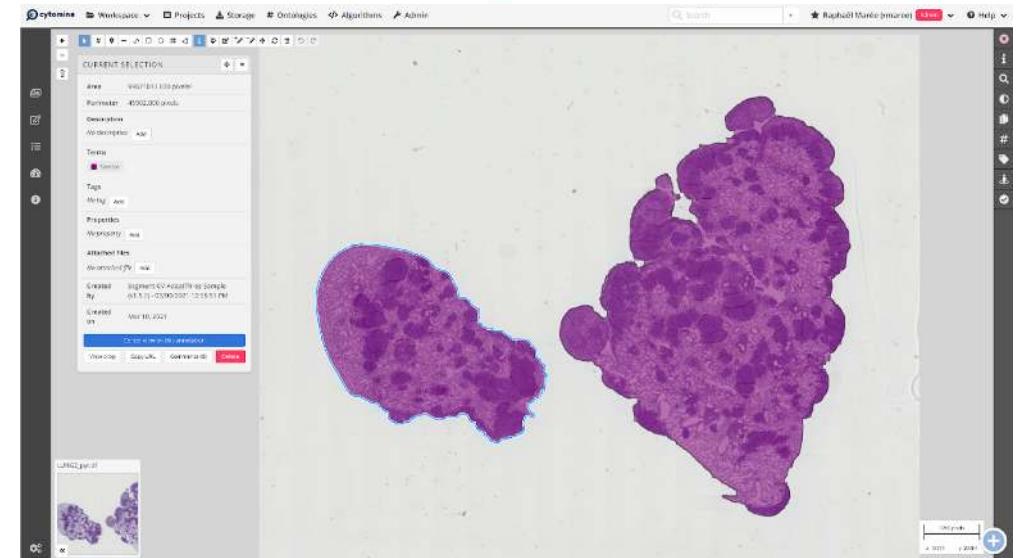
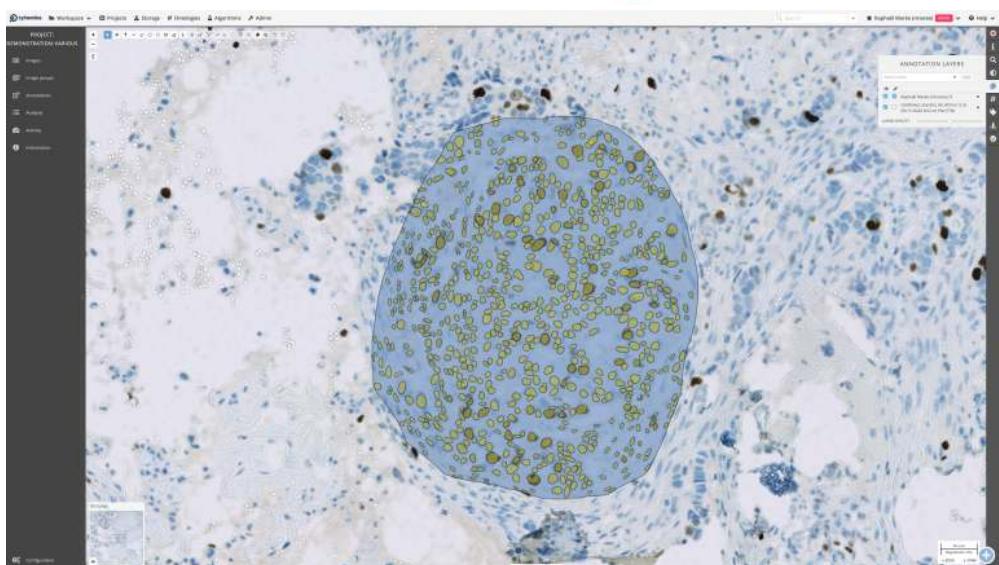
cytominE comes with various « Apps »

e.g. ROI detection using maximum intensity projection in hyperspectral images
(image size : 10K x 7K x 32 bands)
https://github.com/Cytomine-ULiege/S_Segment-CV-Object-Projection

(data: Centre for Cellular Imaging Core Facility, Gothenburg University)



cytominE comes with various « Apps »



Apps for nuclei segmentation:

https://github.com/Cytomine-ULiege/S_CellDetect_Stardist_HE_ROI
https://github.com/Neubias-WG5/W_NucleiSegmentation-Cellpose
https://github.com/Neubias-WG5/W_NucleiSegmentation-UNet
https://github.com/Neubias-WG5/W_NucleiSegmentation-ImageJ

...

Other examples :

<https://github.com/cytomine-uliege>
<https://github.com/neubias-wg5>

Reproducible, online, benchmarking



biaflows.neubias.org

NUCLEI-TRACKING-DIVISION	This project illustrates the 2D tracking of cell nuclei. The time-lapses are derived from Fluo-N2DH-SIM+ datasets from Cell Tracking Challenge .	
GLAND-SEGMENTATION-TRAIN	The images are crops of histopathology slides taken from the 2015 MICCAI challenge of gland segmentation (GLaS 2015). The aim of the problem is to classify pixels as belonging to a gland or not. These images were used to train machine learning based workflows.	
LANDMARKS-DROSO	Landmark detection in Drosophila wings, data from UPMC (Vandaele et al., Nature Scientific Reports, 2018).	
VESSEL-TRACING-3D	This project illustrates the 3D tracing of blood vessels. The images were generated by VascuSynth ITK , a biological image simulator, and some artificial noise was added.	



New workflow run

Workflow

Select options

- NucleiSegmentation-Python (v1.1)
- NucleiSegmentation-CellProfiler (v1.4.1)
- NucleiSegmentation-ImageJ (v1.10.1)
- NucleiSegmentation-MaskRCNN (v1.3)
- NucleiSegmentation-ilastik (v1.0)

1 BIA Problems

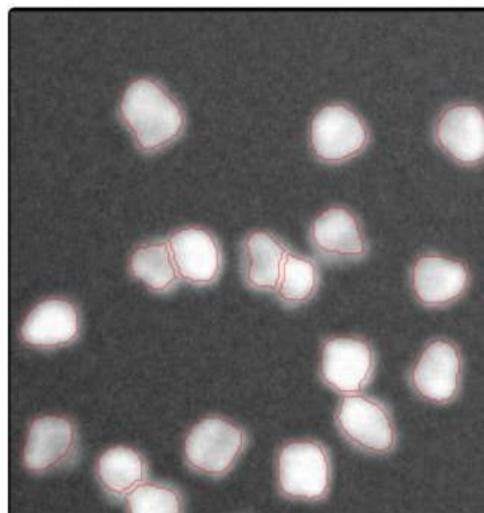
2 Image Datasets

Workflows

6 Benchmarking

5 Results

Aggregated results		Detailed results per image		
Workflow run		Dice coefficient		
		MIN	MAX	AVG
★ NucleiSegmentation-ilastik (v1.0) #1	on Mar 25, 2019 1:19 PM	0.58	0.637	0.614
★ NucleiSegmentation-MaskRCNN (v1.3) #1	on Mar 25, 2019 9:16 AM	0.587	0.649	0.633
★ NucleiSegmentation-ImageJ (v1.10.1) #2	on Mar 19, 2019 10:37 AM	0.613	0.67	0.641
★ NucleiSegmentation-Python (v1.1) #6	on Mar 18, 2019 4:10 PM	0.554	0.613	0.586
★ NucleiSegmentation-CellProfiler (v1.4.1) #2	on Mar 11, 2019 9:22 AM	0.558	0.637	0.595



3 Workflow selection

Workflow runs Run a workflow

4 Set parameters & Run workflow

New workflow run

Workflow

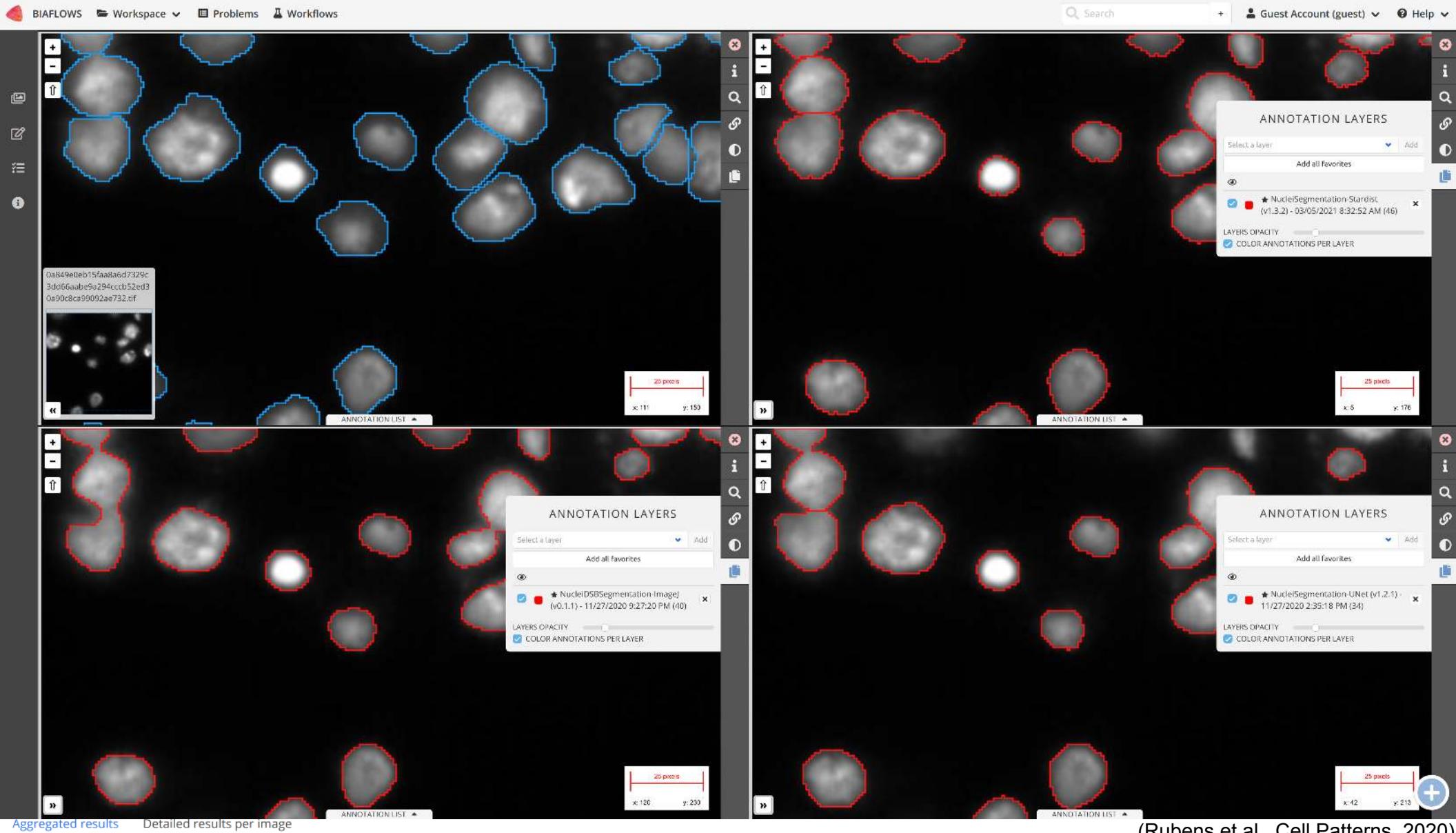
NucleiSegmentation-ImageJ (v1.10.1)

Name Value

Radius 5

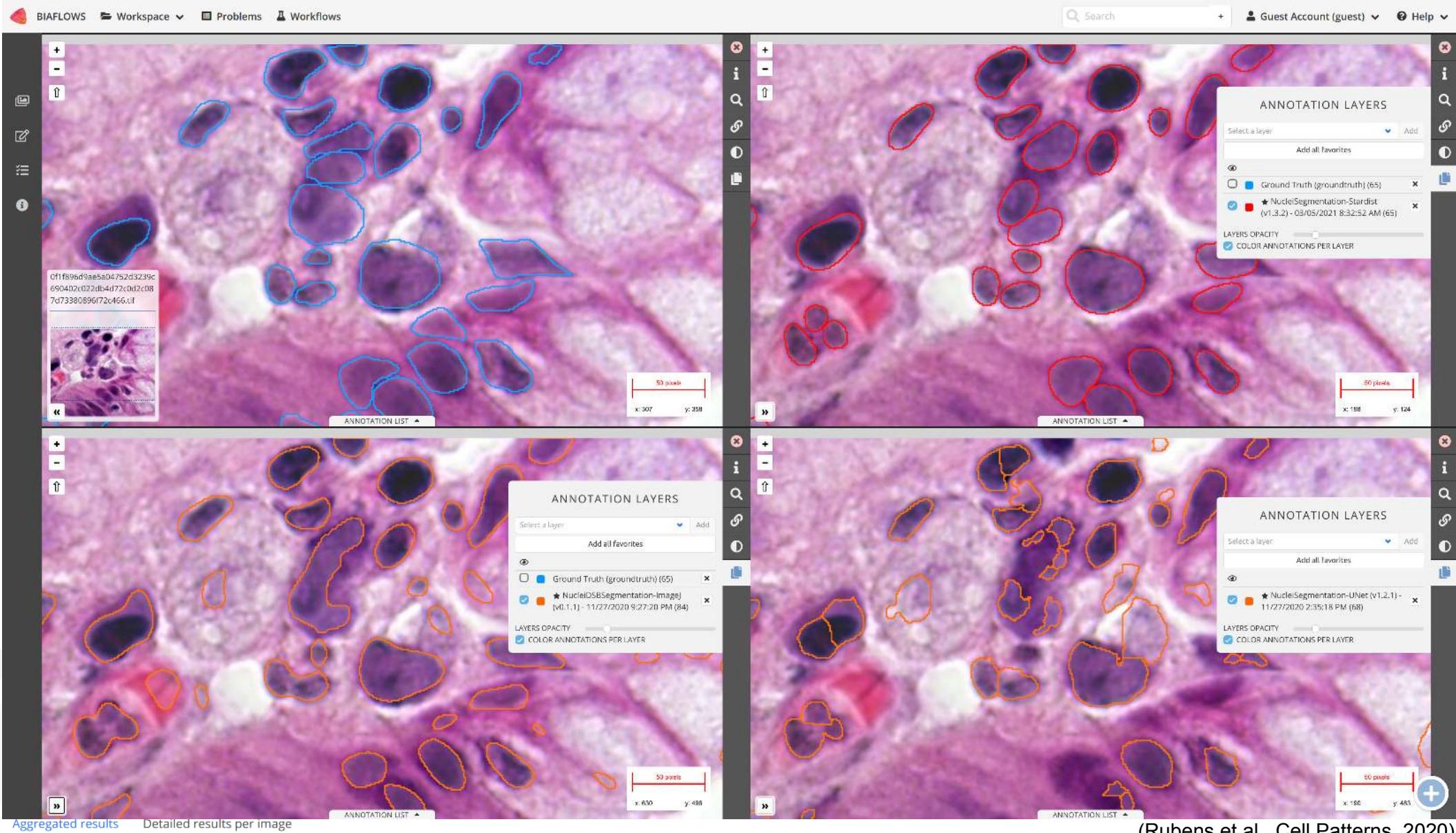
Threshold -0.5

Cancel Run a workflow



(Rubens et al., Cell Patterns, 2020)

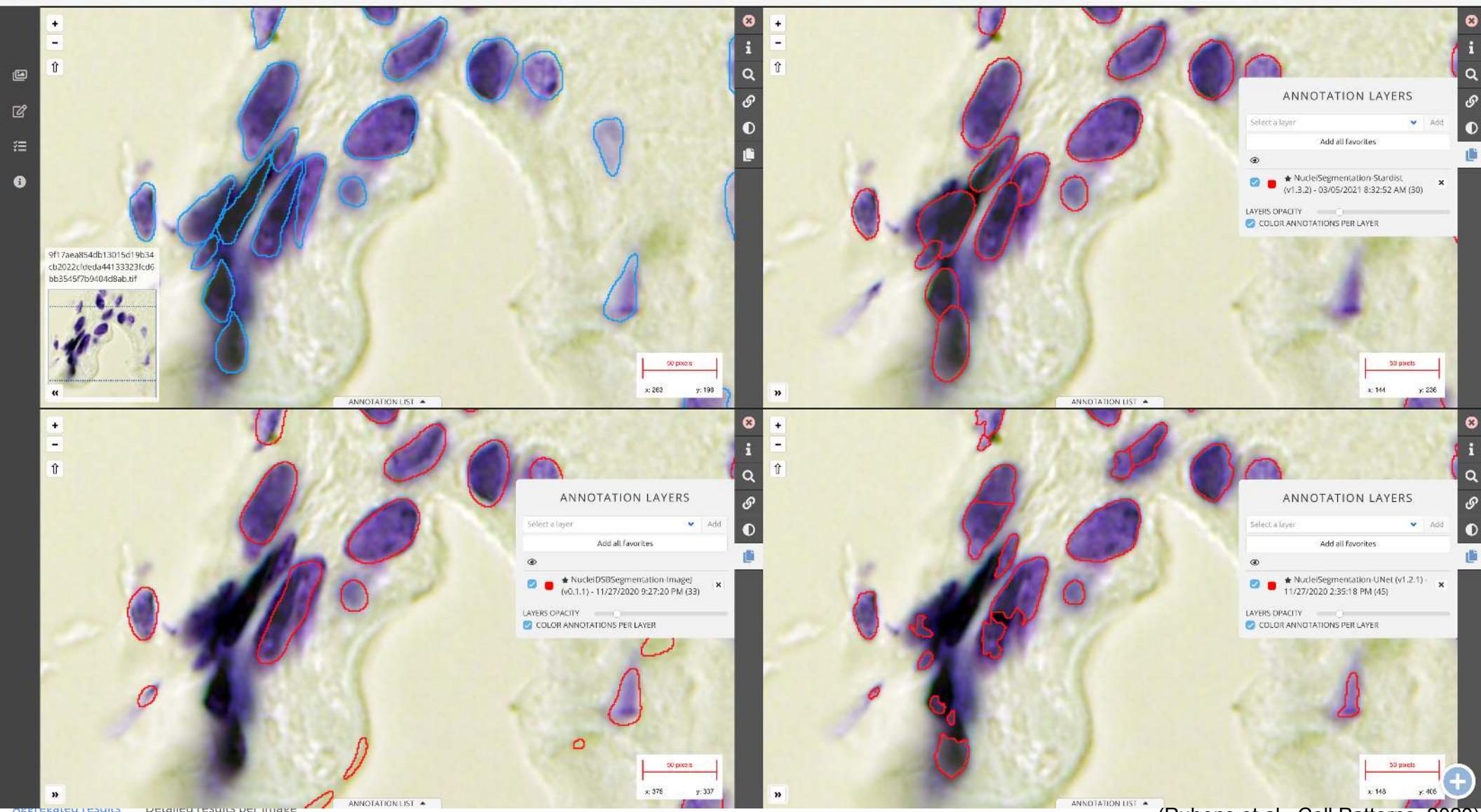
Workflow run	Mean Average Precision [Main metric]	Dice coefficient	Average Hausdorff distance	Fraction Overlap Pred
★ NucleiSegmentation-Cellpose (v1.2.2) #1 on Mar 5, 2021 8:08 PM	0.312	0.701	10.545 *	0.553
★ NucleiSegmentation-Stardist (v1.3.2) #2 on Mar 5, 2021 8:32 AM	0.397	0.845	1.584	0.701
★ NucleiSegmentation-ilastik (v1.4.2) #1 on Nov 28, 2020 11:52 AM	0.208	0.725	3.843	0.502
★ NucleiSegmentation-MaskRCNN (v1.5.4) #1 on Nov 28, 2020 11:35 AM	0.394	0.798	2.702	0.625
★ NucleiDSBSegmentation-ImageJ (v0.1.1) #1 on Nov 27, 2020 9:27 PM	0.235	0.734	3.57	
★ NucleiSegmentation-UNet (v1.2.1) #1 on Nov 27, 2020 2:35 PM	0.282	0.754	8.485	



(Rubens et al., Cell Patterns, 2020)

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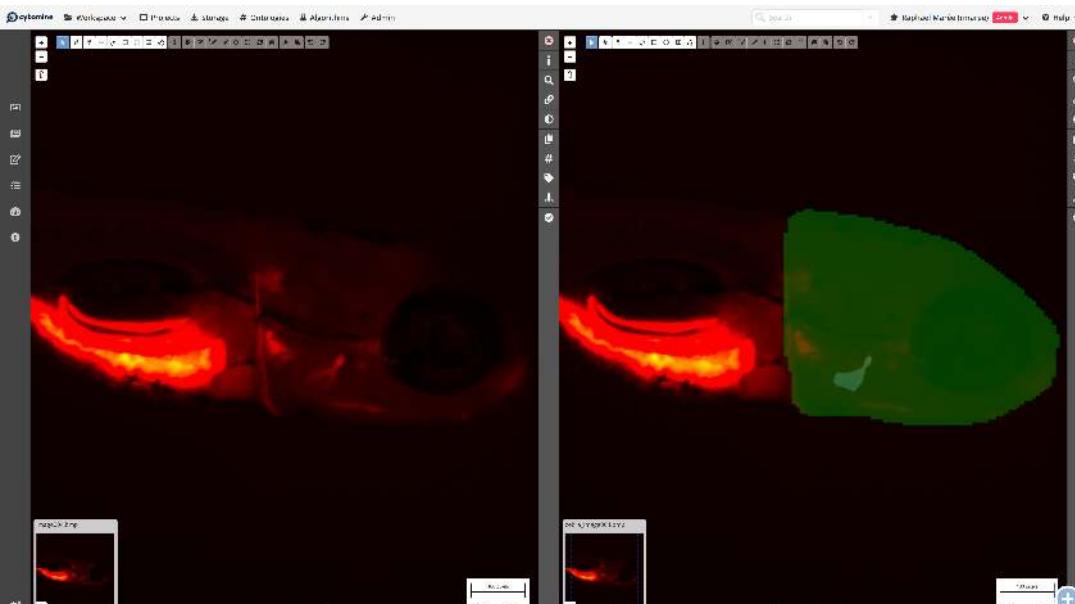


(Rubens et al., Cell Patterns, 2020)

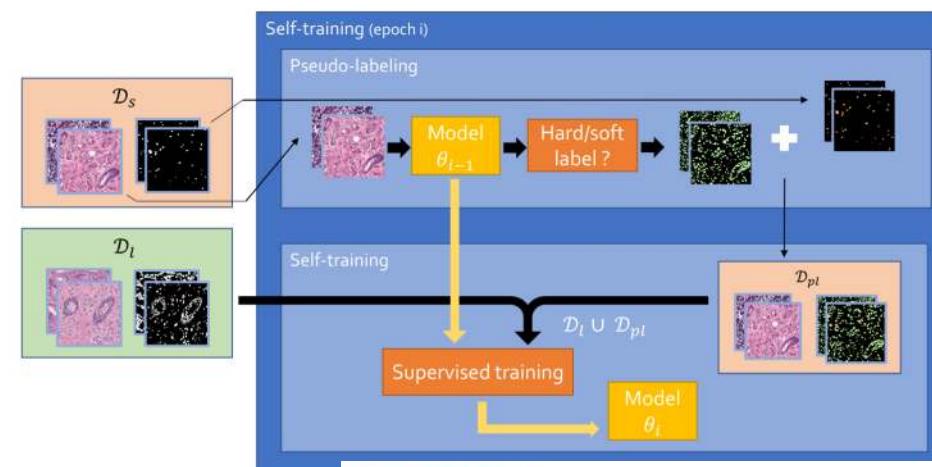
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Applications : Deep Learning-based tissue segmentation

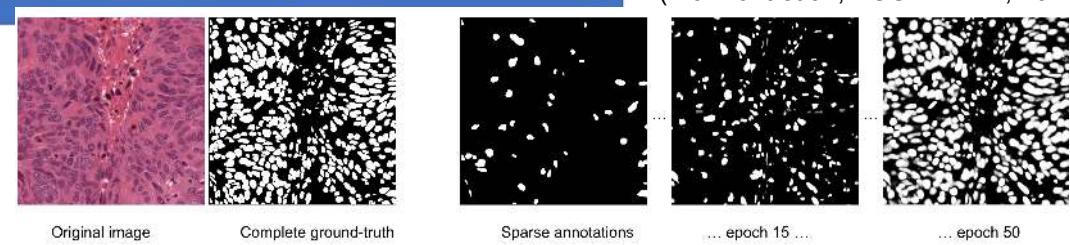
Two-step approach to deal with imbalanced pixel classes



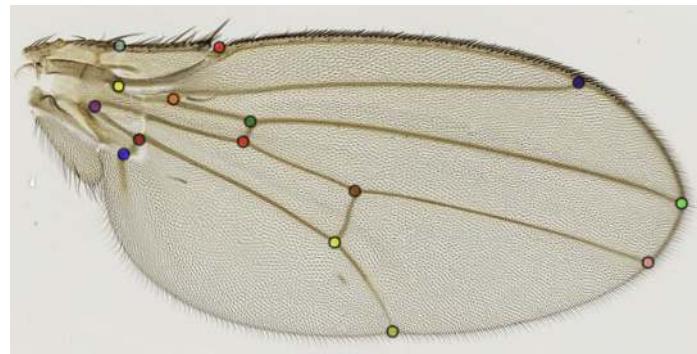
Self-training to relieve labelling effort



(Mormont et al., ECCV AIMIA, 2022)

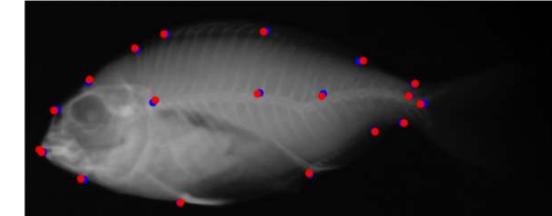
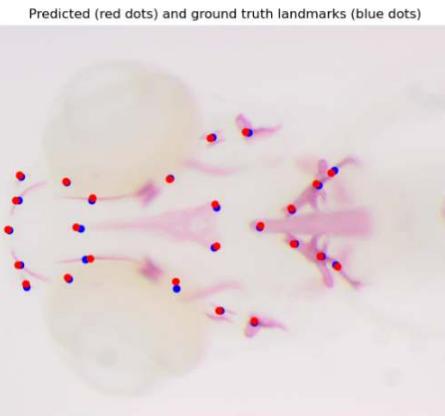
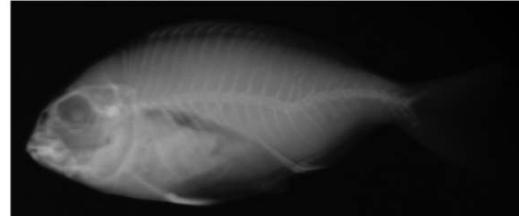
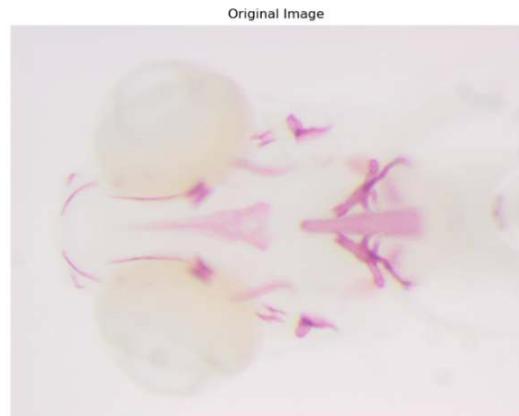


Applications : ML/DL-based landmark detection



(data : GIGA, UPMC, NTUST)
(Vandaele et al., Scientific Reports, 2019)

Heatmap-based deep-learning regression



(data : BioMedAQU : GIGA, CCMR, LESA)

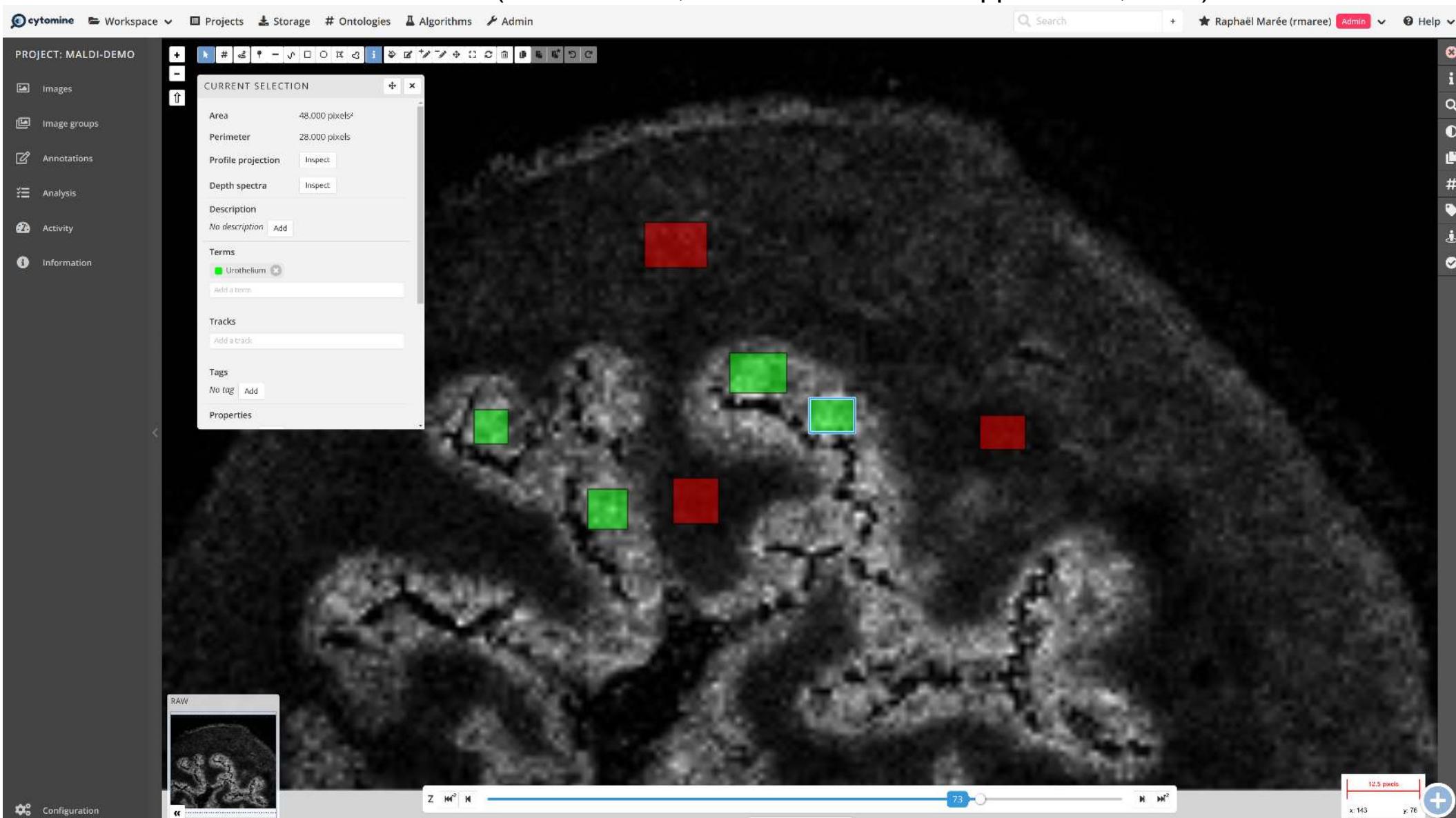
(Kumar et al., ECCV BiolImage Computing, 2022)

Experiments with MALDI-IMS data

Online manual annotations of
positive (urothelium) / negative (stroma) regions of interest

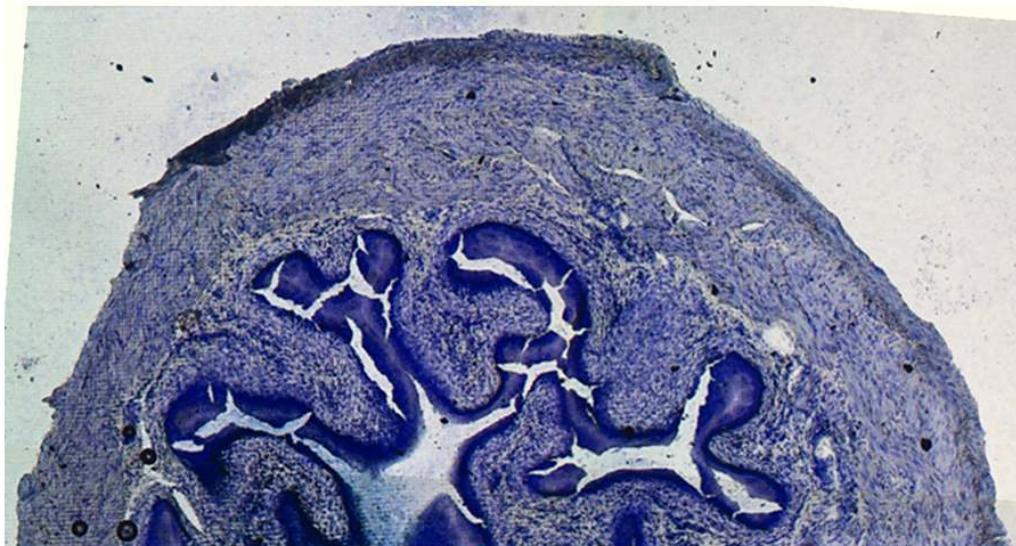
(Rubens et al., Proteomics: Clinical Applications, 2019)

cytominē

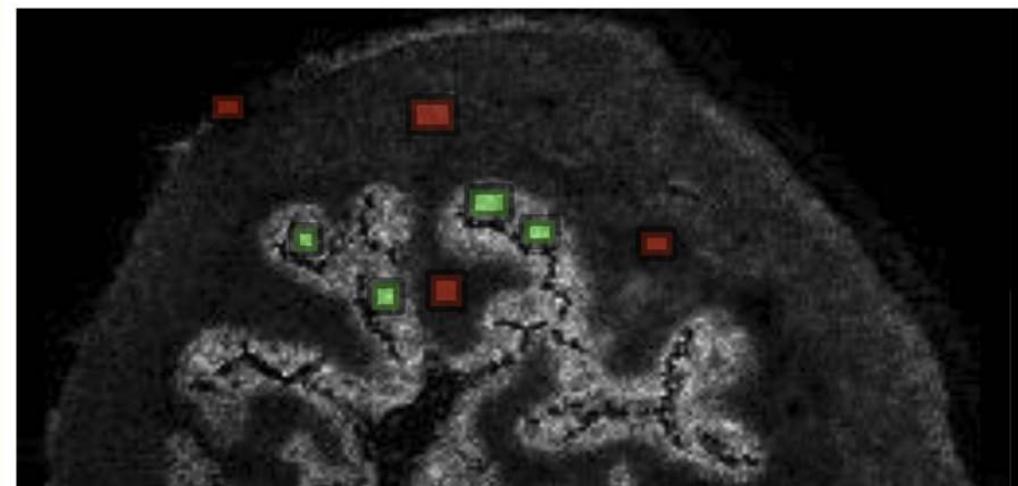


Experiments with MALDI-IMS data

Identification of discriminative spectral bands using randomized trees



A



B

m/z values	ANOVA F-Value	ExtraTree
799.49 (+)	651.918	0.1492940768
798.56 (+)	662.449	0.1211009801
824.53 (+)	564.432	0.0967599441
800.55 (+)	448.28	0.0821023916
812.59 (+)	349.814	0.0768024239
534.29 (+)	406.36	0.0538016408
782.53 (+)	499.857	0.0440587226
826.63 (+)	462.973	0.0408721138
769.54 (-)	213.954	0.0351156839
741.59 (-)	308.67	0.0311644774

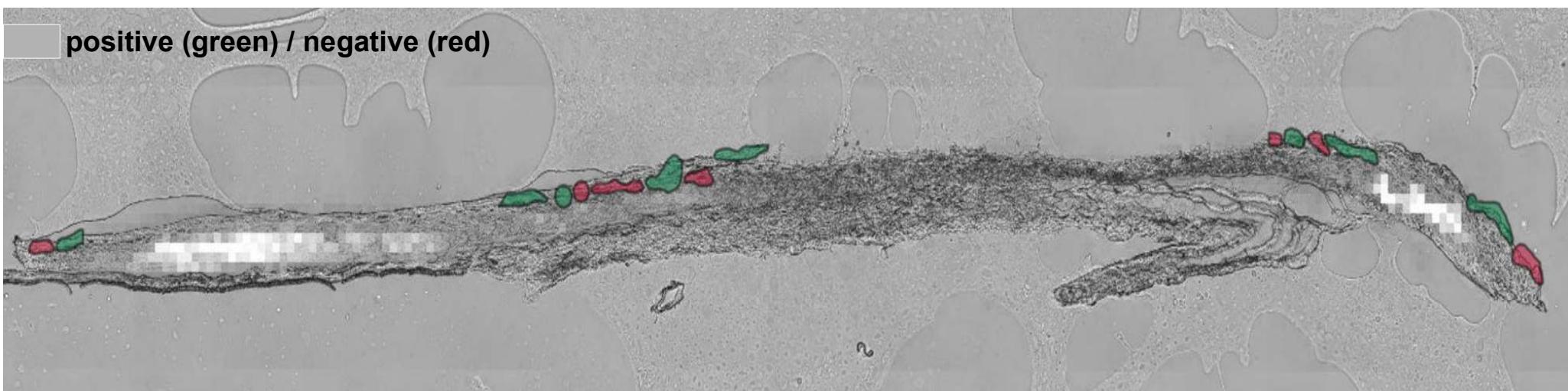
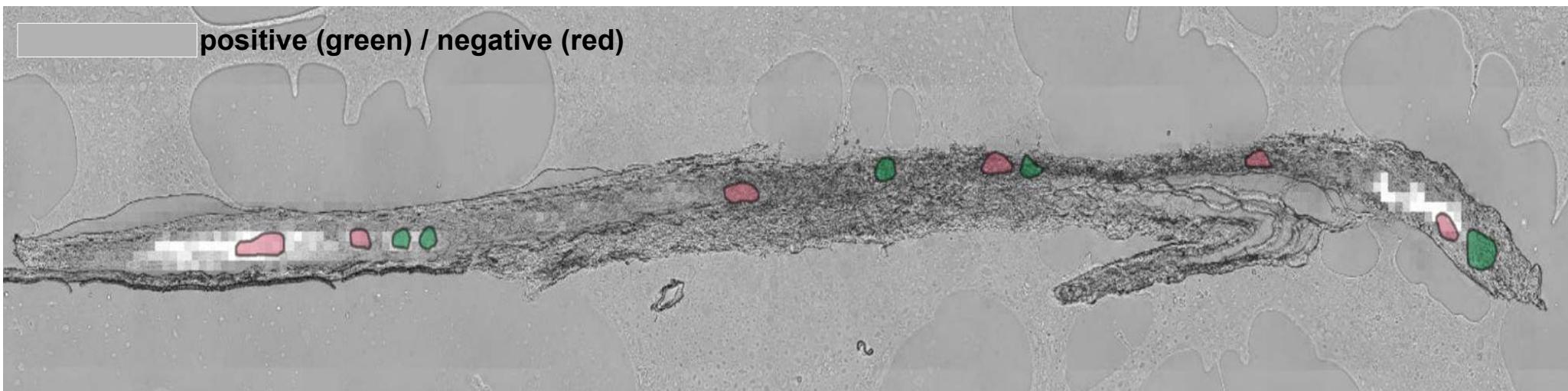
(Rubens et al.,
Proteomics: Clinical
Applications, 2019)

Supplementary Table 3: Ranked m/z values to discriminate between urothelium and stroma regions. (+) indicates that there is positive signal in the urothelium region for this m/z value while (-) indicate there is no signal in the urothelium region but in the stroma region.

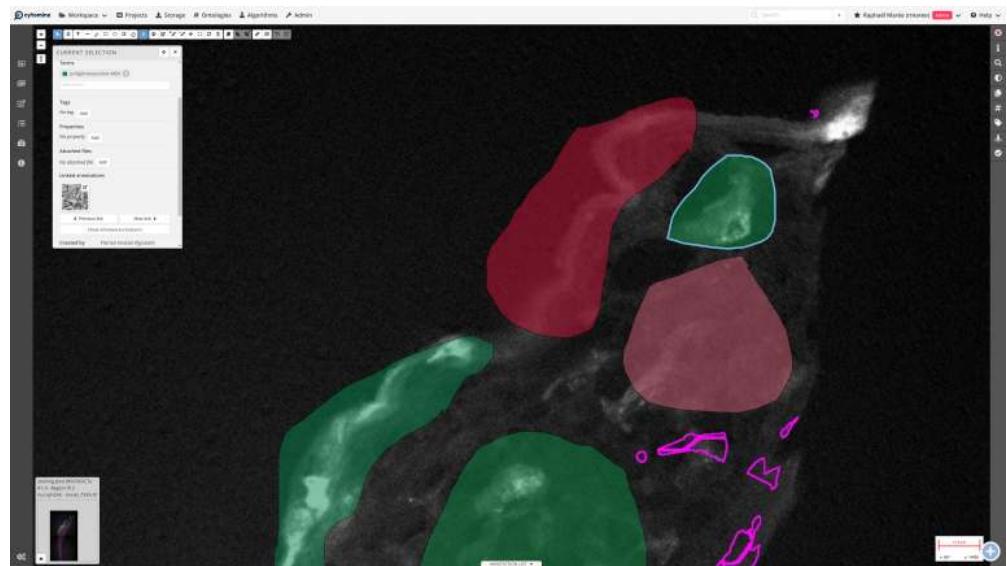
COMULIS multimodal application example

Multiple image acquisition using <> imaging modalities

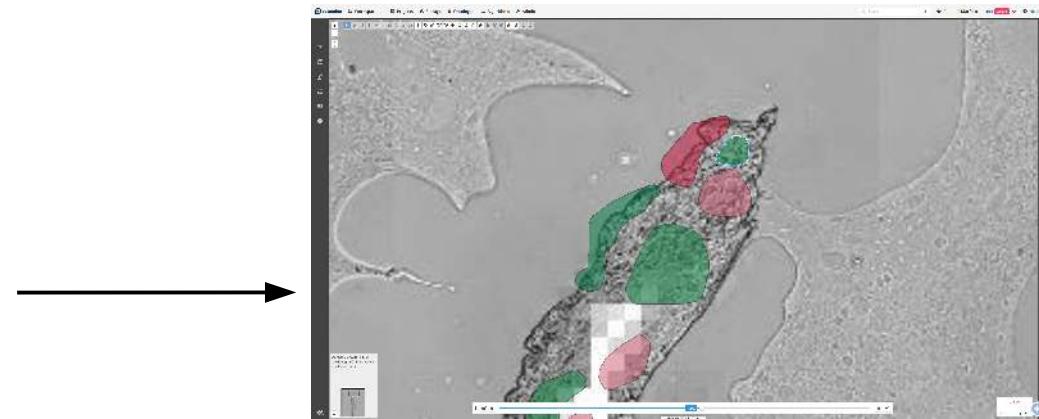
A simple biology question : any features (ions,...) that discriminate + and - ?



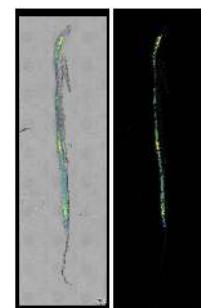
COMULIS multimodal application example



1. Manual annotations in 1st image modality
(high spatial resolution)



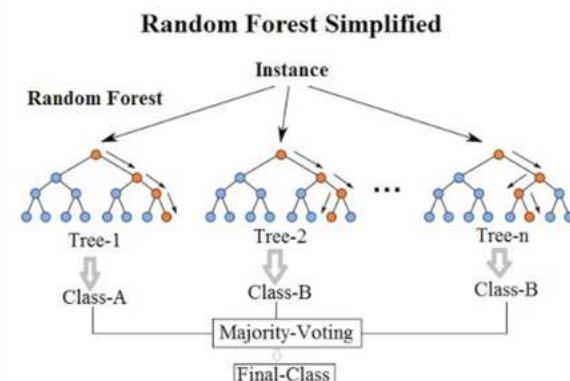
2. « Smart » copy/paste in 2nd image modality
(low spatial, high spectral, resolution)



3. Template matching
with raw data
(imzml/Ome Zarr) to
extract full spectral data

Discriminative features
(ions) ?

4. Binary « pixel » classification
and feature selection



cytominE is documented (doc.cytomine.org)

Cytomine for data and computer scientists:
<https://www.youtube.com/watch?v=FW7M3Ga5wIY>

Getting Started

Concepts

- Roles
- Project
- Image Viewer
- Ontology
- Upload & Storage
- Annotations
- ImageGroups and AnnotationLinks
- Analysis and Algorithms
- Administration

Data scientist Guide ▾

Introduction

Create scripts

Create apps

Interact with Cytomine

Cytomine apps

Concepts

Write a Cytomine App

Release a Cytomine App

JSON descriptor reference

API client for Python ▾

API client for Java ▾

API client for Javascript ▾

API reference

Operations

Introduction

Cytomine Bootstrap

Cytomine containers

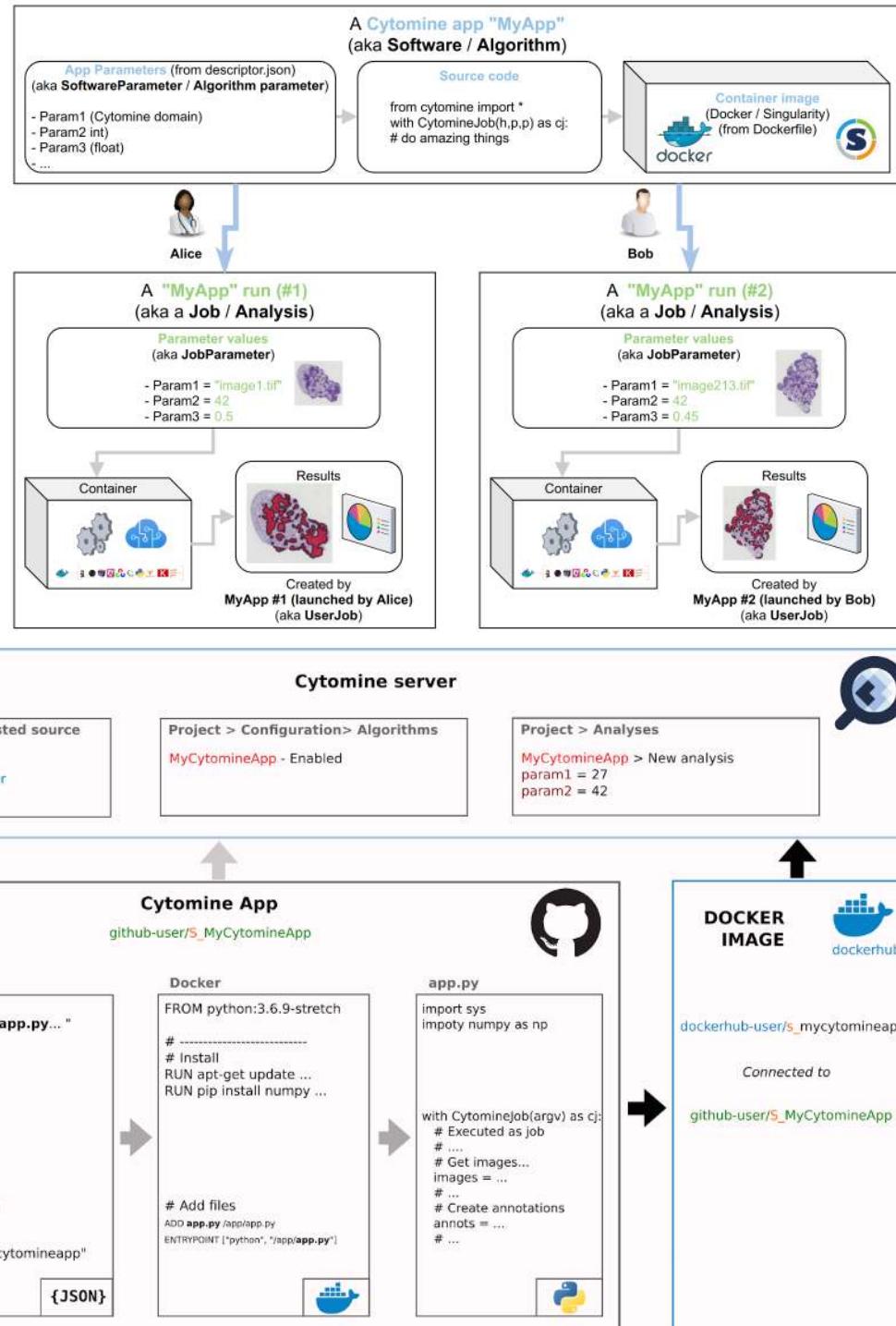
Install

Upgrade

Backup and restore

Troubleshoot

Uninstall



Summary and perspectives

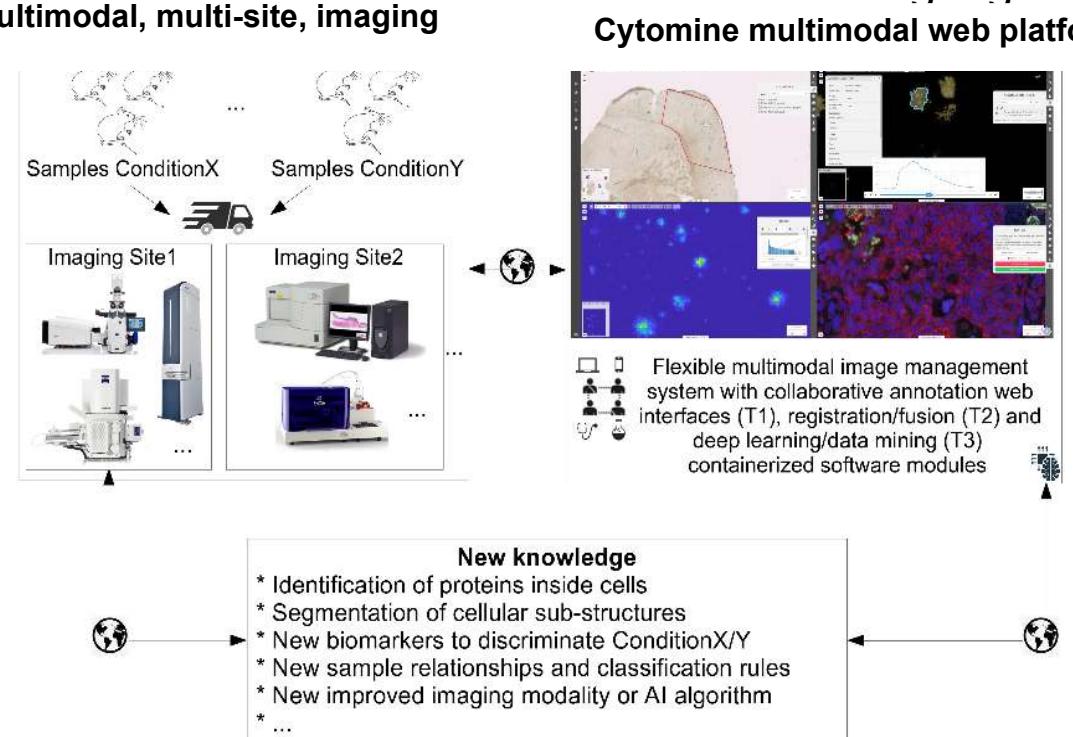
Cytomine for « sharing everything »



- Multimodal images, ground-truth annotations, image analysis/AI source code, quantitative results, ...
- **Cytomine can be installed at your own institute** to start **collaborative** research today
- Ongoing developments for multimodal annotation and analysis

Cytomine ULiège R&D Future plans

- Improve data structures and analysis workflows for multimodal data analysis
- Better support for bigger and distributed datasets with millions of objects
- Deep learning to ease annotation using active/transfer/multi-task/self learning
- Ease the integration of multimodal registration/fusion/data mining algorithms



Acknowledgments

ULiège & Cytomine.com/coop : Ulysse Rubens, Ba Thien Le, Maxime Amodei, Romain Mormont, Navdeep Kumar, Remy Vandaele, Renaud Hoyoux, Grégoire Vincke, Pierre Geurts, Chloé Marchal, Loïc Rollus [cytomine.org]

Comulis & Neubias network : Florian Gruber, Martina Marchetti-Deschmann, Samuele Zoratto, Christopher Kremslehner, Rafael Camacho, Julia Fernandez-Rodriguez, Andreas Walter, Sebastian Munck, Natasa Sladoje, Sebastien Tosi, Benjamin Pavie, Volker Backer, Lassi Paavolainen, ... [comulis.eu & neubias.org]

Funding sources since 2010 :



Contact



cytomine



Community Partners

There are more tickets available for I2K 2022 - so please still register to attend the conference! 😊

Topic	Replies	Views	Activity
Problem with publication of a descriptor.json file • Usage & Issues cytomine	4	34	2h
Cytomine upload error • Usage & Issues cytomine	2	36	4h
How to get properties (key and value) of an annotation via API client for Python • Development cytomine, api	3	51	20h
Error of communication with Cytomine core [Part2] • Usage & Issues cytomine	17	1.0k	1d
Create new terms via the api • Usage & Issues cytomine	1	33	6d
Cytomine ssl with self signed certificates • Usage & Issues cytomine, ssl	2	39	6d
Cytomine backup • Usage & Issues cytomine	6	95	Mar 15
Upload software throws 500 error	n	52	Jan 14



@cytomine

@cytomine_uliege



github.com/cytomine/
github.com/cytomine-uliege
(Apache 2.0 license)



cytomine.org

uliege.cytomine.org

doc.cytomine.org

doc.uliege.cytomine.org



uliege@cytomine.org

Two webinars (May 2021):

https://www.youtube.com/results?search_query=neubias+academy+cytomine



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COMULIS Conference September 21th-22nd, 2022 in Nicosia, Cyprus

<https://www.comulis.eu/comulis-conference-2022>