



MIC-MAQ

Microscopy Images of Cells-Multi Analysis and Quantifications





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## Abstract

- ✓ MIC-MAQ automatically segments cells and/or nuclei on 2D microscopy images
- ✓ The plugin takes Z-stack but works only on 2D projection
- ✓ It provides intensity based and/or morphological measurements in nuclei and/or cells in multi channels experiment
- ✓ The plugin can propose the foci/spots detection

# Workflow

## For MIC-MAQ



Workflow

## Process for analysis:

MIC-MAQ

Select folder of images

Settings ?  
Cells/Nuclei detection  
Quantification

Z stack ? Pre-processing ?

Segmentation

Cellpose  
Model

Analyze Particles

Z stack ? Pre-processing ?

Extract ROIs  
Apply ROIs

Measures

Intensity based

Morphological

Spots

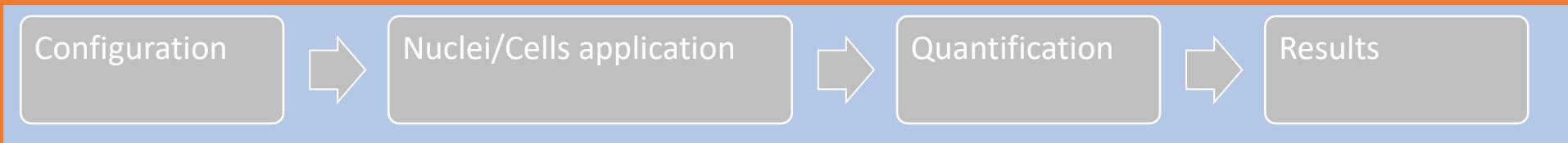
Mean intensity,  
Integrated density,  
...

Area ( $\mu\text{m}^2$ ),  
circularity,...

Find Maxima  
Prominence  
Spots number  
Analyze Particles  
Spots number,  
Mean spots size,  
Mean spots intensity

Table of Results

# How to use the plugin



## Configuration

- Data
- Calibration

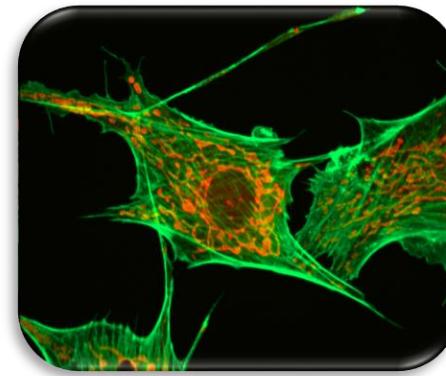
## Nuclei/Cells application

## Quantification

## Results

# Which data can be opened with MIC-MAQ ?

- Classical TIF images
- Any file formats from many life sciences open with the Bio-Format plugin



**.CZI** (Zeiss)  
**.LIF** (Leica)  
**.ND** (Metamorph)  
**.ND2** (Nikon)  
**.VSI** (Olympus)

## Configuration

- Data
- Calibration

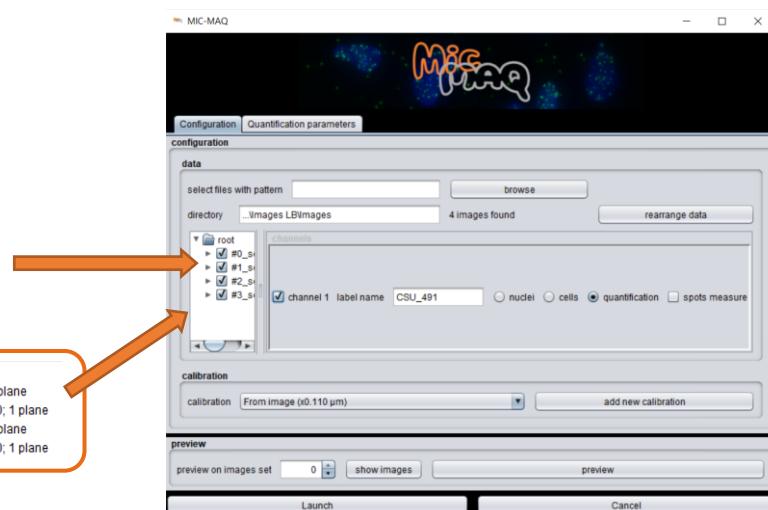
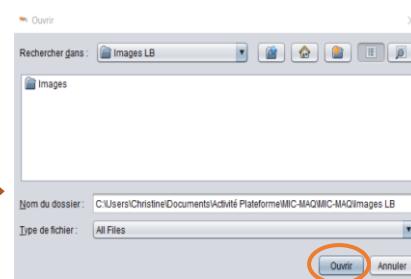
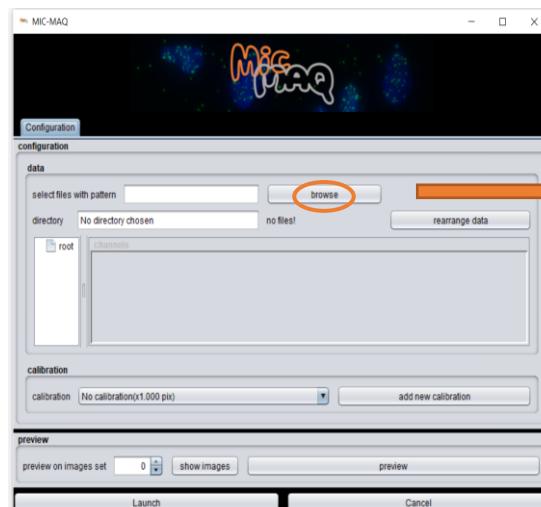
## Nuclei/Cells application

## Quantification

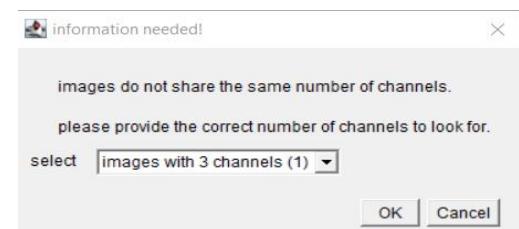
## Results

### A. Open files by selecting directory of images

- Select « **browse** » to choose a directory containing images
- Validate the directory by clicking on **Open/Ouvrir**



During the process of opening, if images do not share the same number of channels, you will be asked to select among the list the number of channels to be used for the analysis.



## Configuration

- Data
- Calibration

## Nuclei/Cells application

## Quantification

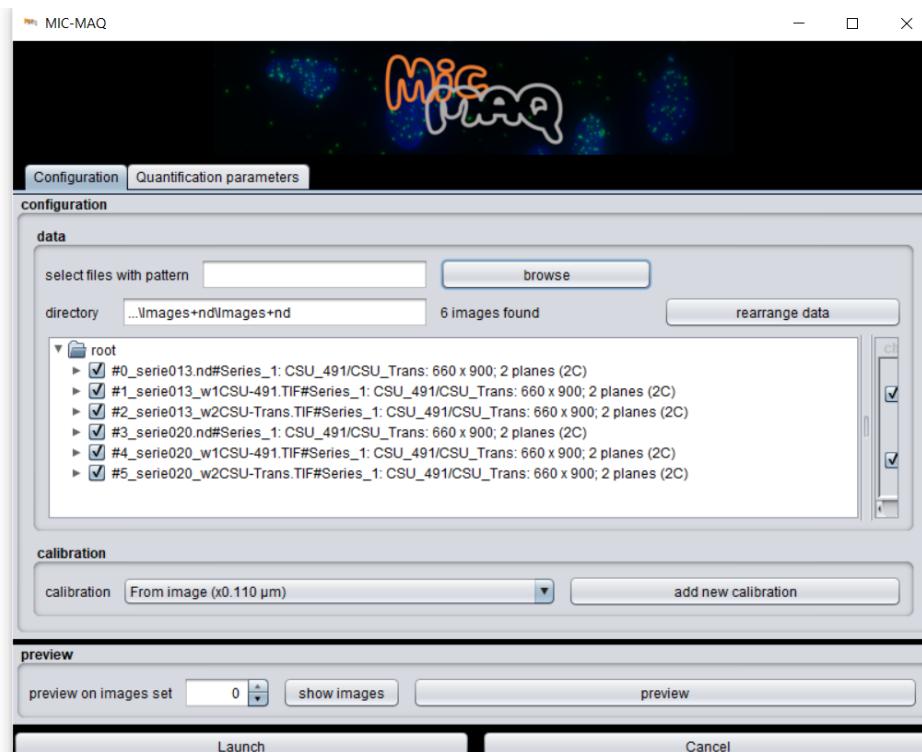
## Results

### B. Open files with pattern

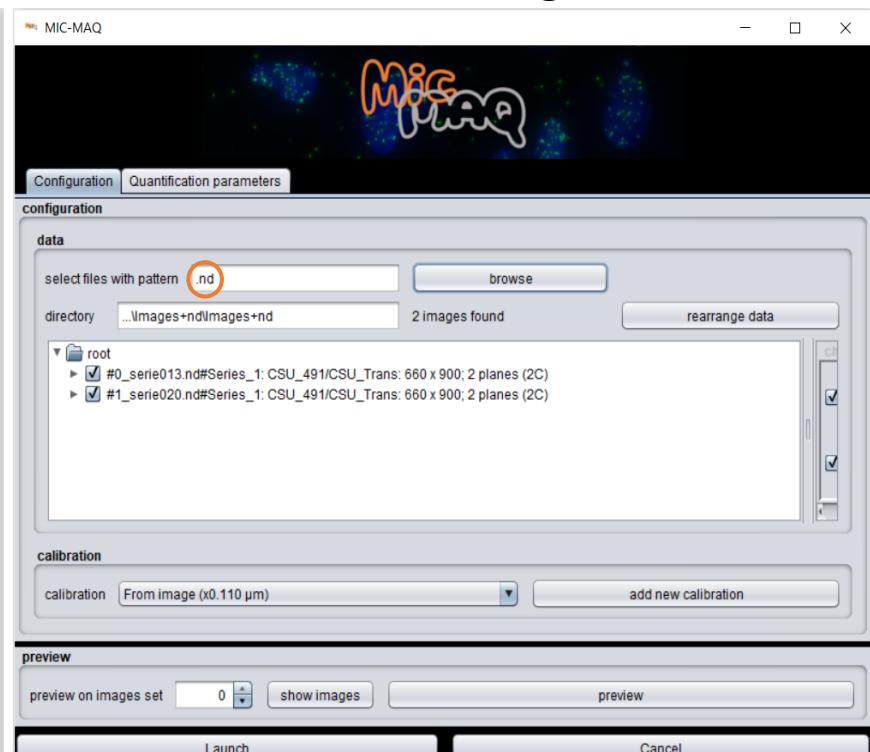
As first step, you can filter the data based on extension file (example: nd, tif) to select only one type of files in the folder of images:

- Enter the extension file in the « select files with pattern box » (example: nd)
- Observe the selected images after filtering in the root box

#### Before filtering



#### After filtering



## Configuration

- Data
- Calibration

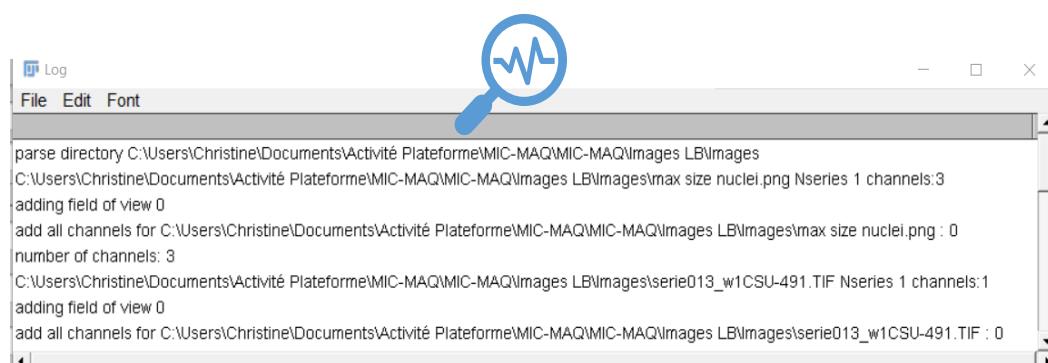
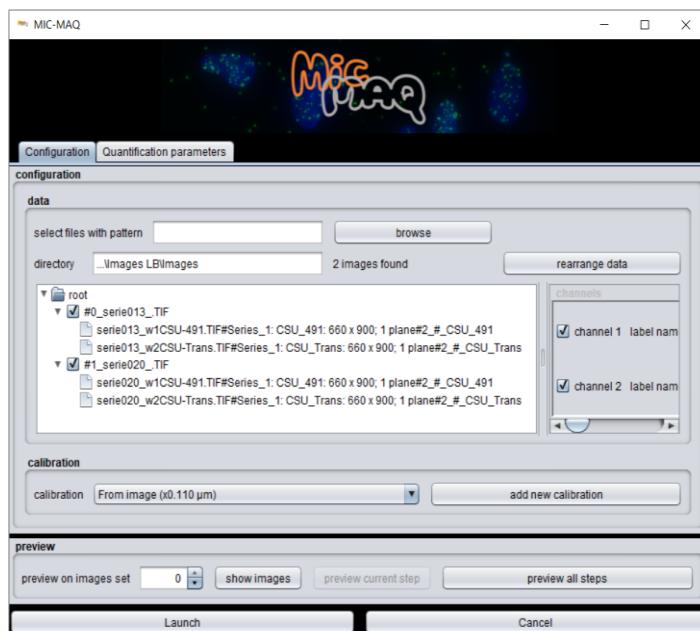
## Nuclei/Cells application

## Quantification

## Results

### Opening process

During the opening process, a window called « log » will appear containing the total number of images. Depend of the number of images, this window can take time to appear.



## Configuration

- Data
- Calibration

## Nuclei/Cells application

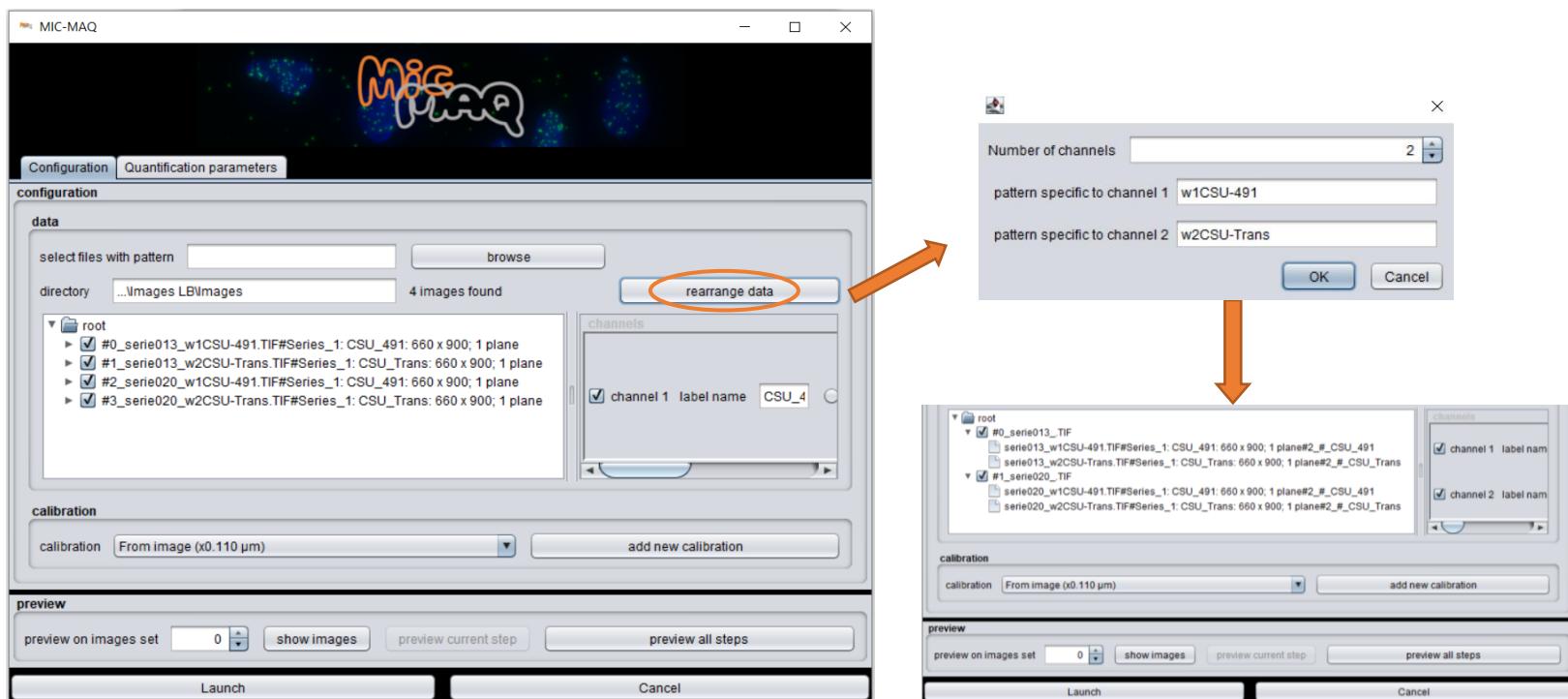
## Quantification

## Results

### Option: Rearrange TIF images by channel association

If you have TIF files with 1 image per channel, you can reorder your data based on the total number of channels and channel name specification:

- Click on « rearrange data »
- Enter the total number of channels in the folder containing images
- Define for each channel the specific filename pattern
- Observe the reorganization of series of images after specifying the filename in the root box



## Configuration

- Data
- Calibration

## Nuclei/Cells application

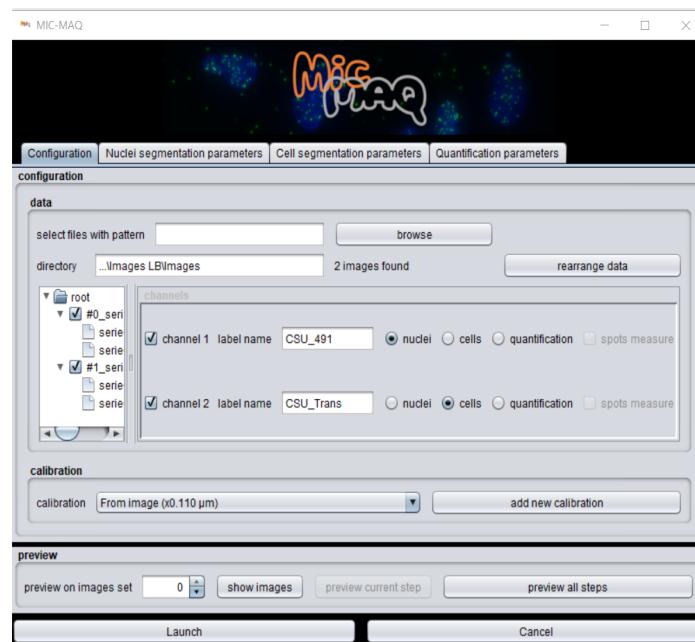
## Quantification

## Results

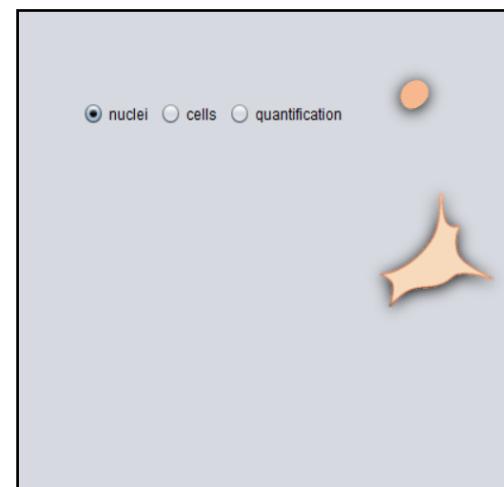
### Configure channels

For each channel:

- Define the label name for the channel
- Choose the application for the channel
  - ✓ « nuclei »: the channel is used to segment nuclei
  - ✓ « cells »: the channel is used to segment cells
  - ✓ « quantification »: the channel is used to measure parameters in nuclei and/or cells regions



*you have only 1 choice for each channel.*



## Configuration

- Data
- Calibration
- 

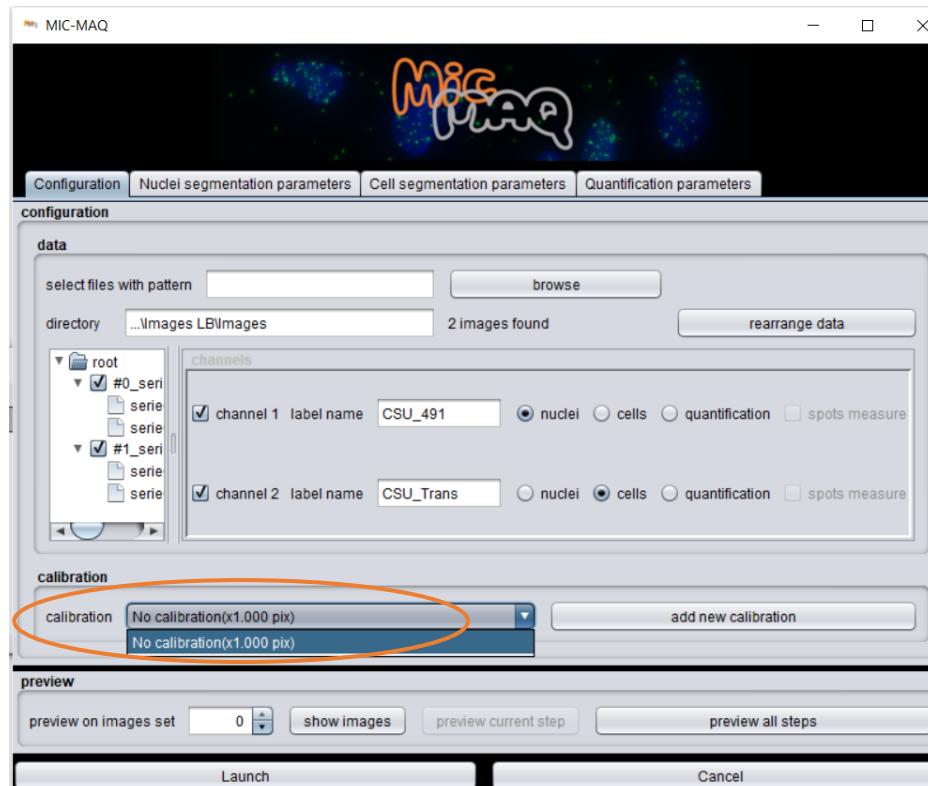
## Nuclei/Cells application

## Quantification

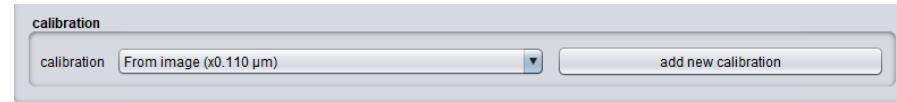
## Results

### Define calibration of images

The default calibration is in pixel (*No calibration (x1.000 pix)*). The measurements (as Area) will be exported in pixels<sup>2</sup>.



If the file format is from a microscope company the calibration directly takes the pixel size recorded in the file metadata (From image (x... µm)).



## Configuration

- Data
- Calibration

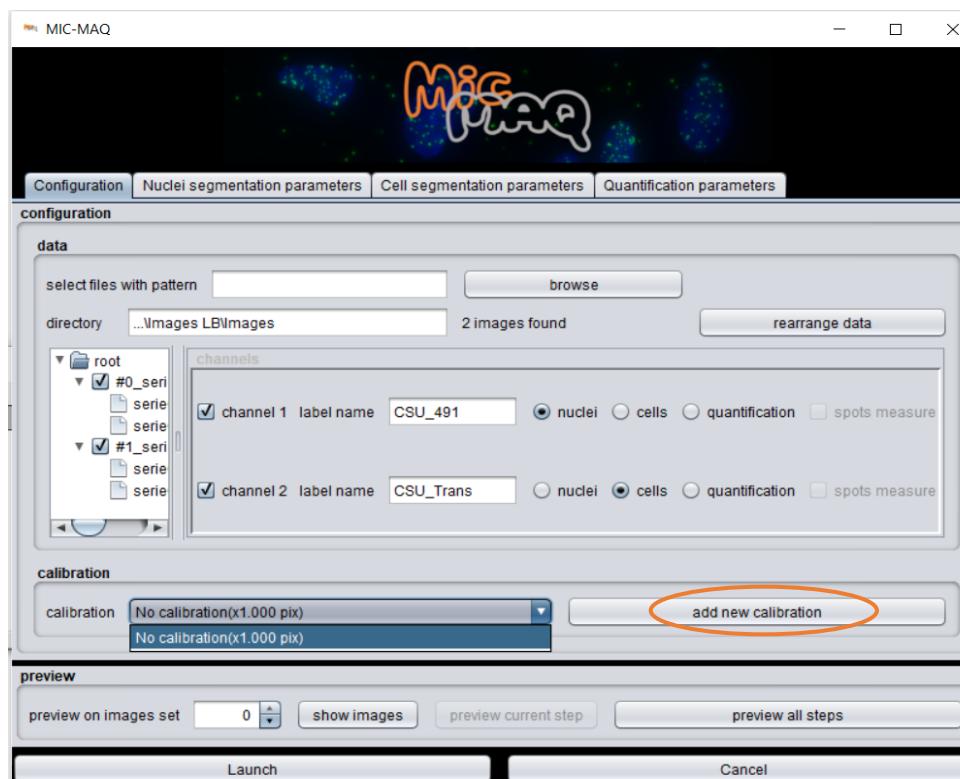
## Nuclei/Cells application

## Quantification

## Results

### Define calibration of images

- i. Click on **Add new measure Calibration**
- ii. A new window « Add a calibration » appears



## Configuration

- Data
- Calibration ● ● ●

## Nuclei/Cells application

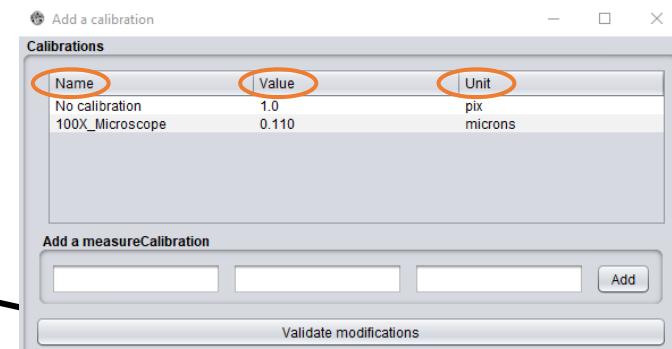
## Quantification

## Results

### Define calibration of images

iii. On this new window, enter a new calibration

- ✓ Name of the calibration
- ✓ The pixel size Value \*
- ✓ The Unit of the length



iv. Click on **Add** to see it on the list

### Pixel size on the microscope ?

Microscope Type	Objective	Pixel size
Ratio 2 Microscope	2.5K	1.82 µm
	5K	0.91 µm
	10K	0.45 µm
	20K	0.23 µm
	40K	0.11 µm
	63K water	0.072 µm
Ratio 1 Microscope	5K	1.82 µm
	10K	0.65 µm
	20K	0.325 µm
	40K	0.163 µm
	63K	0.103 µm
3D SIM Microscope	5K	1.82 µm
	10K	0.65 µm
	20K	0.325 µm
	40K	0.163 µm
	63K	0.103 µm
	100K	0.065 µm
3D Dec Microscope	40K	0.161 µm
	63K	0.102 µm
	100K	0.0645 µm
Spinning-Disk Microscope	10K	1.1 µm
	20K	0.55 µm
	40K	0.275 µm
	60K	0.183 µm
	100K oil	0.11 µm
TIRF Microscope	10K	1.6 µm
	20K	0.8 µm
	40K	0.4 µm
	60K oil	0.266 µm
SPS/SPEX CLSM	Dependant of the Zoom and/or the number of pixels in the image	
	100K oil	0.160 µm

\* <https://institutcurie.sharepoint.com/sites/US43-ImageProcessingAnalysis/SitePages/fr/Calibrer%20une%20image.aspx>

## Configuration

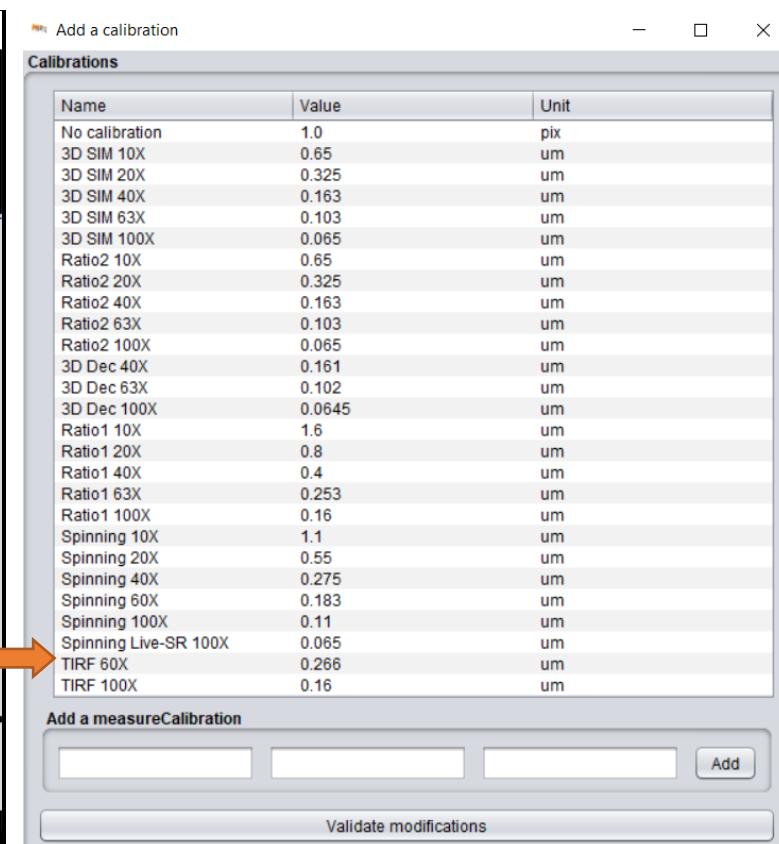
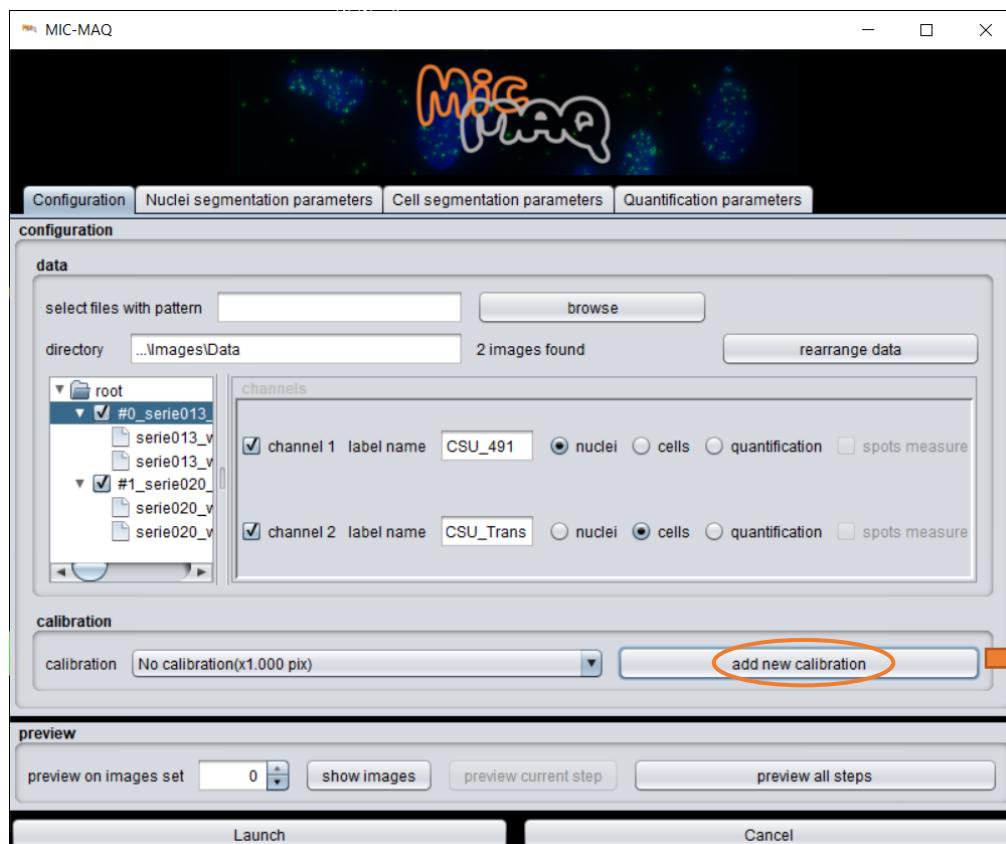
✓ Data  
☐ Calibration ● ●

## Nuclei/Cells application

## Quantification

## Results

- v. Click on **Validate modifications** and close the window « Add a calibration »
- vi. Select the new calibration appearing on the scroll list



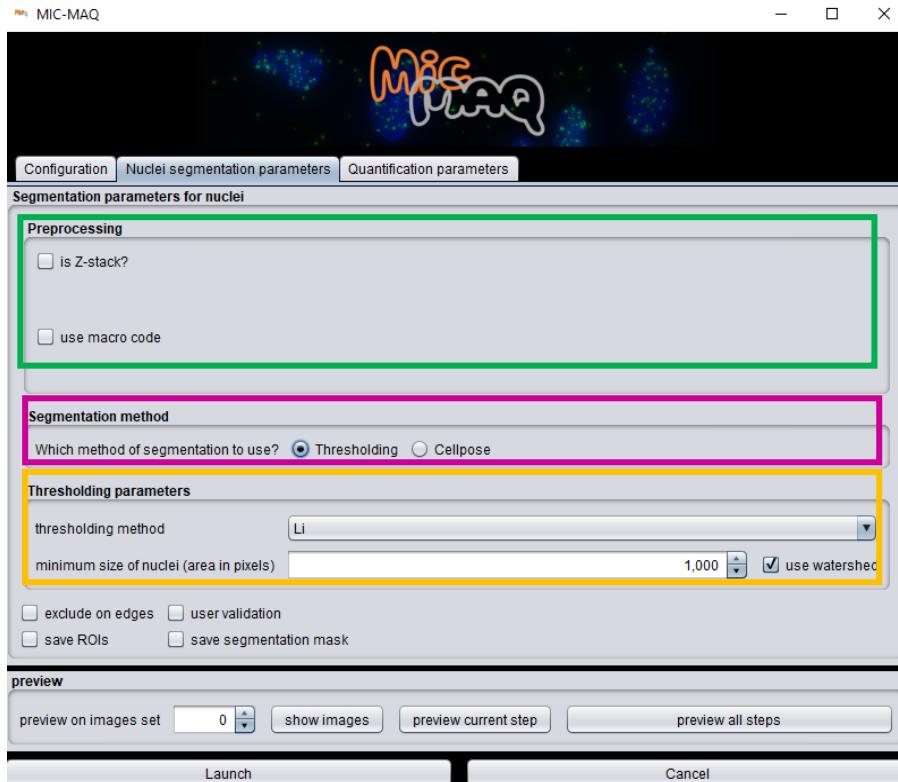
Configuration

Nuclei/Cells application

Quantification

Results

## Nuclei application

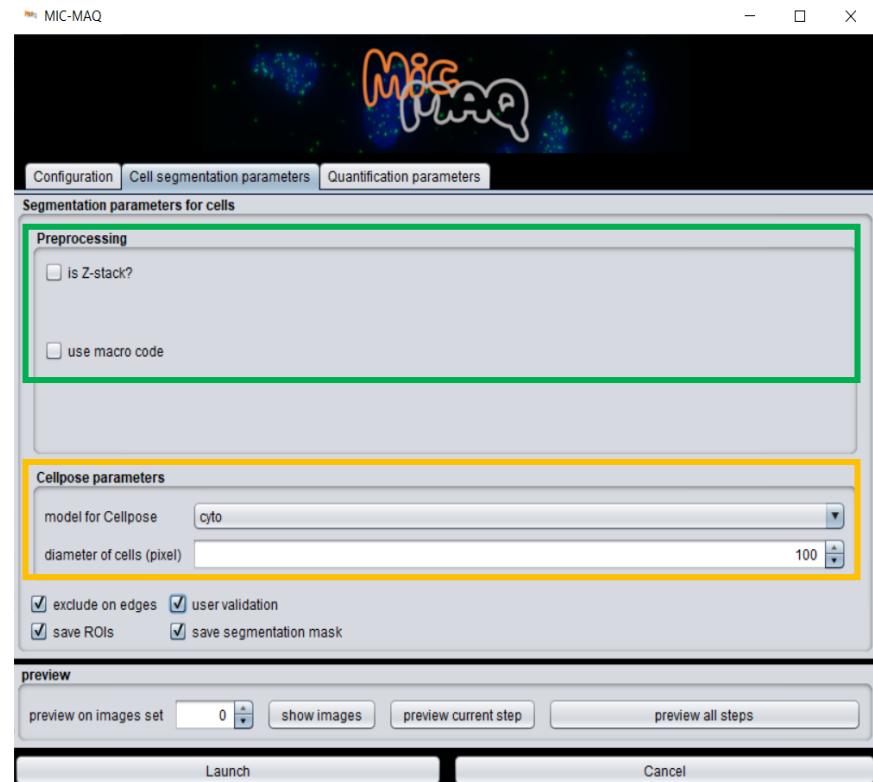


Preprocessing panel

Segmentation algorithm choice

Segmentation algorithm parameters

## Cells application



Configuration

Nuclei/Cells application

Quantification

Results

## Preprocessing: Z-stack



*MIC-MAQ work only on 2D images, if you have Z stack, the stack should be converted into 2D projection.*

### 2D images

Preprocessing

is Z-stack?

use macro code

### 3D images

Preprocessing

is Z-stack?

method of projection

choose slices to use

use macro code

- Untick the box « is a Z-stack ? »
- Tick the box « is a Z-stack ? »
- Choose the method of Z projection in the list

*Optional:* You have the possibility to select slices number to create the 2D projection

choose slices to use

Configuration

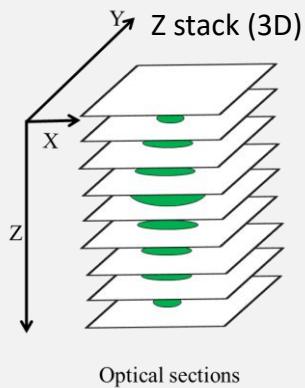
Nuclei/Cells application

Quantification

Results

- Preprocessing** ● ● ●
- Segmentation
- Parameters

## Preprocessing: Z-stack

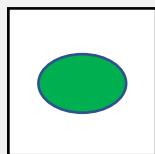


### Method of projection :

- ✓ **Maximum projection** : the 2D projection is calculated based on the maximum voxel value in Z axis
- ✓ **Standard Deviation projection** : the 2D projection is calculated based on the standard deviation value of voxels in Z axis

### Method of projection

Z projection (2D)



Configuration

Nuclei/Cells application

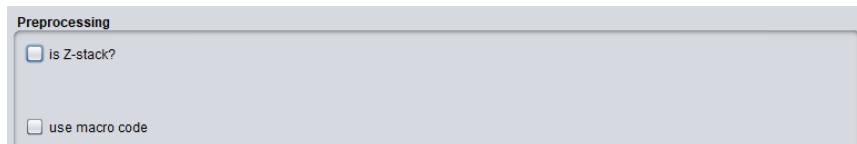
Quantification

Results

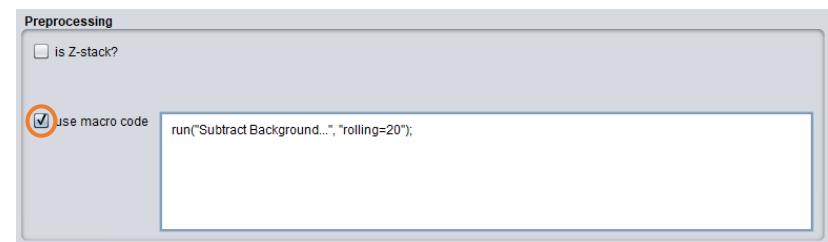
## Preprocessing: use macro code

*MIC-MAQ offers the possibility of applying preprocessing to images using a macro code.*

### Without macro



### With macro



- Untick the box « use macro code »
- Tick the box « use macro code »
- Copy the macro code on the white box

Configuration

Nuclei/Cells application

Quantification

Results

## Nuclei/Cells segmentation methods

- Choose the segmentation method

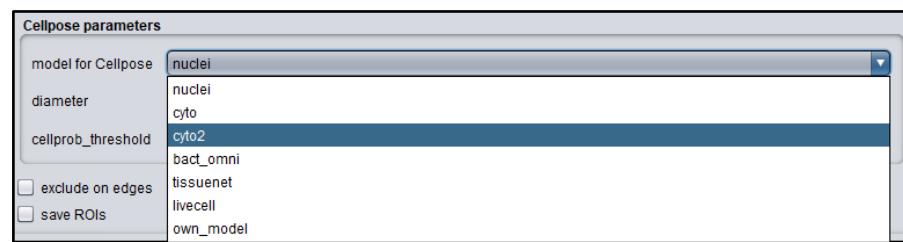
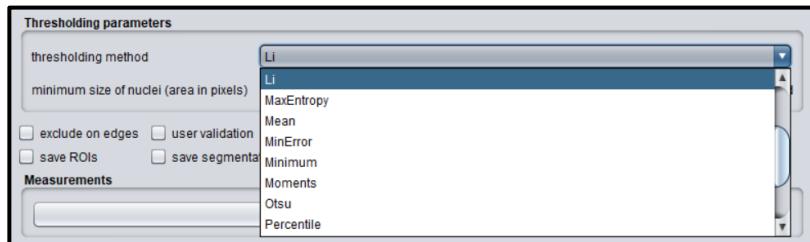
✓ Thresholding

Nuclei

✓ Cellpose

Nuclei

Cells



+ : faster process

+ : close proximity between nuclei

- : close proximity between nuclei,  
intensity variation

- : slow process

Configuration

Nuclei/Cells application

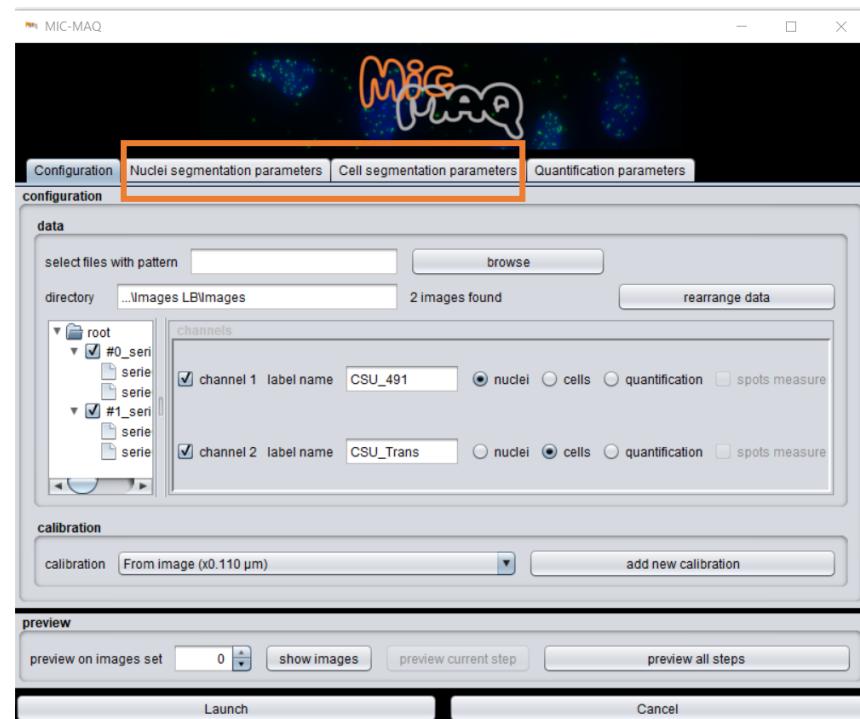
Quantification

Results

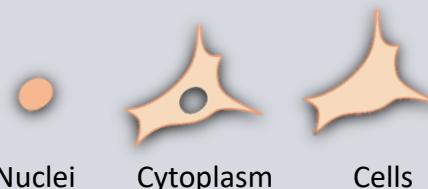
If you have at least 2 channels, one channel for detecting nuclei and another one for detecting cells, the quantification will be done in nuclei, cells and cytoplasm.

Nuclei +  
cells

The cytoplasm regions are obtained by removing nuclei regions from cells.



Measurements are apply on these regions:



Configuration

Nuclei/Cells application

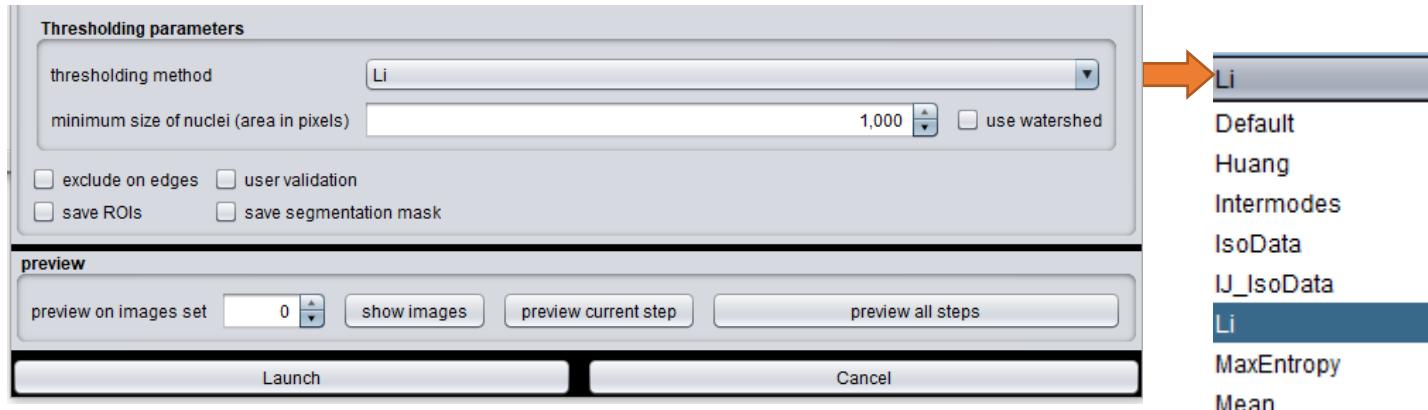
Quantification

Results

- Preprocessing
- Segmentation
- Parameters : Nuclei

## Segmentation parameters: Thresholding

Nuclei



- Choose the thresholding method among the list
- Enter the minimum size of nuclei (defined by the area in pixels<sup>2</sup>)

minimum size of nuclei (area in pixels): 1,000   use watershed

**Optional:** use watershed to separate fused nuclei



Configuration

Nuclei/Cells application

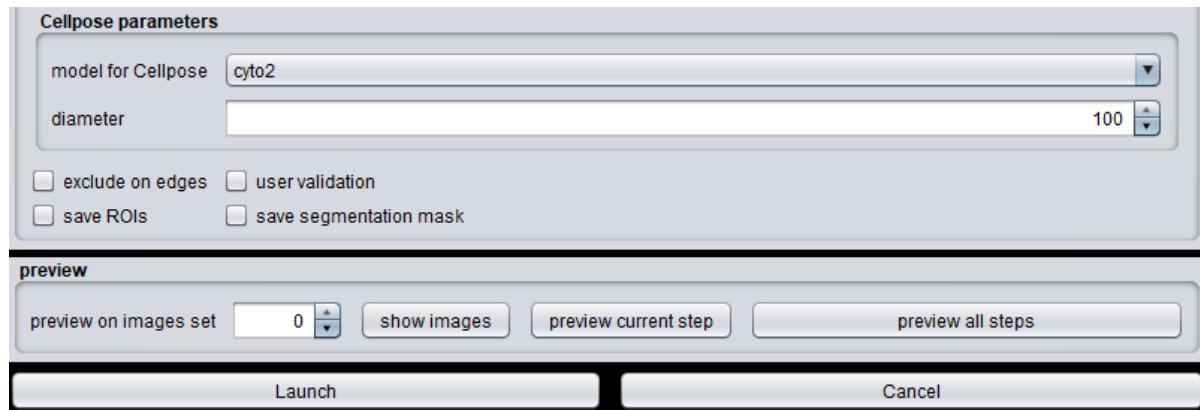
Quantification

Results

## Segmentation parameters: Cellpose

Nuclei

Cells



- cyto2
- nuclei
- cyto
- cyto2
- bact\_omni
- tissuenet
- livecell
- own\_model

- Choose the model for cellpose among the list  
*If you selected « own model », you need to enter the path to select the model with the browse button*



- Enter the mean nuclei diameter to segment (in pixel)



Configuration

Nuclei/Cells application

Quantification

Results

## Cytoplasm extraction parameters

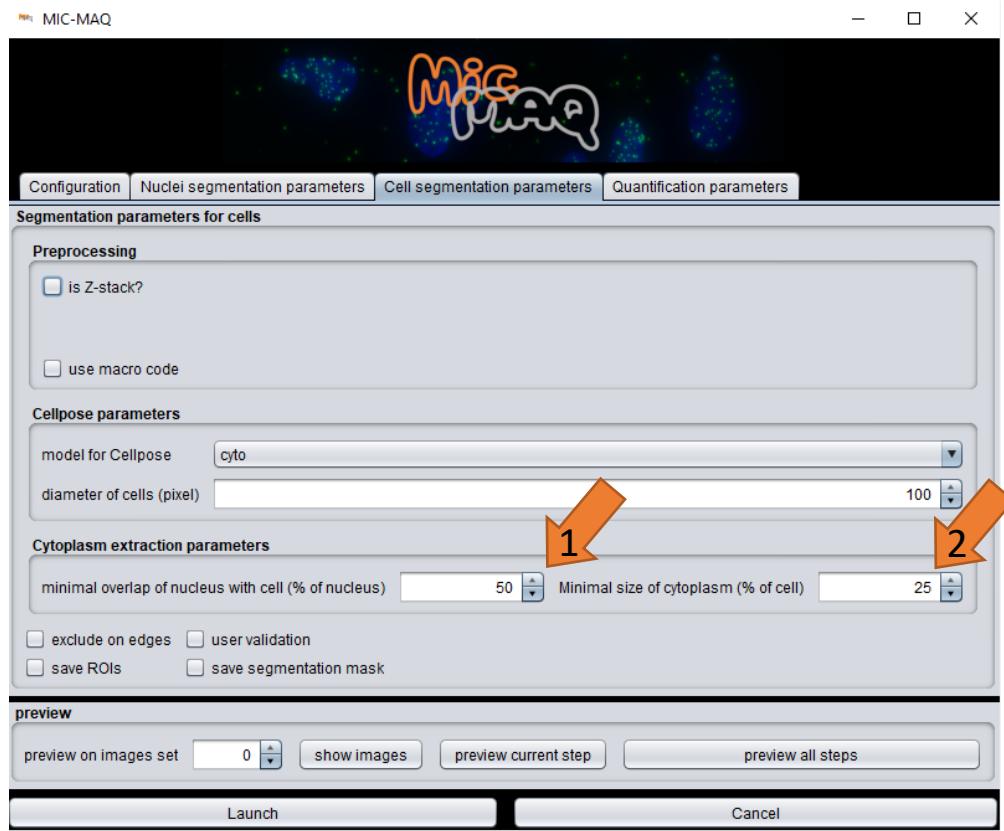
Nuclei +  
cells

In the cell segmentation parameters window:

1. Define the minimal overlap of nucleus with cell to be associated together (% of nucleus) : default value: 50%

2. Enter the minimal size of cytoplasm to be quantify (% of cell) : default value

25%



Configuration

Nuclei/Cells application

Quantification

Results

- Preprocessing
  - Segmentation
  - Parameters**
- 

## Segmentation parameters: Options

<input checked="" type="checkbox"/> exclude on edges	<input checked="" type="checkbox"/> user validation
<input checked="" type="checkbox"/> save ROIs	<input checked="" type="checkbox"/> save segmentation mask

You have the possibility to tick boxes for segmentation:

- **Exclude on edges:** this option will remove automatically regions that touch the edges of the image
- **User validation:** manual step where the user can delete or add regions obtained by segmentation
- **Save ROIs:** this option allows to save automatically the regions of interest obtained by segmentation
- **Save segmentation mask:** this option allows to save automatically the mask of objects obtained by segmentation

Configuration

Nuclei/Cells application

Quantification

Results

- Preprocessing
- Segmentation
- Parameters



## Test the segmentation



1. Select the set number for the preview to test the thresholding parameters
2. Start the analysis on the previous selected series of images with the button « preview current step »

### Thresholding

Thresholding parameters

thresholding method: Li  
minimum size of nuclei (area in pixels): 1,000   
 exclude on edges  user validation  
 save ROIs  save segmentation mask

preview

preview on images set: 0

Launch Cancel

To know the association between the preview number and the image name, check the #value in the root box.

### Cellpose

Cellpose parameters

model for Cellpose: cyto2  
diameter: 100  
 exclude on edges  user validation  
 save ROIs  save segmentation mask

preview

preview on images set: 0

Launch Cancel



root  
►  #0\_serie013\_TIF  
►  #1\_serie020\_TIF

Configuration

Nuclei/Cells application

Quantification

Results

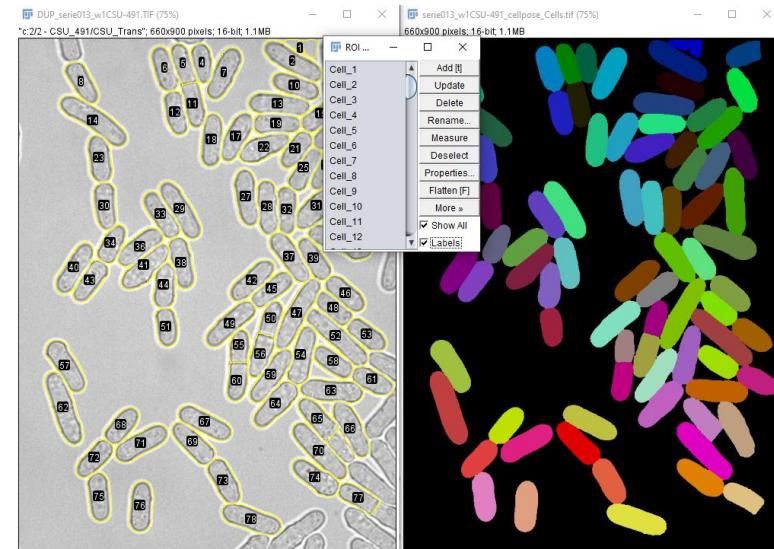
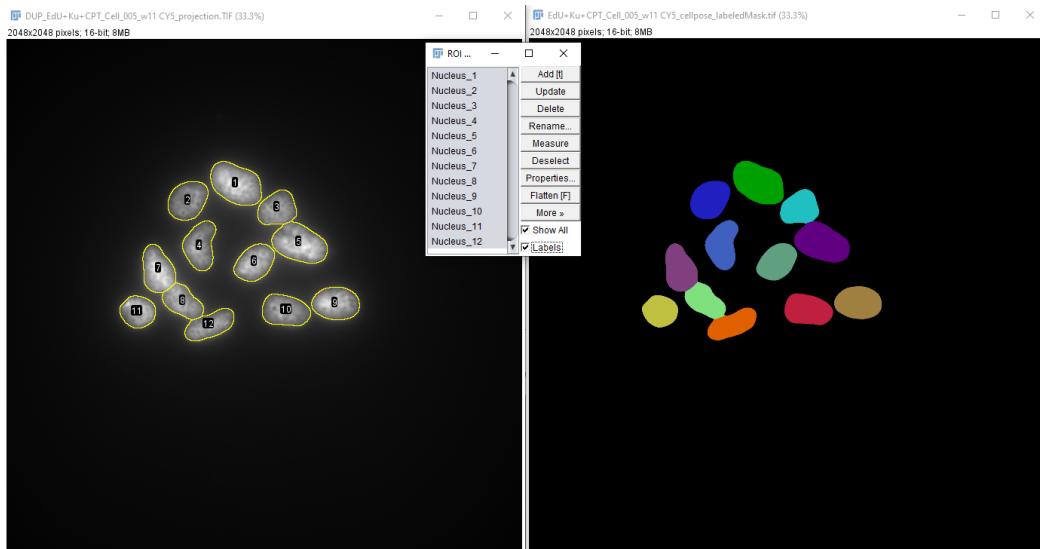
- ✓ Preprocessing
- ✓ Segmentation
- Parameters



## Examples of segmentation

Nuclei

Cells



Configuration

Nuclei/Cells application

Quantification

Results

- Preprocessing** ●●●
- Measurements
- Optional: Spot detection

## Preprocessing: Z-stack



*MIC-MAQ work only on 2D images, if you have Z stack, the stack should be converted into 2D projection.*

**2D images**

Preprocessing

Is Z-stack?

use macro code

**3D images**

Preprocessing

Is Z-stack?

method of projection Maximum projection

choose slices to use Standard deviation projection

use macro code

- Untick the box « Is a Z-stack ? »
- Tick the box « Is a Z-stack ? »
- Choose the method of Z projection in the list

*Optional:* You have the possibility to select slices number to create the 2D projection

choose slices to use 1 10

Configuration

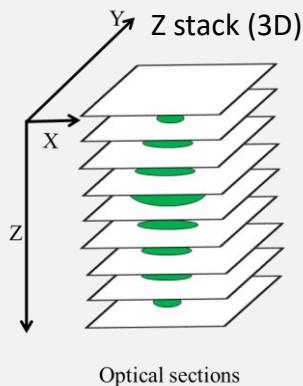
Nuclei/Cells application

Quantification

Results

- Preprocessing** 
- Measurements
- Optional: Spot detection

## Preprocessing: Z-stack

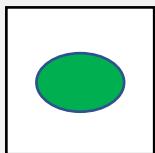


### Method of projection :

- ✓ **Maximum projection** : the 2D projection is calculated based on the maximum voxel value in Z axis
- ✓ **Standard Deviation projection** : the 2D projection is calculated based on the standard deviation value of voxels in Z axis

### Method of projection

Z projection (2D)



Configuration

Nuclei/Cells application

Quantification

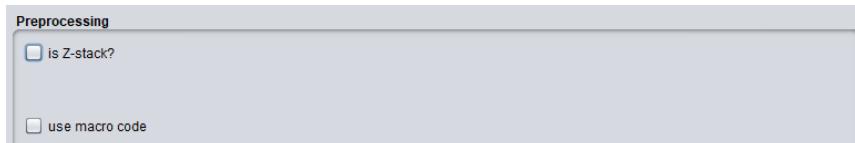
Results

- Preprocessing** ●●●
- Measurements
- Optional: Spot detection

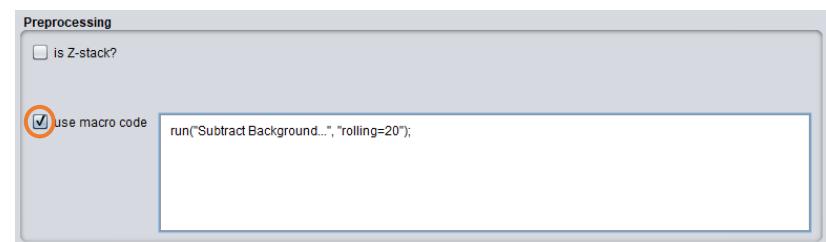
## Preprocessing: use macro code

*MIC-MAQ offers the possibility to apply preprocessing on the images with macro code.*

### Without macro



### With macro



- Untick the box « use macro code »
- Tick the box « use macro code »
- Copy the macro code on the white box

Configuration

Nuclei/Cells application

Quantification

Results

- Preprocessing
- Measurements**
- Optional: Spot detection

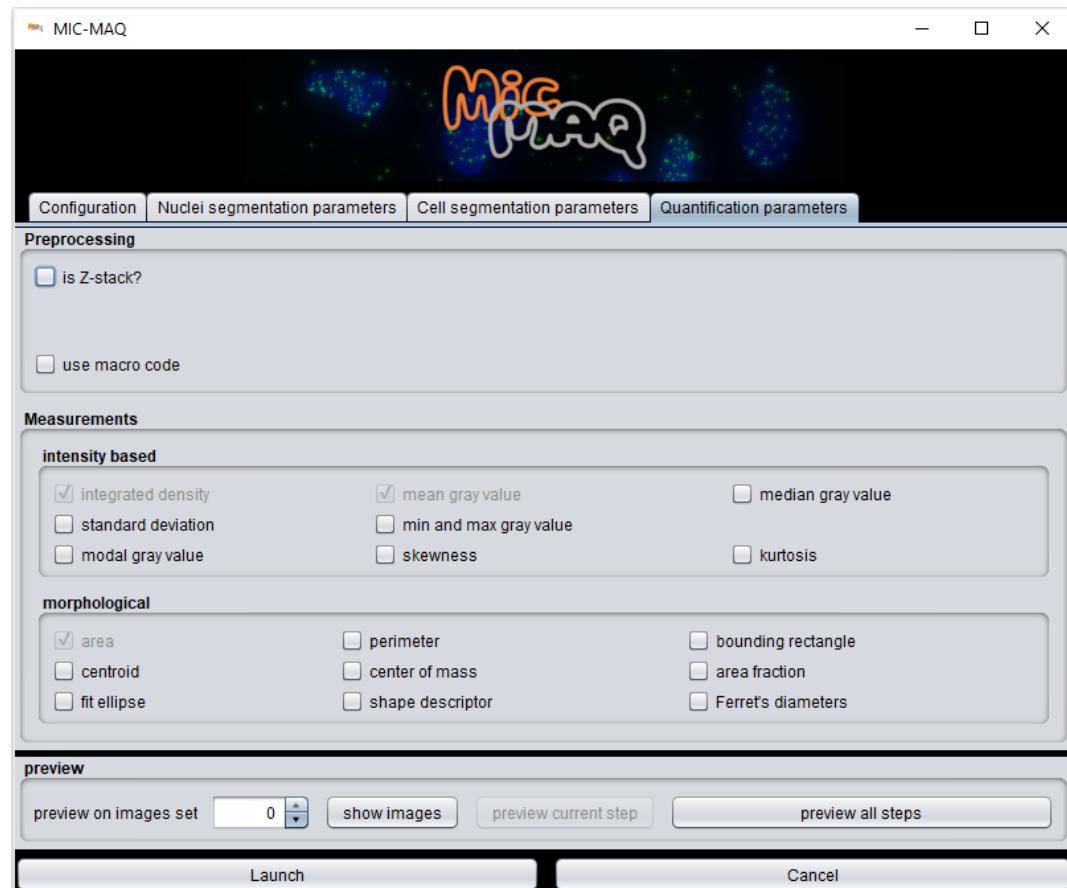
## Quantification parameters

### Measurements

- Among the list, tick the measurement(s) box for the channel(s) used as quantification

Choice of parameters :

- Intensity based**
- Morphological**



*By default, the mean gray value, integrated density and area are automatically measure on the region of nuclei and/or cells for all channel used as quantification.*



Description of measurements: <https://imagej.nih.gov/ij/docs/menus/analyze.html#set>

Configuration

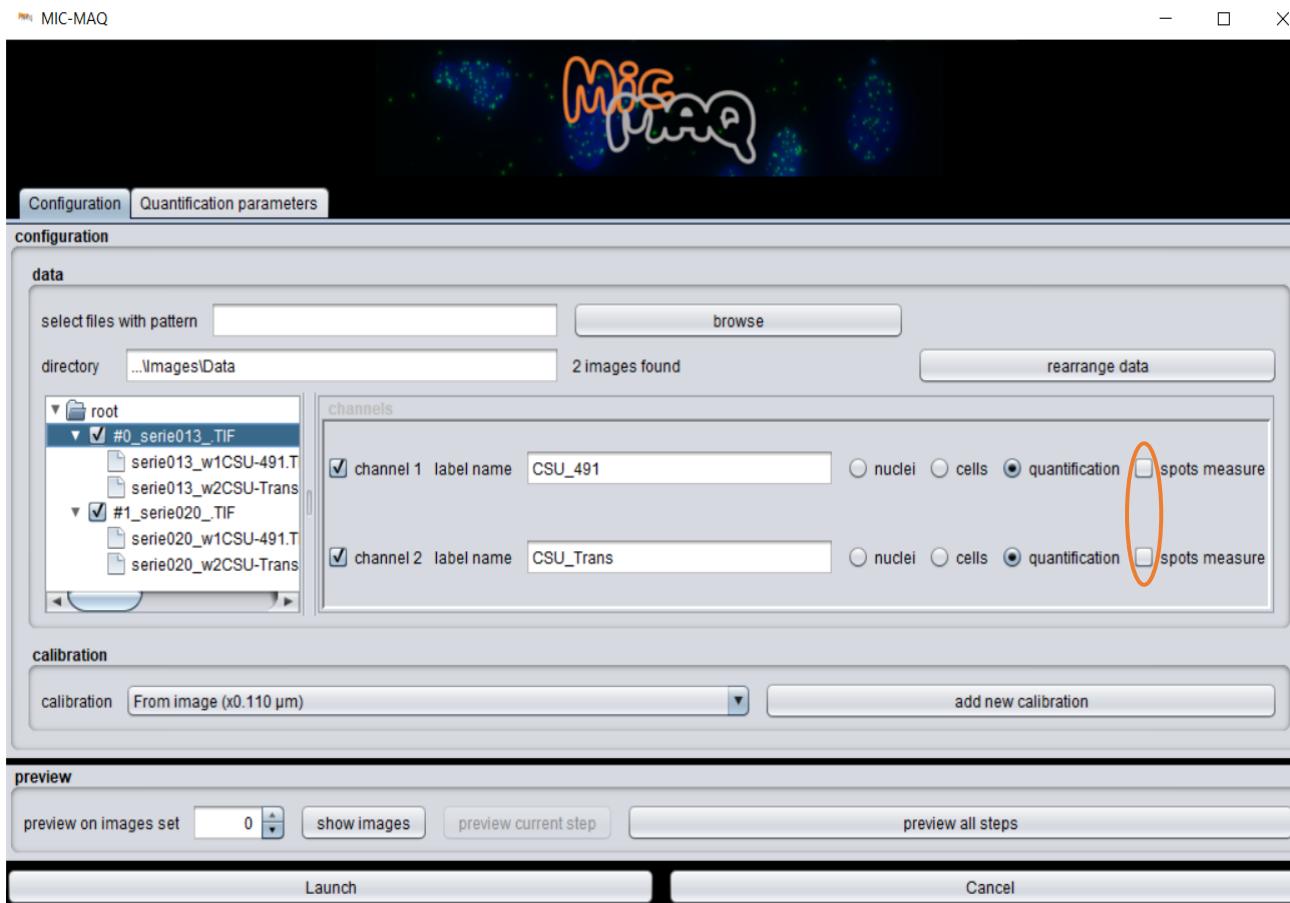
Nuclei/Cells application

Quantification

Results

- Preprocessing
- Measurements
- Optional: Spot detection**

## Spots detection window



Configuration

Nuclei/Cells application

Quantification

Results

- Preprocessing
- Measurements
- Optional: Spot detection**  
● ● ● ● ● ● ● ● ● ●

## Spots detection : Preprocessing Z Stack



*MIC-MAQ work only on 2D images, if you have Z stack, the stack should be converted into 2D projection.*

**2D images**

**3D images**

Preprocessing

is Z-stack?

use macro code

Preprocessing

is Z-stack?

method of projection

choose slices to use

- Untick the box « is a Z-stack ? »
- Tick the box « is a Z-stack ? »
- Choose the method of Z projection in the list

*Optional:* You have the possibility to select slices number to create the 2D projection

choose slices to use

1  10

Configuration

Nuclei/Cells application

Quantification

Results

✓ Preprocessing

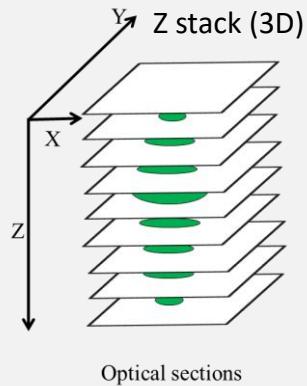
✓ Measurements

**Optional: Spot detection**



## Spots detection :

### Preprocessing: Z-stack

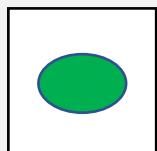


### Method of projection :

- ✓ **Maximum projection** : the 2D projection is calculated based on the maximum voxel value in Z axis
- ✓ **Standard Deviation projection** : the 2D projection is calculated based on the standard deviation value of voxels in Z axis

### Method of projection

Z projection (2D)



Configuration

Nuclei/Cells application

Quantification

Results

- ✓ Preprocessing
- ✓ Measurements
- ❑ **Optional: Spot detection**  
● ● ● ● ● ● ● ● ● ●

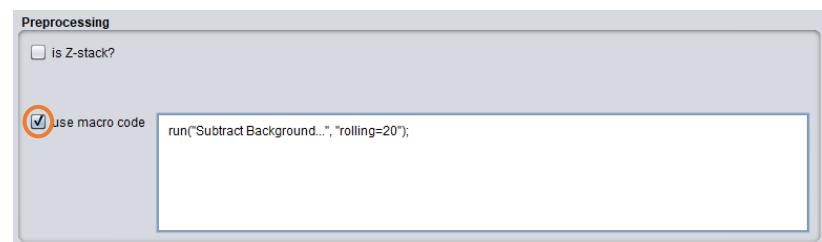
## Spots detection : Preprocessing use macro code

*MIC-MAQ offers the possibility to apply preprocessing on the images with macro code.*

### Without macro



### With macro



- Untick the box « use macro code »
- Tick the box « use macro code »
- Copy the macro code on the white box

Configuration

Nuclei/Cells application

Quantification

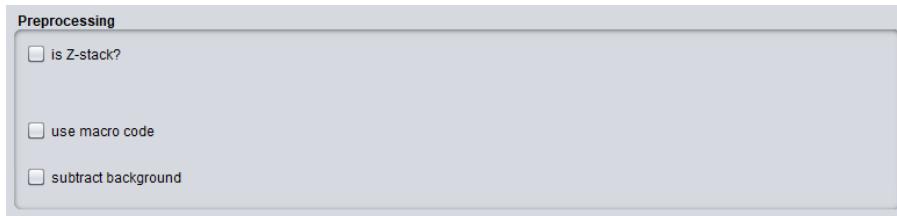
Results

- Preprocessing
- Measurements
- Optional: Spot detection**  
● ● ● ● ● ● ● ● ● ●

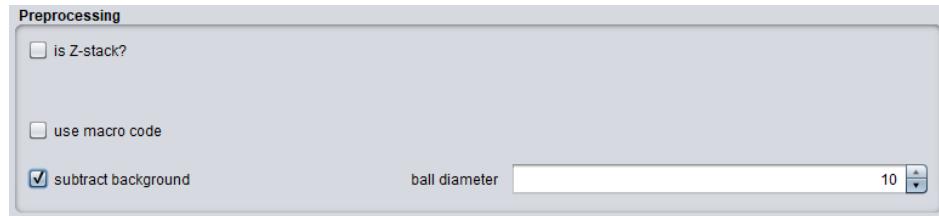
## Spots detection : Preprocessing subtract background

*MIC-MAQ offers the possibility to apply preprocessing on the images to remove background and facilitates the spots detection.*

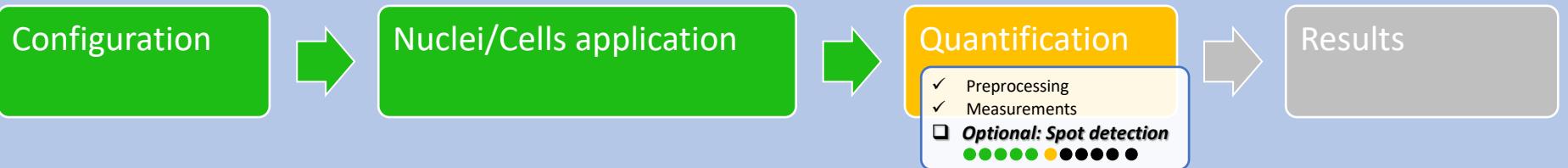
### Without subtract background



### With subtract background



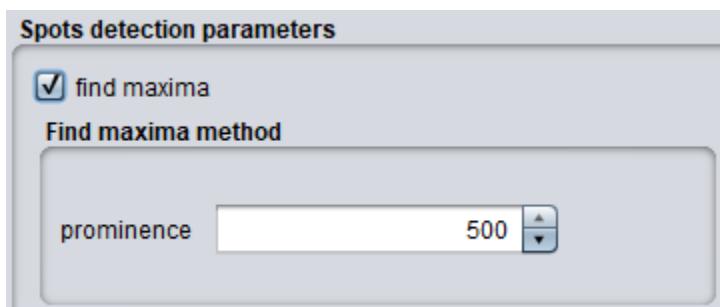
- Untick the box « subtract background »
- Tick the box « subtract background »
- Select the ball diameter



## Spots detection : Methods

- Choose the spots detection method

## ✓ Find maxima



+ : close proximity between spots

- : spot intensity variation

## Quantification

- ✓ Preprocessing
  - ✓ Measurements
  - Optional: Spot detection**  


### ✓ Threshold + Analyze Particles



+ : extract the mean spot size, the  
mean spot intensity

- : close proximity between spots

Configuration

Nuclei/Cells application

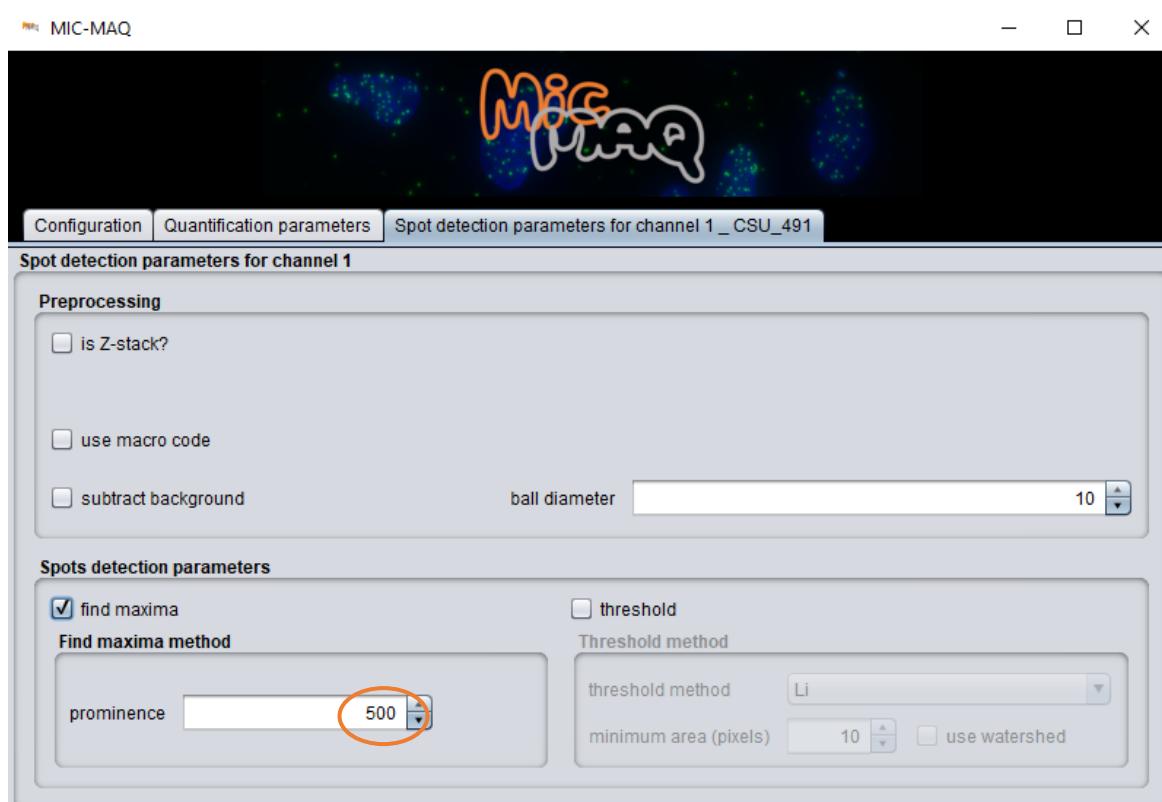
Quantification

Results

- Preprocessing
  - Measurements
  - Optional: Spot detection**
- 

## Spots detection method: find maxima

- Choose the prominence value to define local maxima corresponding to a spot



Configuration

Nuclei/Cells application

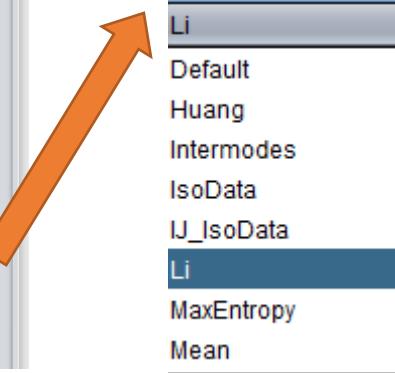
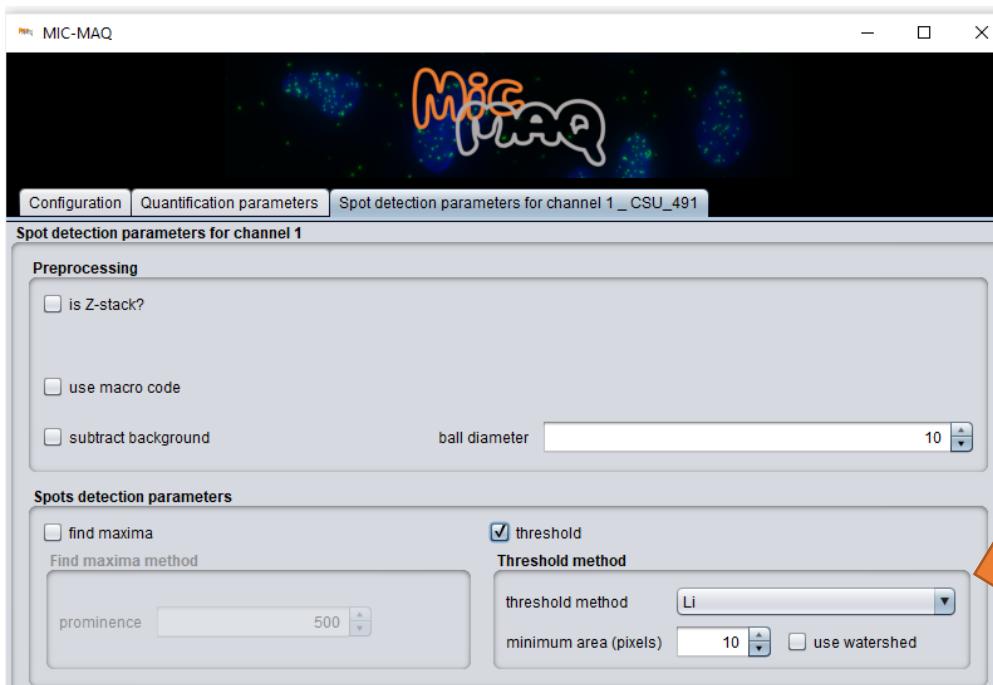
Quantification

Results

- Preprocessing
- Measurements
- Optional: Spot detection**

## Spots detection method: Threshold

- Choose the thresholding method among the list
- Enter the minimum size of spots (defined by the area in pixels<sup>2</sup>)



**Optional:** use watershed to separate fused spots.

minimum area (pixels)   use watershed

Configuration

Nuclei/Cells application

Quantification

Results

- Preprocessing
  - Measurements
  - Optional: Spot detection
- 

## Spots detection : Test the spots detection



1. Select the set number for the preview to test the parameters

2. Start the analysis on the previous selected series of images with the button « preview current step »

### Find Maxima

### Threshold

Spots detection parameters

find maxima       threshold

Find maxima method

prominence: 500

Threshold method

threshold method: Li

minimum area (pixels): 10

use watershed

preview

preview on images set: 0

show images | preview current step | preview all steps

Launch | Cancel

Spots detection parameters

find maxima       threshold

Find maxima method

prominence: 500

Threshold method

threshold method: Li

minimum area (pixels): 10

use watershed

preview

preview on images set: 0

show images | preview current step | preview all steps

Launch | Cancel



To know the association between the preview number and the image name, check the #value in the root box.

- ▼  root
  - #0\_serie013\_.TIF
  - #1\_serie020\_.TIF



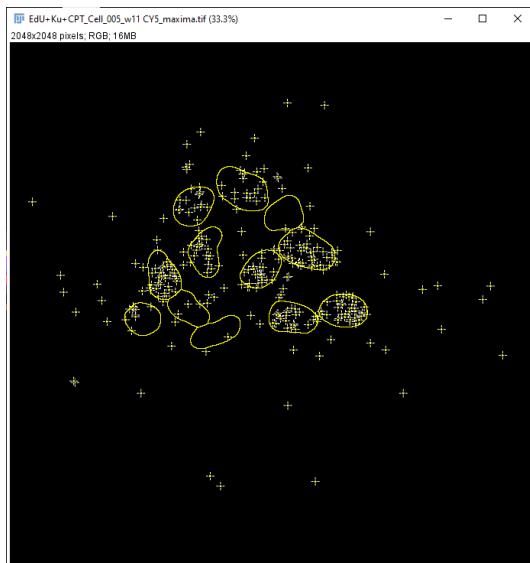
## Examples of spots detection:

# After preprocessing



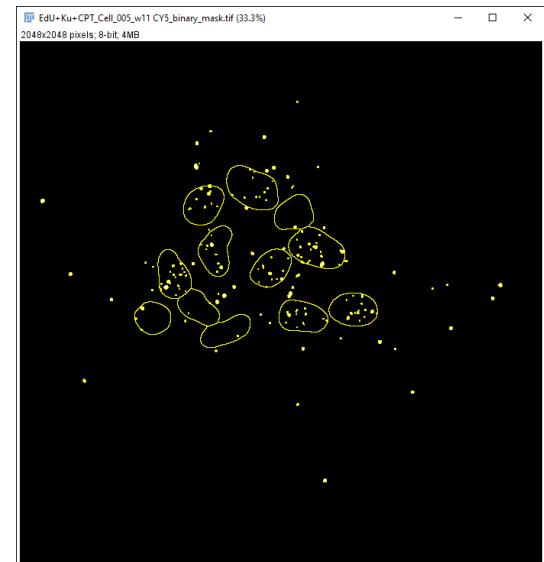
## Find Maxima

An orange arrow pointing diagonally upwards and to the right, containing the word "Analysis".



# Threshold

## Analysis



Configuration

Nuclei/Cells application

Quantification

Results

## Run the analysis on all images

1. Check that all window have been correctly filled in
2. Test all the steps of analysis on the preview
3. Run the analysis on all images in the directory by clicking on the button « Launch »



During the analysis process, check the window « log » to know the progress of the analysis process.

The screenshot shows a 'Log' window with a list of messages indicating the progress of the analysis:

```
out> conda , C:\Users\Christine\anaconda3\envs\cellpose run finished
The binary mask serie020_w2CSU-Trans_cellpose_Cells.tif was saved in C:\Users\Christine\Documents\Activité Plateforme\MIC-MAQ\MIC-MAQ
The cell ROIs of serie020_w2CSU-Trans.TIF were saved in C:\Users\Christine\Documents\Activité Plateforme\MIC-MAQ\MIC-MAQ\Images LB\Im
Quantification channel 1 image:serie020_w1CSU-491.TIF
(cell)number of objects: 100
measurements
Experiment serie020_.TIF is done in :13 seconds
Analysis is done. It took 48 seconds
```

Configuration

Nuclei/Cells application

Quantification

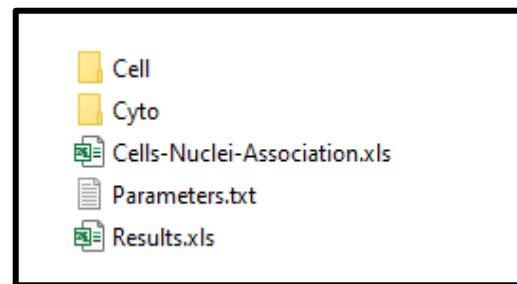
Results

- Summary
- Table
- ROI
- Images

## Explanations about results

After the analysis, a Results folder is automatically created in the folder containing images.

It is composed of :



- **A « Parameters » text file:** resume the parameters used for the analysis
- **One or two « Table » file:** a table of results where all measurements are exported during the analysis
- **several sub-folders :** each contains segmentation of corresponding compartment

Configuration

Nuclei/Cells application

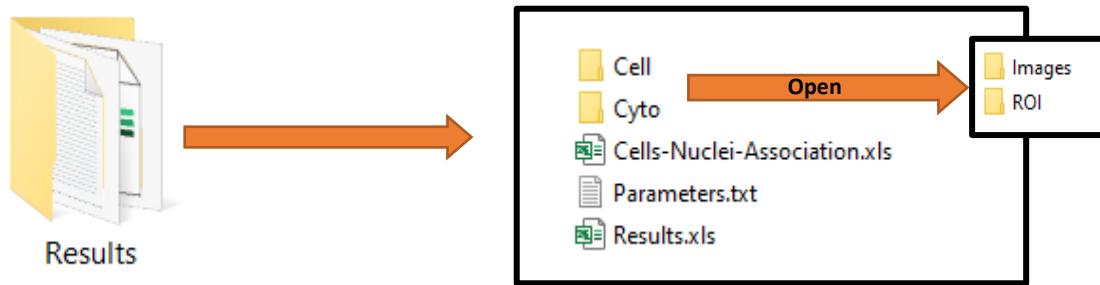
Quantification

Results

- Summary
- Table
- ROI
- Images

## Explanations about results

After the analysis, a Results folder is automatically created in the folder containing images.



Each compartment sub-folder:

- **A sub-folder « Images »:** it contains the mask of objects obtained by segmentation
  - **A sub-folder « ROI »:** it contains compartment's regions of interest for each image in a ZIP file
- For spots
- **Each sub-folder « ROI » and « Images » contains subfolders « findmaxima » and « thresholding »** depending on method used.

Configuration

Nuclei/Cells application

Quantification

Results

- Summary ●●●
- Table
- ROI
- Images

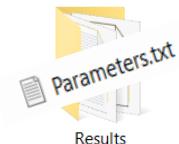
## Explanations about results : Parameters file

It resumes the parameters used for the analysis.

```
Parameters.txt - Bloc-notes
Fichier Edition Format Affichage Aide
The configuration is :
CALIBRATION: 100X_Microscope(x0.110 µm)

CHANNEL 1: used
QUANTIFICATION
Quantification Parameters
Preprocessing:
Measurements (intensity based):
    mean
    integrated density
Measurements (morphological):
    area

CHANNEL 2: used
SEGMENTATION cells
Preprocessing:
Use Cellpose:
    Cellpose model: cyto
    Minimum diameter: 100
    Exclude on edges: yes
    Final user validation: no
Quantification Parameters
Preprocessing:
Measurements (intensity based):
    mean
    integrated density
Measurements (morphological):
    area
```



Parameters.txt

Results

Configuration

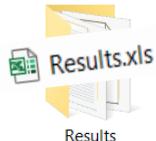
Nuclei/Cells application

Quantification

Results

- Summary
- Table
- ROI
- Images

## Explanations about results : Results table



It is a table where all measurements are compiled during the analysis.

	A	B	C	D	E	F	G	H	I	J	K	L	M
1	Name experiment	Cell nr.	Cell_C2_Area (pixel)	Cell_C2_Area (microns)	Cell_C2_Mean	Cell_C2_Circ.	Cell_C2_RawIntDen	Cell_C2_AR	Cell_C2_Round	Cell_C2_Solidity	Cell_C1_Mean	Cell_C1_RawIntDen	
2	1 serie013_.TIF	1	1177.00	14.24	1353.66	0.48	1593262.00	2.44	0.41	0.88	174.29	205136.00	
3	2 serie013_.TIF	2	3772.00	45.64	1269.72	0.58	4789401.00	3.12	0.32	0.95	190.12	717136.00	
4	3 serie013_.TIF	3	2128.00	25.75	1262.12	0.75	2685782.00	1.75	0.57	0.96	183.95	391447.00	
5	4 serie013_.TIF	4	2094.00	25.34	1289.56	0.74	2700338.00	2.05	0.49	0.96	196.19	410815.00	
6	5 serie013_.TIF	5	2117.00	25.62	1305.75	0.67	2764268.00	2.29	0.44	0.95	197.75	418643.00	
7	6 serie013_.TIF	6	2690.00	32.55	1301.26	0.70	3500383.00	2.16	0.46	0.96	197.65	531685.00	
8	7 serie013_.TIF	7	3353.00	40.57	1261.89	0.67	4231106.00	2.50	0.40	0.96	202.70	679648.00	
9	8 serie013_.TIF	8	2603.00	31.50	1285.35	0.69	3345764.00	2.25	0.44	0.96	196.89	512511.00	
10	9 serie013_.TIF	9	2658.00	32.16	1267.91	0.69	3370104.00	2.24	0.45	0.95	196.60	522570.00	
11	10 serie013_.TIF	10	2682.00	32.45	1285.89	0.67	3448769.00	2.47	0.40	0.95	199.91	536170.00	
12	11 serie013_.TIF	11	2456.00	29.72	1308.34	0.66	3213294.00	2.32	0.43	0.96	206.32	506713.00	
13	12 serie013_.TIF	12	2549.00	30.84	1317.12	0.72	3357340.00	2.13	0.47	0.96	202.15	515268.00	
14	13 serie013_.TIF	13	3474.00	42.04	1321.22	0.61	4589919.00	2.98	0.34	0.95	206.46	717240.00	
15	14 serie013_.TIF	14	4612.00	55.81	1292.44	0.54	5960732.00	3.63	0.28	0.93	203.52	938650.00	
16	15 serie013_.TIF	15	2465.00	29.83	1298.13	0.71	3199897.00	2.29	0.44	0.95	201.59	496929.00	
17	16 serie013_.TIF	16	3021.00	36.55	1320.08	0.64	3993992.00	2.80	0.36	0.93	205.07	619525.00	
18	17 serie013_.TIF	17	2997.00	36.26	1317.19	0.69	3947605.00	2.42	0.41	0.96	207.91	623098.00	
19	18 serie013_.TIF	18	3029.00	36.65	1316.81	0.69	3988612.00	2.53	0.39	0.96	203.48	616326.00	
20	19 serie013_.TIF	19	2564.00	31.02	1336.25	0.71	3426146.00	2.37	0.42	0.96	208.69	535081.00	
21	20 serie013_.TIF	20	2864.00	34.65	1295.11	0.66	3709205.00	2.54	0.39	0.94	214.55	614481.00	
22	21 serie013_.TIF	21	2274.00	27.52	1301.39	0.76	2959371.00	2.09	0.48	0.96	207.78	472493.00	
23	22 serie013_.TIF	22	3046.00	36.86	1319.26	0.67	4018477.00	2.36	0.42	0.96	227.97	694407.00	
24	23 serie013_.TIF	23	2881.00	34.86	1298.81	0.74	3741880.00	2.12	0.47	0.96	210.80	607326.00	
25	24 serie013_.TIF	24	2865.00	34.67	1314.52	0.64	3766087.00	2.60	0.38	0.95	217.54	623263.00	
26	25 serie013_.TIF	25	2429.00	29.39	1317.20	0.64	3199474.00	2.55	0.39	0.95	209.74	509453.00	
27	26 serie013_.TIF	26	3773.00	45.65	1310.74	0.59	4945422.00	3.27	0.31	0.95	214.56	809532.00	
28	27 serie013_.TIF	27	3277.00	39.65	1298.17	0.65	4254103.00	2.68	0.37	0.96	224.06	734259.00	
29	28 serie013_.TIF	28	3045.00	36.84	1350.10	0.67	4111067.00	2.67	0.37	0.96	216.95	660627.00	

Configuration

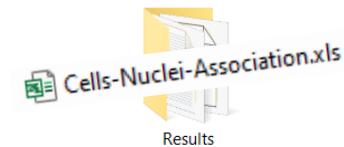
Nuclei/Cells application

Quantification

Results

- Summary
- Table
- ROI
- Images

## Explanations about results : Cell-Nuclei-Association table



Only when Cells and Nuclei are provided, it is a table where correspondence between nucleus and cell is stored as well as nuclei measurements.

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q
1	Name exper	Nucleus nr.	Cell associat	Nuclei_C1	C Nuclei_C1_CSU_491 RawIntDen												
2	serie013_TII	1	34	463.74	670111.00												
3	serie013_TII	2	41	553.15	608465.00												
4	serie013_TII	3	56	335.56	348646.00												
5	serie013_TII	4	63	362.72	428378.00												
6	serie020_TII	1	28	1395.79	1514435.00												
7	serie020_TII	2	40	1023.46	1117619.00												
8	serie020_TII	3	52	628.51	965397.00												
9	serie020_TII	4	64	673.43	868057.00												
10	serie020_TII	5	-1	1102.77	1650849.00												
11																	
12																	
13																	
14																	
15																	
16																	
17																	
18																	
19																	
20																	
21																	
22																	
23																	
24																	

Configuration

Nuclei/Cells application

Quantification

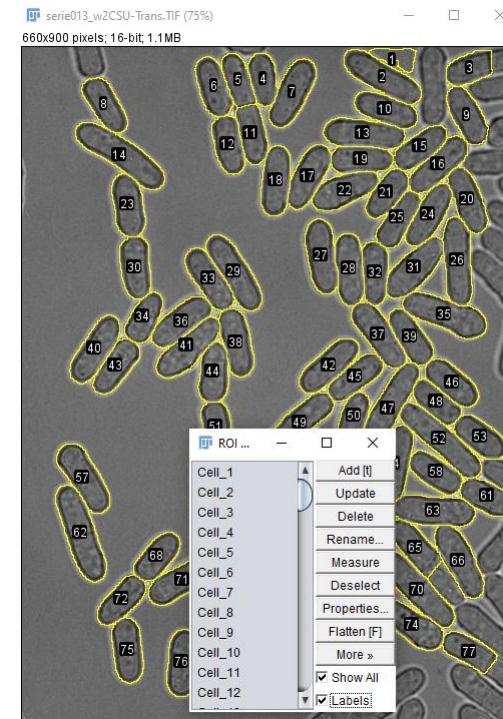
Results

- Summary
- Table
- ROI
- Images

## Explanations about results : A sub-folder « ROI »

It contains nuclei or cells regions for each image in a ZIP file, if the "save ROIs" checkbox was selected in segmentation parameters.

To re-open the nuclei or cells ROI, drag and drop the .Zip file into Fiji. ROI will automatically be loaded to the ROI manager window.



Configuration

Nuclei/Cells application

Quantification

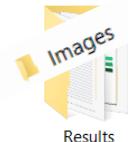
Results

- Summary
- Table
- ROI
- Images**

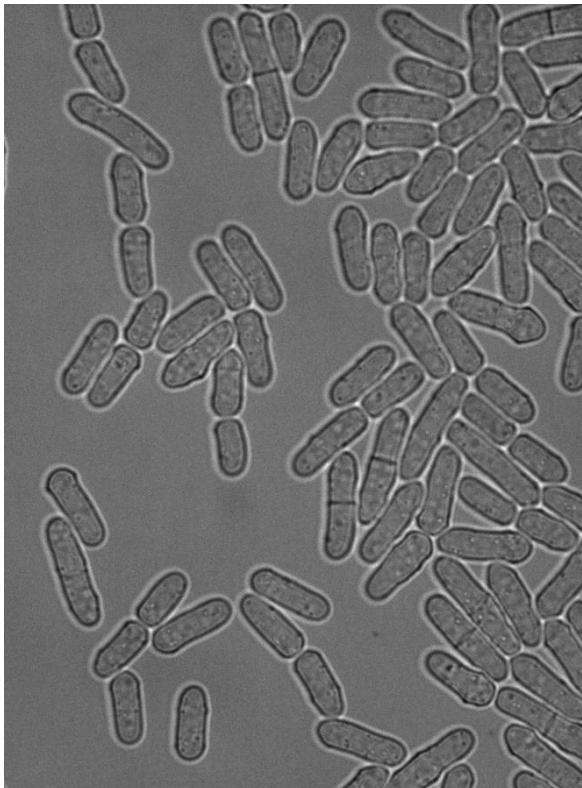
## Explanations about results : A sub-folder « Images »

It contains the mask of objects (nuclei or cells) obtained by segmentation , if the "save segmentation masks" checkbox was selected in segmentation parameters.

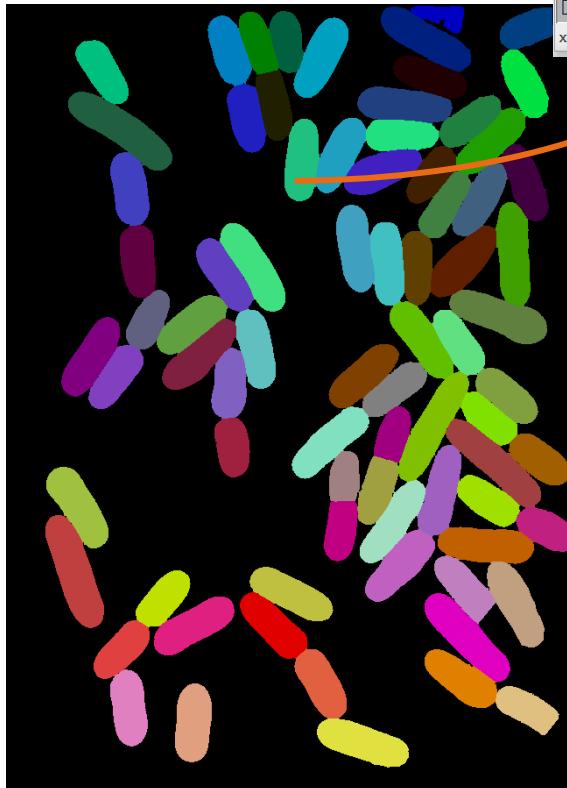
Each detected object is associated to a intensity value on the objects mask image.



Raw data



Objects mask





## Informations

# MIC-MAQ version 1.0.3



<https://github.com/MultimodalImagingCenter/MIC-MAQ>



Images for training

<https://zenodo.org/record/8186508>



If you want to report bugs, ask questions to solve your analyses or request improvements

<https://github.com/MultimodalImagingCenter/MIC-MAQ/issues>