

Development of software tools to foster collaboration with open source & open data:

Cytomine (image analysis) [2010-...]
&
Shareish (citizen mutual aid) [2021-...]

ULiège Open Science Day
27th October 2023

Raphael.Maree@uliege.be

PhD in Computer Science

Senior researcher @ Montefiore Institute, University of Liège

<https://people.montefiore.uliege.be/maree/>

<https://uliege.cytomine.org/> <https://shareish.org/>



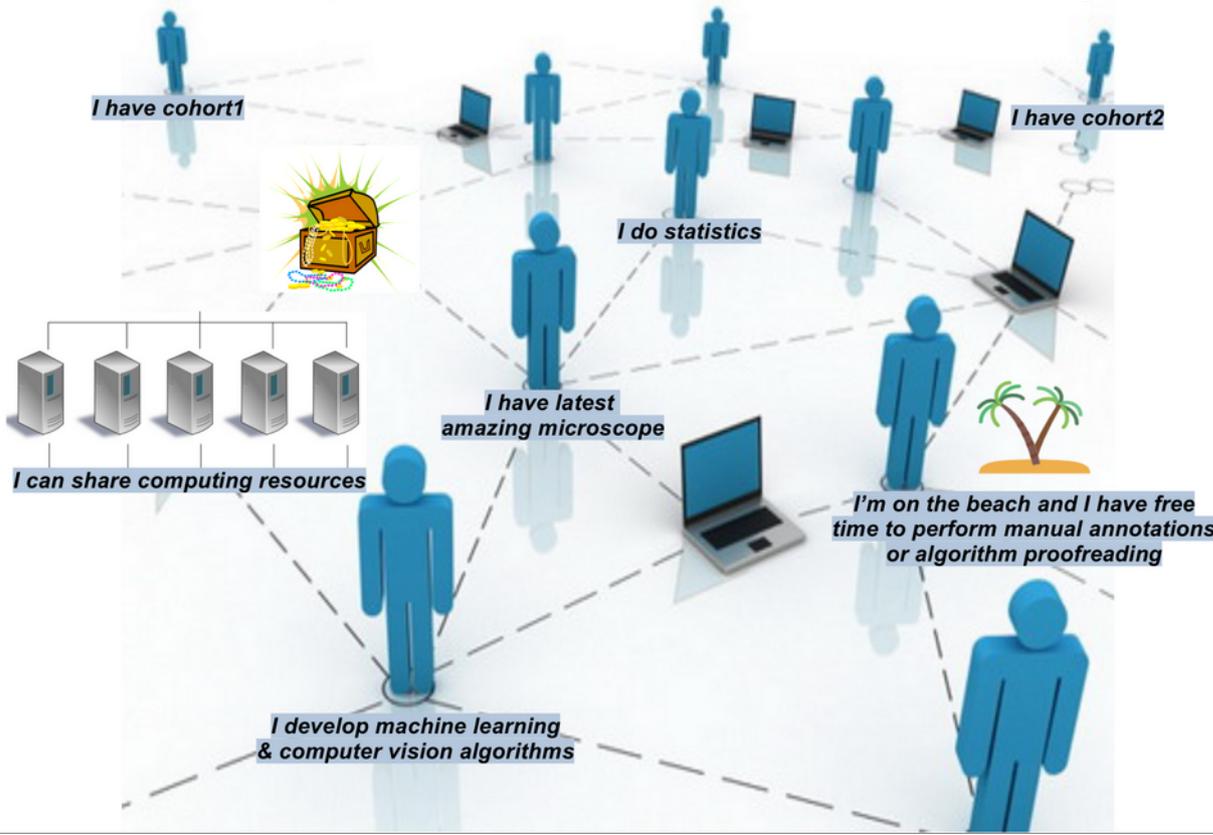
Collaboration tools (Computer-Supported Cooperative Work)

« [...] The goal of CSCW is to help promote and utilize technology in a collaborative way, and help create new tools to succeed in that goal. » (Wikipedia)

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Cytomine for collaborative image-based (biomedical) research



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Cytomine for collaborative image-based (biomedical) research

I have cohort1

I have cohort2

I do statistics

I have latest amazing microscope

I can share computing resources

I develop machine learning & computer vision algorithms

CURRENT SELECTION

Area	156096.850 micron ²
Perimeter	2.009 mm
Description	A nice one.
Terms	Bronche
Tags	No tag
Properties	Intensity 0, Circularity 0.7
Attached files	No attached file

ANNOTATION LAYERS

<input checked="" type="checkbox"/>	Natacha Rocks (nricks) (238)
<input checked="" type="checkbox"/>	Raphaël Marée (rmaree) (18)
<input checked="" type="checkbox"/>	Loïc Rollus (lrollus) (19)
<input type="checkbox"/>	Christine Fink (cfink) (0)

TERMS

<input checked="" type="checkbox"/>	Marquage
<input checked="" type="checkbox"/>	Alpha-smooth
<input checked="" type="checkbox"/>	muscle actin
<input checked="" type="checkbox"/>	Collagen
<input checked="" type="checkbox"/>	Tumeurs
<input checked="" type="checkbox"/>	Adénocarcinomes
<input checked="" type="checkbox"/>	Cellules tumorales
<input checked="" type="checkbox"/>	Foyer hyperplasie

Annotation comments

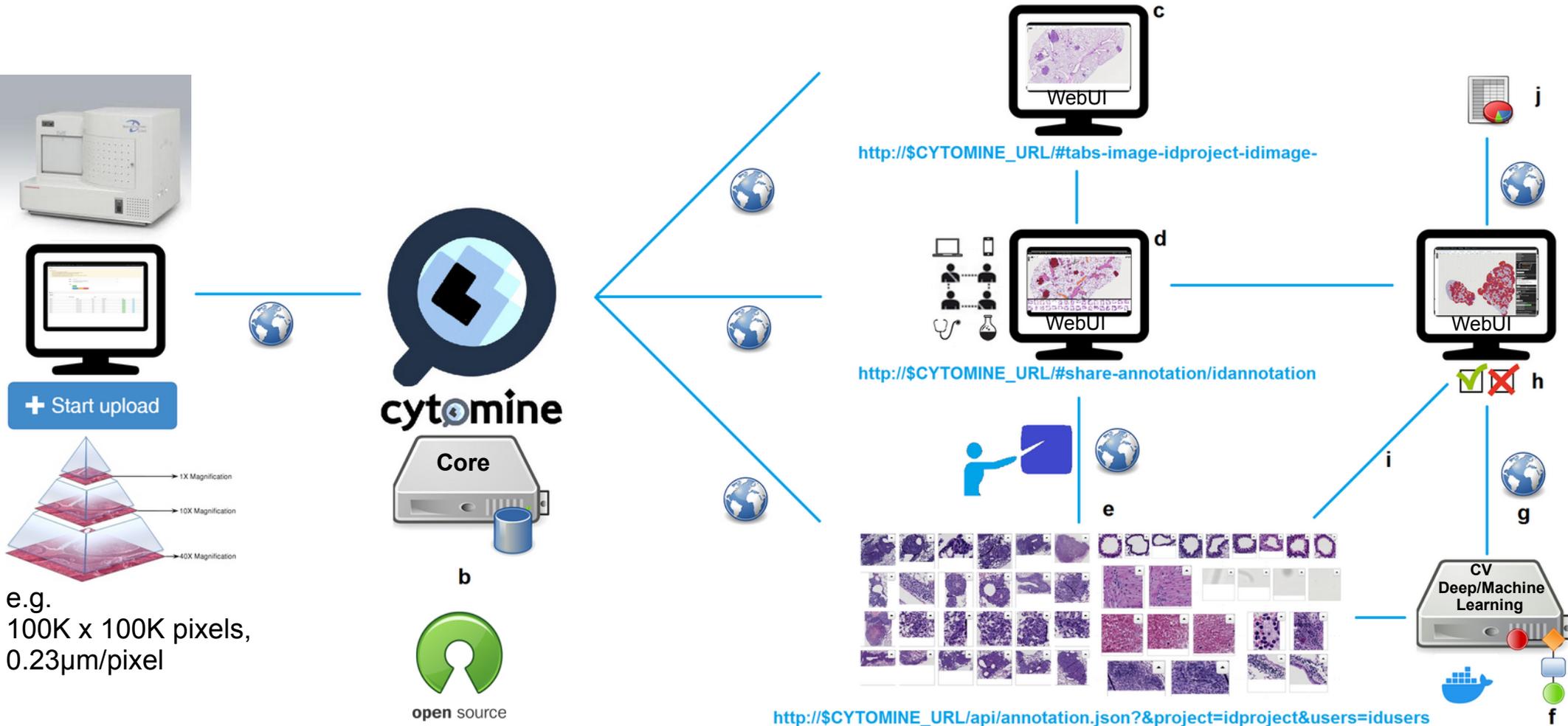
Raphaël Marée Nov 17, 2009 1:52 PM
This is another test comment.2.

Raphaël Marée Nov 17, 2009 1:52 PM
This is a test comment. How are you?

cytomine 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)

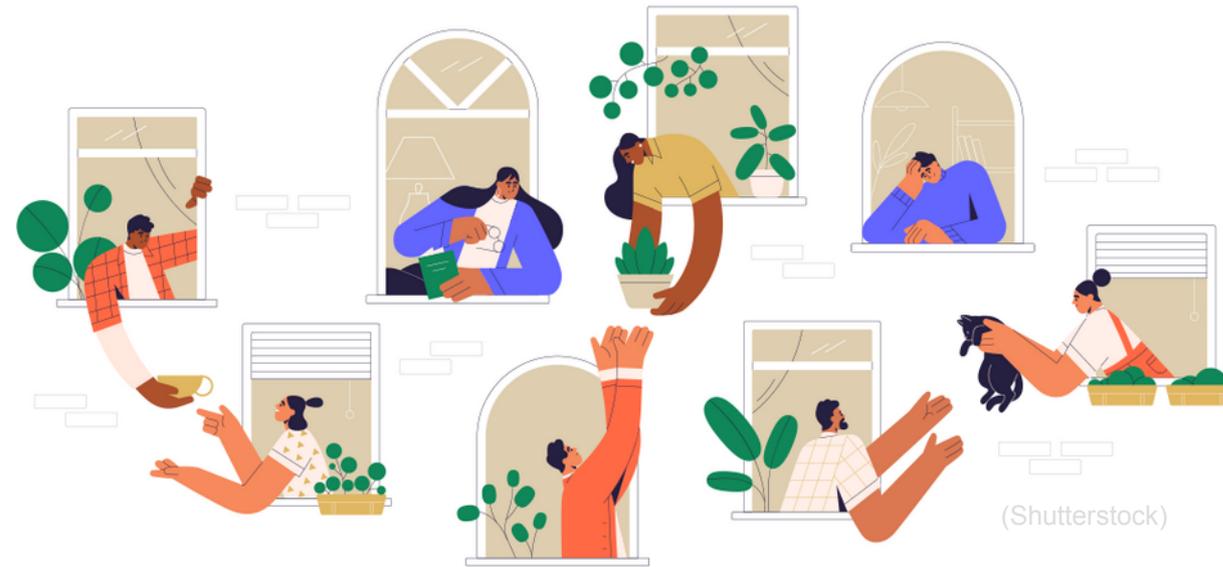


We use `$CYTOMINE_URL = https://research.uliege.cytomine.org/`

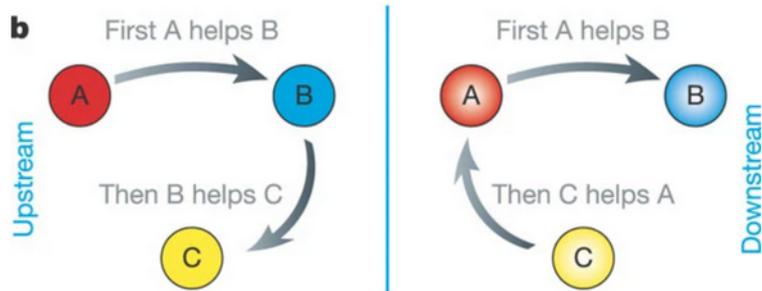
Collaboration tools (Computer-Supported Cooperative Work)

« [...] The goal of CSCW is to help promote and utilize technology in a collaborative way, and help create new tools to succeed in that goal. » (Wikipedia)

Shareish to foster diverse solidarity practices in civil society



(Shutterstock)



[Nowak & Sigmund]

Collaboration tools (Computer-Supported Cooperative Work)

« [...] The goal of CSCW is to help promote and utilize technology in a collaborative way, and help create new tools to succeed in that goal. » (Wikipedia)

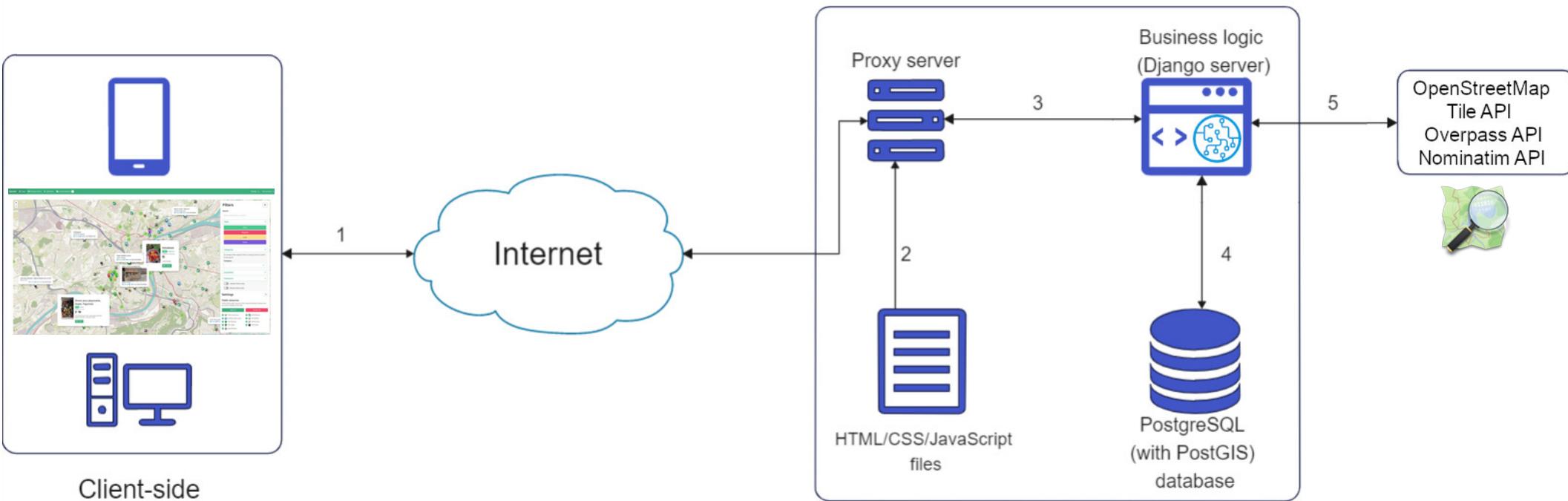
Shareish to foster diverse solidarity practices in civil society

The illustration shows several windows with people engaged in various activities: one person is watering a plant, another is reading, and others are interacting with plants. Below the illustration are two diagrams. Diagram 'b' shows a circular flow of help: A (red) helps B (blue), B helps C (yellow), and C helps A. Diagram 'Nowak' shows a linear flow: A (red) helps B (blue), and then B helps C (yellow).

The screenshot shows the Shareish app interface. It features a map with various markers and pop-up cards for items like 'tomatoes', 'Divers jeux playmobils, Duplo, Figurines', and 'Boîte à livres du Betty Parc'. A 'Filters' panel on the right allows users to search and filter items by type (Offer, Request, Loan, Event), categories, availability, and publication status. The interface also includes a search bar, a map navigation bar, and a settings panel.

Shareish to foster diverse solidarity practices

(non-monetary sharing, mutual aid, network-generalized exchange, gift economy, indirect reciprocity, third party altruism, random acts of kindness, community economy, stooping, gleaning, grafteria/donnerie,...) [Kropotkin; Spade ; Ekeh; Yamagishi and Cook; Lampinen et al. ; Mauss ; Graeber ; Nowak & Sigmund ; Trivers ; Herbert; Bellotti et al. ; Gibson-Graham];



Server-side
<https://shareish.org>



Repair Café Awans
 Repair Café Jeter ? Pas question ! Nos bénévoles vous accueillent à la Maison des Villages d'Awans (Rue Noël Heine,3)....
 Free event by @rm
 Published 12 hours ago
 Available in 2 months
 Ends in 2 months
 At ± 4.76 km
 Do-it-yourself and making
 Helping hands and Manual Labor

Troc de plantes et de graines
 Le jeudi 30 juillet 2023 à partir de 17h
 Free event by @rm
 Published 12 hours ago
 Available in 7 days
 Ends in 7 days
 At ± 4.17 km
 Garden, Nature, and Environment

Glanage haricots verts
 Champ de haricots verts à glâner (raison: surproduction et trop gros calibre pour conserves).
 Chemin du Bois Lasson à Fournes-...
 Gift by @rm
 Published a month ago
 Ends in 12 hours
 At ± 182.84 km
 Food and Supplies
 Garden, Nature, and Environment

Reference address ULiège - Campus de Liège Sart Tilman, Boulevard du Rect

Notification radius (in km) 48

Items	<input checked="" type="checkbox"/> Instantly	<input type="checkbox"/> Daily	<input type="checkbox"/> Weekly	<input type="checkbox"/> Never
Free events	<input checked="" type="checkbox"/> Instantly	<input type="checkbox"/> Daily	<input type="checkbox"/> Weekly	<input type="checkbox"/> Never
Public resources (OSM)	<input checked="" type="checkbox"/> Daily	<input type="checkbox"/> Weekly	<input type="checkbox"/> Monthly	<input type="checkbox"/> Never
Conversations	<input checked="" type="checkbox"/> Instantly	<input type="checkbox"/> Daily	<input type="checkbox"/> Never	
General info	<input checked="" type="checkbox"/> Always	<input type="checkbox"/> Never		

Chatting with Van Anh Hoang-Thu

Repair Café ULiège
 Arbres magiques
 Glanage haricots verts
 Divers jeux playmobils, D...
 Community day LA
 Magazine Grapefruits
 Arbres magiques
 Pommes (Best for demo)

Cytomine & Shareish are



github.com/cytomine-uliege
doc.uliege.cytomine.org/
github.com/shareish

(permissive license)



(opensource.com)

The recipe (source code) is public.

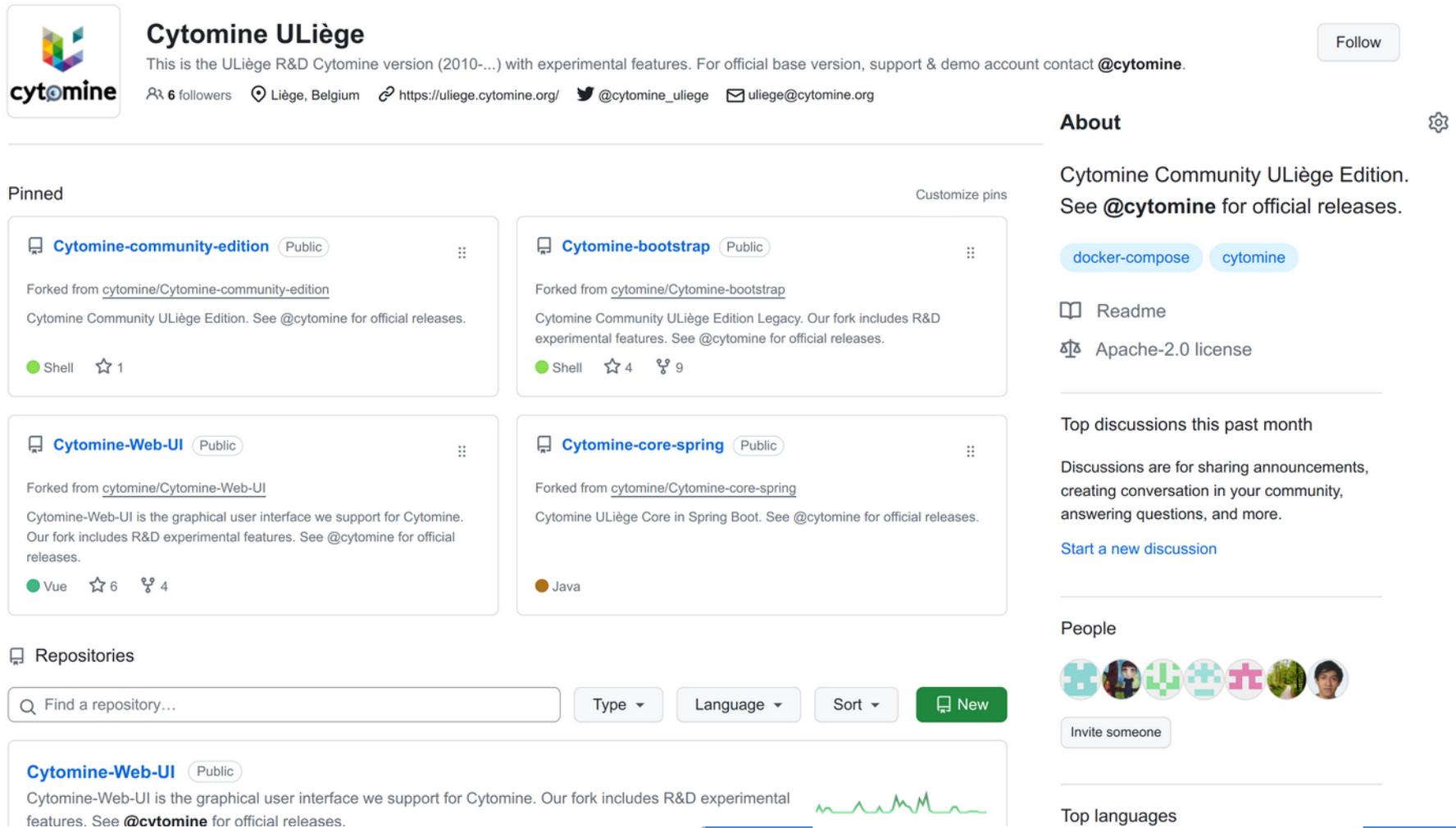
```
all_votes_class = Parallel(n_jobs=n_jobs)(
    delayed(_parallel_confidence_map)(
        pixels[starts[i]:starts[i + 1]],
        _Y[starts[i]:starts[i + 1]],
        starts[i],
        boxes,
        width,
        height,
        pyxit.base_estimator.n_classes_[0],
        pyxit_target_width,
        pyxit_target_height)
    for i in xrange(n_jobs))
```

(figure adapted from opensource.com)

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

Cytomine & Shareish are

² Code: <https://github.com/cytomine-uliege>. Demo server with datasets: <http://research.uliege.cytomine.org/> username: eccv2022bic password: deep-fish.



Cytomine ULIège Follow

This is the ULIège R&D Cytomine version (2010-...) with experimental features. For official base version, support & demo account contact [@cytomine](#).

6 followers Liège, Belgium <https://uliege.cytomine.org/> [@cytomine_uliege](#) uliege@cytomine.org

Pinned

Customize pins

- Cytomine-community-edition** (Public) Shell ☆ 1
Forked from [cytomine/Cytomine-community-edition](#)
Cytomine Community ULIège Edition. See [@cytomine](#) for official releases.
- Cytomine-bootstrap** (Public) Shell ☆ 4 🍴 9
Forked from [cytomine/Cytomine-bootstrap](#)
Cytomine Community ULIège Edition Legacy. Our fork includes R&D experimental features. See [@cytomine](#) for official releases.
- Cytomine-Web-UI** (Public) Vue ☆ 6 🍴 4
Forked from [cytomine/Cytomine-Web-UI](#)
Cytomine-Web-UI is the graphical user interface we support for Cytomine. Our fork includes R&D experimental features. See [@cytomine](#) for official releases.
- Cytomine-core-spring** (Public) Java
Forked from [cytomine/Cytomine-core-spring](#)
Cytomine ULIège Core in Spring Boot. See [@cytomine](#) for official releases.

Repositories

Find a repository... Type Language Sort New

- Cytomine-Web-UI** (Public)
Cytomine-Web-UI is the graphical user interface we support for Cytomine. Our fork includes R&D experimental features. See [@cvtomine](#) for official releases.

About

Cytomine Community ULIège Edition. See [@cytomine](#) for official releases.

[docker-compose](#) [cytomine](#)

[Readme](#)
[Apache-2.0 license](#)

Top discussions this past month

Discussions are for sharing announcements, creating conversation in your community, answering questions, and more.

[Start a new discussion](#)

People

[Invite someone](#)

Top languages

```
pyxit_target_height)
for i in xrange(n_jobs))
```

(figure adapted from opensource.com)

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Why open-source ?

A need for research/civil community autonomy while existing tools were proprietary and subject to arbitrary/unpredictable decisions (« vendor lock-in », « data lock-in », limited impact, ...)

<https://optics.org/news/3/10/16>

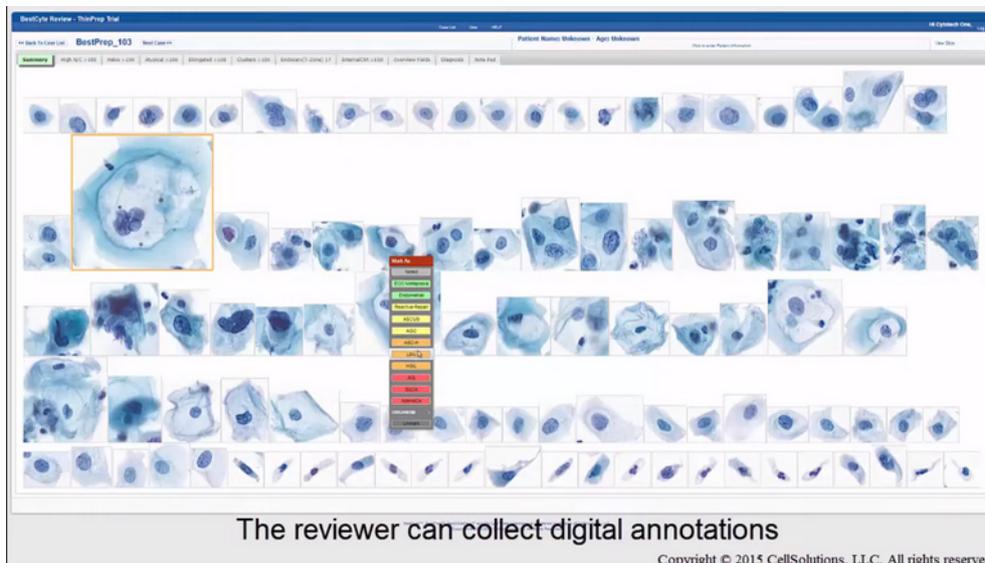
Definiens closes funding round for digital pathology expansion

15 Oct 2012 ... Investment of €10 million proves that image analysis techniques have potential to transform cancer diagnosis, company believes.

<https://www.astrazeneca.com/media-centre/press-releases/2014/medi...>

MedImmune completes acquisition of Definiens - AstraZeneca

26 Nov 2014 ... **Definiens** is the leading provider of image analysis and data mining solutions for tissue diagnostics and clinical **digital pathology**. **Definiens** ...



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¹E.g. the Jaspr Trades for "cash-free swap community in Berlin" suddenly ended its activity, the renting platform Usitoo in Belgium did not find a sustainable business model and was discontinued, the Kassi online forum "with the aim of linking those who can give something to those who are in need" [41] became as a start-up company the "Sharetribe online marketplace to sell, buy, and lend stuff", ...

Twitter announces new API pricing, posing a challenge for small developers



/ After announcing it would be changing its API rules in February, Twitter has now detailed how free access to its API will work in the future.

Home > Tech

Twitter's API keeps breaking, even for developers paying \$42,000

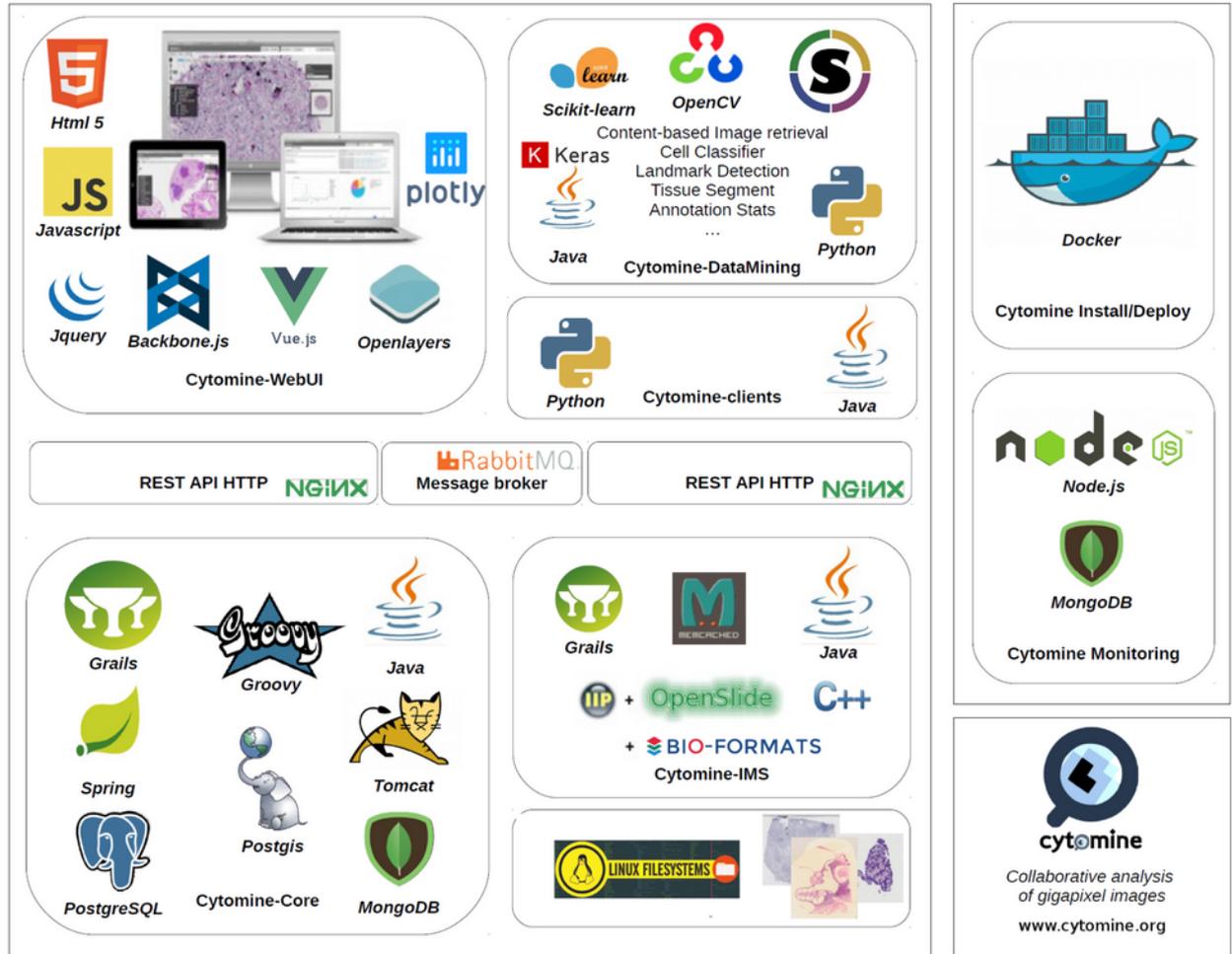
Everything worked fine until Elon Musk took over.

By [Matt Binder](#) on June 29, 2023



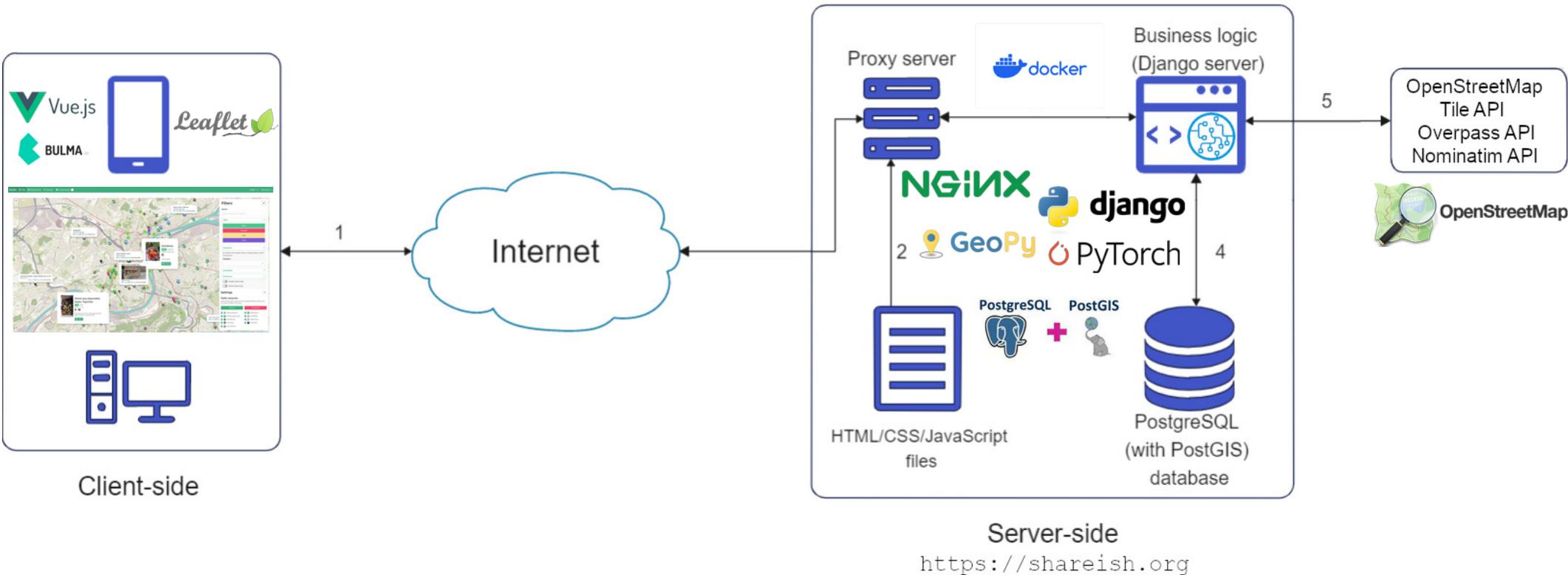
Why open-source ?

Direct way to « give back » to society (« commons ») as we relied on public funds and we re-used many existing open-source libraries / open data



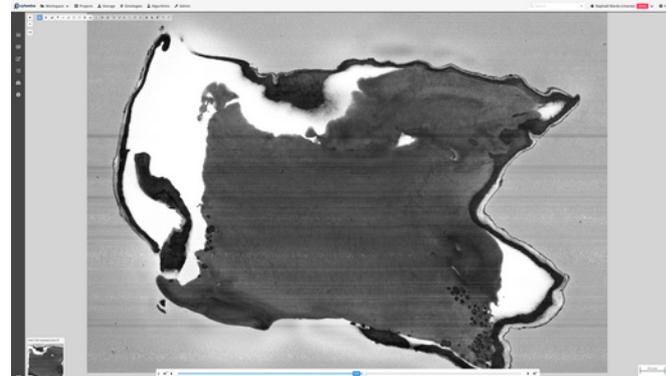
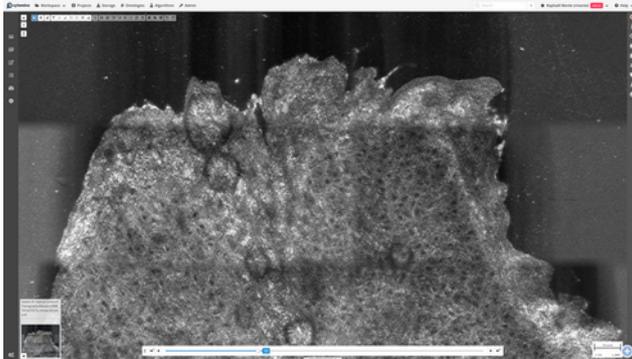
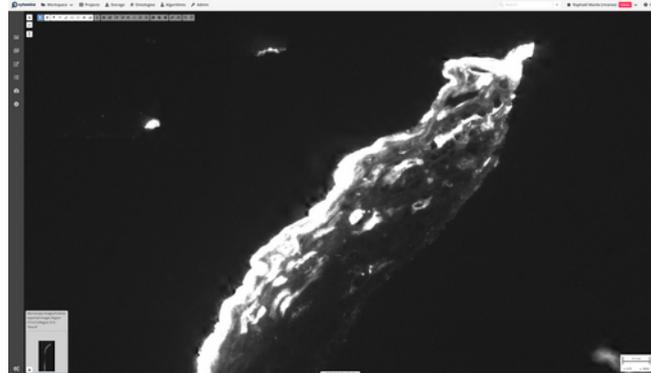
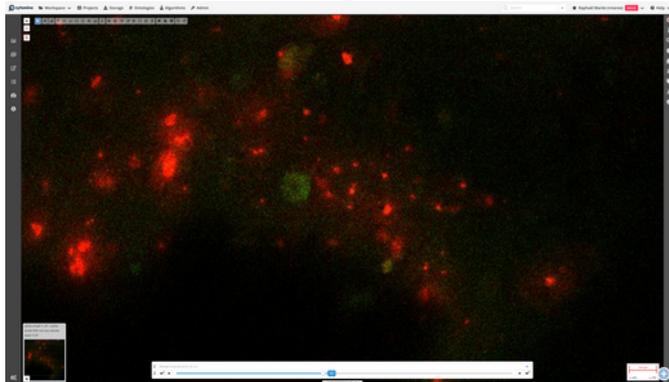
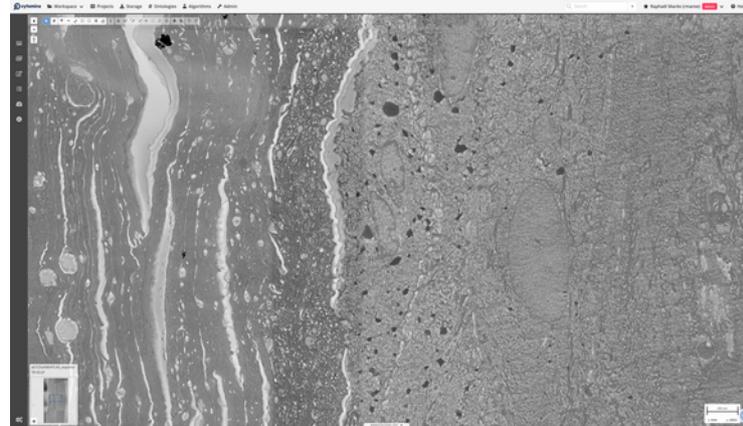
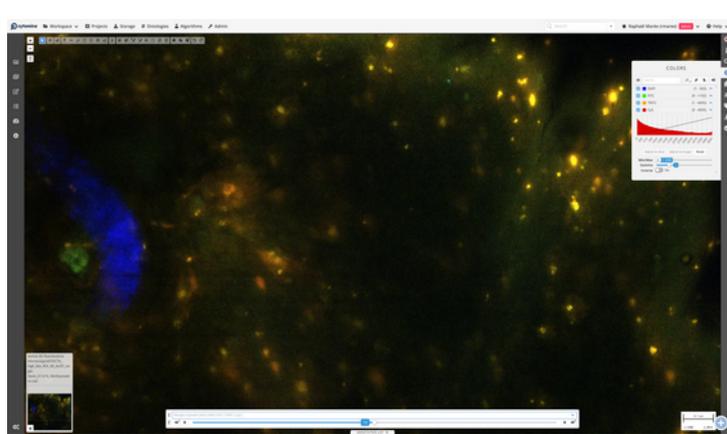
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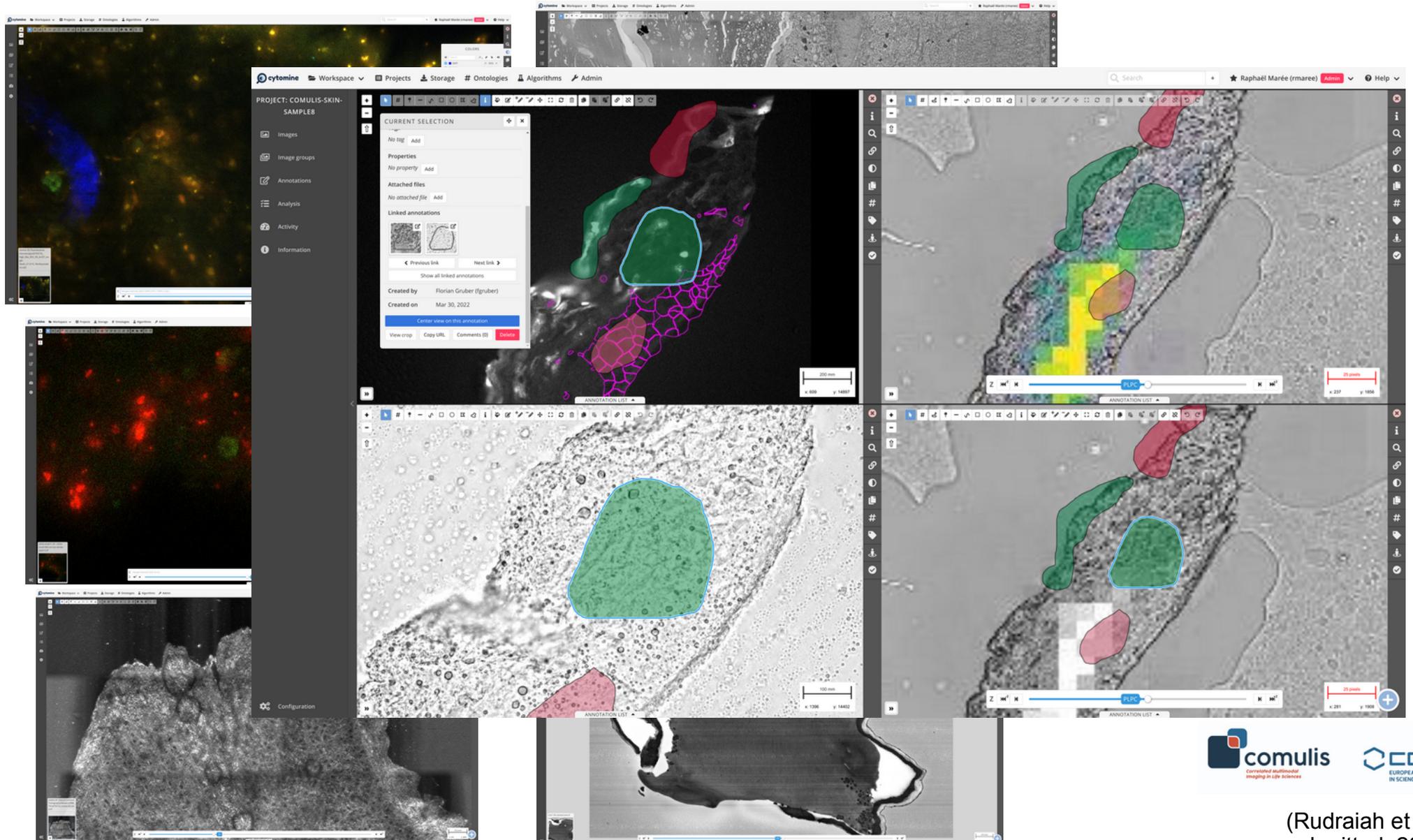
Open-source impact

Eases collaboration, adoption and replication by other researchers, and extension to other application domains (beyond initial scope, by others)



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NUCLEI-TRACKING-DIVISION
This project illustrates the 2D tracking of cell nuclei. The time-lapses are derived from Fluor-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.

img_0005_Nuc_Norm.tif

img_0003_Nuc_Norm.tif

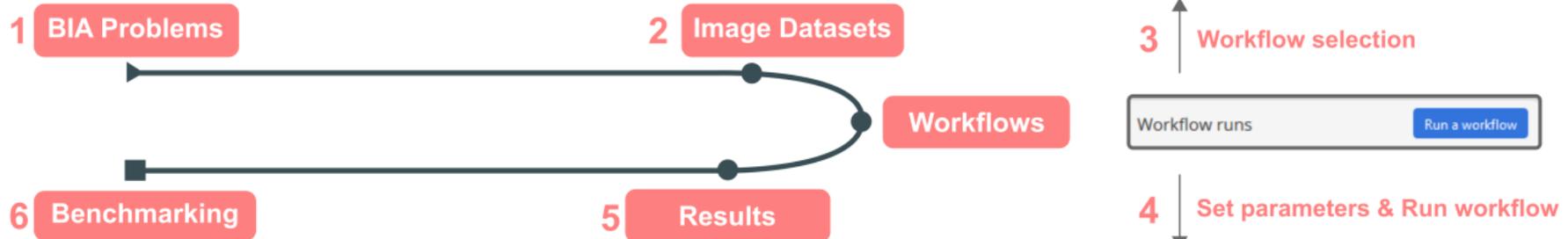
img_0004_Nuc_Norm.tif

img_0002_Nuc_Norm.tif

New workflow run

Workflow: Select options

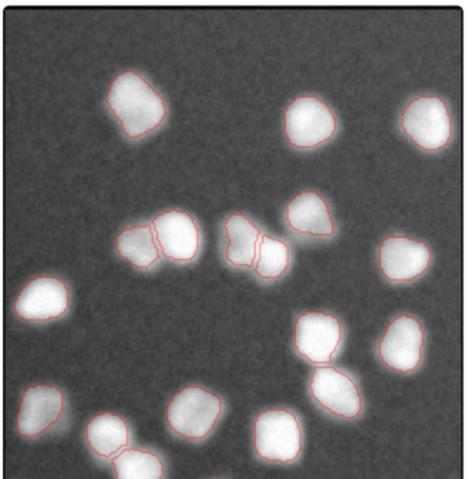
- NucleiSegmentation-Python (v1.1)
- NucleiSegmentation-CellProfiler (v1.4.1)
- NucleiSegmentation-ImageJ (v1.10.1)
- NucleiSegmentation-MaskRCNN (v1.3)
- NucleiSegmentation-ilastik (v1.0)



Workflow runs Run a workflow

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



New workflow run

Workflow: NucleiSegmentation-ImageJ (v1.10.1)

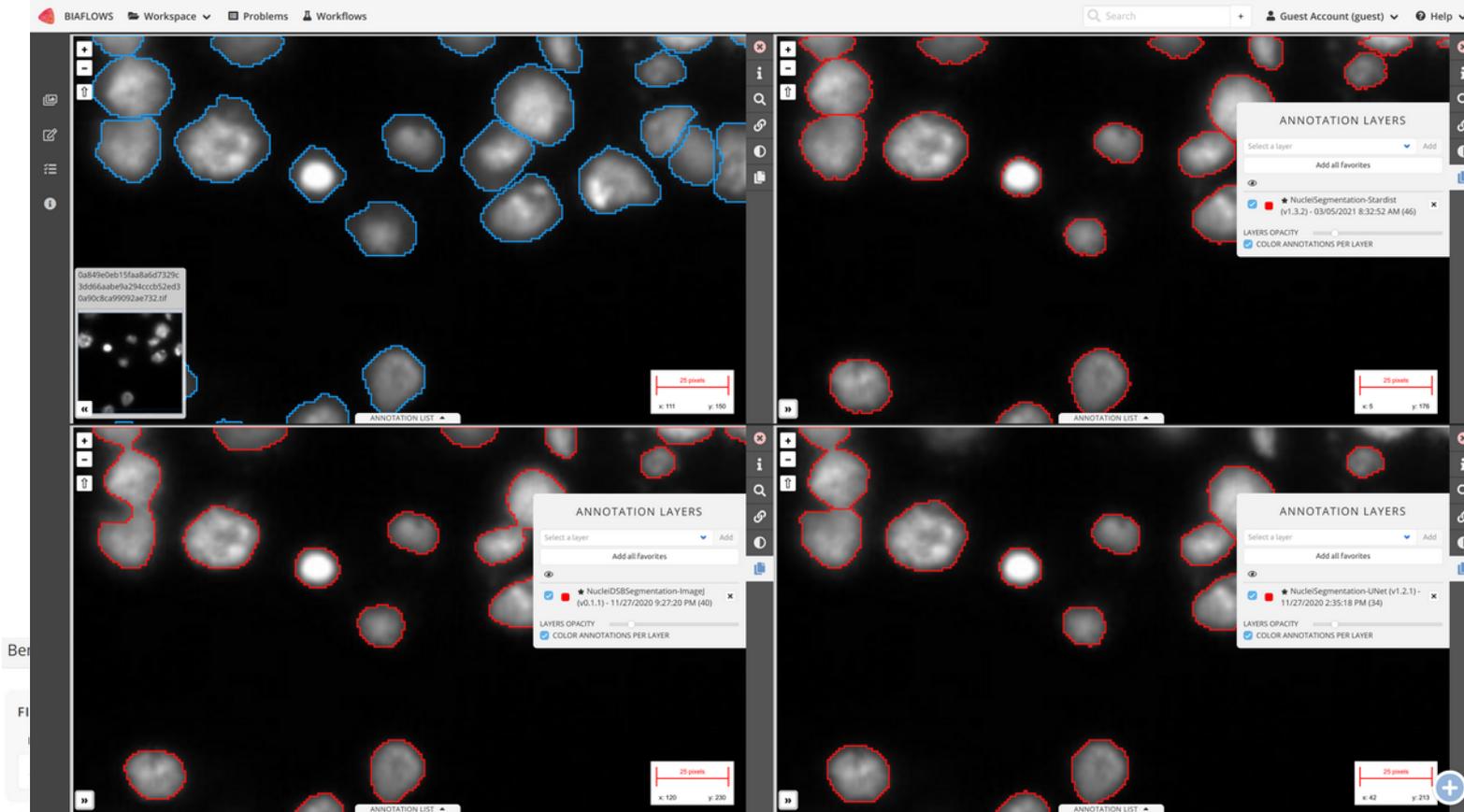
Name	Value
Radius	5
Threshold	-0.5

Cancel Run a workflow



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Aggregated results Detailed results per image

Workflow run	Mean Average Precision [Main metric]	Dice coefficient	Average Hausdorff distance	Fraction Overlap Pred
	AVG	AVG	AVG	AVG
★ NucleiSegmentation-Cellpose (v1.2.2) #1 on Mar 5, 2021 8:08 PM	0.312	0.701	10.545*	0.552
★ NucleiSegmentation-Stardist (v1.3.2) #2 on Mar 5, 2021 8:32 AM	0.397	0.845	1.584	
★ NucleiSegmentation-Ilastik (v1.4.2) #1 on Nov 28, 2020 11:52 AM	0.208	0.725	3.843	
★ NucleiSegmentation-MaskRCNN (v1.5.4) #1 on Nov 28, 2020 11:35 AM	0.394	0.798	2.702	
★ 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	

Patterns

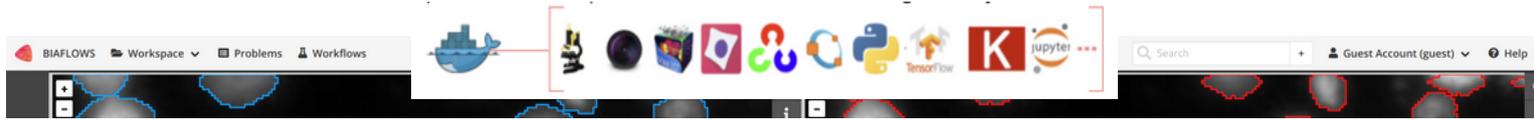
CellPress
OPEN ACCESS

Descriptor
BIAFlows: A Collaborative Framework to Reproducibly Deploy and Benchmark Bioimage Analysis Workflows

Ulysse Rubens,^{1,10} Romain Mormont,^{1,10} Lassi Paavolaianen,² Volker Bäcker,³ Benjamin Pavie,⁴ Leandro A. Scholz,⁵ Gino Michels,⁶ Martin Maska,⁷ Devrim Ünay,⁸ Graeme Ball,⁹ Renaud Hoyoux,¹⁰ Rémy Vandaele,¹¹ Ofra Golani,¹¹ Stefan G. Stanciu,¹² Natasa Sladoje,¹³ Perrine Paul-Gilloteaux,¹⁴ Raphaël Maréchal,¹⁵ and Sébastien Tosi^{15,17,18,*}

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cytomine / S_CellDetect_Stardist_HE_ROI

Code Issues Pull requests Actions Projects Wiki Security Insights

FROM cytomine/software-python3-base:v2.2.0

Dockerfile

```

# -----
# Install Stardist and tensorflow
RUN pip install tensorflow==2.2.0
RUN pip install stardist==0.6.0
RUN mkdir -p /models && \
    cd /models && \
    mkdir -p 2D_versatile_HE
ADD config.json /models/2D_versatile_HE/config.json
ADD thresholds.json /models/2D_versatile_HE/thresholds.json
ADD weights_best.h5 /models/2D_versatile_HE/weights_best.h5
RUN chmod 444 /models/2D_versatile_HE/config.json
RUN chmod 444 /models/2D_versatile_HE/thresholds.json
RUN chmod 444 /models/2D_versatile_HE/weights_best.h5

# -----
# Install scripts
ADD descriptor.json /app/descriptor.json
RUN mkdir -p /app
ADD run.py /app/run.py

ENTRYPOINT ["python3", "/app/run.py"]
    
```

geektortoise integration to cytomine repository

- Dockerfile: integration to cytomine repository (7 months ago)
- LICENSE: Initial commit (11 months ago)
- README.md: Update README.md (11 months ago)
- config.json: CellDetection with Stardist (initial version with models) (11 months ago)
- descriptor.json: integration to cytomine repository (7 months ago)
- run.py: Batch mode to process multiple images (11 months ago)
- screenshot-detections.jpg: better illustrative screenshots (11 months ago)
- screenshot-launch.jpg: better illustrative screenshots (11 months ago)
- screenshot.jpg: Example screenshot (11 months ago)
- thresholds.json: CellDetection with Stardist (initial version with models) (11 months ago)
- weights_best.h5: CellDetection with Stardist (initial version with models) (11 months ago)

README.md

S_CellDetect_Stardist_ROI

Descriptor

```

{
  "id": "stardist_prob_t",
  "value-key": "@ID@",
  "command-line-flag": "--@id@",
  "name": "Stardist Probability Threshold",
  "description": "Probability Threshold in range [0.0, 1.0] - higher values lead to fewer segmented objects, but will likely miss some objects.",
  "default-value": 0.5,
  "set-by-server": false,
  "optional": true,
  "type": "Number"
},
{
  "id": "stardist_nms_t",
  "value-key": "@ID@",
  "command-line-flag": "--@id@",
  "name": "Stardist Non-Maximum Suppression Overlap threshold",
  "description": "Overlap threshold in range [0.0, 1.0] - higher values allow segmented objects to overlap substantially.",
  "default-value": 0.5,
  "set-by-server": false,
  "optional": true,
  "type": "Number"
},
}
    
```

Code (e.g. Python)

```

#Stardist model prediction with thresholds
labels, details = model.predict_instances(img,
                                         prob_thresh=conn.parameters.stardist_prob_t,
                                         nms_thresh=conn.parameters.stardist_nms_t)

print("Number of detected polygons: %d" % len(details['coord']))
cytomine_annotations = AnnotationCollection()
#Go over detections in this ROI, convert and upload to Cytomine
for pos, polygroup in enumerate(details['coord'], start=1):
    #Converting to Shapely annotation
    points = list()
    for i in range(len(polygroup[0])):
        #Cytomine cartesian coordinate system, (0,0) is bottom left corner
        #Mapping Stardist polygon detection coordinates to Cytomine ROI in whole slide image
        p = Point(minx+polygroup[1][i], miny-polygroup[0][i])
        points.append(p)

    annotation = Polygon(points)
    #Append to Annotation collection
    cytomine_annotations.append(Annotation(location=annotation.wkt,
                                          id_image=id_image, #conn.parameters.cytomine_id_image,
                                          id_project=conn.parameters.cytomine_id_project))
    
```

	AVG	AVG	AVG	AVG
★ NucleiSegmentation-Cellpose (v1.2.2) #1 on Mar 5, 2021 8:08 PM	0.312	0.701	10.545*	0.552
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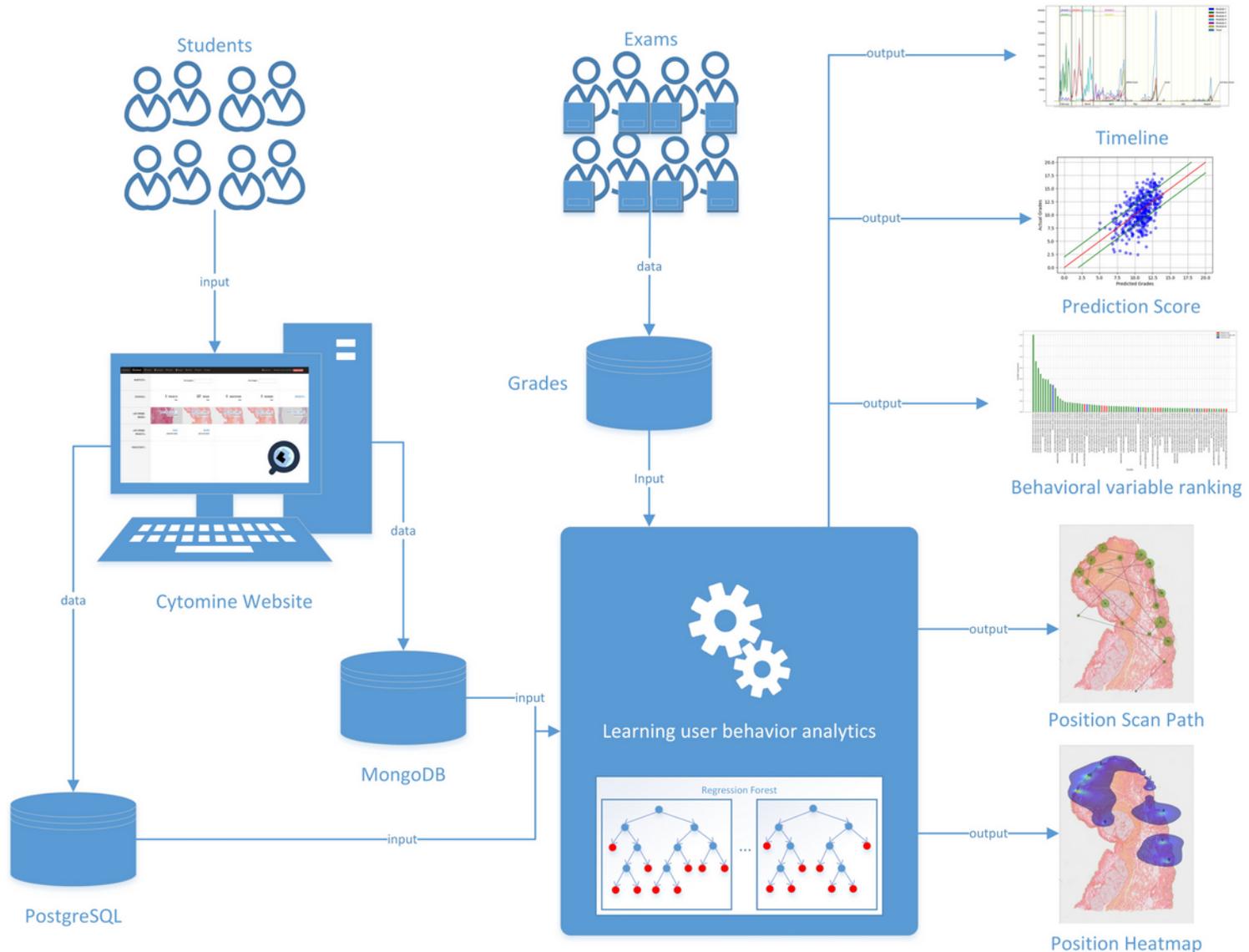
BIAFLOWS: A Collaborative Framework to Reproducibly Deploy and Benchmark Bioimage Analysis Workflows

Ullyse Rubens,^{1,10} Romain Mormont,^{1,10} Lassi Paavolaianen,² Volker Bäcker,³ Benjamin Pavie,⁴ Leandro A. Scholz,⁵ Gino Michiels,⁶ Martin Maska,⁷ Devrim Ünay,⁸ Graeme Ball,⁹ Renaud Hoyoux,¹⁰ Rémy Vandaele,¹⁰ Ofra Golani,¹¹ Stefan G. Stanciu,¹² Natasa Sladoje,¹³ Perrine Paul-Giloteaux,¹⁴ Raphaël Maréchal,¹⁵ and Sébastien Tosi^{15,17,18*}

CellPress
OPEN ACCESS

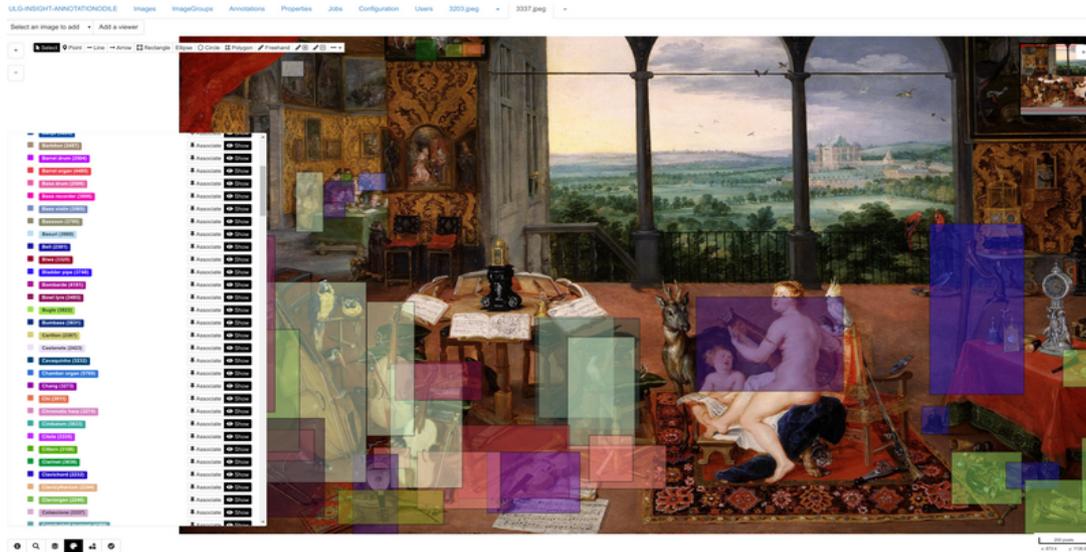
Open-source impact

Eases collaboration, adoption and replication by other researchers, and extension to other application domains (beyond initial scope, by others)

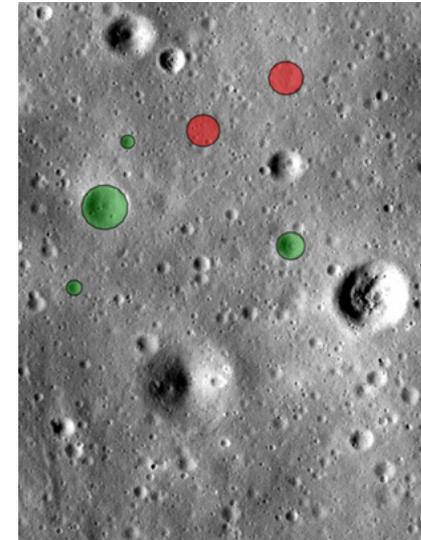


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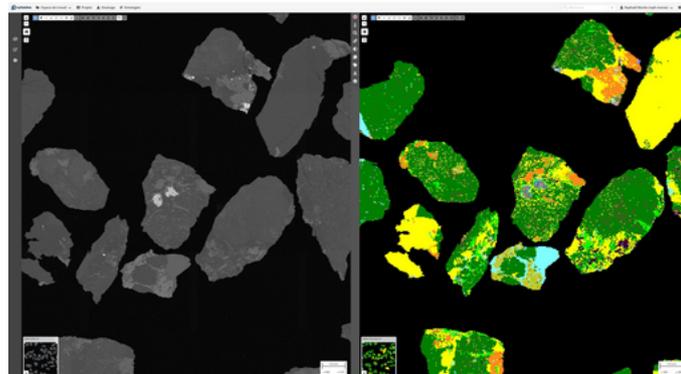
(Sabatelli et al., DHQ 2021)



(Q. Glaude, Master Thesis 2017)



(SpaceBel, X. Song, Master Thesis 2019)



(Mineralogy/geology, E. Pirard & H. Bouzahzah)



(X-Ris, ADRIC project)

Open-source + open data (FAIR)

IMI2

18th Call for proposals



Topic 1: Central repository of digital pathology slides to support the development of artificial intelligence tools

- developed open-source, cross-platform software tools to:
 - upload, search and access slides and associated metadata;
 - visualise and annotate the slides;
 - download slide for data mining and model development.



BigPicture project (2021-2027) : building the largest european GDPR-compliant open-access repository of digital pathology slides (clinical & non-clinical) to support the development of artificial intelligence tools
(incl. hardware, software, legal, and ethical issues)

Open-source & valorization

- Permissive open-source licence eases scientific collaboration with researchers and companies
 - Researchers' international mobility and entrepreneurial activities
 - Commercial proprietary / non-proprietary releases
 - *Cytomine SCES* (<https://doc.cytomine.org>) [2017,...]
 - Open-source « Community edition » code maintenance, documentation, and community management
 - *Cytomine corporation* (<https://cytomine.com>) [2021, ...]
 - Services and development of software modules on top of the open-source software for diverse clients :



Other thoughts

- Cytomine might be useful @ ULiège level to share imaging data ?
 - Who ? How ? Image viewer for Dataverse & Oliver ?
- How to improve open-source practice & impact @ ULiège ?
 - Need for permanent research software engineers ?
- Share/mutualize open-source best practices ?
 - Code hosting, documentation
 - Attract contributors, organize hackathons & mini-conference, manage community,...
 - Target specific funding for open source software development & maintenance (NLNet Foundation,...)
 - → Jérémie Fays « Open Source academy » !

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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]

Shareish : Adrien Guilliams, Ulysse Rubens, Florent Banneux, Pierre Chapeau

Cytomine funding sources since 2010 :

