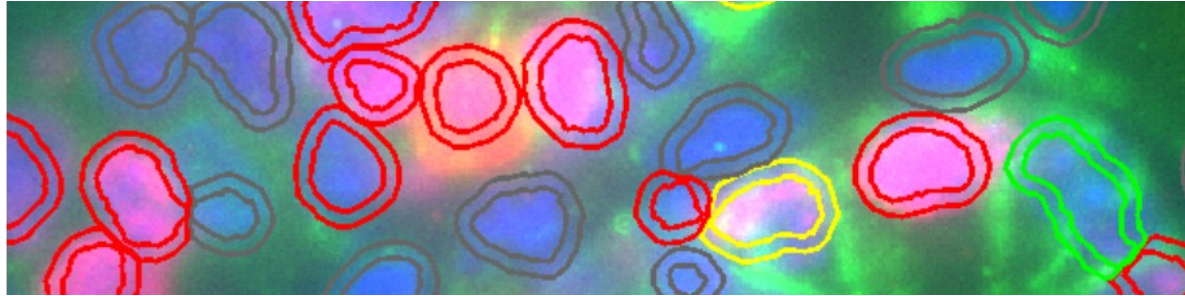




Chapter 7

Multiplex Analysis



VII. Multiplex Analysis

Multiplex Analysis

Stained nuclei

- For cell detection

DAPI, C1, C2, C3

Number of cells positive for

Different stains

- Count cells positive for each stain
- Count cells positive for any combination of stains

- C1, C2, C3,
C1C2, C2C3, C1C3, C1C2C3

VII. Multiplex Analysis

Multiplex Analysis

Plan

- Set channel names and colors
 - Detect all cells
 - Train classifiers for each stain
 - Create a combined classifier
- Apply the combined classifier to the project
 - Reorganize the output data
 - Count each positive detection whether single or in combination

$$c1_total = c(C1) + c(C1C2) + c(C1C3) + \dots + c(C1C2C3)$$

Set channel names and colors

We will first set the channel names

They correspond to the markers of interest

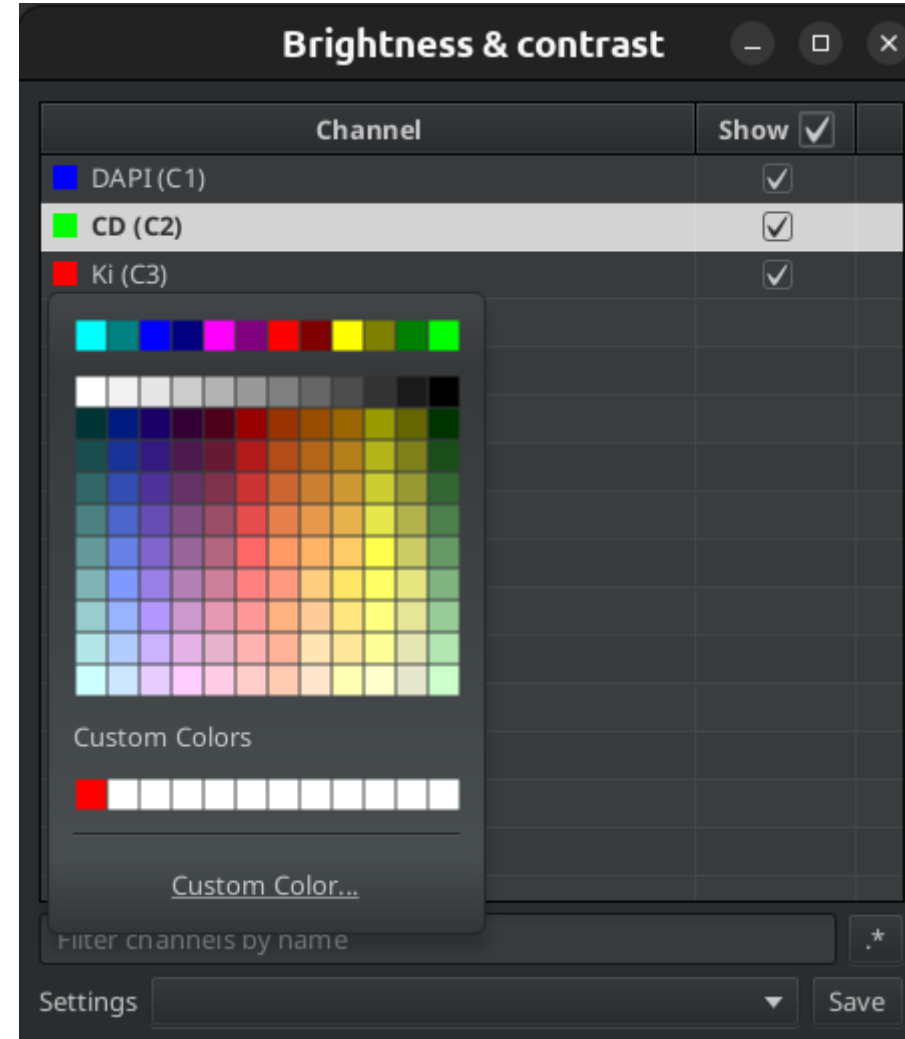
We will create classifiers from them

For one image, use B&C tool

Hoover over the color and note the hex-string of the color

For example

- #ff0000 (red),
- #00ff00 (green)
- #0000ff (blue)



Set channel names and colors

Use a script to apply to all images
in the project

0, 1, 2, ... A, B, C, D, E, F
0, 10, 15

Run for project

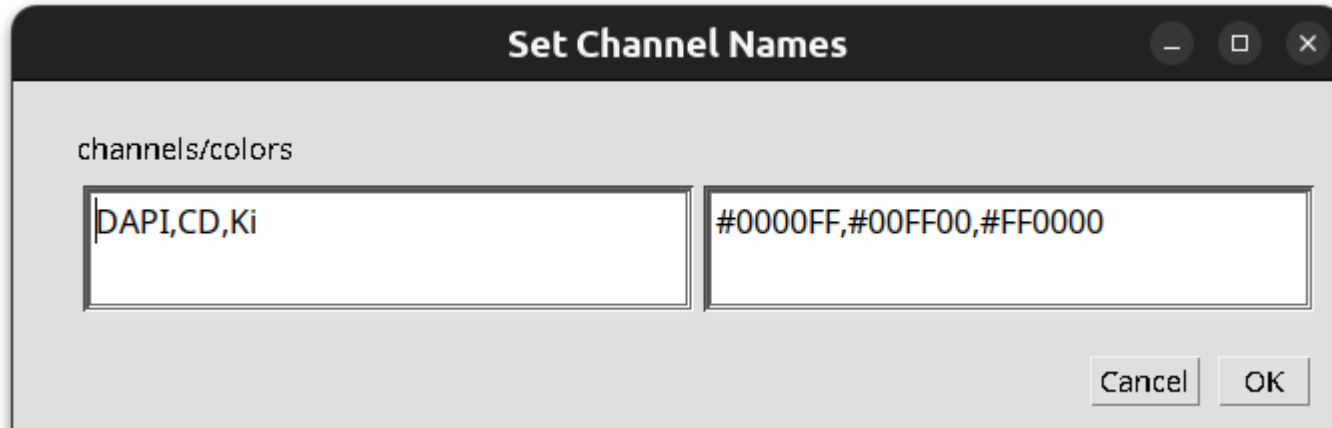
$D_2D_1 \text{ base } 16 = D_2 * 16 + D_1 * 1$

For example $F5 = 15 * 16 + 5 = 245$

```
setChannelNames("PDL1", "CD8", "FoxP3", "CD68", "PD1", "CK", "DAPI", "AF")
setChannelColors(
    getColorRGB(255, 255, 255),
    getColorRGB(0, 255, 0)
)
setChannelDisplayRange("CD8", 0, 5)
```

Set channel names and colors

Download and run (for project) `set_channel_names.groovy` from https://github.com/MontpellierRessourcesImagerie/qupath_multiplex_analysis



VII. Multiplex Analysis

Cell detection

Analyze>

Cell Detection>

Cell Detection or

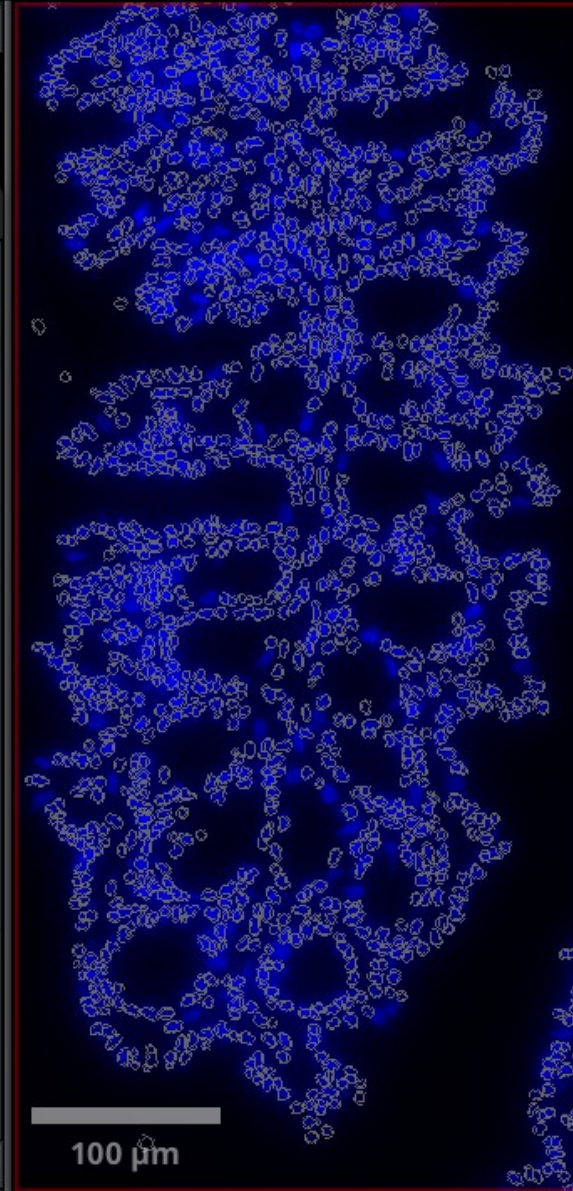
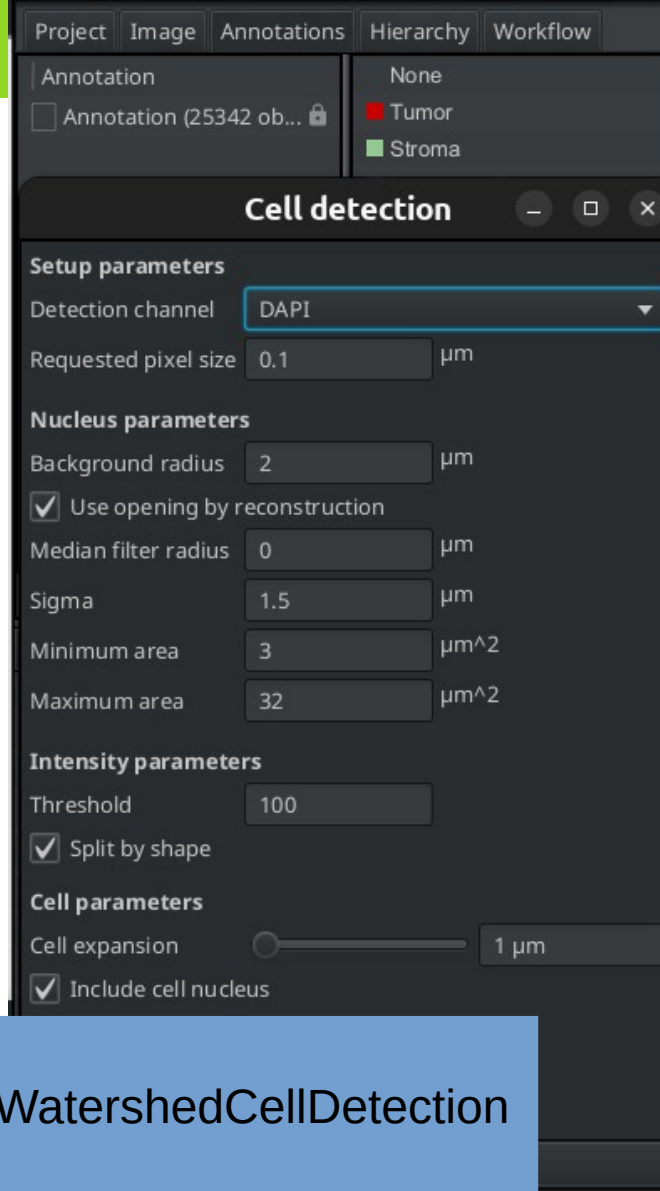
Cellpose

Stardist

Apply to whole project

- Create command history script
- Run for project

```
setImageType('FLUORESCENCE');  
runPlugin('qupath.imagej.detect.cells.WatershedCellDetection',
```

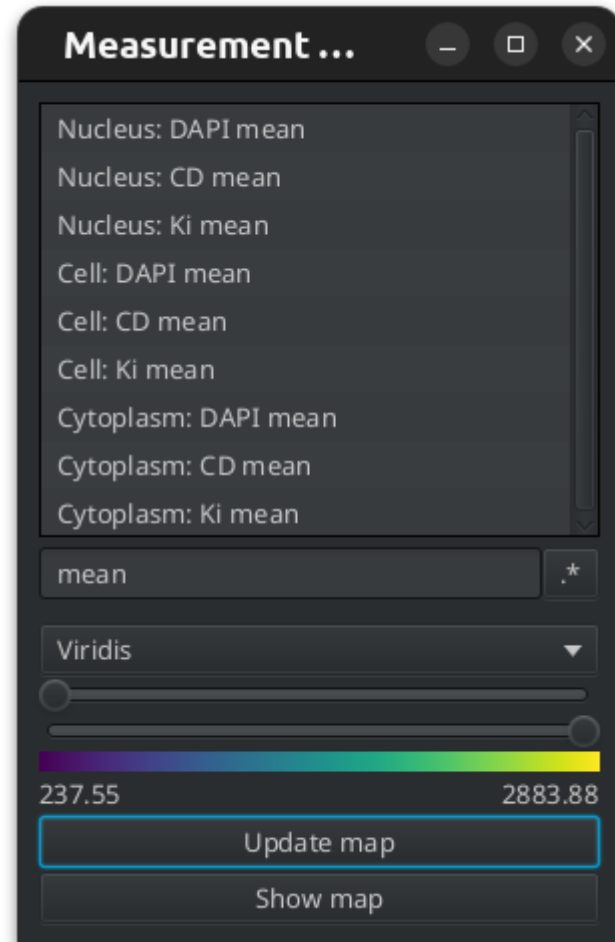


Cell Detection Measurements

Cell Detection

- Automatically measures features for
 - cell
 - cytoplasm
 - nucleus

We will train the classifiers with these features

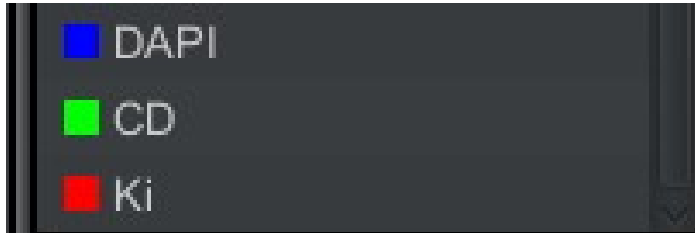


VII. Multiplex Analysis

Train a classifier per channel

Populate from image channels

- Creates a class for each channel



project not for an image

- No need to create a script and “run for project” in this case

The screenshot shows the QuPath software interface. The top menu bar includes File, Edit, Tools, View, Objects, TMA, Measure, Automate, Analyze, Classify, and Extensions. The main window is divided into several panes. The left pane shows the Project, Image, Annotations, Hierarchy, and Workflow tabs. The Hierarchy pane shows a single annotation with 10890 objects. The right pane shows a histology image with blue, green, and red channels, and yellow outlines representing cell nuclei. The bottom pane shows a table of object properties.

Key	Value
Image	image004.lif - A1 R 1_Merged
Object ID	96403d95-67d1-48e3-8475-...
Object type	Annotation
Name	
Classification	
Parent	Root object (Image)

The classification menu is open, showing the following options:

- Add/Remove...
- Populate from existing objects
- Populate from image channels
- Reset to default classes
- Import classes from project
- Show/Hide...
- Select objects by classification

Train a classifier for each marker

Project Image Annotations Hierarchy Workflow

- Annotation (6981 objects)
- Annotation (Ignore*) (13 points)
- Annotation (Ki) (13 points)

Points

- None
- Tumor
- Stroma
- Immune cells
- Necrosis
- Other
- Region*
- Ignore* (1)
- Positive
- Negative
- DAPI
- CD
- Ki (1)**

Filter classifications:

Set s... A... :

Value

lif - A1 R 4_Merged
t (Image)

Add Edit Delete :

Show point convex hull

Highlight selected objects by color

Point size

Convert detections to points

Load points Save points

Delete individual points by clicking on them with the 'Alt' key pressed

Measurements Description



Train object classifier

Object fil... Detections (all)

Classifier Random trees (RTrees) Edit

Features Selected measurements Select

Classes All classes Select

Training All annotations

Load training Advanced options

Live update

Training data

● Ignore*
● Ki

Classifie... Ki Save

VII. Multiplex Analysis

Train a classifier for a marker

Select measurements

- Select mostly measurements of the marker

Filtered by output class

- Selects all measurements containing the class name

Name	Selected
Cell: CD min	<input type="checkbox"/>
Cell: Ki mean	<input checked="" type="checkbox"/>
Cell: Ki std dev	<input checked="" type="checkbox"/>
Cell: Ki max	<input checked="" type="checkbox"/>
Cell: Ki min	<input checked="" type="checkbox"/>
Cytoplasm: DAPI mean	<input type="checkbox"/>
Cytoplasm: DAPI std dev	<input type="checkbox"/>
Cytoplasm: DAPI max	<input type="checkbox"/>
Cytoplasm: DAPI min	<input type="checkbox"/>
Cytoplasm: CD mean	<input type="checkbox"/>
Cytoplasm: CD std dev	<input type="checkbox"/>
Cytoplasm: CD max	<input type="checkbox"/>
Cytoplasm: CD min	<input type="checkbox"/>
Cytoplasm: Ki mean	<input checked="" type="checkbox"/>
Cytoplasm: Ki std dev	<input checked="" type="checkbox"/>

Object fil... Detections (all)

Classifier Random trees (RTrees) Edit

Features Selected measurements Select

Classes All measurements Select

Training Selected measurements Filtered by output classes

Load training Advanced options

Live update

Training data

● Ignore*
● Ki

Classifie... Ki Save

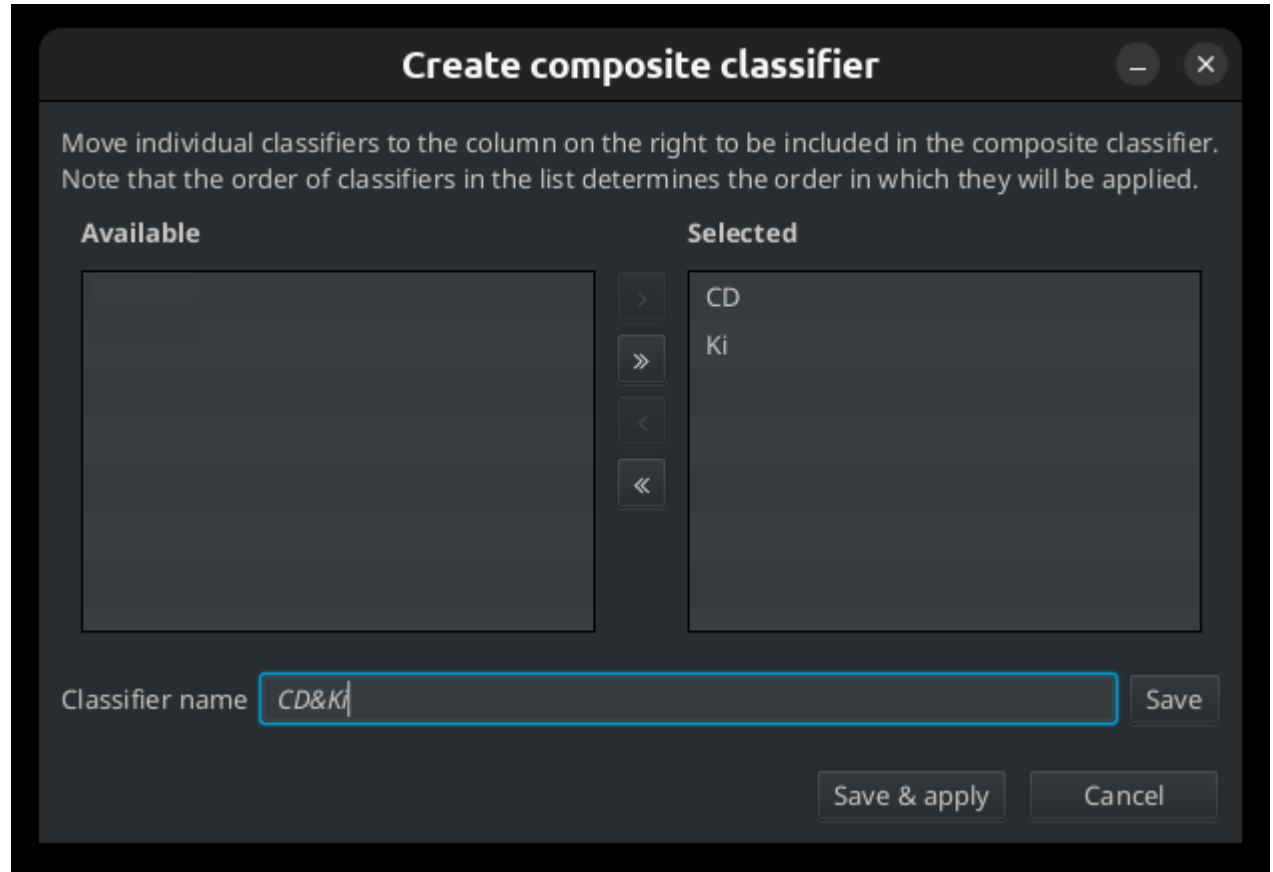
Composite Classifier

Create and save a composite classifier

Classify>

Object Classification>

Create composite classifier

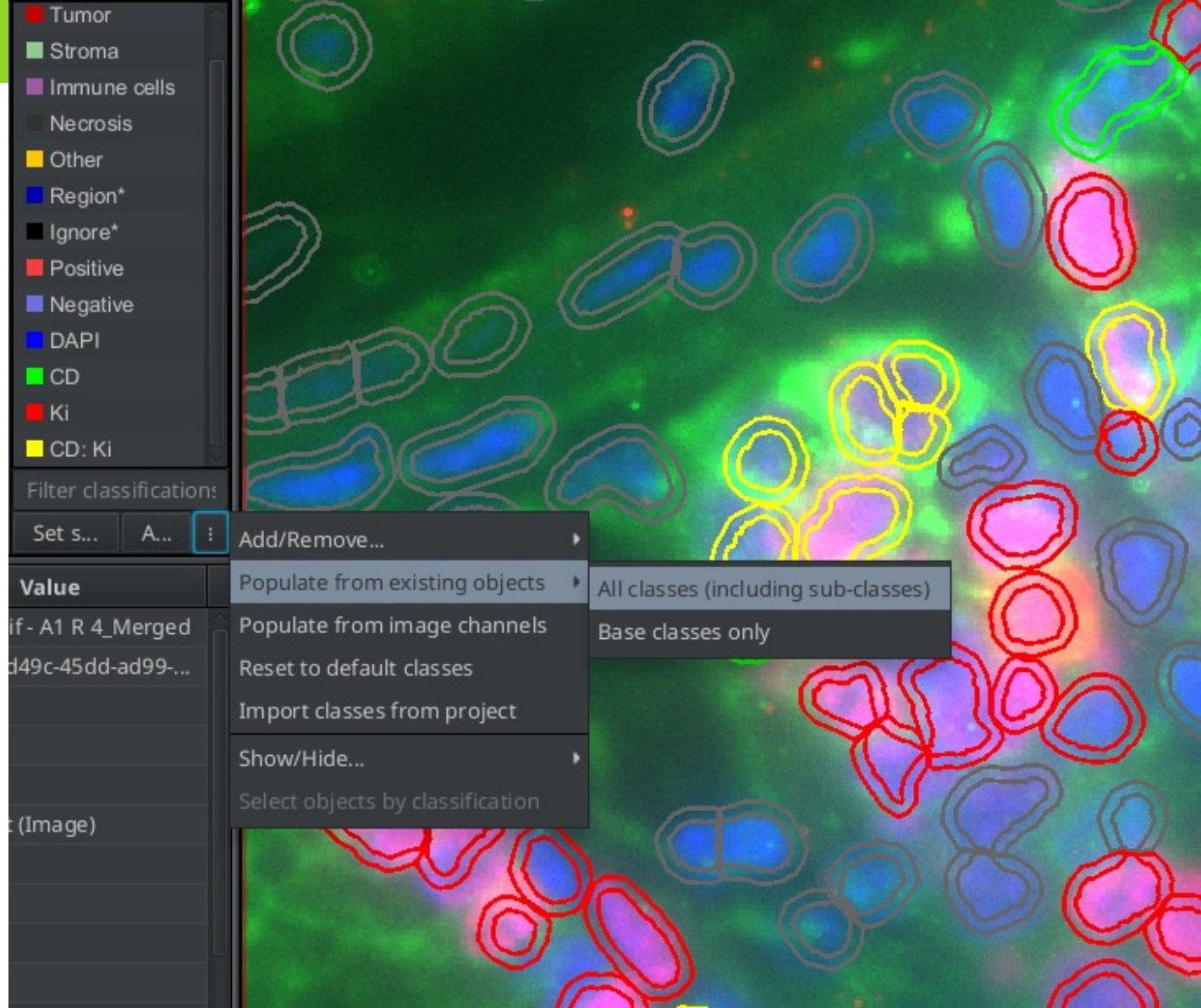


VII. Multiplex Analysis

View classifications

Populate from existing objects>all classes

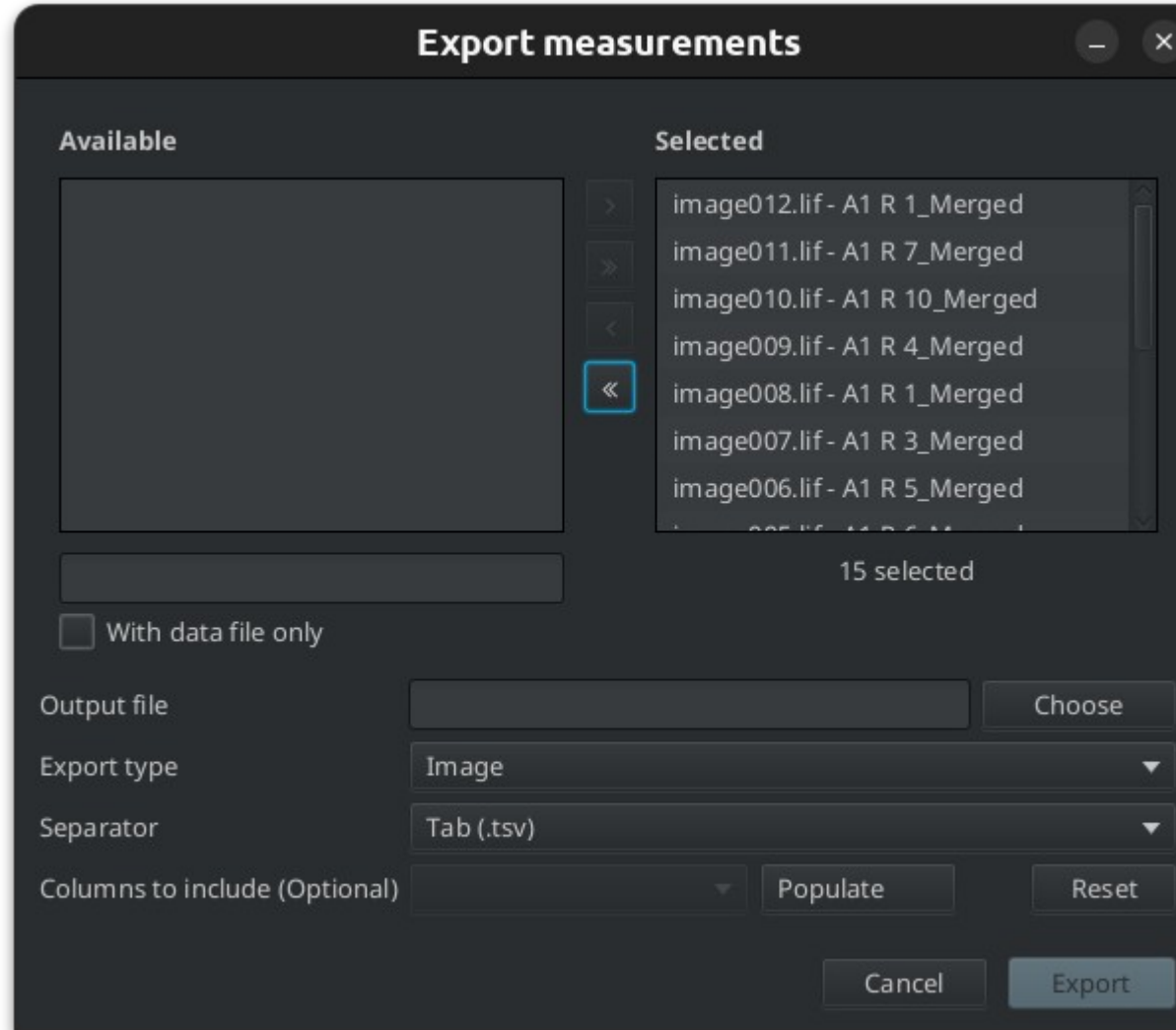
- Will add the combined class(es)
- You can change colors
 - To distinguish them from ignored cells



Run on project

Automate>Create command history script

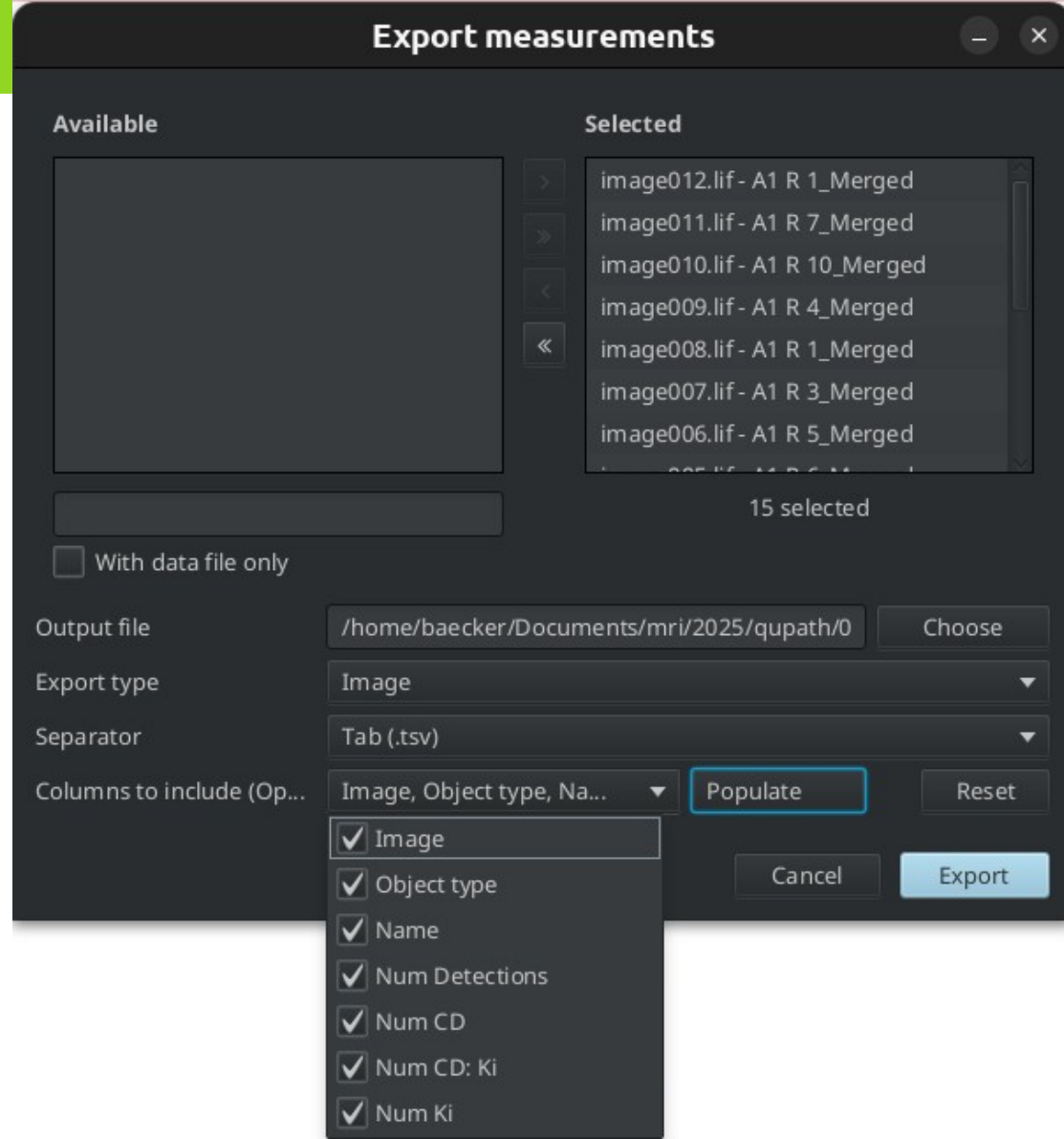
run for project
`runObjectClassifier("CD&Ki");`



Export Measurements

Measure>Export Measurements

Export Image or Annotations or
Detections



VII. Multiplex Analysis Measurements

Problem

- Num CD counts CD positive cells that are not Ki positive

- Add sum of columns in excel or
- run the script

Image	<u>Num Detections</u>	<u>Num CD</u>	<u>Num CD: Ki</u>	<u>Num Ki</u>
image012.lif - A1 R 1_Merged	3905	206	175	148
image011.lif - A1 R 7_Merged	9351	6600	1102	6
image010.lif - A1 R 10_Merged	8068	261	307	505
image009.lif - A1 R 4_Merged	6981	324	248	336
image008.lif - A1 R 1_Merged	50684	29686	2490	52
image007.lif - A1 R 3_Merged	5403	211	158	162
image006.lif - A1 R 5_Merged	71469	21271	8528	1380
image005.lif - A1 R 6_Merged	8047	6180	1198	1
image004.lif - A1 R 1_Merged	10890	635	736	373
image003.lif - A1 R 2_Merged	23788	6887	2967	526

convert_table.groovy

<https://github.com/MontpellierRessourcesImagerie/>

VII. Multiplex Analysis

Total Numbers per class

Image	<u>Num Detections</u>	<u>Num CD</u>	<u>Num CD: Ki</u>	<u>Num Ki</u>	Total CD	Total Ki
image012.lif - A1 R 1_Merged	3905	206	175	148	381	323
image011.lif - A1 R 7_Merged	9351	6600	1102	6	7702	1108
image010.lif - A1 R 10_Merged	8068	261	307	505	568	812
image009.lif - A1 R 4_Merged	6981	324	248	336	572	584
image008.lif - A1 R 1_Merged	50684	29686	2490	52	32176	2542
image007.lif - A1 R 3_Merged	5403	211	158	162	369	320
image006.lif - A1 R 5_Merged	71469	21271	8528	1380	29799	9908
image005.lif - A1 R 6_Merged	8047	6180	1198	1	7378	1199
image004.lif - A1 R 1_Merged	10890	635	736	373	1371	1109
image003.lif - A1 R 2_Merged	23788	6887	2967	526	9854	3493
image002.lif - A1 R 1_Merged	33157	24476	6663	47	31139	6710
image001.lif - A1 R 5_Merged	14977	3721	1507	343	5228	1850