

About open science and

cytomine

A generic open-source software for collaborative image analysis

uliege.cytomine.org



cytome_uliege

Raphael.Maree@uliege.be

Scientific coordinator @ University of Liège, Belgium (since 2010)
Co-founder of Cytomine not-for-profit cooperative (since 2017)

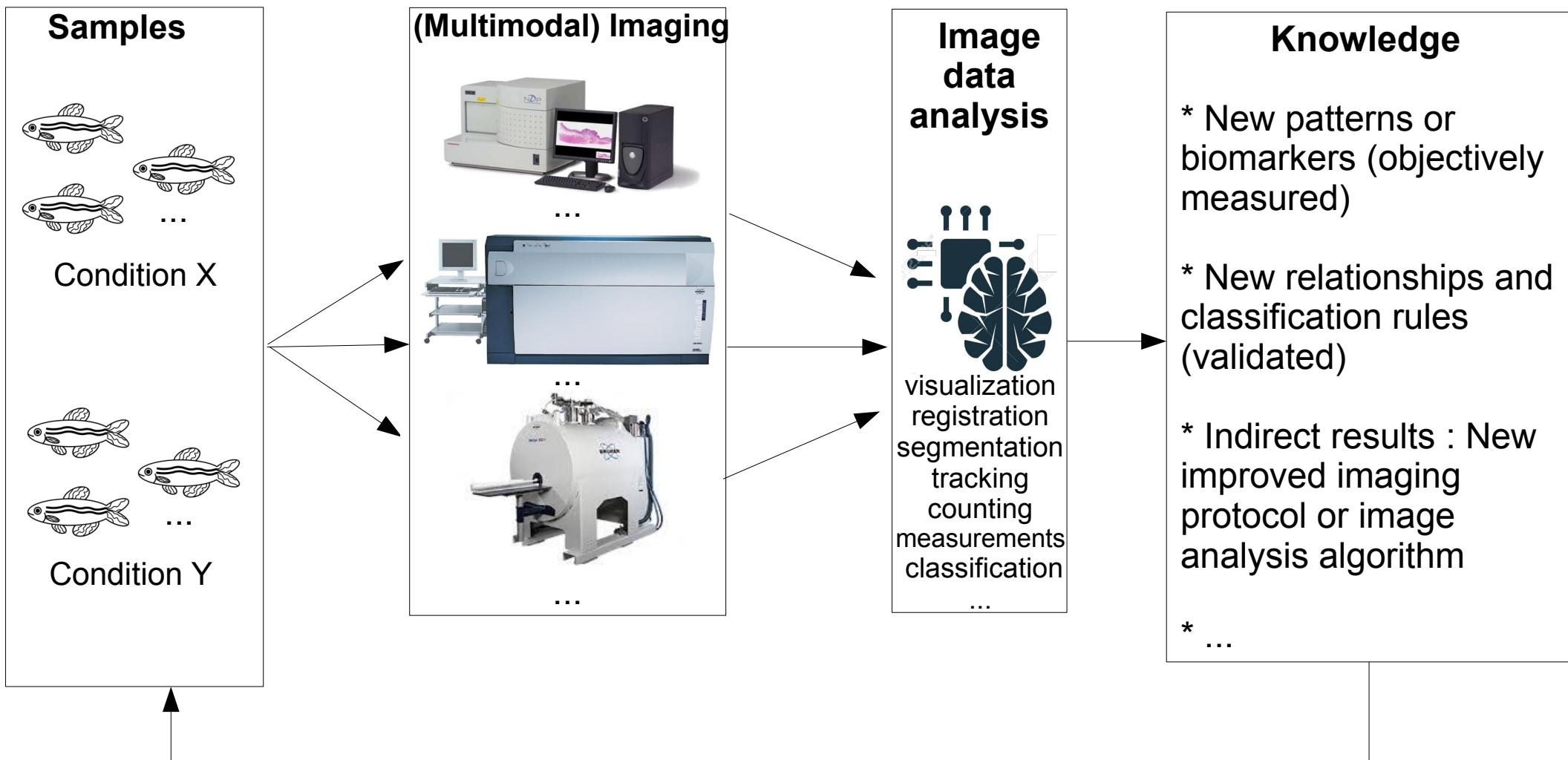


MONTEIRO INSTITUTE

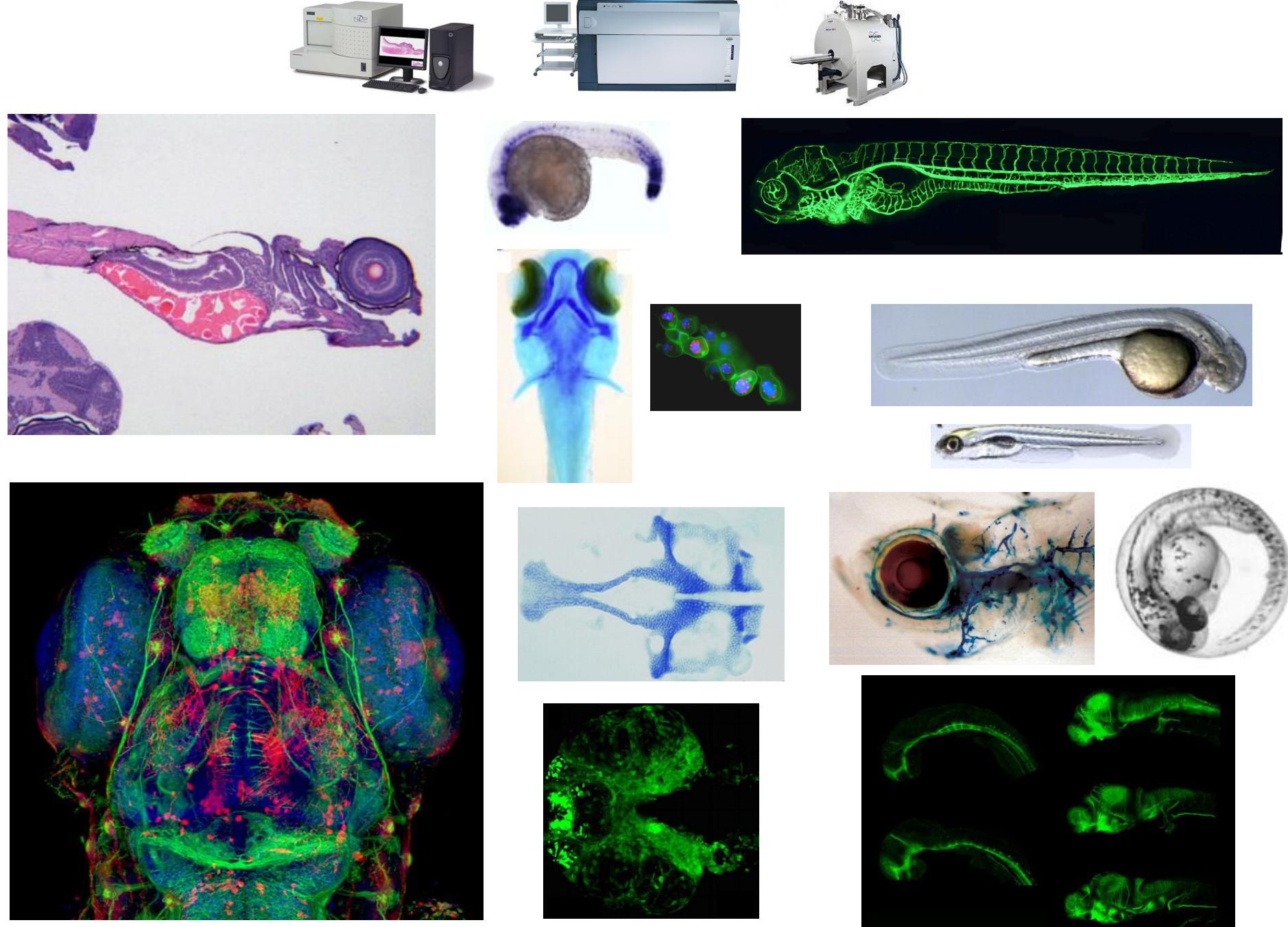
Department of Electrical
Engineering and Computer Science

Life science research heavily relies on images

(Exploratory analysis / Biomarker discovery / Classification of samples)

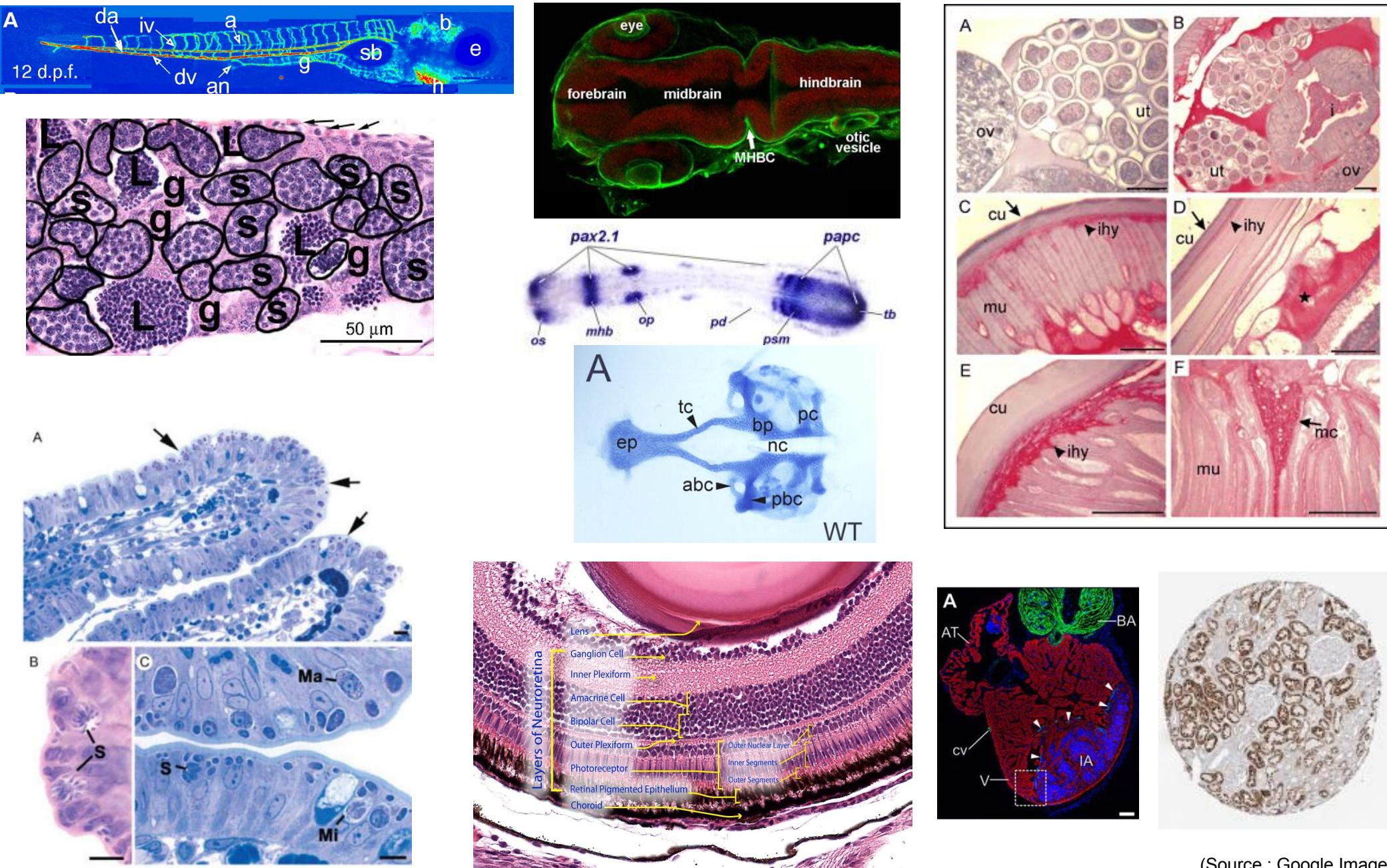


e.g. many Zebrafish imaging screens

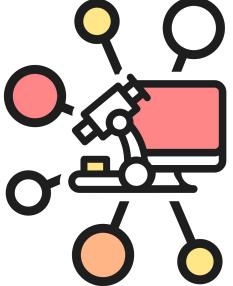


(Source : Google Images & GIGA)

A multiplicity of image analysis tasks



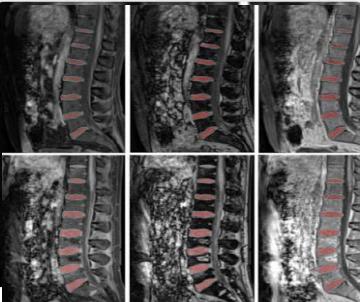
A multiplicity of image analysis tools



BiiI
Bioimage
Informatics
Index

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

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



(e.g. intervertebral disc localization)

Medical Image Segmentation

57 benchmarks

113 papers with code

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



GitHub

<https://github.com/search?q=zebrafish>
(> 400 zebrafish code repositories)

Automated Processing of Zebrafish Imaging Data:
A Survey (Mikut et al., 2013)

+ Navdeep's survey

...

Image analysis practices are not ideal (1/2)

Image analysis is still often :

- Qualitative (seeing is believing?) or performed (semi-)manually
- Performed within tissue subregions or in small sample groups
(might not be statistically significant or one might miss specific patterns)
- Performed by isolated experts and stored locally
(sometimes lost)
- Not saved, or in closed formats so hardly reusable
(e.g. Photoshop draws for paper figures)

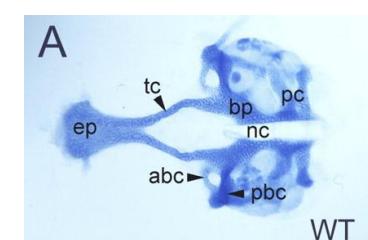


Image analysis practices are not ideal (2/2)

Challenges for biologists:

« Not easy to reuse previous work on my images because ... »
... many nice biology papers do not come with a tool or few details
... which algorithm to choose in the zoo ? How can I trust it ?
... best algorithms might not be implemented in user-friendly software
... many algorithms are not interpretable (black box)
... 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 because ... »
... so many imaging techniques & combinations
... few annotated (ground-truth) datasets available (proprietary formats)
... meaningful results ? expert's proofreading ?
... publish & perish... validation only on 1-2 (small) dataset(s) : ad hoc

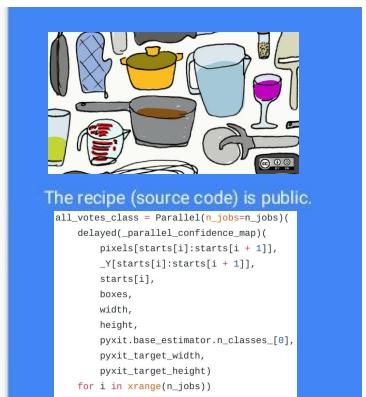
→ **suboptimal science practices** (reproducibility issues, waste of time, ...)

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

Let's try to **collaborate** more effectively towards **more generic** and **reproducible** image analysis workflows and biomedicine research.

Practical suggestions to improve our situation :

- **Image sharing**
- **Image annotation (ground truths) sharing**
- **Image analysis workflows sharing and benchmarking**
- **Open science** (open data access, open source code, ...)



→ Freedom to install, inspect, extend, improve, reproduce, redistribute

(see also Brito et al., Gigascience 2020)

Existing image sharing solutions

Centralized repositories



www.ebi.ac.uk/bioimage-archive/



www.oasis-brains.org/



bossdb.org/projects



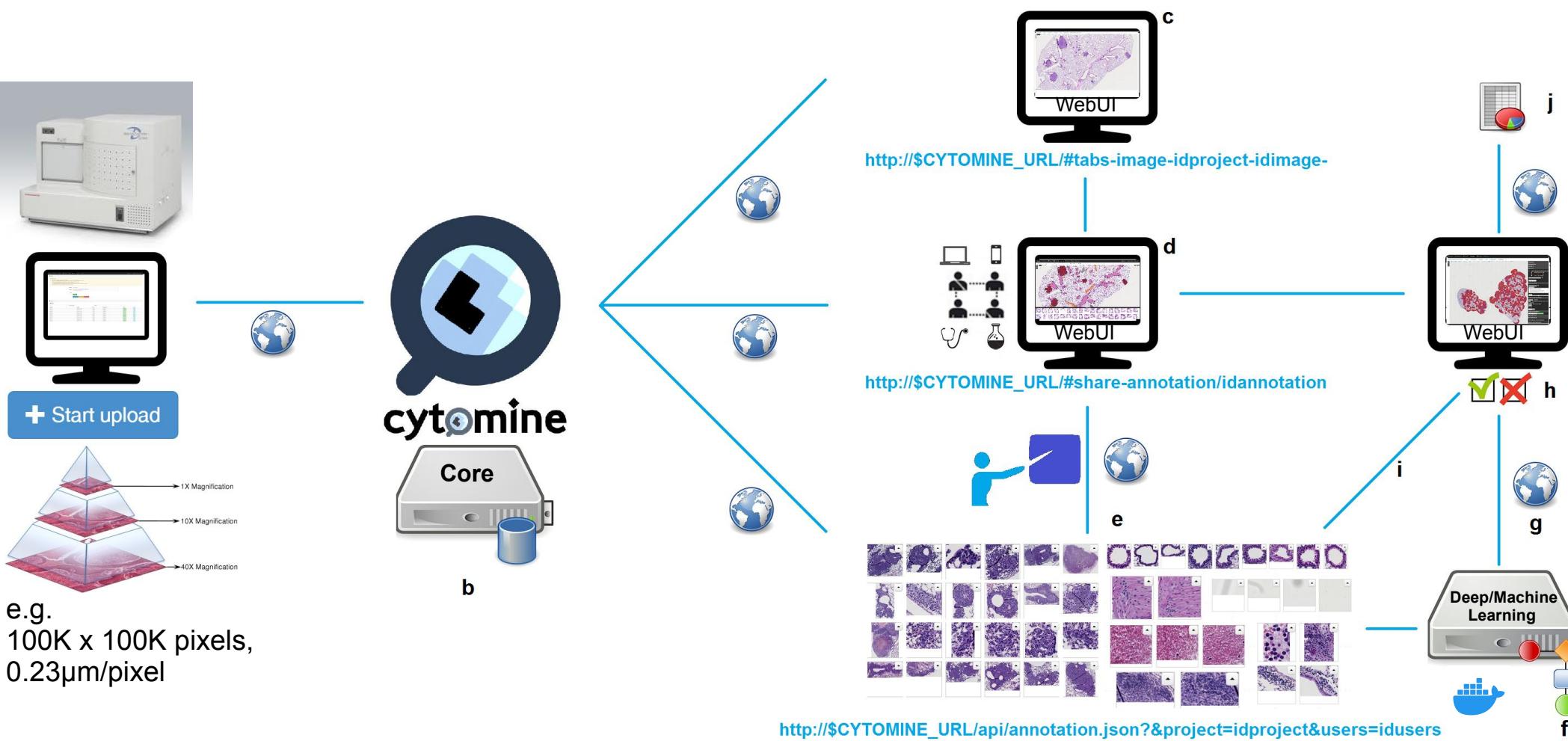
www.cancerimagingarchive.net/



Overview of main features

cytome.org (official version)
uliege.cytome.org (ULiège R&D version)

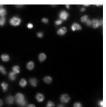
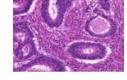
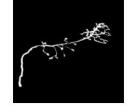
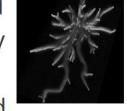
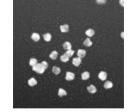
cytominne enables collaboration through the web (Sharing of images, annotations, algorithms, results)



cytominE: organize your images, securely, on the web

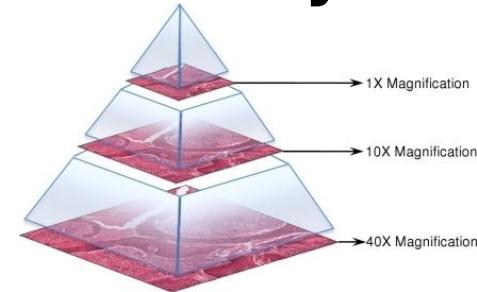
Create and manage multiple **projects**:

- Support **various digital pathology, microscopy & other image formats**
- 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 BBC038v1 , available from the Broad Bioimage Benchmark Collection [Ljosa et al., Nature Methods, 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 : visualize large images, remotely

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

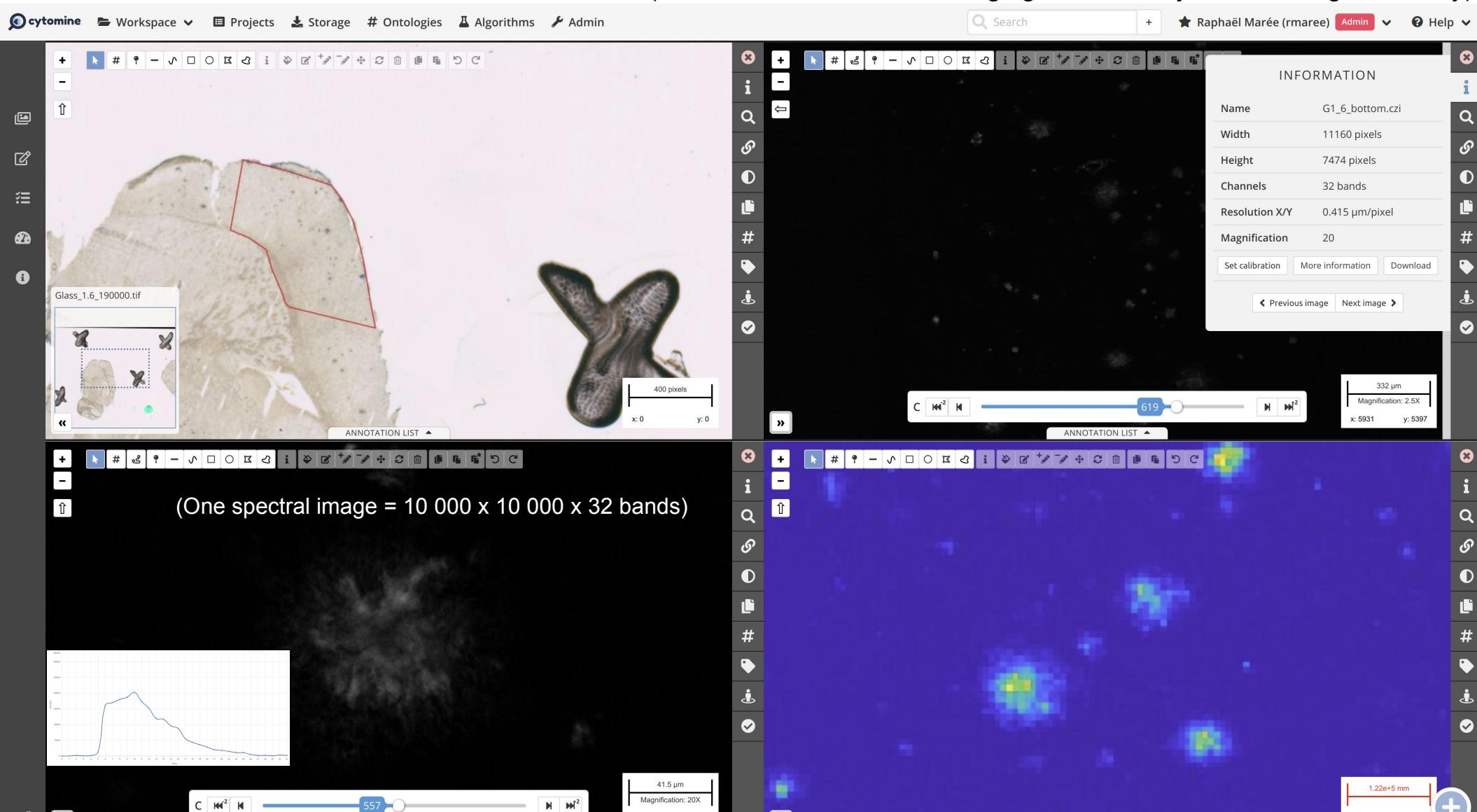


The screenshot shows the cytominE software interface. At the top, there is a navigation bar with links for 'cytominE', 'Workspace', 'Projects', 'Storage', 'Ontologies', 'Algorithms', and 'Admin'. On the right side, there is a user profile for 'Raphaël Marée (rmaree)' with an 'Admin' button. Below the navigation bar, there is a search bar and a help icon. The main area displays a large tissue slice image. A text overlay on the left side of the image states: 'One tissue slice = 40000 x 30000 pixels (0.23µm/pixel)'. The image itself shows a complex tissue structure with various cellular components and architectural features. In the bottom left corner of the main image, there is a small inset image and some text: 'PGP POUMON PB55 1 - 2012-08-07 11.39.07.jp2'. The bottom right corner of the main image also has some small text and icons. On the far left, there is a vertical toolbar with various icons for image manipulation. On the far right, there is another vertical toolbar with icons for different functions.

... and multidimensional, multimodal images

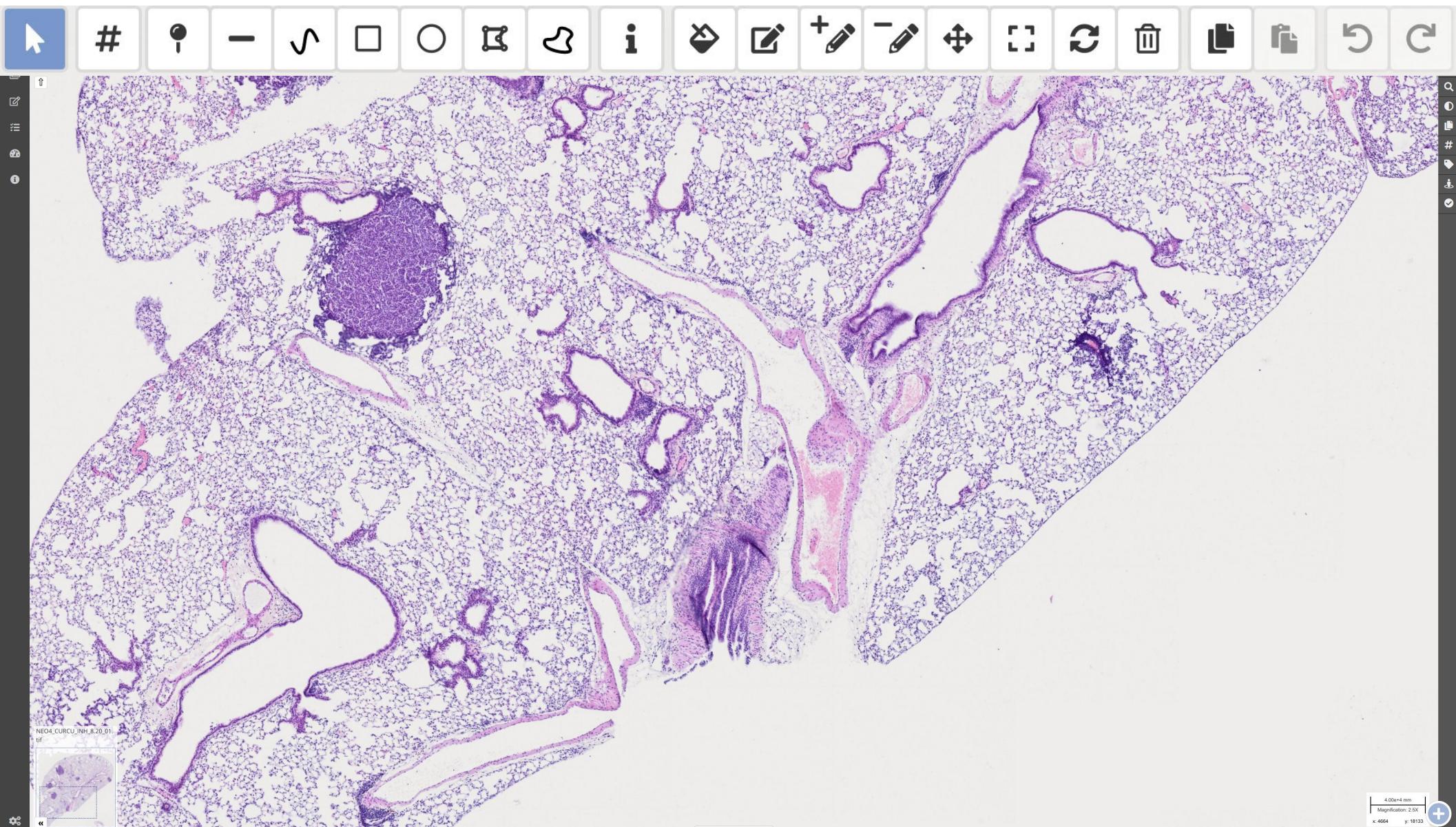
- Explore **2D+c+z+t slices**
- Explore **spectral profiles**
- Side-by-side comparison of multiple views

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



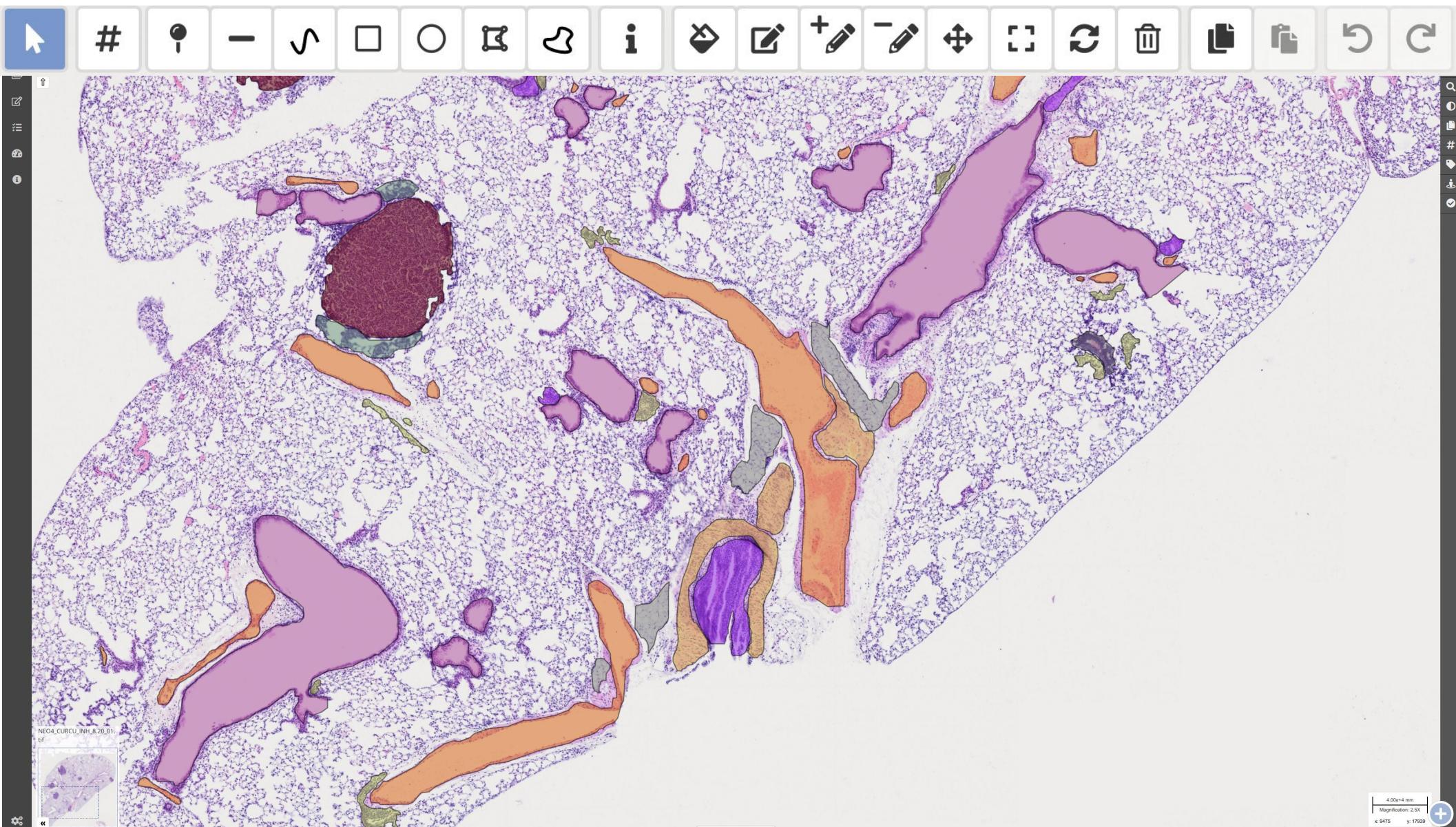
cytominE : annotate semantically, collaboratively

- 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**



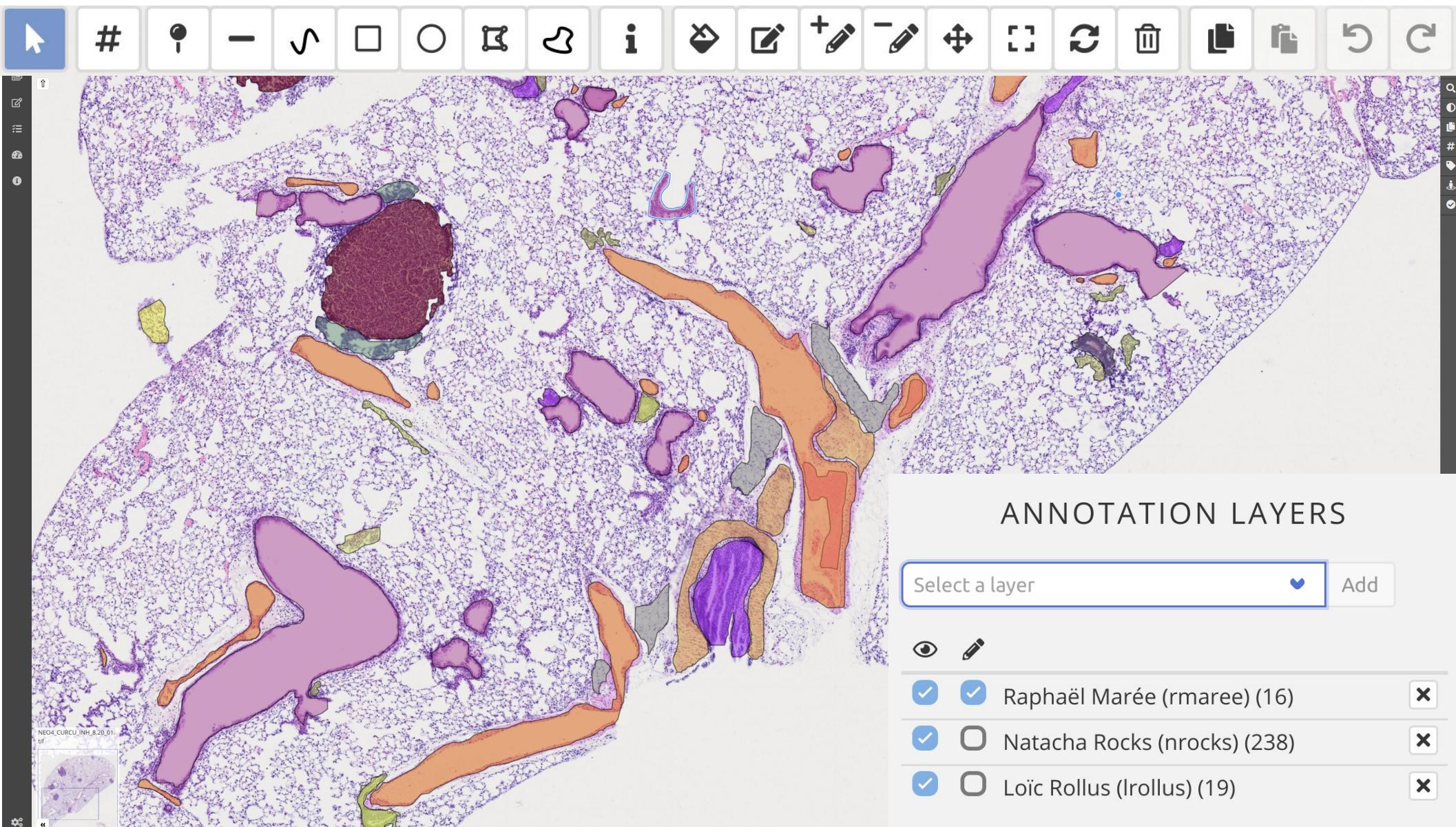
cytominE : annotate semantically, collaboratively

- 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**



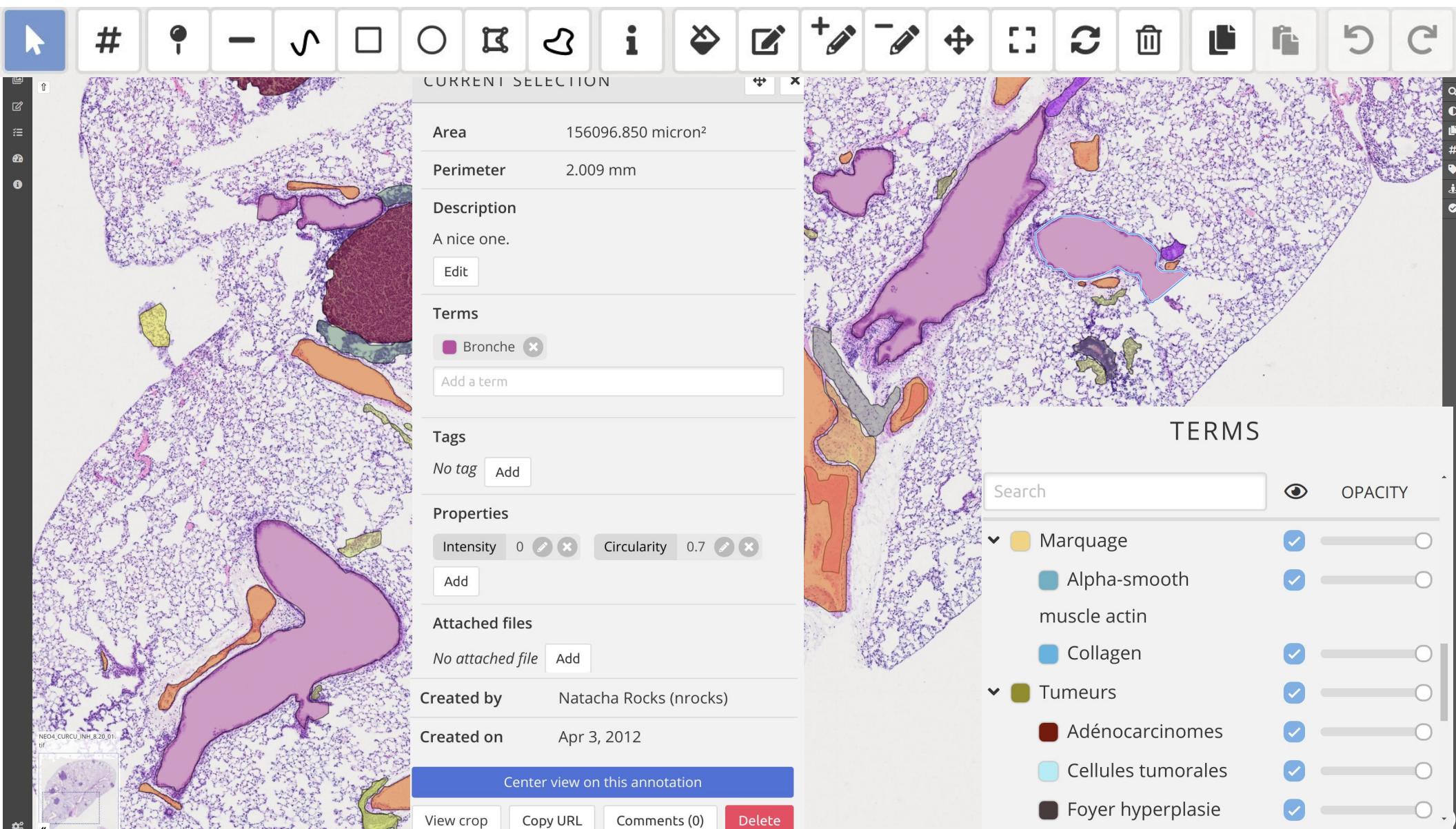
cytominE : annotate semantically, collaboratively

- 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**



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**



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**

The screenshot shows the cytominE interface for semantic annotation. At the top, a toolbar contains various drawing tools: arrow, hash, circle, square, rectangle, freehand, selection, text, polygon, plus, minus, cross, crop, trash, copy, and paste. Below the toolbar, a status bar displays "CURRENT SELECTION" and "Area 156096.850 micron²". A green notification box in the center says "Your comment was successfully send by email". The main area shows a histology image with several purple-stained regions. On the left, a sidebar lists "Annotation comments". The first comment is from "Raphaël Marée" on Nov 17, 2020 at 1:52 PM, reading "This is another test comment.2.". The second comment is also from "Raphaël Marée" on Nov 17, 2020 at 1:52 PM, reading "This is a test comment. How are you ?". At the bottom center is a blue button labeled "Add comment". In the bottom right corner, there is a legend for "Tumeurs" with three categories: "Adénocarcinomes" (dark red), "Cellules tumorales" (light blue), and "Foyer hyperplasie" (black). The bottom navigation bar includes "Center view on this annotation", "View crop", "Copy URL", "Comments (0)", and "Delete". On the far right, there are sliders for "OPACITY" and a vertical list of other semantic layers.

Annotation comments

Raphaël Marée Nov 17, 2020 1:52 PM
This is another test comment.2.

Raphaël Marée Nov 17, 2020 1:52 PM
This is a test comment. How are you ?

Add comment

Created by Natacha Rocks (nrocks)

Created on Apr 3, 2012

Center view on this annotation

View crop Copy URL Comments (0) Delete

Tumeurs

- Adénocarcinomes
- Cellules tumorales
- Foyer hyperplasie

cytominE : annotate semantically, collaboratively

Subject:Cytomine: Raphaël Marée (rmaree) commented an annotation

Date:Tue, 17 Nov 2020 12:52:57 +0000 (UTC)

From:cytominE.uliege@gmail.com

Reply-To:noreply@cytominE.org

To:info@cytominE.be



Hi,

Raphaël Marée (rmaree) shared an annotation with you and commented : "This is another test comment.2."

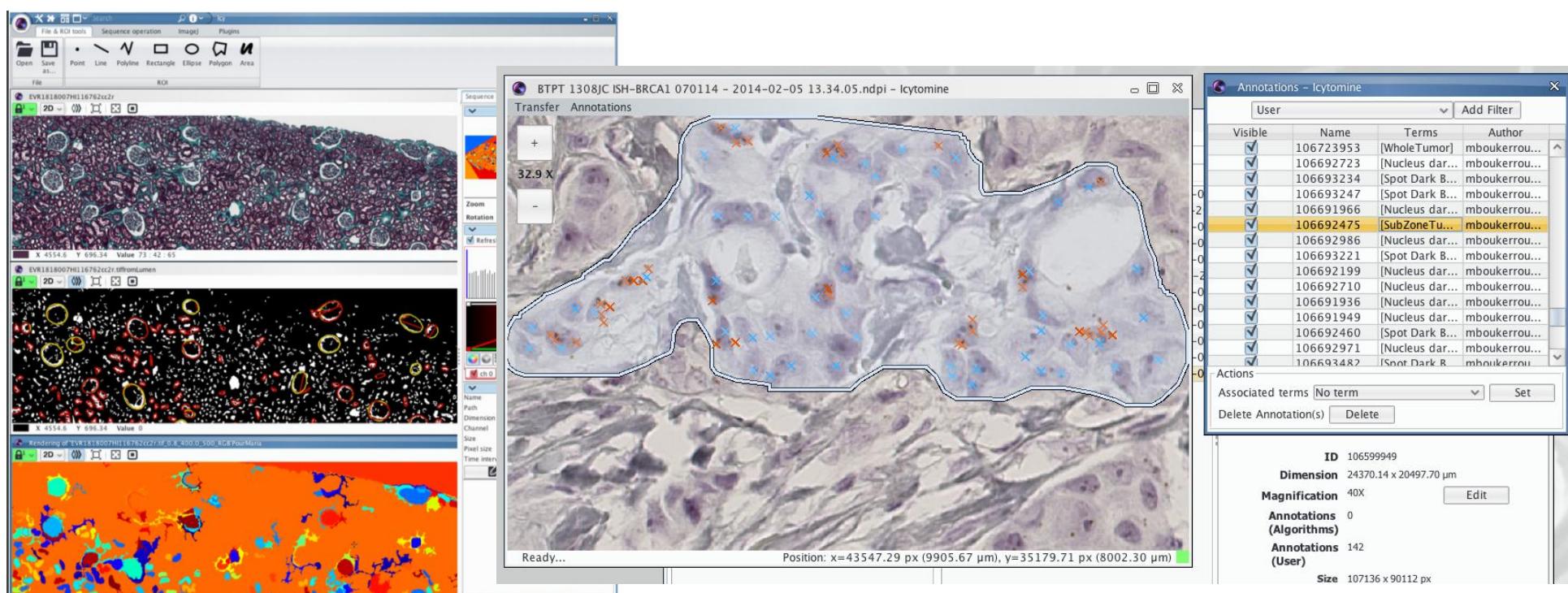
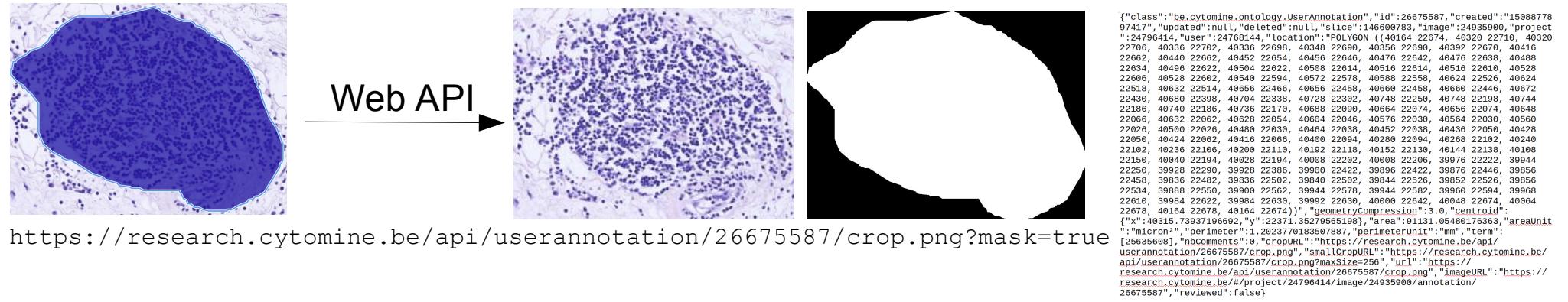


Navigate to <https://research.cytominE.be/#/project/51066666/image/51068020/annotation/51079563?action=comments> in order to reply.

Navigate to <https://research.cytominE.be/#/project/51066666/image/51068020/annotation/51079563> in order to view the annotation within its context, or click on the thumbnail.

cytominE is highly interoperable

RESTful API to easily import/export all data through Internet

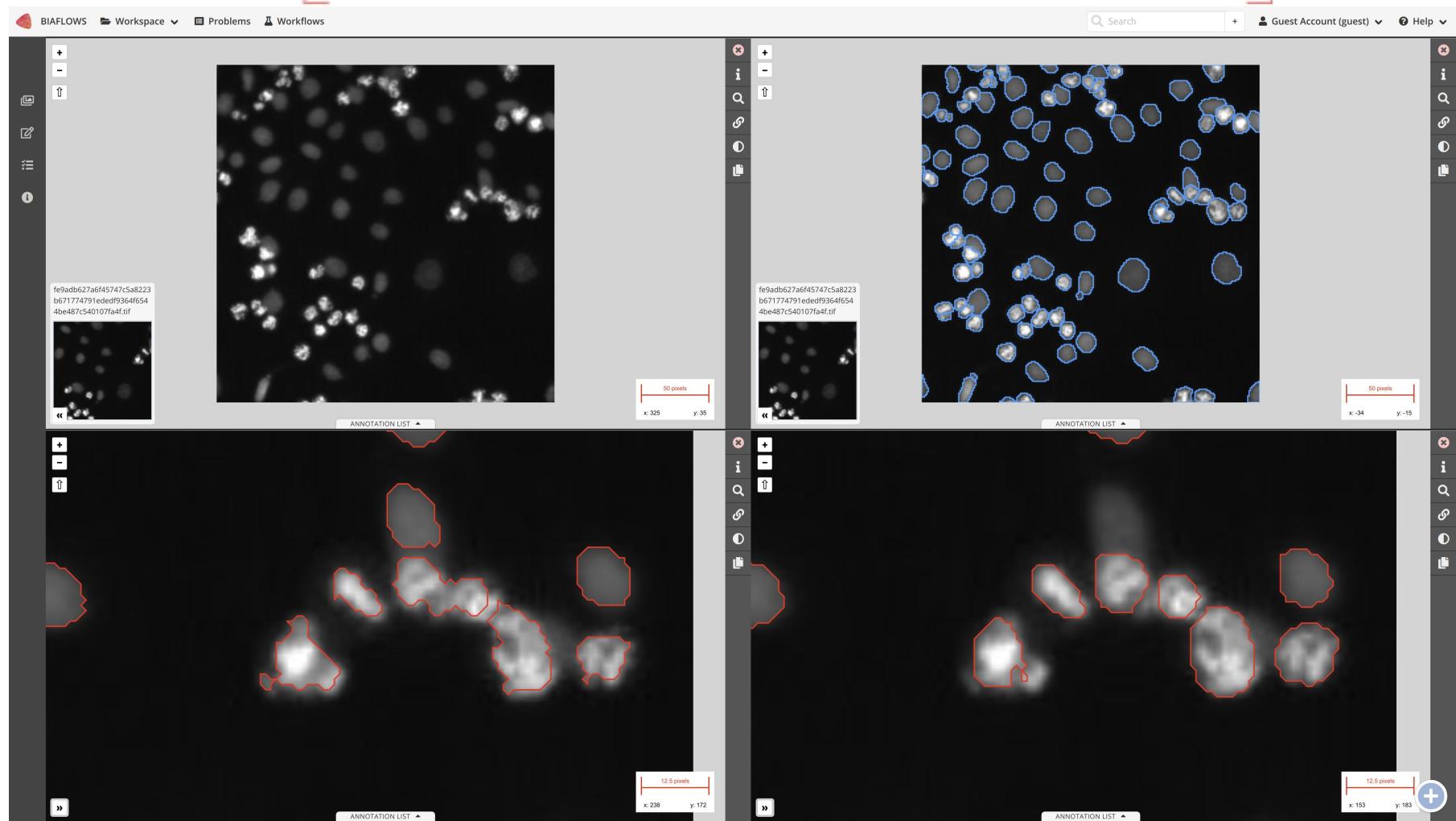


Institut Pasteur

cytominE is highly extensible

(Rubens et al., Cell Patterns, 2020)

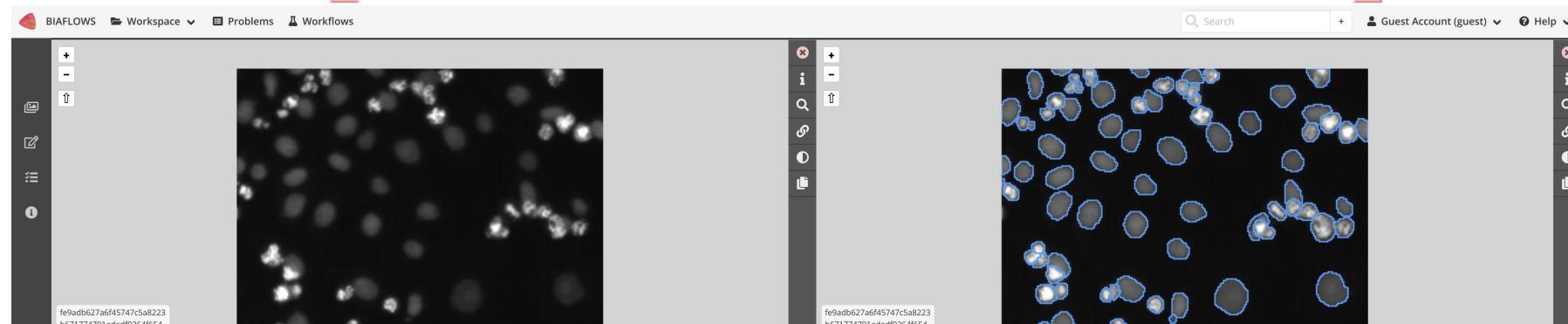
- **Integrate** algorithms **from any other tool** (ImageJ, Fiji, Icy, CellProfiler, ilastik, Vaa3D, Python, Keras/Tensorflow, OpenCV, ...) using **containers** (Docker/Singularity)
- **Reproducibility** : saving parameter values, versioned source code and libraries,...



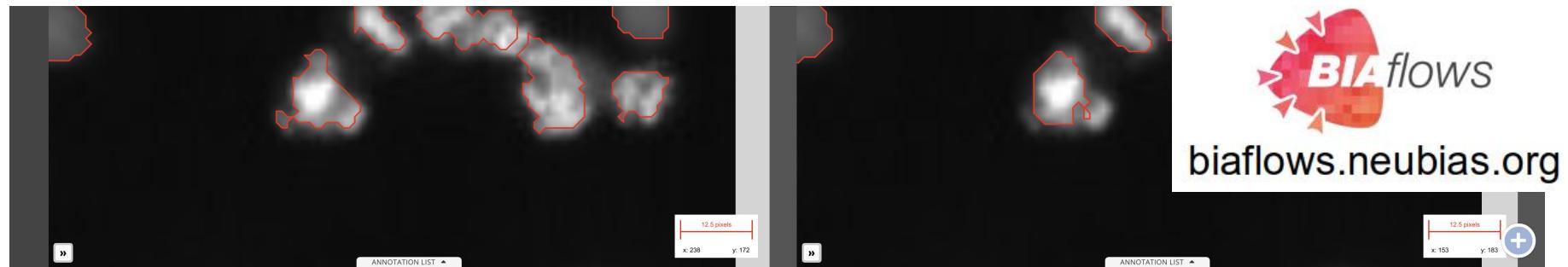
cytominE is highly extensible

(Rubens et al., Cell Patterns, 2020)

- **Integrate** algorithms **from any other tool** (ImageJ, Fiji, Icy, CellProfiler, ilastik, Vaa3D, Python, Keras/Tensorflow, OpenCV, ...) using **containers** (Docker/Singularity)
- **Reproducibility** : saving parameter values, versioned source code and libraries, ...



Workflow run	Mean Average Precision [Main metric]				Dice coefficient				Average Hausdorff distance				Fraction Overlap Pred			
	MIN	MAX	AVG	SD	MIN	MAX	Avg	SD	MIN	MAX	Avg	SD	MIN	MAX	Avg	SD
★ NucleiSegmentation-MaskRCNN (v1.5.0) #1 on Mar 28, 2020 7:49 PM	0.058	0.9	0.394	0.174	0.452	0.963	0.798	0.119	0.07	31.054	2.702	4.846	0.195	0.934	0.625	0.186
★ NucleiSegmentation-ilastik (v1.4.0) #2 on Mar 27, 2020 4:57 PM	0	0.82	0.208	0.195	0.215	0.944	0.725	0.164	0.056	34.331	3.843	6.527	0.046	0.902	0.502	0.181
★ NucleiSegmentation-UNet (v1.1.1) #7 on Mar 27, 2020 2:37 PM	0	0.85	0.282	0.177	0.075	0.948	0.754	0.193	0.053	128.964	8.485	20.924	0.044	0.934	0.542	0.177





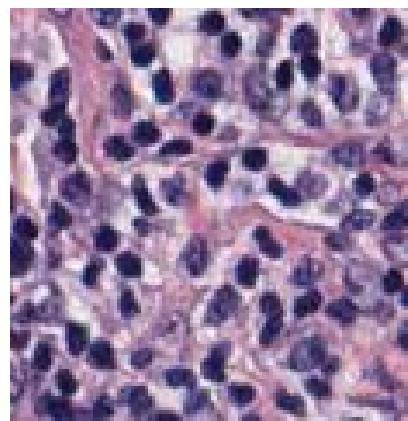
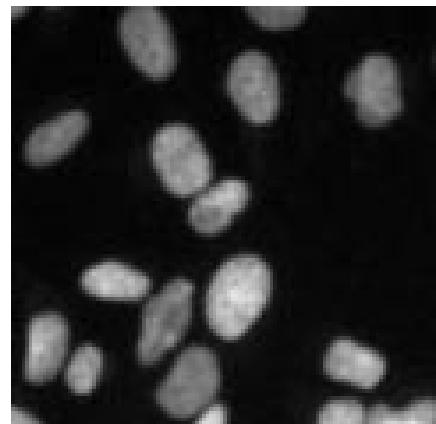
Examples and applications
1. Cell segmentation and counting

uliege.cytomine.org

An example of the potential benefits of an open science « sharing » approach

StarDist cell segmentation algorithm (Schmidt et al., 2018)

- Was trained on **public datasets** (images+ground-truths) : TCGA, DSB 2018 and Monuseg 2018 challenges
- It is **open-source** (<https://github.com/mpicbg-csbd/stardist>)
- It is a promising « generic » candidate (originally tested on fluorescent nuclei and H&E)



An example of the potential benefits of an open science « sharing » approach

StarDist integrated into cytominer

Launch new analysis

Algorithm CellDetect_Stardist_HE_ROI (v1.0.3) ▾

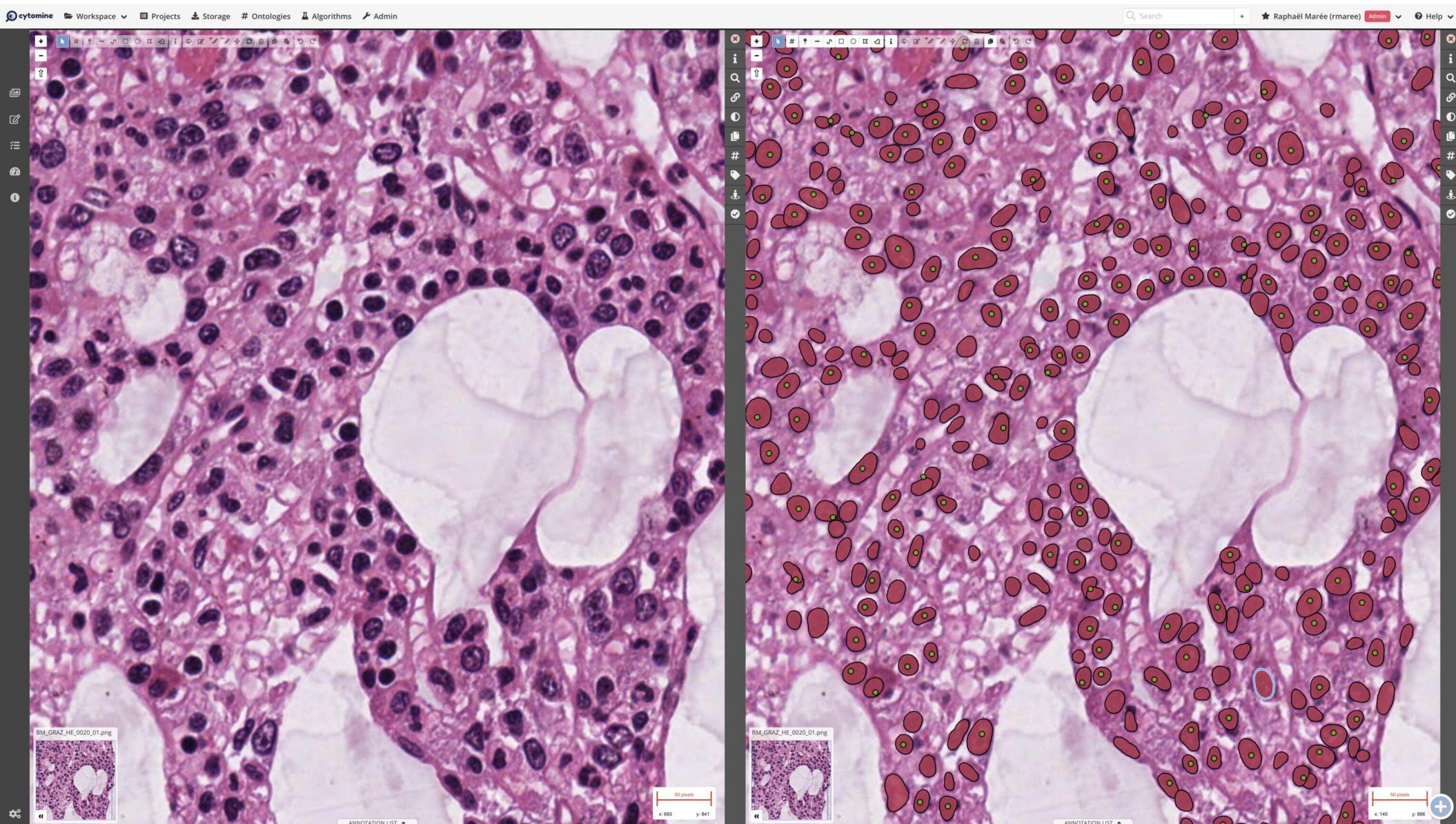
Name	Value
Cytomine Image IDs	CMU-1.svs
Cytomine ROI term ID	ROI
Cytomine Cell term ID	Nuclei_predict

Pre-filled parameters Hide

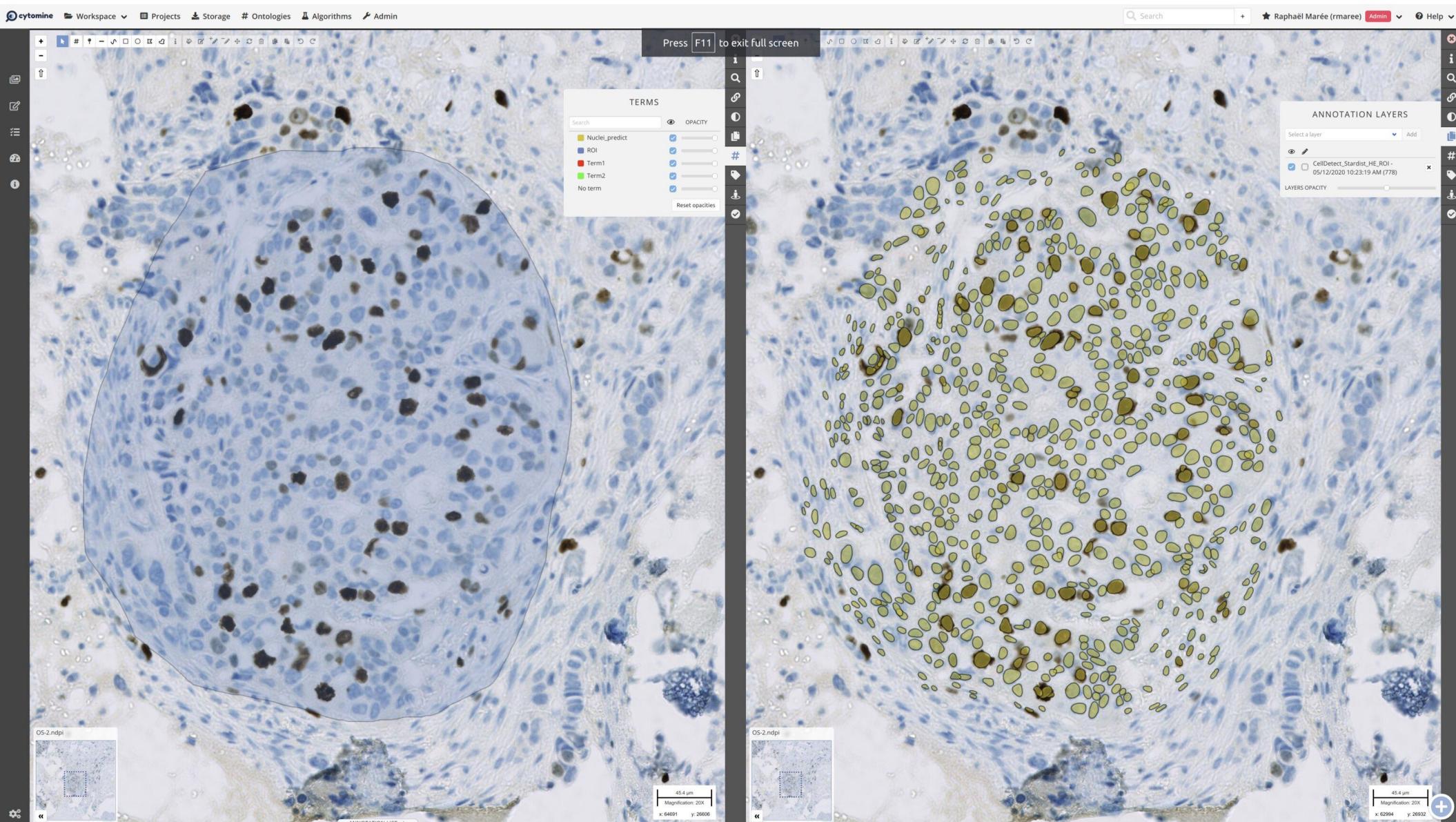
Stardist Probability Threshold	0.5
Stardist Non-Maximum Suppression Overlap threshold	0.5
Stardist Image Normalization Percentile Low	1
Stardist Image Normalization Percentile High	99.8

Cancel Launch new analysis

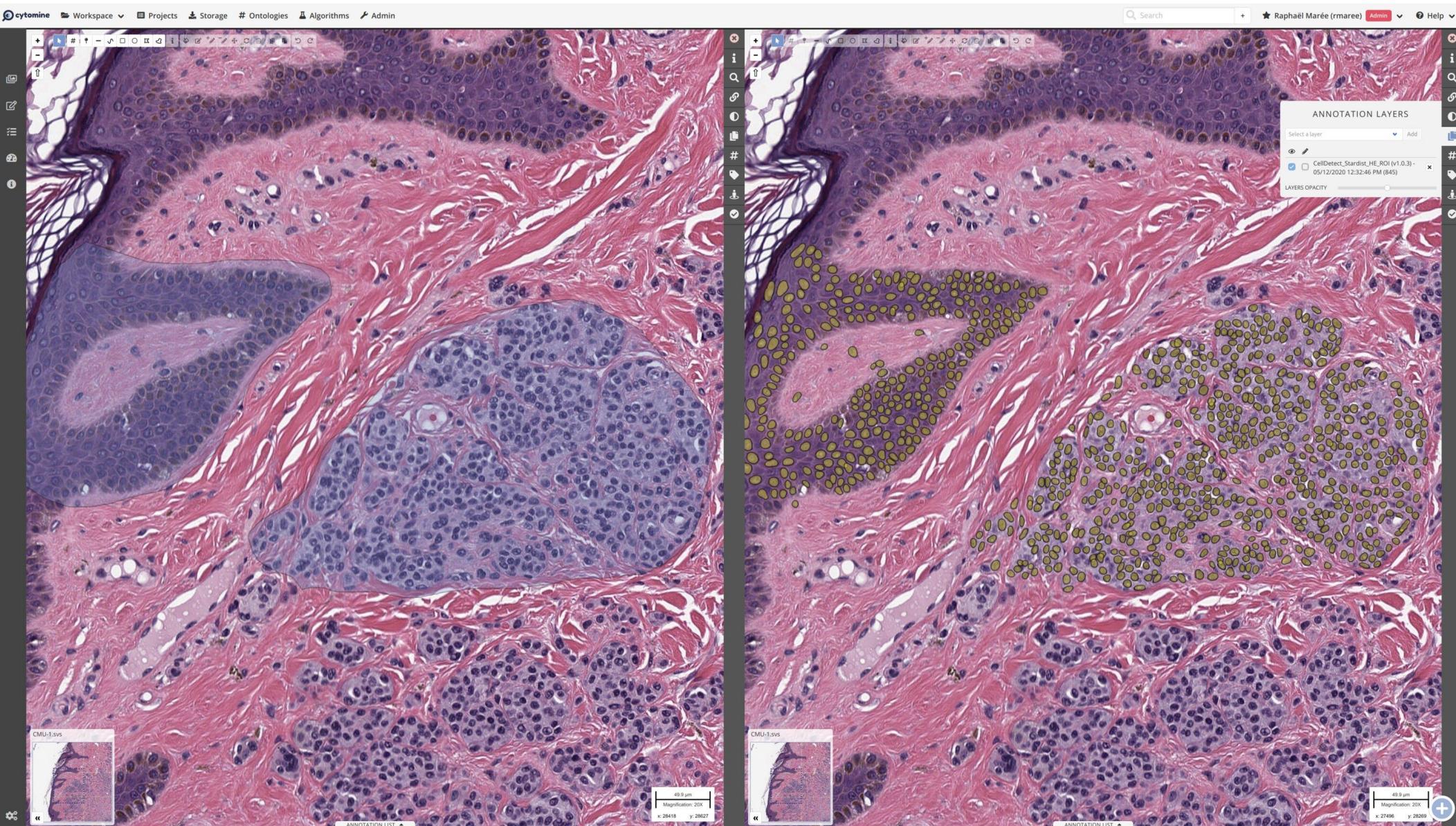
An example of the potential benefits of an open science « sharing » approach



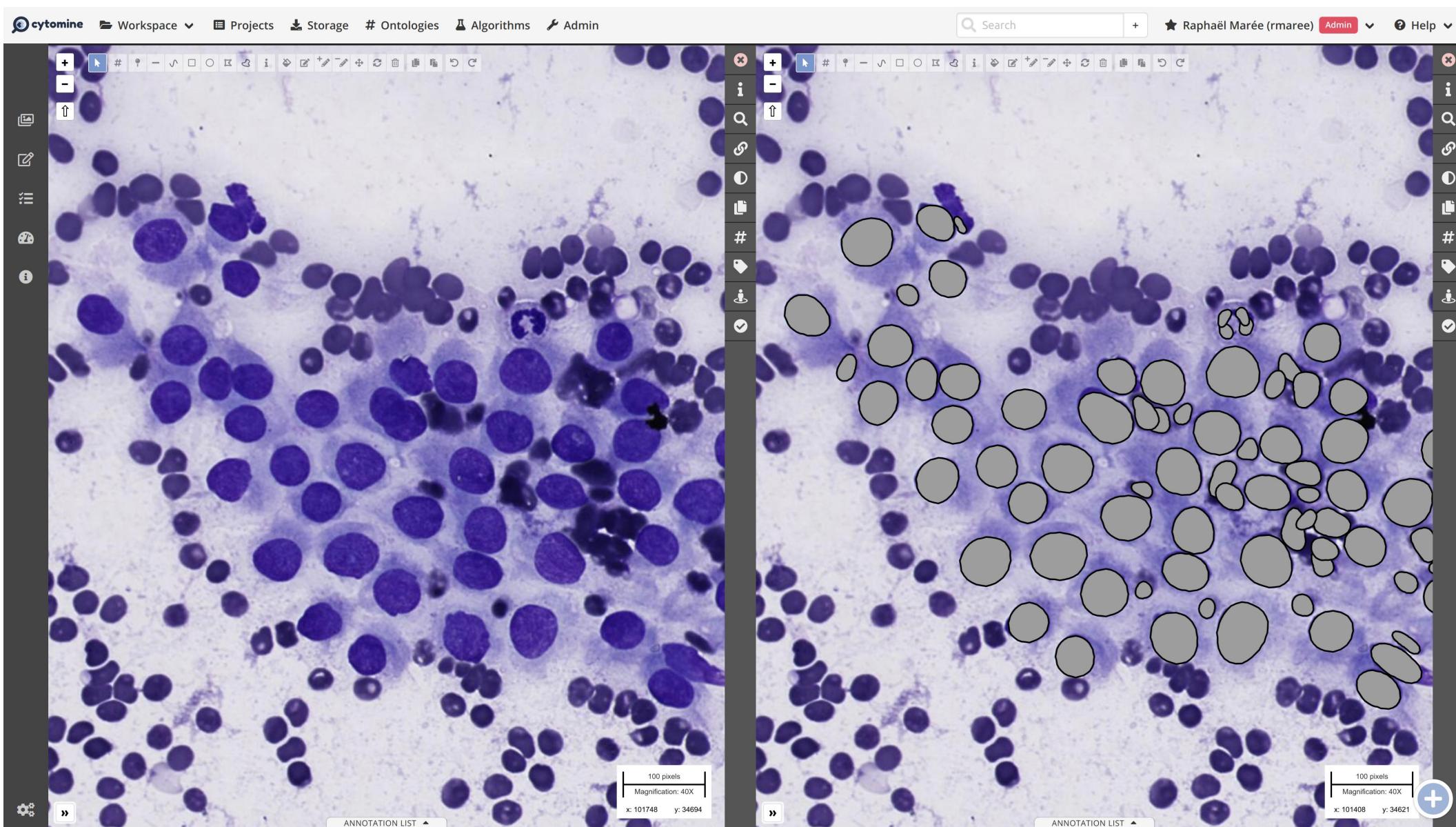
An example of the potential benefits of an open science « sharing » approach



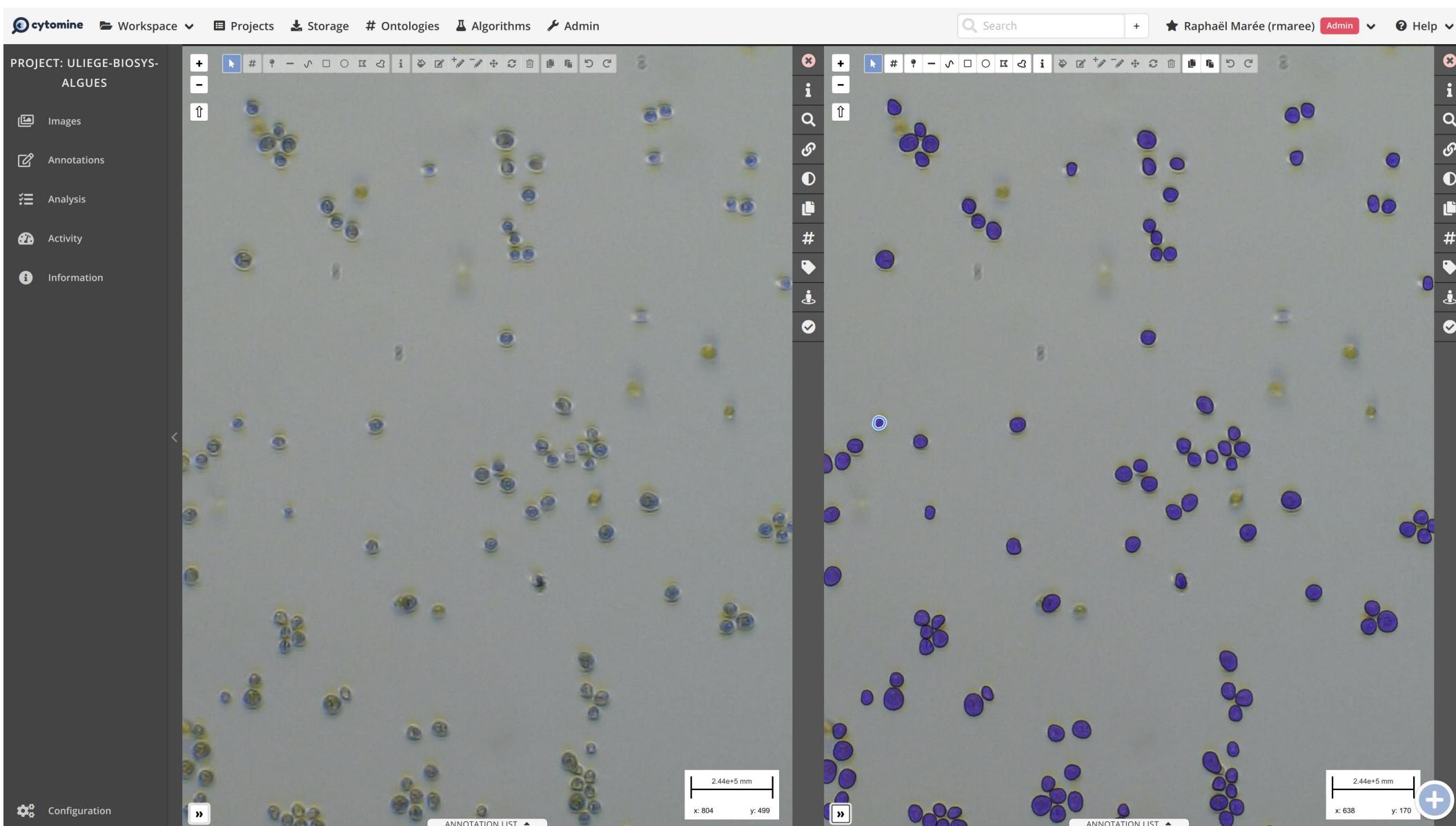
An example of the potential benefits of an open science « sharing » approach



An example of the potential benefits of an open science « sharing » approach



An example of the potential benefits of an open science « sharing » approach



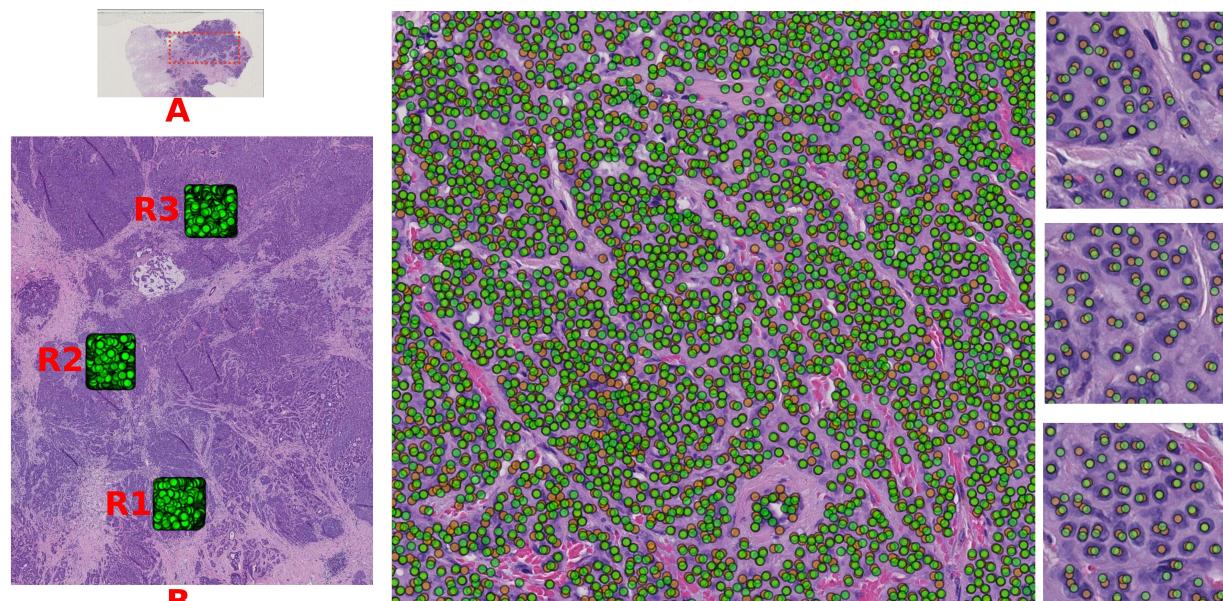
Qualitative vs Quantitative evaluation

Choosing an algorithm (e.g. for cell segmentation) only by **visual examination** of its predictions on a small subset of images is **unsafe** : no algorithm is perfect, bias, image variations and artefacts, ...

Ideally, **benchmarking** (quantitative evaluation) should drive image analysis method choice :

- Preselects methods that have good results on « similar », large datasets
- Evaluate quantitatively and tune methods on your own images + ground truths, proofread results

(ongoing empirical
evaluation on >500K nuclei)





Examples and applications

2. Landmark detection

uliege.cytomine.org

Morphometric description of head cartilage and bone skeleton in Zebrafish

> 900 images, manual positioning of > 25000 landmarks
Export of statistics (distances, angles)

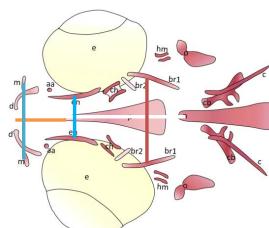
Distance between:	Vit D3	PTH
angulo articular up and angulo articular down	=	N D
anterior and notochord	++	=
anterior and parasphenoid a	++	+++
branchiostegal ray1 up and branchiostegal ray1 down	=	+++
entopterygoid up and entopterygoid down	=	+++
maxilla up and maxilla down	+++	N D
opercul up and opercul down	=	=
triangle area (parasphenoid a-b-c)	=	---

Treatments with VitD3:

Head longer (orange and white)
Maxillary wider (green-blue)

Treatments with PTH:

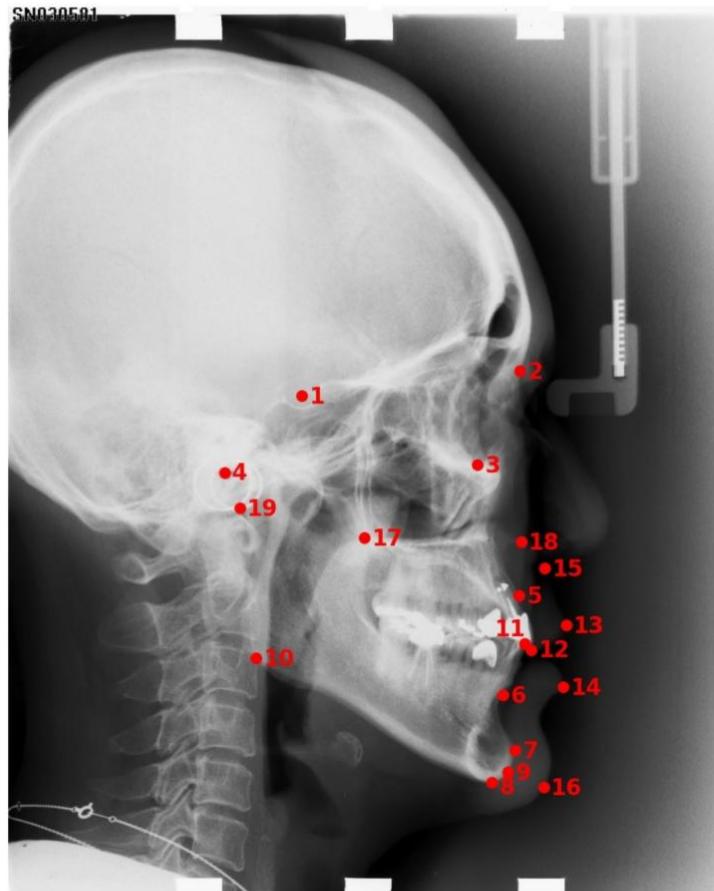
Missing structures => ND
Increased distance between entopterygoids (blue) and branchiostegals (red)
Decrease of parasphenoid (triangle)



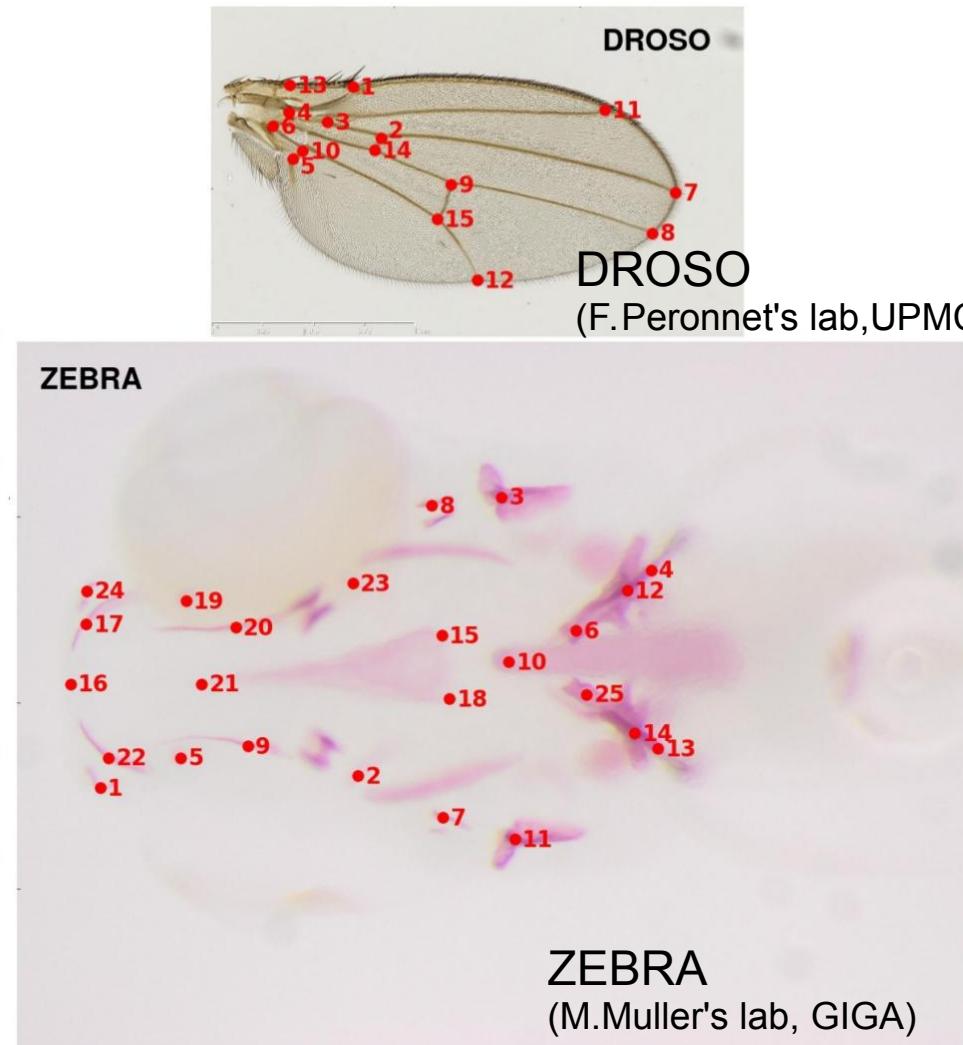
Gravitational effects on zebrafish bone and general physiology are revealed by hypergravity studies

Jessica Aceto, Rasoul Nourizadeh-Lillabadi, Raphaël Marée, Nathalie Jeanray, Louis Wehenkel, Peter Alestrom, Jack van Loon, Marc Muller. *PLOS ONE*, 2015

Towards automated landmark detection



CEPHA
(C-T Huang's lab, NTUST)

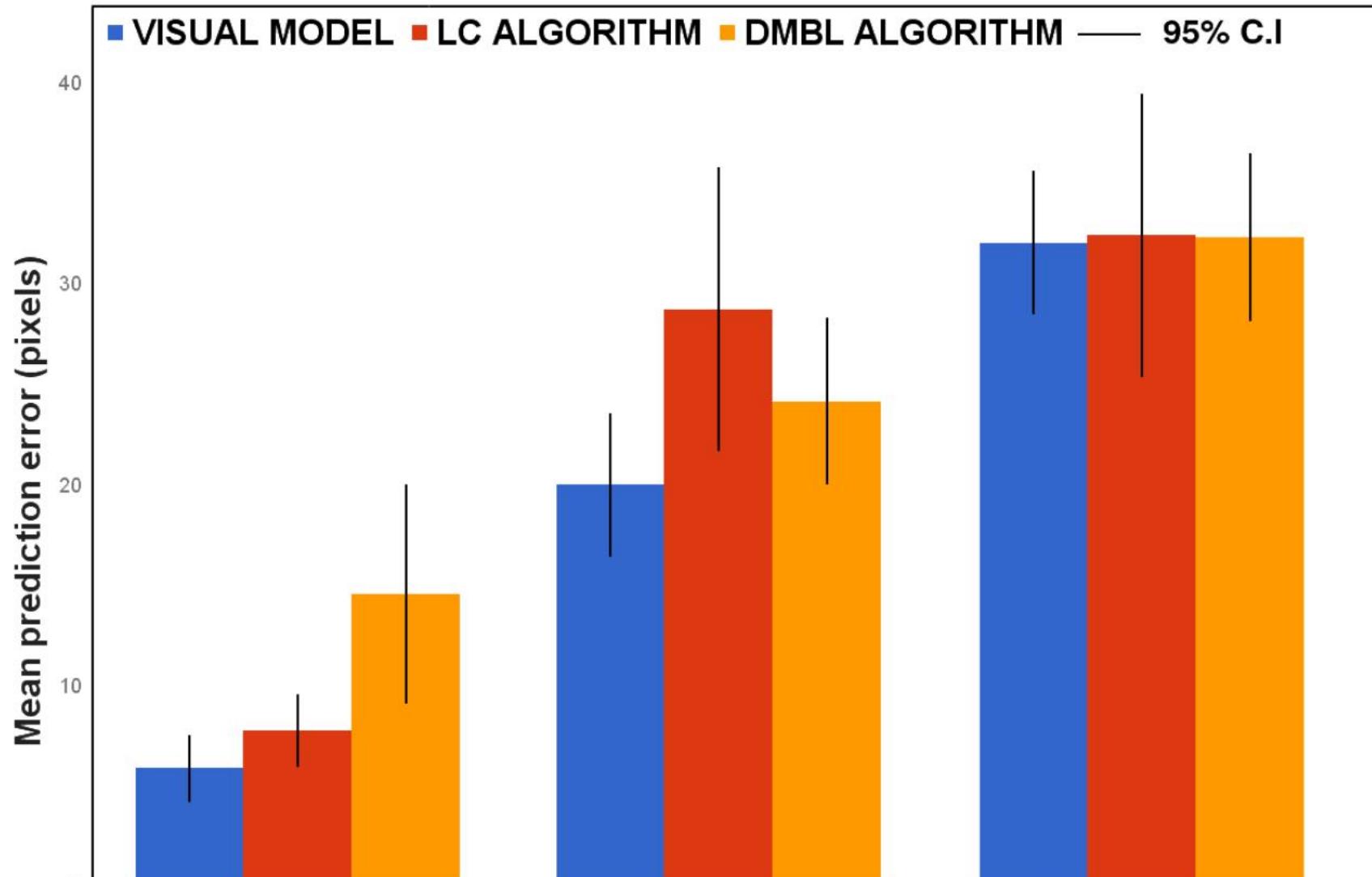


ZEBRA
(M.Muller's lab, GIGA)

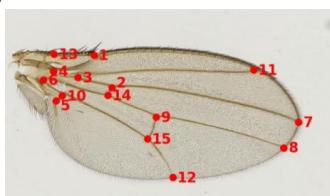
Dataset	# images	# landmarks	Size
DROSO	138	15	900×1440
CEPHA	100	19	2400×1900
ZEBRA	113	25	1972×2536

Vandaele et al.,
Scientific Reports, 2018

Comparing algorithm predictions with humans

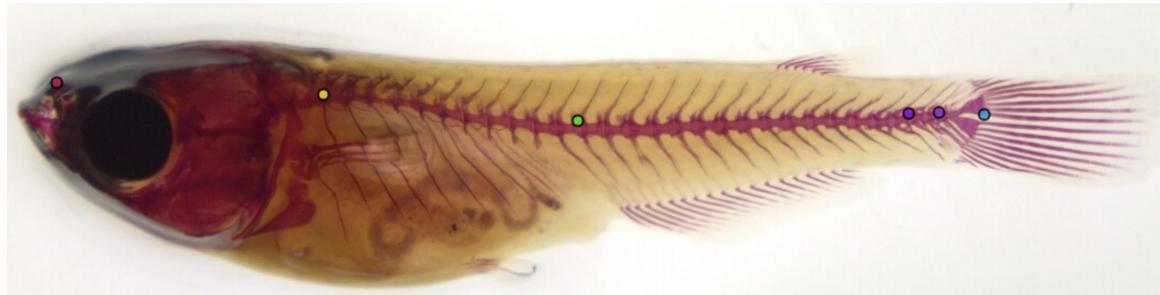


Vandaele et al.,
Scientific Reports, 2018



.... to be continued (Navdeep)

- Improve localization accuracy with novel deep learning approaches on previous and newly acquired datasets



Claudia @ LESA

- Improve user interfaces for more efficient proofreading hence fasten studies

A screenshot of the Cytomine software interface. The main view shows a detailed image of a fly wing with several green and red circular landmarks placed on specific features. On the left, there are several panels: 'CURRENT SELECTION' showing annotation details like area and perimeter; 'ANNOTATION PREVIEW' showing a zoomed-in view of the wing with a red crosshair; 'SIMILARITIES' suggesting a 'Suggested term'; and a bottom row of thumbnail images labeled 'Annotation'. On the right, there are various toolbars and panels for 'OVERVIEW', 'INFORMATIONS', 'POSITION', 'ONTOLOGY', 'REVIEW | LAYERS', 'REVIEW | ACTION SELECTION', 'REVIEW | ACTION IMAGE', 'JOBS TEMPLATE', 'MULTIDIMENSION', and 'ANNOTATIONS PROPERTIES'. The top navigation bar includes 'Cytomine', 'Dashboard', 'Projects', 'Explore', 'Storage', 'Activity', and user information.

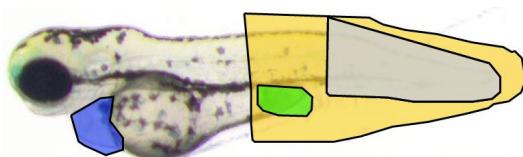


Examples and applications

3. Phenotype classification

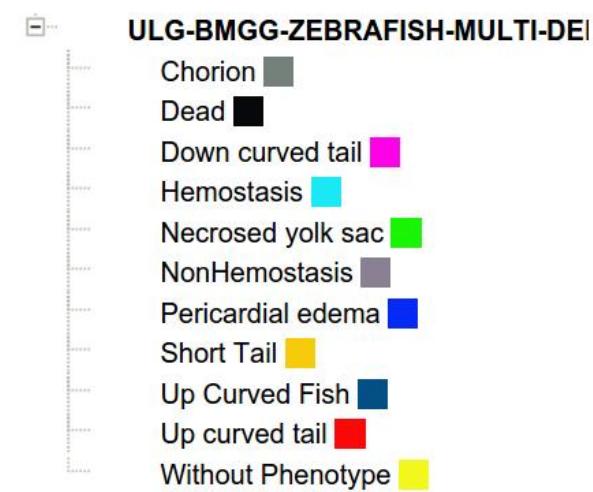
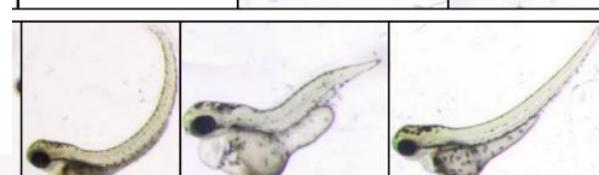
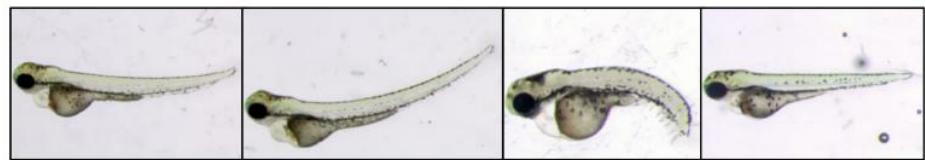
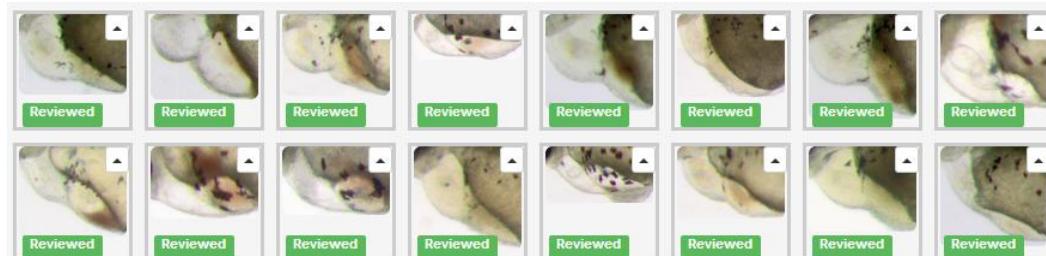
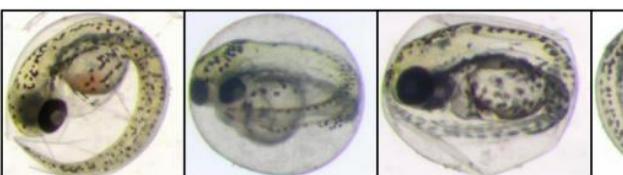
uliege.cytomine.org

Zebrafish embryo phenotype recognition

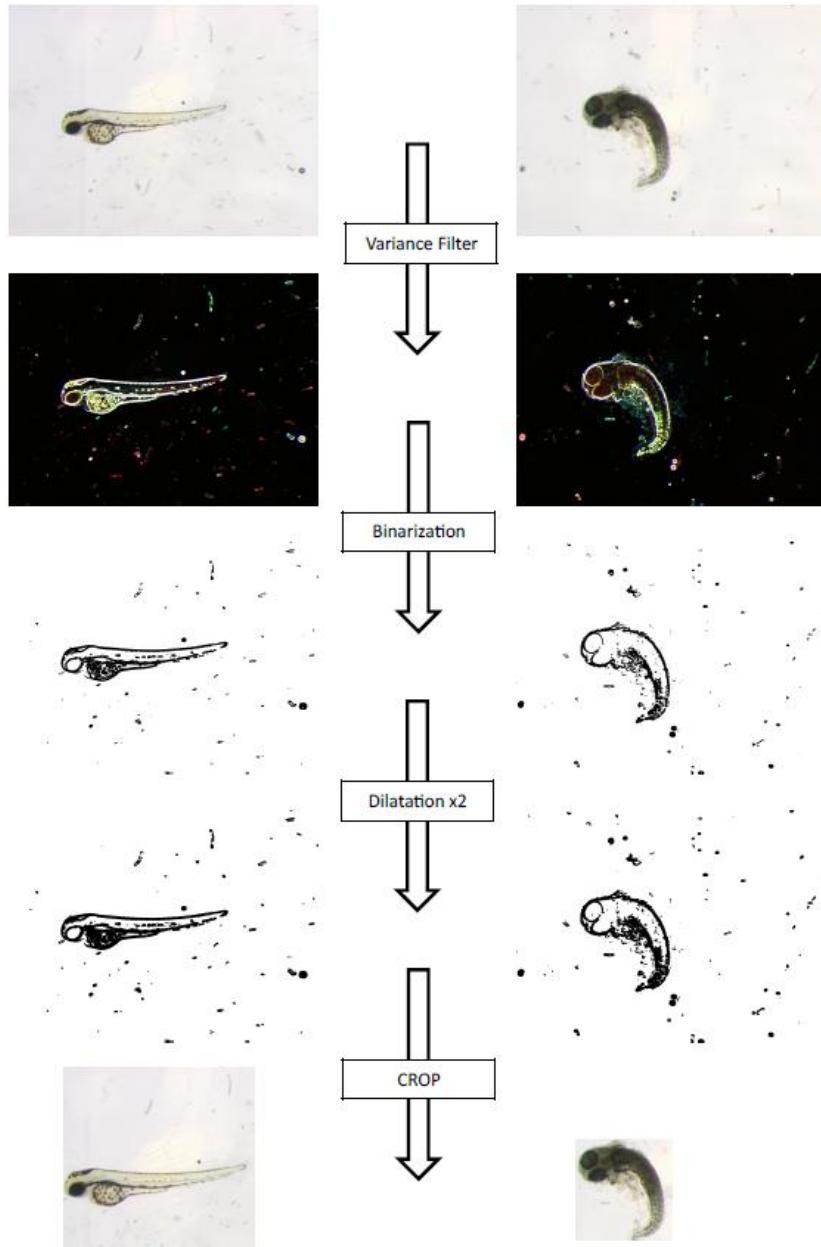


Training :

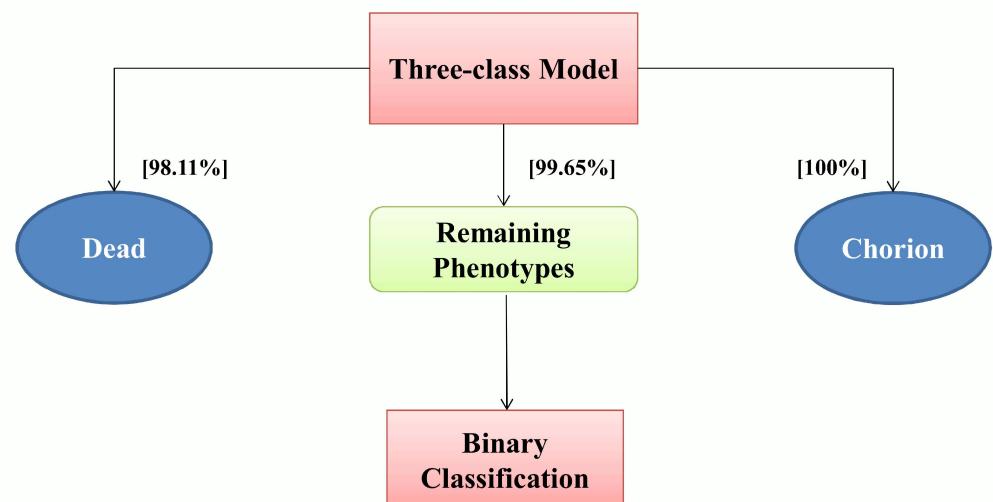
Expert's manual annotations using CYTOMINE
3 experts (consensus voting)
870 annotated training images, 11 phenotypes



Zebrafish embryo phenotype recognition



Two-tier classification



Phenotype	Rate
Chorion	100%
Dead	99.47%
Down Curved Tail	89.82%
Necrosed Yolk Sac	89.94%
Pericardial Edema	74.42%
Short Tail	89.74%
Up Curved Fish	99.26%
Up Curved Tail	84.85%
Up Curved Tail/Fish	89.50%
Hemostasis	52.58%
Without Phenotype	91.18%

1191 validation images



Examples and applications

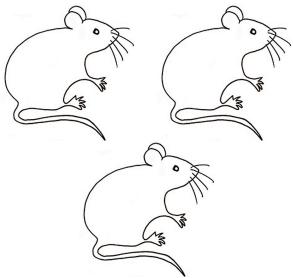
4. Tissue segmentation

uliege.cytomine.org

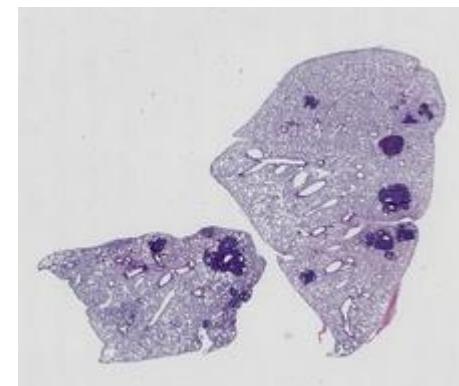
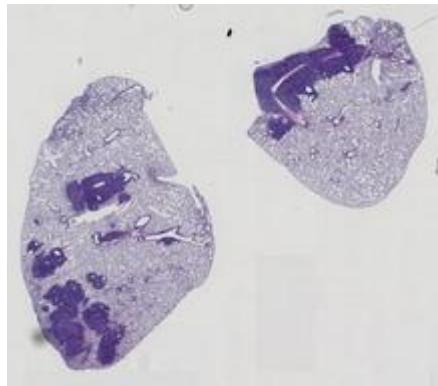
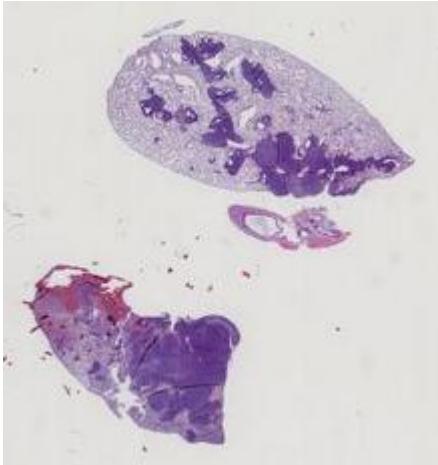
LUNG tumor tissue quantification

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

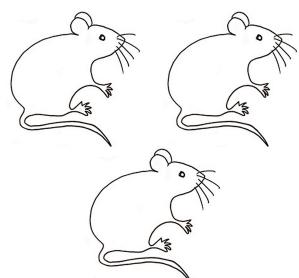
What is the impact of condition X/Y/... on lung tumor onset and progression ?
(measurements : ratio tumor area / lung area)



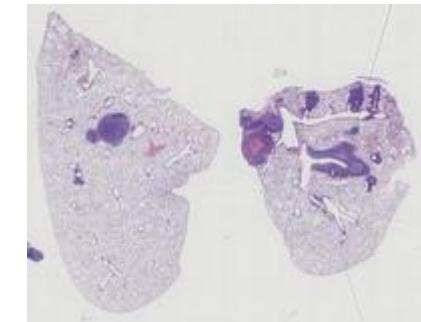
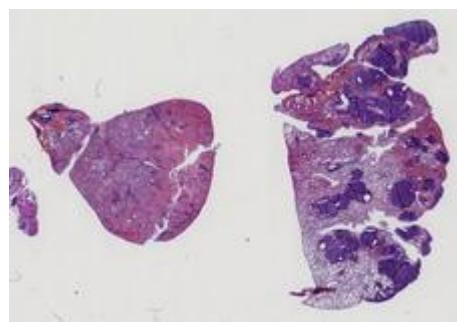
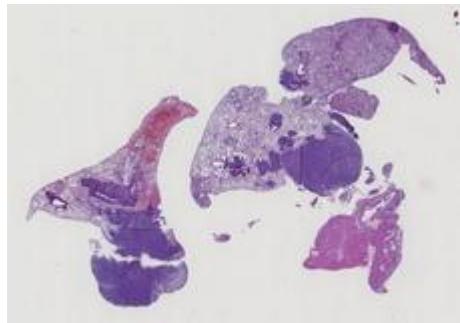
Condition X



...



Condition Y

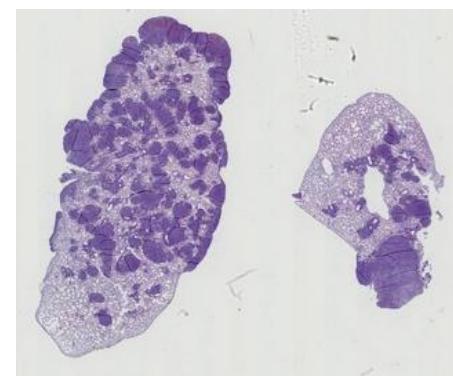
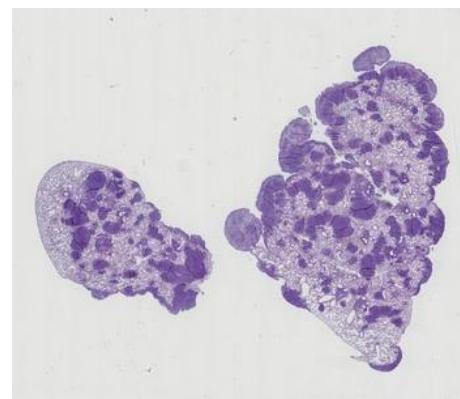
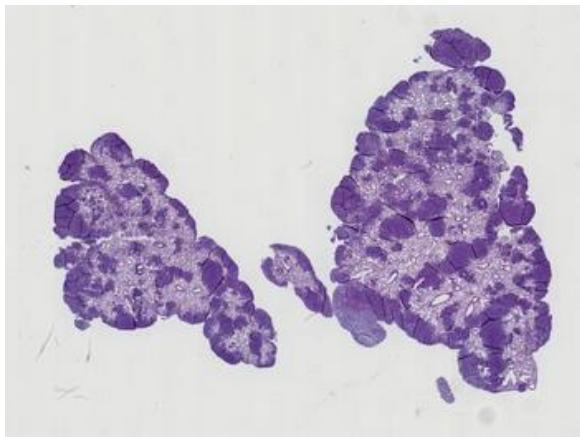


...

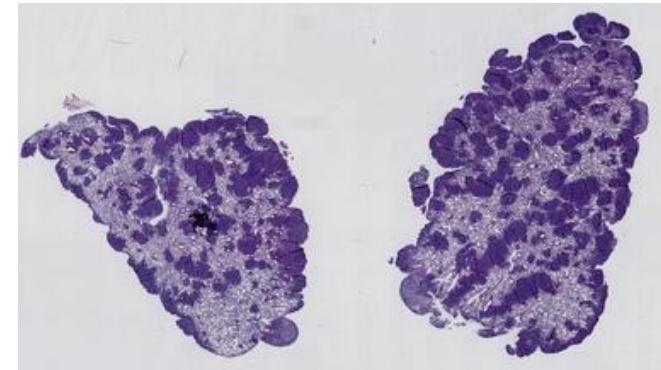
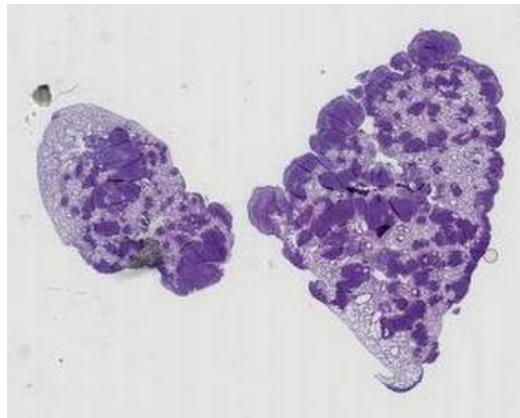
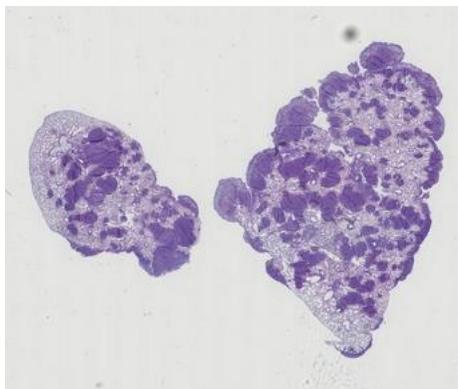
(H&E-stained histological lung sections, one image ~ 40K x 30K pixels, 0.23µm/pixel)

:

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

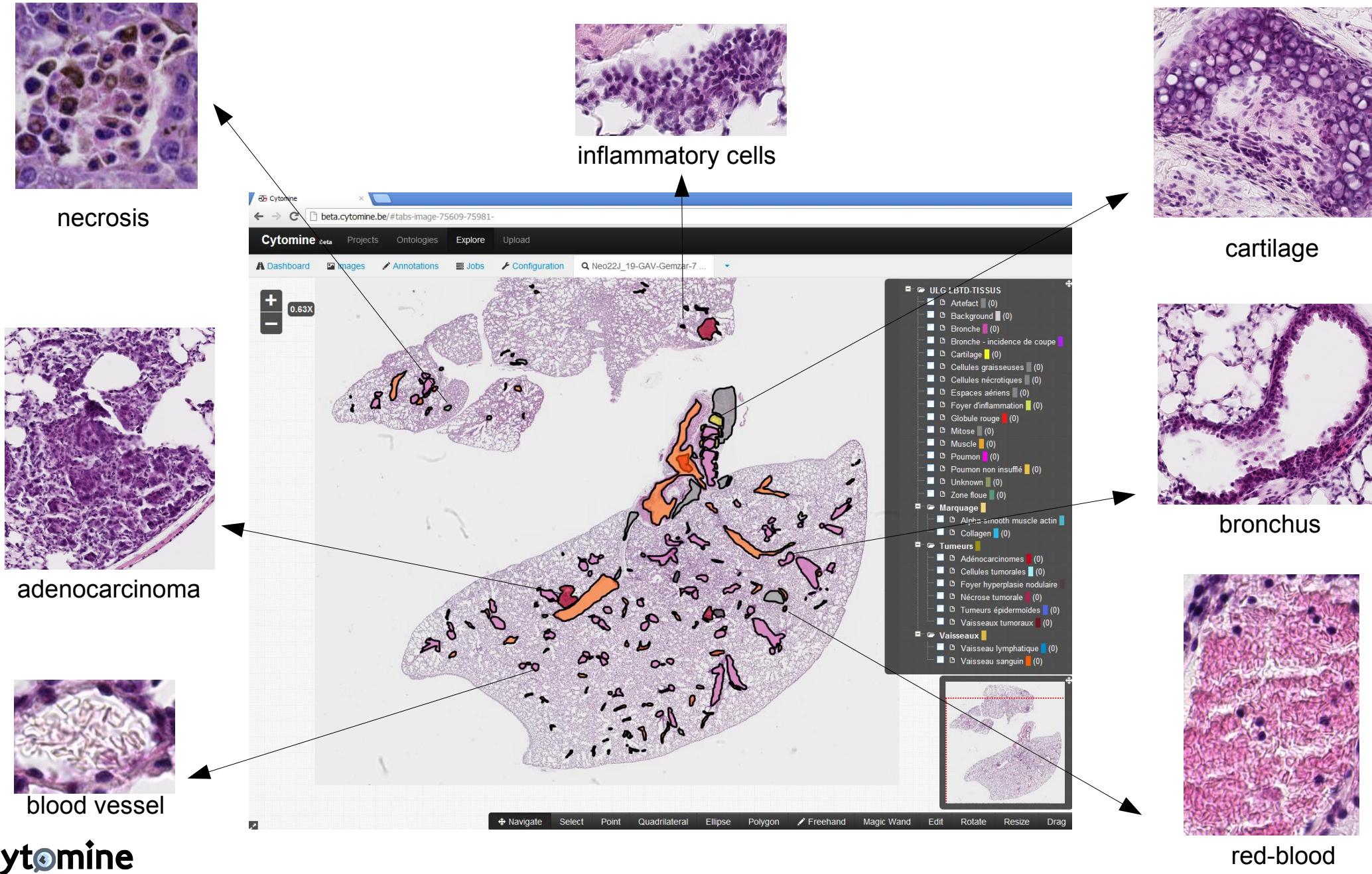


...



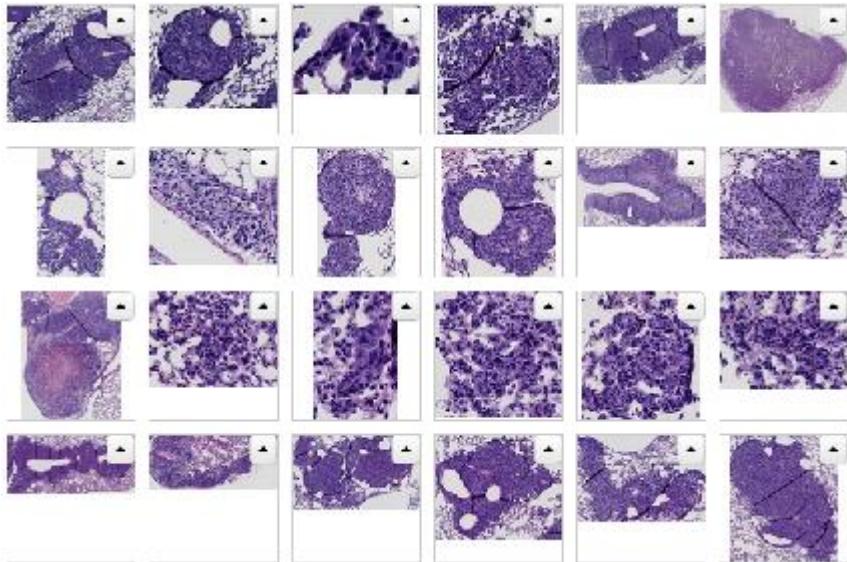
Hybrid human-computer workflow

1. Manual region contouring and labelling to provide training examples



Hybrid human-computer workflow

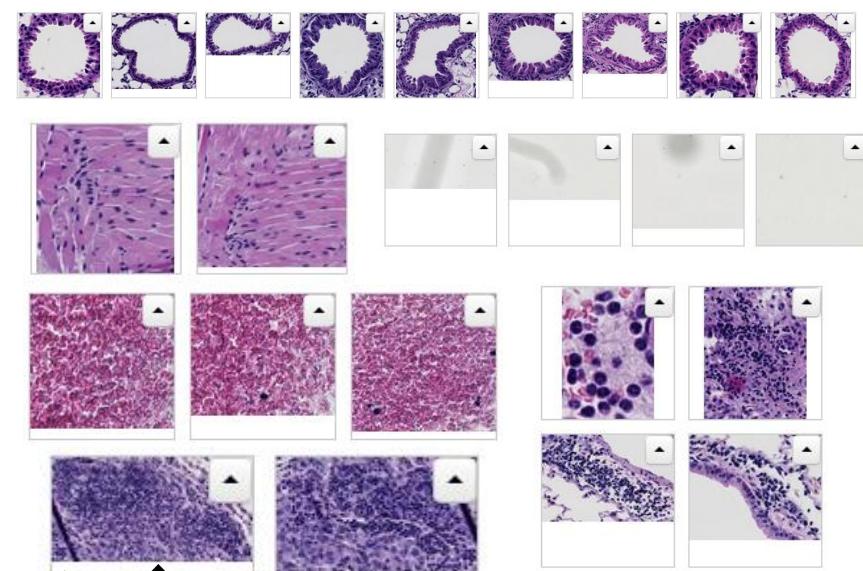
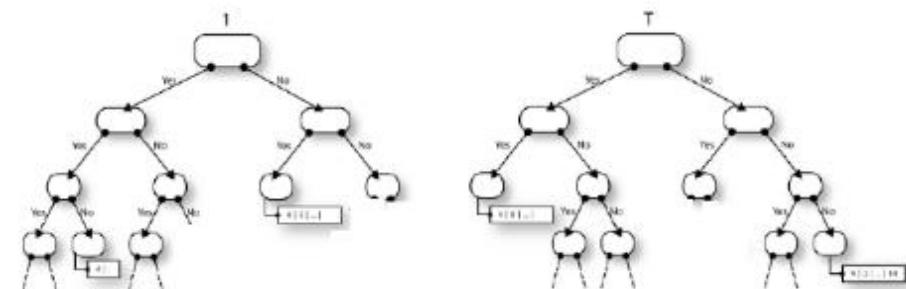
2. Automatic training of image recognition model based on training examples



VS



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

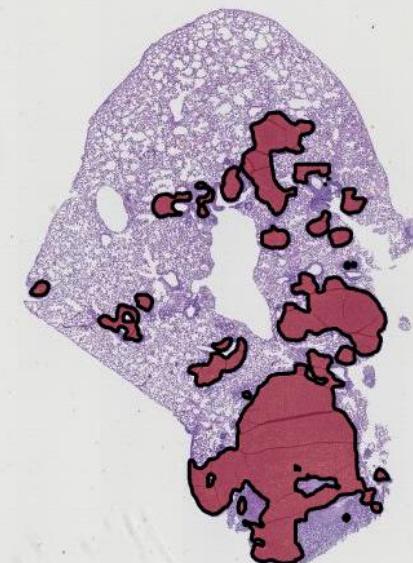
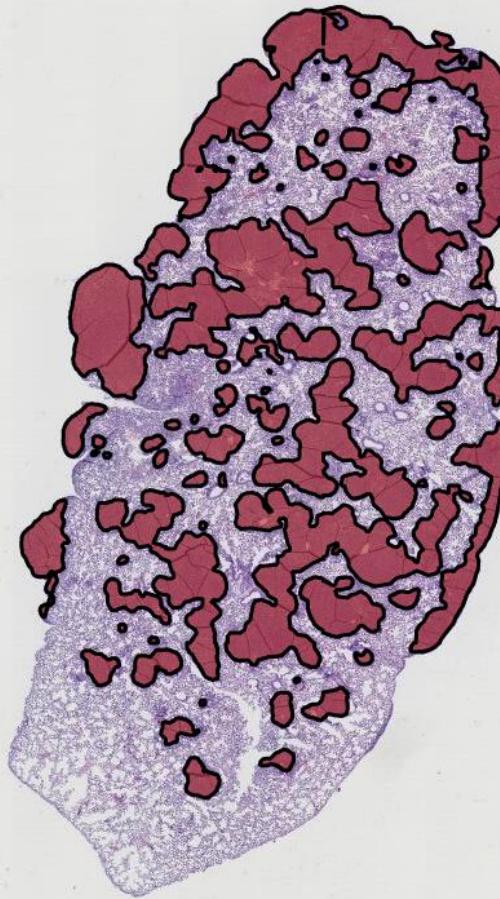
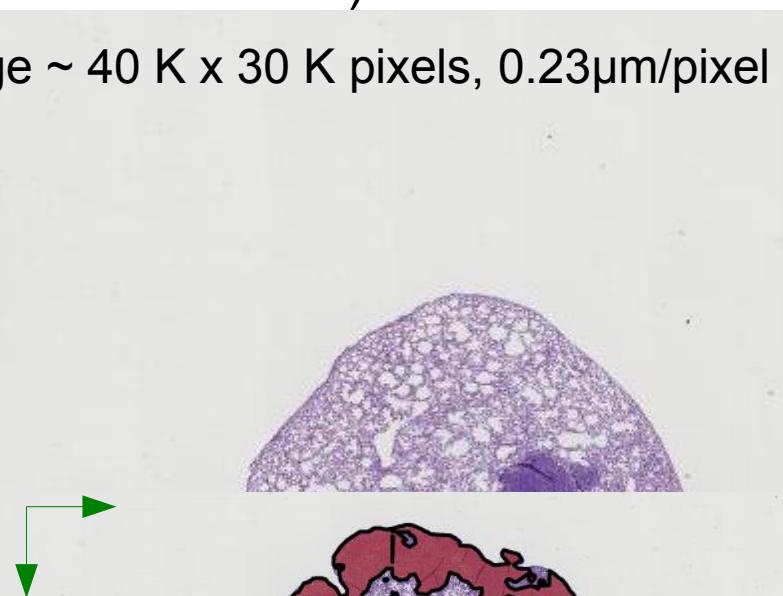


A hybrid human-computer approach for large-scale image-based measurements using web services and machine learning,
Marée et al. Proc. IEEE ISBI, 2014

Hybrid human-computer workflow

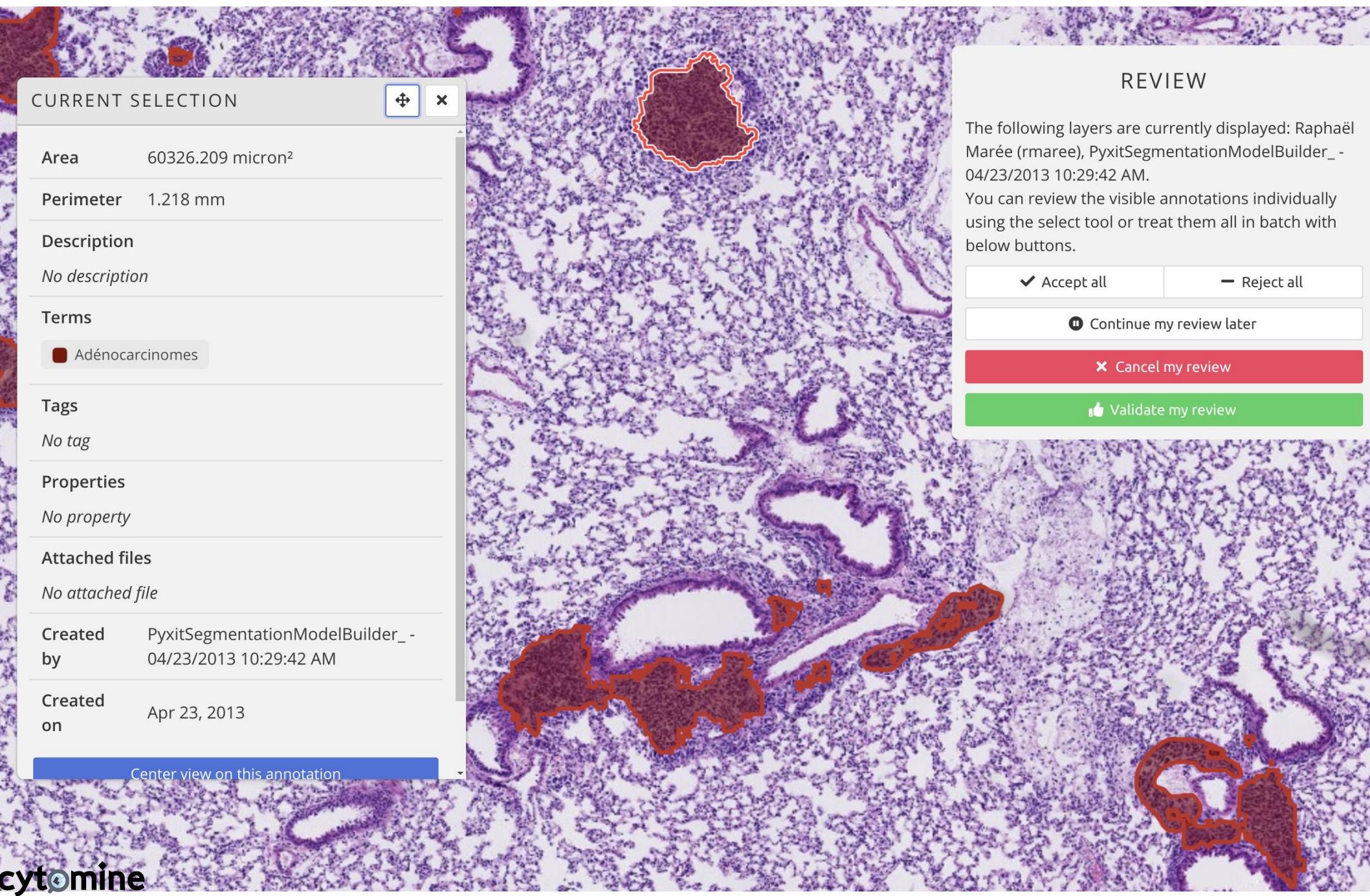
3. Automatic segmentation (pixel classification) of tumors in new images

One image ~ 40 K x 30 K pixels, 0.23 μ m/pixel



Hybrid human-computer workflow

4. Proofreading automatic segmentations (corrections are stored in database)



The image shows a digital pathology slide with a purple-stained tissue background. Several regions are highlighted with red, irregularly shaped polygons, representing automated segmentation results. A large rectangular selection box is visible at the top left.

CURRENT SELECTION

Area 60326.209 micron²

Perimeter 1.218 mm

Description

No description

Terms

Adénocarcinomes

Tags

No tag

Properties

No property

Attached files

No attached file

Created by PyxitSegmentationModelBuilder_- 04/23/2013 10:29:42 AM

Created on Apr 23, 2013

[Center view on this annotation](#)

REVIEW

The following layers are currently displayed: Raphaël Marée (rmaree), PyxitSegmentationModelBuilder_- 04/23/2013 10:29:42 AM.

You can review the visible annotations individually using the select tool or treat them all in batch with below buttons.

Accept all

Reject all

Continue my review later

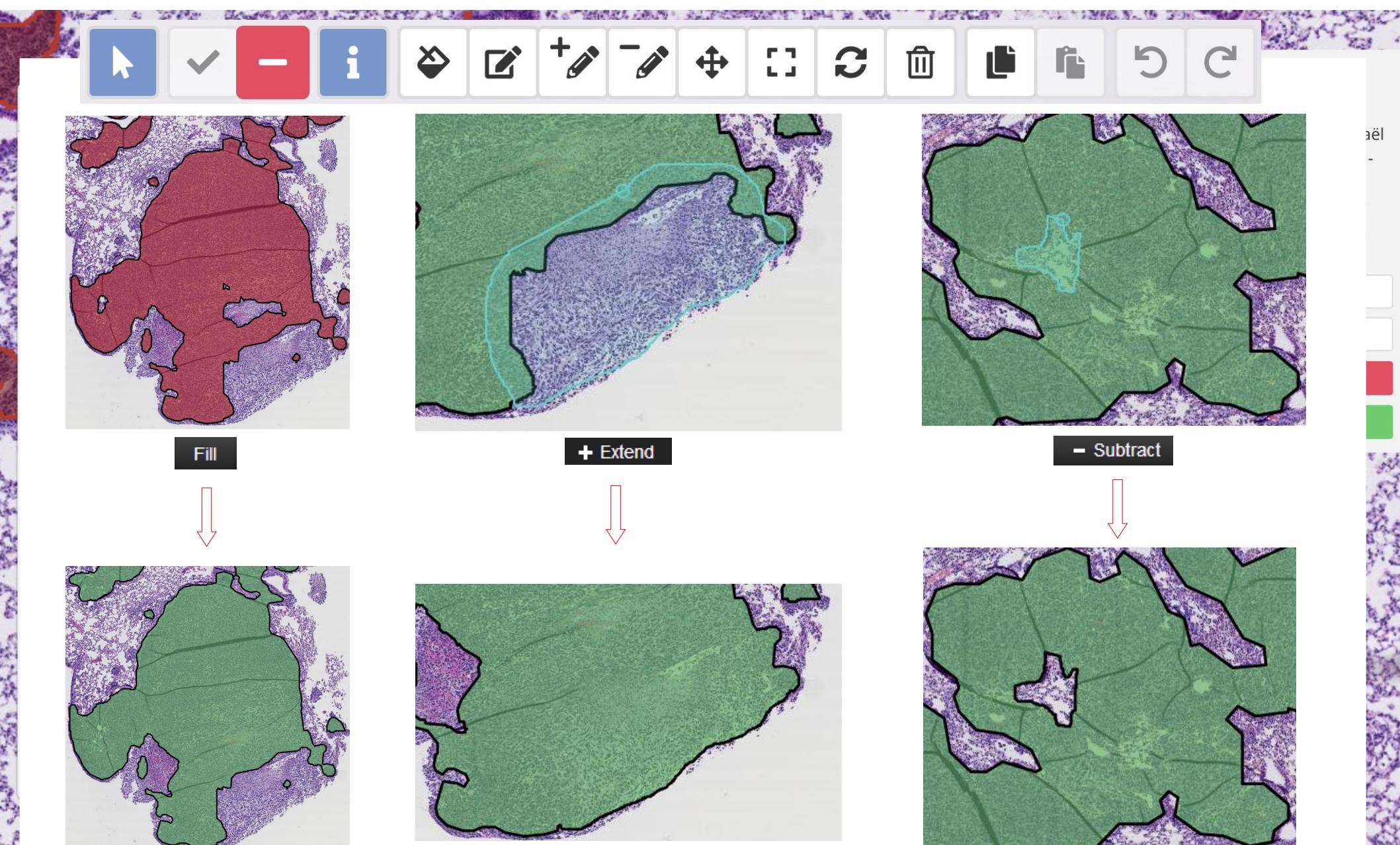
Cancel my review

Validate my review

cytominE

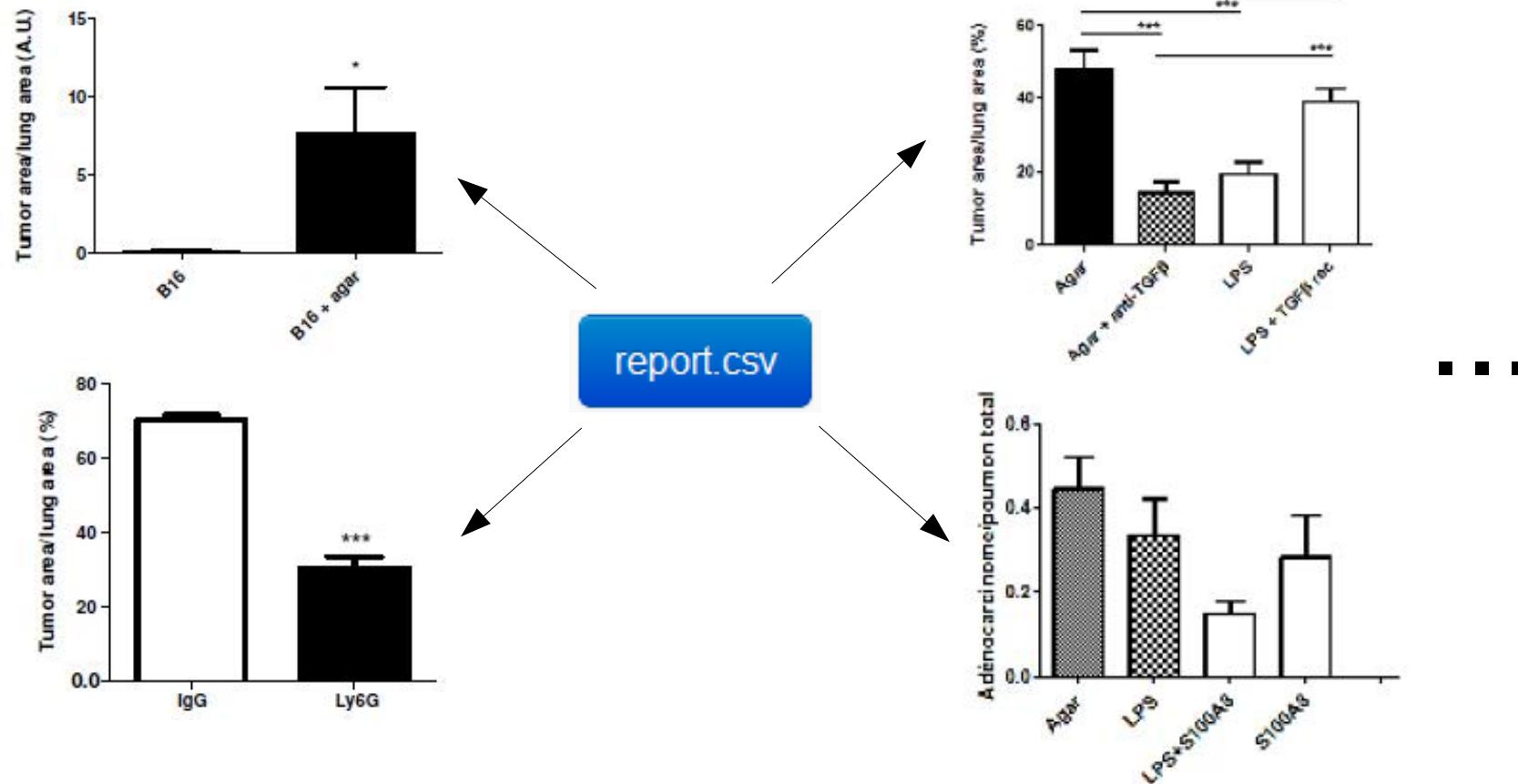
Hybrid human-computer workflow

4. Proofreading automatic segmentations (corrections are stored in database)



Hybrid human-computer workflow

... new (faster) biomedical insights in lung tumor onset and progression...

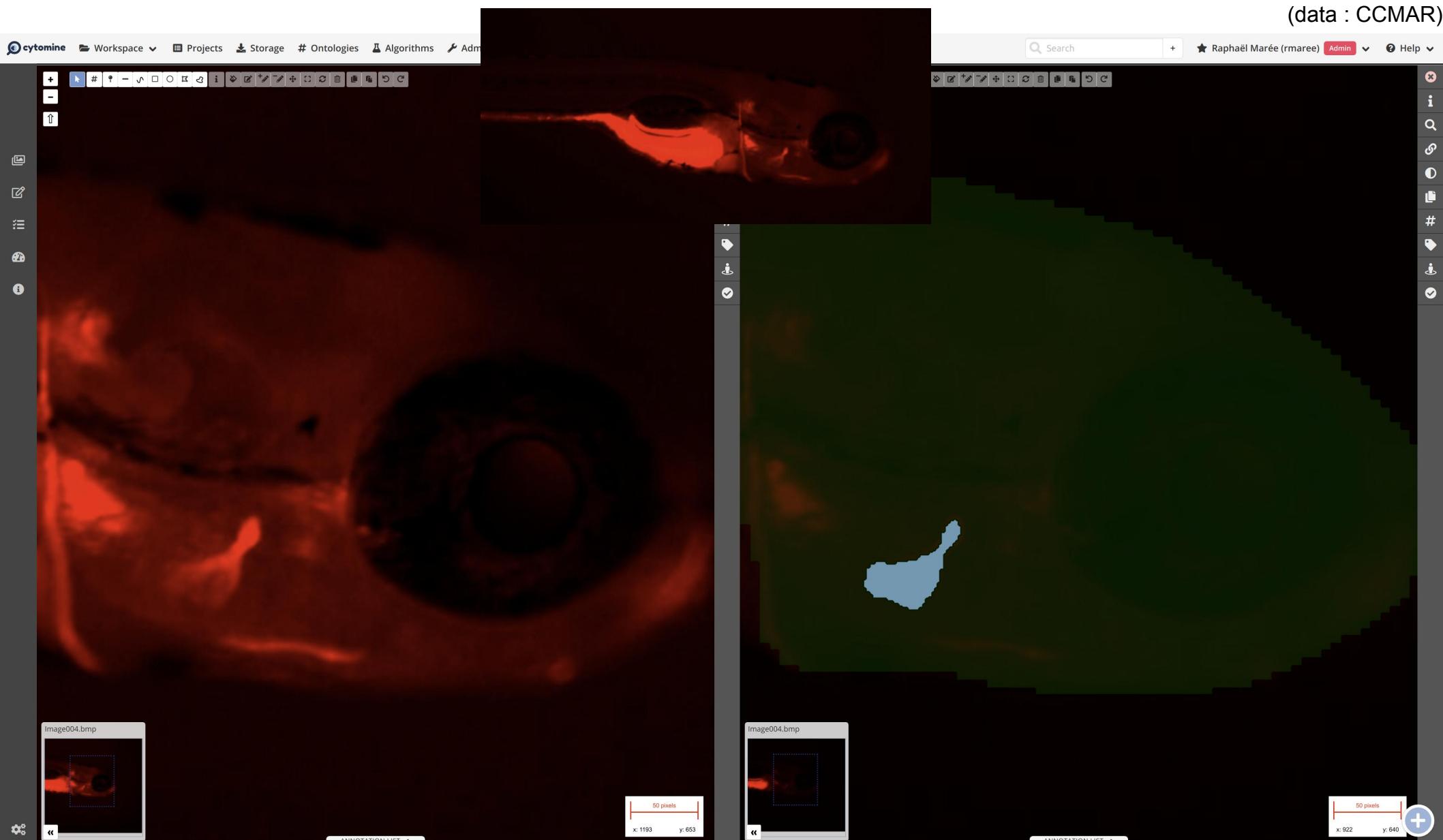


> 1500 whole-slide images analyzed with > 50 000 validated tumoral islets (proofreading)

(Bekaert et al., Cancer Growth and Metastasis, 2017 ; Rocks et al., Thorax, 2019)

Automated head/operculum segmentation

Training head/operculum deep learning models from expert's annotations (imported)



(Live demo today at 3.30 PM)

(Kumar et al., Submitted)

Automated head/operculum segmentation

Training head/operculum deep learning models from expert's annotations (imported)

The screenshot shows the Cytomine software interface. On the left, a large fluorescence microscopy image of a fish head is displayed with red staining. A blue button labeled "report.csv" is overlaid on the image. A green arrow points from this button towards a table on the right. On the far left, there is a small inset image labeled "Image004.bmp". At the bottom left, there is an "ANNOTATION LIST" button. At the bottom right, there is another "ANNOTATION LIST" button. The top of the screen has a navigation bar with various icons and the text "cytome". The right side of the screen features a detailed table of annotations:

	A	B	C
1	Total annotation area per image and per term		
2	Image	Operculum	Head
3	Image030.bmp	2200	156135
4	Image015.bmp	2151	189414
5	Image034.bmp	1957	165021
6	Image033.bmp	1200	165705
7	Image031.bmp	2086	170787
8	Image035.bmp	1408	153904
9	Image017.bmp	2217	192100
10	Image025.bmp	2244	178211
11	Image027.bmp	3170	286588
12	Image008.bmp	1215	162091
13	Image007.bmp	1754	161037
14	Image029.bmp	1423	182799
15	Image006.bmp	1210	158340
16	Image032.bmp	1784	161361
17	Image026.bmp	2872	255769
18	Image011.bmp	2021	167056
19	Image014.bmp	1838	180773
20	Image016.bmp	2016	180965
21	Image013.bmp	1520	170154
22	Image012.bmp	1612	144903
23	Image010.bmp	1338	162090
24	Image023.bmp	1170	168653
25	Image009.bmp	1482	155890
26	Image028.bmp	2261	171252
27	Image036.bmp	2250	169930
28	Image022.bmp	1802	184578
29	Image005.bmp	2190	174425
30	Image024.bmp	1733	175343
31	Image020.bmp	1837	189214
32	Image004.bmp	2066	168014

(Live demo today at 3.30 PM)

(Kumar et al., Submitted)

Summary

- Sharing images, annotations, algorithms and results could improve both biomedicine/aquaculture research (more quantitative results) and computer science research (more generic, accurate algorithms)
- We illustrated several AI/machine/deep learning algorithms that exploit expert's annotations to speedup quantitative studies



- Cytomine open-source tool eases open science and enables reproducibility on the web

- + demo today at 3.30 PM
- + G.Vincke cooperative talk on Monday

Acknowledgments

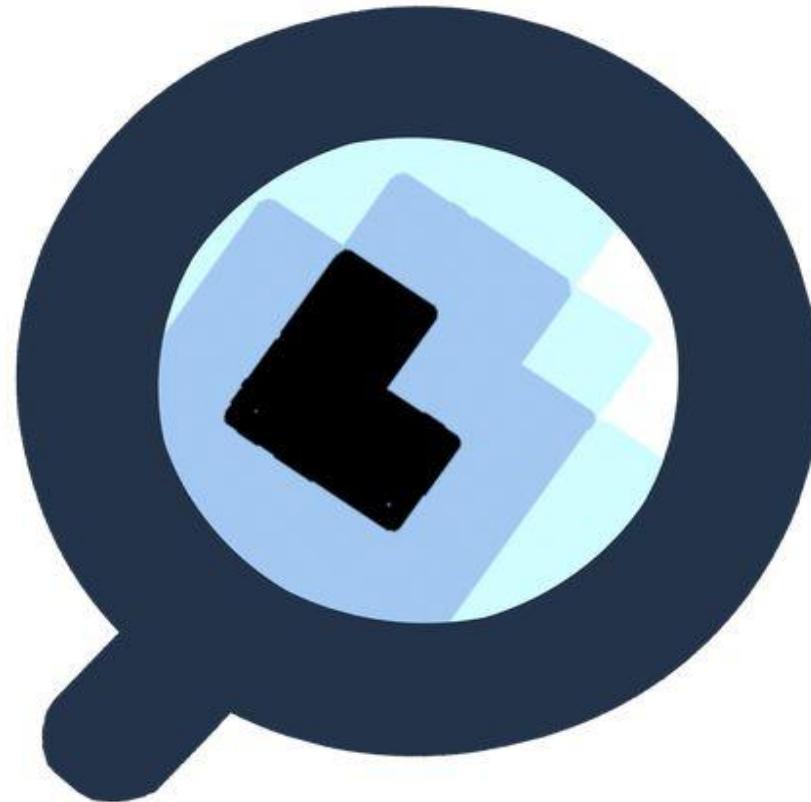
ULiège & Cytomine.coop : Ulysse Rubens, Romain Mormont, Navdeep Kumar, Remy Vandaele, Renaud Hoyoux, Grégoire Vincke, Pierre Geurts [cytomine.org]

GIGA : Marc Muller, Sing-E Lee

Neubias and Comulis EU network : Sebastien Tosi, Benjamin Pavie, Volker Backer, Natasa Sladoje [neubias.org & comulis.eu]



Contact Cytomine ULiège R&D team



cytomine



@cytome_uliege



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



uliege.cytomine.org
doc.uliege.cytomine.org



uliege@cytomine.org

Raphael.Maree@uliege.be