

OASIS 1.0 Manual

(Osteoclast Image Analysis s/w)

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Introduction

OASIS is a software for analyzing multi-spectral microscopy images of osteoclasts

OASIS can segment osteoclasts based on the membrane fluorescent markers

OASIS can detect nucleus marked by Dapi, and calculate # of nucleus for each osteoclast

OASIS can calculate morphological features of osteoclast, and give quantification of protein level

OASIS is implemented in 100% Python

Installation

Python interpreter and package manager

- Download Anaconda Python2 (<https://www.continuum.io/downloads>)
- Install with the default settings

Necessary Packages, install using conda install, type the command in 'cmd' prompt

- PyQt (conda install -c anaconda pyqt=4.11.4)
- Matplotlib 1.5.1 (conda install -c conda-forge matplotlib=1.5.1)
- Scikit-learn (conda install -c anaconda scikit-learn=0.18.1)
- Scikit-image (conda install -c anaconda scikit-image=0.12.3)
- SimpleITK (conda install -c <https://conda.anaconda.org/simpleitk> SimpleITK)
- VTK (conda install -c anaconda vtk=6.3.0)
- OPENCV (conda install -c menpo opencv=2.4.11)

Running OASIS (0)

Before running OASIS, make sure that the image data are ready

The original sample images provided by Ankit are color images with RGB channel

Run `python OASIS_Data.py` to convert the images to standard format

- Need to Specify the original and destination data path in the script
- Make sure `dst_path` does not exist before conversion

Running OASIS (1)

The Program Folder Containing these python Scripts

- ❏ OASIS.py
- ❏ OASIS_Adjust.py
- ❏ OASIS_Display.py
- ❏ OASIS_ScatterPlot.py
- ❏ OASIS_Table.py

In the cmd prompt, change to the directory where python scripts located, and type: (3 means total number of image stacks in this dataset)

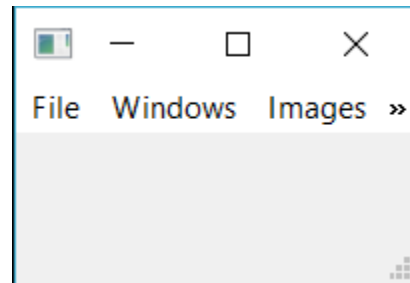


```
C:\Windows\system32\cmd.exe
C:\LAB\Osteoclast\OASIS 1.0>python OASIS.py 3
```

The image shows a screenshot of a Windows command prompt window. The title bar at the top reads 'C:\Windows\system32\cmd.exe'. The command prompt itself has a black background with green text. The current directory is 'C:\LAB\Osteoclast\OASIS 1.0' and the command being executed is 'python OASIS.py 3'.

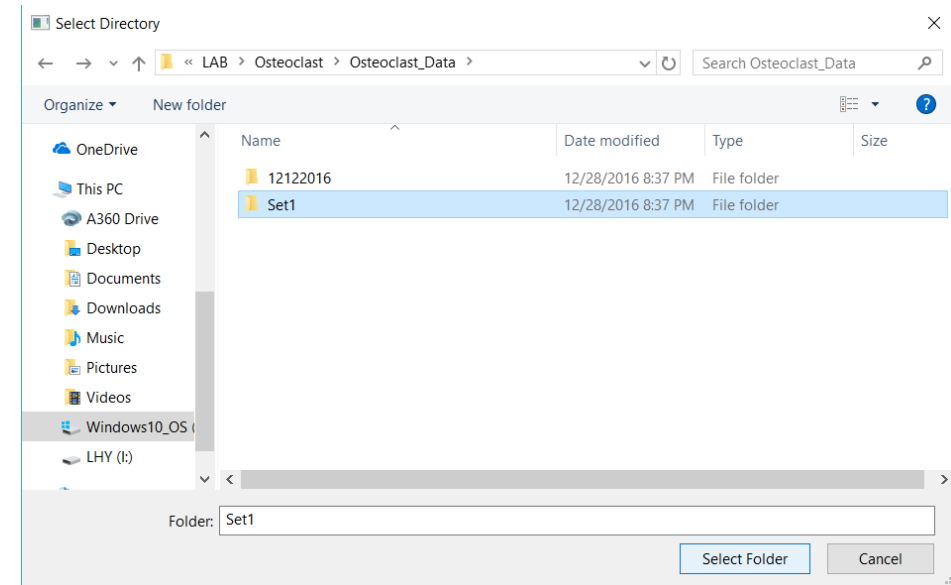
Running OASIS (2)

The Main Program Window will prompt:



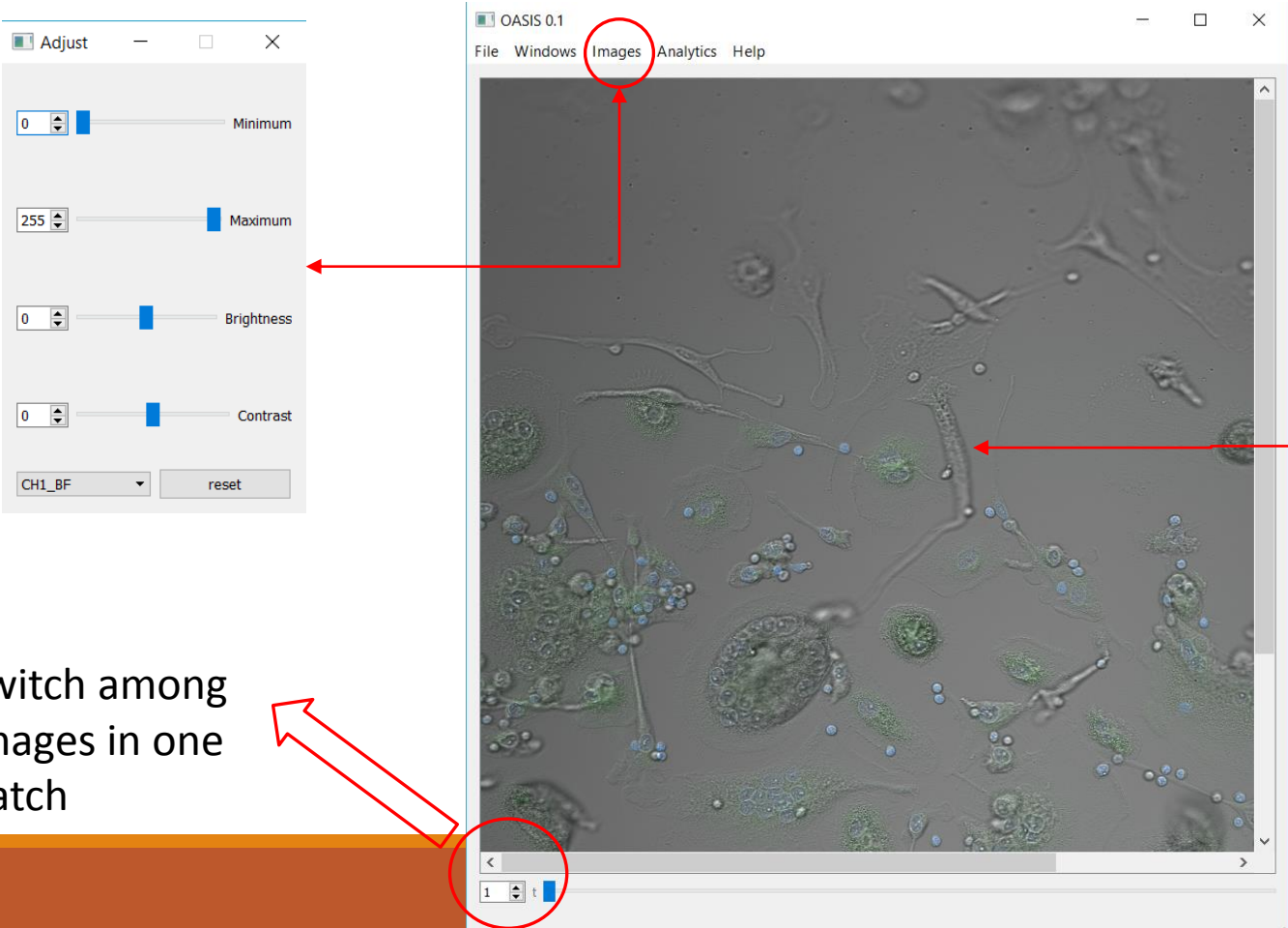
Click “File” Menu and Load images,

In Osteoclast_Data folder, select sample data Set1



Running OASIS (3)

Sample Data Set1 contain 3 images



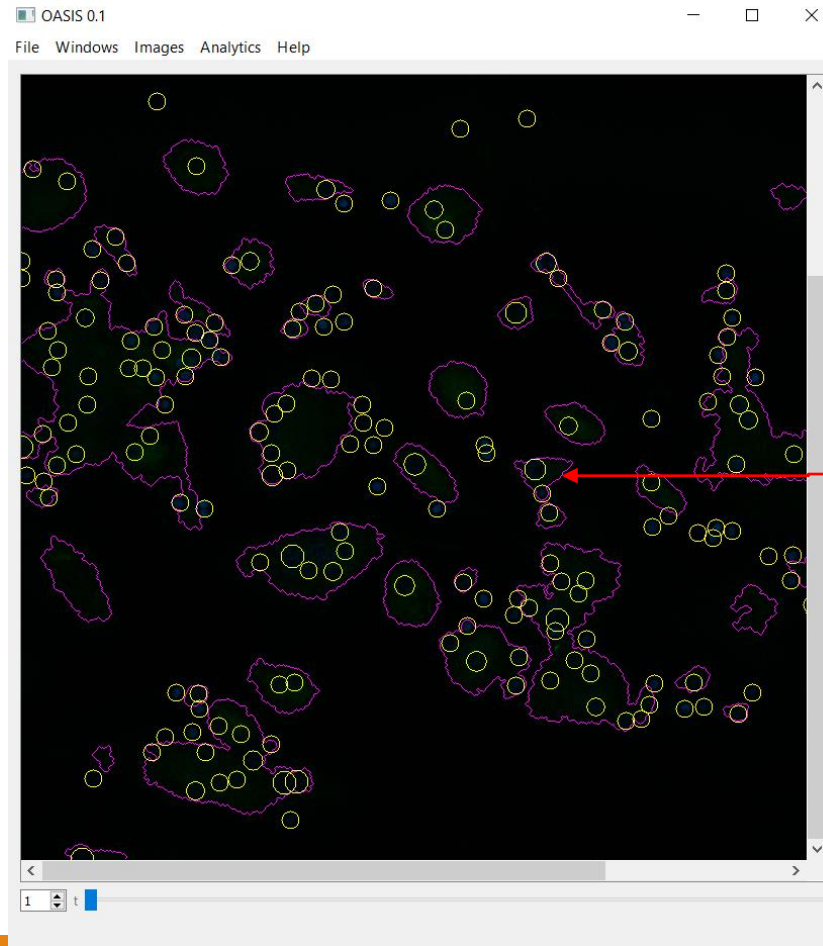
The screenshot shows the OASIS 0.1 software interface. On the left is an 'Adjust' panel with sliders for Minimum (0), Maximum (255), Brightness (0), and Contrast (0). Below these is a dropdown menu set to 'CH1_BF' and a 'reset' button. The main window displays a grayscale microscopy image of cells. A red circle highlights the 'Images' menu item in the top bar. A red arrow points from this menu to the 'Adjust' panel. Another red arrow points from the 'Images' menu to the main image area. A third red arrow points from the bottom-left corner of the main image window to the text 'Switch among images in one batch'. A fourth red arrow points from the main image area to the list of channel options on the right. At the bottom of the main window, a small panel shows a slider set to '1'.

Click on the Image Area first, then use number keypad to control on/off of channels

- 0: BF Channel
- 1: CH 488
- 2: CH Dapi
- 3: CH Protein
- 4: Segmentation of 488
- 5: Detection of Dapi

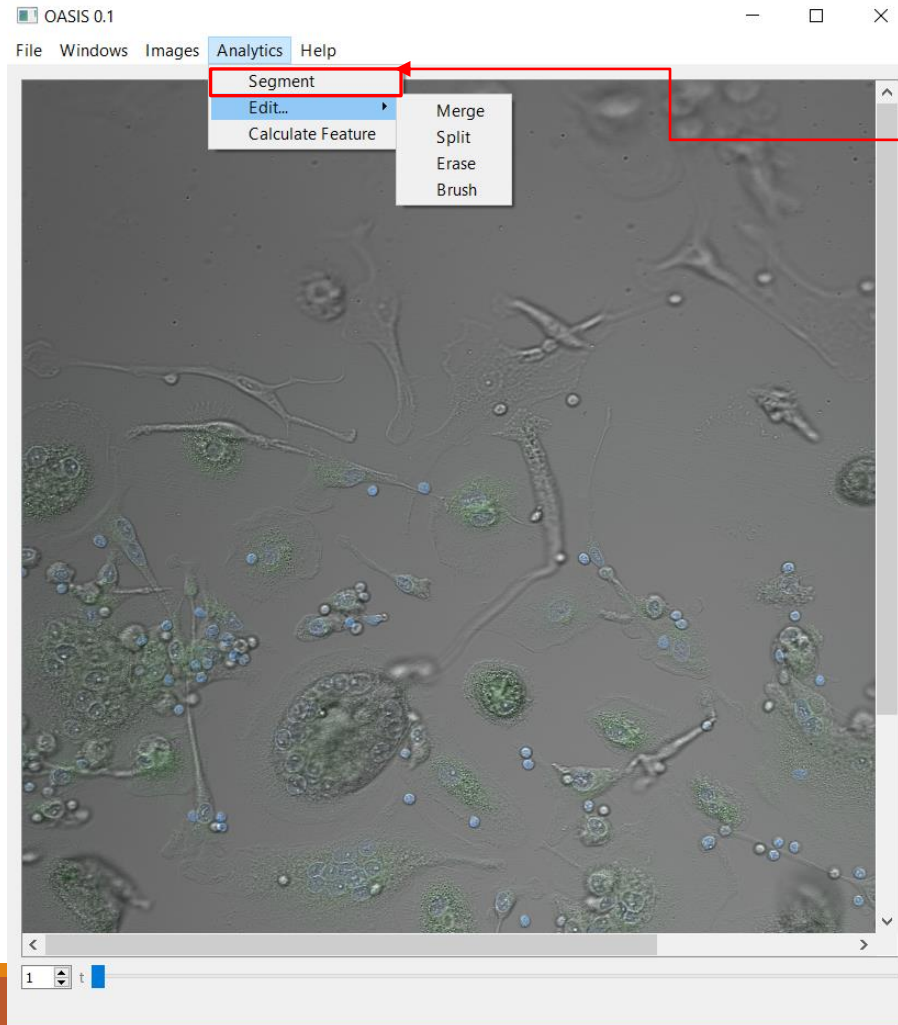
Switch among images in one batch

Running OASIS (4)

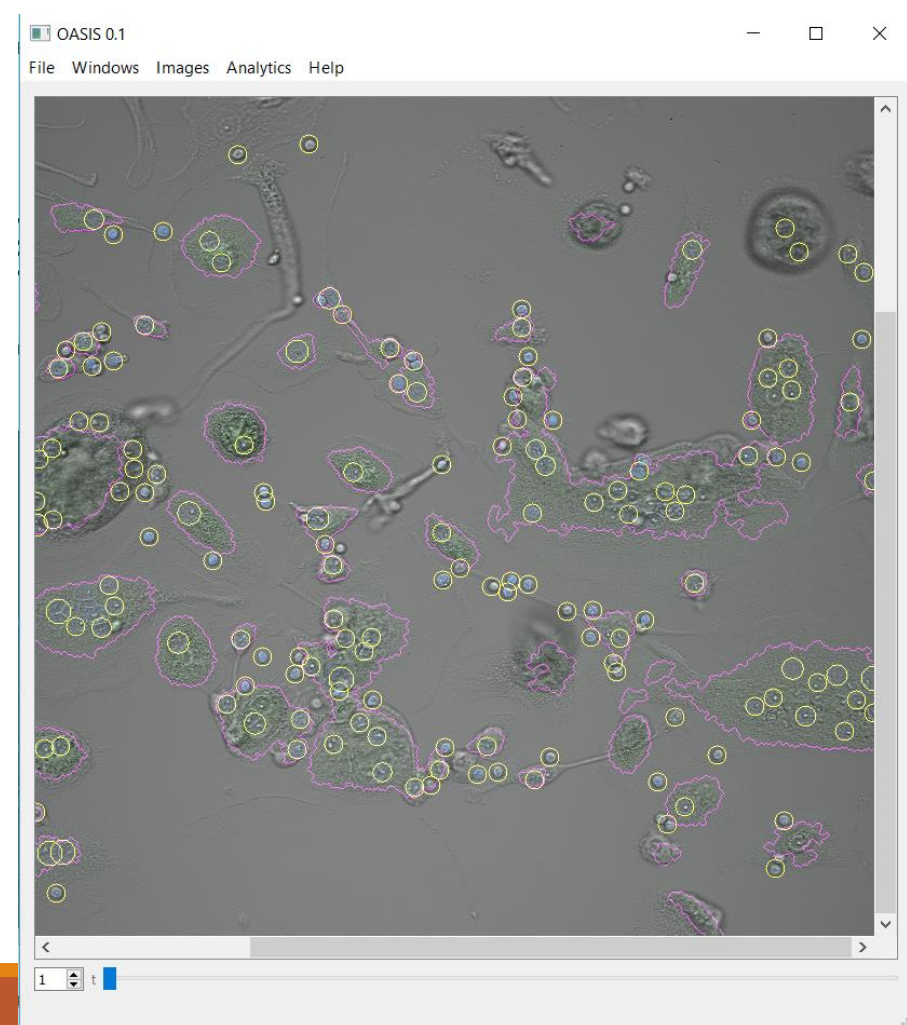
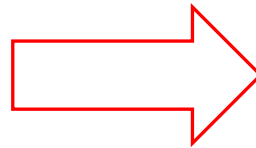


Press '0', turning off
Bright field channel, the
speed of on/off
channels is optimized in
OASIS 1.0

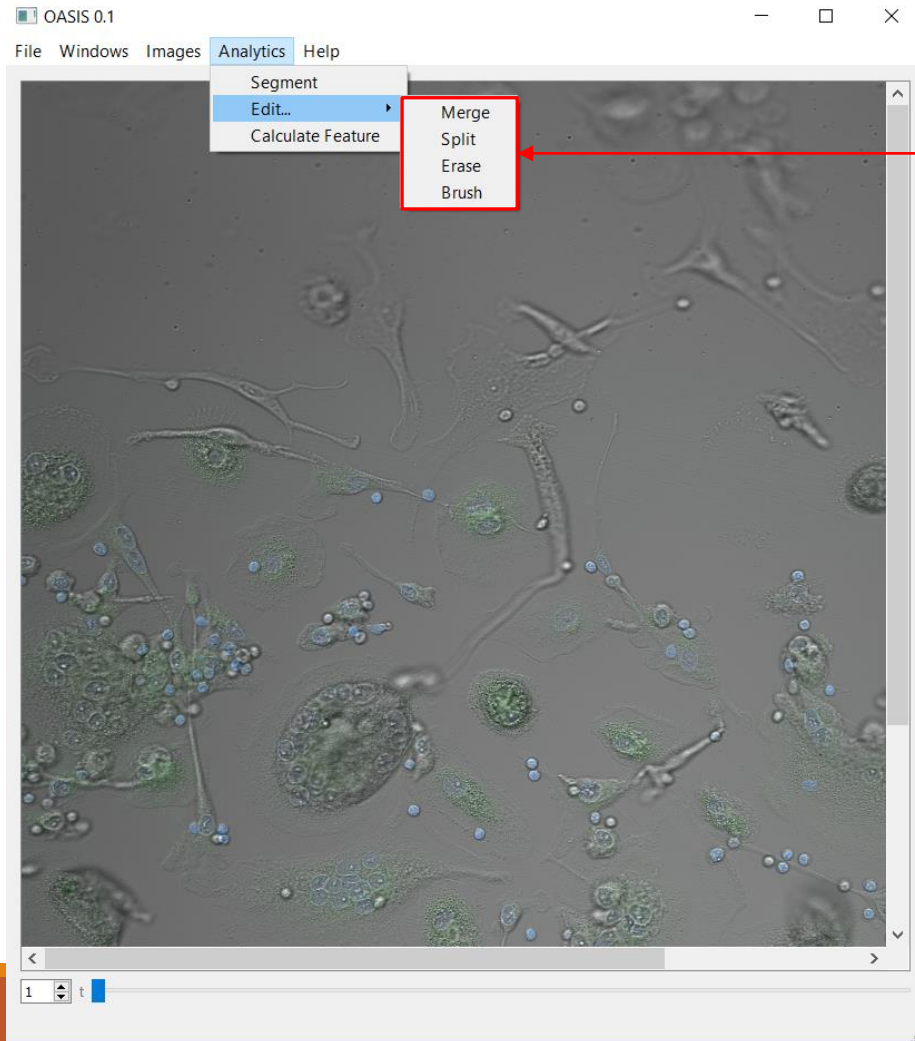
Running OASIS (5)



Segmentation for cells and nucleus, it takes 15 to 20 seconds for 1 image

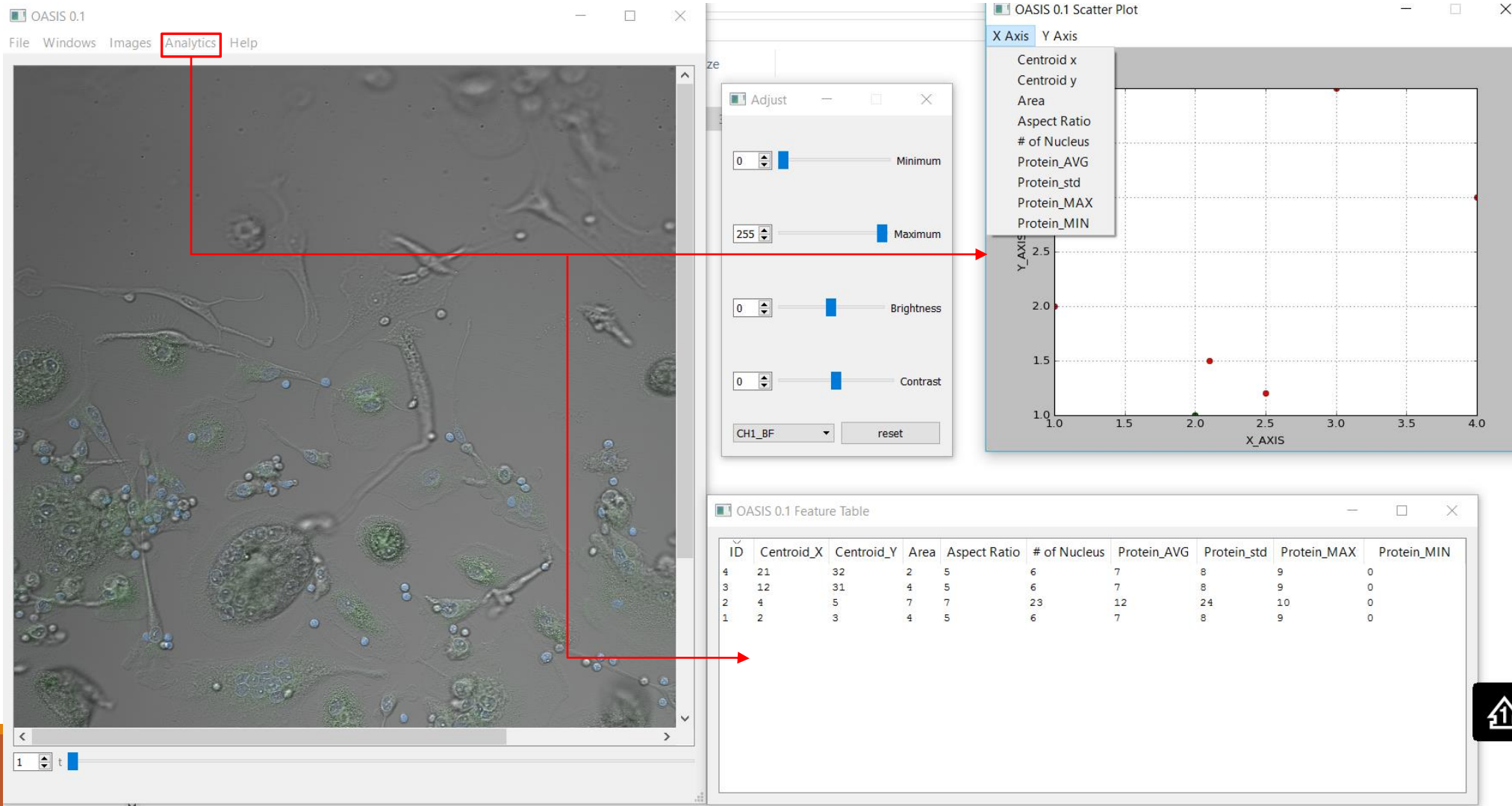


Running OASIS (6)



With editing functions, user can do manual editing of segmentation, including merging and splitting of cells and freely correcting cell contours with erase and brush, these functions hasn't been fully supported, but will come in OASIS 2.0

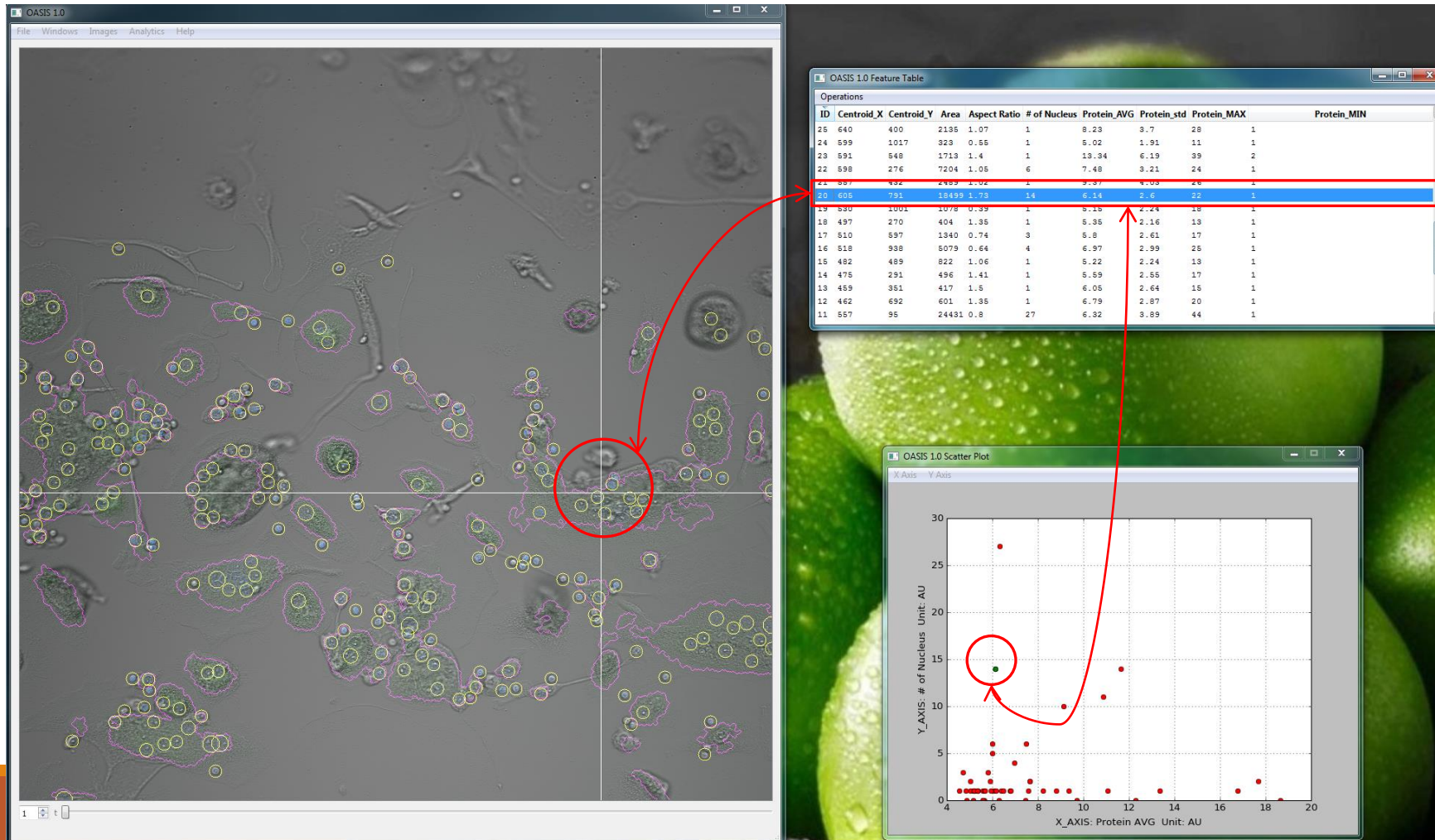
Running OASIS (7)



Click Calculate Features in Analytics Menu, the feature will be shown in Feature table and Scatter plot, If feature windows are closed, just click Calculate features again



Running OASIS (8)



Cells in Image Panels are linked to the items in Feature Table and Scatter Plot. Users can click the cells or select the rows in Feature Table to highlight the target, the corresponding scatter point will be green.

Running OASIS (9)

The feature table can be sorted by any feature, just click the cell with column names, and it will toggle between ascending and descending order

Feature Table can be exported to a feature_table.txt file. User need to click the Export Table button, and then select the path to save the table.

OASIS 1.0 Feature Table

Operations

Export Table

Ctrl+E

Area

Aspect Ratio

of Nucleus

Protein_AVG

Protein_std

Protein_MAX

Protein_MIN

25

640

400

2135

1.07

1

8.23

3.7

28

1

24

599

1017

323

0.55

1

5.02

1.91

11

1

23

591

548

1713

1.4

1

13.34

6.19

39

2

22

598

276

7204

1.05

6

7.48

3.21

24

1

21

557

432

2489

1.02

1

9.37

4.03

26

1

20

605

791

18499

1.73

14

6.14

2.6

22

1

19

530

1001

1078

0.39

1

5.15

2.24

18

1

18

497

270

404

1.35

1

5.35

2.16

13

1

17

510

597

1340

0.74

3

5.8

2.61

17

1

16

518

938

5079

0.64

4

6.97

2.99

25

1

15

482

489

822

1.06

1

5.22

2.24

13

1

14

475

291

496

1.41

1

5.59

2.55

17

1

13

459

351

417

1.5

1

6.05

2.64

15

1

12

462

692

601

1.35

1

6.79

2.87

20

1

11

557

95

24431

0.8

27

6.32

3.89

44

1

Future Work in OASIS 2.0

Main Function of OASIS 1.0 is to do cell segmentation and nucleus detection, feature calculation and link analysis.

In OASIS 2.0, following functions will be added

- Dynamic image quality adjustment
- Save and Quick results Reloading
- Cell editing function, Merge, Split, Paint and Erase.
- Machine learning Packages of scikit-learn and tensorflow

Thank You!

