



User guide Cytomine version 1.0
(Version: 20160116)

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This document covers the main functionalities of our software. The software can be tested at <http://demo.cytomine.be/> with one of these 3 accounts, using a modern web browsers (Google Chrome (preferred choice), Safari, Mozilla Firefox):

Username	Password	Role
jsnow	jsnow	User
clannister	clannister	User
estark	estark	User

The software can also be installed automatically on desktop/server computers using the procedure described in Section 6.1. In both cases, our installation procedure installs "toy data", namely five projects for testing main functionalities.

6.1 Installation

The automated installation procedure is described at: <http://doc.cytomine.be/x/goCj>

It basically requires the edition of a single configuration file (Bootstrap/configuration.sh) and the execution of a few command lines. The procedure will automatically create virtual environments (using Docker deployment system) for each Cytomine components and download, compile, and install all the required libraries, and start all servers. The whole process takes approximately 2 hours without user intervention. The web user interface is then directly accessible at the `http://$SCORE_URL$` location (e.g. `http://demo.cytomine.be`) using modern web browsers (we recommend using Google Chrome).

6.2 Usage (Cytomine-WebUI)

This guide explains how to:

- Visualize and annotate manually images
- Configure projects and manage users
- Upload new images
- Apply Cytomine-DataMining analysis modules and proofread them
- Perform textual search
- Follow online users
- Blind assessment (including IRIS: the Inter-observer study module)

In this guide, we assume using the "jsnow" account.

Please refer to your web browser documentation for basic navigation operations (e.g. "F5" key might be useful to reload pages).

6.2.1 Visualization and manual annotations

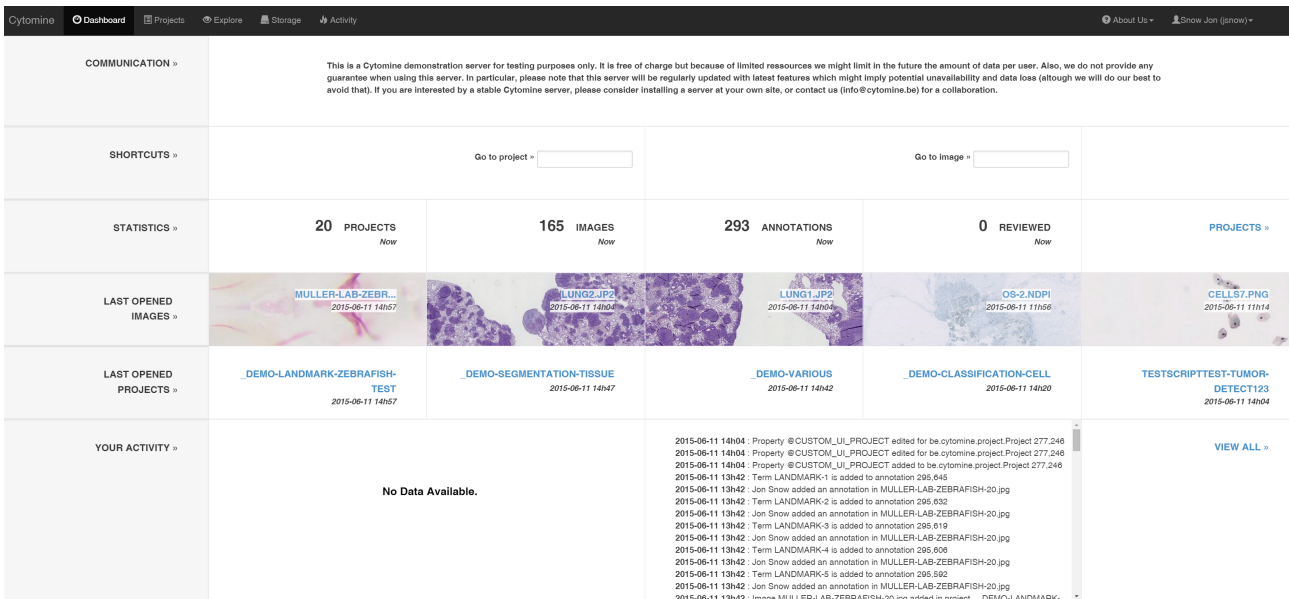
Users log into Cytomine using the login panel:

Sign in to Cytomine

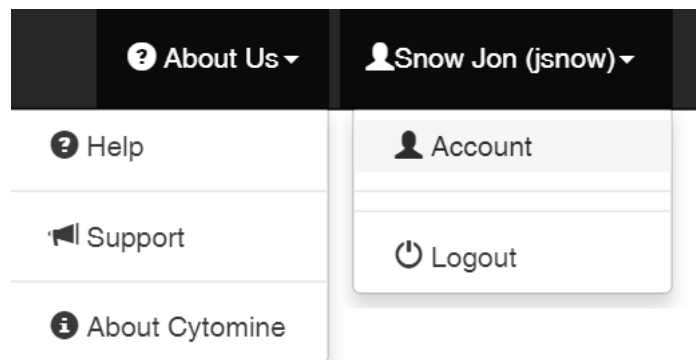
Remember me

[Forgot your username](#) or your [password](#) ?

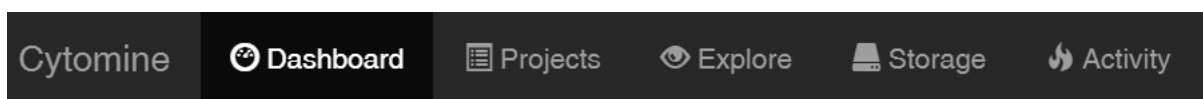
Once connected, the user has access to its user dashboard which summarizes global information (number of projects, images, annotations) and it also shows latest opened projects, images, and activities:



The menu on the top right (black bar) gives access to Account information (under the user name) where the user can change its password and get its public/private keys. The help sub-menu lists main shortcuts applicable when exploring images:



The menu on the top left (black bar) gives access to the User dashboard, the listing of Projects, the Storage panel (to upload new images through the web interface), and the Activity panel which summarizes latest user activities:



The project listing displays boxes where each box corresponds to a specific project. Project listing can be filtered (box at the top left) by names, number of annotations, images, disciplines, ontology names:



Cytomine Dashboard Projects Explore Storage Activity About Us Snow Jon (jnow)

Filters

Name:

Images: 0-20

Annotations: 0-100

Discipline: All

Ontology: All

[Reset filters](#)

DEMO-EMPTY

Name: DEMO-EMPTY
Discipline: Undefined
Ontology: DEMO-EMPTY

Number of images: 0
Number of user annotations: 0
Number of job annotations: 0
Number of validated annotations: 0

[Info](#) [Edit](#) [Delete](#) [Open](#)

DEMO-LANDMARK-Z...

Name: DEMO-LANDMARK-ZEBRAFISH-TEST
Discipline: Undefined
Ontology: DEMO-LANDMARK-Z...

Number of images: 20
Number of user annotations: 4
Number of job annotations: 4
Number of validated annotations: 4

[Info](#) [Edit](#) [Delete](#) [Open](#)

DEMO-VARIOUS

Name: DEMO-VARIOUS
Discipline: Undefined
Ontology: DEMO-VARIOUS

Number of images: 2
Number of user annotations: 4
Number of job annotations: 4
Number of validated annotations: 4

[Info](#) [Edit](#) [Delete](#) [Open](#)

TESTSCRIPTDEMO...

Name: TESTSCRIPTDEMO-CELLS123
Discipline: Undefined
Ontology: TESTSCRIPTDEMO...

Number of images: 9
Number of user annotations: 4
Number of job annotations: 4
Number of validated annotations: 4

[Info](#) [Edit](#) [Delete](#) [Open](#)

Clicking on the project name (e.g. `_DEMO_SEGMENTATION_TISSUE`) or on the Open button will open the project and shows the Project dashboard with basic information (textual description on the top right, users currently online) and various statistics about the project (including number of images, annotations, various statistics of annotations by ontology terms, users, images, ...).

`_DEMO_SEGMENTATION_TISSUE` Images Annotations Properties Configuration

_DEMO_SEGMENTATION_TISSUE

Ontology: `_DEMO_SEGMENTATION_TISSUE-ONTOLOGY`

User annotations: 20
Job annotations: 0
Reviewed annotations: 0

[See users](#) [Lock project](#)

ONLINE USERS

Snow Jon (jnow)

ACTIVITY

Last commands Last tasks

11/6/2015 11:42:58 :
Image LUNG2.jp2 added in project `_DEMO_SEGMENTATION_TISSUE` by jsnow

- 11/6/2015 11:42:38 : Term Tumor is added to annotation 278,747 by jsnow
- 11/6/2015 11:42:37 :
Jon Snow added an annotation in LUNG1.jp2 by jsnow

- 11/6/2015 11:42:37 : Term Tumor is added to annotation 278,734 by jsnow
- 11/6/2015 11:42:37 :
Jon Snow added an annotation in LUNG1.jp2 by jsnow

- 11/6/2015 11:42:37 : Term Tumor is added to annotation 278,721 by jsnow
+ 11/6/2015 11:42:32 :

ANNOTATIONS VS TERM

● Tumor ● Negative

ANNOTATIONS VS TERM

Term	Tumor	Negative
Tumor	10.00	0.00
Negative	0.00	10.00

ANNOTATIONS BY USER

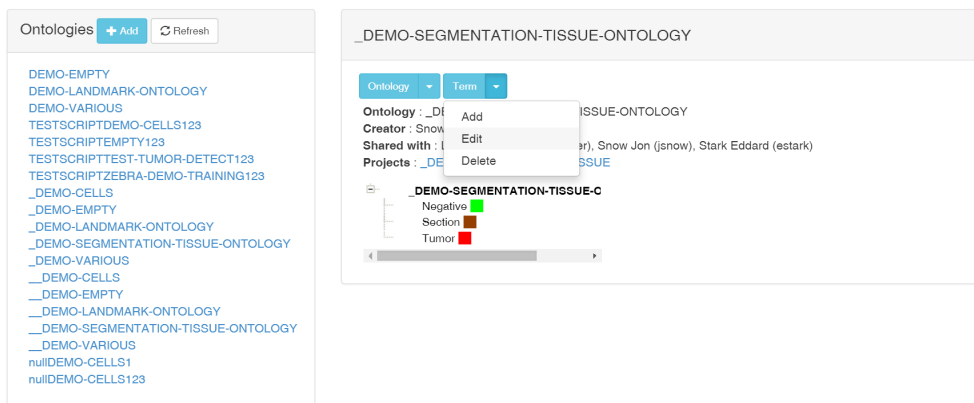
User	Tumor	Negative
Edouard Spink	0.00	0.00
Jon Snow	10.00	0.00
Didier Lemaire	0.00	10.00

ANNOTATED SLIDES BY TERM

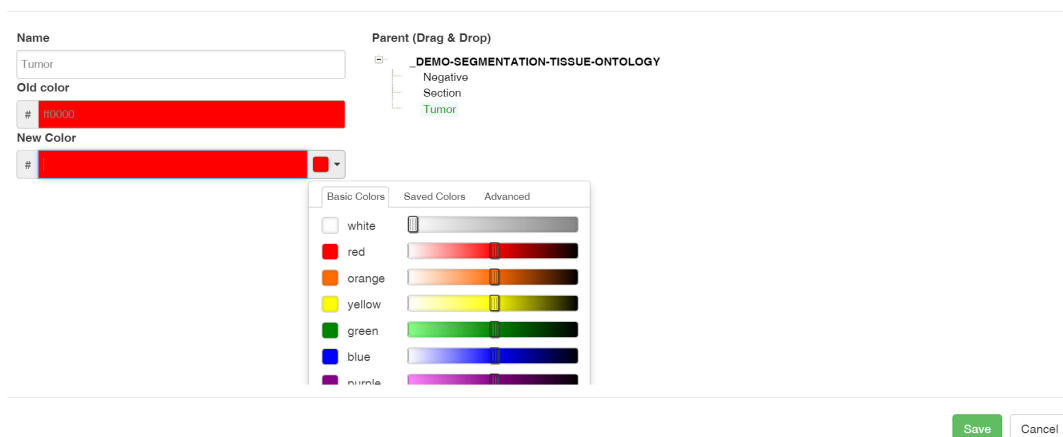
Slide	Tumor	Negative
Slide 1	1.00	0.00
Slide 2	1.00	0.00
Slide 3	0.00	1.00



One key concept of Cytomine is the Ontology, a structured vocabulary of user-specified terms used for the semantic annotation of regions of interest in images. Each project has a single ontology. It can be either an existing ontology (it can be associated with the project when a user creates it) or a new ontology that can be edited online. Editing the ontology can be done by clicking on its name (first line under the project name) which opens the Ontology editor. The editor allows to rename the ontology, add/edit/delete terms from the ontology. In this "toy" project where life scientists are interested to quantify the sizes of tumor islets with respect to the size of tissue sections, the Ontology is simplified and has only three terms: Section (to delimit the tissue section, in brown), Tumor (for tumoral islets, in red), and Negative (for all other tissue substructures, in green):

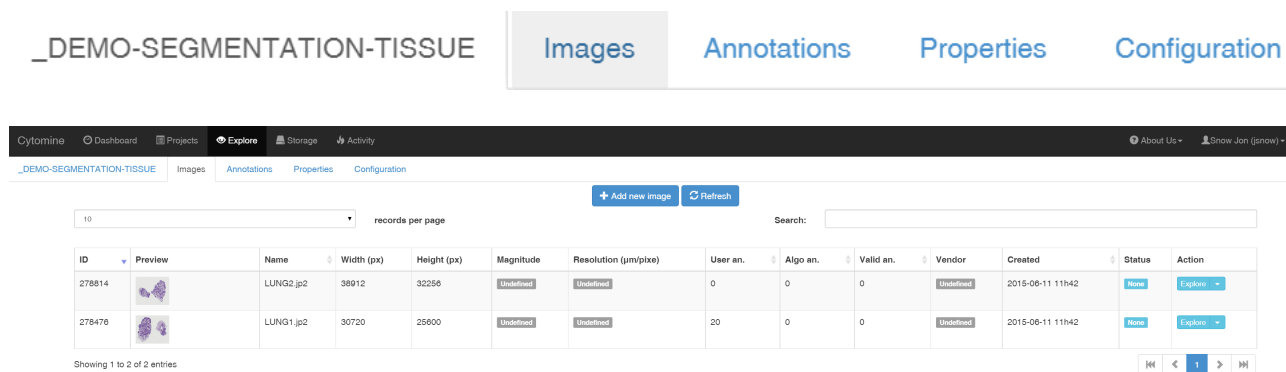


Edit term

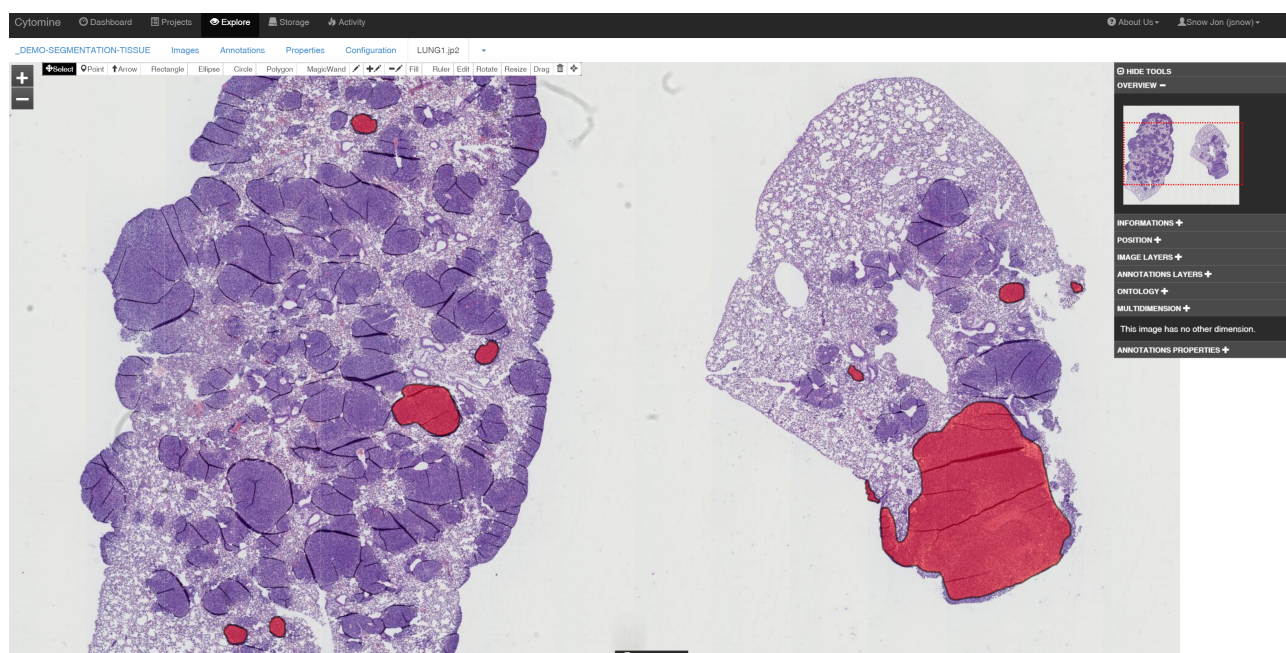


Once

the ontology is defined, one can start semantically annotating whole-slide images. It has to be noted that Term names and colors can be changed afterwards, only term identifiers are linked to annotations in the database. To start annotation, the user goes back to the Project dashboard and clicks on the "Images" tab which opens a page with the Image listing of this project:



This project contains only 2 images whose characteristics are listed. Image "LUNG1.jp2" already contains 20 user annotations. One can open the image by clicking on its thumbnail or on the blue Explore button at the right. Note that the arrow at the right of the Explore button gives access to supplementary information and operations (e.g. download the image, describe it, start reviewing it (see below), importing annotations from another project, ...). The explore view is then displayed. It is a zoomable viewer for gigapixel images, with various tools for annotation. Note that multiple images can be opened in parallel, each one having its own tab. By default (this can be configured in the "Configuration" tab of the project), the viewer also displays current user's annotations (in red here, corresponding to the color of the Tumor term):




Annotations can be selected , edited, and drawn manually by using tools on the top bar:







It includes geometries such as:

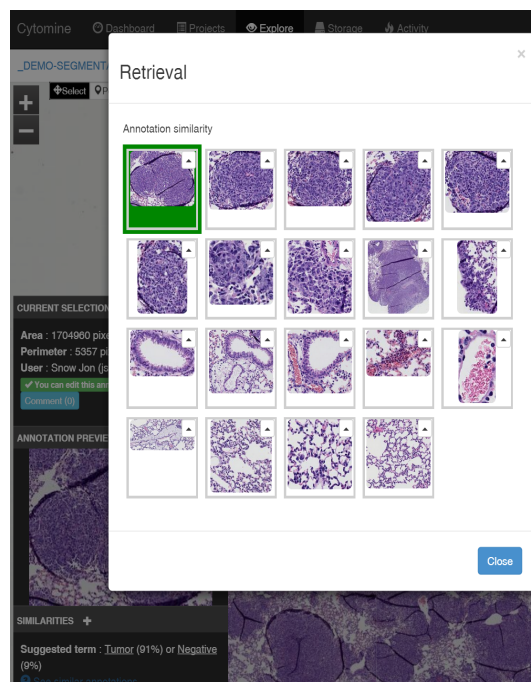
- Point, Rectangle, Ellipse, Circle, Polygon,

- Freehand 
- Magic Wand (which parameters have to be configured in Project Configuration tab)

And operations such as:

- Rotate,  Resize, Drag,
- Delete 
- Fill
- Complement (performs the union of a new geometry with an intersecting, existing, geometry) 
- Subtract  (subtracts the intersection of a new geometry with existing geometry)

Selecting an annotation opens the Current Selection Annotation panel (at the bottom left) which gives basic information (e.g. annotation area based on image resolution) about the currently selected annotation and launch the content-based image retrieval algorithm. This algorithm suggests ontology terms based on visual similarity. The most similar annotations can be visualized by clicking on "See Similar Annotations" (they are ranked according to their computed similarity):



It is possible to click on these "similar" annotations to jump directly at their locations within their original image.

Properties (key-value pairs) and keywords can be added to Annotations by clicking on the "Add property" link (at the bottom of the Current Selection panel).

Add a property

Key Value

Add a keyword

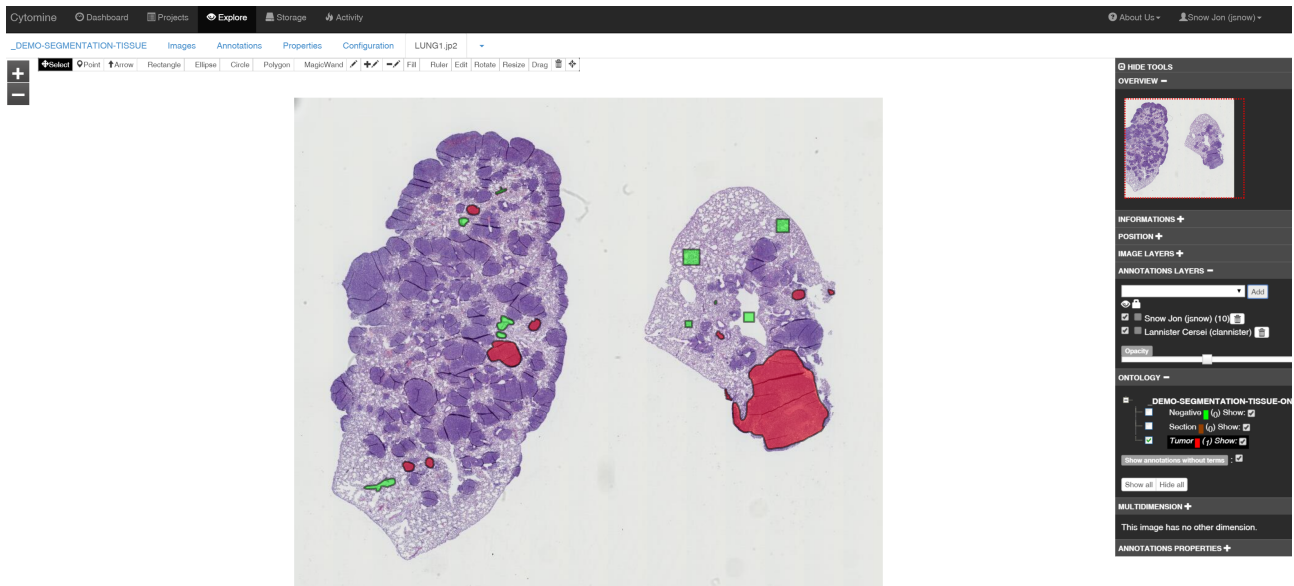
Properties

Key	Value	Delete
Info: To edit a property, double-click on the key or the value. Valid with Enter.		
No data to display		

Rich text descriptions can also be added in a similar way as for Projects and Images.

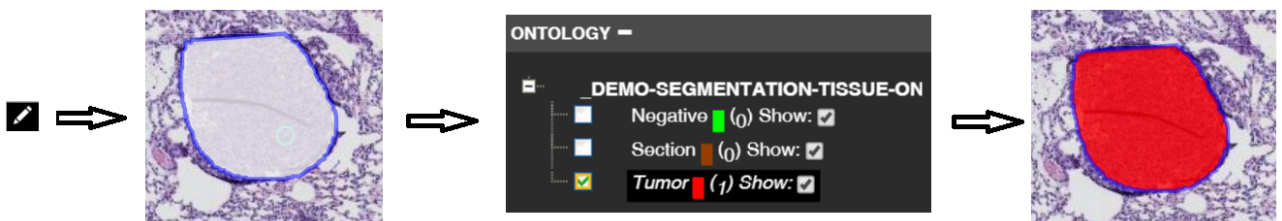
On the right side of the Explore view, the "Tools" panel can be activated to show an overview (thumbnail with red square corresponding to the active view), image information, image layers (which allow to apply on the fly image processing filter to tiles, see Configuration page of the project), annotation layers (containing user layers, userjob layers, and the review layer), ontology, and multi-dimensional browser.

Selecting and adding another user layer will display its layer of annotations in the whole-slide images in addition to current user annotations (in this case, the user clannister only created annotations with the Negative term, in green):



Multiple user annotations can then be displayed. A blinded mode allows to hide other user layers if needed (see Project Configuration page).

Adding an annotation requires the user to draw it, then eventually associate a term from the Ontology (the color of the Annotation thus changes):



All annotations created in a project are visible in filtered galleries in the Project Annotations tab:



Annotations can be filtered according to images they come from, terms from the Ontology, Users from the project and types (user/job/reviewed). Filters can be saved and reused later. The user can click on any of these annotations to jump to its actual location in whole slide images.

Annotation descriptions can be exported as tabular files containing annotation information (area, user who created them, direct link to it,...):

Cytomine Dashboard | Projects | Explore | Storage | Activity | About Us | Show Jon (snow)

_DEMO-SEGMENTATION-TISSUE Images | Annotations | Properties | Configuration | LUNG1.jp2

Filters

- Search in uselabel annotations
- Search in reviewed annotations

_DEMO-SEGMENTATION-TISSUE

- Annotations without terms
- Annotations with several terms

_DEMO-SEGMENTATION-TISSUE-ONTOLOGY

- Image
- Section
- Tumor

Users

- Lannister Cersel (clannister)
- Show Jon (snow)
- Chuck Eckhart (eckhart)

_DEMO-SEGMENTATION-TISSUE

- 0segmentation_Model_Builder
- 1segmentation_Model_Builder
- 2segmentation_Model_Builder
- 3segmentation_Model_Predict
- 4segmentation_Model_Predict
- 5segmentation_Model_Predict
- 6segmentation_Model_Predict
- 7segmentation_Model_Predict
- 8segmentation_Model_Predict
- 9segmentation_Model_Predict
- 10segmentation_Model_Predict
- 11segmentation_Model_Predict
- 12segmentation_Model_Predict
- 13segmentation_Model_Predict
- 14segmentation_Model_Predict
- 15segmentation_Model_Predict
- 16segmentation_Model_Predict
- 17segmentation_Model_Predict
- 18segmentation_Model_Predict
- 19segmentation_Model_Predict
- 20segmentation_Model_Predict
- 21segmentation_Model_Predict
- 22segmentation_Model_Predict

Predefined Filters

Undefined

Multiple

Negative

Section

Tumor

Download

Download CSV | Download Excel | Download PDF

A	B	C	D	E	F	G	H	I	J	K
id	Area (microns ²)	Perimeter (mm)	X	Y	Image Id	Image Filename	User	Term	View annotation picture	View annotation on image
2	302661554624.0	2958.0	7046.116321532636	4725.001467744019	278476.LUNG1.jp2		jsnow	Tumor	http://demo.cytomine.be/api/annotation/302661/crop.png	http://demo.cytomine.be/#tabs-image-278366-278476-302661
3	278747175230.0	1594.0	7069.32970381784	6572.665609009112	278476.LUNG1.jp2		jsnow	Tumor	http://demo.cytomine.be/api/annotation/278747/crop.png	http://demo.cytomine.be/#tabs-image-278366-278476-278747
4	278734227312.0	1880.0	5960.75249290256	6390.173060228526	278476.LUNG1.jp2		jsnow	Tumor	http://demo.cytomine.be/api/annotation/278734/crop.png	http://demo.cytomine.be/#tabs-image-278366-278476-278734
5	278721253480.0	1946.0	12556.091504918204	13743.268813052706	278476.LUNG1.jp2		jsnow	Tumor	http://demo.cytomine.be/api/annotation/278721/crop.png	http://demo.cytomine.be/#tabs-image-278366-278476-278721
6	278708251696.0	1973.0	9331.685970376962	19742.053609645496	278476.LUNG1.jp2		jsnow	Tumor	http://demo.cytomine.be/api/annotation/278708/crop.png	http://demo.cytomine.be/#tabs-image-278366-278476-278708
7	2786951704960.0	5357.0	11001.564964964966	12278.455656565656	278476.LUNG1.jp2		jsnow	Tumor	http://demo.cytomine.be/api/annotation/278695/crop.png	http://demo.cytomine.be/#tabs-image-278366-278476-278695
8	27868271540.0	1605.0	10794.882024042494	20723.60314975305	278476.LUNG1.jp2		clannister	Negative	http://demo.cytomine.be/api/annotation/278682/crop.png	http://demo.cytomine.be/#tabs-image-278366-278476-278682
9	278669162990.0	1568.0	8824.732830234983	19137.8159396282	278476.LUNG1.jp2		clannister	Negative	http://demo.cytomine.be/api/annotation/278669/crop.png	http://demo.cytomine.be/#tabs-image-278366-278476-278669
10	278656434896.0	4195.0	4590.964963270912	5427.768220448107	278476.LUNG1.jp2		clannister	Negative	http://demo.cytomine.be/api/annotation/278656/crop.png	http://demo.cytomine.be/#tabs-image-278366-278476-278656
11	278643129030.0	1419.0	10797.546918104317	13221.16901500511	278476.LUNG1.jp2		clannister	Negative	http://demo.cytomine.be/api/annotation/278643/crop.png	http://demo.cytomine.be/#tabs-image-278366-278476-278643
12	278630373352.0	2724.0	10976.037383845094	13842.707638046769	278476.LUNG1.jp2		clannister	Negative	http://demo.cytomine.be/api/annotation/278630/crop.png	http://demo.cytomine.be/#tabs-image-278366-278476-278630
13	27861714602.0	527.0	21993.5566817331	14925.346299593662	278476.LUNG1.jp2		clannister	Negative	http://demo.cytomine.be/api/annotation/278617/crop.png	http://demo.cytomine.be/#tabs-image-278366-278476-278617
14	278604117600.0	1372.0	20585.0	13798.0	278476.LUNG1.jp2		clannister	Negative	http://demo.cytomine.be/api/annotation/278604/crop.png	http://demo.cytomine.be/#tabs-image-278366-278476-278604
15	278591681792.0	3304.0	20730.0	17282.0	278476.LUNG1.jp2		clannister	Negative	http://demo.cytomine.be/api/annotation/278591/crop.png	http://demo.cytomine.be/#tabs-image-278366-278476-278591
16	278578443232.0	2664.0	25496.0	18924.0	278476.LUNG1.jp2		clannister	Negative	http://demo.cytomine.be/api/annotation/278578/crop.png	http://demo.cytomine.be/#tabs-image-278366-278476-278578
17	278564266760.0	2069.0	23736.0	14159.0	278476.LUNG1.jp2		clannister	Negative	http://demo.cytomine.be/api/annotation/278564/crop.png	http://demo.cytomine.be/#tabs-image-278366-278476-278564
18	27854516290496E7	18271.0	25461.181634248594	9723.086243496413	278476.LUNG1.jp2		jsnow	Tumor	http://demo.cytomine.be/api/annotation/278545/crop.png	http://demo.cytomine.be/#tabs-image-278366-278476-278545
19	278532279788.0	1982.0	26318.944643801737	15324.092674930067	278476.LUNG1.jp2		jsnow	Tumor	http://demo.cytomine.be/api/annotation/278532/crop.png	http://demo.cytomine.be/#tabs-image-278366-278476-278532
20	27851996759.0	1279.0	22222.987084750086	13198.88393277524	278476.LUNG1.jp2		jsnow	Tumor	http://demo.cytomine.be/api/annotation/278519/crop.png	http://demo.cytomine.be/#tabs-image-278366-278476-278519
21	27850675715.0	942.0	28014.469363828004	15463.157382540645	278476.LUNG1.jp2		jsnow	Tumor	http://demo.cytomine.be/api/annotation/278506/crop.png	http://demo.cytomine.be/#tabs-image-278366-278476-278506
22	27849276746.0	1585.0	22618.569549137515	10065.900478421101	278476.LUNG1.jp2		jsnow	Tumor	http://demo.cytomine.be/api/annotation/278492/crop.png	http://demo.cytomine.be/#tabs-image-278366-278476-278492

In addition to ontology terms, properties, keywords, and rich text descriptions, Comments can be associated to Annotations and send through e-mail to project's users (using e-mail addresses encoded in the User account). E-mails contain the textual comment and a direct link to the actual location of the annotation within its gigapixel image for direct visualization. The user has to click on the blue "Comment" button in the Current selection panel, then select recipients and then click on the green "Share" button:

Comment/Share an annotation

CURRENT SELECTION +

Area : 554624 pixels²

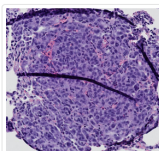
Perimeter : 2958 pixels

User : Snow Jon (jsnow)

✓ You can edit this annotation

Comment (0)

→



Comments

Share with

- Everyone
- Email
- Some users

Lannister Cersel (clannister)

Your comment

What do you think ?

Cancel Share

6.2.2 Project

configuration and user management

Each project can be configured through the Configuration page:

_DEMO-SEGMENTATION-TISSUE

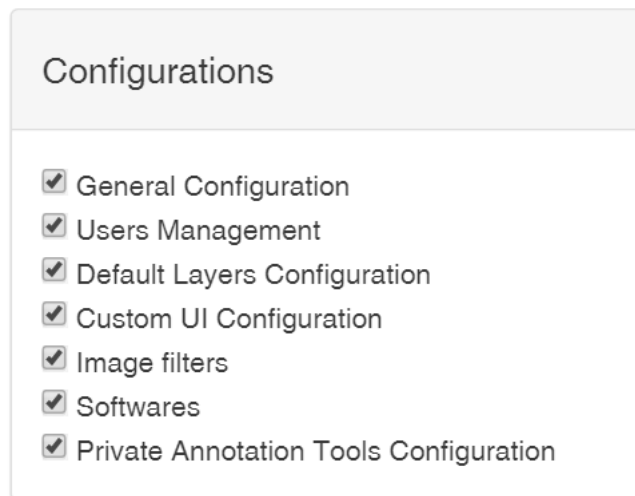
Images

Annotations

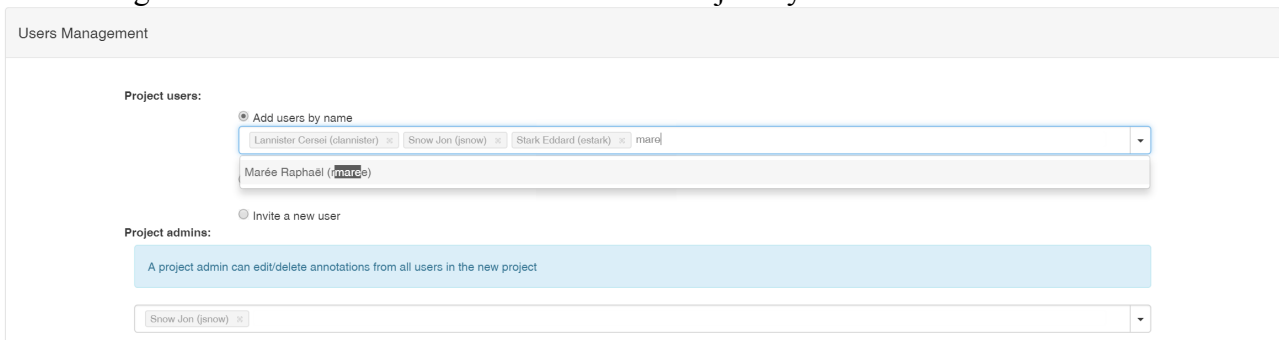
Properties

Configuration

Admins of a project can configure all options including general configuration (e.g. blind mode which hides image names, enable/disable the content-based image retrieval algorithm,...), user management (add/delete users from this project), configure the default annotation layer in the Explore view, customize the user interface to enable/disable graphical tools and displayed information (such as the drawing tools and panels), the image filters (that can be applied on-the-fly to image tiles), the softwares to be associated (e.g. the Cytomine-DataMining modules or any other third-party softwares registered to the database), and some other visual configuration (e.g. the magic wand tolerance parameter or the size of Point annotations, configurable by a regular User).



An existing user in the database can be added to the Project by an admin.



To add new user into the database through the web user interface, admins or super admins have to enter into the Cytomine admin area where they can add new user or edit existing ones (including their role):

id	username	lastname	firstname	email	created	updated	action
37	admin	ADMIN	Just an	info@cytomine.be	2015-04-22	2015-04-22	View Edit
263700	clannister	LANNISTER	Cersei	admin@ulg.ac.be	10 hours ago		View Edit
263688	estark	STARK	Eddard	estark@ulg.ac.be	10 hours ago		View Edit
30	imageServer1	SERVER	Image	info@cytomine.be	2015-04-22	Yesterday	View Edit
263676	jsnow	SNOW	Jon	johnsnow@ulg.ac.be	10 hours ago		View Edit

Note: on our demo instance, we do not provide admin codes to avoid issues due to unintentional operations. If you install the software on your servers, an admin user will be created by our automated installation procedure (username/password is requested during installation).

6.2.3 Upload and manage images

A user can upload images to its storage and then associate images to project(s). The user has to click on the "Storage" button (top black bar) to access the Storage panel where he can select (drag & drop or "Add files" dialog box) images from its local computer and link them automatically to a given project. If multiple files are to be uploaded, start upload will upload five of them in parallel:

Filename	Created	Size	Content Type	Status	Action
MULLER-LAB-ZEBRAFISH-20.jpg	2015-06-11 13h42	0.19Mo	application/octet-stream	DEPLOYED	Delete
MULLER-LAB-ZEBRAFISH-19.jpg	2015-06-11 13h41	0.18Mo	application/octet-stream	DEPLOYED	Delete
MULLER-LAB-ZEBRAFISH-18.jpg	2015-06-11 13h41	0.18Mo	application/octet-stream	DEPLOYED	Delete
MULLER-LAB-ZEBRAFISH-17.jpg	2015-06-11 13h41	0.17Mo	application/octet-stream	DEPLOYED	Delete
MULLER-LAB-ZEBRAFISH-16.jpg	2015-06-11 13h41	0.17Mo	application/octet-stream	DEPLOYED	Delete
MULLER-LAB-ZEBRAFISH-15.jpg	2015-06-11 13h41	0.18Mo	application/octet-stream	DEPLOYED	Delete
MULLER-LAB-ZEBRAFISH-14.jpg	2015-06-11 13h40	0.18Mo	application/octet-stream	DEPLOYED	Delete
MULLER-LAB-ZEBRAFISH-13.jpg	2015-06-11 13h40	0.18Mo	application/octet-stream	DEPLOYED	Delete

The bottom table lists all images uploaded to the Cytomine instance and their current status. Once it is "Deployed", an image will appear in the user storage and selected (if any) project image list. Some images require additional conversion steps (e.g. non-pyramidal TIFF, or multidimensional microscopy formats supported by Bio-Formats) and will take longer than natively supported formats. The uploaded image will also be available for other projects and the User can associate it



to another project through the "Add Image" (blue) button in the specific Project image list:

DEMO-VARIOUS

10 records per page Search:

id	Preview	Name	Created	Action
264100		cells1.png	2015-06-11 09h26	+ Add
265148		cells1.png	2015-06-11 10h41	+ Add
265317		cells2.png	2015-06-11 10h41	+ Add
265471		cells5.png	2015-06-11 10h41	+ Add
265569		cells4.png	2015-06-11 10h41	+ Add
265667		cells3.png	2015-06-11 10h41	+ Add
265761		cells6.png	2015-06-11 10h42	+ Add
265869		cells8.png	2015-06-11 10h42	+ Add
265975		cells7.png	2015-06-11 10h42	+ Add
266423		LUNG1.jp2	2015-06-11 10h48	+ Add

Showing 1 to 10 of 175 entries

An image can be removed from a project through the "Delete image" option in the drop down list (Arrow at the right of the explore button):

DEMO-VARIOUS

10 records per page Search:

ID	Preview	Name	Width (px)	Height (px)	Magnitude	Resolution (µm/px)	User an.	Algo an.	Valid an.	Vendor	Created	Status	Action
305162		test_upload.png	1287	720	Undefined	Undefined	0	0	0	Undefined	2015-06-11 20h00	None	Explore
287484		OS-2.ndpi	128976	73728	40 X	0.227	0	0	0	HAMAMATSU	2015-06-11 19h18	None	Explore
287147		CMU-1.evs	48000	32814	20 X	0.499	0	0	0	aperio	2015-06-11 19h17	None	Explore

Showing 1 to 3 of 3 entries

6.2.4 Apply Cytomine-DataMining analysis modules and proofreading

Our Cytomine-DataMining analysis modules can be launched from Cytomine-WebUI. It has to be



noted that other third-party modules can be similarly launched, provided they are registered as Software into the Cytomine-Core and described by a template of Software parameters.

Here we only illustrate the basic principles of these workflows on small ("toy") datasets. Obtaining satisfactory recognition performances on real-world applications depends on many factors including image variations (due to image acquisition and sample preparation protocols), and the quality and quantity of annotations provided for training. To obtain validated training sets by multiple experts, one might use the Inter-observer module (see below Section 6.2.5). Overall, our tool allows to rapidly prototype such applications by using our generic algorithms described in Supplementary Note 4. Additional research in machine learning and image analysis might produce algorithms better suited for specific applications. Our modules allow to build models by tree-based supervised learning, apply them on new images, edit results, and re-apply learning procedures based on enhanced training sets.

6.2.4.1 Tissue Detection and Semantic segmentation

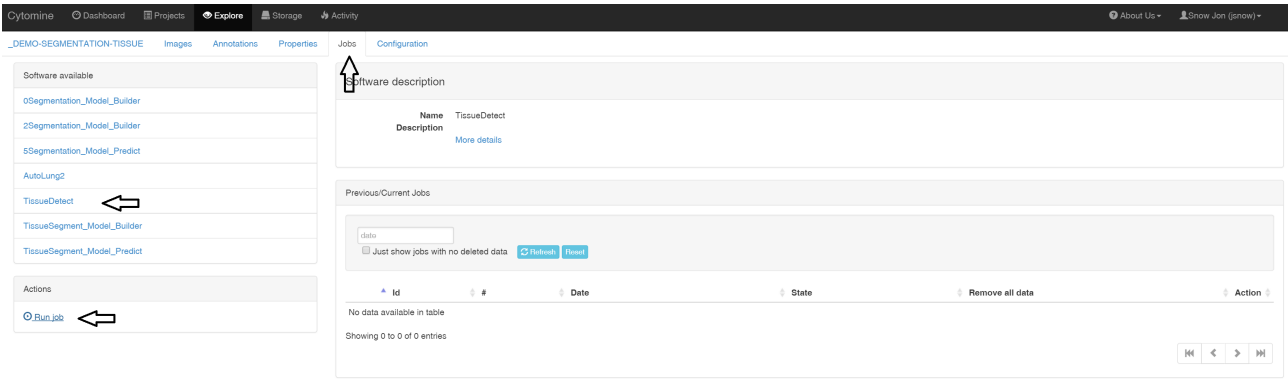
In this example, we want to quantify the size (area) of tumor islets with respect to section sizes in whole slide (gigapixel) images. In order to produce these quantification results, we will apply four registered softwares: a Tissue Section Detector, a Tumor detector learning procedure, a Tumor detector prediction procedure, and a final procedure to output statistics (ComputerTermArea). We use the toy project DEMO-SEGMENTATION-TISSUE.

The first step (if not already done) is to associate the Software to the Project in the Project Configuration page (bottom of the page), in our case we begin with the TissueDetect software:

The image shows two screenshots of the Cytomine web interface. The top screenshot is the 'Configuration' page for the project '_DEMO-SEGMENTATION-TISSUE'. It features a 'Softwares' section with a dropdown menu listing various software modules. 'TissueDetect' is selected and highlighted in blue. To the right of the dropdown is an 'Add' button (with a left-pointing arrow) and a vertical stack of 'Remove' buttons. A downward arrow points from the 'Configuration' tab to this screenshot. The bottom screenshot is the 'Custom UI Configuration' page. It shows a table of 'Project tabs' with columns for 'project admin', 'project user', and 'project guest user'. The 'Jobs' tab is highlighted with a green background, while the 'Config' tab is highlighted with a red background. A right-pointing arrow points to the 'Jobs' tab. A downward arrow points from the 'Configuration' tab to this screenshot.

The user also has to activate (green) the "Jobs" tab in the "Custom UI" panel (if not already done): Now let's consider the User wants to apply the "Detect Sample" analysis module to detect its tissue sections. The user first click on the "Jobs" tab of the project, then on the "TissueDetect" software,

then on the "Run Job":



It opens a "Launch new job" dialog box to allow the User to configure the Software parameter values (the form is automatically build based on software parameter definition in the database). Here, we want to associate the term "Section" to objects detected by the procedure, and we keep default values for the thresholding algorithm:

Launch new job

Run TissueDetect on project _DEMO-SEGMENTATION-TISSUE

Name	Value	Required
cytomine_predict_term	<input type="text" value="Section"/>	<input type="checkbox"/>
cytomine_max_image_size	<input type="text" value="2000"/>	<input type="checkbox"/>
cytomine_erode_iterations	<input type="text" value="3"/>	<input type="checkbox"/>
cytomine_dilate_iterations	<input type="text" value="3"/>	<input type="checkbox"/>
cytomine_athreshold_blocksize	<input type="text" value="951"/>	<input type="checkbox"/>
cytomine_athreshold_constant	<input type="text" value="5"/>	<input type="checkbox"/>

Preview

This will add an entry to the "Previous/Current jobs" panel. The job will be executed and Status is displayed and updated during execution. It can be seen by clicking on the "Details" blue button. This also displays parameter values of the running job:

Cytomine Dashboard Projects Explore Storage Activity About Us Show Jon (jnow)

Software available

- 0Segmentation_Model_Builder
- 2Segmentation_Model_Builder
- 5Segmentation_Model_Predict
- AutoLung2
- TissueDetect
- TissueSegment_Model_Builder
- TissueSegment_Model_Predict

Actions

- Run job

Software description

Name: TissueDetect

Description: [More details](#)

Previous/Current Jobs

data

Just show jobs with no deleted data [Refresh](#) [Reset](#)

Id	#	Date	State	Remove all data	Action
305384	1	2015-06-11 20h37	Success	Delete data	View

Showing 1 to 1 of 1 entries

Job details

Name: Job 1

Launched by: jnow

Date: 2015-06-11 20h37

Status: [Success](#)

Data: [Annotations](#)

Parameters

Search:

Name	Value	Type
cytomine_attneshold_blocksize	951	Number
cytomine_attneshold_constant	5	Number
cytomine_dilate_iteations	3	Number
cytomine_erode_iteations	3	Number
cytomine_id_project	278306	Number

Once the job has reached the "Success" status (in roughly one minute for the two images of our toy project running on our demo instance), one can see (by scrolling down) the objects detected by this job by clicking on "View Predicted galleries" (blue button) that will open the Annotations tab with the filter corresponding to this UserJob. In our case, Sections of the lung are well detected automatically:



Cytomine Dashboard Projects Explore Storage Activity About Us Show Job (arrow)

Parameters

Name	Value	Type
cytomine_athreshold_blocksize	951	Number
cytomine_athreshold_constant	5	Number
cytomine_dilate_iterations	3	Number
cytomine_erode_iterations	3	Number
cytomine_id_project	278366	Number

Showing 1 to 5 of 11 entries

Selected Job results

Recognition rates

- For Section (success 100 %), algo suggest:
- Average : 100.00
- Average (per class) : 100.00

[View confusion matrix](#) [View predicted galleries](#)

Filters

Search in usatfgo annotations
Search in reviewed annotations

DEMO-SEGMENTATION-TISSUE
[Check all](#) [Uncheck all](#)

Annotations without terms
Annotations with several terms

DEMO-SEGMENTATION-TISSUE-ONTOLOGY
 Tissue
 Bone
 Tumor
[Check all](#) [Uncheck all](#)

Users
 Lannister Corsari (dannister)
 Snow Jon (snow)
 Stark Eddard (ostank)
[Check all](#) [Uncheck all](#)

DEMO-SEGMENTATION-TISSUE
0Segmentation_Model_Builder
Autolung2
2segmentation_Model_Builder
TissueDetect
110020161837266

0Segmentation_Model_Predict
TissueSegment_Model_Builder
TissueSegment_Model_Predict

Predefined Filters
[Select](#) [Delete](#) [Save current selection](#)

Negative

Section

Tumor
[Download CSV](#) [Download Excel](#) [Download PDF](#)

Download

The user can then validate annotations produced by this module in all project images by using proofreading (Review) tool from the Project Image listing:

DEMO-SEGMENTATION-TISSUE Images Annotations Properties Jobs Configuration

10 records per page

ID	Preview	Name	Width (px)	Height (px)	Magnitude	Resolution (µm/pixe)	User an.	Algo an.	Valid an.	Vendor	Created	Status	Action
278614		LUNG2.jp2	38912	32258	Undefined	Undefined	0	2	0	Undefined	2015-08-11 11h42	None	Explore
278476		LUNG1.jp2	30720	25600	Undefined	Undefined	21	2	0	Undefined	2015-08-11 11h42	None	Explore

Showing 1 to 2 of 2 entries

↑ [Add new image](#) [Refresh](#)

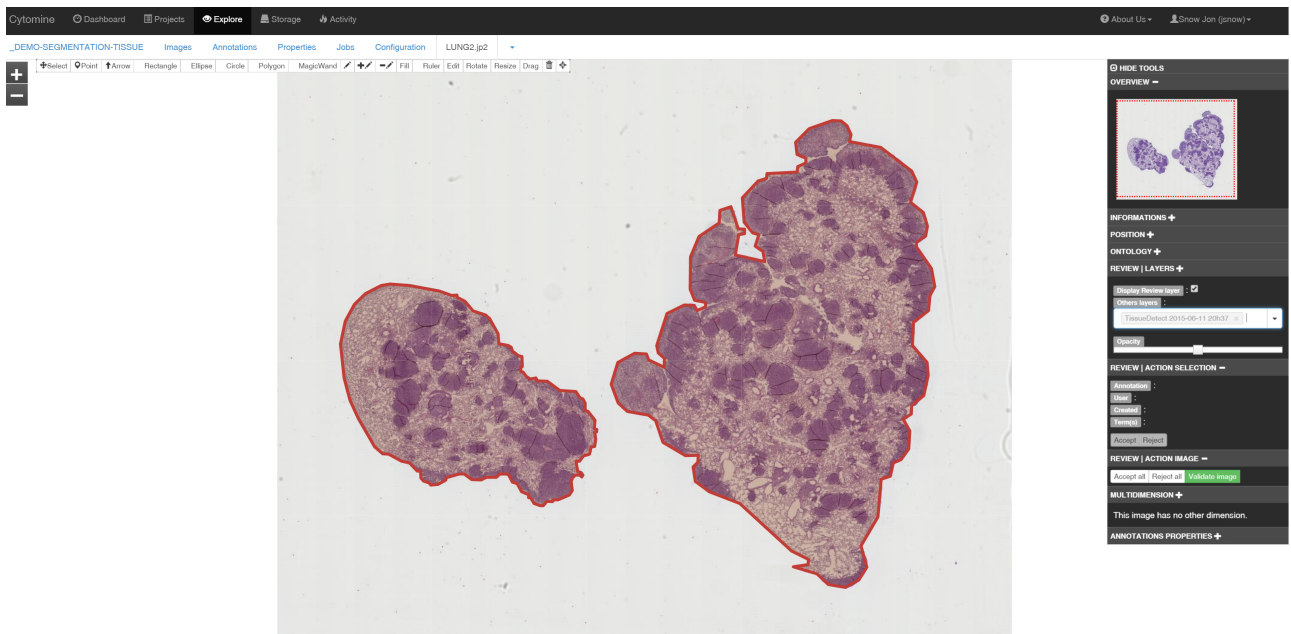
Search:

Explore
Start reviewing
Start reviewing (Cyto)
Copy image and annotations
Import user annotations
Description
Download
Rename
Delete
More info

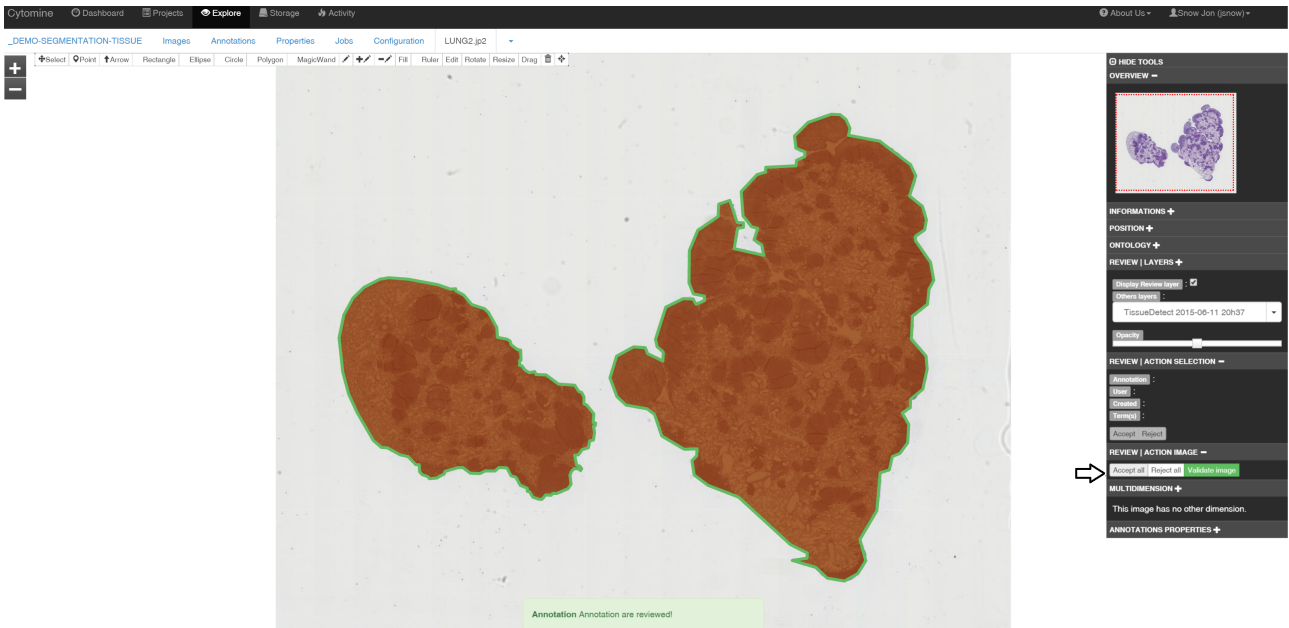
"Start reviewing" (using LUNG2 image) opens the Explore view with additional "Review" tools in the right Panel. The user can then first select the Job (or User) layer from which he wants to validate annotations:



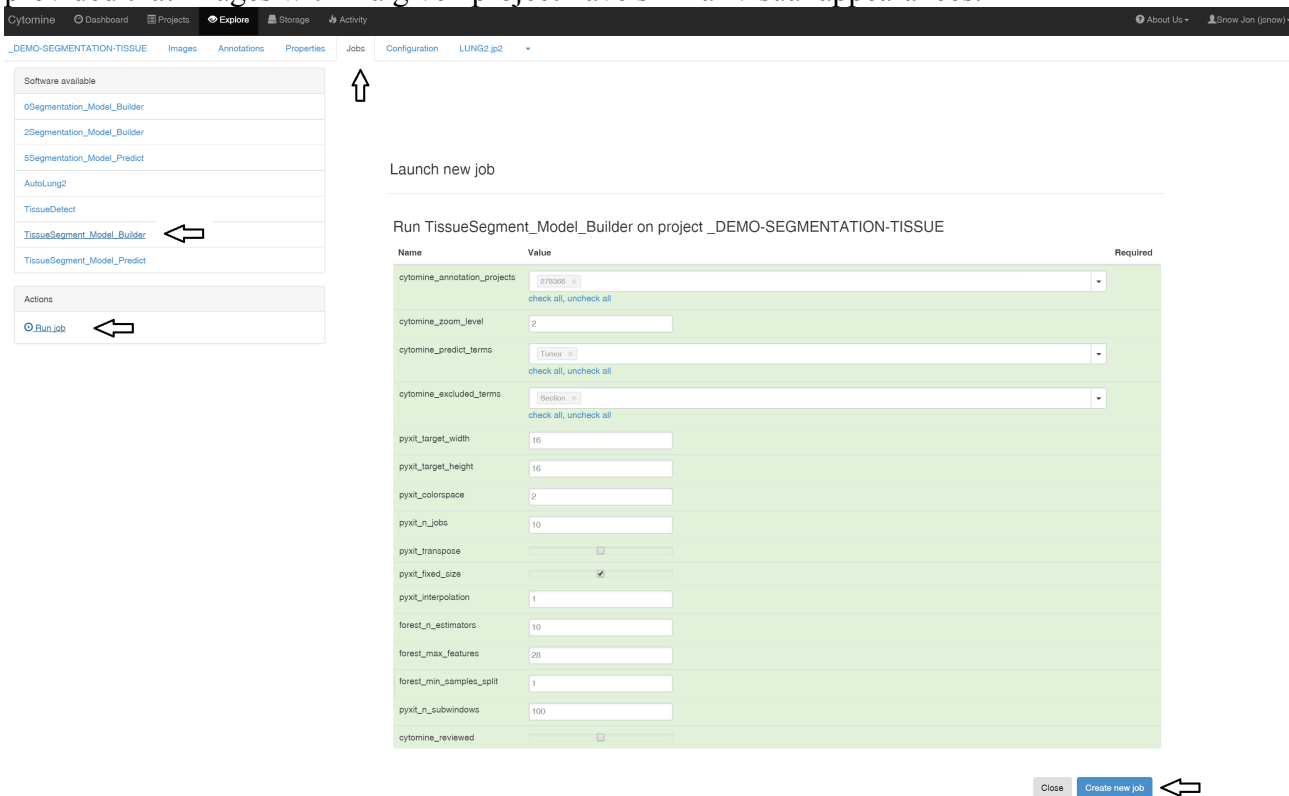
It displays the unvalidated annotations with a lighter opacity and red borders:



The user can then accept annotations one by one (by selecting the annotation, then click on "Accept" or press "A" on the keyboard) or all at one (by clicking on "Accept all"). Validated annotations are colored with the original color of the ontology Term and have green borders. Concretely, these annotations are copied into the "Reviewed" annotations of that image:



Once sections have been detected (e.g. to compute section Area), a typical application might be to detect tumor islets within them. For that, we use the Cytomine-DataMining Semantic Segmentation analysis module. We will exploit Tumor and Negative manual annotations to build a Tumor detection model, then we will use the model to segment whole slide images. As for the TissueDetect module, the software has to be added to the Project (if not already done) in the Project Configuration panel. Then the TissueSegmentModel_builder has to be run using appropriate parameter values (in our case select the current Project identifier to download annotations, the "Tumor" as predicted terms, the "Section" as excluded terms, and zoom level = 2). Learning is in general only performed once in a project (using annotations coming from this project or other ones), provided that images within a given project have similar visual appearances.

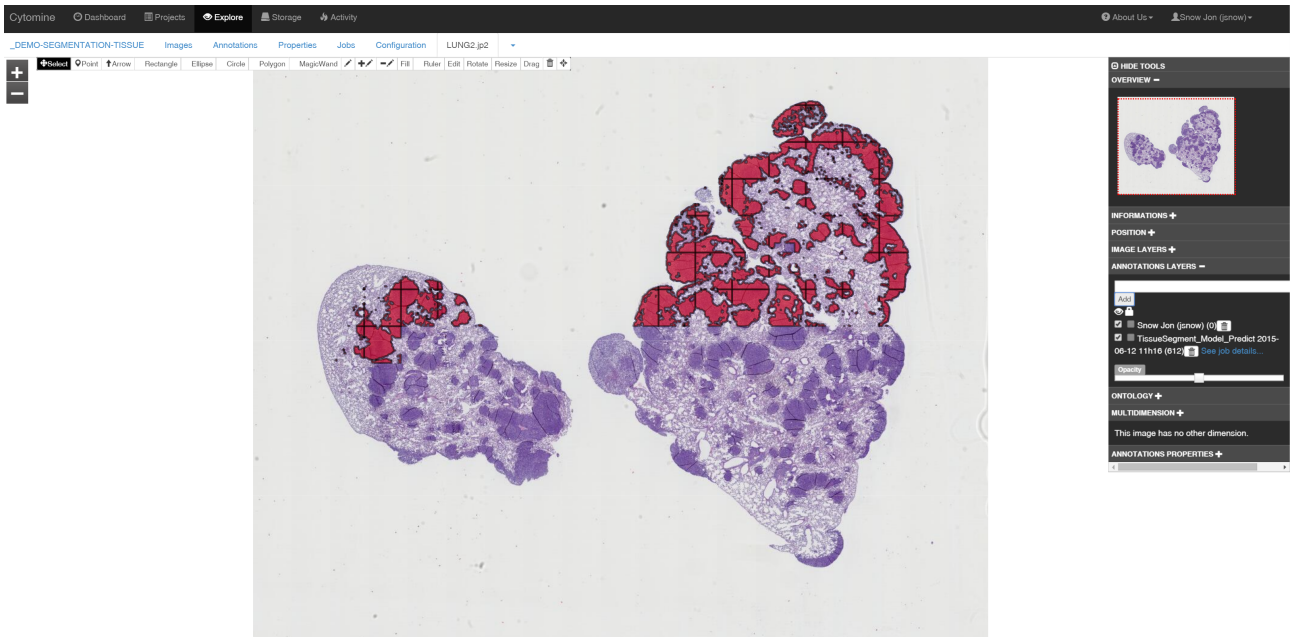


Once the Job reaches the "Success" status (in roughly one minute using our "toy" data on the demo instance), the Tumor detection model is ready to be applied to whole-slide images. The user then launch the TissueSegment_Prediction Job using appropriate parameter values (the image identifier, identifier of the TissueSegmentModel_builder job which created the model, the "Tumor" as predict term, the "Section" ROI term and activate the cytomine_reviewed_roi to only apply the model within validated Sections, zoom_level = 2):

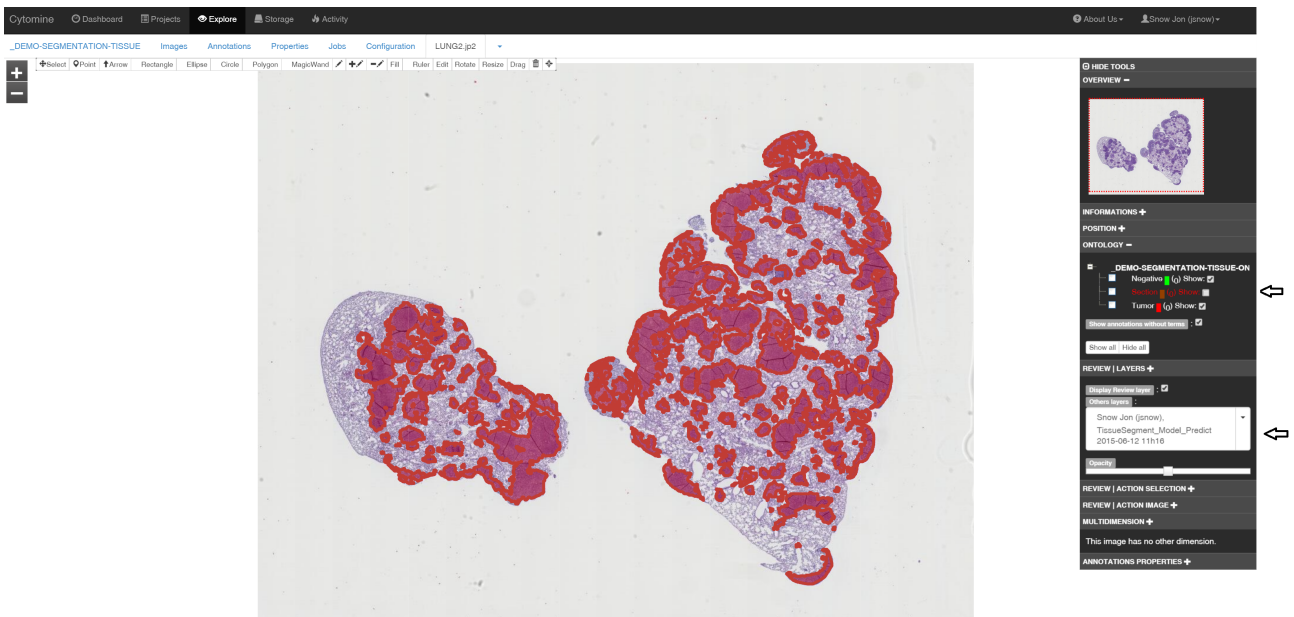
The screenshot shows the Cytomine web interface with the 'Launch new job' dialog box open. The dialog is titled 'Run TissueSegment_Model_Predict on project _DEMO-SEGMENTATION-TISSUE'. It contains a list of parameters to be configured for the job. The parameters are organized into two identical sections. The first section includes parameters like cytomine_id_image, model_id_job, cytomine_zoom_level, cytomine_title_size, cytomine_title_min_stddev, cytomine_title_max_mean, cytomine_startx, cytomine_starty, cytomine_endx, cytomine_endy, cytomine_nb_jobs, cytomine_predict_term, cytomine_roi_term, cytomine_reviewed_roi, pyxif_target_width, pyxif_target_height, pyxif_colospace, and pyxif_nb_jobs. The second section includes cytomine_predict_term, cytomine_roi_term, cytomine_reviewed_roi, pyxif_target_width, pyxif_target_height, pyxif_colospace, pyxif_nb_jobs, cytomine_predict_step, cytomine_union, cytomine_postproc, cytomine_min_size, cytomine_union_min_length, cytomine_union_bufferoverlap, cytomine_union_area, cytomine_union_min_point_for_simplify, cytomine_union_min_point, cytomine_union_max_point, cytomine_union_nb_zones_width, cytomine_union_nb_zones_height, cytomine_mask_internal_holes, cytomine_count, cytomine_max_size, pyxif_post_classification, and pyxif_post_classification_save_to. The 'cytomine_reviewed_roi' parameter is checked in both sections. The 'cytomine_union' and 'cytomine_postproc' parameters are also checked. The 'cytomine_mask_internal_holes' parameter is unchecked. The 'cytomine_count' parameter is unchecked. The 'cytomine_max_size' parameter is set to 10000000. The 'pyxif_post_classification' parameter is set to 'tumor'. The 'pyxif_post_classification_save_to' parameter is set to '/tmp'. The dialog has a 'Close' button and a 'Create new job' button.

This procedure can take time (from minutes to hours) depending on model complexity, image sizes, resolution level, and allocated computing resources. It will create progressively annotations in tiles of the image. The process is running in the background and the user can perform other tasks meanwhile. The progress can be seen visually by opening the image and selecting in the "Annotation layer" tool the running Job, as illustrated below:

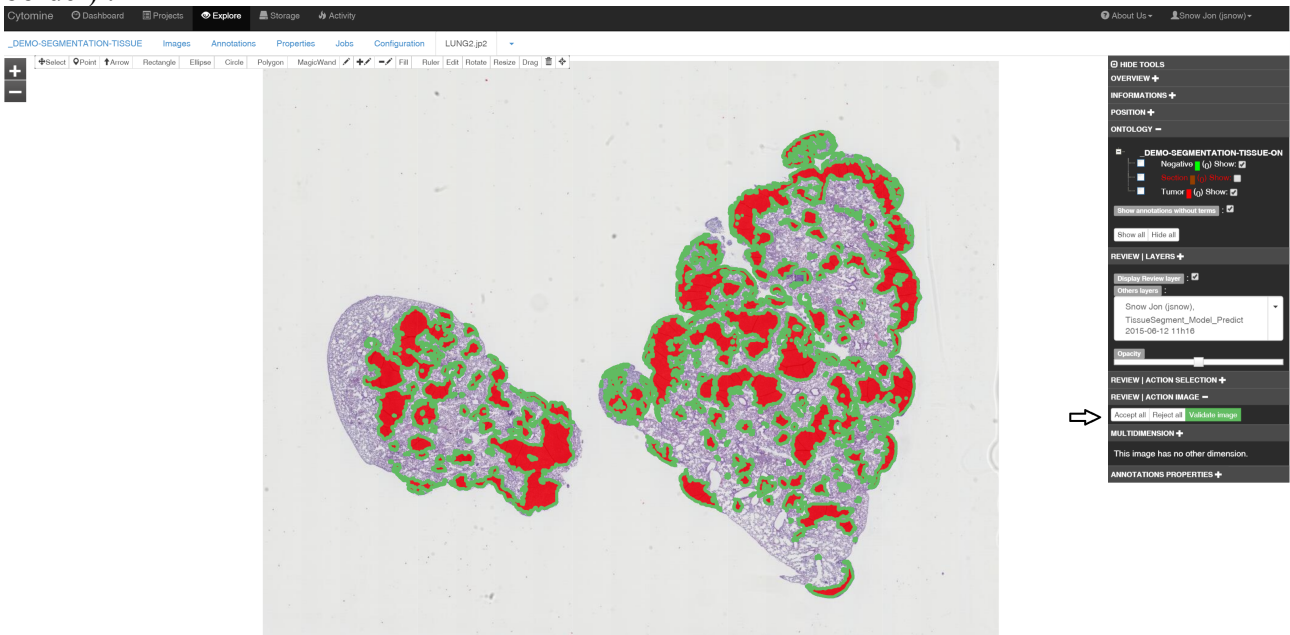




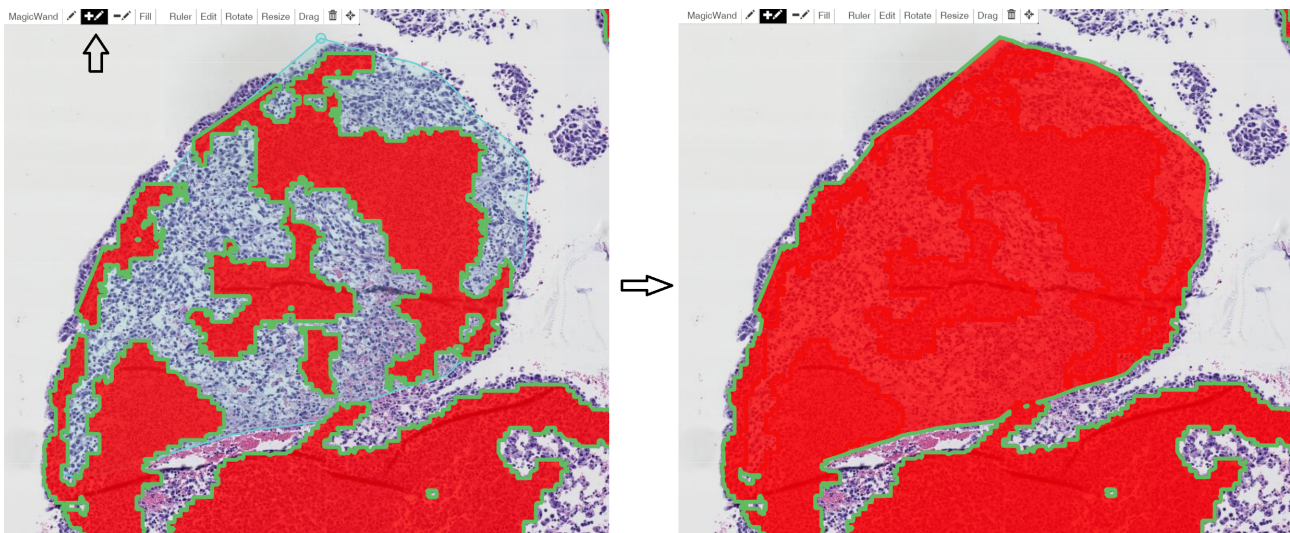
Then once all tiles are processed, the module will apply post-processing and an union procedure of all overlapping geometries. Once the whole process is done (it displays the "Success" status in the Job panel, it can take roughly 40 minutes to process this "toy" image on our demo instance), the user can review these tumor annotations using the same Reviewing procedure as for Tissue detection, by selecting the corresponding TissueSegment_Prediction job (the "Section" annotations can be hidden to ease reviewing by unselecting the box "Show" in the Ontology panel):



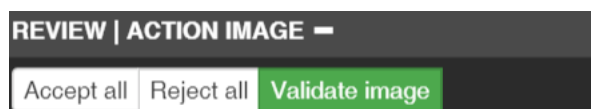
When most of the annotations are correct, we recommend to use the "Accept all" operations that will validate all annotations at once (they now take visually the original term color and have a green border) :



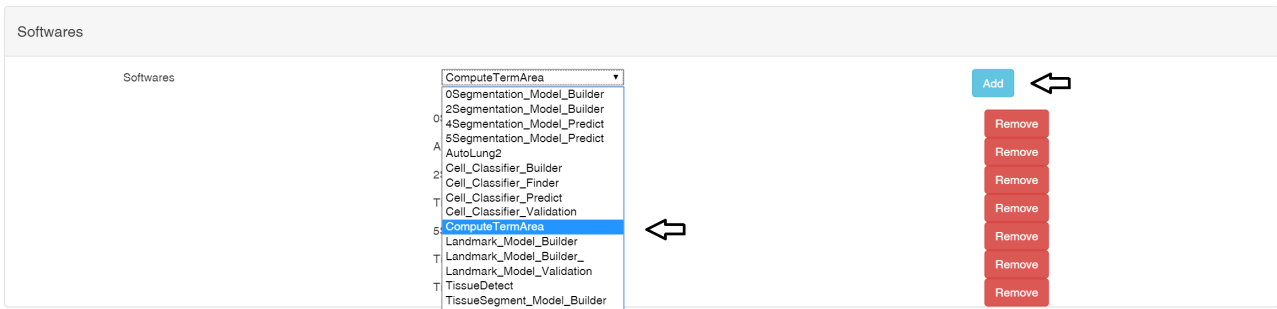
If annotations are not satisfactory at all, we recommend to annotate manually more examples (corresponding to observed predictions errors) and re-train a model. If only some annotations do not fit well the regions of interest (e.g. it misses portions of several tumor islets), the user can use proofreading tools to edit their geometries (or reject objects, e.g. tissue subtypes that are not tumor islets). Using the "t" keyboard or the "Display review layer" checkbox, the user can switch the display of the review layer for further inspection to look at the original tissue, and refine tumor contours using +/-/Fill polygon operations (+ operates an union of the draw polygon with the reviewed polygon, - subtract it):



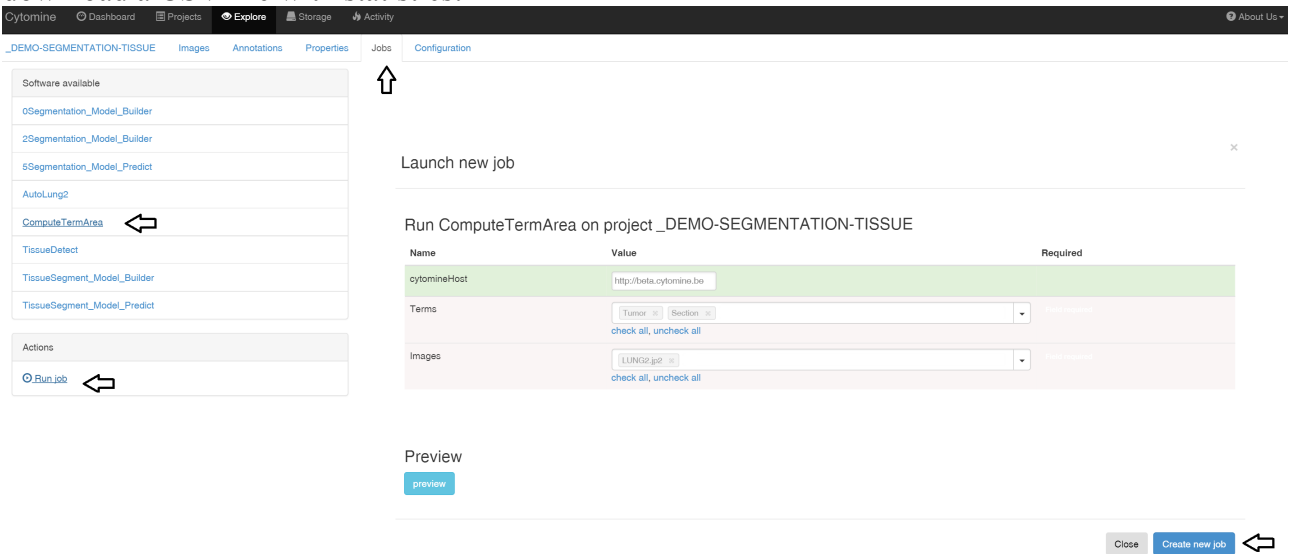
Once the whole image is proofread, the user has to Validate the image (green button) in the right Tool panel:



Now, it is possible to use the "ComputerTermArea" software to generate statistics about Section and Tumor area and ratios. Add the software to the project (once) in the Project configuration Panel, and run the Job:



Then run the job, select "Tumor" and "Section" as Terms, and your image, in order to generate and download a CSV file with statistics:



#	Date	State	Remove all data	Action
17	2015-06-12 14:09		Delete data	Details
16	2015-06-12 14:07		Delete data	Details
15	2015-01-15 11:16		Delete data	Details
14	2014-01-25 01:53		Delete data	Details
13	2013-12-19 09:08		Delete data	Details

Showing 1 to 5 of 17 entries

Job details

Name: Job 17
 Launched by: mjaire
 Date: 2015-06-12 14:09
 Status: Not launch
 Data: Annotations

Parameters

Name	Value	Type
cytomineHost	http://beta.cytomine.be	String
Images	14/1350548372140/PGP_POUMON_PGPT_41_..._2012-08-07_12.13.50.jp2_...	ListDomain
Terms	Adenocarcinomes, Poumon	ListDomain

Showing 1 to 3 of 3 entries

Selected Job results

Filename	Comment	Size	View	Download
report2.csv	Report	5 KB	report.csv	report.csv

Summary Area	Tumor	Section	Total
Image			
14/1350548372140/LUNG2.jp2	4742018	11852289	16594287
Total	4742018	11852289	16594287
Summary Number			
Image			
14/1350548372140/LUNG2.jp2	139	3	142
Total	139	3	142
Ratio Data			
Image			
14/1350548372140/LUNG2.jp2	0.285763	0.714237	1.000000
Details			
Image 1			
14/1350548372140/PGP_POUMON_PGPT_41_..._2012-08-07_12.13.50.jp2			

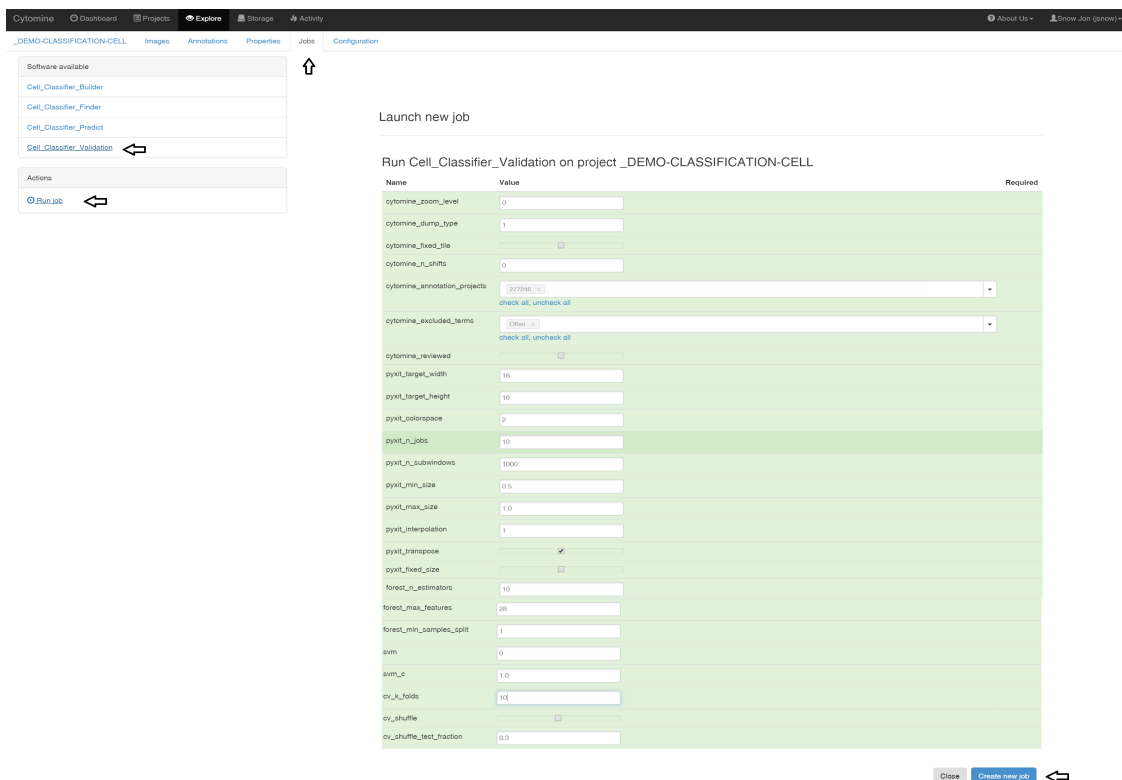
Tumor			
Created	2012.11.29 14:10:06	Area	223442.0
	2012.11.29 14:10:06		161401.0



6.2.4.2 Object detection and classification

In this guide, we explain how to apply an object finder procedure followed by an object classification step, e.g. to classify positive and negative cells in cytology images. This example uses four softwares from the Cytomine-DataMining analysis modules: classification validation, classification model builder, object finder, and classification prediction. The provided "toy" demo project (DEMO-CLASSIFICATION-CELL) contains two main classes of cells (10 positive in red, 10 negative in blue). The goal is to build a workflow to detect and classify these cells automatically.

First, the classification validation module allows to evaluate by cross-validation classification performances of the image classification algorithm, given its parameter values and manual annotations with semantic terms. It is launched as other modules through the Jobs panel of the Project:



Once the process reaches the "Success" state, it is possible to view recognition rates, misclassified objects, and an interactive confusion matrix of the classifier in the Job Details (click on the Blue "Details" button, then scroll down and click on the blue "View confusion matrix"). It is possible to click on the confusion matrix numbers to view galleries of cell classifications. In our example, the classifier reaches 100% recognition rate for both cell types:

Cytomine Dashboard Projects Explore Storage Activity About Us Show Jon (jnow)

Id	#	Date	State	Remove all data	Action
410923	8	2015-06-12 14h41	Success	Delete data	Details
413222	7	2015-06-12 11h47	Success	Delete data	Details
411065	6	2015-06-12 11h38	Running	Delete data	Details
410042	5	2015-06-12 11h38	Running	Delete data	Details
403686	4	2015-06-12 11h36	Running	Delete data	Details

Showing 1 to 5 of 8 entries

Job details

Name: Job 0
 Launched by: jnow
 Date: 2015-06-12 14h41
 Status: success
 Data: Annotations

Parameters

Name	Value	Type
cv_k_folds	5	Number
cv_shuffle	<input type="checkbox"/>	Boolean
cv_shuffle_test_fraction	0.3	Number
cytomine_annotation_projects	277246	ListDomain
cytomine_dump_type	1	Number

Showing 1 to 5 of 30 entries

Selected Job results

Recognition rates

- For Negative (success 100 %), also suggest:
- For Positive (success 100 %), also suggest:
- Average : 100.00
- Average (per class) : 100.00

View confusion matrix View predicted galleries

	X	Nega.	Othe.	Posl.	total
Nega.		10			100%
Othe.			10		100%
Posl.				10	100%

Suggest Term Positive for annotation Positive

The classification validation module only evaluates classification models without saving them. Once satisfactory results are obtained, the user can build with corresponding parameter values and save a classification model by using the classification model builder module. It will save a model on the processing server that can be later reused by the classification prediction module (it takes less than one minute on our demo instance using our small "toy" data):

Cytomine Dashboard Projects Explore Storage Activity About Us

_DEMO-CLASSIFICATION-CELL Images Annotations Properties Jobs Configuration

Software available

- Cell_Classifier_Builder
- Cell_Classifier_Finder
- Cell_Classifier_Predict
- Cell_Classifier_Validation

Actions

- Run job

Launch new job

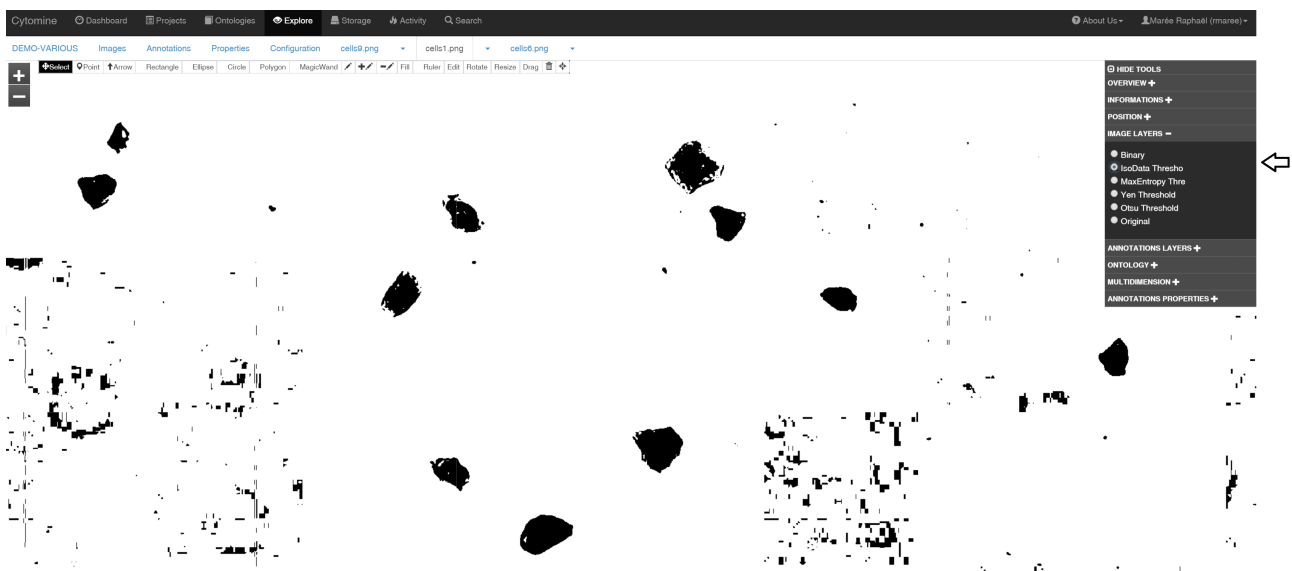
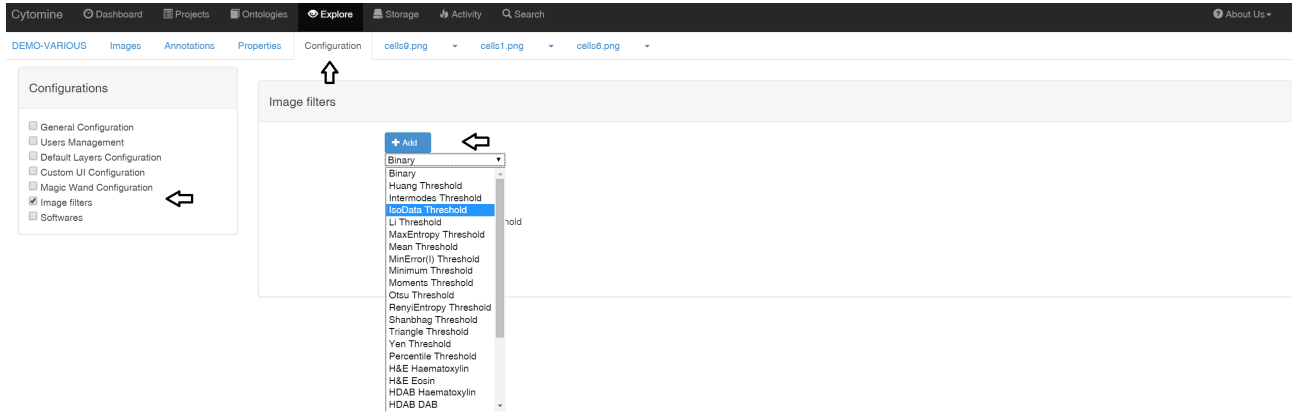
Run Cell_Classifier_Builder on project _DEMO-CLASSIFICATION-CELL

Name	Value	Required
cytomine_annotation_projects	277246	
cytomine_zoom_level	0	
cytomine_excluded_terms	Other	
pyxit_target_width	16	
pyxit_target_height	16	
pyxit_colorspace	2	
pyxit_n_jobs	10	
pyxit_min_size	0.5	
pyxit_max_size	1	
pyxit_interpolation	2	
forest_n_estimators	10	
forest_max_features	28	
forest_min_samples_split	1	
pyxit_n_subwindows	1000	
svm	1	
cytomine_dump_type	1	
cytomine_reviewed	<input type="checkbox"/>	
pyxit_transpose	<input checked="" type="checkbox"/>	
cytomine_predict_terms	Positive	
pyxit_fixed_size	<input type="checkbox"/>	
forest_shared_mem	<input type="checkbox"/>	
svm_c	1.0	

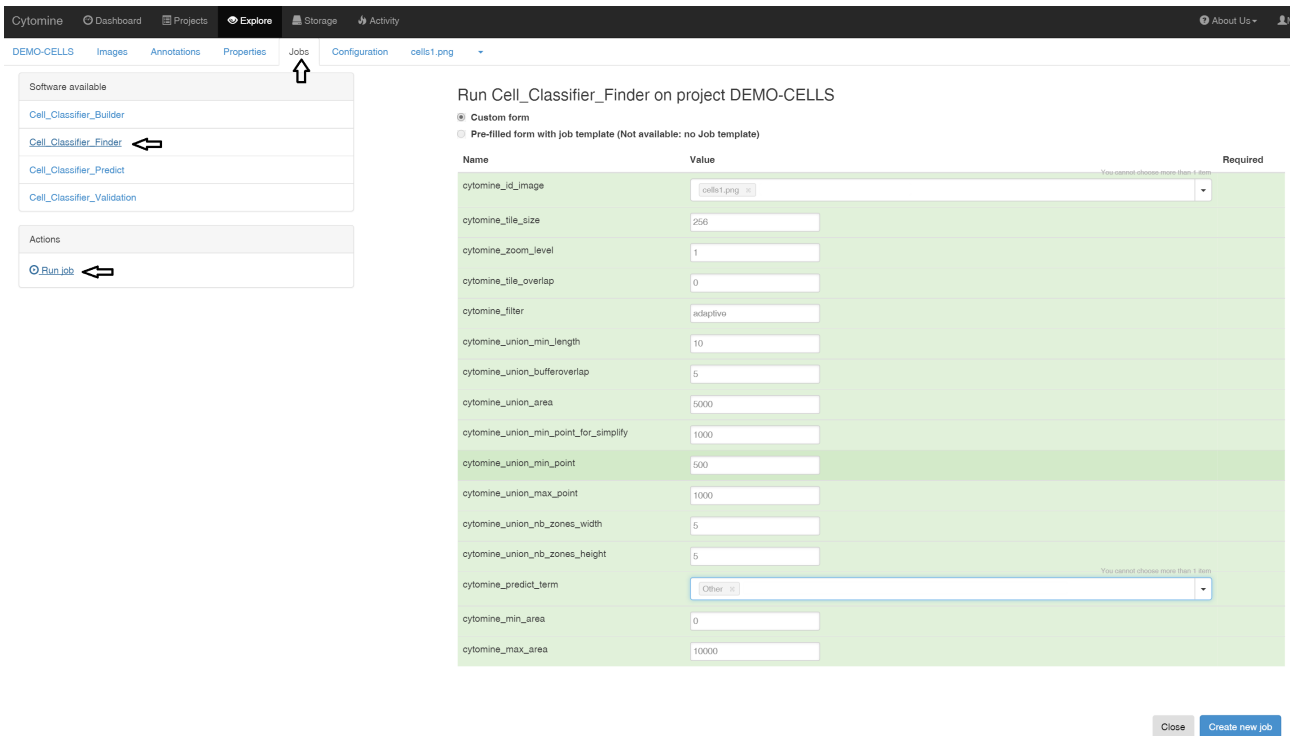
Close Create new job



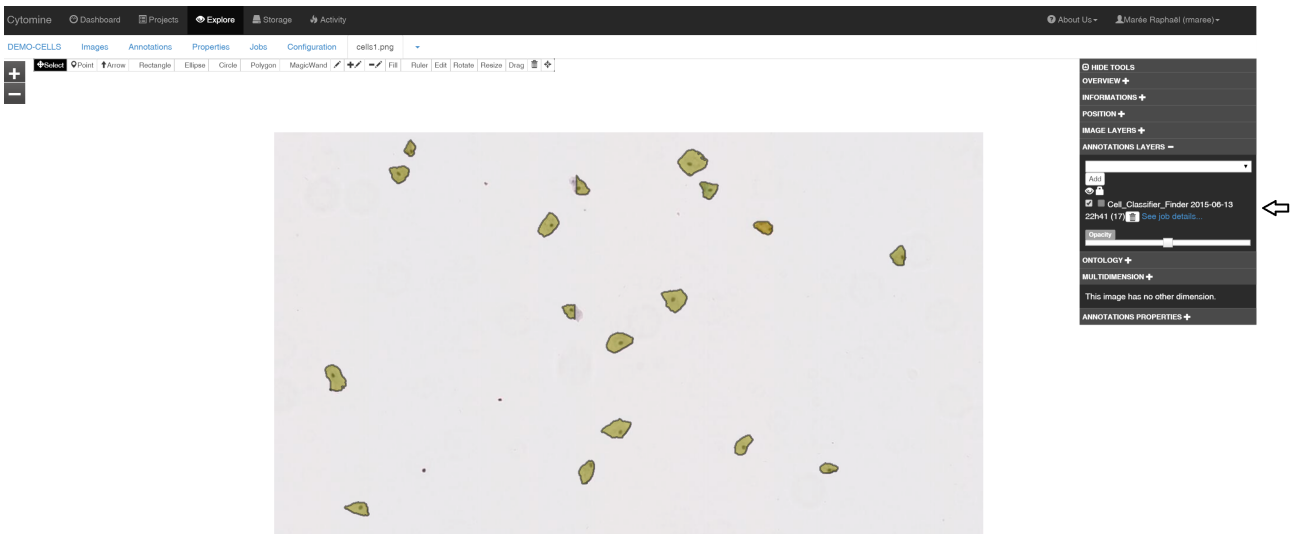
Now it is possible to apply this model to classify annotations of an image. We thus need before to apply an object finder to the image to create annotations corresponding to candidate objects. To ease the choice of a thresholding algorithm, it is first possible to apply standard algorithms on-the-fly, tile per tile, in the Cytomine-WebUI image explore view. The user needs first to add the image layer (in the Project Configuration panel), then apply it using the "Image Layers" panel at the right of the image Explore view:



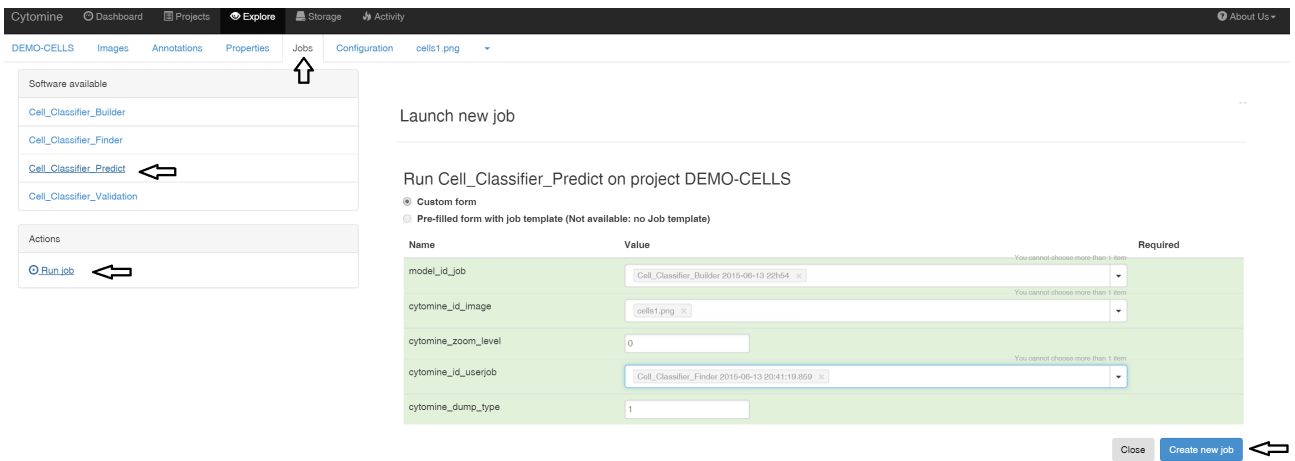
To apply the Object finder module on an image to create annotations, the user needs to add the software to the project (once), then launch it. It will create annotation objects in the corresponding job layer (here we use zoom level=1 and adaptive thresholding algorithm on cells1 image):



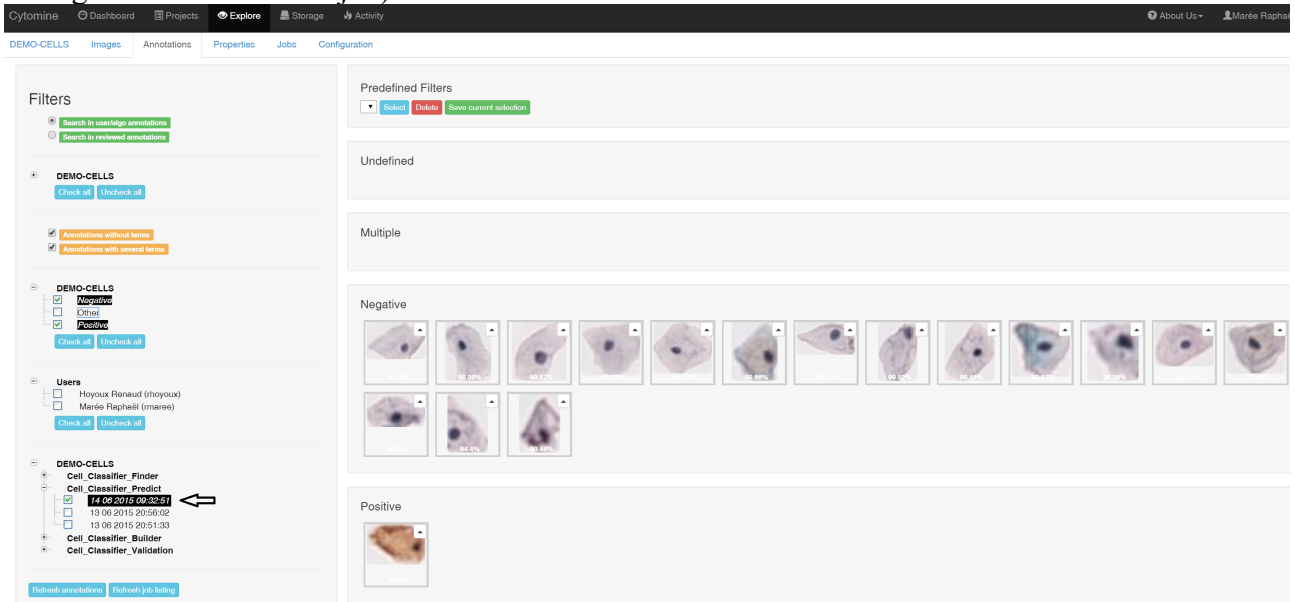
Once the job has reached its "Success" (less than one minute for one image on our demo instance) status, detected objects can be seen in "View predicted galleries" (blue button in the "Details" of the job) or directly in the Explore view of that image:



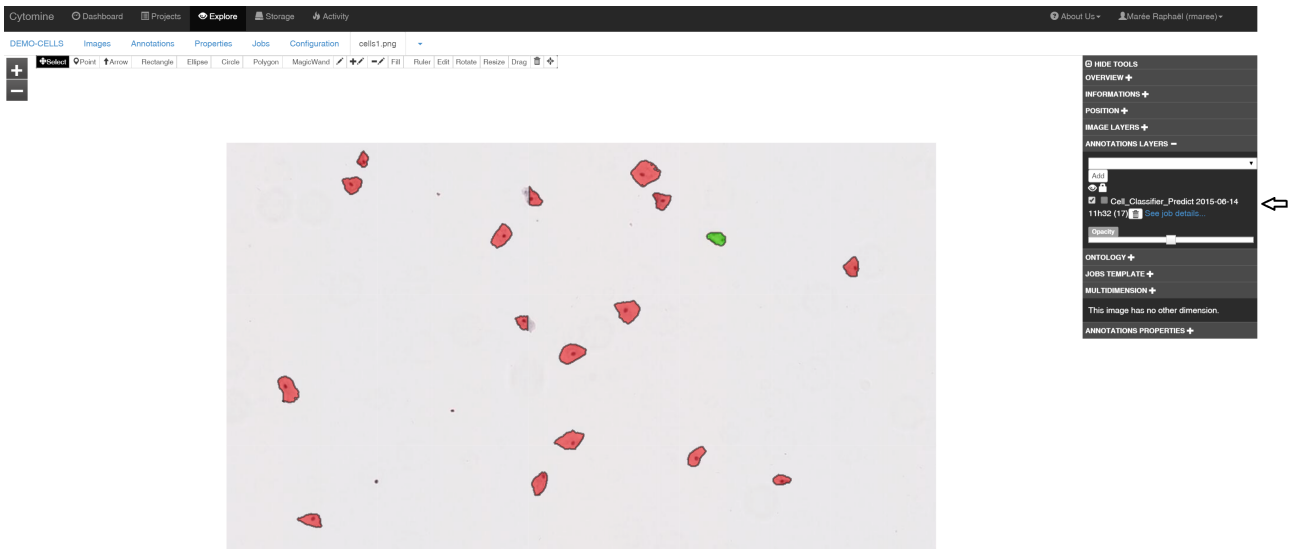
Now, we can apply a classifier to these detected objects in the image, by launching the classification prediction module (Cell_Classifier_Model_Predict), using the previously built classifier model, and the previously found candidate annotations (using the identifier of the job which generated these objects):



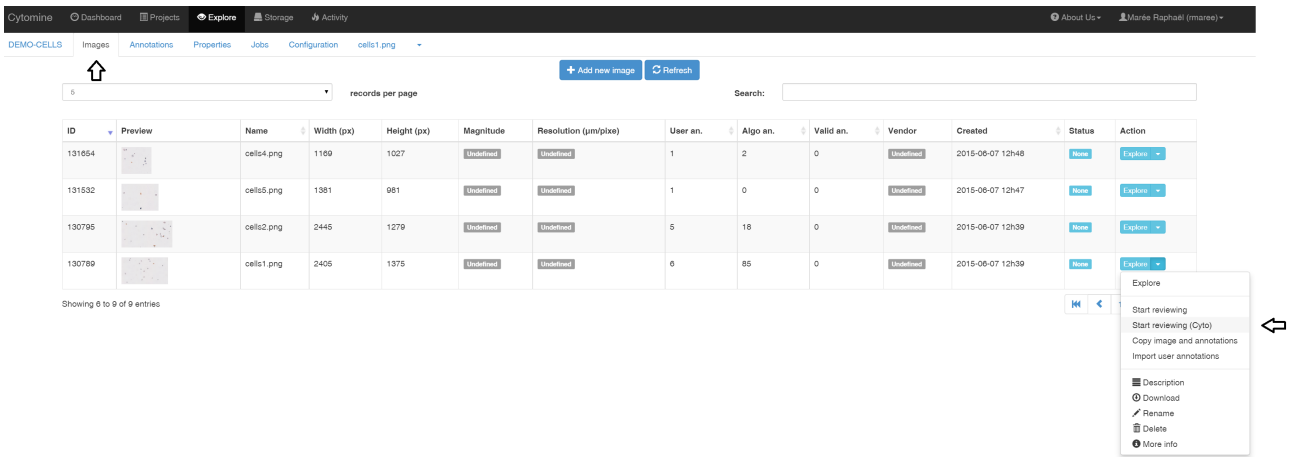
Once the classifier has reached its "Success" status (it takes less than one minute on our demo instance using annotations detected in cells1.png image), it is possible to visualize its classifications (as another job layer, either in the Explore view, or as "Predicted galleries" in the Annotation tab through the Details of the job).



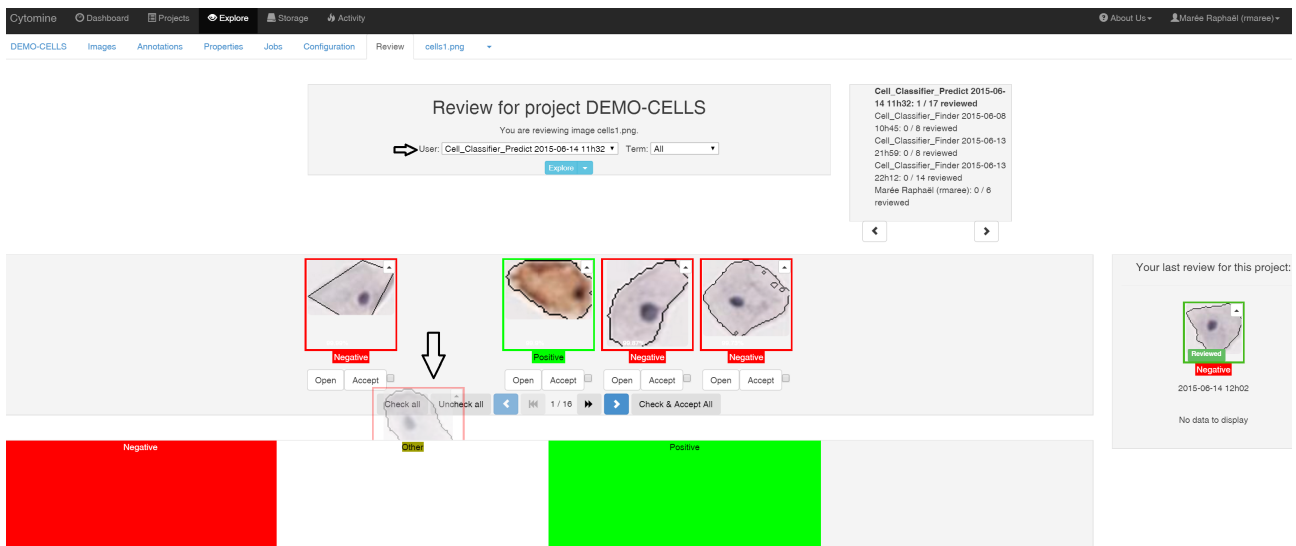
In this toy example, the classifier perfectly classifies cells (one positive in green, others negative).



As in the tissue detection application, these annotations can be reviewed by an expert. We have developed a specific "Review (Objects)" module to review object classifications in a more efficient way. It can be launched from the Project image listing:



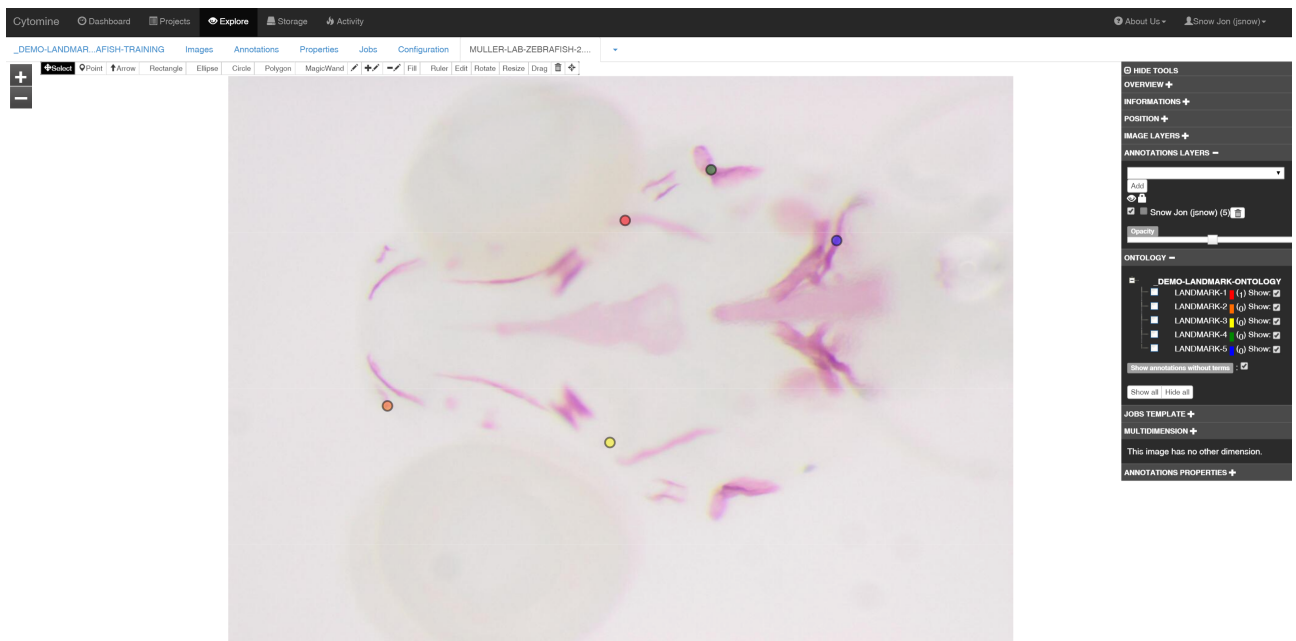
This module allows to select a user/job layer and displays galleries of its predictions (using pagination across all annotations). The user can then either accept these classifications, or correct them by drag'n'drop into visual boxes corresponding to the correct term. Validated and corrected annotations are copied to the Review layer of that image.



6.2.4.3 Landmark detection

In this guide, we explain how to use the landmark detection module on a "toy" dataset of Zebrafish embryo images. This example uses two softwares from the Cytomine-DataMining analysis modules: Landmark_Builder and Landmark_Predict. The provided "toy" demo project (DEMO-LANDMARK-ZEBRAFISH) contains five landmarks for 20 images, and 10 unlabelled images. The goal is to build a workflow to detect these landmarks automatically in the unlabelled images.

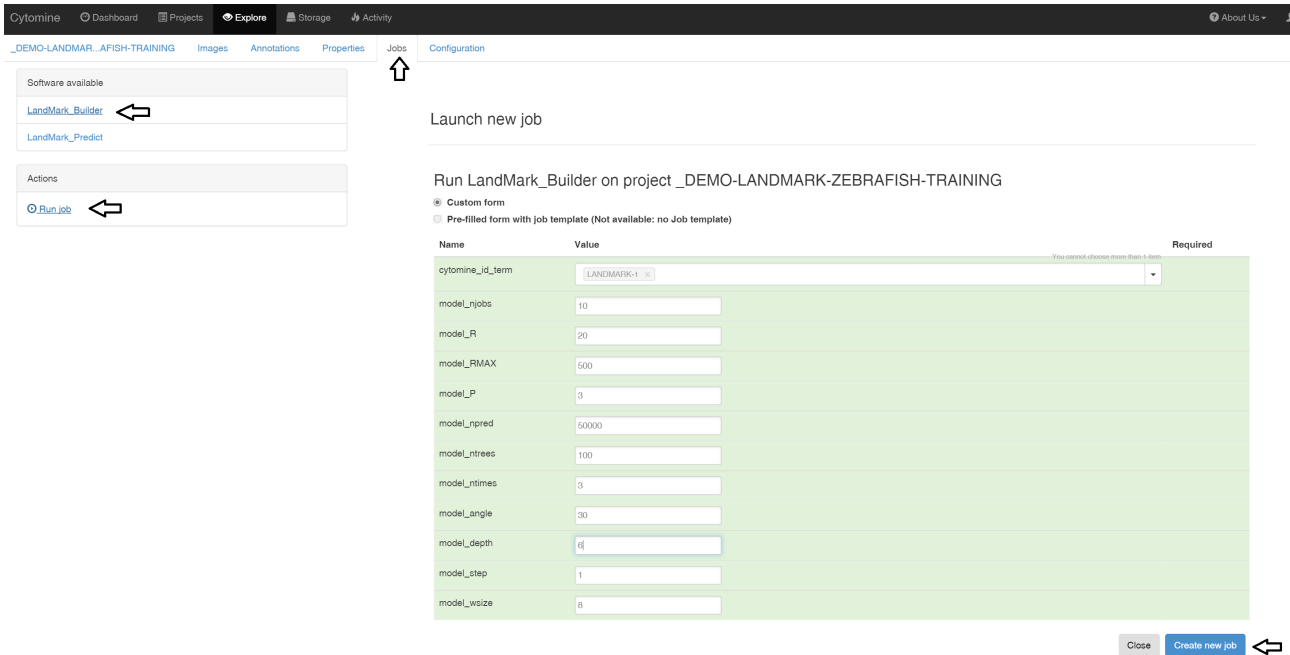
This module uses examples of landmarks positioned in images to build landmark recognition models. Here is an example of 5 manual landmarks on Zebrafish alizarin red images:



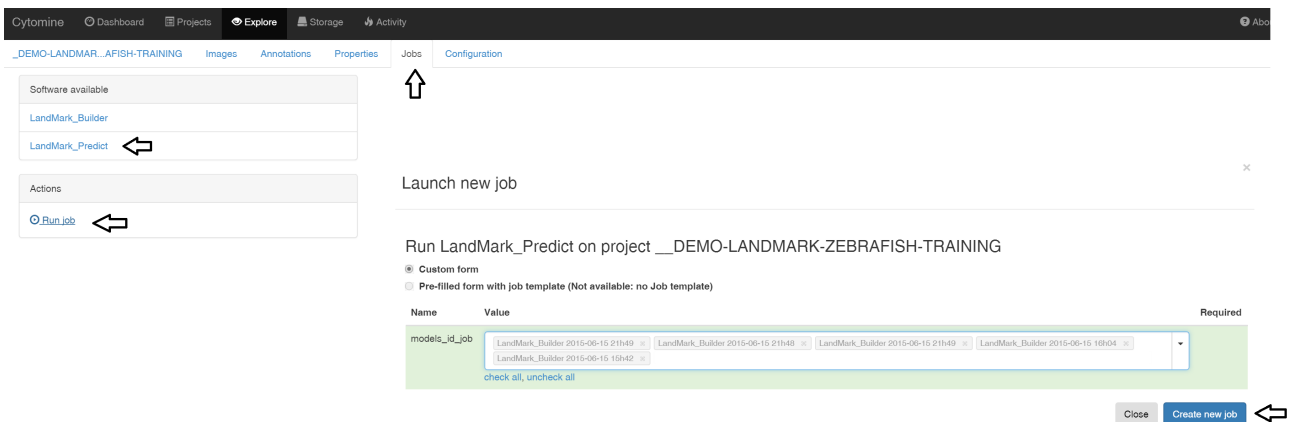
As previously, to launch the learning procedure, the user first needs to add the software Landmark_Model_Builder to its project (if not already done) in the Project Configuration panel:



Then, it launches the training algorithm (the algorithm will use all landmark UserAnnotations from images of this project):

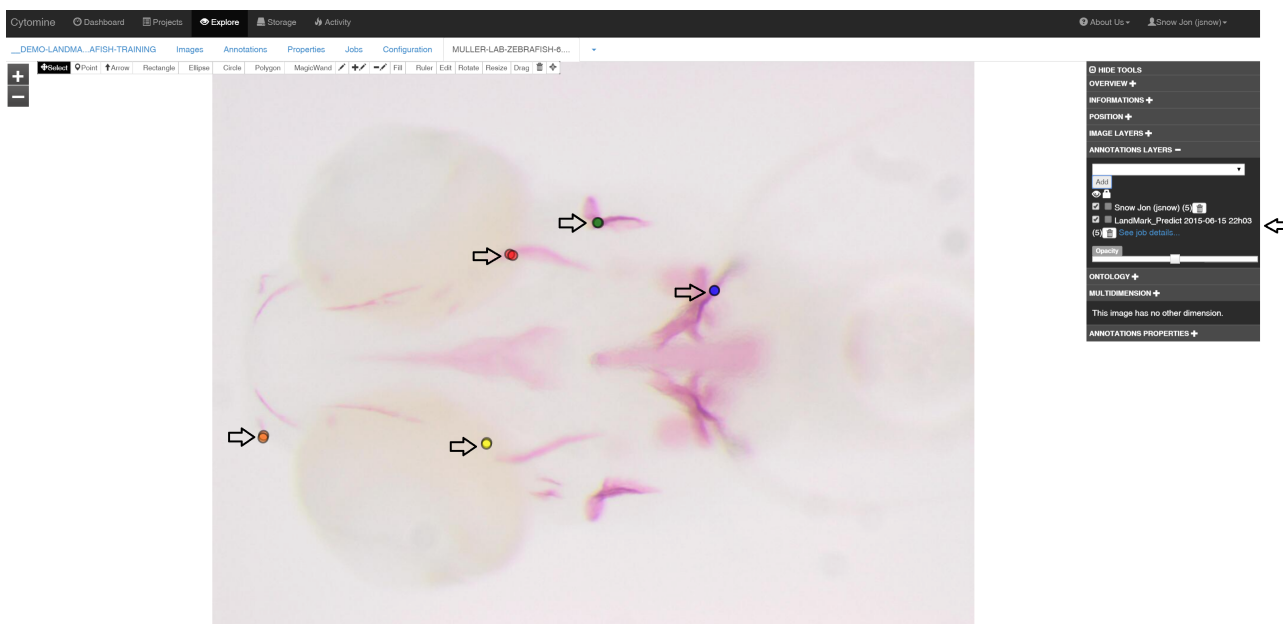


This procedure will generate a model to detect a single landmark. If multiple landmarks have to be detected, the training procedure should be repeated for other landmarks. Once a job has reached the "Success" status (it takes roughly 5 minutes per landmark on our demo instance with default parameter values), its model can be used to predict landmarks in other images. In this guide, we created models for landmark_1 to landmark_5 using 20 manually annotated images. Applying models to predict landmarks is done by launching the Landmark_Model_Predict module and by selecting the previously build models:

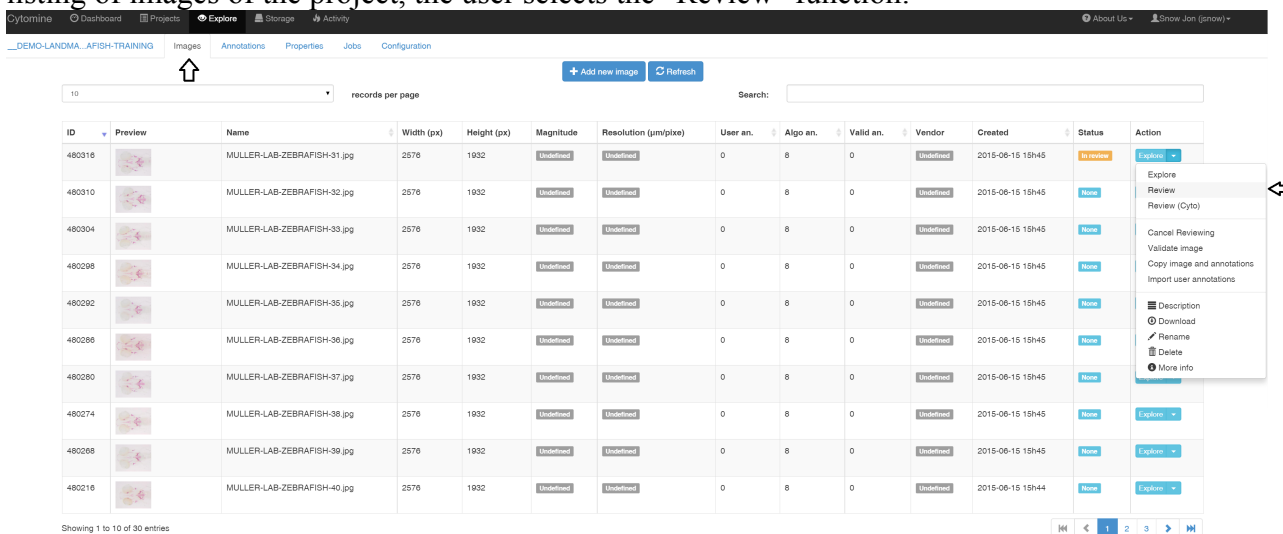


In our case, it will create Point annotations corresponding to the five predicted landmark positions in all 30 project images (it takes roughly 12 minutes on our demo instance with default parameter

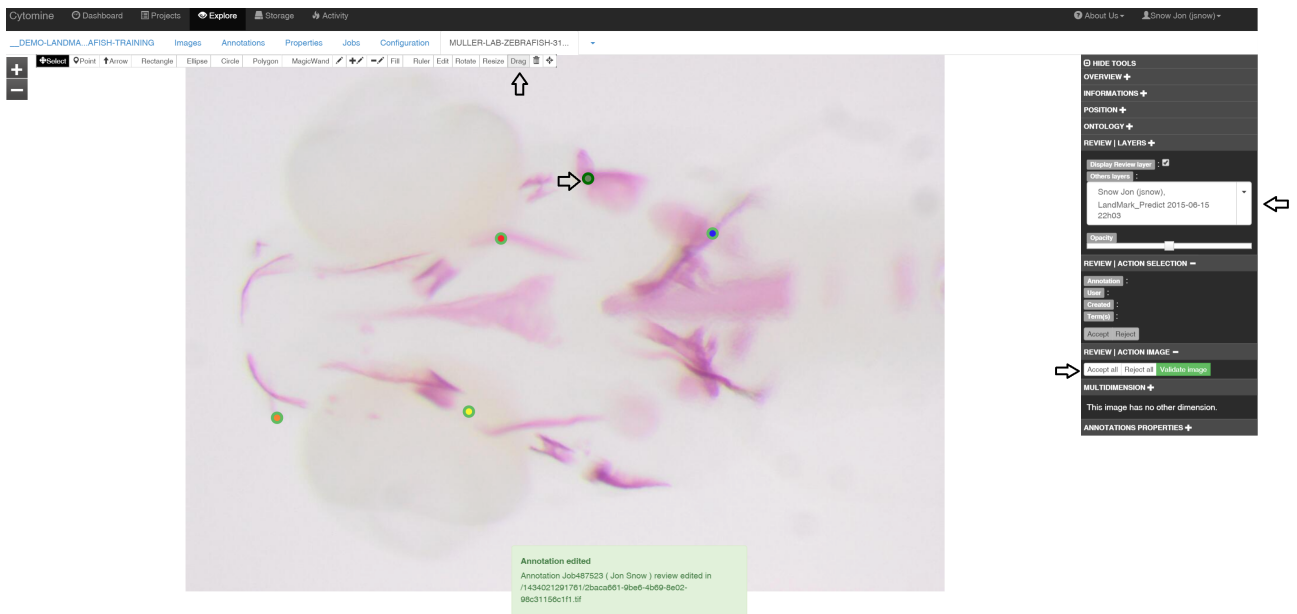
values). Here we illustrate predictions for a training image (the Figure shows both manual and predicted landmarks to assess position precision, one can observe slight shifts only) and an unlabelled image for which no manual annotation was provided for training the model:



As with other modules, the user can now proofread these detections on new images. From the listing of images of the project, the user selects the "Review" function:



It opens the image in the Explore view with reviewing tools activated. The user first selects the UserJob layer in the right panel. When most of the landmarks are well detected, we recommend to use the "Accept all" function (Points now have a green border) and then use the "Drag" tool (click on the landmark to edit) to move landmarks that are not well detected only:

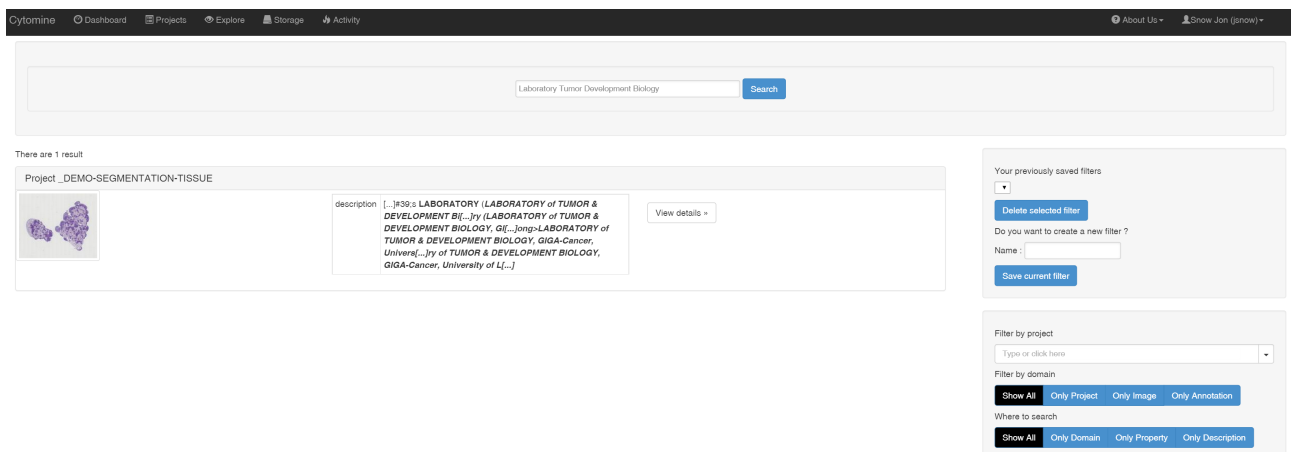


Once all landmarks are well positioned, the user validates the image (green button). Reviewed landmark positions can later be exported to derive morphometric measurements.

6.2.5 Textual search

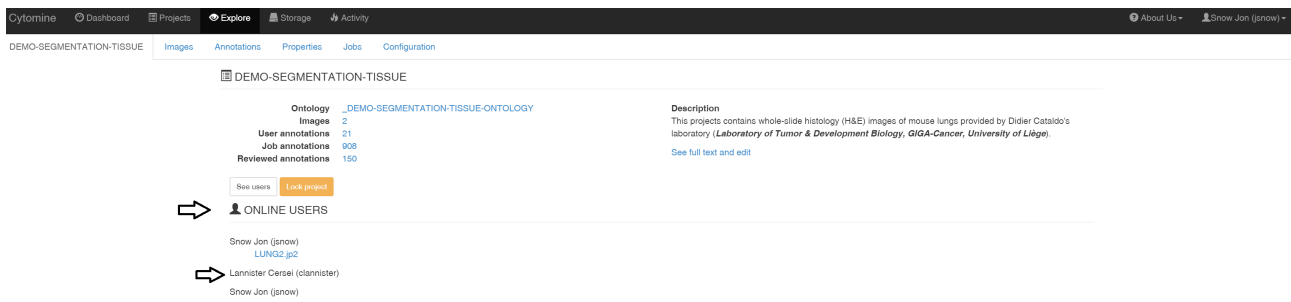
In addition to content-based image searching and user interface tools to filter annotation based on semantic terms, it is possible to perform textual searches through Cytomine-WebUI using <http://demo.cytomine.be/#search->

Searching will be performed across data entities (projects, images, annotations, domains, properties, descriptions) that are accessible by the user. In the example below, the user looks for “Laboratory Tumor Development Biology” and the search engine displays a project that contains these words in its description:

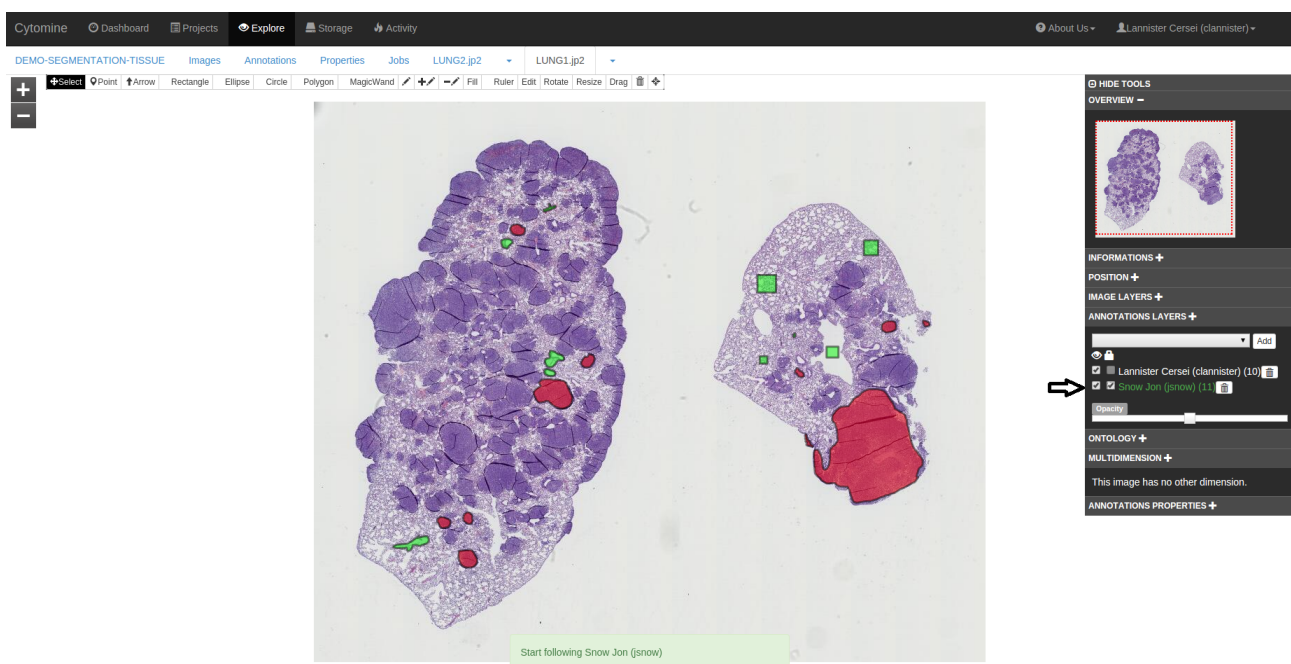


6.2.6 Online users

Cytomine can perform the tracking of all user activities (user positions in images are stored in the database) that e.g. allows multiple users to follow remotely another user observation paths and actions. Online users appear in the project dashboard, and in the Explore Annotation layers panel.



It is possible to follow another online user (in green) by checking the closest box next to the user name. Once the followed user moves in the gigapixel image or creates an annotation, the following user explore view will move to the same position and display novel annotations. Geographically distributed users can thus discuss remotely in front of the same image areas (using e.g. instant messaging or phone calls).



6.2.7 Blind assessment

6.2.7.1 Blind configuration

Cytomine has a blind mode that can be activated by administrators of a project in its Configuration Panel. This option will hide (for non-admin users) in Cytomine-WebUI image names (in the Image listing, the Explore view, ...) so that the user quantifying experimental outcomes is blinded to the experimental setting that might appear in original filenames. This option also hides user activities and annotation statistics. This option might be used to reduce bias in analyzing imaging data.

The screenshot shows the 'General Configuration' page in Cytomine. On the left, a sidebar lists configuration categories: General Configuration, Users Management, Default Layers Configuration, Custom UI Configuration, Image filters, Software, and Private Annotation Tools Configuration. The main area is titled 'General Configuration' and contains several settings:

- Hide admins layers: If you check "hide admin layers", a "simple" project user will not be able to see the layer of a project admin. A project admin will still be able to see all layers.
- Hide users layers: If you check "Hide user layers", a "simple" project user will not be able to see a layer from another user. A project admin will still be able to see all layers.
- Blind Mode: If blind mode is enabled, a user will not see image filename. The filename will not influence his work. Filename potentially contains the type of experiment.
- Read-Only project: If you check read-only project, a "simple" project user will not be able to add/edit or delete data except annotation on his own layer. A project admin will still be able to see to add/edit or delete data for this project.

The screenshot shows the 'Jobs' page in Cytomine. It features a table with columns for job details and a search bar. The table contains two entries:

ID	Preview	Name	Width (px)	Height (px)	Magnitude	Resolution (um/pixe)	User an.	Algo an.	Valid an.	Vendor	Created	Status	Action
278814		[BLIND]278814	38812	32256	Undefined	Undefined	0	900	150	Undefined	2015-06-11 11:42	In review	Expire
278476		[BLIND]278476	30720	25600	Undefined	Undefined	21	2	0	Undefined	2015-06-11 11:42	None	Expire

Showing 1 to 2 of 2 entries.

The screenshot shows the 'Activity' page in Cytomine. It displays a list of activity items under the heading 'ACTIVITY'. The items are:

- Last commands: Last tasks
- Not available in blind mode!
- ANNOTATIONS VS TERM: Not available in blind mode!
- ANNOTATIONS VS TERM: Not available in blind mode!

6.2.7.2 Cytomine-IRIS: Measuring Inter-observer Reliability

In contrast to the intentionally collaborative nature of the Cytomine-Core and Cytomine-WebUI annotation modules, Cytomine-IRIS, the inter-observer reliability study module, provides an intuitive web interface for blind assessment of annotations. It is based on the public Cytomine REST API described in section 6.3 to leverage existing Cytomine backend functionality like project and user management, or annotation services for manipulating ontology terms of annotations. On the other hand, it provides a completely decoupled user interface. In addition to the basic project configuration done using the regular Cytomine-WebUI, particular projects and images can be disabled per user on IRIS, such that for example within existing projects only few images are used for assessing the inter-observer reliability among particular users.

IRIS Installation

Since Cytomine-IRIS is an additional module, multiple instances of IRIS running on different servers can be connected to a single Cytomine-Core server. Thus, the installation of IRIS differs a bit and is detailed on <https://github.com/cytomine/Cytomine-IRIS>.



In contrast to previous sections, this user guide is based on larger dataset not yet publicly available and therefore it is not directly reproducible on our demo instance (<http://demo-iris.cytomine.be/iris/index.html#/>) but main functions are presented here to allow users to apply these concepts on a reduced “toy” dataset or on their own data.

Annotation Labeling and Reviewing

The structure of a standard Cytomine project is reflected in the workflow of IRIS: once a user logs into IRIS, a list of available projects is shown, where particular projects may be disabled just for this IRIS instance. In order to start labeling, the user opens a project and views a list of available images which contain the annotations:

You are working on: Project [IRIS_DEMO] > Image [[BLIND]151637994] > Annotation [151638900]

Refresh

You have access to 1 project on IRIS.

Name	Created	# Images	# Annotations	Mode	Actions	Info
IRIS_DEMO	2014-12-21	14	155	Blind Mode	Open	
IRIS_EMPTY-PROJECT	2014-12-04	0	0	Regular	Open	
MEDUNIGRAZ-BONE-MARROW	2014-10-03	56	4171	Blind Mode	Open	
SVS-J2K	2014-02-04	5	1	Regular		
MEDUNIGRAZ-BONE-MARROW-DEV	2014-01-14	4	144	Blind Mode		

Showing project 1 to 5 (5 in total)

- Statistics Dashboard
- Settings
- Coordinator Request
- Request Access

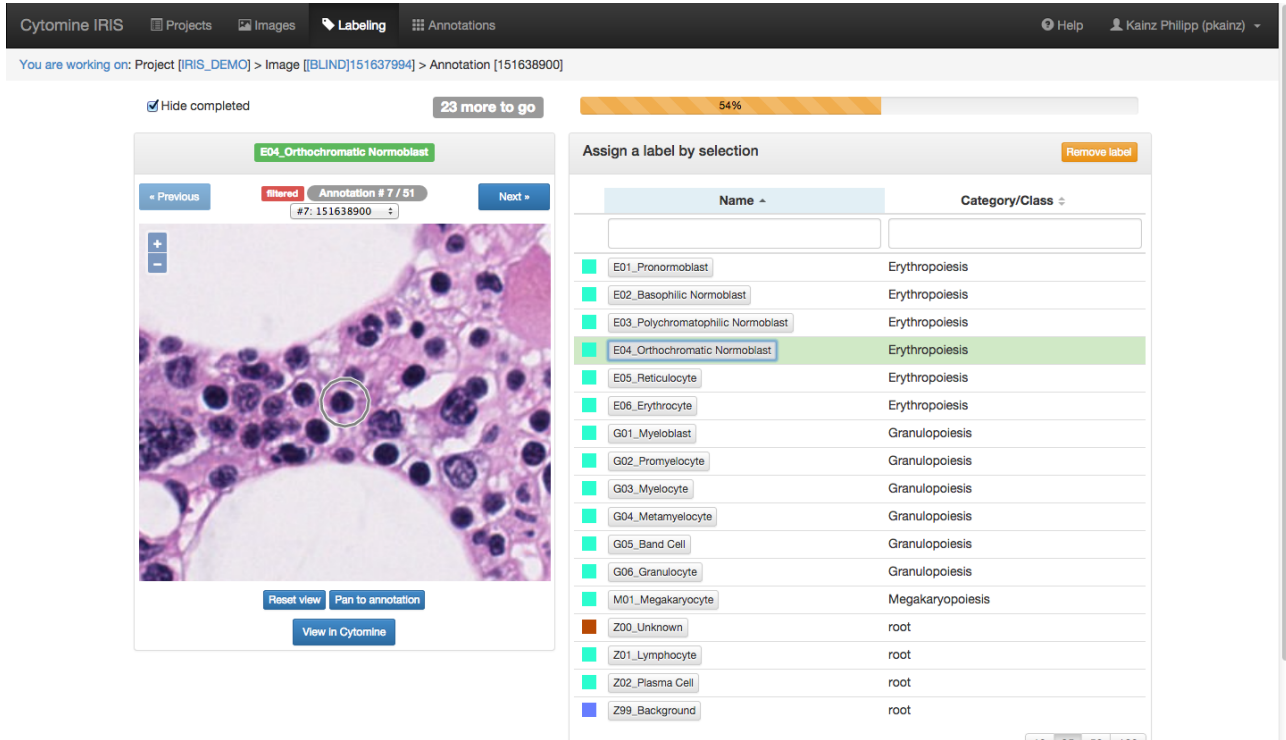
The image table also reflects the overall labeling progress within each image and provides functions for sorting and filtering. For example, this enables the user to filter out all images, where annotations are left to be labeled. This is particularly useful in situations where the study protocol requires all users to label all annotations, or when there are lots of images in a project.

You are working on: Project [IRIS_DEMO]

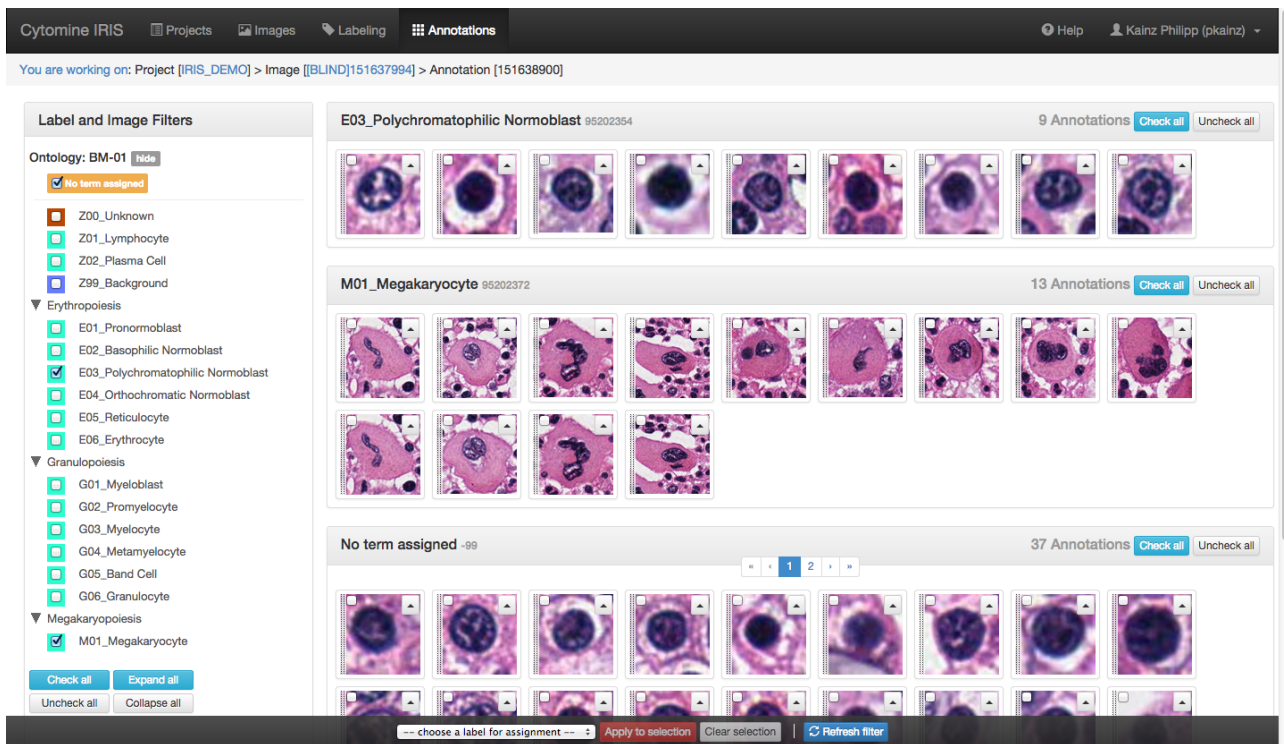
ID	Preview	Name	Magnification	Progress	Actions
151637961		[BLIND]151637961 50,455 x 31,589 px	40 X	100% finished	Start Labeling
151637967		[BLIND]151637967 40,935 x 32,578 px	40 X	100% finished You labeled 8 of 8 annotations.	Start Labeling
151637987		[BLIND]151637987 51,407 x 35,368 px	40 X	100% finished	Start Labeling
151665529		[BLIND]151665529 56,640 x 39,163 px	40 X	100% finished	Start Labeling
151637955		[BLIND]151637955 55,215 x 36,845 px	40 X	62% 3 more to go	Start Labeling
151637994		[BLIND]151637994 42,839 x 18,942 px	40 X	52% 24 more to go	Start Labeling
151637949		[BLIND]151637949 51,407 x 26,989 px	40 X	35% 11 more to go	Start Labeling

The annotation labeling can be performed per image in a dedicated view by selecting “Start Labeling” from the rightmost column. Image zooming and panning is available like in the main Cytomine-WebUI, allowing proper exploration of the image context of an annotation in order to

make an informed decision about the label. The user can hide annotations where a label already exists and thus just navigates through unlabeled annotations, while their order is preserved. Navigation among annotations can be done either using the buttons above the image view or by pressing the keys “n” for the next, or “p” for the previous annotation. A label is assigned by simply selecting the term in the table on the right hand side, which is basically a flat representation of a possible hierarchical ontology:



It is convenient to view annotations in a gallery-like view per ontology term, which can be done by selecting “Annotations” from the menu bar at the top. This enables users to visually filter out outliers that do not comply e.g. with the appearance of the majority of annotations having the same label. Moreover, the gallery can display annotations across different images in a project and provides several methods to correct the label either directly or by navigating to the labeling view, if more context around the annotation is required. Multiple objects can also be re-assigned labels at once, which drastically reduces the time of manually navigating to the corresponding images and finding these annotations in the labeling view.



IRIS Sessions

In some scenarios, a single image may contain hundreds of annotations that sometimes cannot be assessed at once. Finding the exact annotation to continue is tedious and thus, IRIS preserves the current status of labeling across logins in sessions, such that the user can continue labeling at the exact same point where the application has been left last time. This can be done by simply going to any IRIS page and clicking on the current image name below the menu bar, or pressing the “r” key on the keyboard, which takes the user back to the labeling view in order to resume the labeling.

Interface Documentation: Help Pages

Each view in IRIS has a dedicated help page that is accessible from the main menu bar (top right corner) or by pressing the “h” key. The pages contain instructions on how to handle the interface.

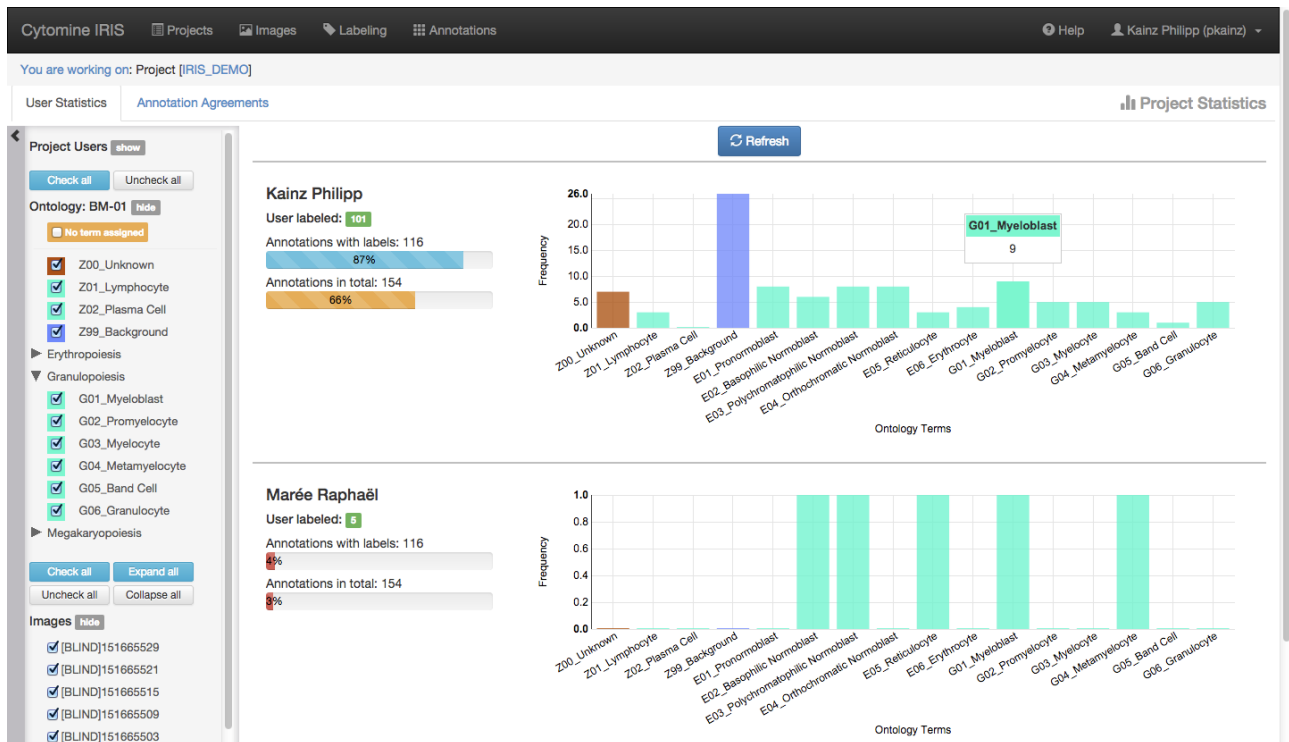
IRIS Project Coordination

The standard Cytomine user management is extended in IRIS by granting special rights to particular users: the IRIS project coordinators. Each user can request to become a project coordinator and they are authorized once as such by the administrator of the IRIS instance. Coordinators are able to view and visualize project statistics such as histograms of assigned ontology terms for all users or annotation agreements. Each of these visualizations also comes with a variety of filters for particular users, ontology terms and images. Moreover, they can manage project and image access settings for all users and authorize other users to become a project coordinator. Communication among access request and authorization is handled via email, using the email address encoded in the Cytomine User Account page.

Dashboard: User Statistics

The distribution of assigned terms can be evaluated for one or more users in the Statistics Dashboard of each project from the project table (project coordinators). This enables a quick

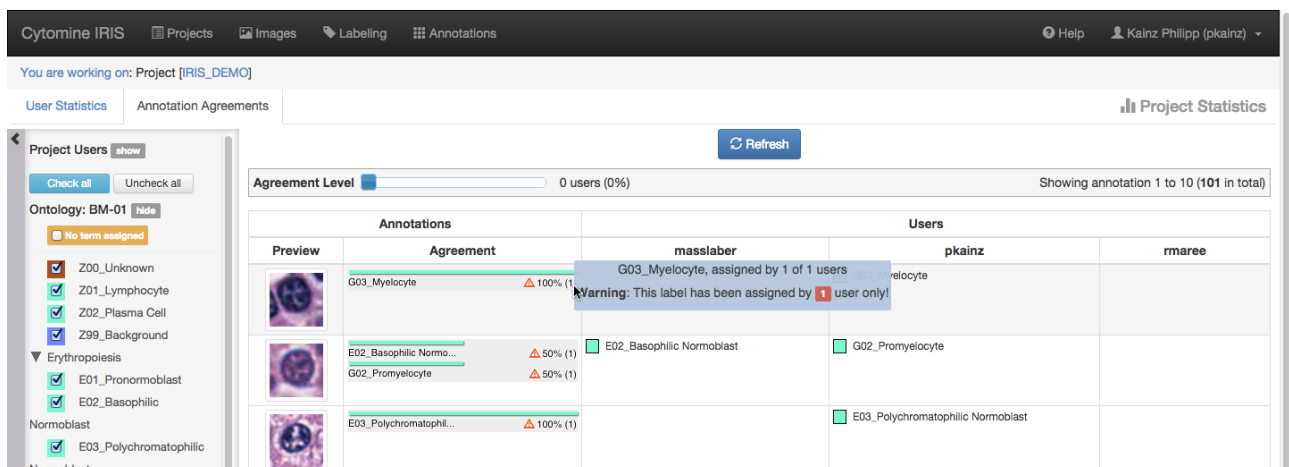
examination, for example, of whether one or more users are biased towards assigning a particular label. This also gives a clear picture of how many terms have already been assigned by the users with respect to the total number of assigned terms and the total number of available annotations.



The coordinator can combine several filters (users, ontology terms, images) to meet the current requirements of the query.

Dashboard: Observer Agreements per Annotation

Inter-observer variability of labeled annotations can be visualized in the Statistics Dashboard of a project by selecting the tab titled “Annotation Agreements”.



From the filter panel on the left hand side, a coordinator can construct the query and a list of annotations is shown. In addition, this result list can be filtered by annotation agreements using the “Agreement Level” slider at the top of the list. This slider's maximum value corresponds to the total

number of observers that assigned any label in the query. So if the slider is moved to the right, the agreement level increases and filters out annotations, where at least n or more observers are agreeing on one or more terms. Moving it to the right usually shrinks the list and hence all annotations in the smaller list have a higher level of inter-observer agreement.

The screenshot shows the Cytomine IRIS web interface. At the top, there are navigation tabs: Projects, Images, Labeling, Annotations, Help, and a user profile for Kainz Philipp (pkainz). Below this, it indicates the current project is [IRIS_DEMO]. There are tabs for User Statistics and Annotation Agreements, with Project Statistics on the right. A 'Project Users' sidebar on the left shows a list of ontology terms with checkboxes, including Z00_Unknown, Z01_Lymphocyte, Z02_Plasma Cell, Z99_Background, Erythropoiesis (E01_Pronormoblast, E02_Basophilic), and Normoblast (E03_Polychromatophilic). The main area features an 'Agreement Level' slider set to 2 users (67%) and a 'Refresh' button. Below the slider is a table with columns for 'Annotations' and 'Users'. The 'Annotations' column has sub-columns for 'Preview' and 'Agreement'. The 'Users' column has sub-columns for 'masslabe', 'pkainz', and 'rmaree'. The table lists several annotations with their agreement percentages and the number of users who assigned them. For example, E04_Orthochromatic Normoblast has a 67% agreement (2 users), and E02_Basophilic Normoblast has a 100% agreement (2 users). A tooltip for E01_Pronormoblast indicates it is assigned by 2 of 3 users.

6.3 Usage (API documentation)

Cytomine documentation is available on <http://doc.cytomine.be/>

A documented RESTful API is continuously updated and accessible online at

http://demo.cytomine.be/restApiDoc/?doc_url=http://demo.cytomine.be/restApiDoc/api#

If you install your own Cytomine instance, this documentation is also automatically installed on your server by our automated installation procedure and then available at:

[http://SCORE_URL\\$/restApiDoc/?doc_url=http://SCORE_URL\\$/restApiDoc/api#](http://SCORE_URL$/restApiDoc/?doc_url=http://SCORE_URL$/restApiDoc/api#)

This API is used both by Cytomine-WebUI (including Cytomine-IRIS) and Cytomine-DataMining analysis modules. It can also be used by third-party software. Code examples that encapsulate http requests in Java and Python are provided here:

- <https://github.com/cytomine/Cytomine-java-client/tree/master/src/main/java/be/cytomine/client/sample>
- <https://github.com/cytomine/Cytomine-python-client/tree/master/client/examples>

Web users can inspect communications between their web browser and Cytomine components through the "Network" tab in the "Inspect Element" (Google Chrome)/"Inspector" (Mozilla Firefox) module of their web browser:

The screenshot displays the Cytomine web application interface. At the top, there are navigation tabs for Dashboard, Projects, Explore, Storage, and Activity. Below this, the main content area is divided into several sections:

- Filters:** A sidebar on the left containing search filters for user logs, ontology terms, and users. The 'Users' section is expanded, showing 'Laminator_Corsor (Laminator)' and 'Stark Eckhard (stark)'.
- Predefined Filters:** A section with 'Selected' and 'Save current selection' buttons.
- Undefined:** A section for undefined filters.
- Multiple:** A section for multiple filters.
- Negative:** A section displaying a grid of image thumbnails, likely representing negative results for a search query.
- Network Traffic:** A central pane showing a network traffic analysis with a timeline and a table of requests. The table includes columns for Name, Method, Status, Type, Initiator, Size, Time, and Timeline.

In addition, the API online documentation includes a "Playground" for each web service that allows the user to test server responses according to user input (e.g. here we use the service to get annotation description given an annotation identifier):

The screenshot shows the JSONDoc API documentation for the Cytomine REST API. The interface is divided into three main sections:

- API INFO:** Provides the base path (`http://beta.cytomine.be/restApiDoc/api`) and version (`0.1`).
- USER ANNOTATION SERVICES:** Details the `/api/userannotation/{id}.json` endpoint. It lists the `GET` method, path parameters (`id`), and response object structure. It also includes a list of error codes (400, 401, 403, 404) and their descriptions.
- PLAYGROUND:** A section for testing the API. It shows the `Accept` header (`application/json`) and the `Path parameters` section with an input field for the `id` parameter (value: `152928410`). Below this, there are buttons for 'Submit', 'Response text', 'Response info', and 'Request info'. The 'Response text' section displays a JSON object representing the API response.

The following table give some examples of URLs to export data (using jsnow username account on demo.cytomine.be):

URL example	Description
http://demo.cytomine.be/api/user.json	List of users (JSON)
http://demo.cytomine.be/api/user/263676.json	Description of a specific user (JSON)
http://demo.cytomine.be/api/project.json	List of projects (JSON)
http://demo.cytomine.be/api/project/528050.json	Description of a specific project (JSON)
http://demo.cytomine.be/api/project/528050/imageinstance.json	List of images in a specific project (JSON)
http://demo.cytomine.be/api/imageinstance/528460.json	Description of a specific image (JSON)
http://demo.cytomine.be/api/abstractimage/528120/thumb.png?maxSize=1024	Thumbnail of a specific image (PNG)
http://demo.cytomine.be/api/annotation.json?&project=528050	List of annotations in a specific project (JSON)
http://demo.cytomine.be/api/annotation.json?&project=528050&term=528044&users=263676&images=528132	List of annotations of a specific ontology term, in a specific project, for a specific user (human or userjob), in a specific image (JSON)
http://demo.cytomine.be/api/annotation/528401.json	Description of a specific annotation (JSON)
http://demo.cytomine.be/api/userannotation/528401/crop.png	Crop image of a specific annotation (PNG)
http://demo.cytomine.be/api/userannotation/528401/crop.png?increaseArea=2	Crop image of a specific annotation (PNG) with context
http://demo.cytomine.be/api/userannotation/528401/crop.png?zoom=2	Crop image of a specific annotation at zoom level 2 (PNG)
http://demo.cytomine.be/api/userannotation/528401/crop.png?zoom=2&mask=true	Crop binary mask of a specific annotation at zoom level 2 (PNG)
http://demo.cytomine.be/api/userannotation/528401/crop.png?zoom=2&alphaMask=true	Crop alpha mask of a specific annotation at zoom level 2 (PNG)
http://demo.cytomine.be/api/imageinstance/528460/window-23181-14285-1000-1000.png	Tile of size 1000x1000 at a specific location (23181,14285) in a specific image (PNG)
http://demo.cytomine.be/api/imageinstance/528460/window-23181-14285-1000-1000.png?mask=true&review=true&terms=528044	Tile reviewed mask of size 1000x1000 at a specific location (23181,14285) for a specific ontology term in a specific image (PNG)
http://demo.cytomine.be/api/job/1939560.json	Description of a specific job (JSON) including software parameter values