

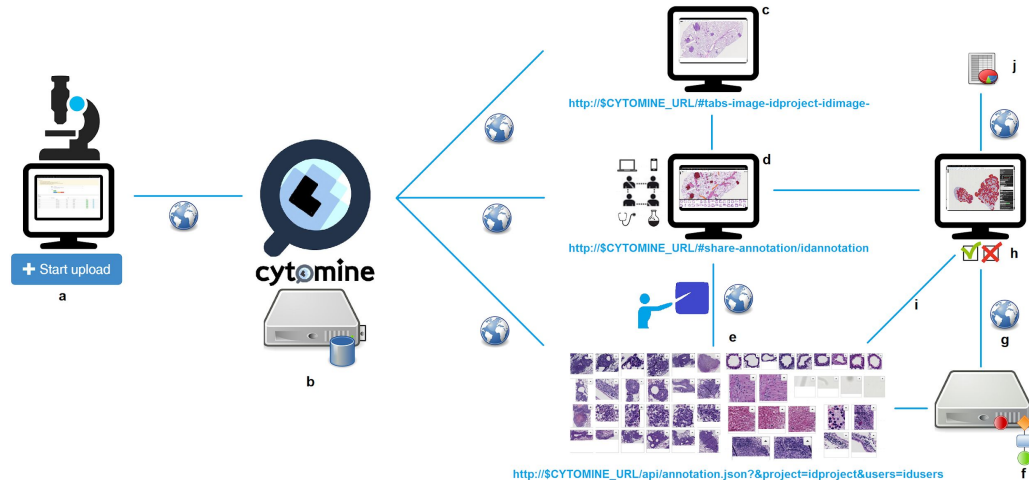


**Open-source rich internet application for collaborative analysis of
multi-gigapixel images**

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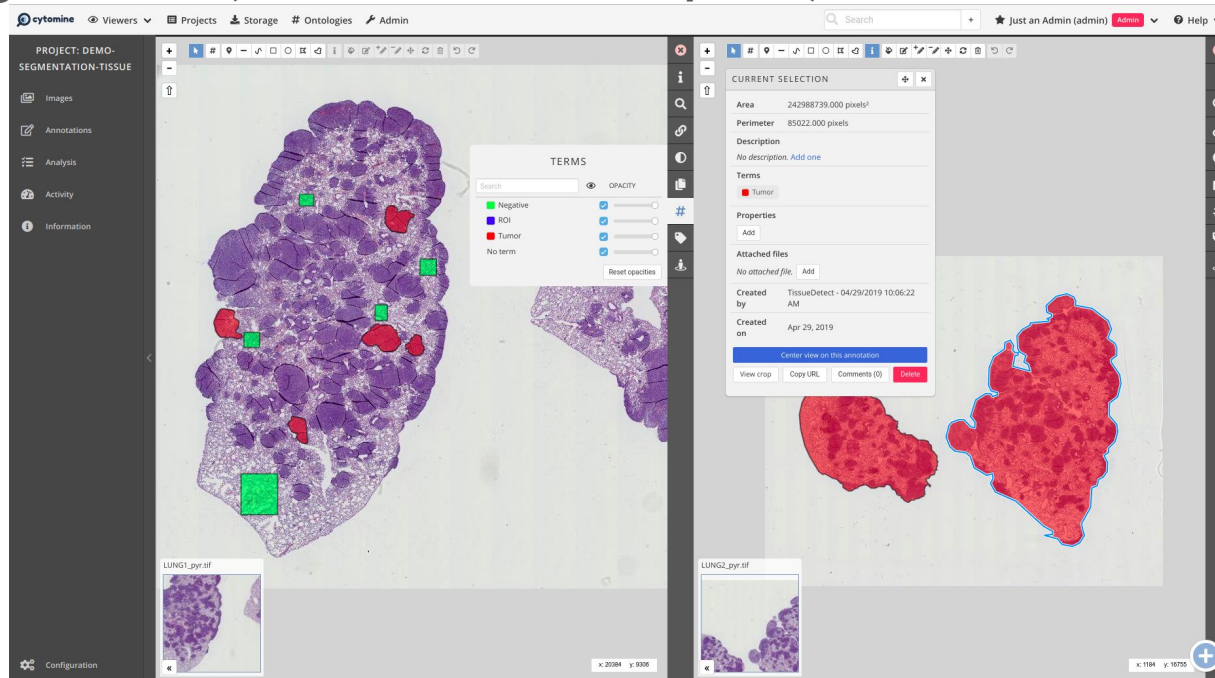
Cytomine - Overview

- Open-source rich internet application for collaborative analysis of multi-gigapixel images
- Initiated at Montefiore (& GIGA), ULiège (<https://uliege.cytomine.org>)



Cytomine - Application example

Histological slides (> 100 000 x 100 000 pixels)



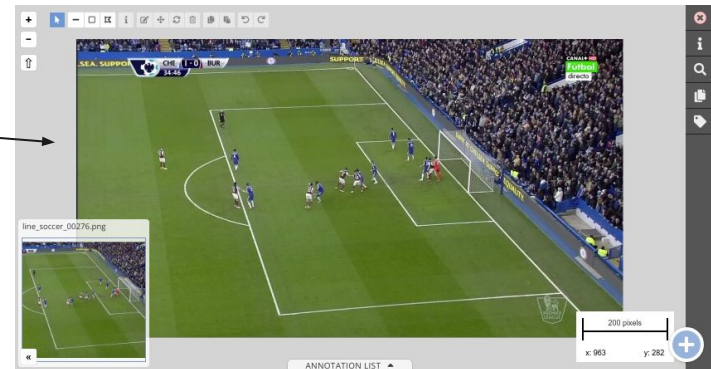
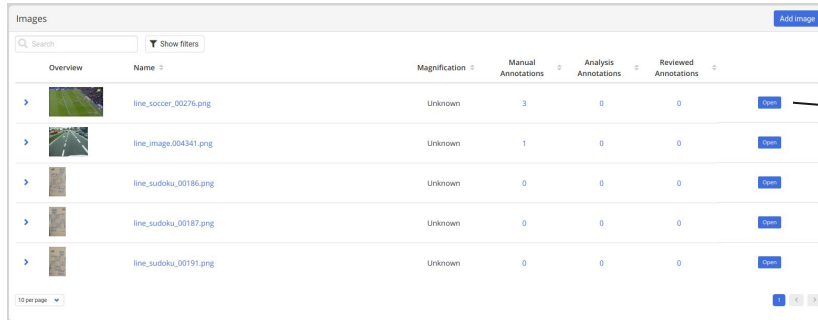
Connect to Cytomine



- URL: <https://learn.cytomine.be>
- Username: sXXXXXX
- Password: your student email address in lowercase
 - (e.g: john.doe@student.uliege.be)
- (if not working, try “Forgot my password” on login page)
- Once connected: **update your password !**
 - Go to “Account” in top-right dropdown.

Project in Cytomine

- 1 Cytomine project per group
 - CV2019_PROJECT_TEAM01, ...
- The project contains the set of images you have to annotate
 - Click on “Open” to open an image viewer



Annotate in Cytomine

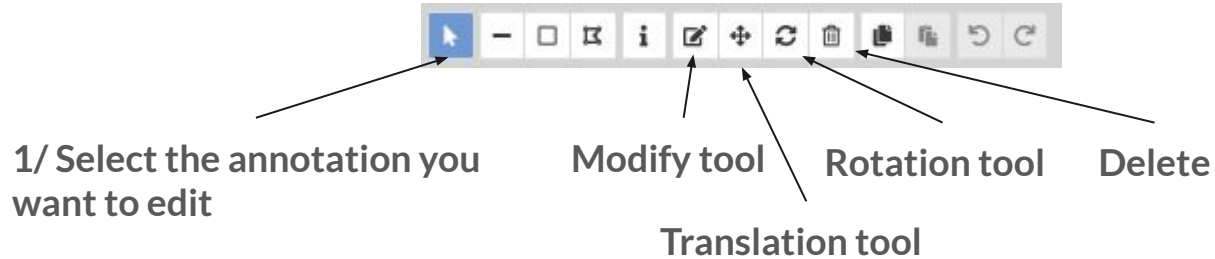
- For your project, 3 kinds of annotations

- **Line** : use line tool
- **Bounding box** : use rectangle tool
- **Ellipsis** :
 - Use polygon tool
 - Create polygon with 5 vertices
 - In your code, create ellipsis from the 5 coordinates



Annotate in Cytomine

- Edit an annotation



- With modify tool:
 - Add/Move vertex: simply click on contour
 - Delete vertex: Alt + click on vertex

Retrieve Cytomine data



- Cytomine Python client

- Library wrapping HTTP requests to Cytomine API

- Installation

- <https://github.com/Cytomine-ULiege/Cytomine-python-client>
- From Github:
 - `wget`
<https://github.com/Cytomine-ULiege/Cytomine-python-client/releases/download/v2.4.0/Cytomine-Python-Client-2.4.0.zip>
 - `unzip Cytomine-Python-Client-2.4.0.zip`
 - `cd Cytomine-Python-Client-2.4.0`
 - `pip install .`
- Other installation methods in README on Github.

Retrieve Cytomine data - Authentication

- Authentication with Python client

- host = <https://learn.cytomine.be>
- public/private keys: Get them in your Account page

```
from cytomine import Cytomine
```

```
host = "https://learn.cytomine.be"
```

```
public_key = "123-456"
```

```
private_key = "abc-def"
```

```
conn = Cytomine.connect(host, public_key, private_key)
```

```
print(conn.current_user)
```

- Good practice: use command-line arguments for host, public key and especially private key !

Retrieve Cytomine data - Images

- Example: Get images from your project

- Find project ID: <https://learn.cytomine.be/#/project/1234/...>
- Full example in [Cytomine-python-client/examples/get_images.py](https://github.com/cytomine/cytomine-python-client/blob/master/examples/get_images.py)

```
from cytomine import Cytomine
from cytomine.models import ImageInstanceCollection, ImageInstance

host = "https://learn.cytomine.be"
public_key = "123-456"
private_key = "abc-def"
id_project = 1234

conn = Cytomine.connect(host, public_key, private_key)

image_instances = ImageInstanceCollection().fetch_with_filter("project", id_project)
for image in image_instances:
    assert (type(image) == ImageInstance)
    print("Image ID: {} | Name: {} | Width: {} | Height: {}".format(
        image.id, image.originalFilename, image.width, image.height))
```

Retrieve Cytomine data - Annotations

- Example: Get annotations from your project
 - Find project ID: <https://learn.cytomine.be/#/project/1234/...>
 - Full example in [Cytomine-python-client/examples/get_annotations.py](#)

```
# Connect to Cytomine...
```

```
# Get image instances...
```

```
annotations = AnnotationCollection()
```

```
annotations.project = id_project
```

```
annotations.showMeta = True
```

```
annotations.showWKT = True
```

```
annotations.fetch()
```

```
for annot in annotations:
```

```
    print("Annotation ID: {} | Image ID: {} | WKT: {}".format(annot.id, annot.image,  
        annot.location))
```

Retrieve Cytomine data - Remarks

- **Geometry (annot.location) is in WKT format**
 - **Line:** LINESTRING (30 10, 40 40)
 - **Rectangle:** POLYGON ((20 10, 40 10, 40 30, 20 30, 20 10))
 - **Polygon:** POLYGON ((30 10, 40 40, 20 40, 10 30, 10 20, 30 10))
 - https://en.wikipedia.org/wiki/Well-known_text_representation_of_geometry
- **Use Shapely library (installed with Python client)**
 - To read WKT format
 - `shapely.wkt.loads(annot.location)`
 - To get list of coordinates
- **!! Cytomine uses a cartesian coordinate system**
 - \neq OpenCV coordinate system
 - See 'affine_transform' in Shapely if you need to convert

Cytomine documentation



- Web interface documentation: <https://doc.cytomine.org>
- Cytomine concepts: <https://doc.cytomine.be>
- Python client:
 - [Data access using Python client](#)
 - <https://github.com/Cytomine-ULiege/Cytomine-python-client>
 - https://github.com/Cytomine-ULiege/Cytomine-python-client/blob/master/examples/get_images.py
 - https://github.com/Cytomine-ULiege/Cytomine-python-client/blob/master/examples/get_annotations.py