

Collaborative analysis of multimodal imaging data with **cytominē** web platform

Gdr MAGIS

September 27th, 2022

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uliege.cytomine.org



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

Automated tissue bioimaging (digital pathology)

Sample preparation

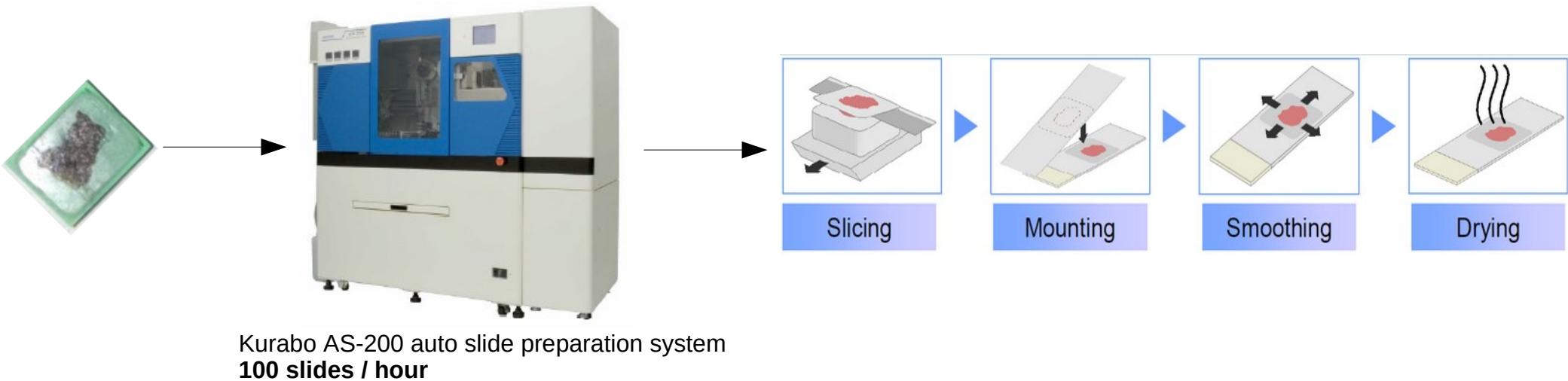
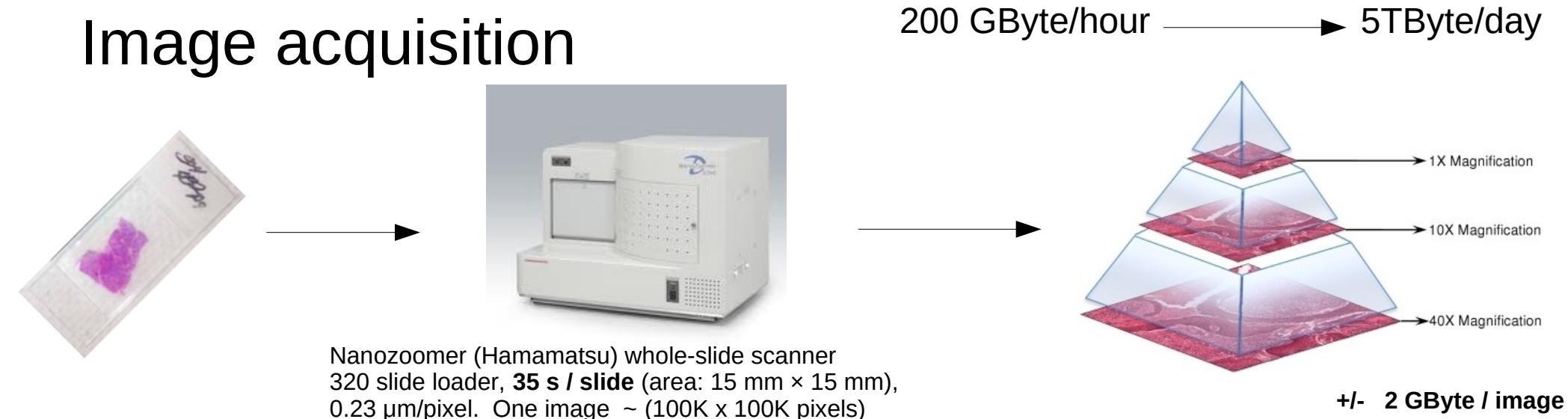
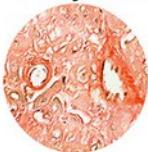


Image acquisition

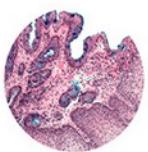


Heterogeneity of histology images

Amyloid

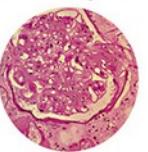


Congo Red
Cat # 24614



Alcian Blue/ PAS
Cat # 25086

Carbohydrates



PAS
Cat # 24200



Rapid Mucin
Cat # 24208

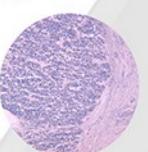
Neuronal Tissue



Cresyl Violet
Cat # 21063

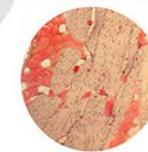


Bielschowsky
Cat # 25994



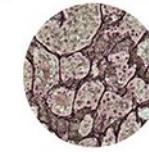
Luxol® Fast Blue
Cat # 24611

Triglycerides & Lipids

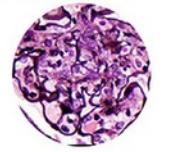


Oil Red O
Cat # 25962

Reticulin Fibers



Reticulin
Cat # 25094

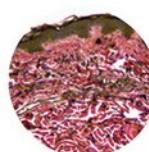


Jones PAS-M
Cat # 25091

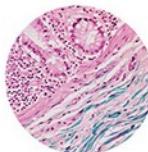
Connective Muscle Tissue



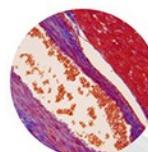
Picosirius Red
Cat # 24901



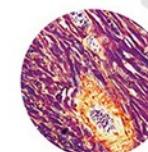
Verhoeff Van Gieson
Cat # 25089



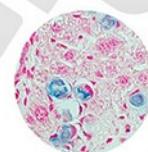
Gomori's Trichrome
Cat # 24205



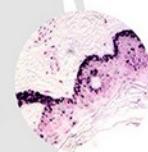
Masson's Trichrome
Cat # 25088



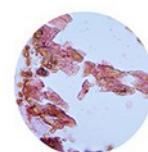
Rapid PTAH
Cat # 25715



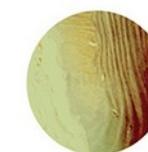
Prussian Blue Iron
Cat # 24199



Fontana Masson
Cat # 25104

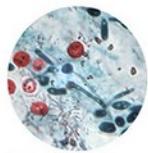


Von Kossa Method
Cat # 24633

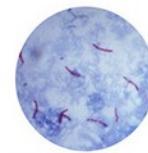


Villanueva Osteochrome Bone
Cat # 16280

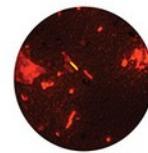
Microorganisms



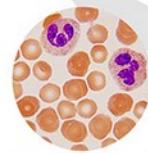
AFB Kinyoun
Cat # 25765



AFB Ziehl-Neelson
Cat # 24669



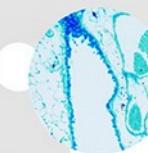
Auramine O
Cat # 24665



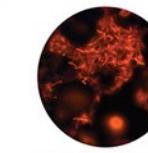
Differential Quik
Cat # 24606



Fungi-Fluor®
Cat # 17442



Grocott Methenamine
Silver
Cat # 25462



TB Fluorostain
Cat # 22422



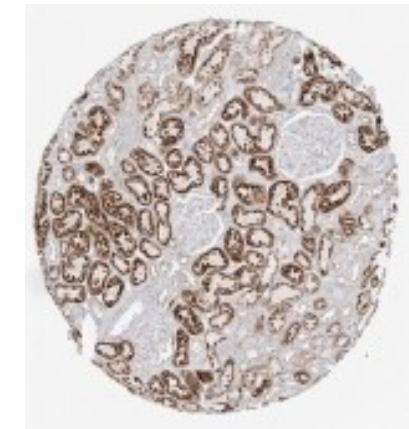
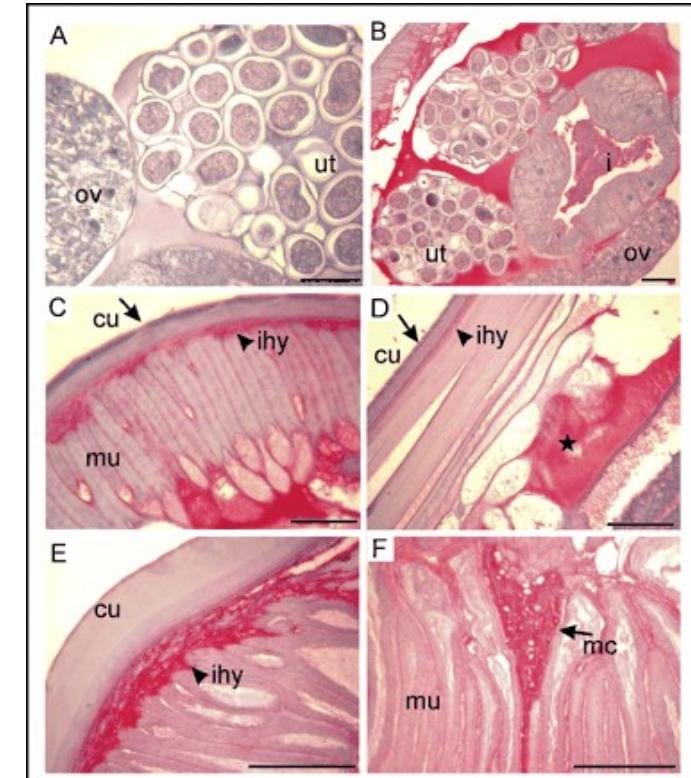
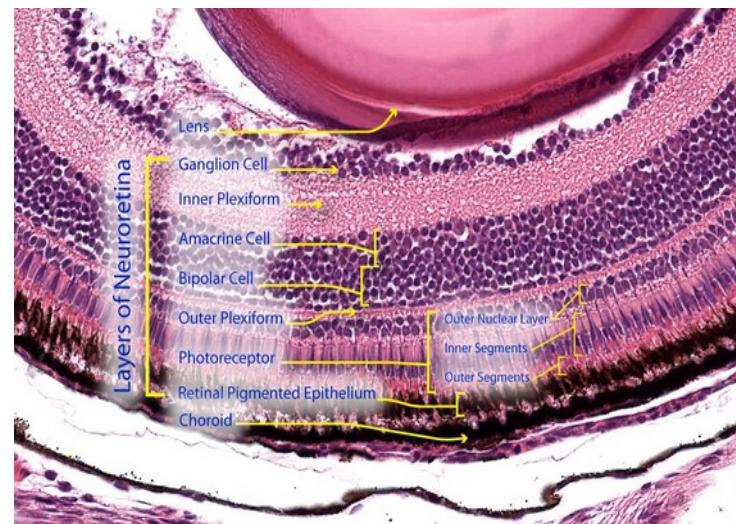
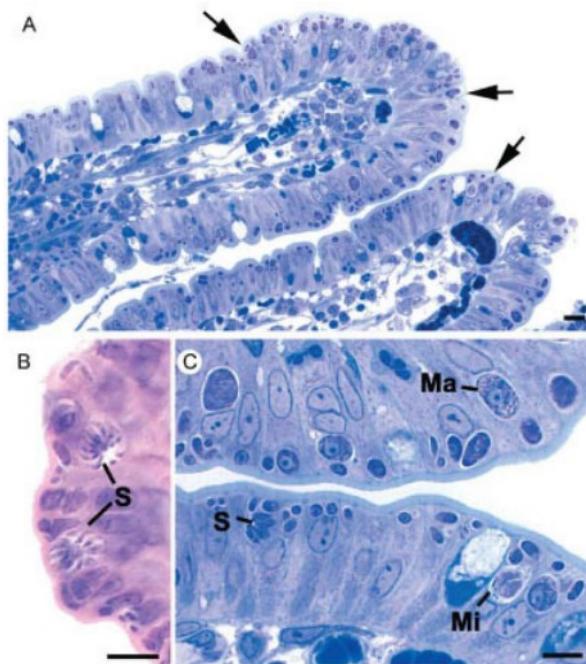
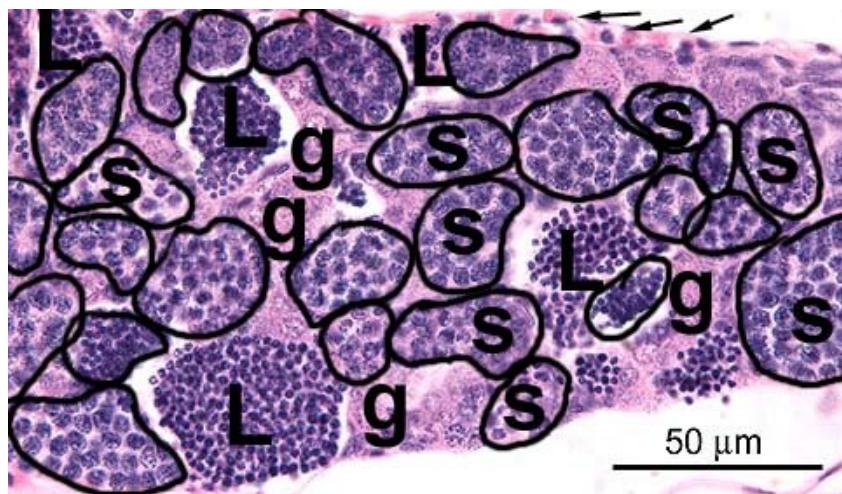
Warthin-Starry
Cat # 25093



Gram's Stain
Cat # 24668

Special Stains

Heterogeneity of histology images



(Source : Google Images)

Heterogeneity in multimodal imaging

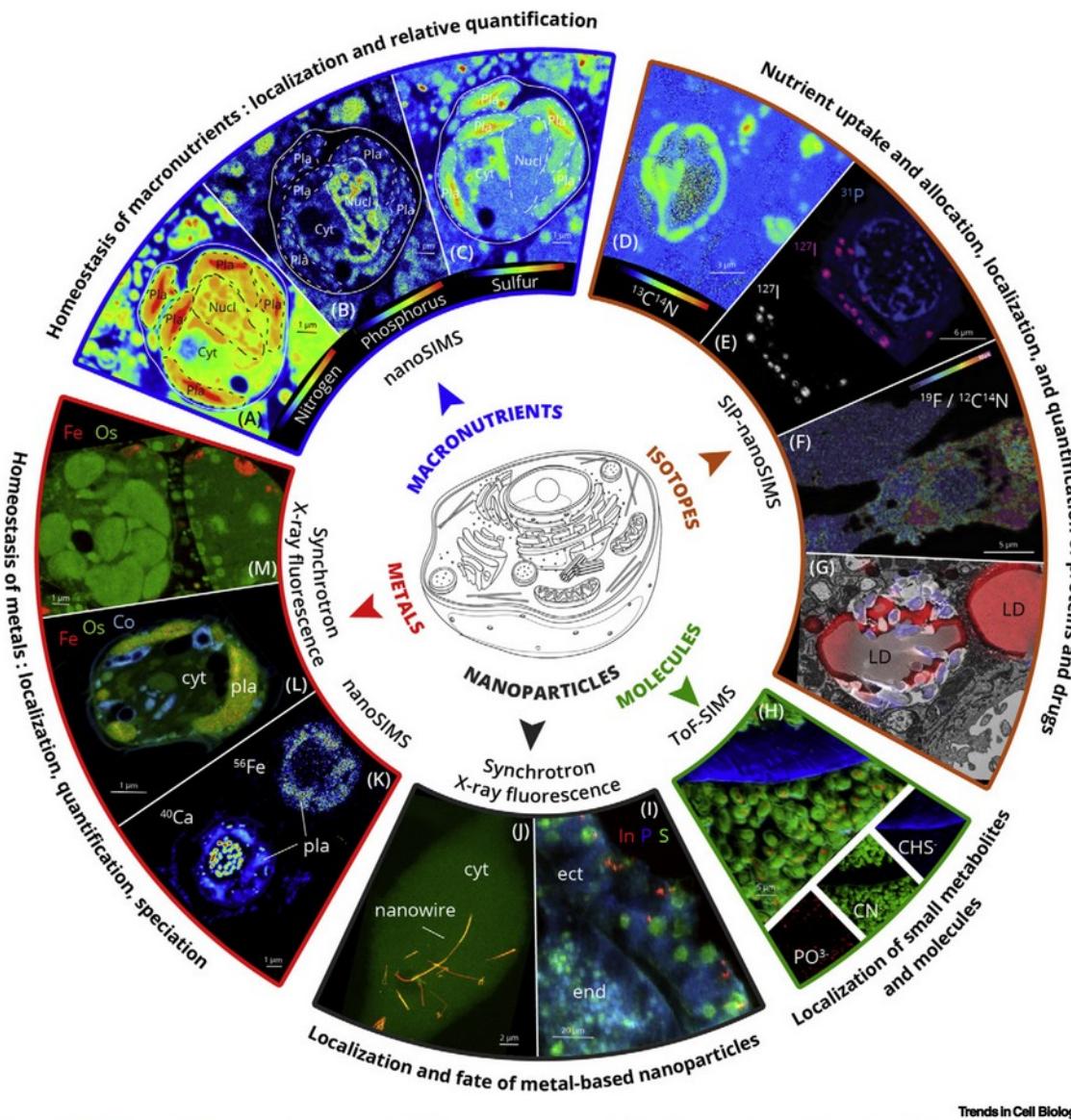


Figure 2. The Potential of Chemical Imaging to Unveil the Chemical Landscape of a Cell: Composition and Distribution of Elements, Isotopes, and Molecules at the Nanoscale. (A–C) Nano-secondary ion mass spectrometry (nanoSIMS) images showing the distribution of the macronutrients nitrogen [(A)]

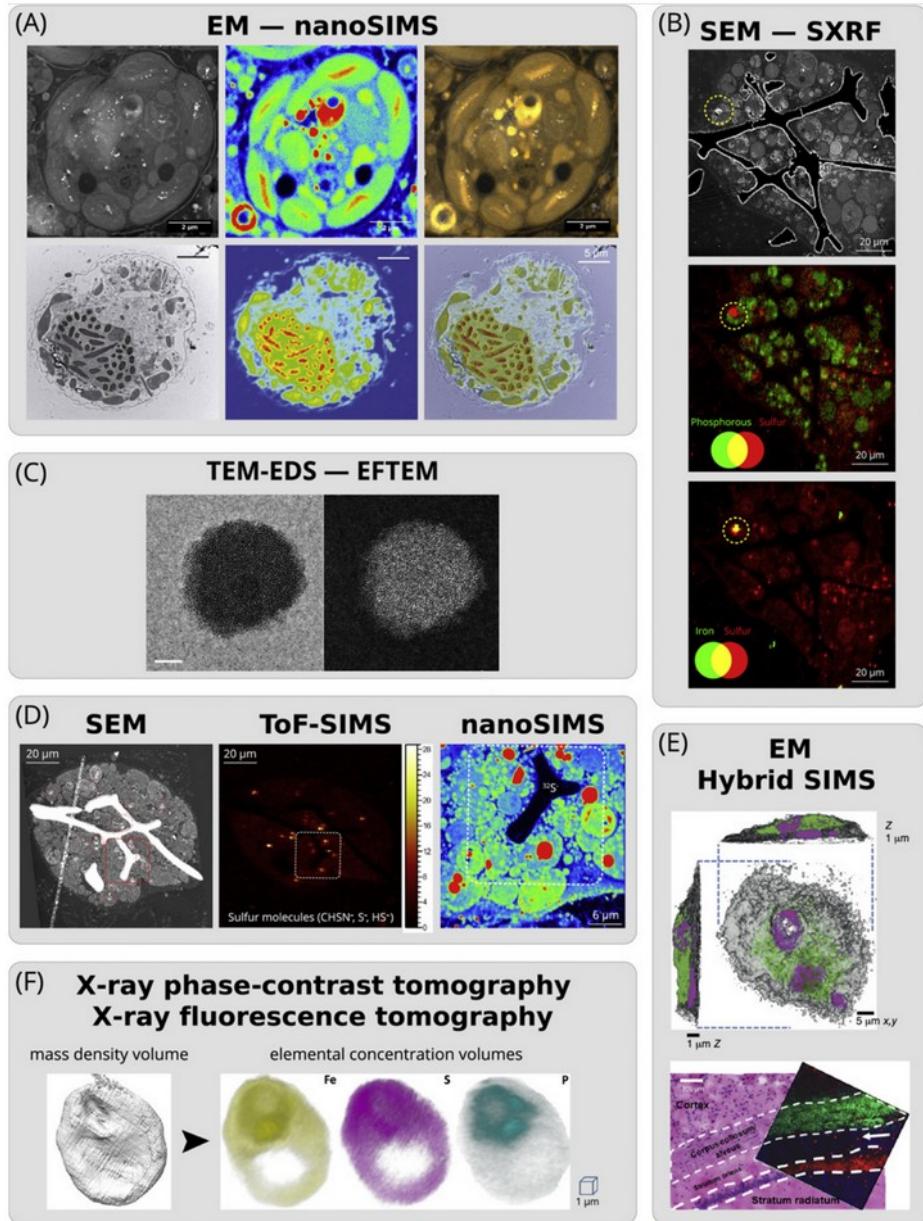
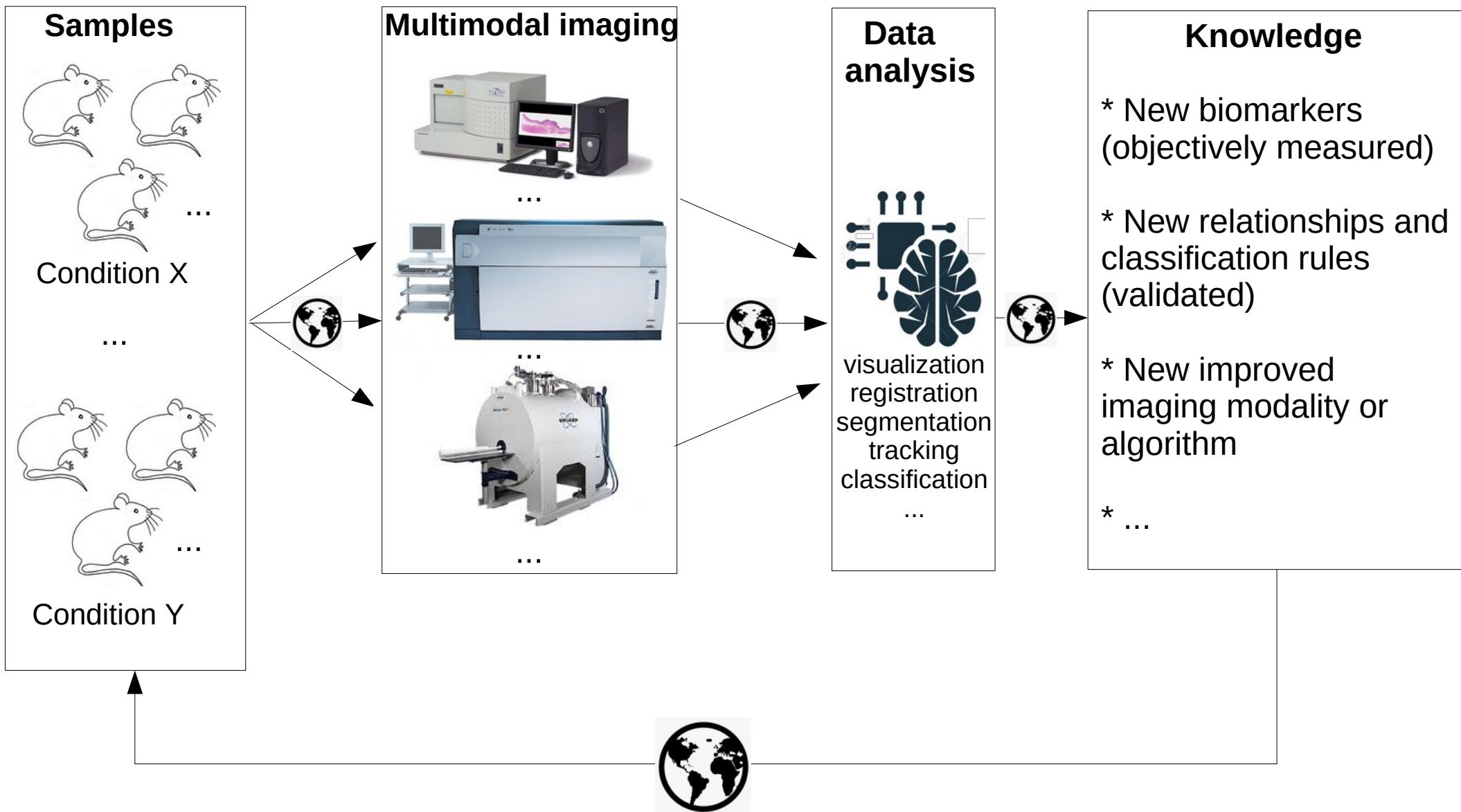


Figure 3. Examples of Correlated Electron Microscopy (EM) and Chemical Imaging. (A) Correlation between EM

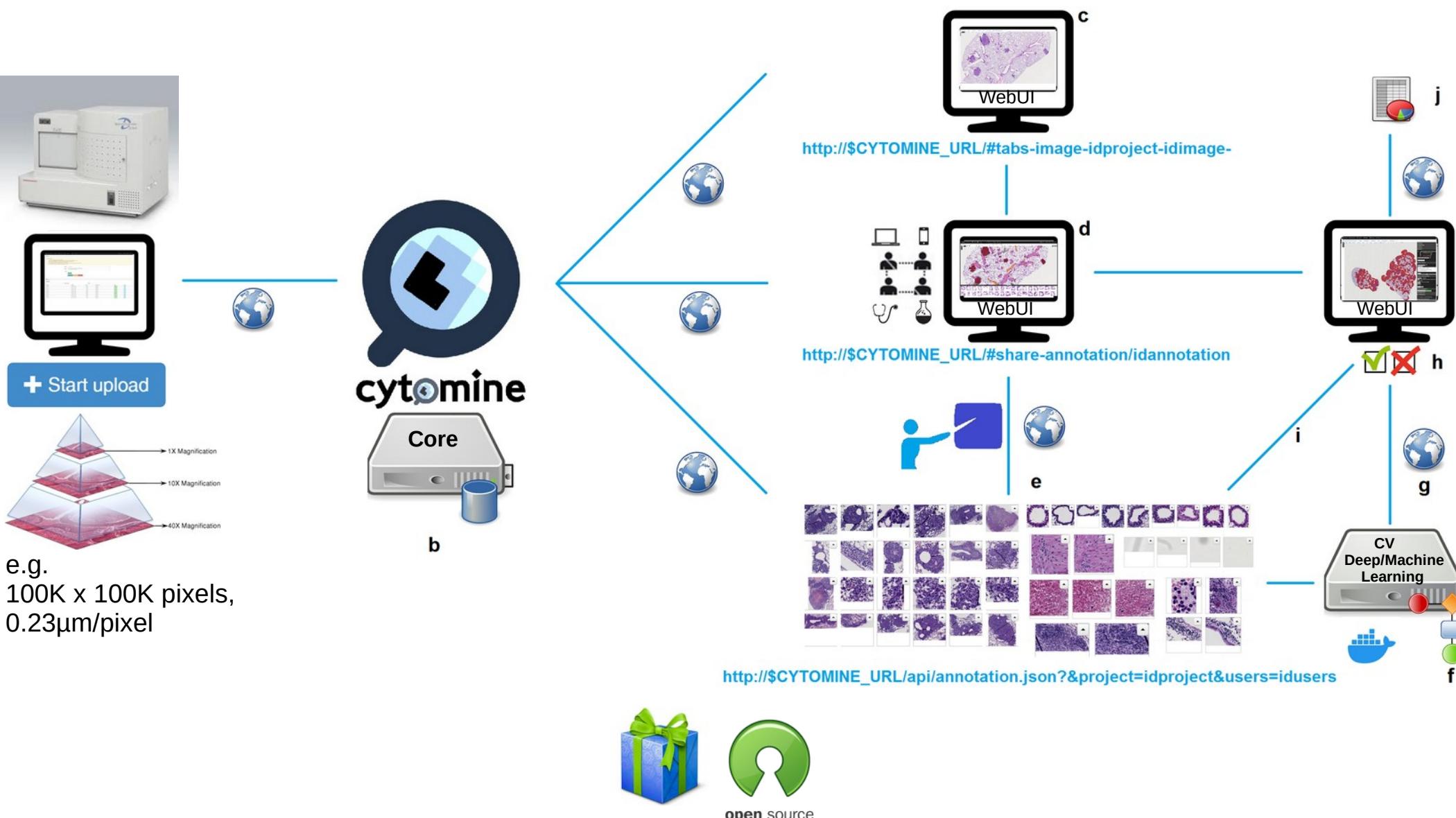
Ideal correlative/multimodal workflow

(Exploratory analysis / Biomarker discovery / Classification of samples)



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)

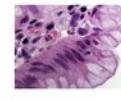
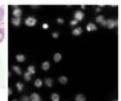
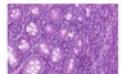
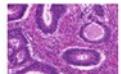
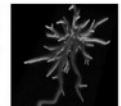
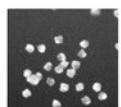


Note : Cytomine-Core can be installed on Linux-based servers or on a desktop/laptop (but then without collaborative features)

cytominE : organize your images on the web

Create and manage multiple **projects** :

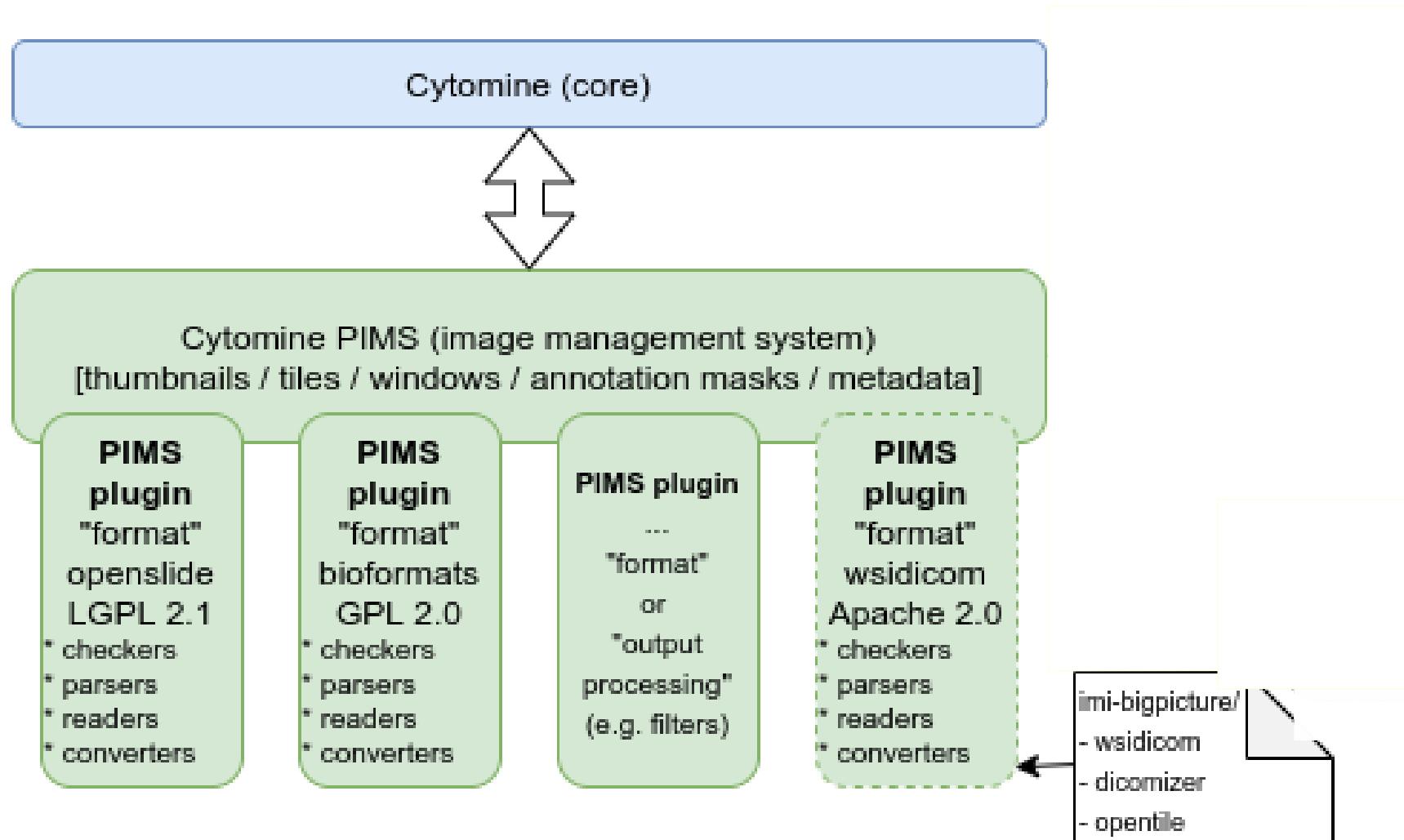
- Users with **authentification** (e.g. LDAP), **access rights**, and **roles**

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

cytominē : extensible image management system

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

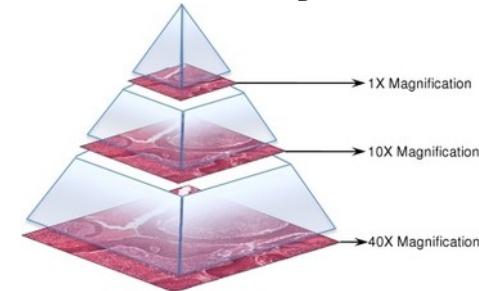
- Support **various digital pathology, microscopy & other image formats** (Pyramidal TIFF, WSI-DICOM, OME-TIFF, ...)
- **Flexible architecture** with plug-ins (using various libraries e.g. OpenSlide, BioFormats, Zarr, WSIDicom, VIPS, ...)



cytominE : visualize large 2D images, remotely

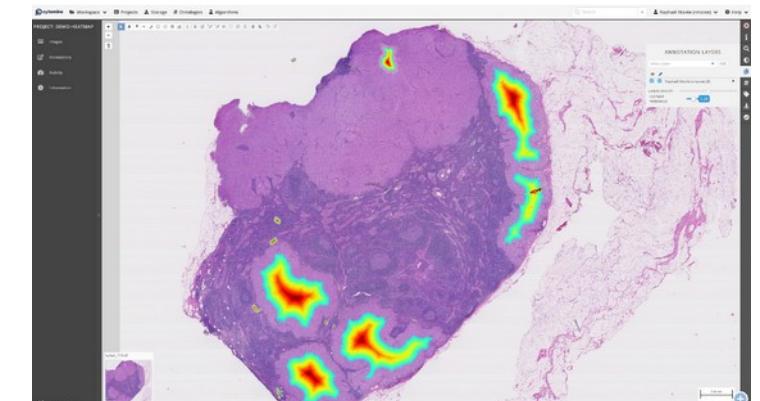
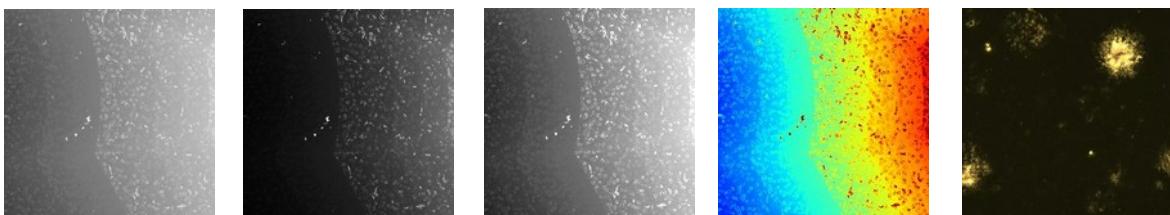
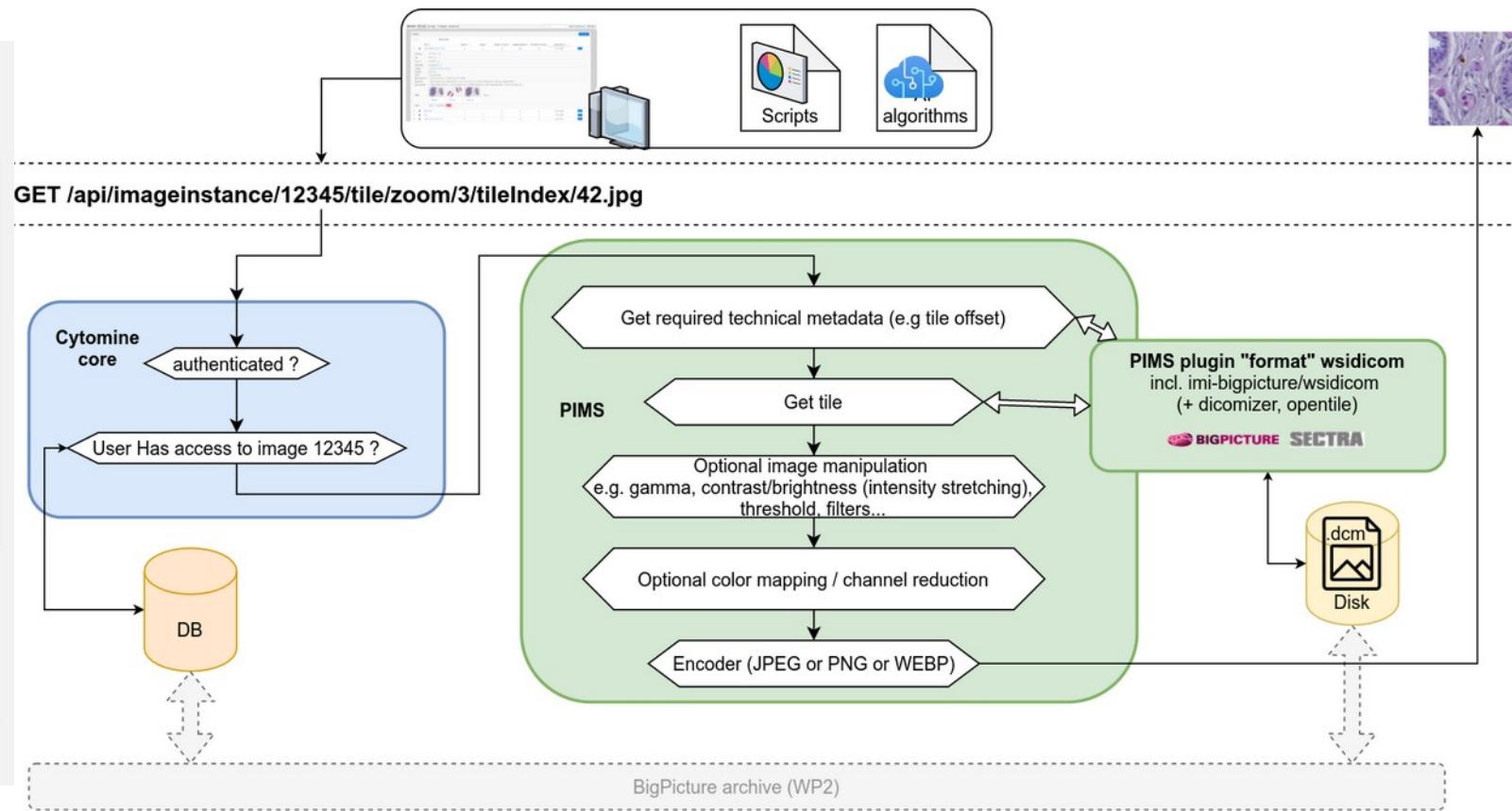
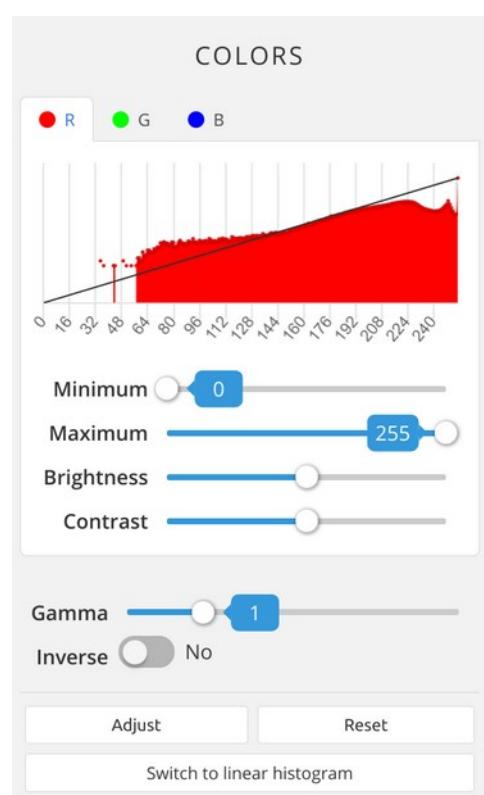
- Explore **large** (multi-gigapixel) images at multiple resolutions, **remotely**
- OpenStreetMaps browsing style (zoom in/out, pyramid tile-based)

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



The image shows the cytominE software interface. At the top, there is a navigation bar with links for 'cytominE', 'Workspace', 'Projects', 'Storage', 'Ontologies', 'Algorithms', 'Admin', 'Search', and a user profile for 'Raphaël Marée (rmaree)'. Below the navigation bar, there are two main windows. The left window displays a large, low-magnification view of a tissue sample, showing several large, irregularly shaped clusters of cells stained purple against a light background. The right window shows a much higher magnification view of a specific area within the tissue, focusing on a dense cluster of cells. Both windows have toolbars along their top edges with various icons for image manipulation. In the bottom left corner of the left window, there is a small thumbnail image and some text: 'PGP POUMON PB55 1 - 2012-08-07 11.39.07.jp2'. The overall interface is designed for remote visualization of large-scale microscopy images.

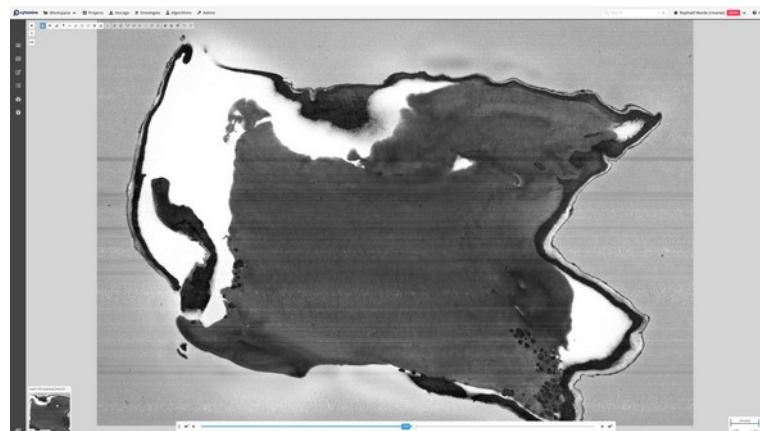
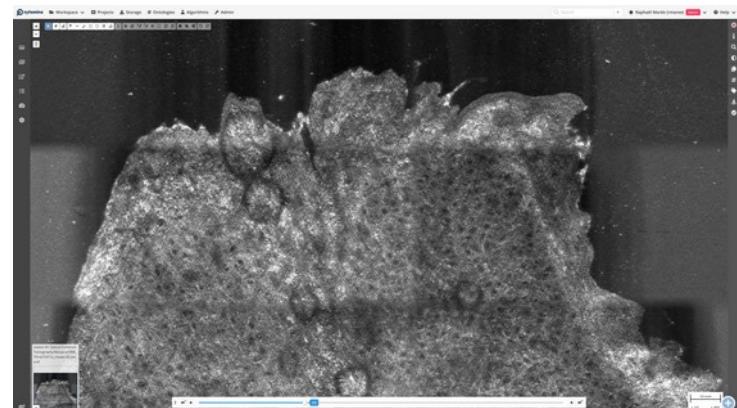
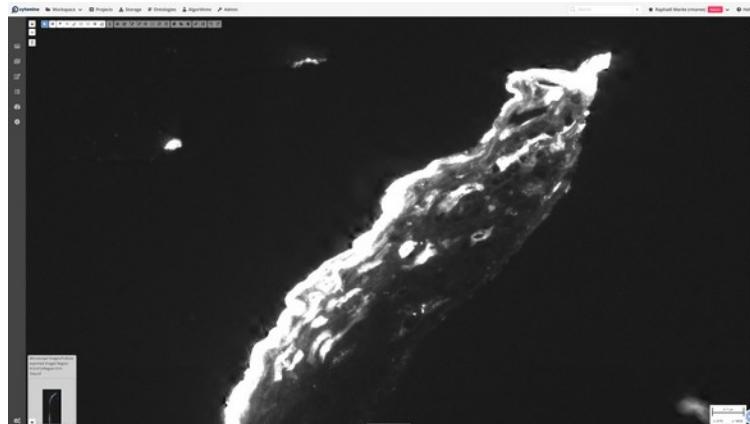
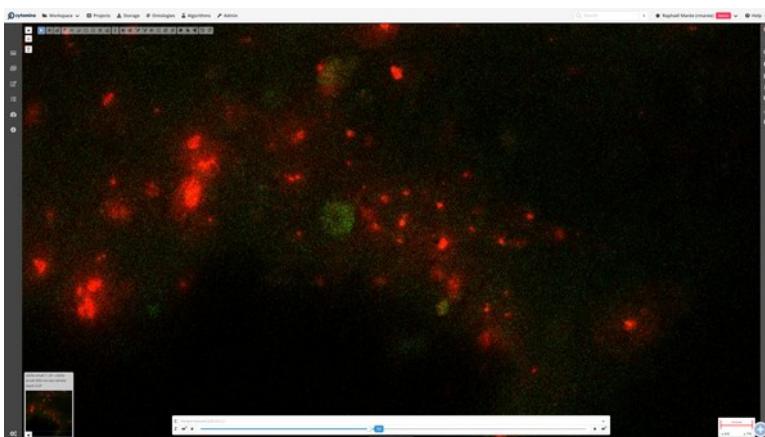
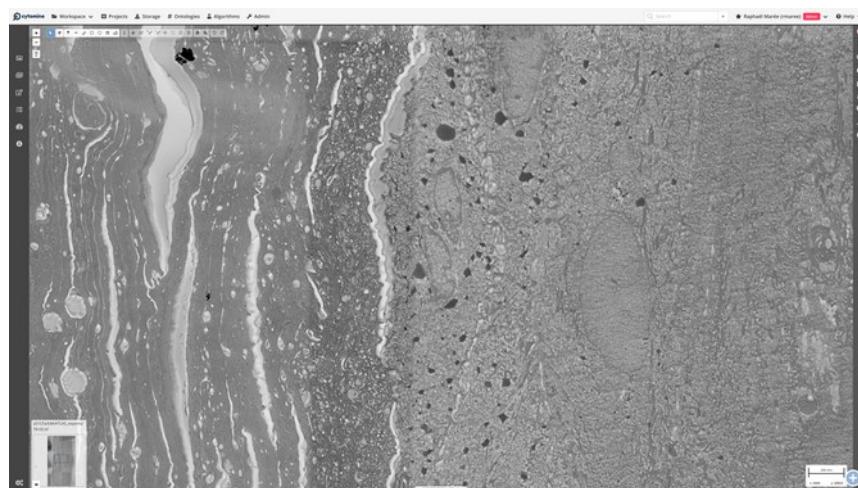
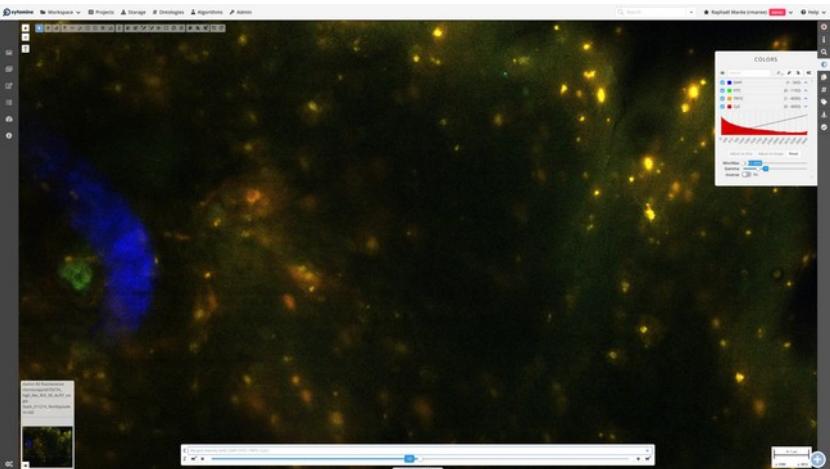
cytominE PIMS on-the-fly (tile) image operations



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

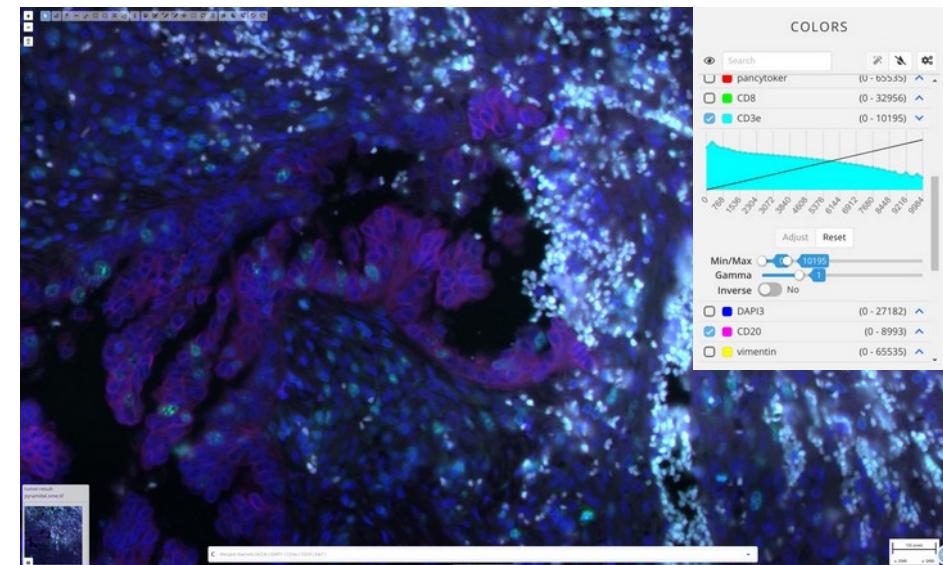
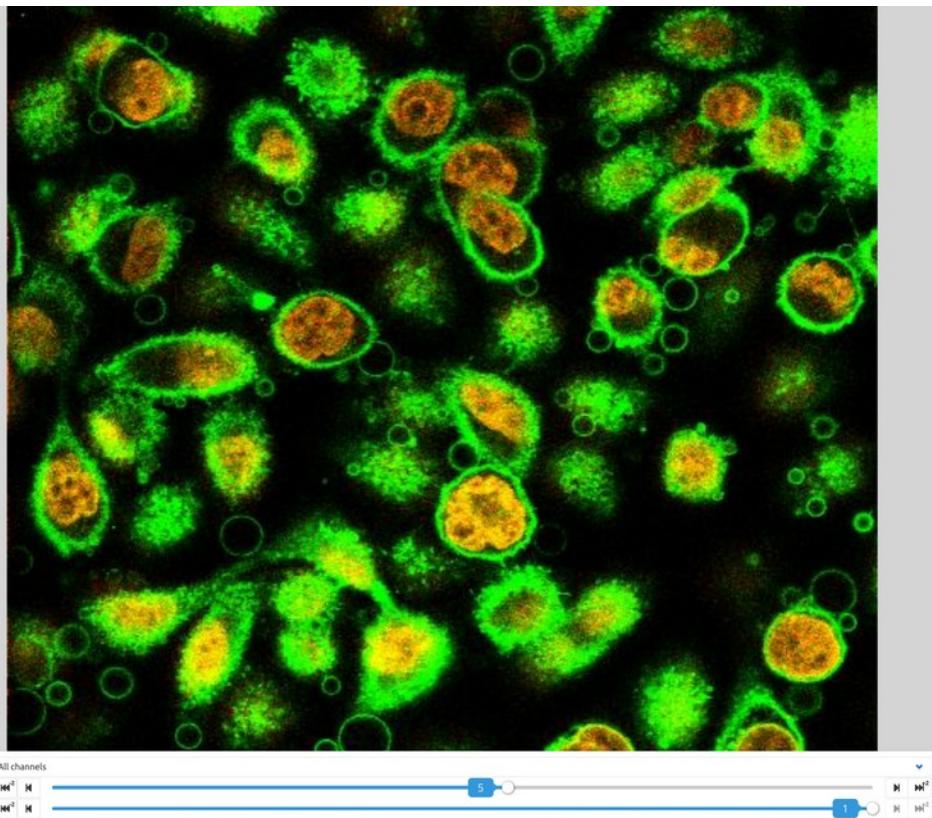
cytominE : Support of 2D+c+z+t image formats

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



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

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



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

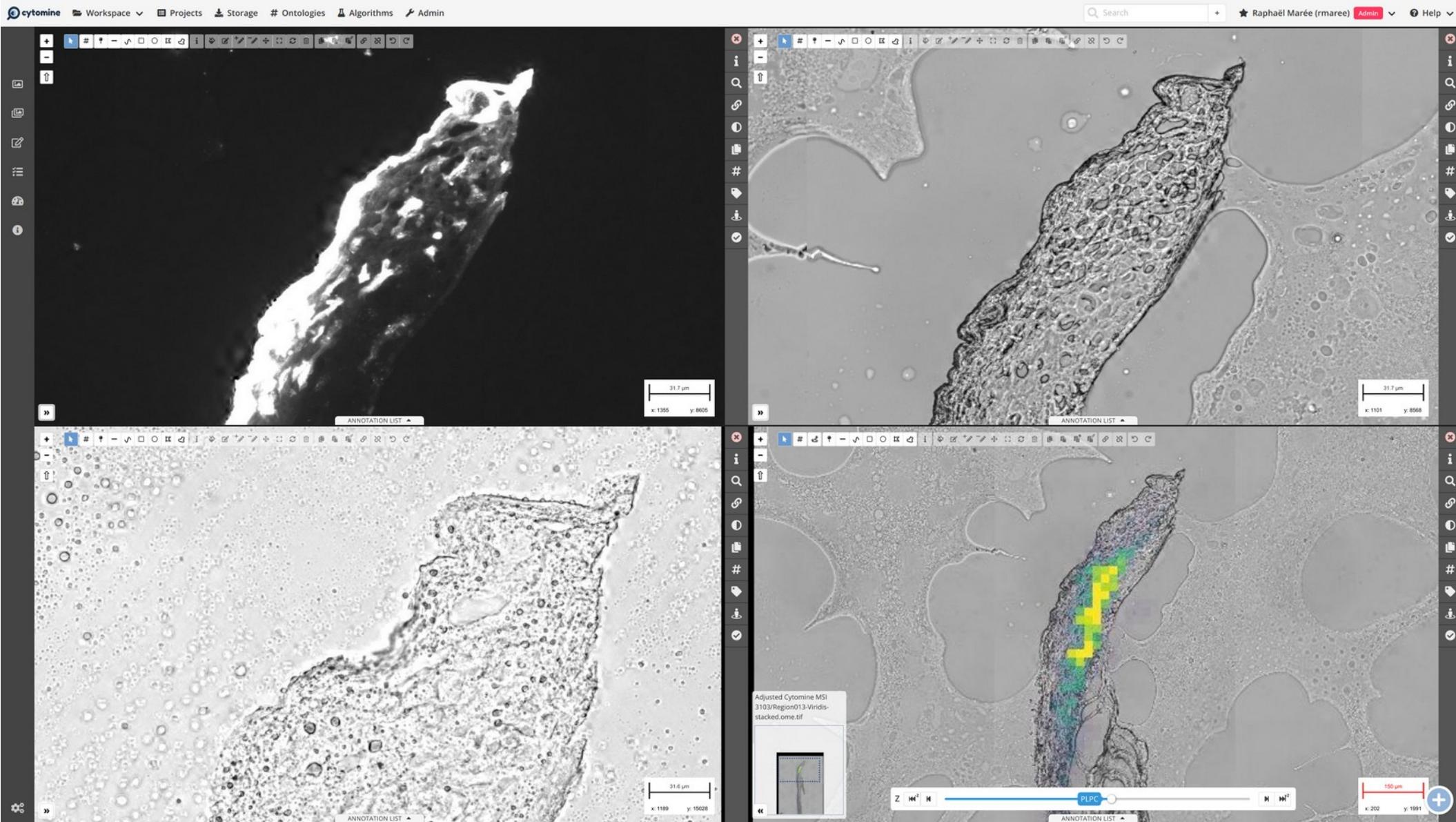


cytominE: joint visualization of multimodal datasets

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

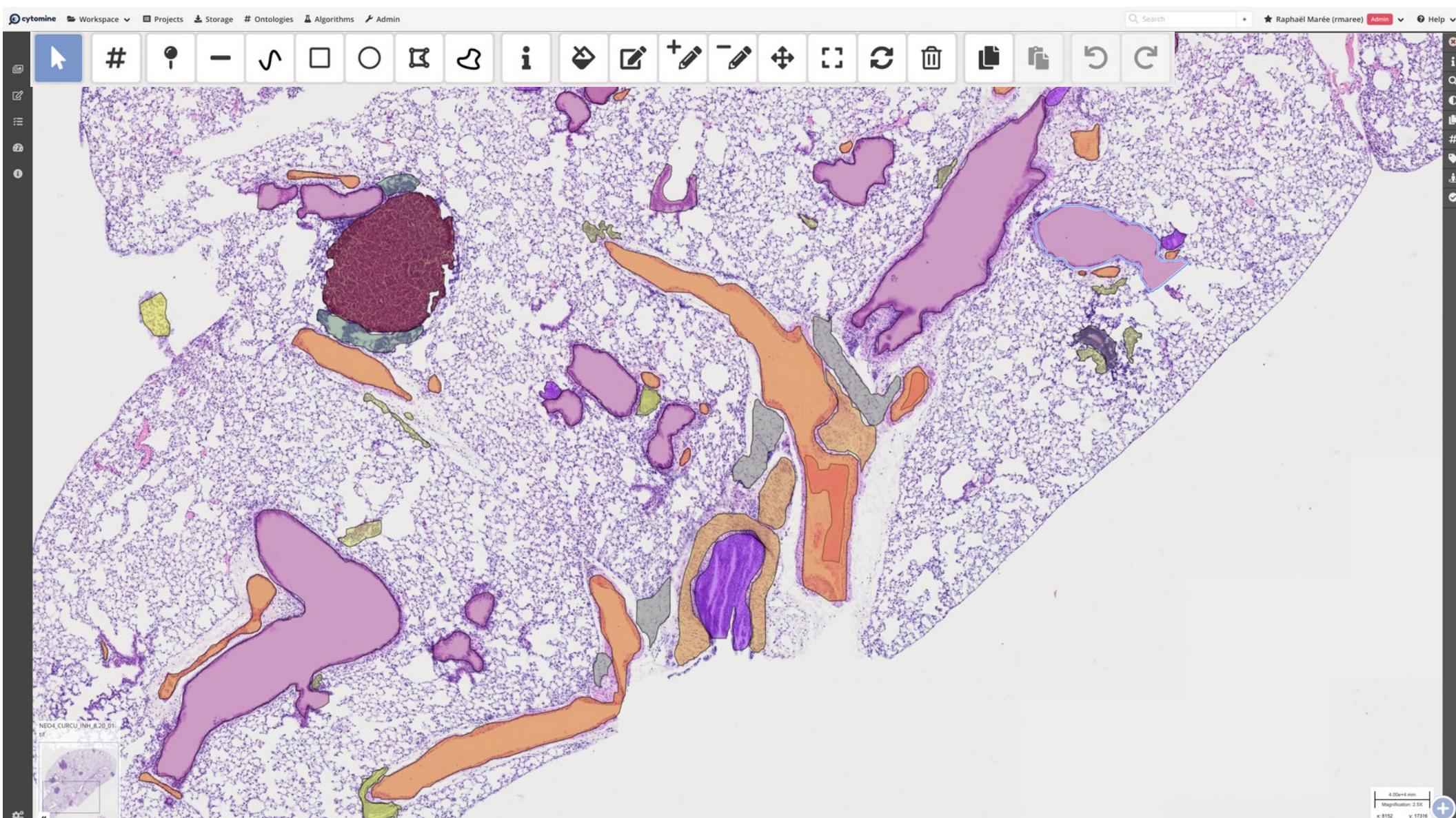


(data : COMULIS)



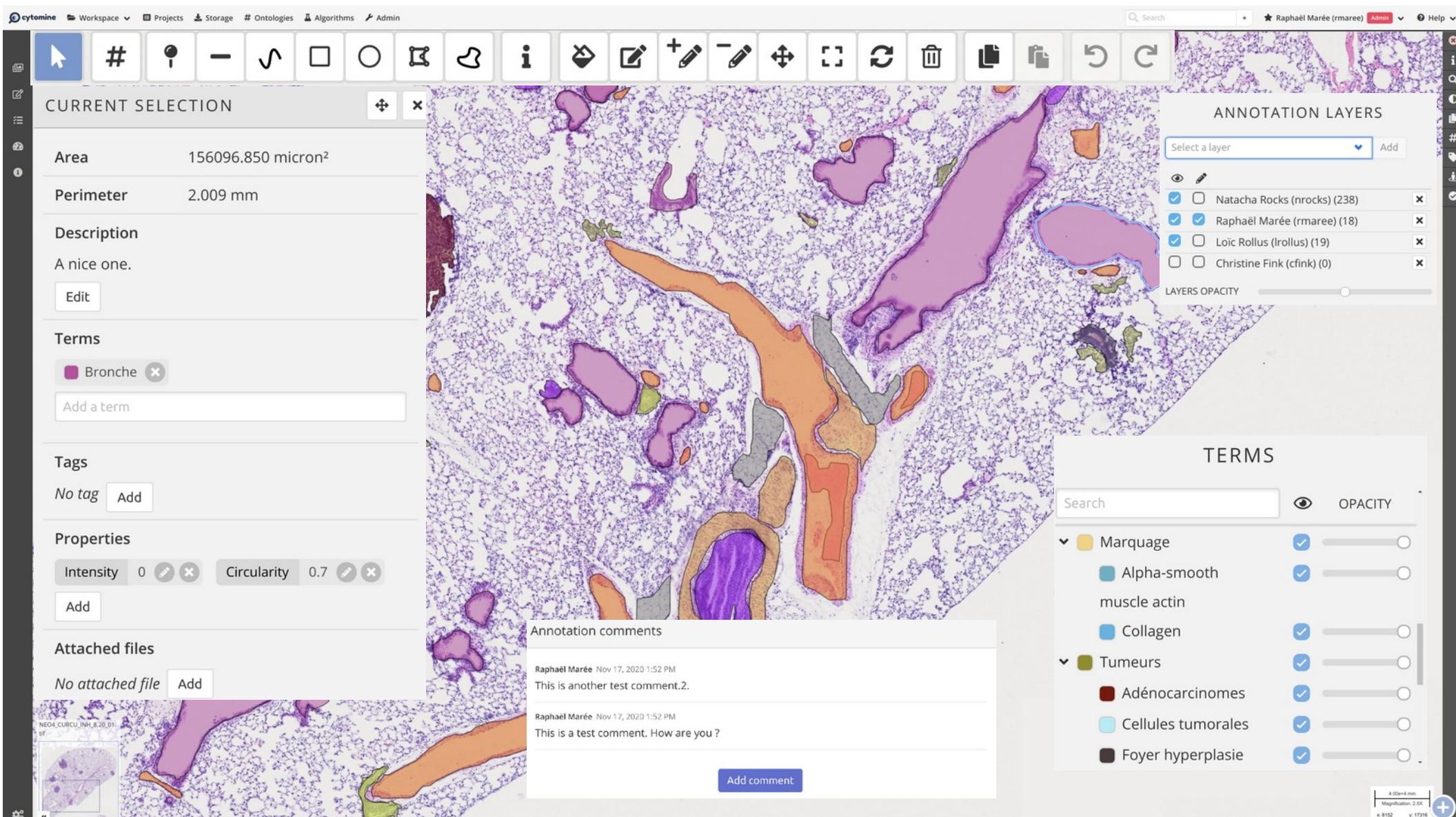
cytominE : annotate semantically, collaboratively

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



cytominE : annotate semantically, collaboratively

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



cytominE : online editor for user-defined vocabularies

Ontologies

New ontology

Search

- BIOMEDAQU-LESA-MEDAKA-CLAUDIA
- BIOMEDAQU-LESA-MEDAKA-LANDMARKS
- BIOMEDAQU-LESA-SAURATA-XRAYS-ZACH
- BIOMEDAQU-LESA-SAURATA-ZACK
- BIOMEDAQU-SUMMERSCHOOL
- BIOMEDAQU-UGENT-XRAYS-VERTEBRAE MEASURMENTS-LUCIA
- BIOMEDAQU-UGHENT-XRAY-DEF-LUCIA
- BIOMEDAQU-UGHENT-XRAY-LUCIA
- BIOMEDAQUE-CCMR-ZEBRA
- BIOMEDAQUE-GIGA-ZEBRAFISH-MICROSCOPIC
- BM-01
- BUDÉSONIDE 1 BALF
- BUDÉSONIDE 1 SCORE

ULG-LBTD-TISSUS

- Globule rouge
- Mitose
- Muscle
- NotAdeno
- Poumon
- Poumon non insufflé
- Unknown
- Zone floue
- Marquage
 - Alpha-smooth muscle actin
 - Collagen
- Tumeurs
 - Adénocarcinomes
 - Cellules tumorales
 - Foyer hyperplasie nodulaire
 - Nécrose tumorale
 - Tumeurs épidermoïdes
 - Vaisseaux tumoraux
- Vaisseaux
 - Vaisseau lymphatique
 - Vaisseau sanguin

Ontologies

New ontology

Search

BIOMEDAQU-LESA-MEDAKA-CLAUDIA

BIOMEDAQU-LESA-MEDAKA-LANDMARKS

BIOMEDAQU-LESA-SAURATA-ZACH

BIOMEDAQU-LESA-SAURATA-ZACH

BIOMEDAQU-SUMMERSCHOC

BIOMEDAQU-UGENT-XRAYS-VMEASURMENTS-LUCIA

BIOMEDAQU-UGHENT-XRAY-D

BIOMEDAQU-UGHENT-XRAY-L

BIOMEDAQUE-CCMR-ZEBRA

BIOMEDAQUE-GIGA-ZEBRAFISMICROSCOPIC

BM-01

BUDÉSONIDE 1 BALF

BUDÉSONIDE 1 SCORE

ULG-LBTD-TISSUS

Globule rouge

Mitose

Muscle

NotAdeno

Poumon

Update term

Name

Adénocarcinomes

Color picker interface:

- Hex code: 840303
- RGB sliders: R: 132, G: 3, B: 3
- Color swatches: Red, Orange, Yellow, Green, Cyan, Blue, Magenta, Black, Gray, White

Cancel Save

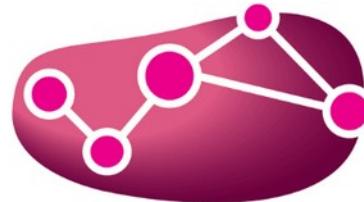
Vaisseaux tumoraux

Vaisseaux

Vaisseau lymphatique

Vaisseau sanguin

Icons for each vocabulary item (e.g., edit, delete, etc.)



BIGPICTURE

European Digital Pathology Platform

(2021-2027)



« For each Image

- in a clinical dataset there must be at least one Observation of type ‘Diagnosis’. There must be at least one ontology used to code its statement, coming from a set of generally defined Ontologies (**SNOMED CT, ICD-O *, ICD-10, ICD-11**).
- In a non-clinical dataset, the Observation must be of type ‘Finding’ and the **SEND/CDISC** terminology must be used to code it. » (BigPicture Metadata Task Force, August 2022)

cytominE : towards use of standardized ontologies ?

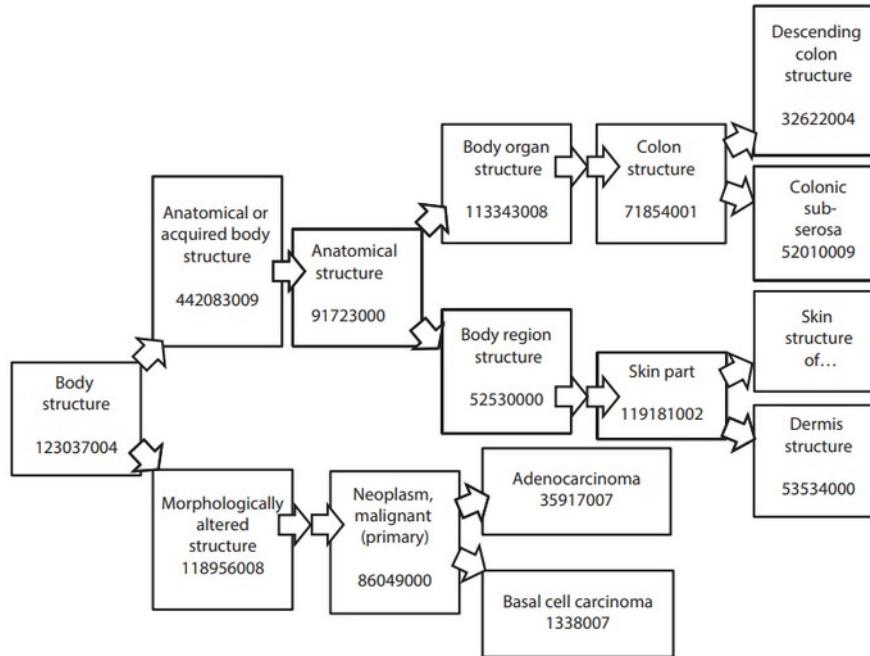


Table 1: Summary of pros and cons of each ontology

Ontology	Pros	Cons
NCIt	Well-known and evolving reference terminology/biomedical ontology Good coverage for cancer	Not a formal ontology Do not cover all other abnormalities except cancer Lack some morphological structures No coverage for the pathology laboratory process
FMA	Well-known and evolving reference ontology Good coverage for anatomical structures	No coverage for disease, terms as abnormal, normal, or artifact No coverage for the pathology laboratory process
MeSH	Well-known and evolving vocabulary thesaurus Good coverage for diseases, anatomy, and tissue subcompartments	No ontology No coverage for all concepts needed No logical hierarchy when it comes to anatomy and tissue sub compartments Low coverage for the pathology laboratory process
SNOMED CT	Well-known and evolving hierarchy of concepts/ontology Includes all concepts needed	Low formality Low coverage for the pathology laboratory process

SNOMED CT: Standardized nomenclature of medicine clinical terms, MeSH: Medical subject headings, FMA: Foundational model of anatomy,

NCIt: National Cancer Institute thesaurus

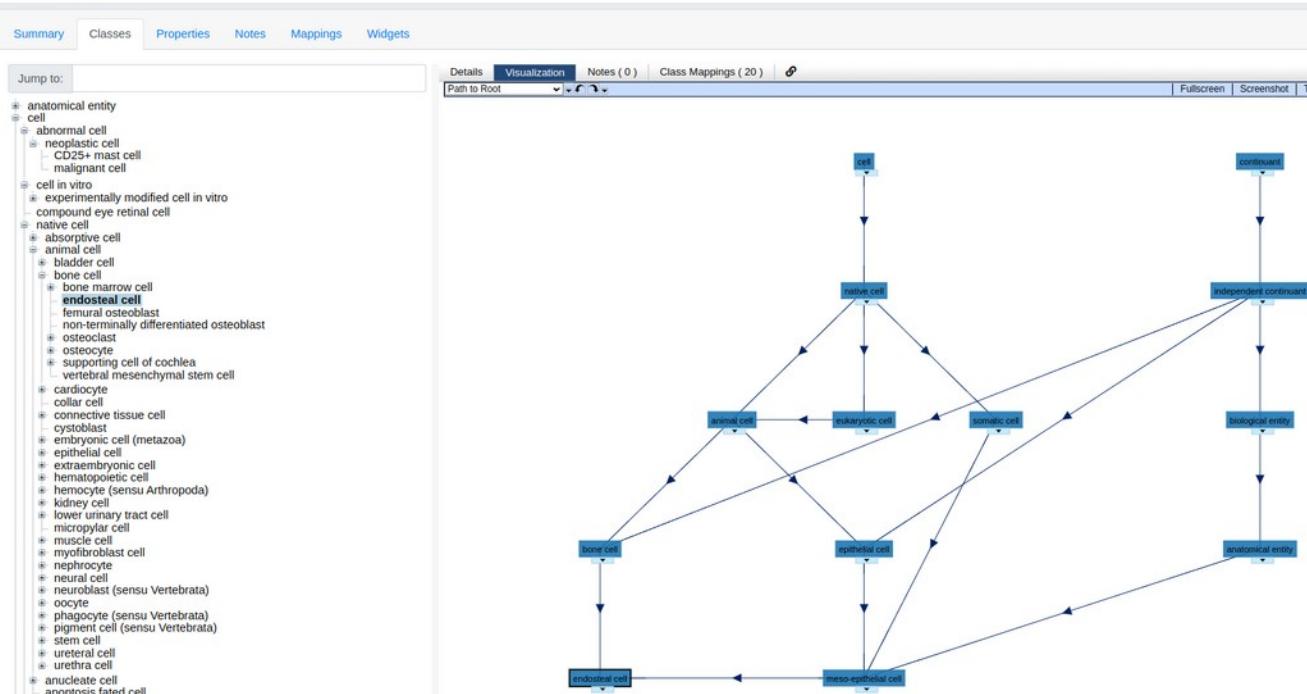
Lindman et al., Annotations, Ontologies, and Whole Slide

Images – Development of an Annotated Ontology-Driven Whole

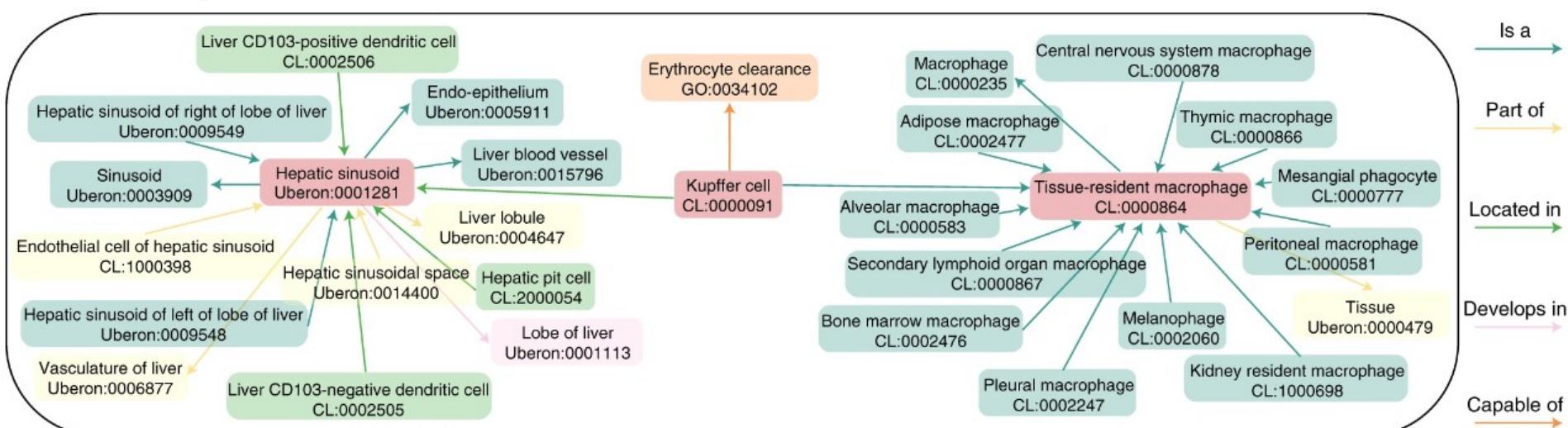
Slide Image Library of Normal and Abnormal Human Tissue, Journal of Pathology Informatics, 2019

cytominE : towards use of standardized ontologies ?

Cell Ontology



<https://bioportal.bioontology.org/ontologies/CL/>



A graph showing the relationships between terms for anatomical structures (for example, hepatic sinusoid), cell types (for example, macrophage) and functional roles (for example, erythrocyte clearance). The following relationships are shown: 'is a', which records the classification; 'part of', which relates cells to their tissues and organs; 'located in', which relates cells to spaces such as the hepatic sinusoid; 'develops in', which records the developmental origin; and 'capable of', which records the function. Osumi-Sutherland et al., Cell type ontologies of the Human Cell Atlas, *Nature Cell Biology* 2021

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

Show filters

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

Region 13

9 Open

Images

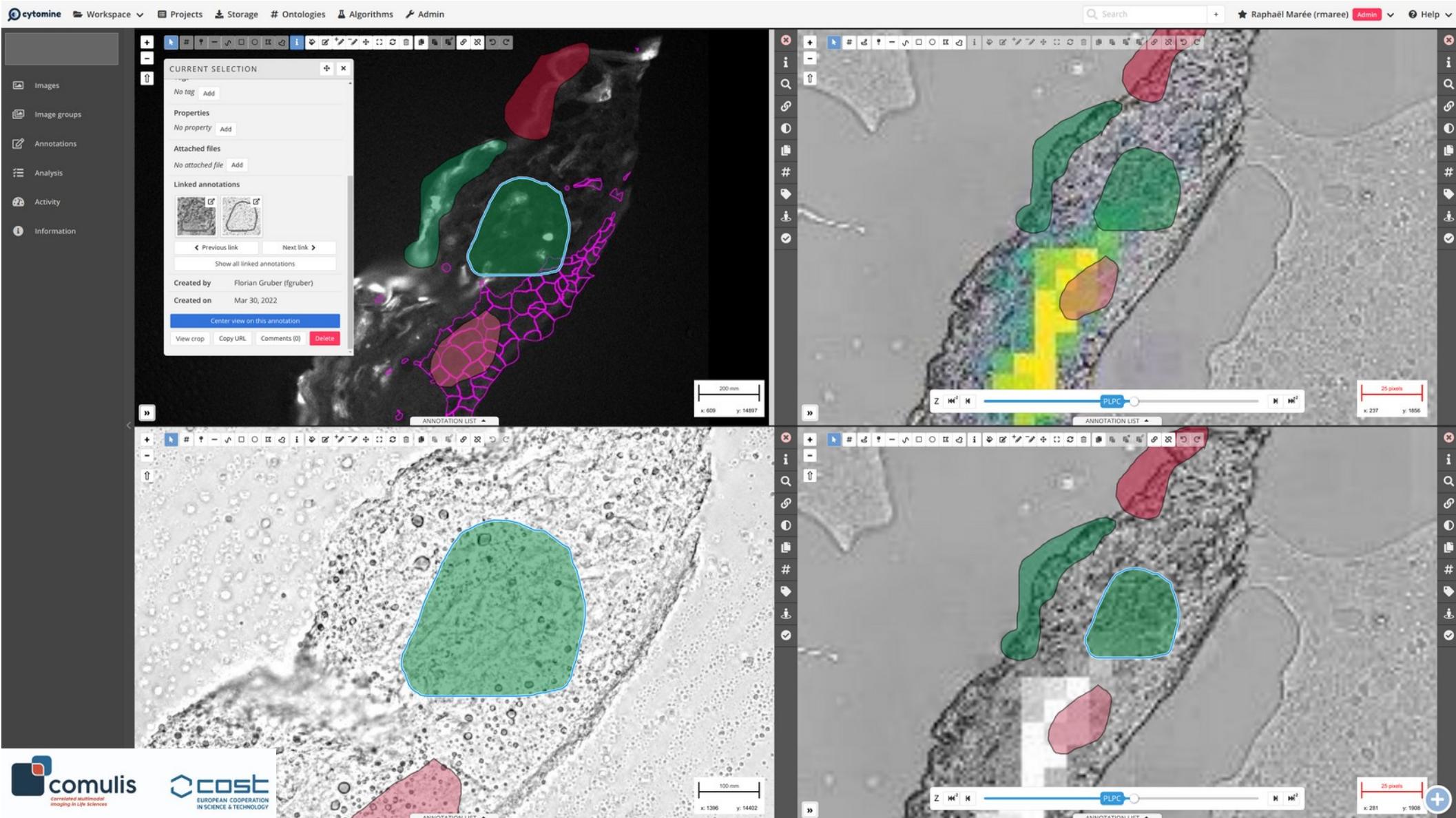
Adjusted Cytomine MSI 3103/Laserspot- position-mask.jpg	Adjusted Cytomine MSI 3103/Mask-Exp- v2.png	Adjusted Cytomine MSI 3103/Mask- Exp.jpg	Adjusted Cytomine MSI 3103/Region013- Grayscale- stacked.ome.tif	Microscope Images/Regions 013-015/2021-07- 06- aS80CTa_S8OCTa- Region-013-- Texa.jpg	Microscope Images/Regions 013-015/2021-07- 06- aS80CTa_S8OCTa- Region-013- Tran.jpg	staining post MSI/Region 013 nuc+gh2AX - Tran.tif	staining post MSI/S8OCTa #1-3 - Region 013 nuc+gh2AX - masks_TEWA.tif
Remove	Remove	Remove	Remove	Remove	Remove	Remove	Remove

Actions

Rename Add images Delete

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

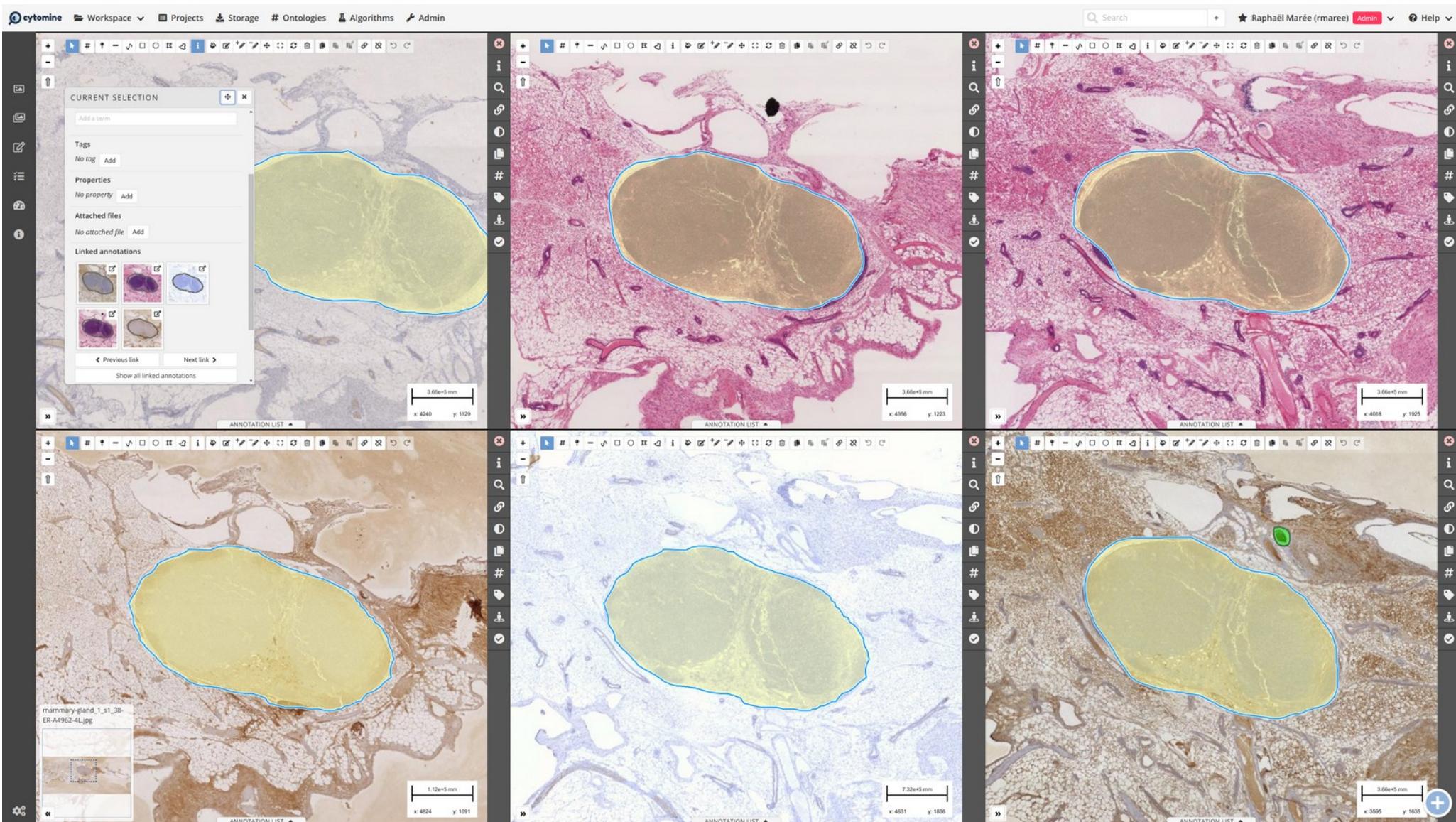


(image data: COMULIS COST Action)

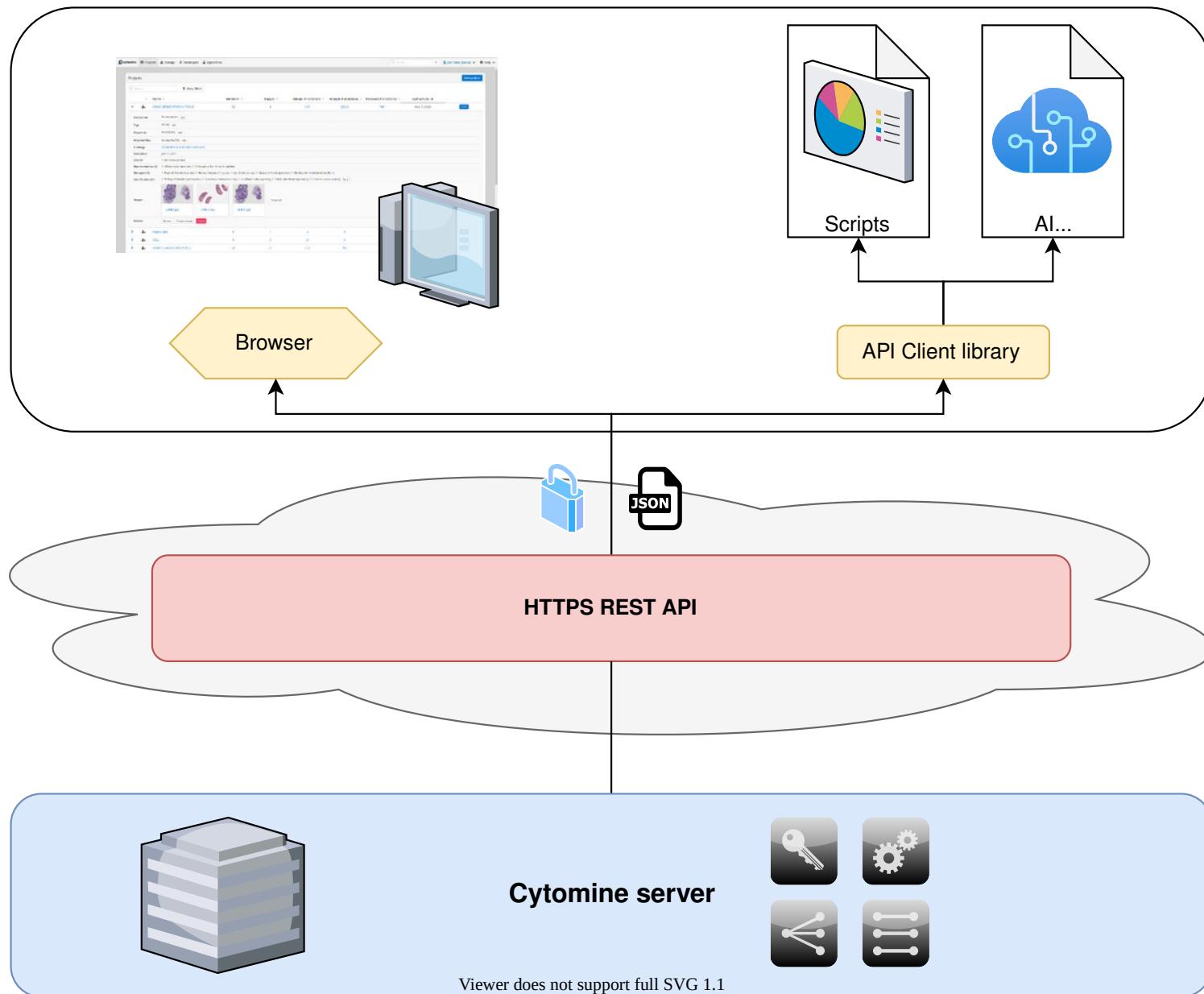
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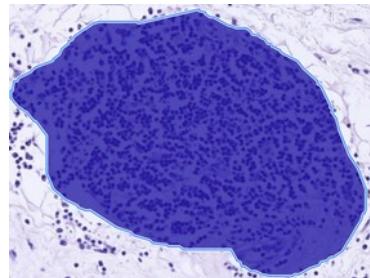
(image data: ANHIR challenge)



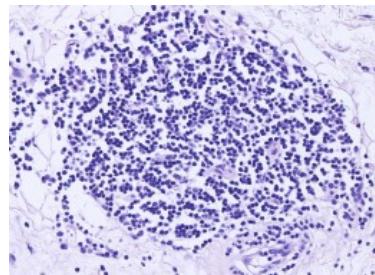
cytominē is highly interoperable : API (web services) to share/import/export all data



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



RESTful API →



```
{"class": "be.cytomine.ontology.UserAnnotation", "id": 26675587, "created": "150887789417", "updated": "null", "deleted": "null", "slice": "146600783", "image": "24935900", "project": "24796414", "user": "24768144", "location": "POLYGON ((40164 22674, 40320 22710, 40320 22706, 40336 22702, 40336 22698, 40348 22690, 40356 22690, 40392 22670, 40416 22662, 40440 22662, 40452 22654, 40454 22646, 40476 22642, 40476 22638, 40488 22634, 40496 22622, 40504 22622, 40508 22614, 40516 22614, 40516 22610, 40528 22606, 40528 22602, 40540 22594, 40572 22578, 40588 22558, 40624 22552, 40624 22518, 40632 22514, 40654 22466, 40656 22458, 40668 22446, 40672 22438, 40680 22398, 40704 22338, 40728 22302, 40748 22259, 40748 22198, 40744 22186, 40749 22186, 40733 22170, 40688 22090, 40664 22074, 40656 22074, 40648 22066, 40632 22062, 40624 22054, 40664 22046, 40576 22030, 40564 22030, 40560 22026, 40484 22030, 40464 22038, 40452 22038, 40436 22050, 40428 22050, 40424 22062, 40416 22066, 40498 22094, 40288 22094, 40268 22102, 40240 22102, 40236 22106, 40200 22110, 40192 22118, 40152 22130, 40144 22138, 40108 22150, 40040 22194, 40028 22194, 40008 22202, 40008 22206, 39976 22222, 39944 22250, 39928 22290, 39928 22386, 39998 22422, 39896 22422, 39876 22446, 39856 22458, 39836 22482, 39836 22502, 39848 22502, 39844 22526, 39852 22526, 39856 22534, 39888 22550, 39908 22562, 39944 22578, 39944 22582, 39960 22594, 39968 22610, 39984 22622, 39984 22630, 39992 22630, 40000 22642, 40048 22674, 40064 22678, 40164 22678, 40164 22674))", "geometryCompression": "3.0", "centroid": {"x": 40315.73937196692, "y": 22371.35279565198}, "area": 91131.05480176363, "areaUnit": "micron", "perimeter": 1.2023770183507887, "perimeterUnit": "mm", "term": "[25635608]", "nbComments": 0, "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/26675587/crop.png", "imageURL": "https://research.cytomine.be/#/project/24796414/image/24935900/annotation/26675587", "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)

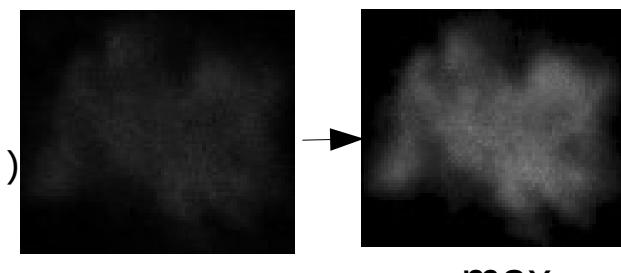


Get maximum projection of an annotation as an image:

<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")
```



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

<https://research.cytomine.be/api/project/77150529.json>

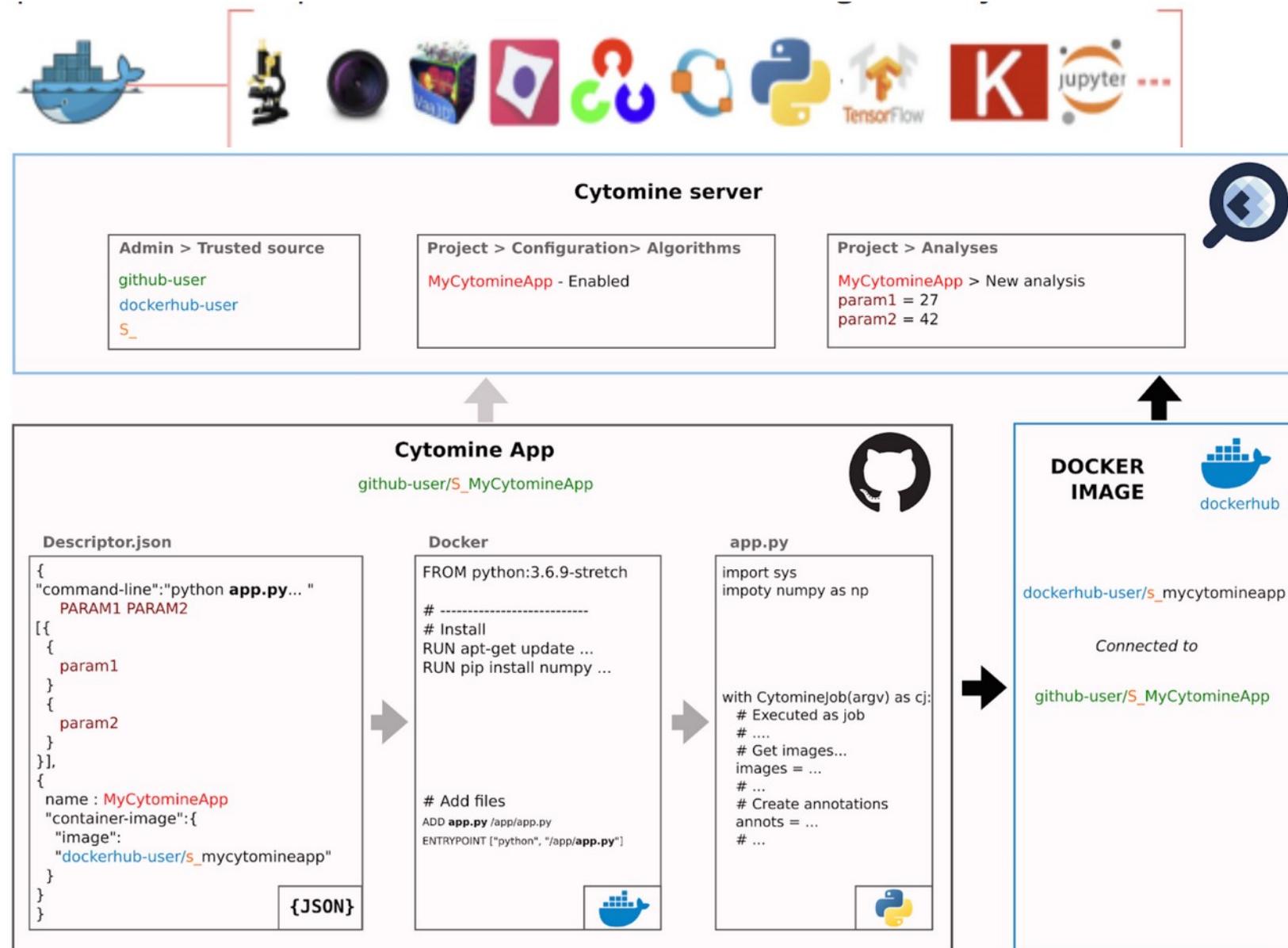
```
{  
    "class": "be.cytomine.project.Project",  
    "id": 77150529,  
    "created": "1344956458986",  
    "updated": "1375969879937",  
    "deleted": null,  
    "name": "ULB-ANAPATH-THYROID-FNAB (6)",  
    "ontology": 35777301,  
    "ontologyName": "ULB-ANAPATH-THYROID-FNAB",  
    "discipline": null,  
    "blindMode": false,  
    "disciplineName": null,  
    "numberOfSlides": 0,  
    "numberOfImages": 85,  
    "numberOfAnnotations": 7340,  
    "numberOfJobAnnotations": 3040390,  
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    "retrievalDisable": false,  
    "retrievalAllOntology": true,  
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    "isReadOnly": false,  
    "isRestricted": false,  
    "hideUsersLayers": false,  
    "hideAdminsLayers": false  
}
```

```
{  
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    "title": "Architectural patterns",  
    "data": "Architectural patterns",  
    "color": "#000000",  
    "class": "be.cytomine.ontology.Term",  
    "parent": null,  
    "attr": {  
        "id": 35777417,  
        "type": "be.cytomine.ontology.Term"  
    },  
    "checked": false,  
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    "children": [  
        {  
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            "id": 35777351,  
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            "data": "Normal follicular architectural pattern",  
            "color": "#9bf8e",  
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            "attr": {  
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                "type": "be.cytomine.ontology.Term"  
            },  
            "checked": false,  
            "key": 35777351,  
            "children": [],  
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        {  
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            "id": 35777321,  
            "title": "Proliferative follicular architectural pattern",  
            "data": "Proliferative follicular architectural pattern",  
            "color": "#a43232",  
            "class": "be.cytomine.ontology.Term",  
            "parent": 35777417,  
            "attr": {  
                "id": 35777321,  
                "type": "be.cytomine.ontology.Term"  
            },  
            "checked": false,  
            "key": 35777321,  
            "children": [],  
            "isFolder": false,  
            "hideCheckbox": false  
        }  
    ]  
}
```

<https://research.cytomine.be/api/ontology/35777301.json>

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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Launch new analysis

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)

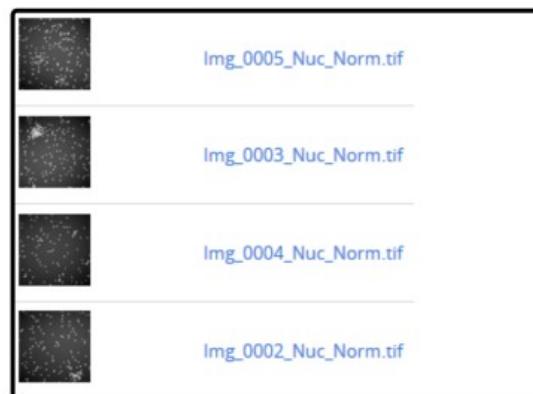
Cancel Launch new analysis

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

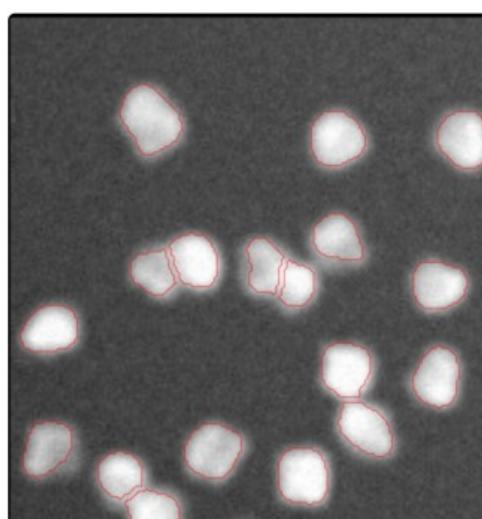
Workflows

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



Workflow runs Run a workflow

4 Set parameters & Run workflow

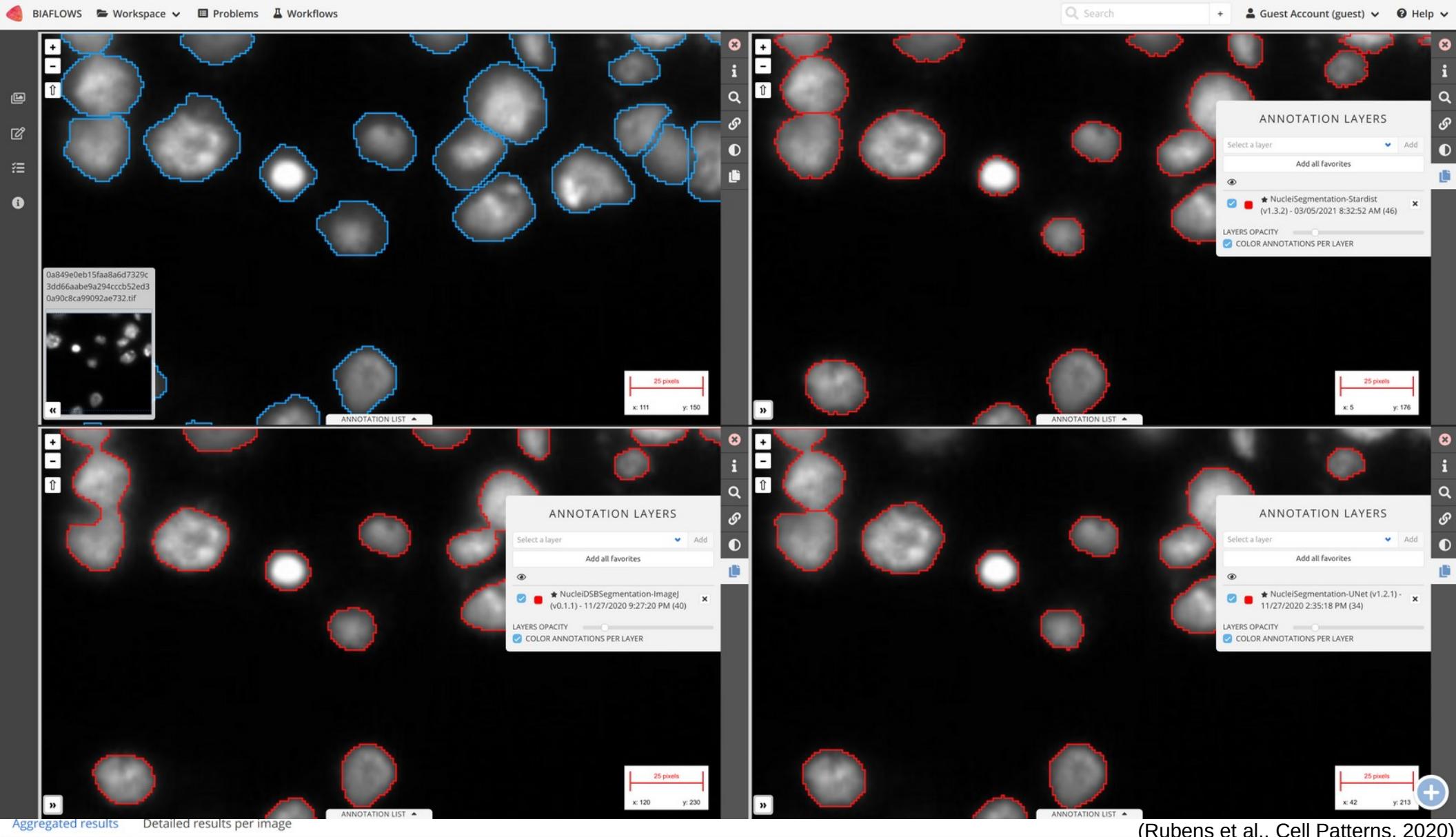
New workflow run

Workflow

NucleiSegmentation-ImageJ (v1.10.1)

Name	Value
Radius	5
Threshold	-0.5

Cancel Run a workflow

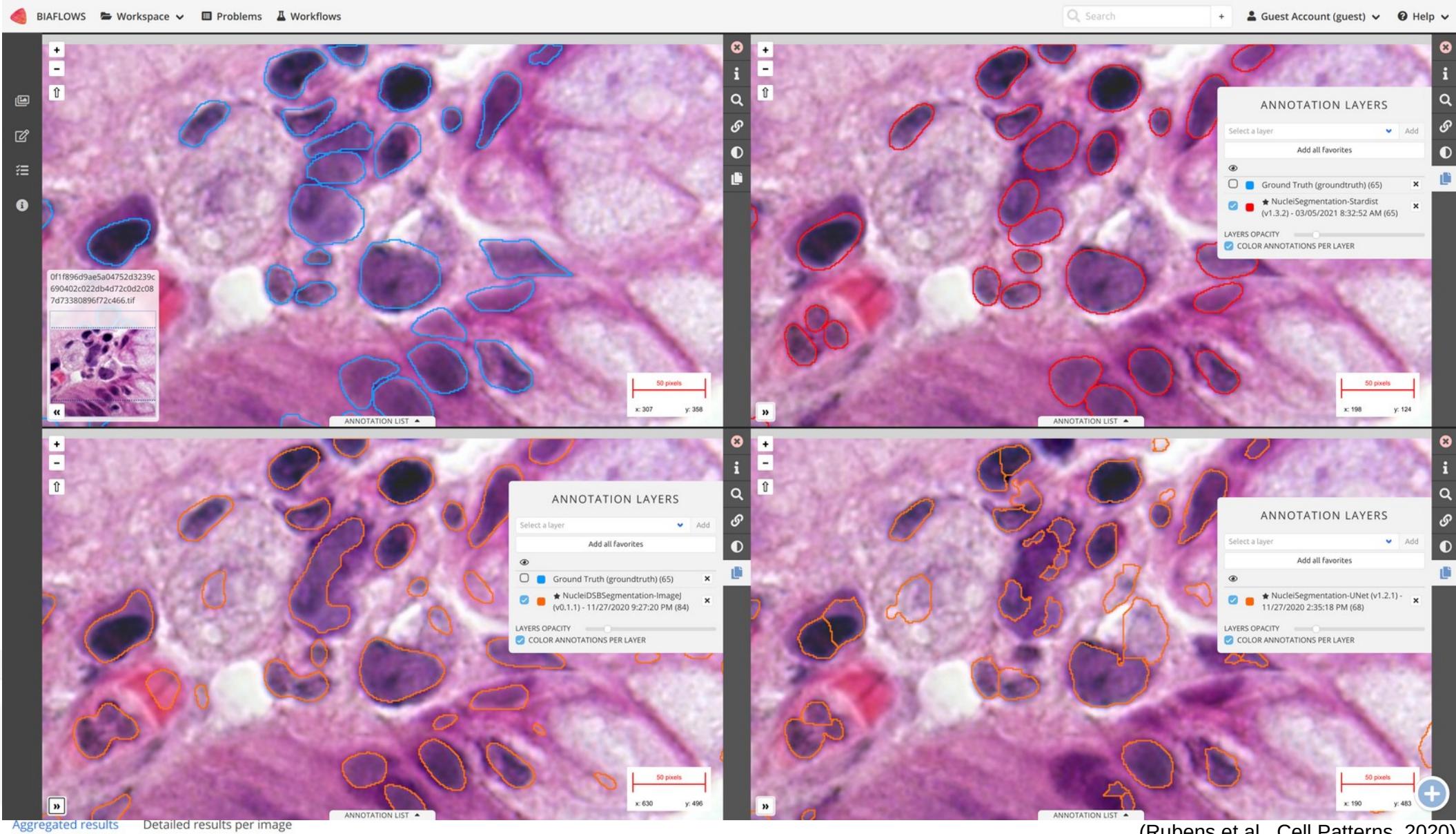


(Rubens et al., Cell Patterns, 2020)

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	

BIAflows biaflows.neubias.org



(Rubens et al., Cell Patterns, 2020)

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★ NucleiSegmentation-UNet (v1.2.1) #1 on Nov 27, 2020 2:35 PM	0.282	0.754	8.485	

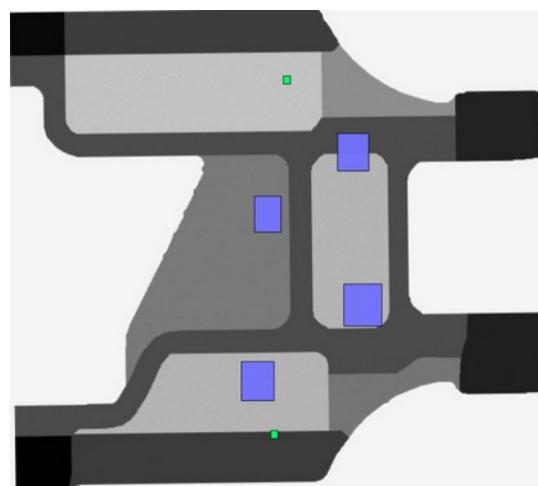
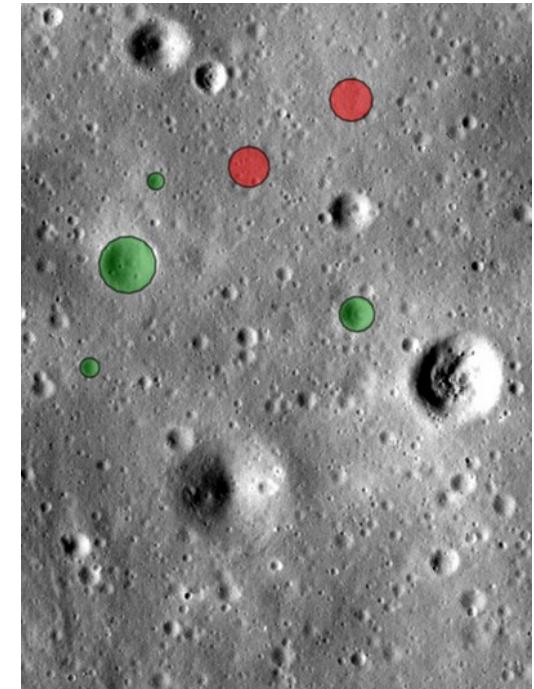
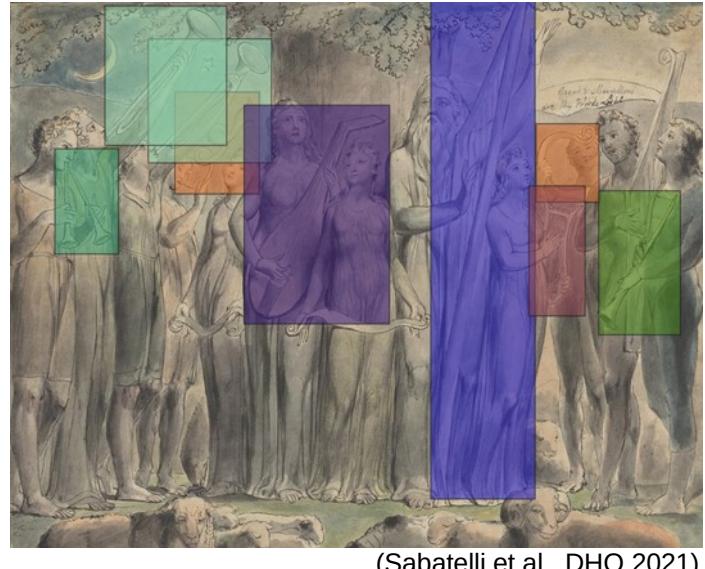




Applications

<http://uliege.cytomine.org/>

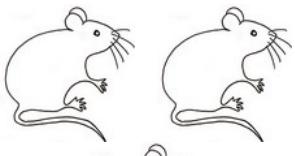
cytomin is not only meant for histology



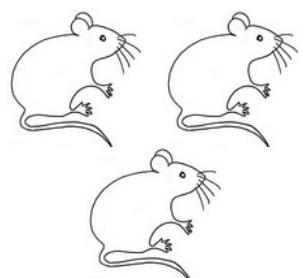
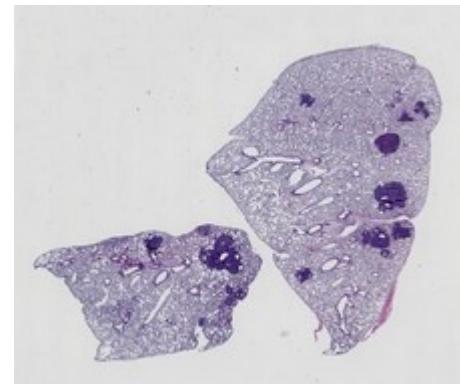
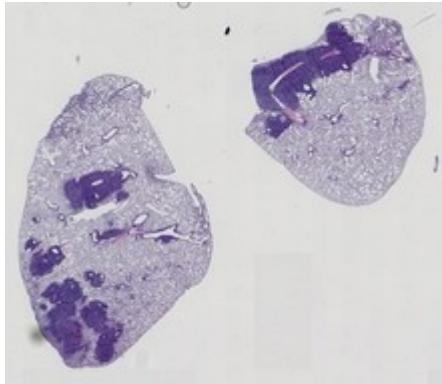
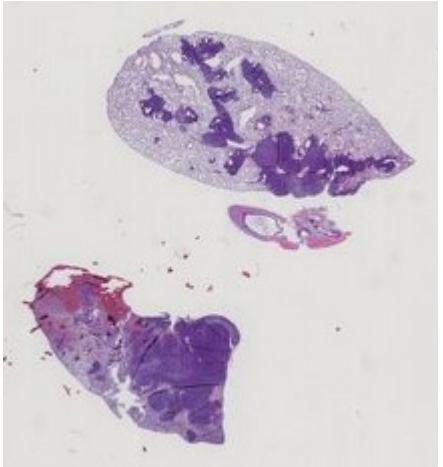
LUNG tumor tissue quantification

(Collaboration with D. Cataldo, N. Rocks, at LBTD, GIGA)

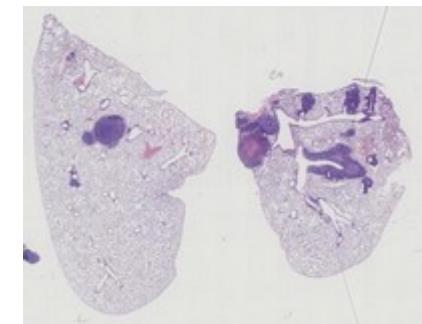
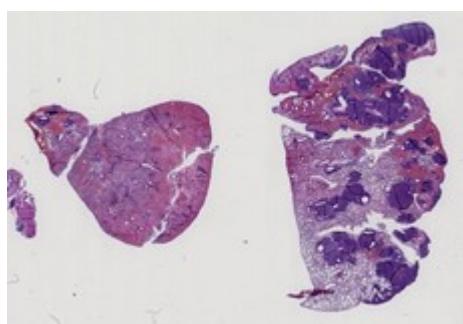
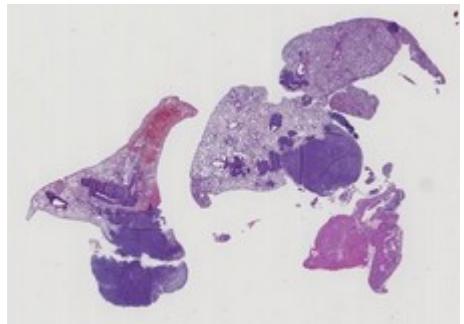
What is the impact of condition X/Y/... on lung tumor onset and progression ?



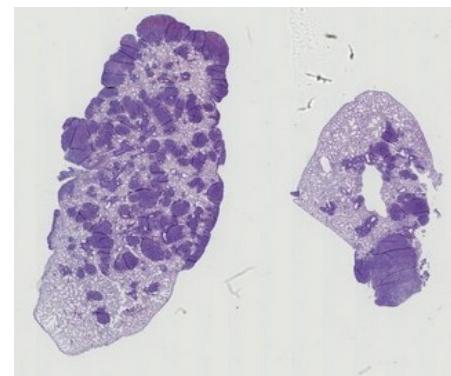
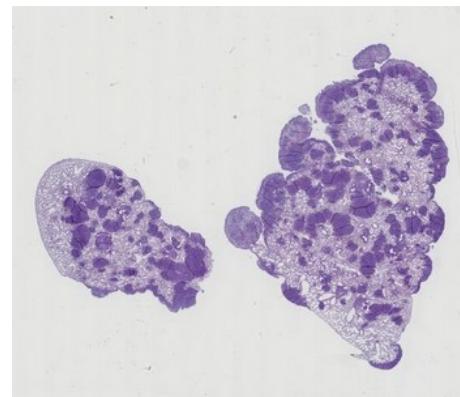
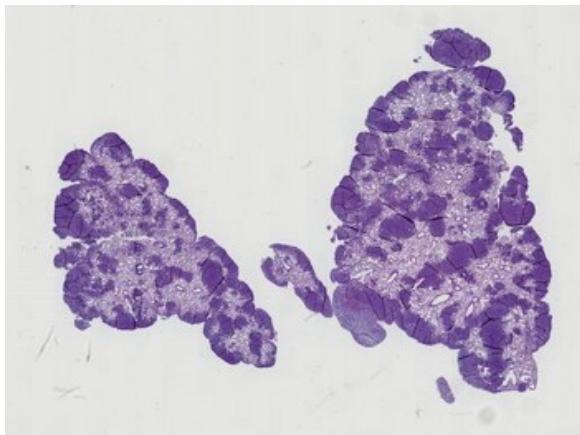
Condition X



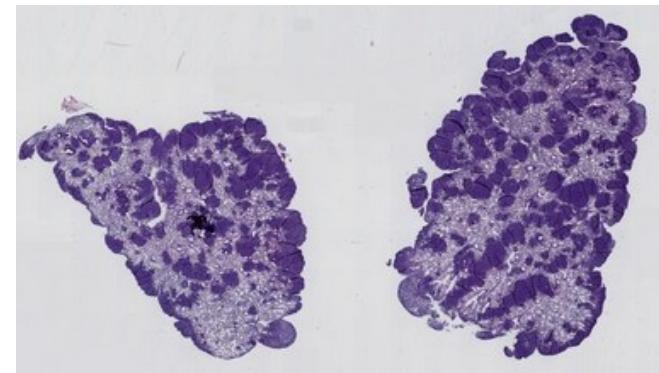
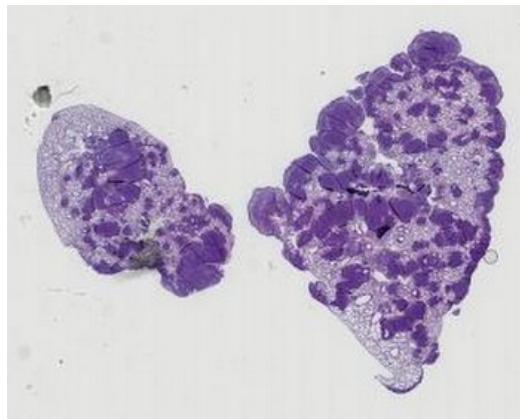
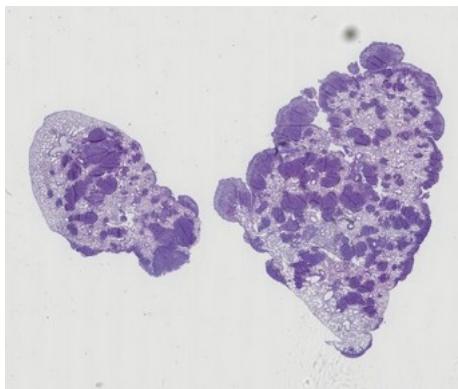
Condition Y



Tens or hundreds of glass slides to be quantified per study...

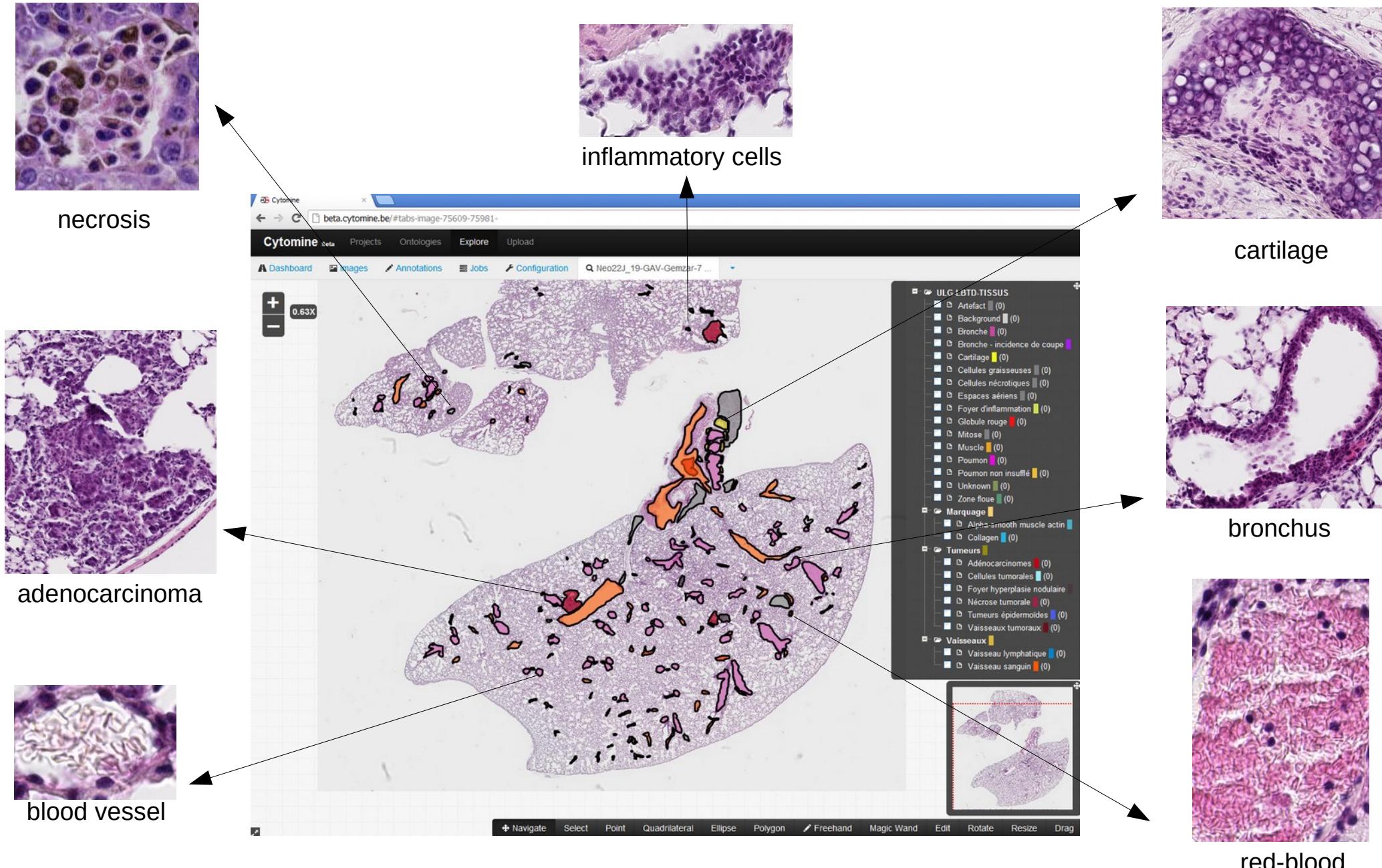


...



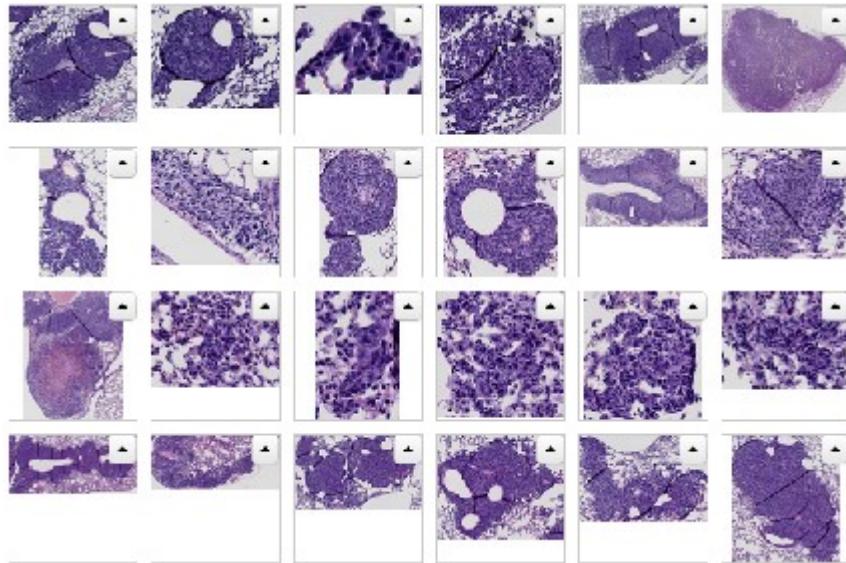
Hybrid human-computer workflow

1. Manual region contouring and labelling to provide training examples



Hybrid human-computer workflow

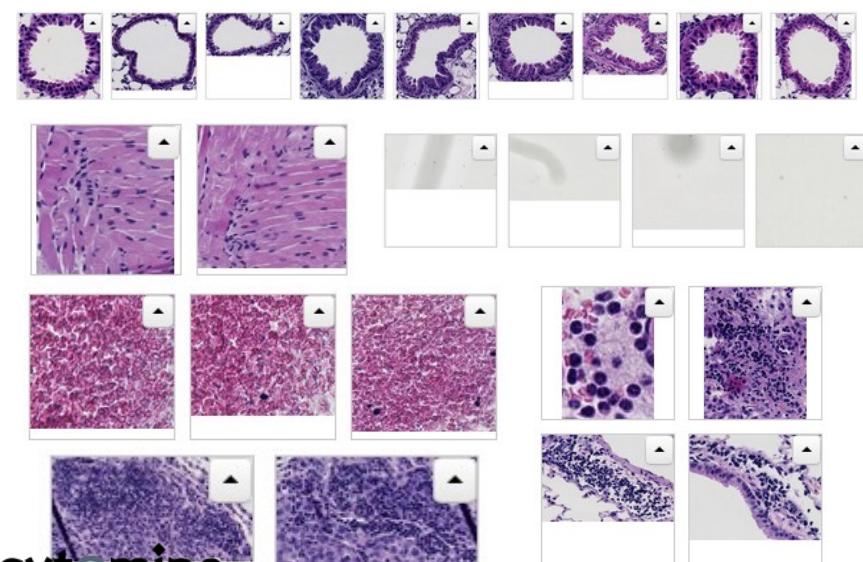
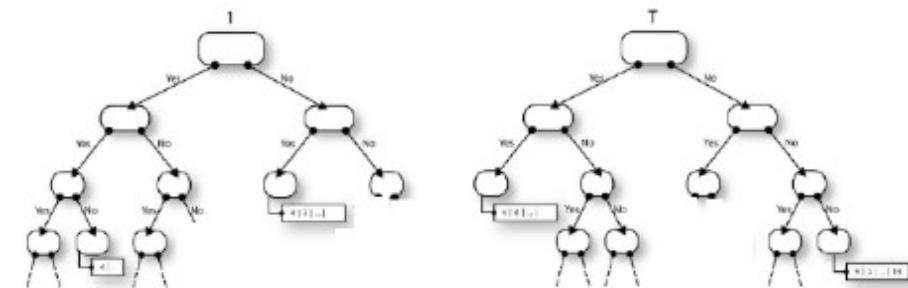
2. Automatic training of image recognition model based on training examples



VS

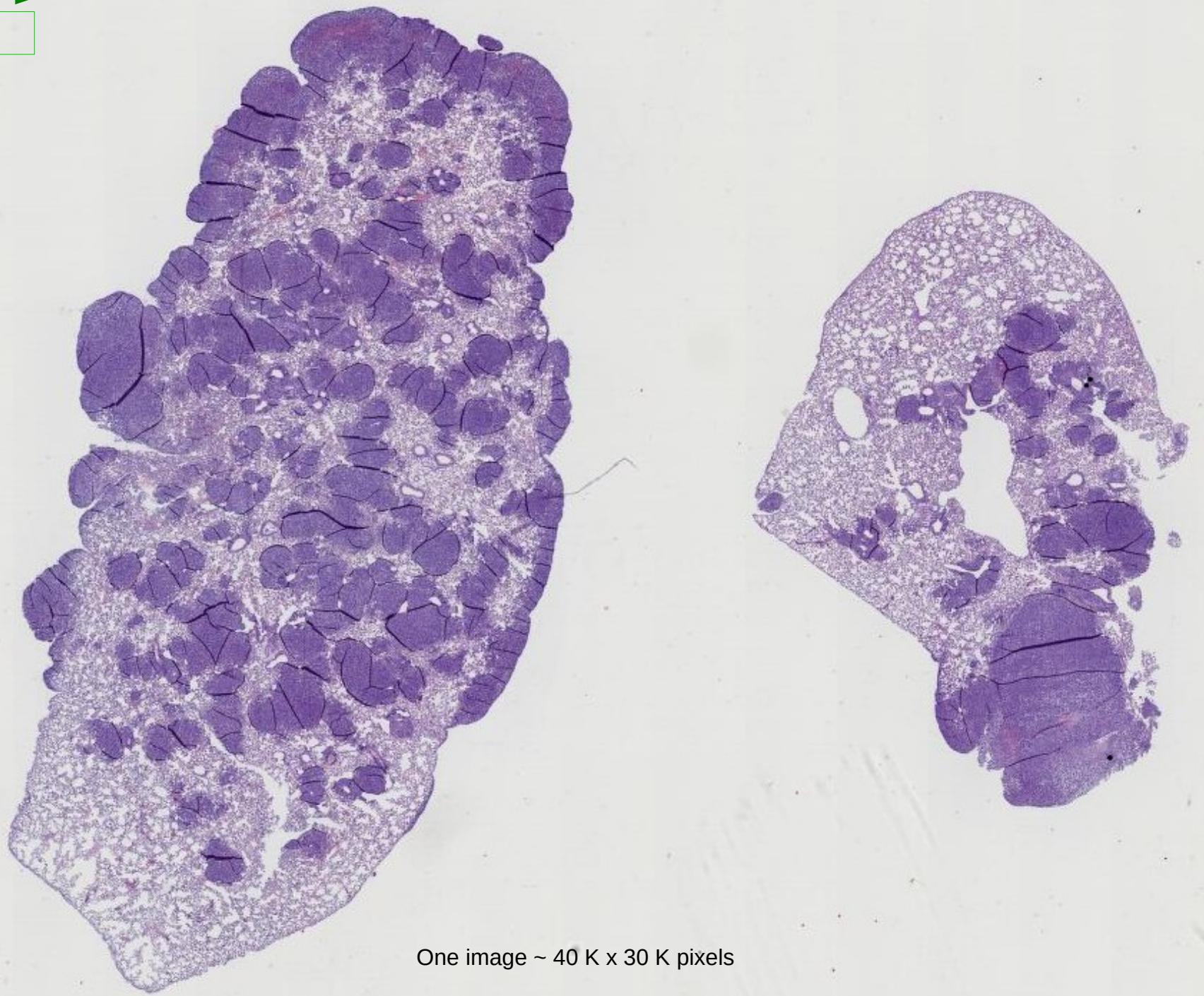


A machine-learnt classifier that recognizes tumor/nontumor pixels using **local patches**



Hybrid human-computer workflow

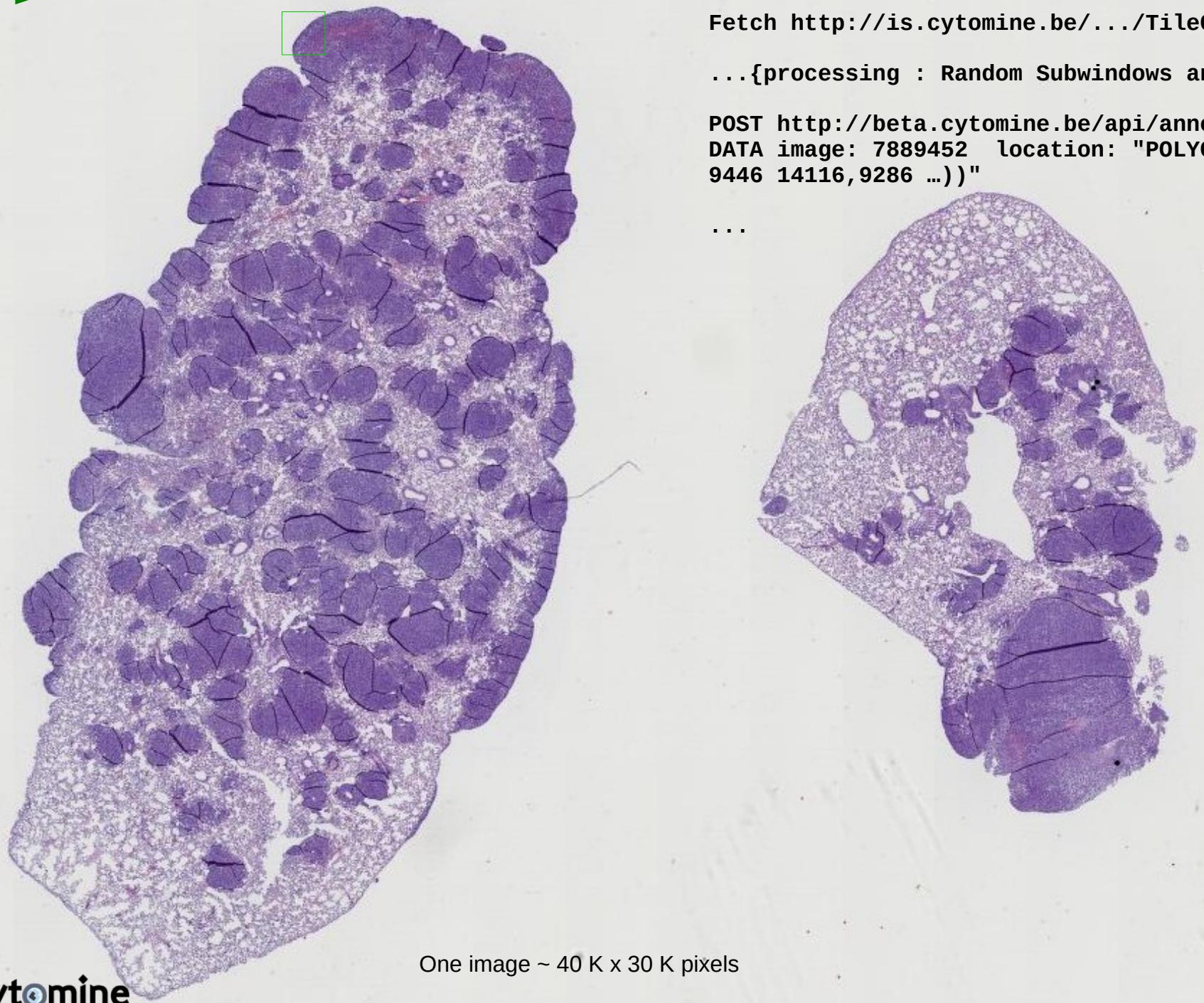
3. Automatic segmentation (pixel classification) of tumors in new images



One image ~ 40 K x 30 K pixels

Hybrid human-computer workflow

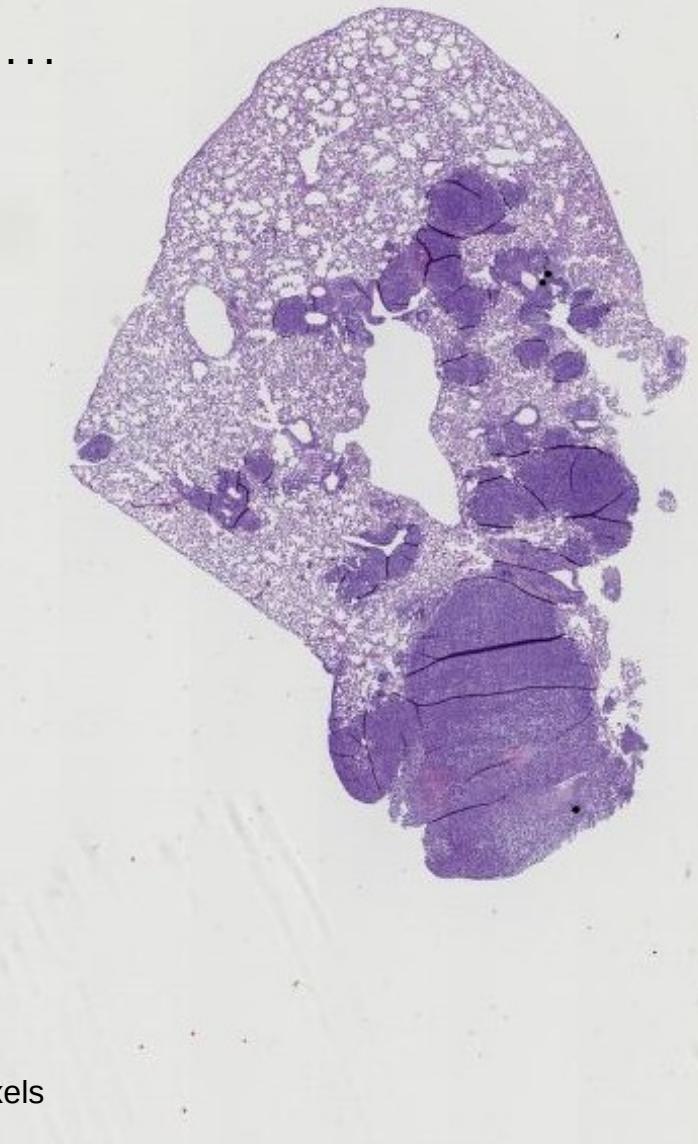
3. Automatic segmentation (pixel classification) of tumors in new images



```
Fetch http://is.cytomine.be/.../TileGroup39/9-16-48.jpg
```

```
...{processing : Random Subwindows and Extra-Trees}...
```

```
POST http://beta.cytomine.be/api/annotation.json  
DATA image: 7889452 location: "POLYGON((9479 14179,  
9446 14116,9286 ...))"
```



One image ~ 40 K x 30 K pixels

Hybrid human-computer workflow

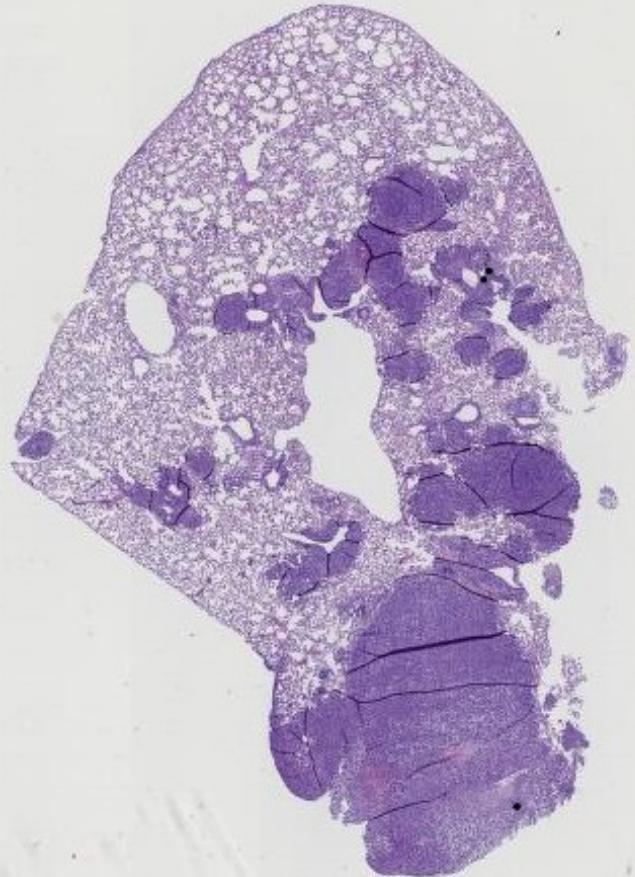
3. Automatic segmentation (pixel classification) of tumors in new images



```
Fetch http://is.cytomine.be/.../TileGroup67/6-12-27.jpg
```

```
...{processing : Random Subwindows and Extra-Trees}...
```

```
POST http://beta.cytomine.be/api/annotation.json  
DATA image: 7889452 location: "POLYGON((10475 15176,  
9840 15112,10280 ...))"
```



One image ~ 40 K x 30 K pixels

Hybrid human-computer workflow

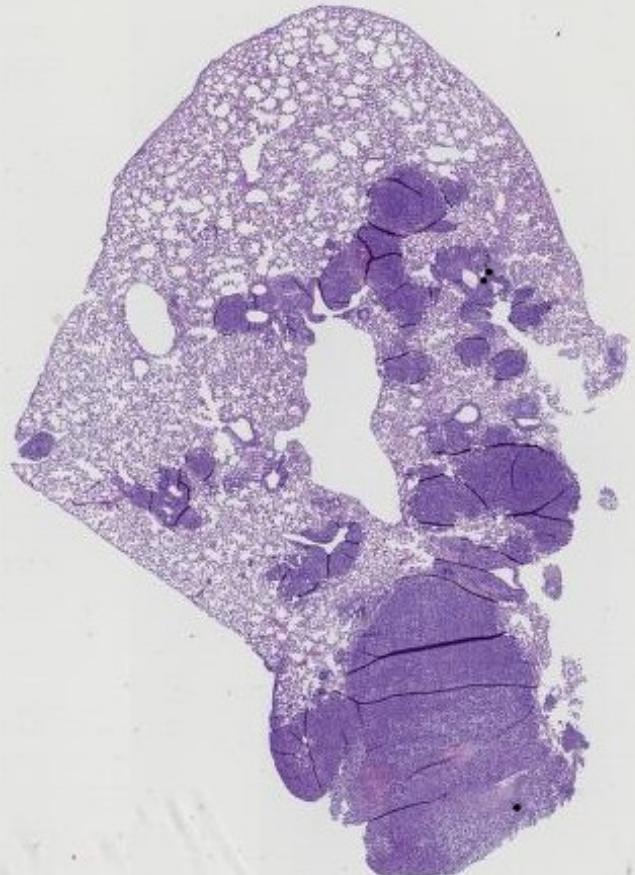
3. Automatic segmentation (pixel classification) of tumors in new images



```
Fetch http://is.cytomine.be/.../TileGroup78/8-15-47.jpg
```

```
...{processing : Random Subwindows and Extra-Trees}...
```

```
POST http://beta.cytomine.be/api/annotation.json  
DATA image: 7889452 location: "POLYGON((23472 23176,  
9440 24112,9280 ...))"
```



One image ~ 40 K x 30 K pixels

Hybrid human-computer workflow

3. Automatic segmentation (pixel classification) of tumors in new images



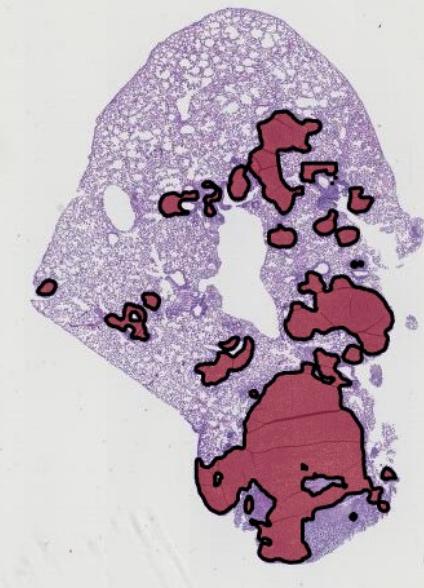
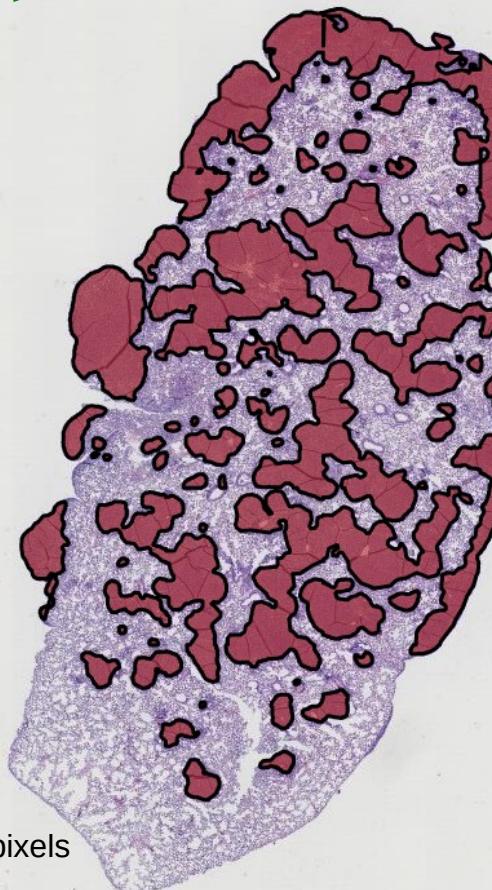
Fetch <http://is.cytomine.be/.../TileGroup97/2-1-7.jpg>

...{processing : Random Subwindows and Extra-Trees}...

POST <http://beta.cytomine.be/api/annotation.json>
DATA image: 7889452 location: "POLYGON((29672 26176,
34980 24902,29580 ...))"

...

Union of POLYGONS + Simplification of Geometries
(JTS Topology Suite)

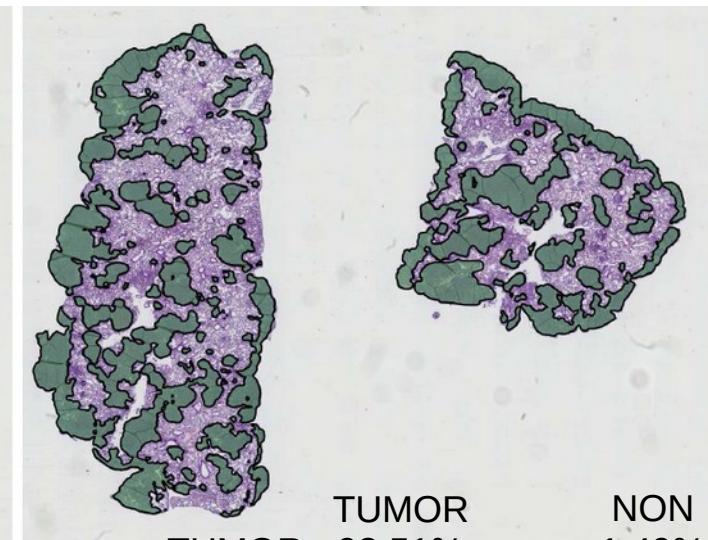
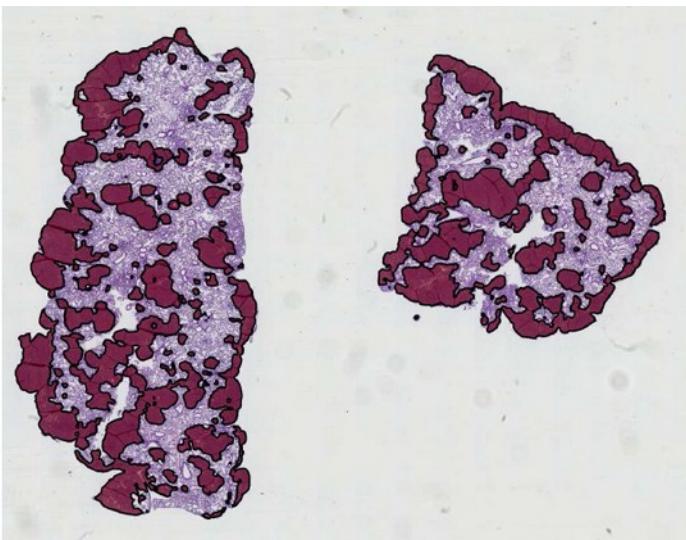
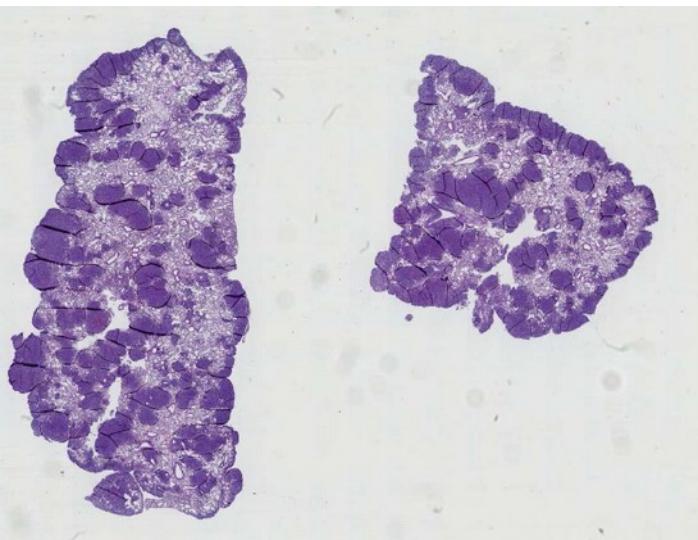


One image ~ 40 K x 30 K pixels

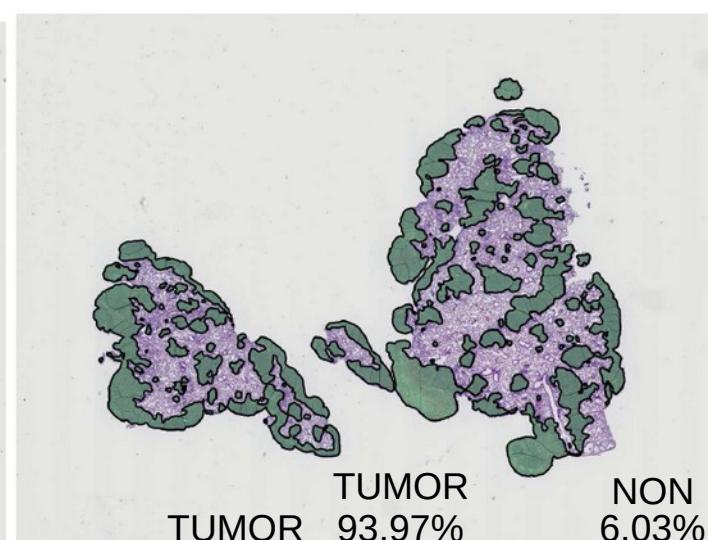
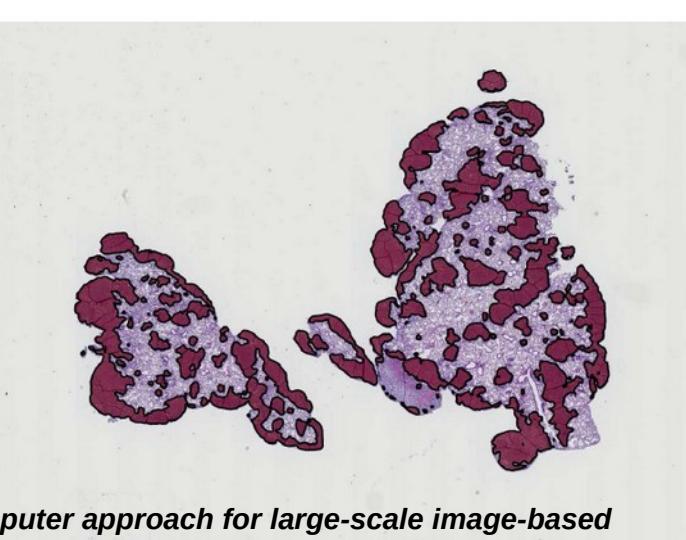
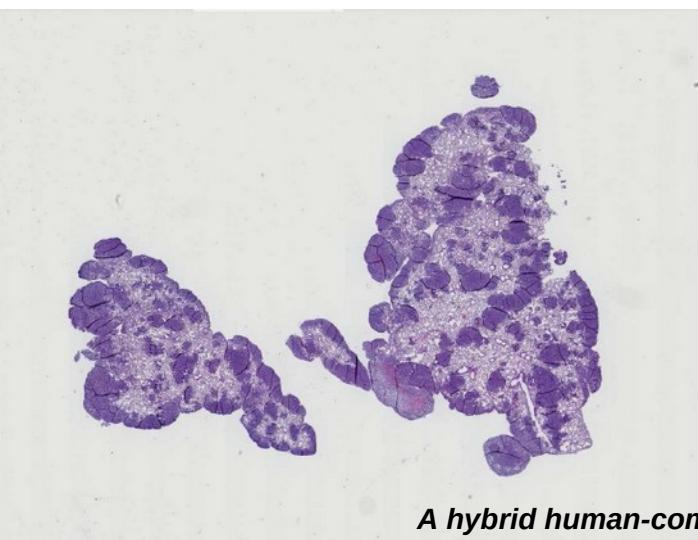


Hybrid human-computer workflow

5. Recognition performances



TUMOR	98.51%	TUMOR	NON
NON	2.78%	97.22%	1.49%



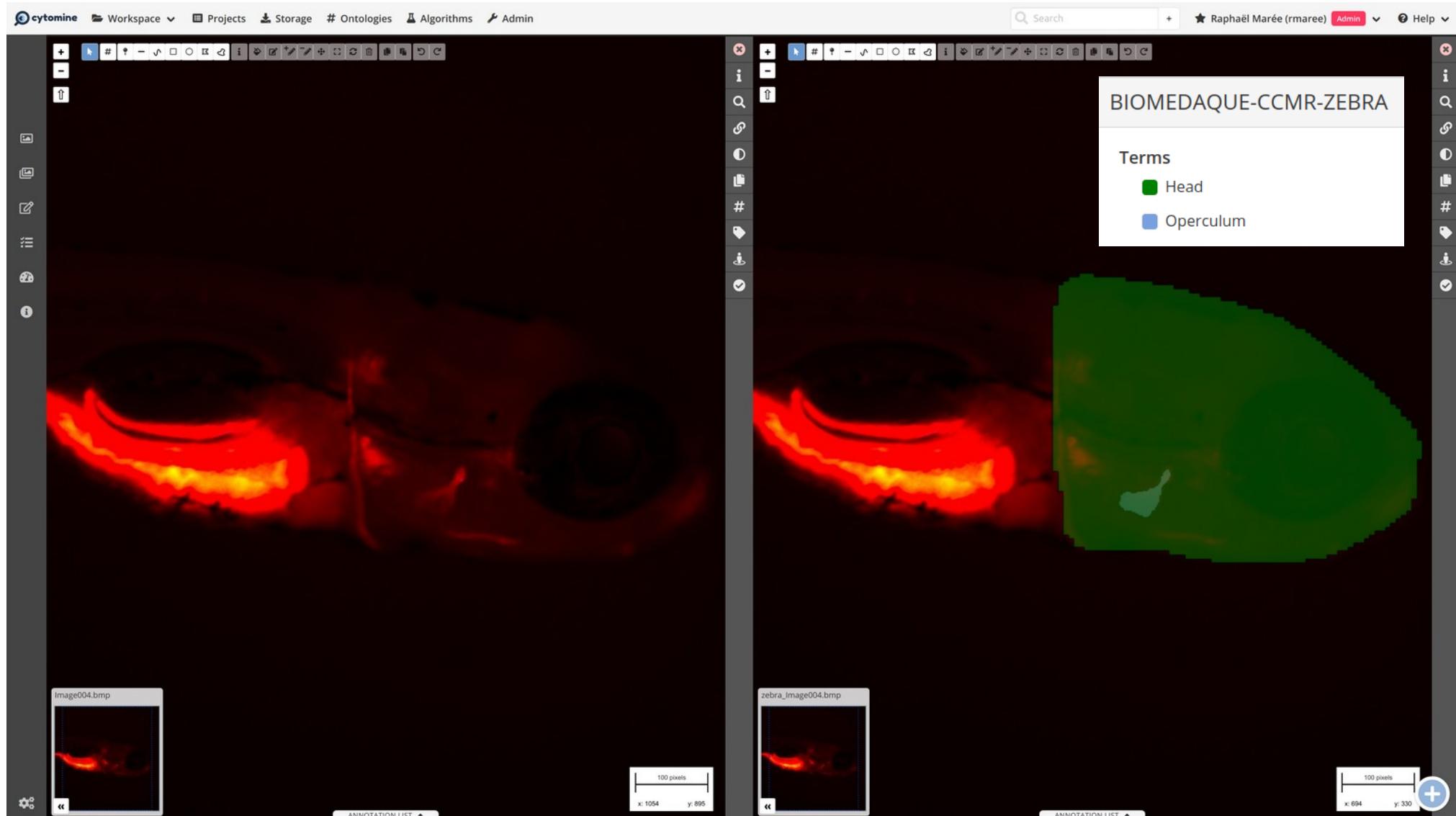
TUMOR	93.97%	TUMOR	NON
NON	6.03%	0.01%	99.99%

A hybrid human-computer approach for large-scale image-based measurements using web services and machine learning,
Marée et al. Proc. IEEE ISBI, 2014

Deep Learning-based tissue segmentation

« Polygon » annotations for segmentation and measurements

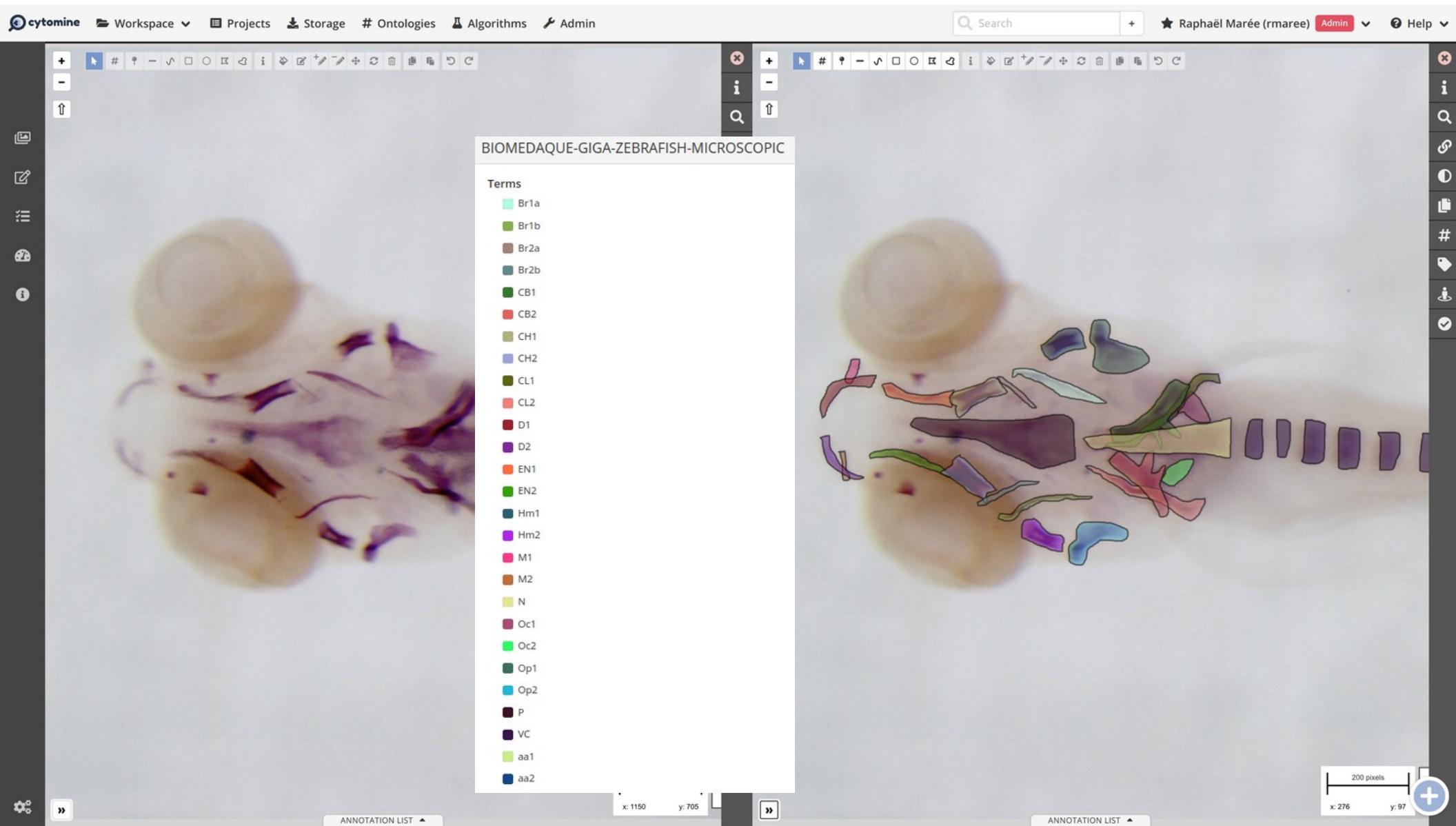
Two-step approach to deal with imbalanced pixel classes



Deep Learning-based tissue segmentation

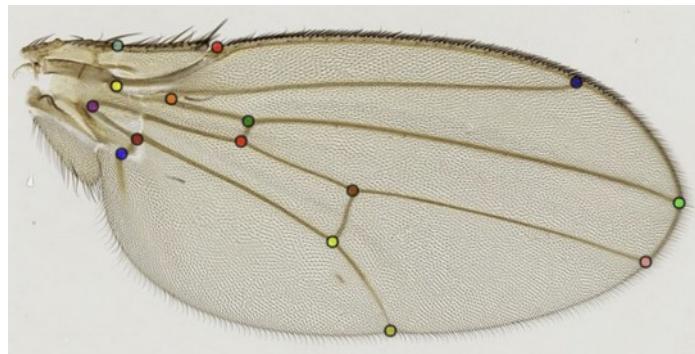
« Polygon » annotations for segmentation and measurements

(data : GIGA, BioMedAQu)



Machine / Deep Learning-based landmark detection

« Point » annotations for landmark detection



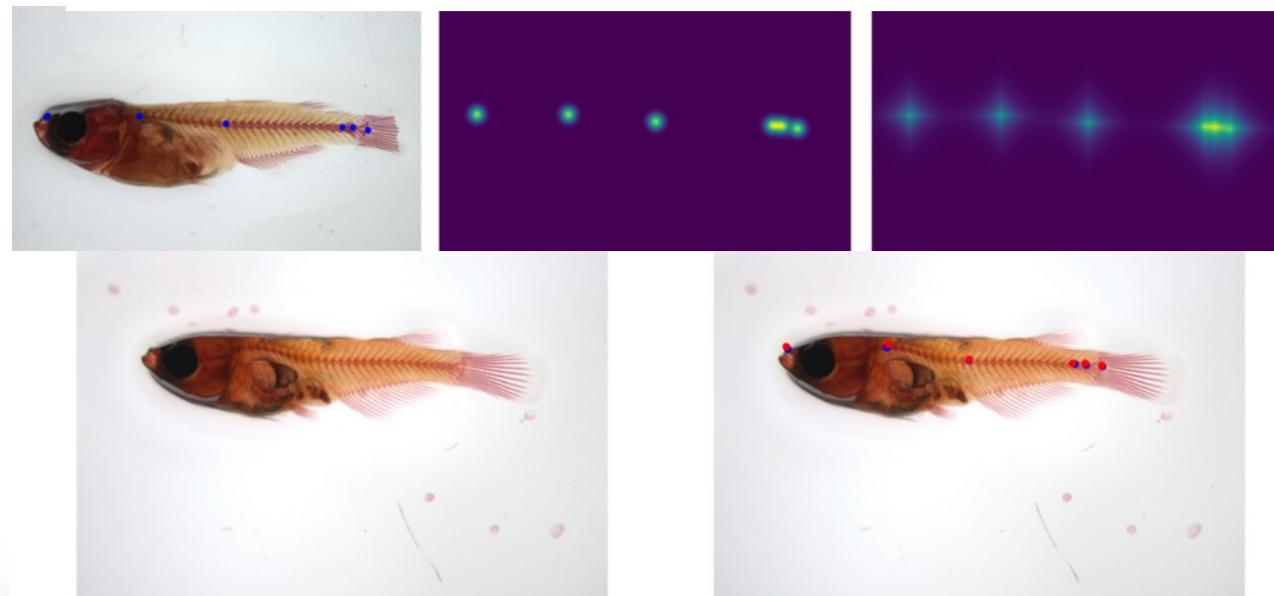
(Vandaele et al., Scientific Reports, 2019)

Heatmap-based deep-learning regression

BIOMEDAQU-LESA-MEDAKA-LANDMARKS

Terms

- AV
- HV
- HY
- PU2
- PUX
- ST



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

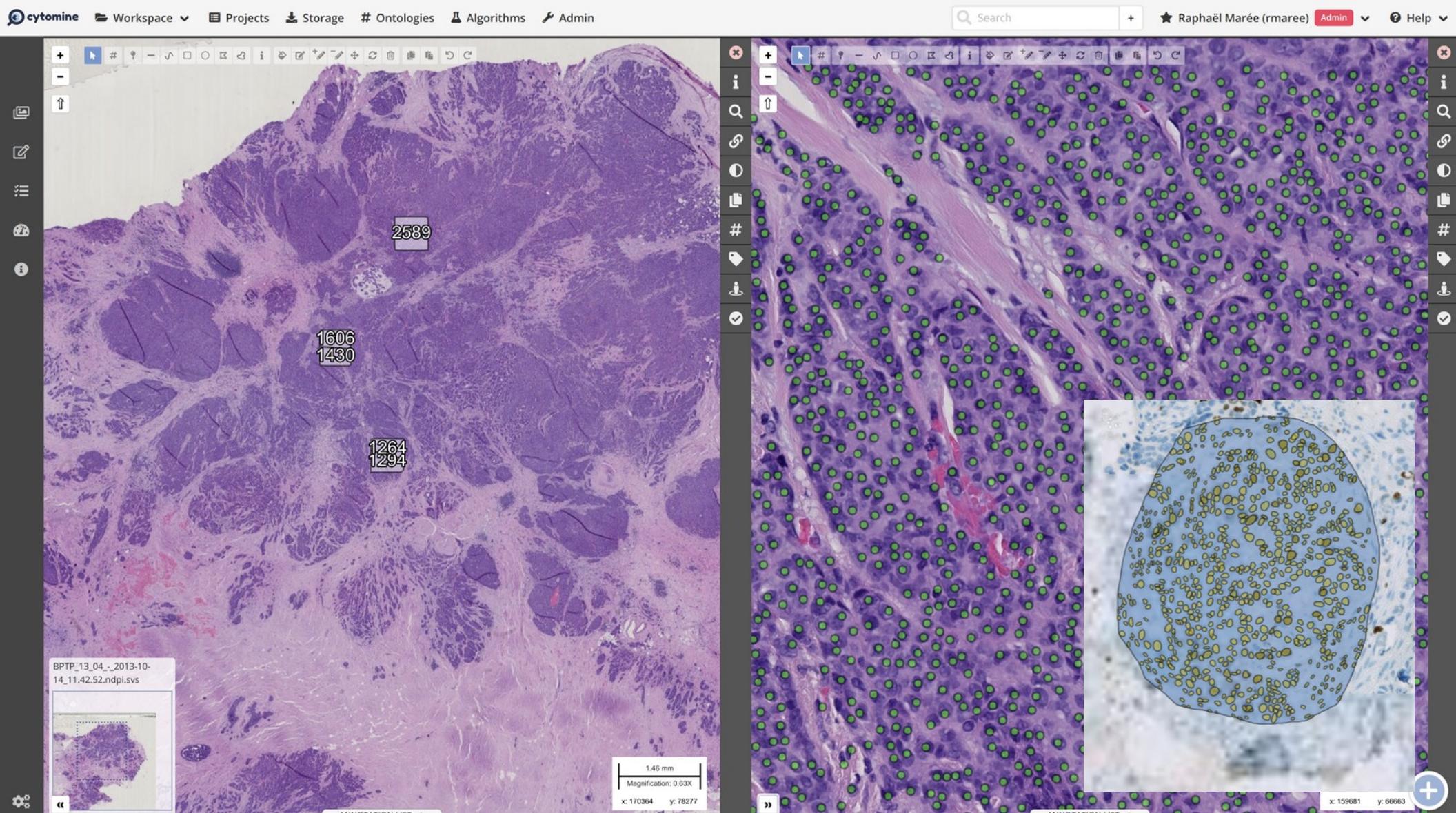


(Evomorpho, L. Marganne, Master Thesis 2022)

Machine / Deep Learning-based cell counting

« Point » annotations for cell counting

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

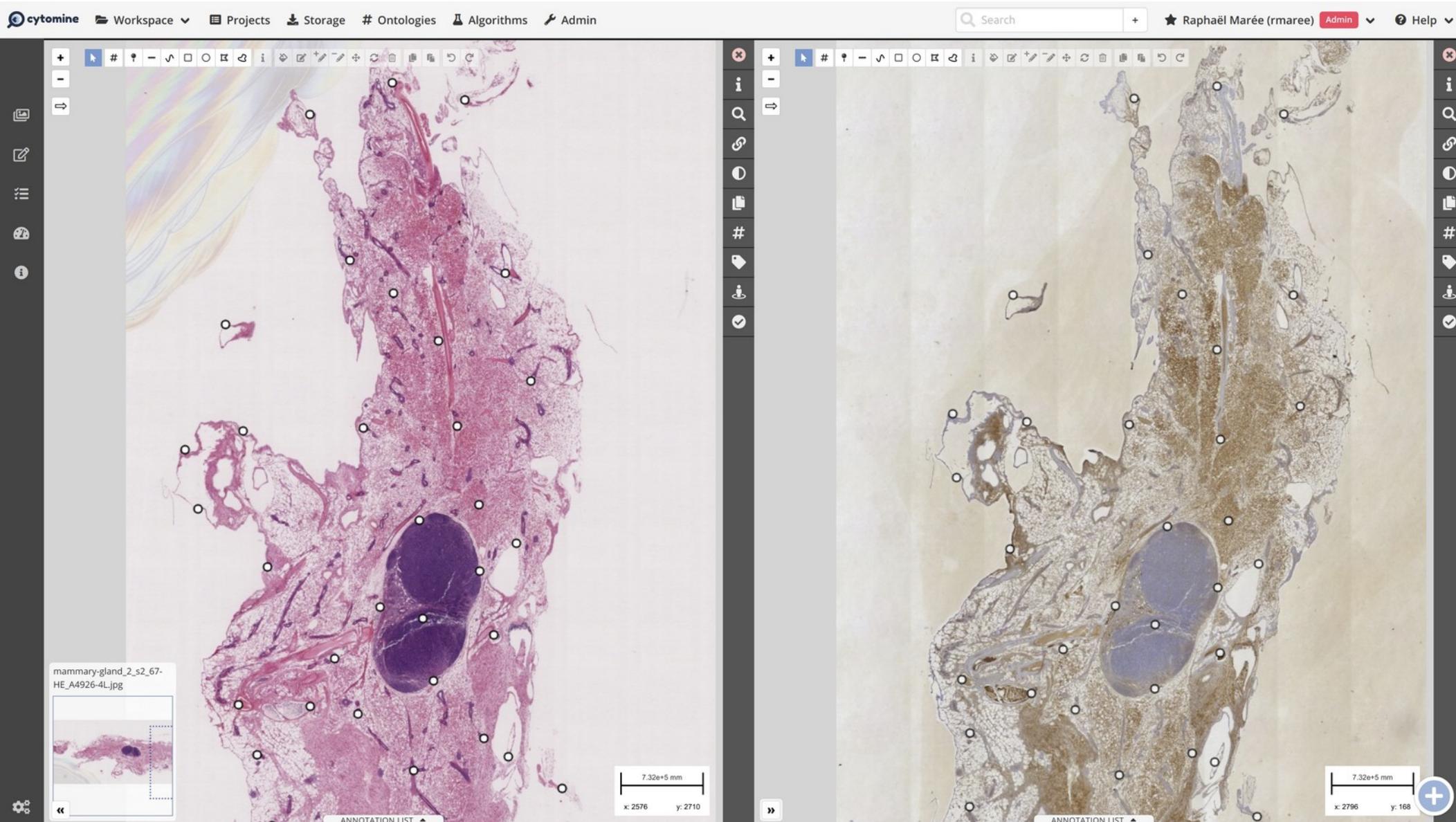


Other potential use of point annotations

Image registration

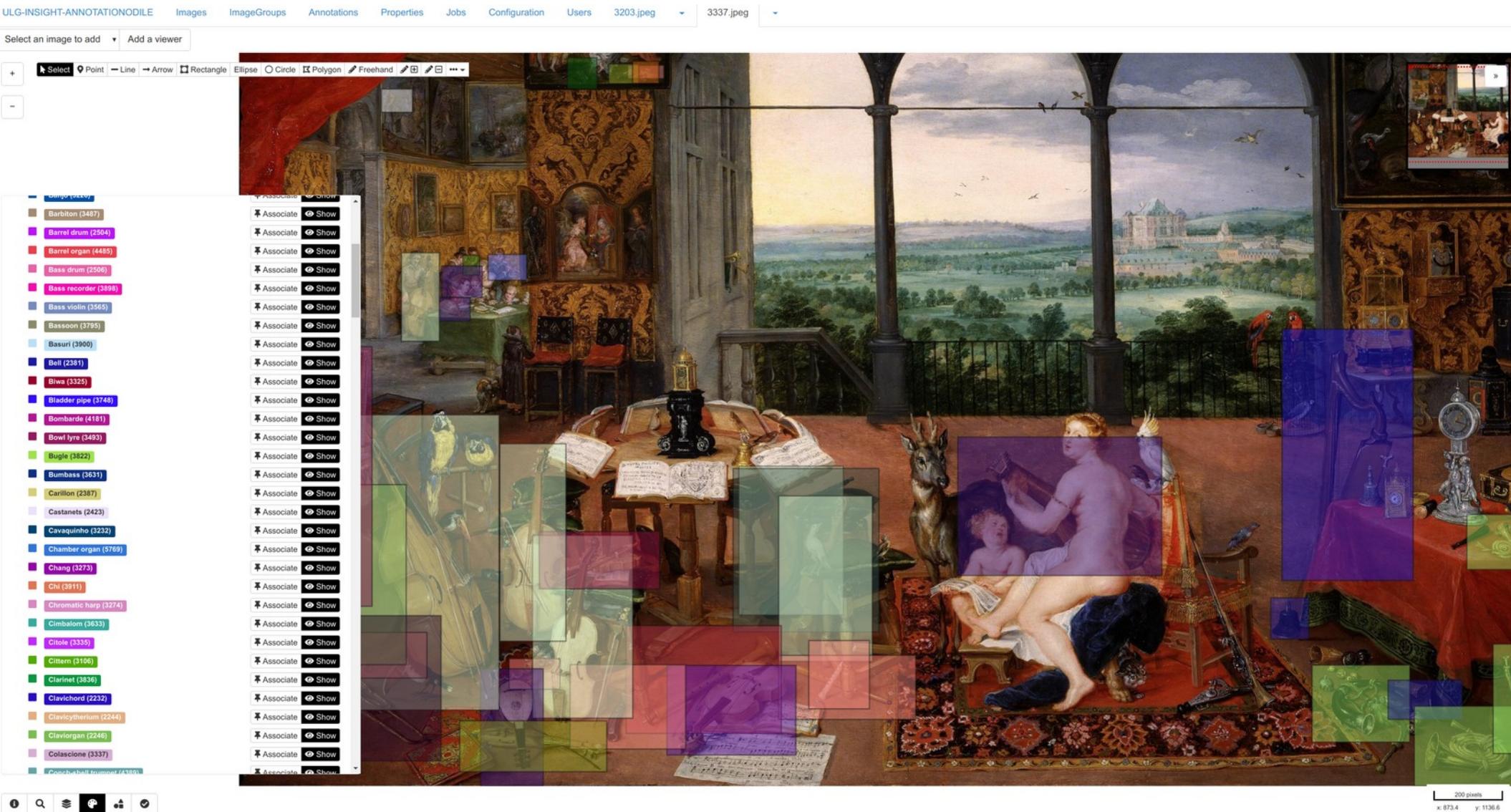
(data : ANHIR challenge)

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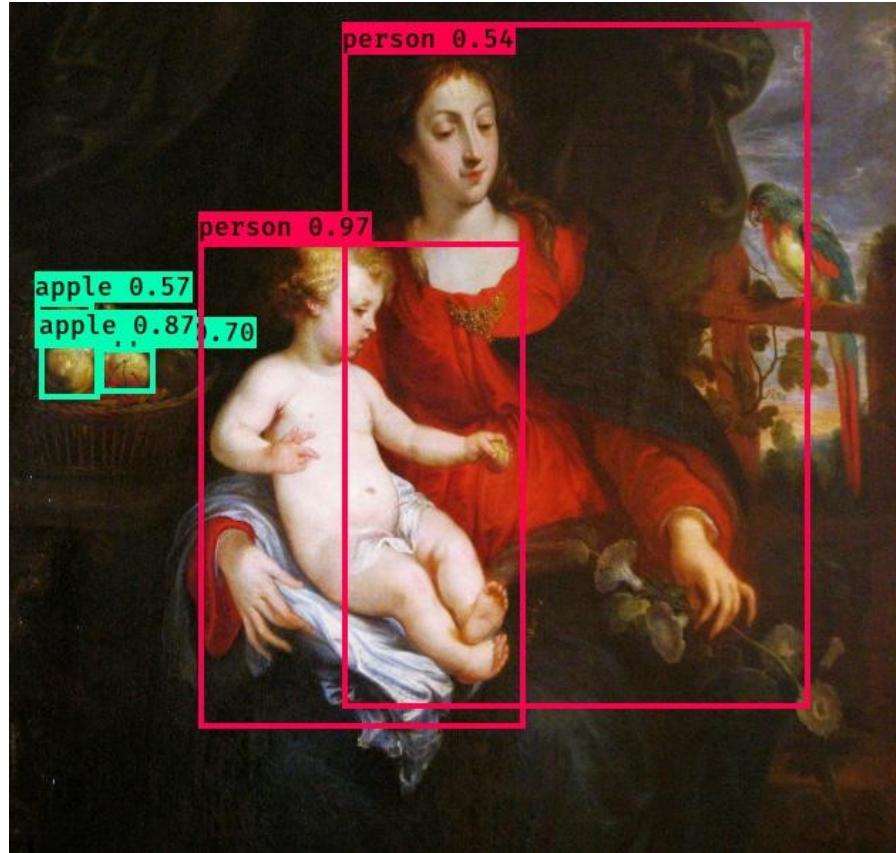
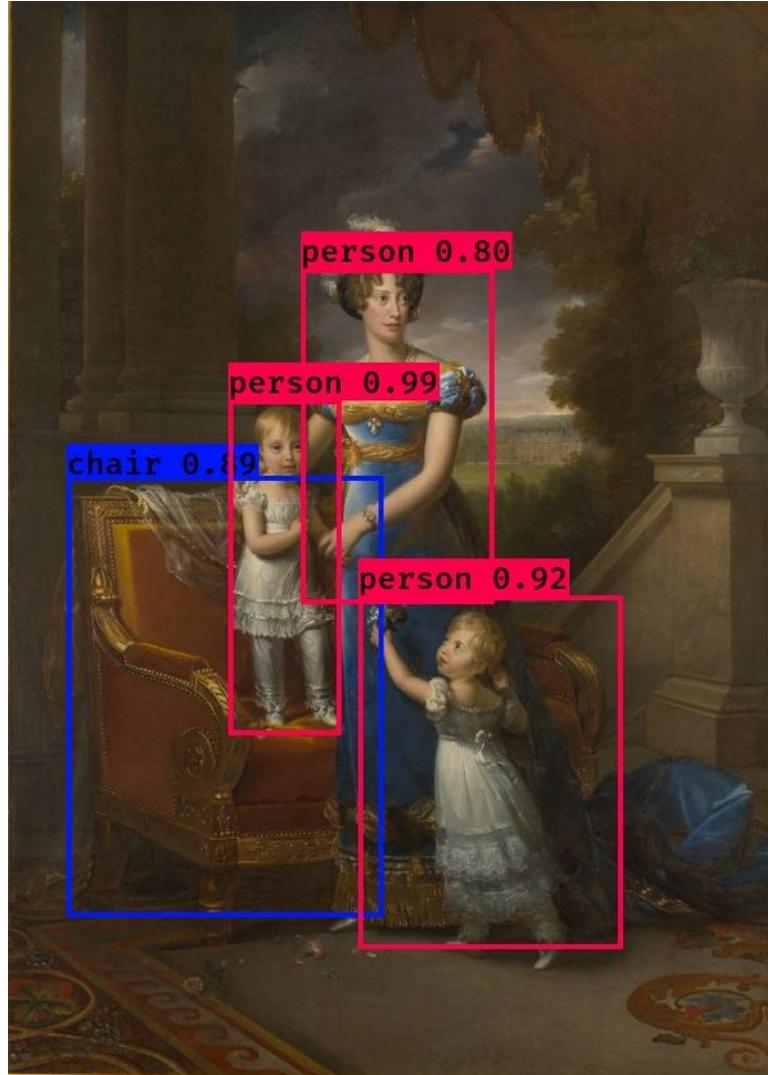
Deep Learning-based object detection

« Rectangle » (bounding box) annotations for object detection

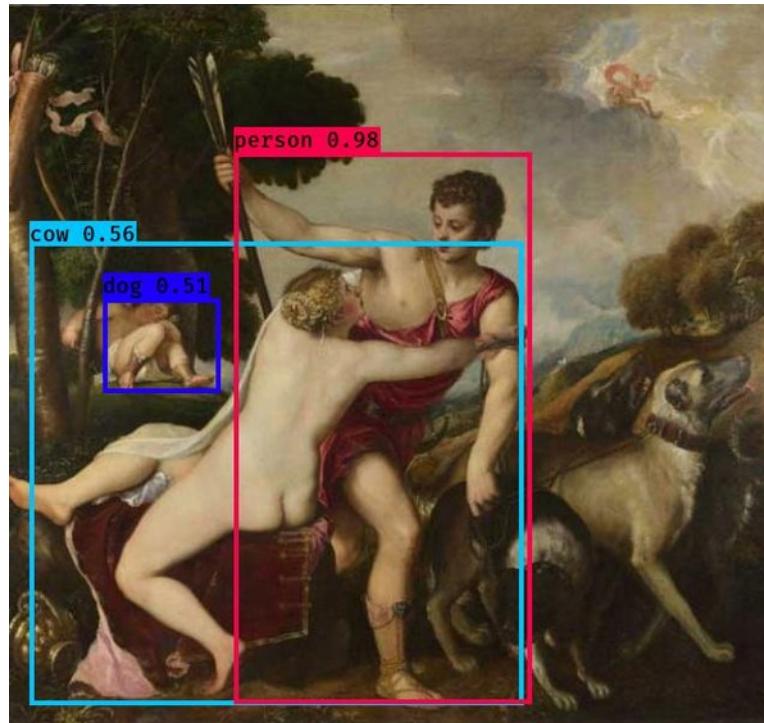


Sabatelli et al., Benchmarking the detection of musical instruments in unrestricted, non-photorealistic images from the artistic domain, Digital Humanities Quarterly, 2021

Deep Learning-based object detection



Deep Learning-based object detection

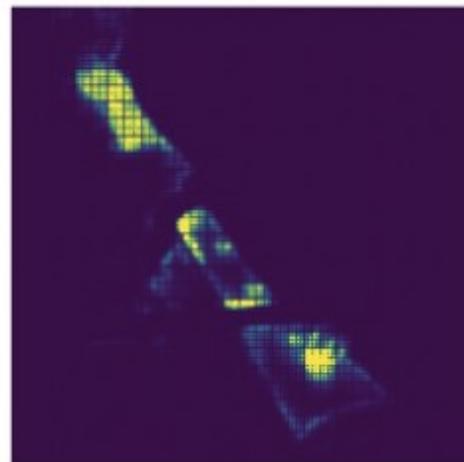


Sabatelli et al., Benchmarking the detection of musical instruments in unrestricted, non-photorealistic images from the artistic domain, Digital Humanities Quarterly, 2021

Interpretability (saliency maps)

(e)

Saliency Map from a trained model

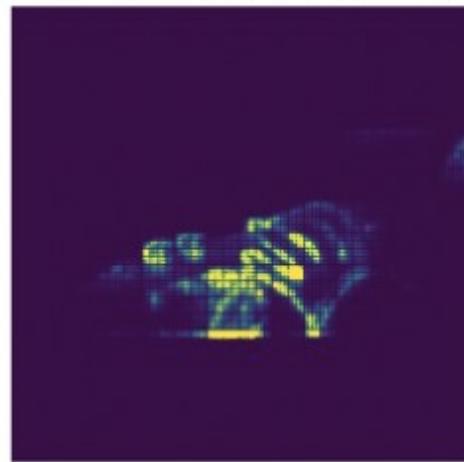


Original Image



(f)

Saliency Map from a trained model



Original Image

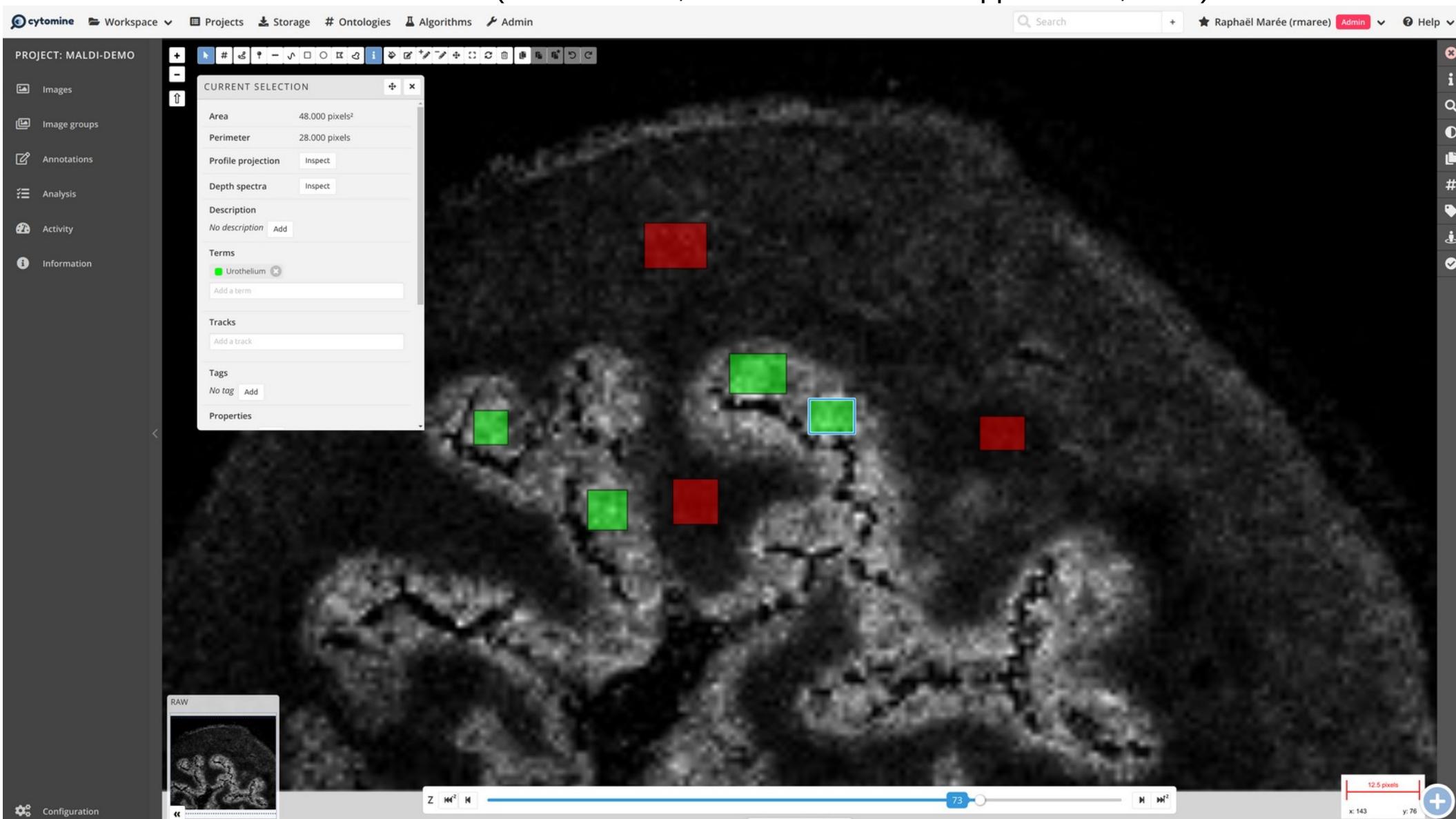


Interpretability (experiments with MALDI-IMS data)

Manual annotations of
positive (urothelium) / negative (stroma) regions of interest

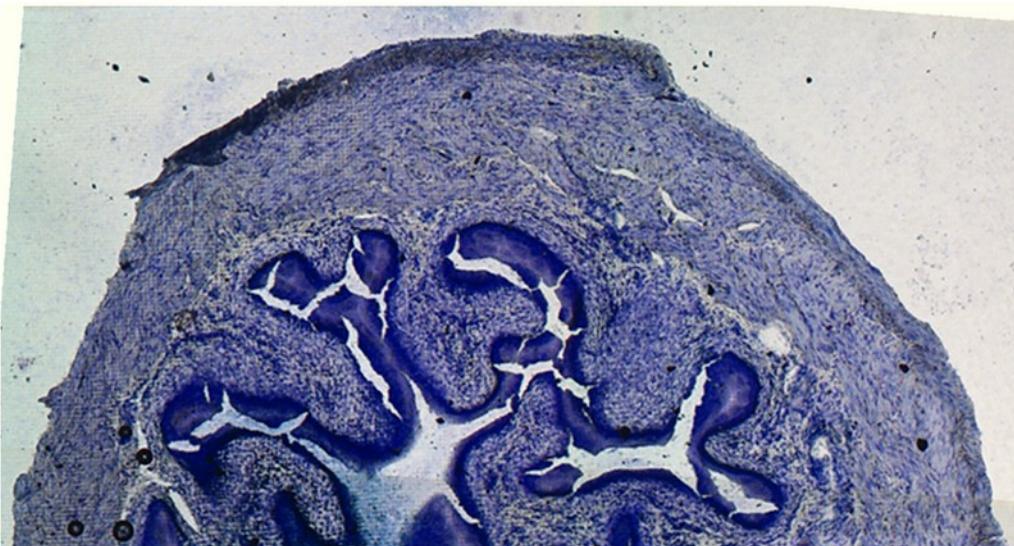
(Rubens et al., Proteomics: Clinical Applications, 2019)

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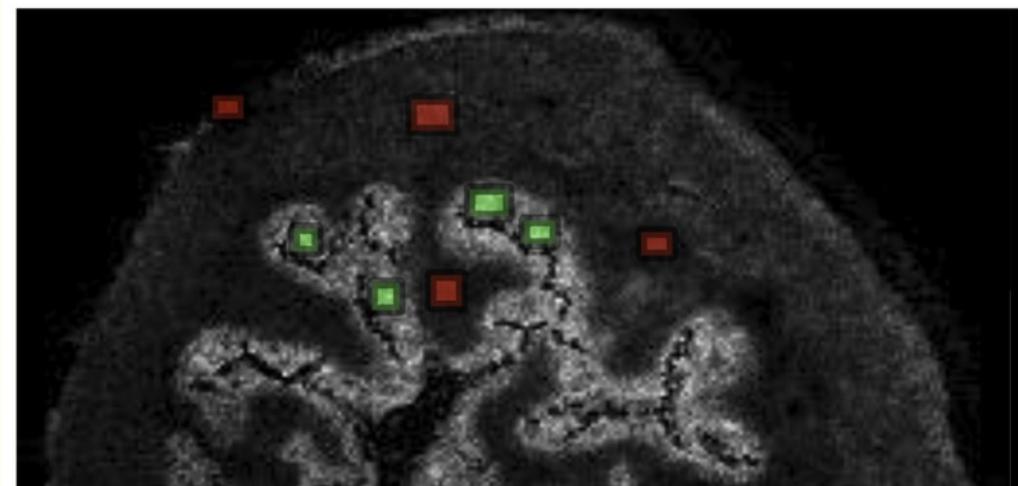


Interpretability (experiments with MALDI-IMS data)

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.

Summary and perspectives

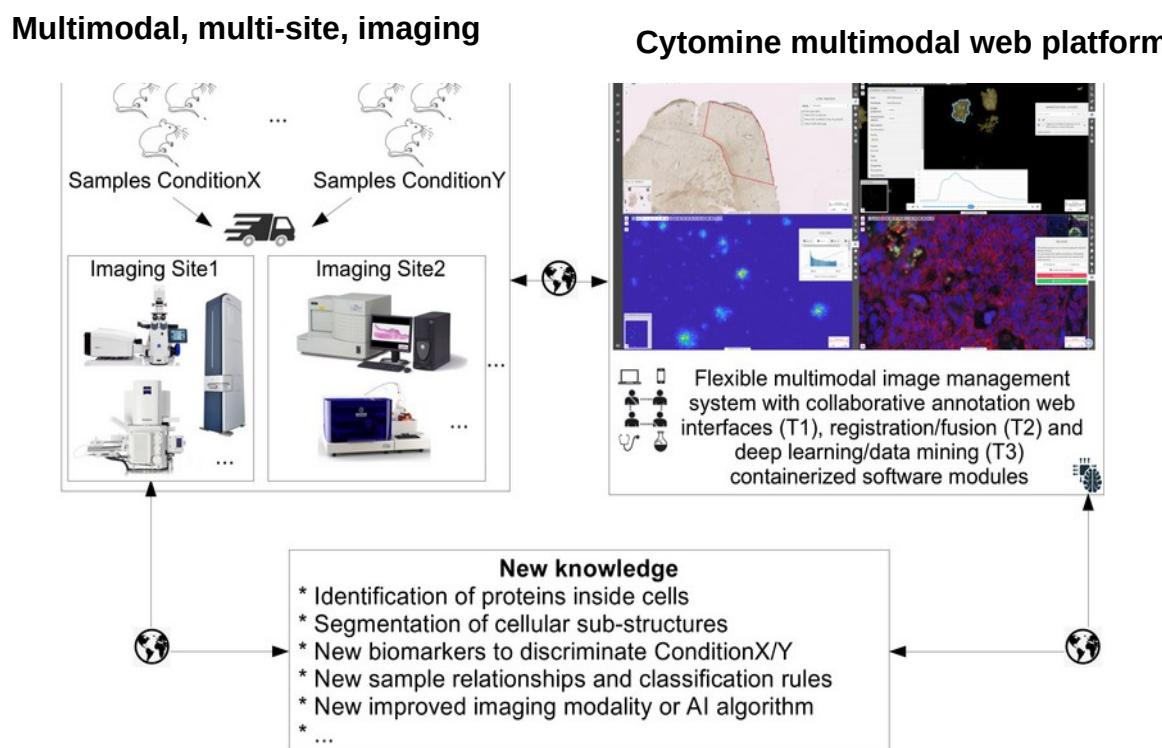


Cytomine for « sharing everything »

- Multimodal images, ground-truth annotations, source code, quantitative results, ...
- **Cytomine can be installed at your own institute** to start **collaborative** research today
- We use user-defined vocabularies.

Cytomine ULiège R&D Future plans

- Better support for bigger and distributed multimodal datasets with millions of objects
- Ease the integration of multimodal registration/fusion/data mining algorithms
- Support of standardized ontologies



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 [cytome.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 us

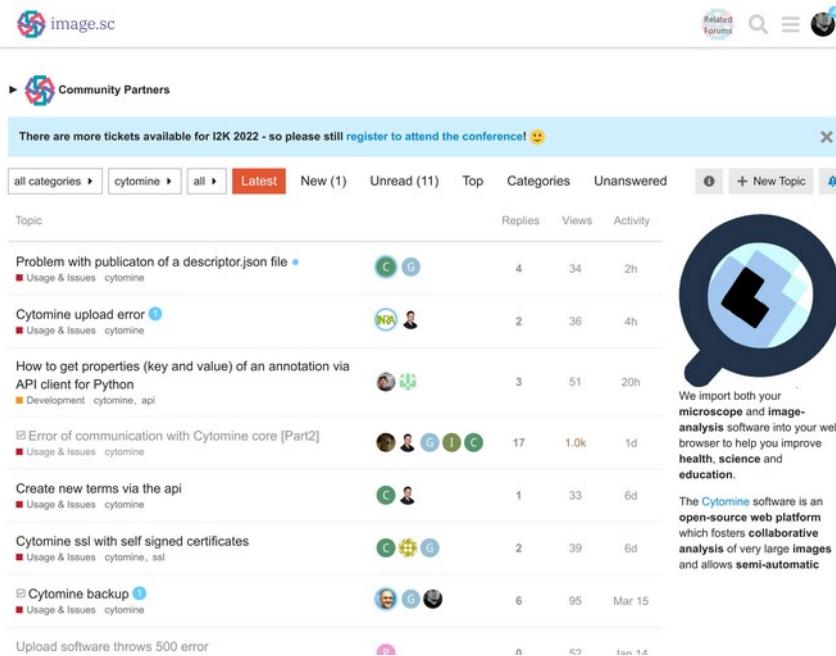


@cytome

@cytome_ulei



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



The screenshot shows a forum interface with a header bar including 'Related Forums', a search bar, and a navigation menu. Below the header, a message box says 'There are more tickets available for I2K 2022 - so please still register to attend the conference! 😊'. The main area displays a list of forum topics:

- Problem with publication of a descriptor.json file • 4 replies, 34 views, 2h ago
- Cytomine upload error ① • 2 replies, 36 views, 4h ago
- How to get properties (key and value) of an annotation via API client for Python • 3 replies, 51 views, 20h ago
- Error of communication with Cytomine core [Part2] • 17 replies, 1.0k views, 1d ago
- Create new terms via the api • 1 reply, 33 views, 6d ago
- Cytomine ssl with self signed certificates • 2 replies, 39 views, 6d ago
- Cytomine backup ① • 6 replies, 95 views, Mar 15
- Upload software throws 500 error • 0 replies, 49 views, Jan 1d

A sidebar on the right contains promotional text about Cytomine's features and its open-source nature.

cytome.org



ulei.cytome.org

doc.cytome.org



info@cytome.org

ulei@cytome.org

Webinars (May 2021 & July 2022):

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

https://www.youtube.com/results?search_query=cytome+correlated+imaging+series

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

Operations

Introduction

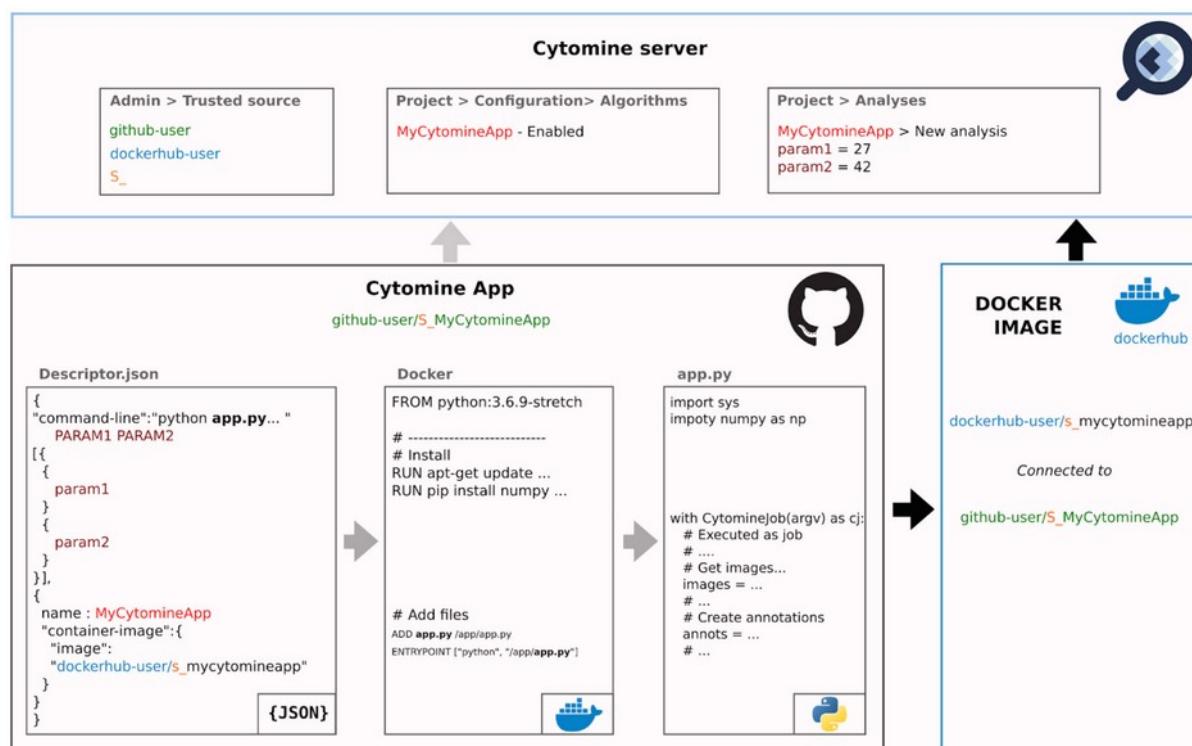
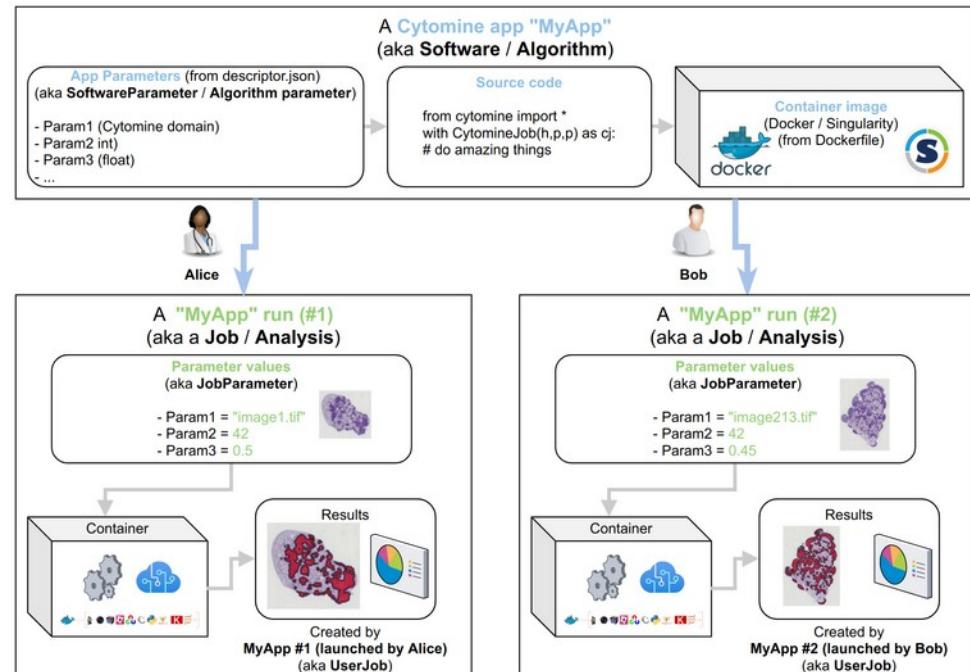
- Cytomine Bootstrap
- Cytomine containers
- Install
- Upgrade
- Backup and restore
- Troubleshoot
- Uninstall

API client for Python ▶

API client for Java ▶

API client for Javascript ▶

API reference



cytominē worldwide installations

Numerous Cytomine server installations around the world



UNIL | Université de Lausanne



Ecole Nationale
Vétérinaire, Agroalimentaire et de l'Alimentation



Universiteit
Antwerpen



UNIVERSITÉ
DE REIMS
CHAMPAGNE-ARDENNE



HELSE VEST IKT



LABORATORIO DE
PATOLOGÍA
DR. NOY



SAAB
TECHNOLOGY



Fédération Française de Cancérologie Digestive



UNIVERSITÉ
DE GENÈVE
FACULTÉ DE MÉDECINE



REVEAL
BIOSCIENCES



Enva
École nationale vétérinaire d'Alfort



VetAgro Sup
Campus Vétérinaire de Lyon

(see <https://cytomine.com>)



Université
numérique
en santé et sport.



BIGPICTURE

European Digital Pathology Platform

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

