

1. This program is developed in-house for the use of our lab. Do not distribute without permission.
2. The program is a compiled run-time on IDL. IDL must be installed first, at least version 8.2.3 The installation file can be downloaded from Exelis VIS for free (after registration), or can be found on Laksa
3. For Error report, be as detailed as possible, i.e. include Error Message, Screenshot, and the data file that is causing the error.

Workflow

Acquire images on the microscope,
make sure to note **objective**,
magnification & camera pixel size

Organize the images (single
channel) into folder:
e.g. One condition per folder

Create **FA mask or Cell mask or**
both, either ***manually*** or by using a
script

Save in ***morph.sav** file

Calculate statistics, analyze FA or
cell properties or create
visualization

Batch mode

Single mode

Open image in MorphometryFA

Create **FA mask or Cell mask or**
both

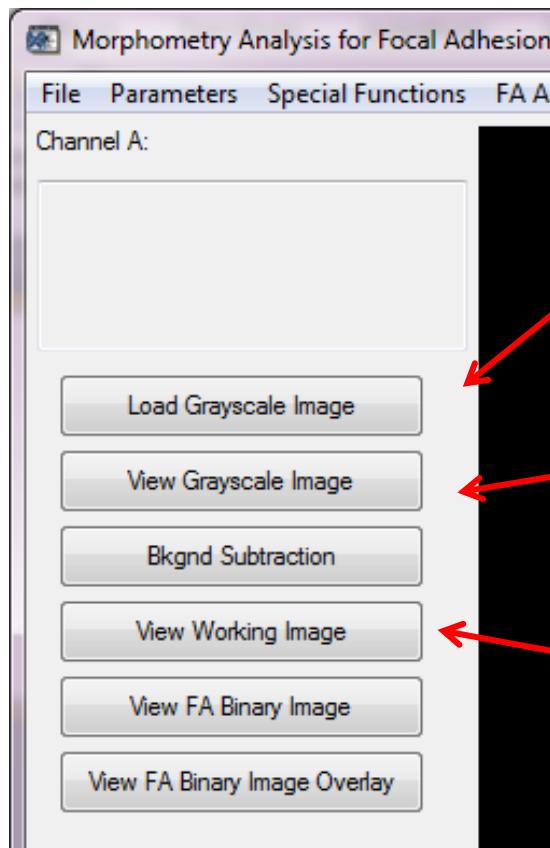
Save in ***morph.sav** file

Analyze or create visualization

Layout



General

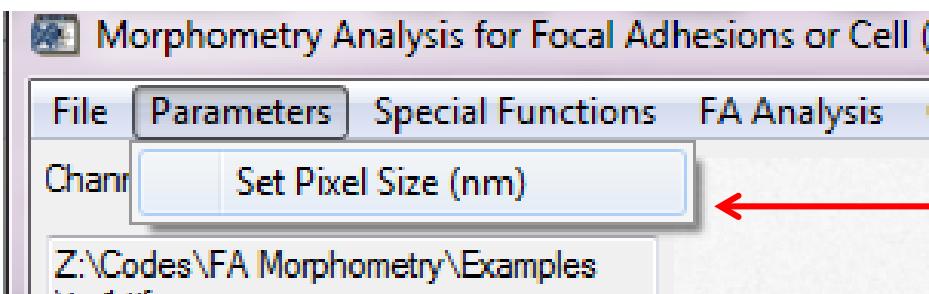


Click to load raw data (TIFF file)

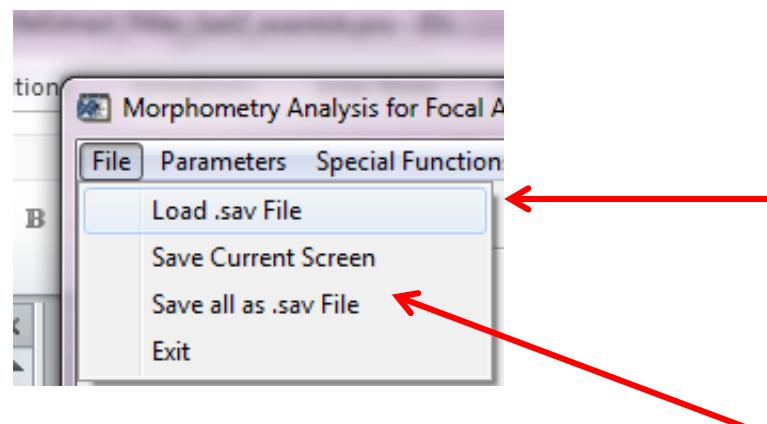
Click here any time to view the original data

Image that is processed for use is called **Working Image**

General



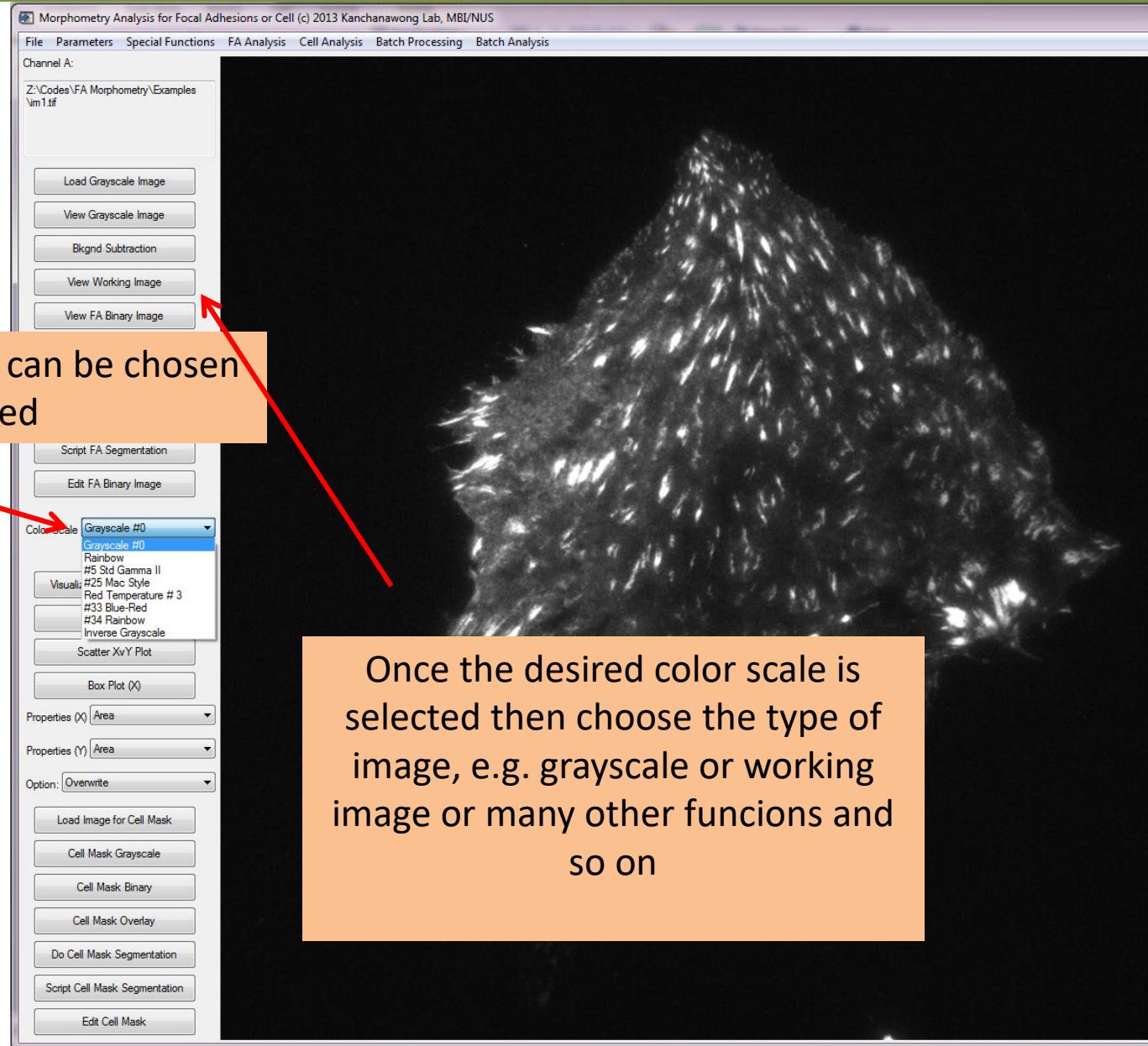
Make sure the correct pixel size is set for every file



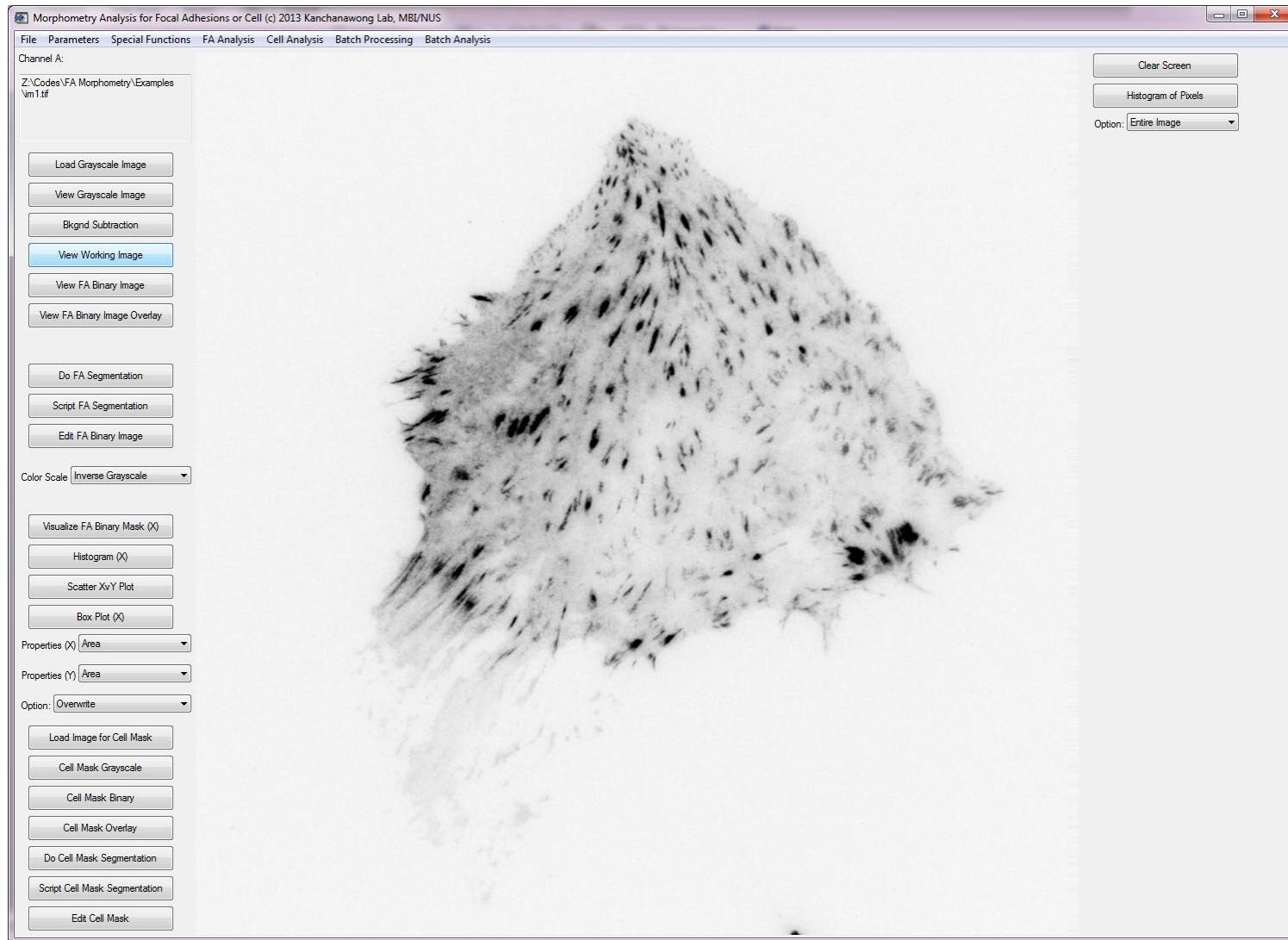
To load a previously saved
***morph.sav** file

To save everything to a ***morph.sav** file

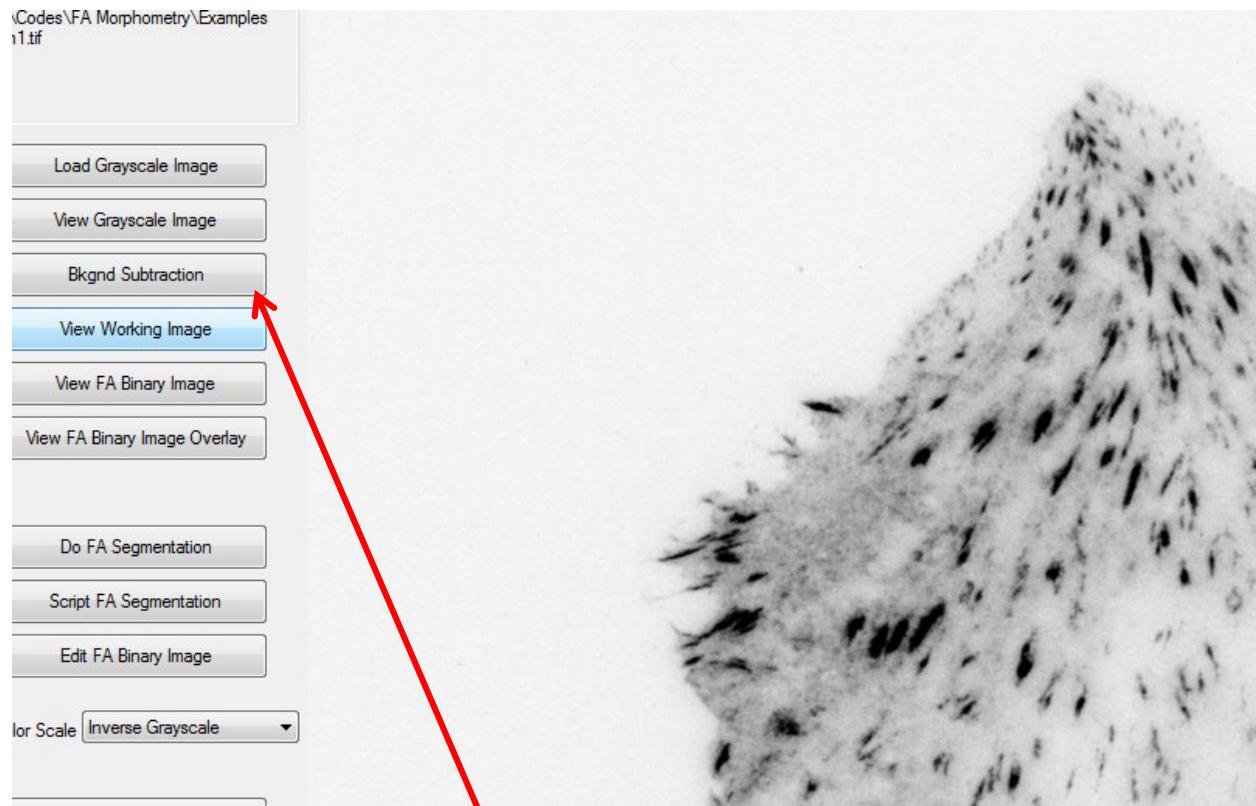
General



General



Background Subtraction



Generally for FA it is useful to subtract the background before FA segmentation

Background Subtraction

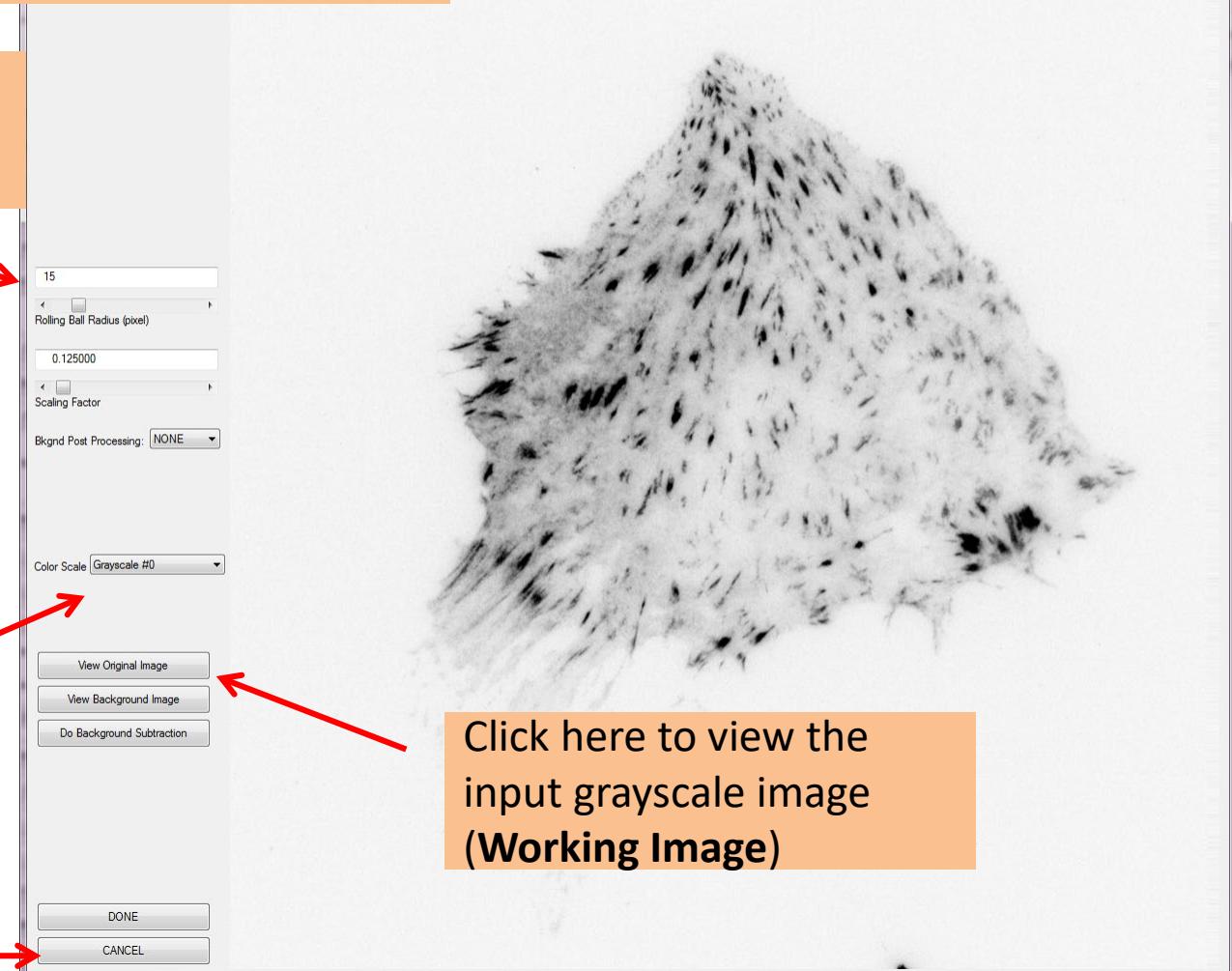
This will load a new window for background subtraction. This use Sternberg rolling ball algorithm as ported from the Java version in ImageJ

The ball radius can be adjusted as needed

For large image, a smaller scaling factor, around 0.1 can help speed up

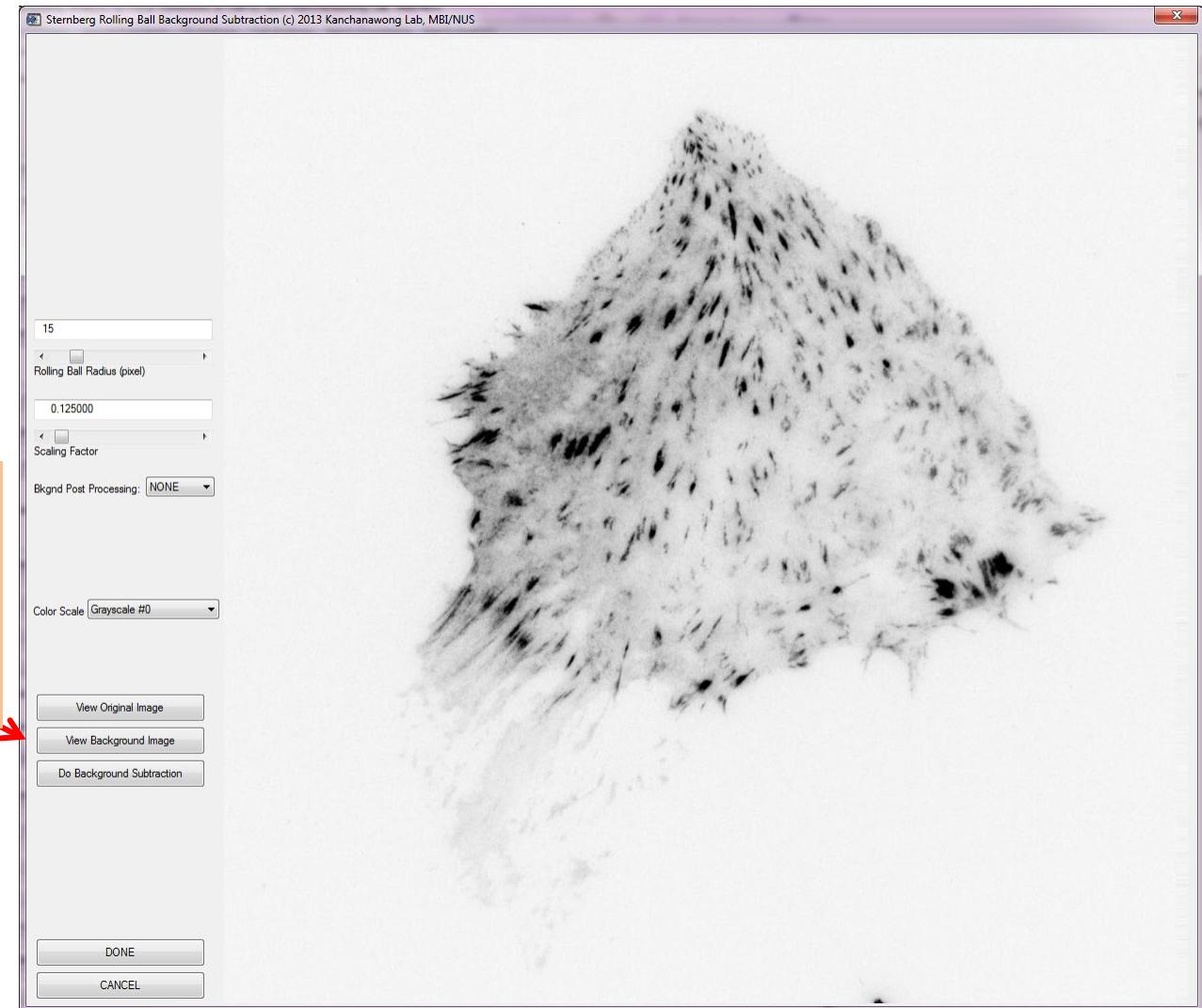
Different color scale can be used

To exit without subtracting background click cancel



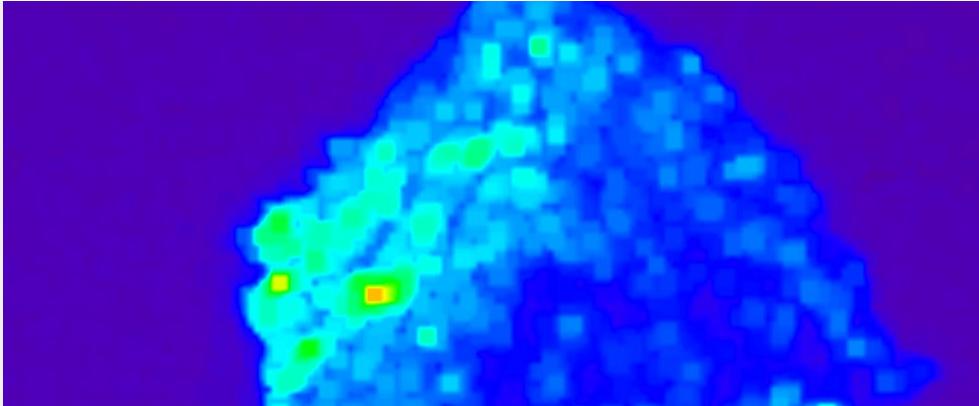
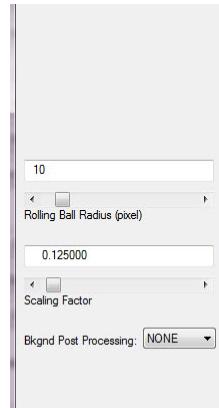
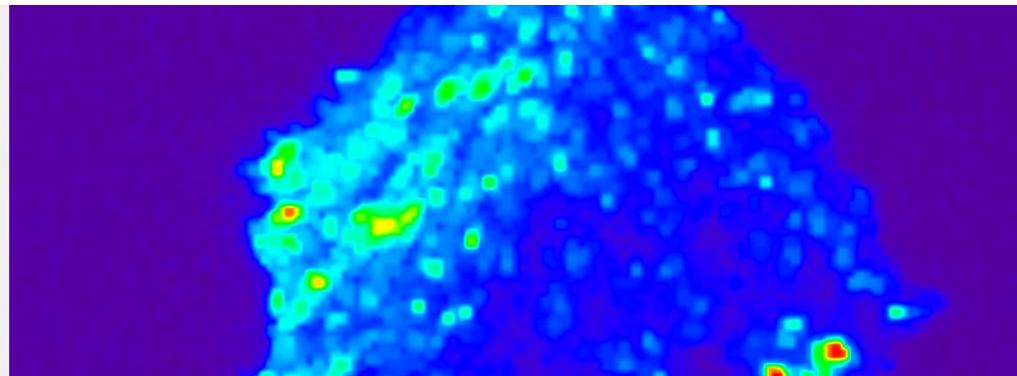
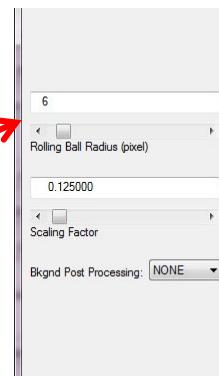
Background Subtraction

Click here to view the **background image** that will be subtracted from the **working image**

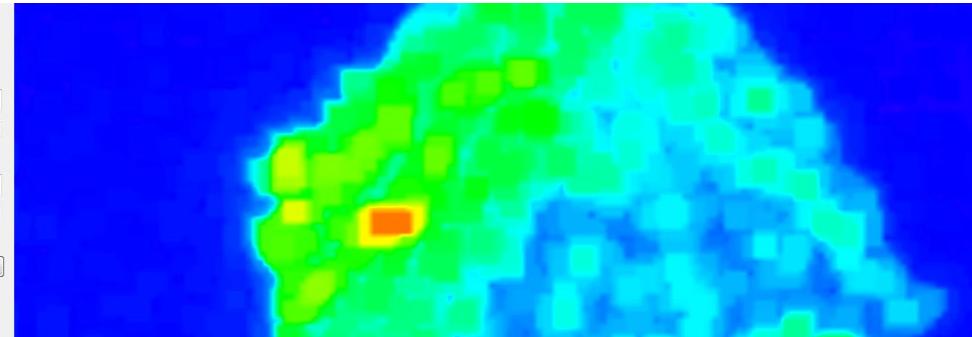
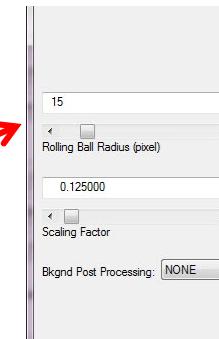


Background Subtraction

Background using small ball radius

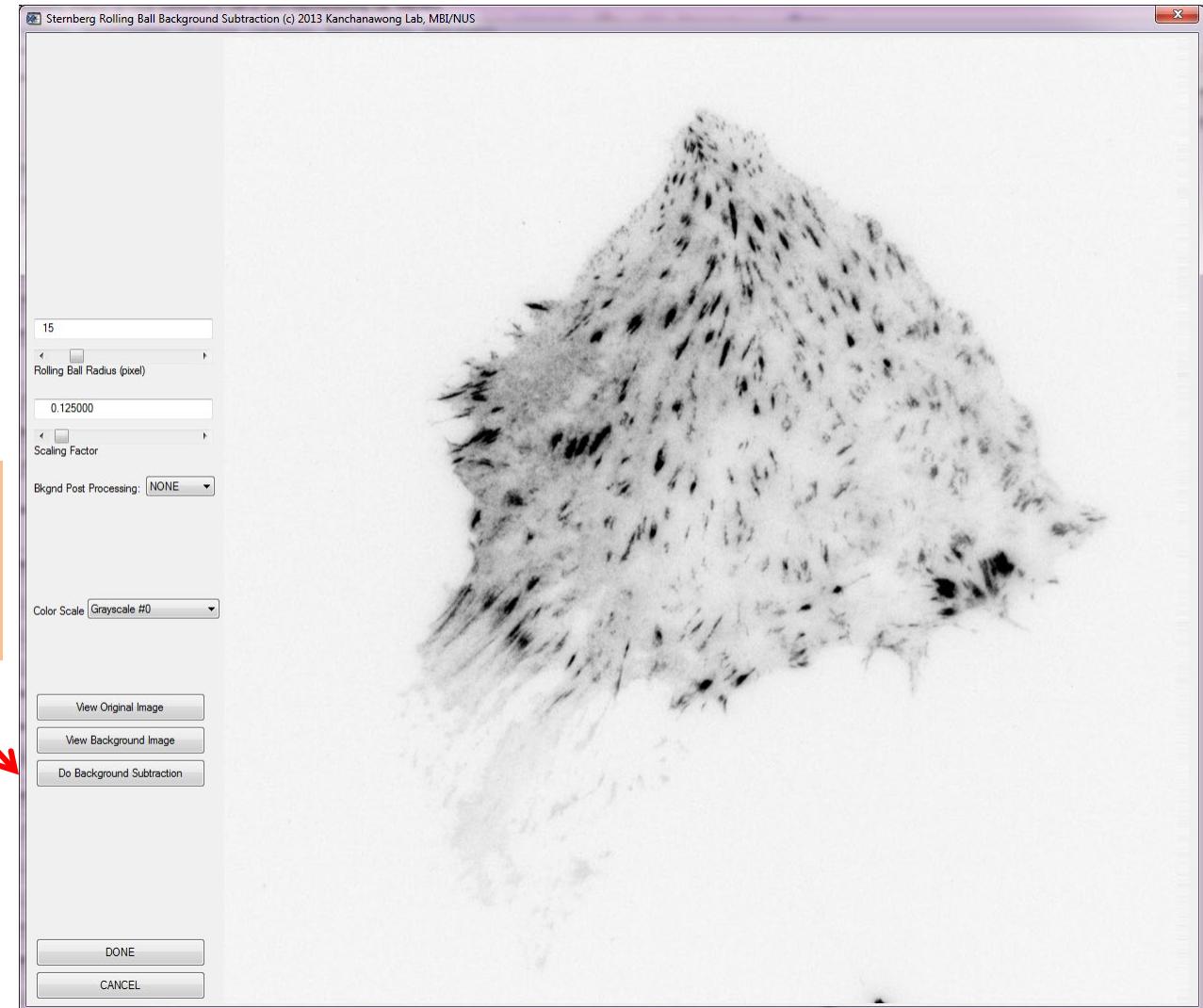


Background using large ball radius

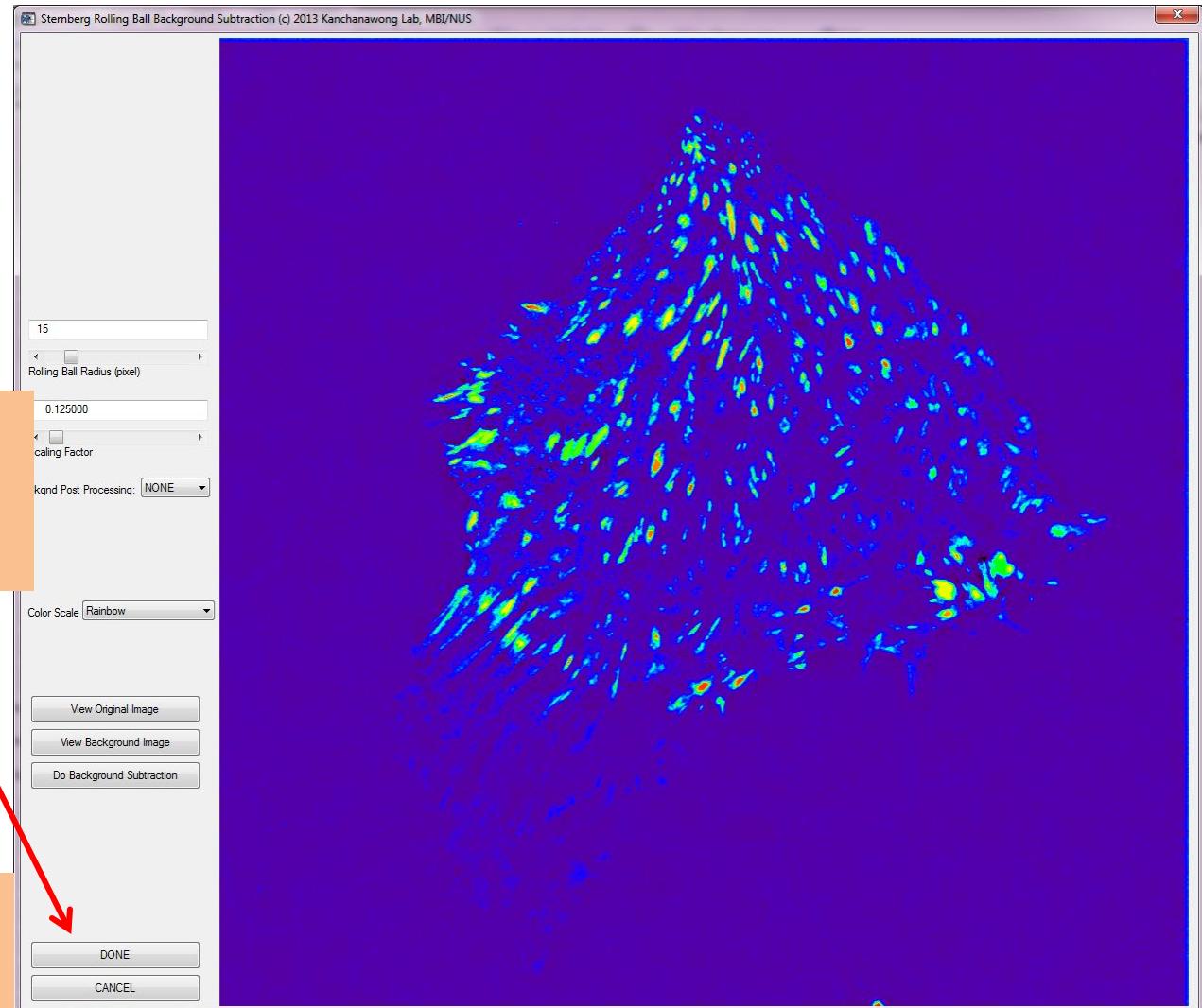


Background Subtraction

Click here to view the
background-subtracted
image



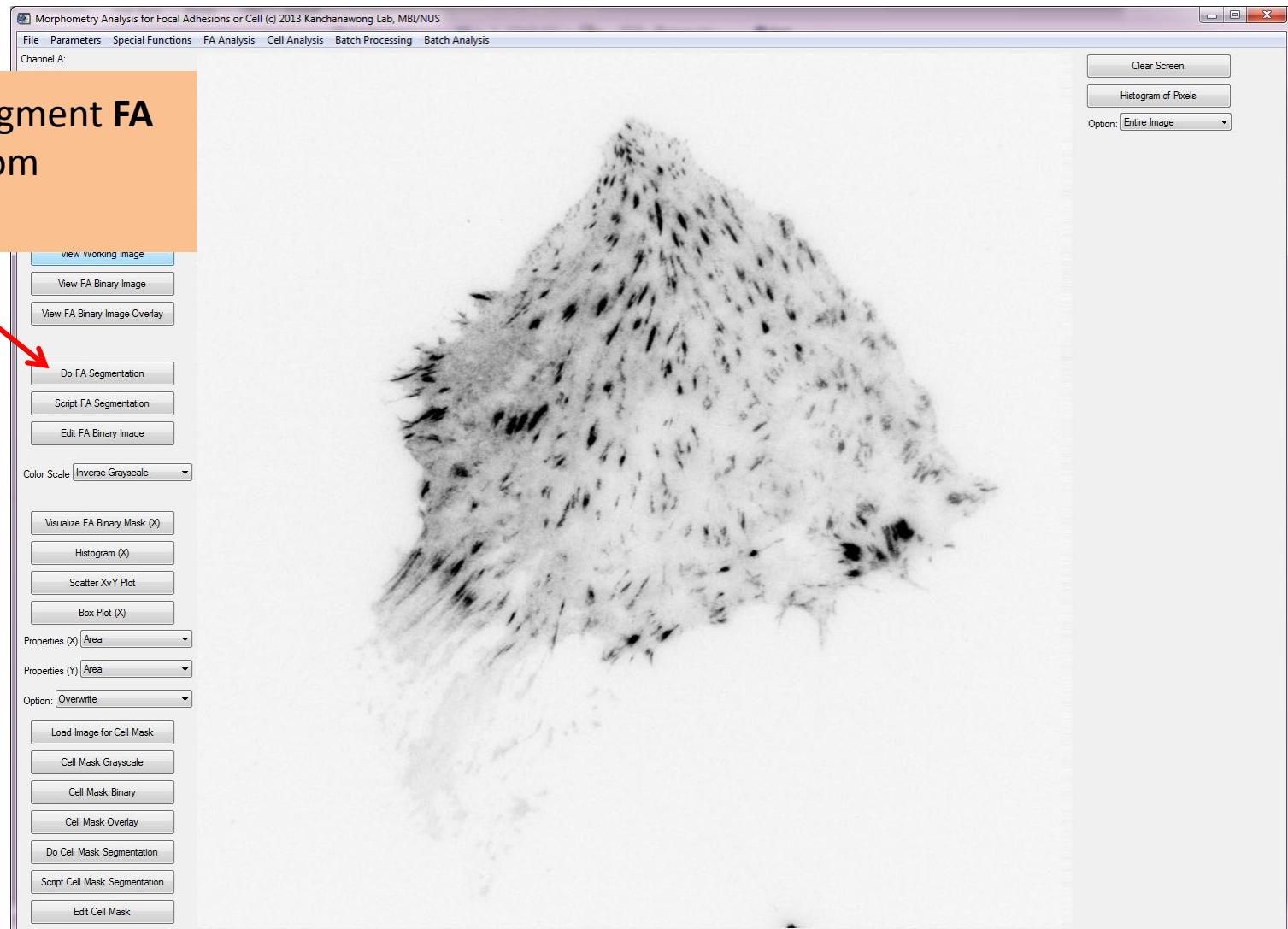
Background Subtraction



Click here if satisfied with
the **background-**
subtracted image

This window will close
and the **background-**
subtracted image will
become the **working**
image

Segmentation of Binary Mask

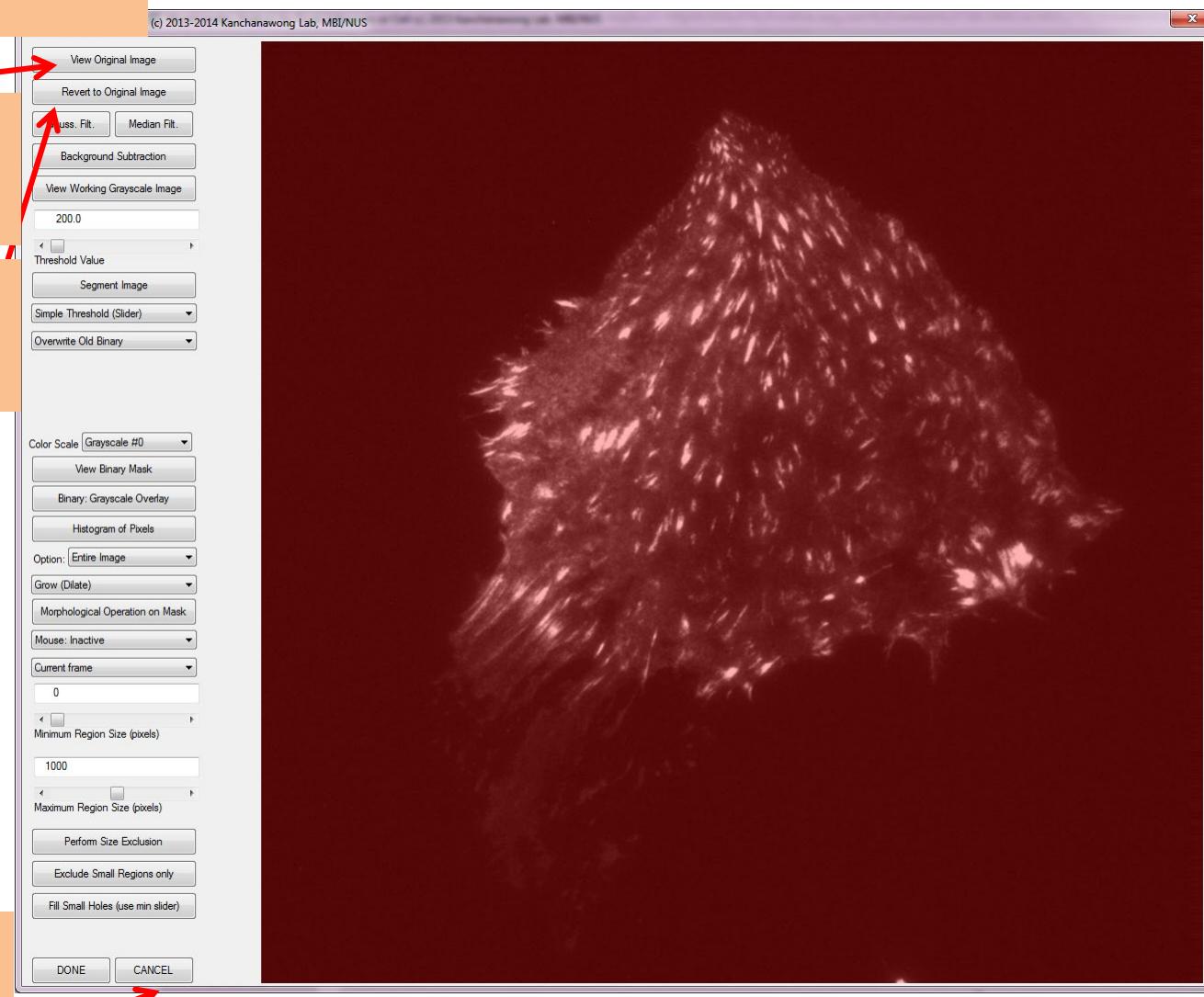


Segmentation of Binary Mask

Segmentation will be performed on **working image**

To view current **working image**

To revert back to input **working image**



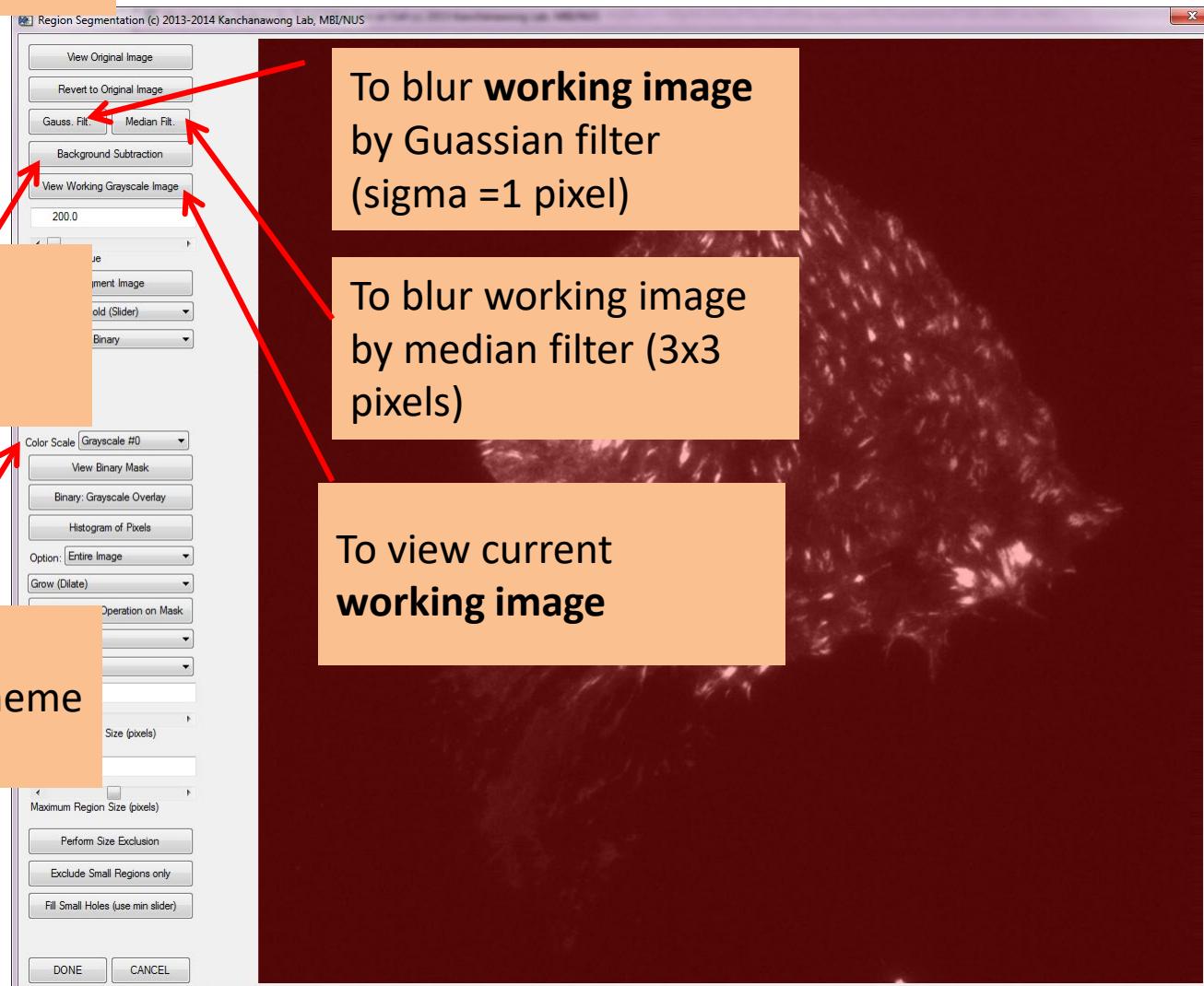
To exit this window without changing the FA mask, click cancel

Manipulation of
working image can also
be done in this window

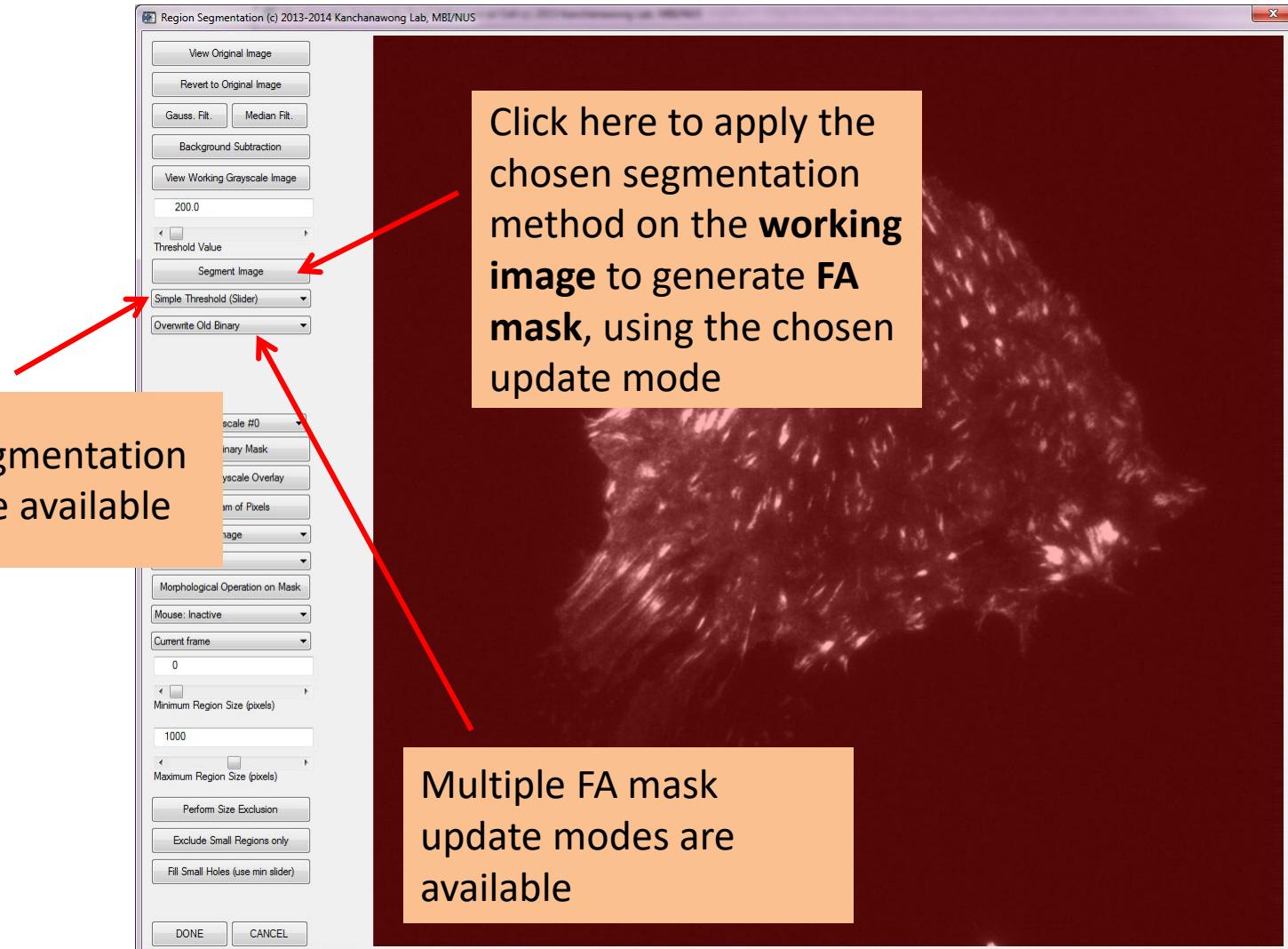
Segmentation of Binary Mask

To do background subtraction

To change color scheme



Segmentation of Binary Mask



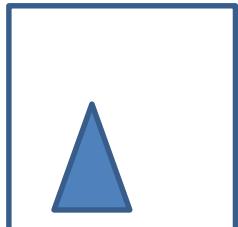
Segmentation of Binary Mask

Multiple mask update modes are available

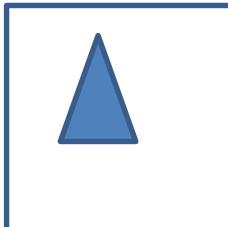
Overwrite will replace everything with the new mask

Add to will add new mask with existing mask

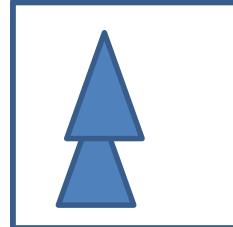
Existing mask



Mask from new segmentation



New mask



Simple Threshold (Slider)

Overwrite Old Binary

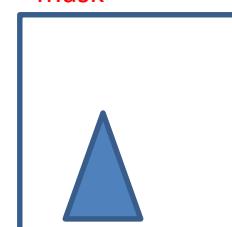
Overwrite Old Binary

Add to (OR operation)

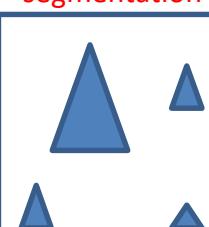
Keep new blob, Ignore overlap

The new object (blob) will be added to existing mask. Object that overlap with existing mask will be unchanged

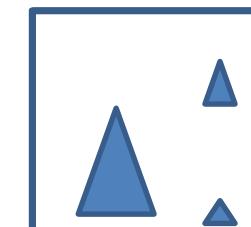
Existing mask



Mask from new segmentation

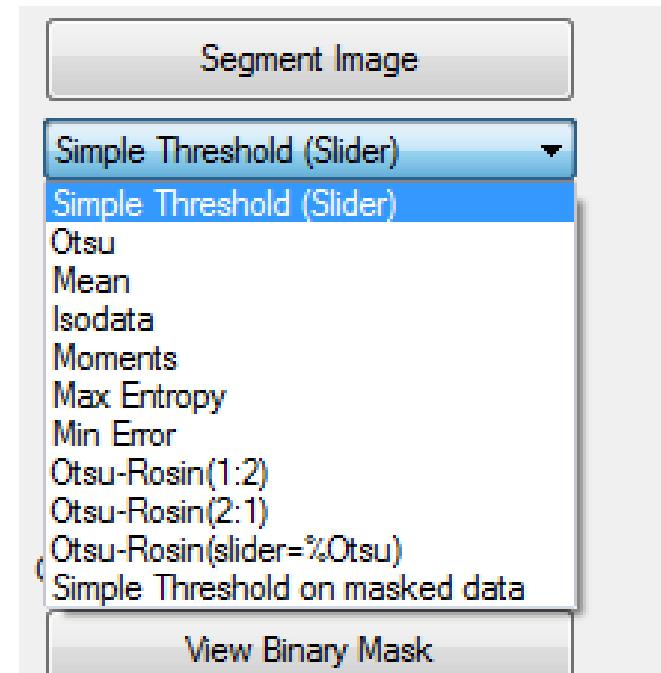


New mask

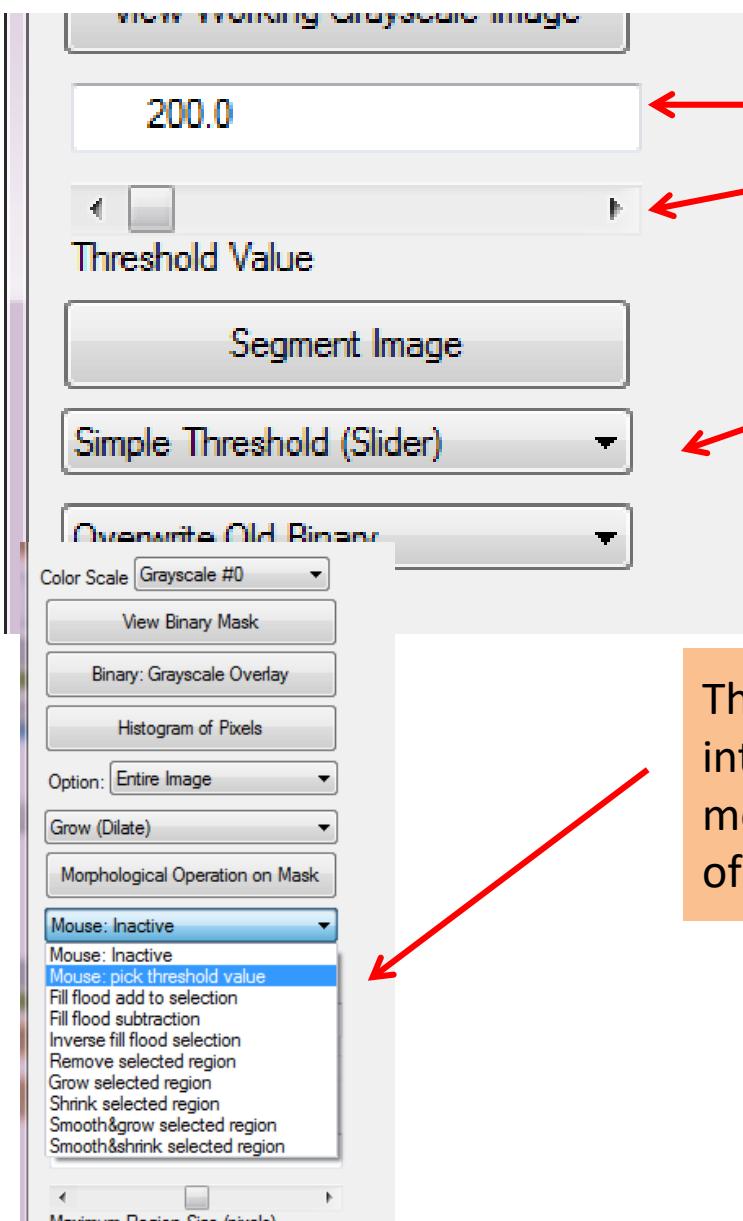


Segmentation of Binary Mask

Multiple Segmentation methods are available



Segmentation of Binary Mask



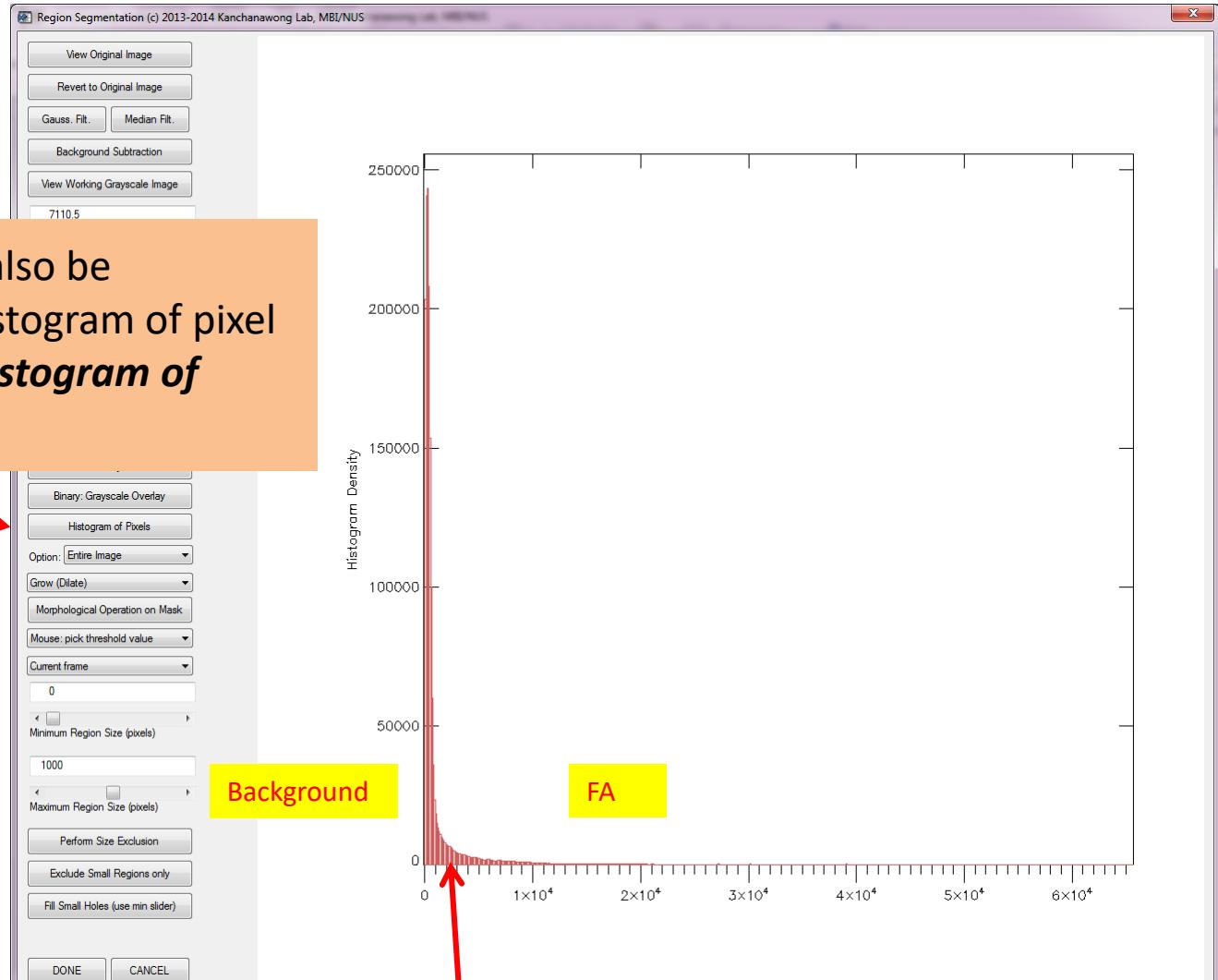
Threshold values can be adjusted by slider or type into the box

Simple thresholding will select any pixels with value above the specified threshold

Threshold values can also be picked interactively by choosing the proper mouse mode, and then click on the region of **working image**

Segmentation of Binary Mask

Threshold values can also be estimated from the histogram of pixel intensity by clicking **Histogram of Pixels**

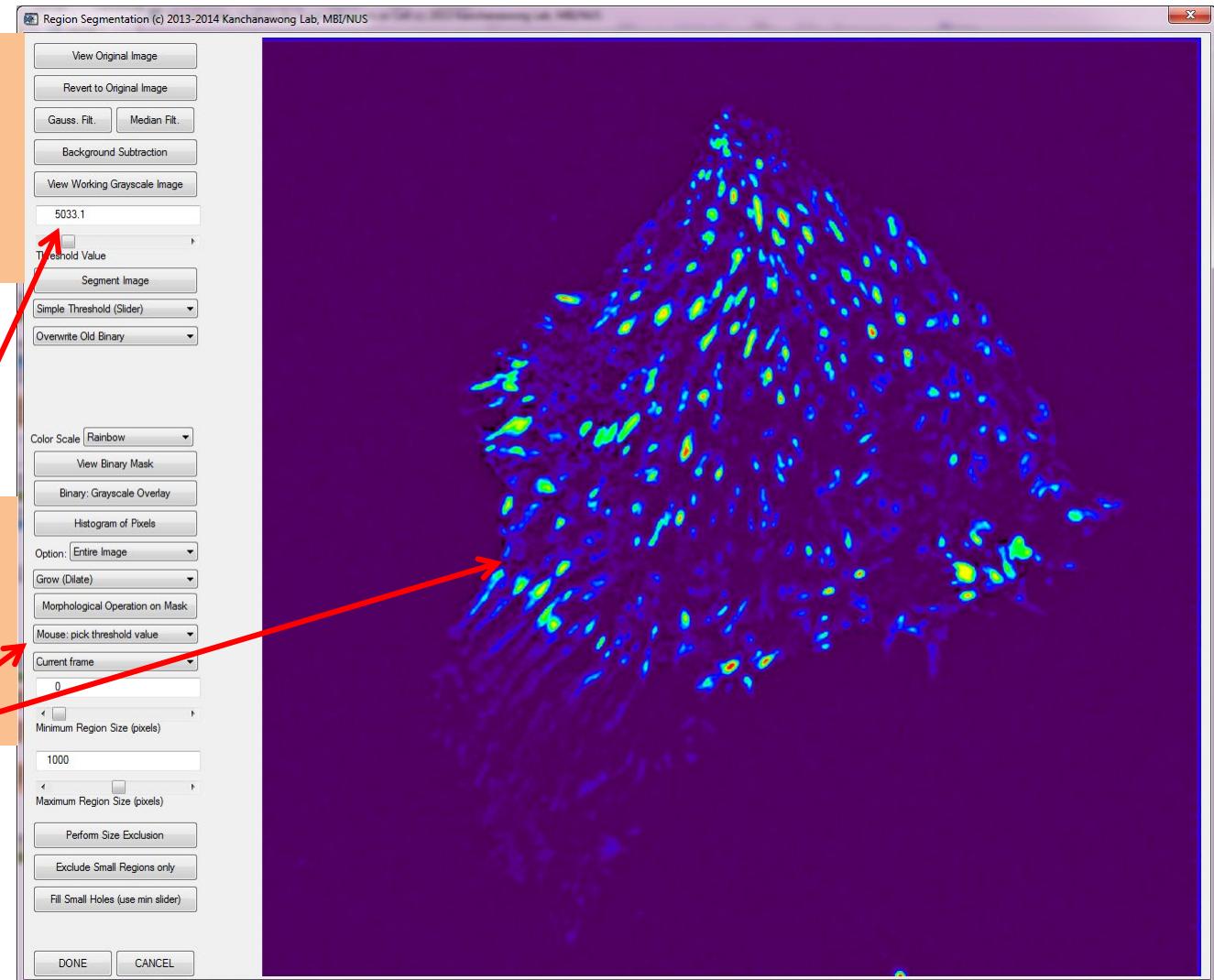


Approximate threshold

Segmentation of Binary Mask

In this example, the image is first Gaussian filtered 2-3 times, then background subtracted

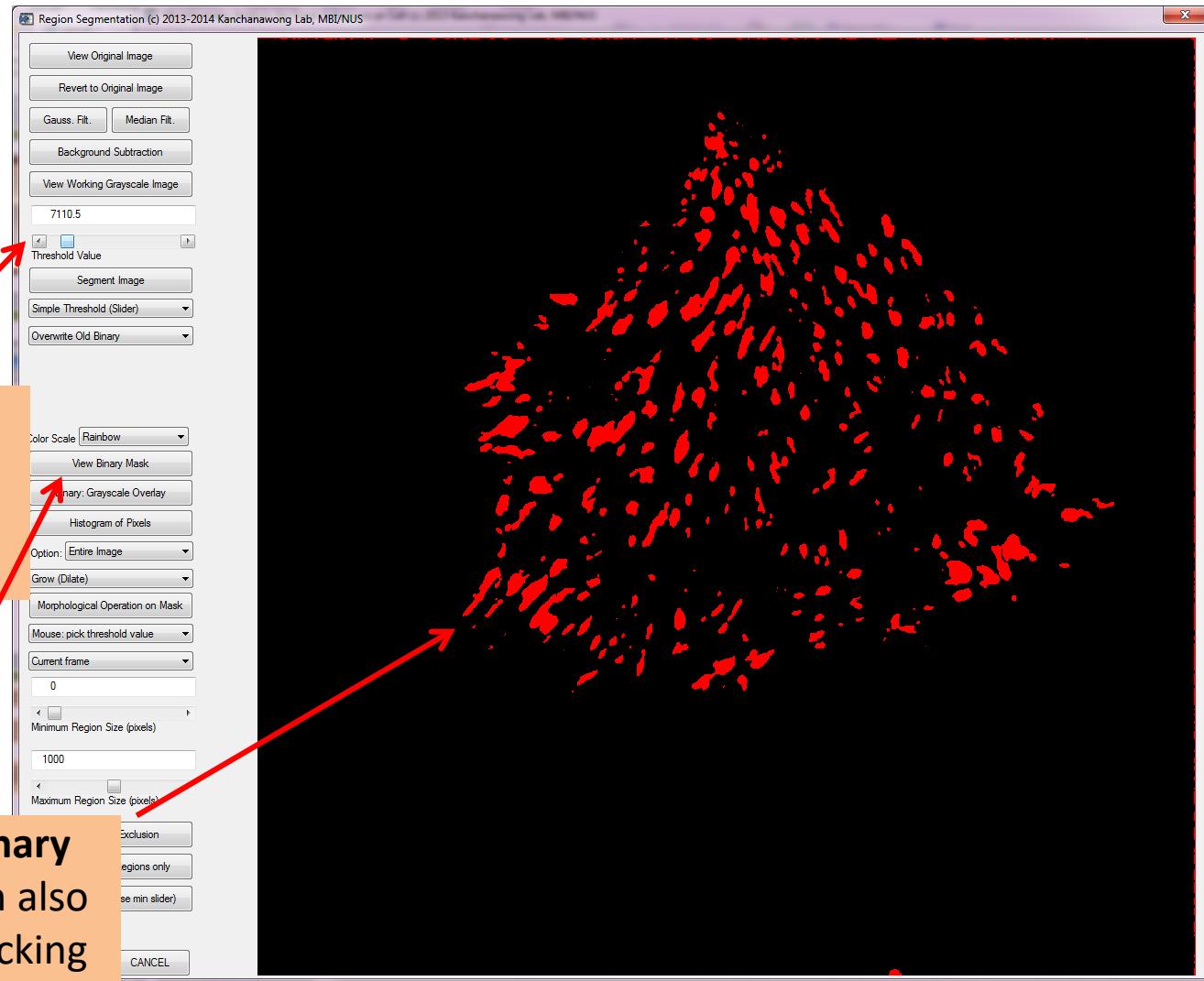
Then the mouse is used to estimate the background level by picking on the region close to but not in FA



Segmentation of Binary Mask

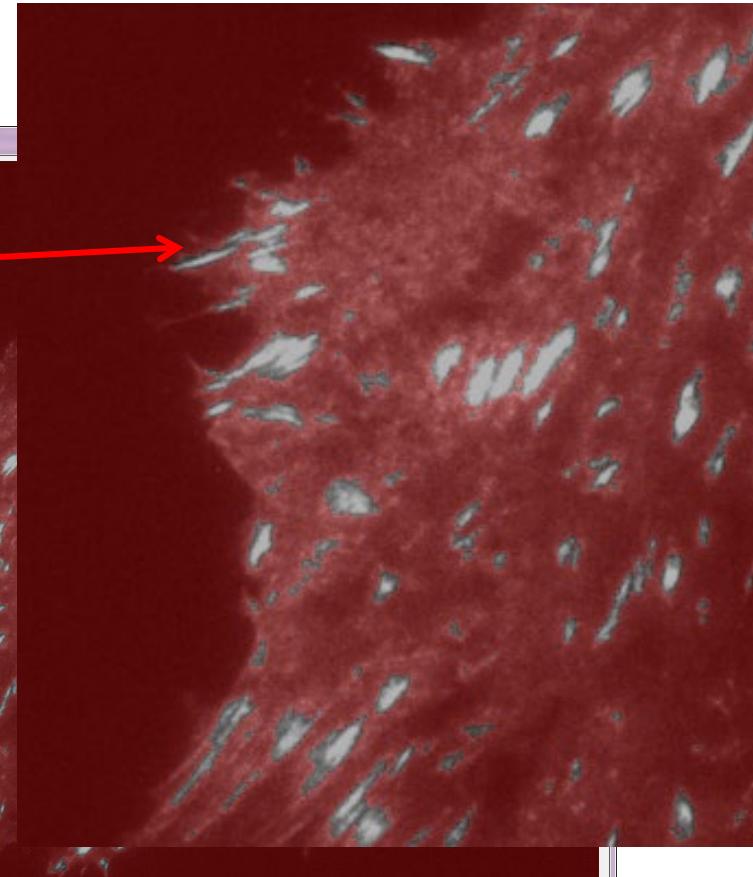
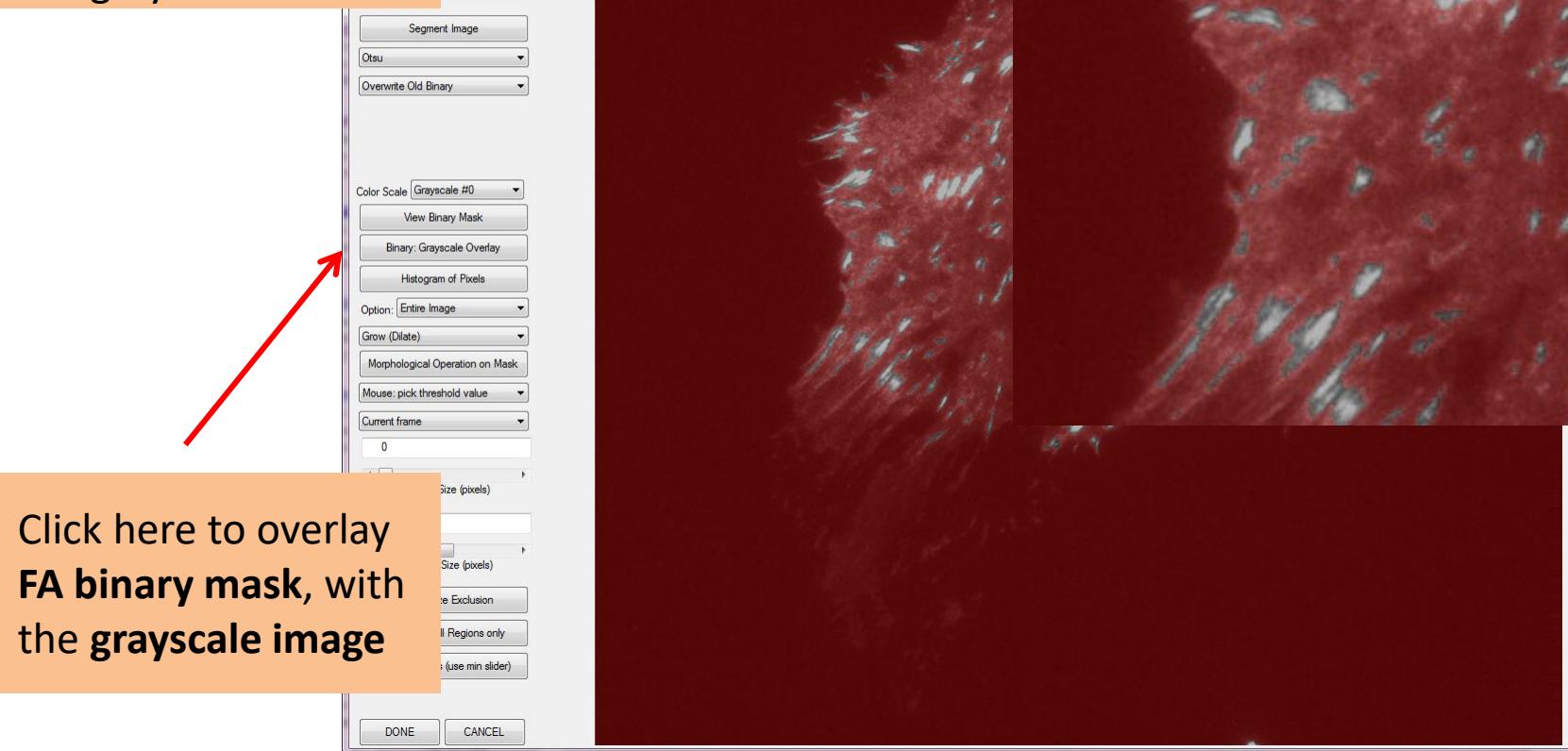
Slider can be adjusted to get the proper threshold levels

This is the **FA binary mask**, which can also be viewed by clicking here



Segmentation of Binary Mask

The quality of the mask can be checked by comparing with the grayscale data



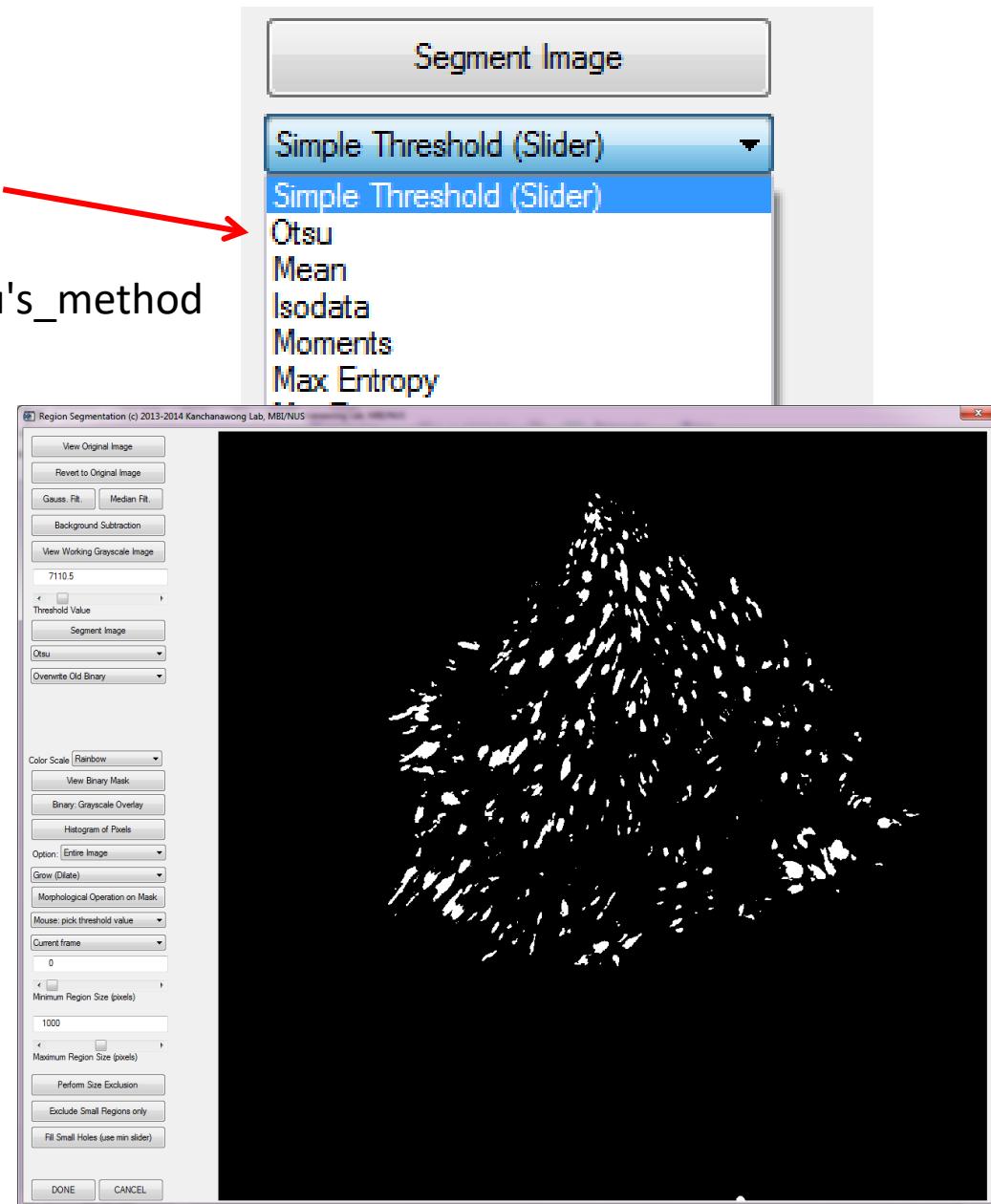
Segmentation of Binary Mask

Segmentation methods commonly useful for FA is the Otsu segmentation. For more info see the following URL

http://en.wikipedia.org/wiki/Otsu's_method

For example, this mask is generated by

1. Gaussian filter 1X
2. subtract background
3. Otsu thresholding



Mask Refinement

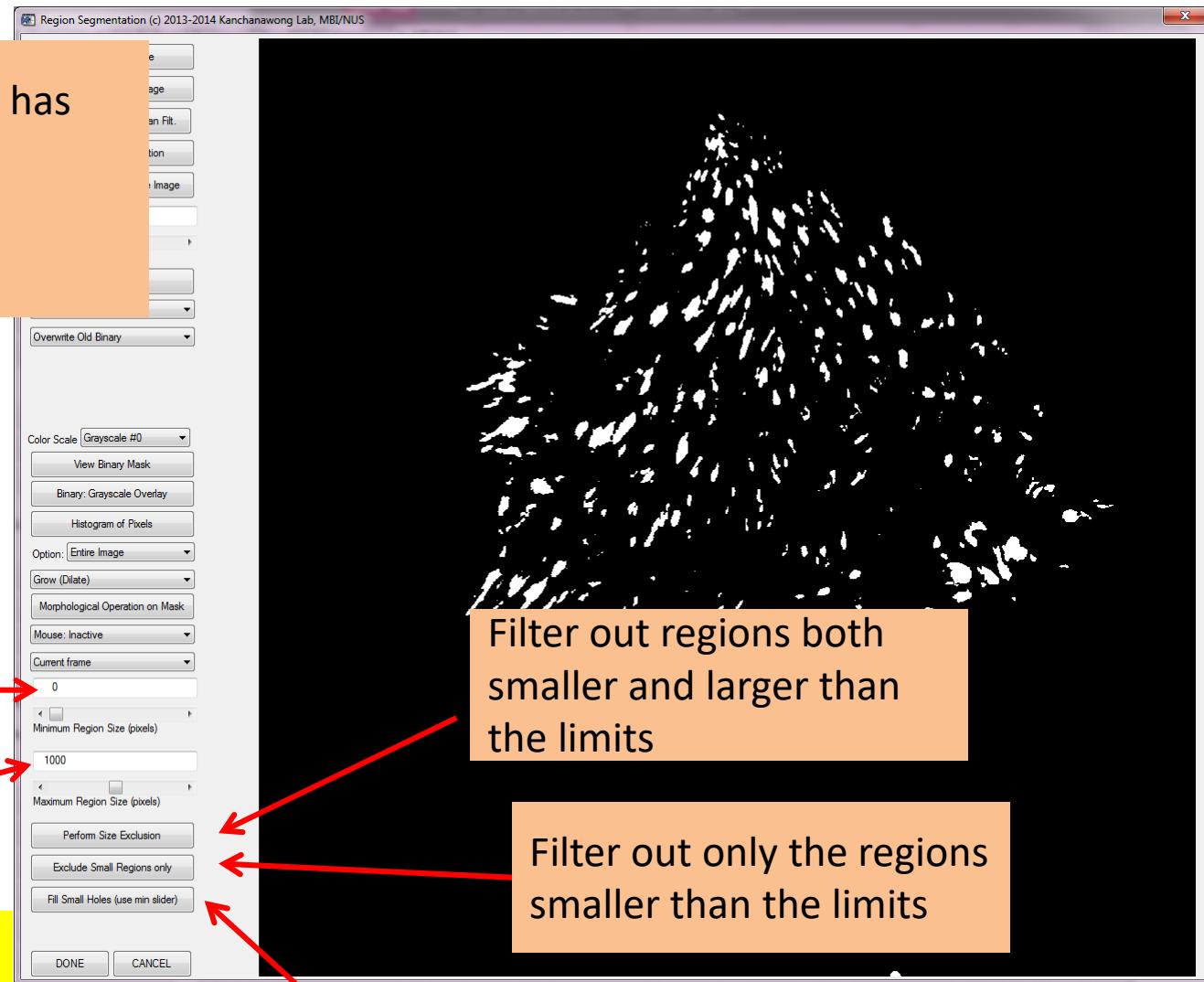
Once the initial FA mask has been created, there are multiple options for refinement.

The size of the regions can be filtered

Minimum region size

Maximum region size

Note that the value larger than the slider can be put in by typing into the box directly



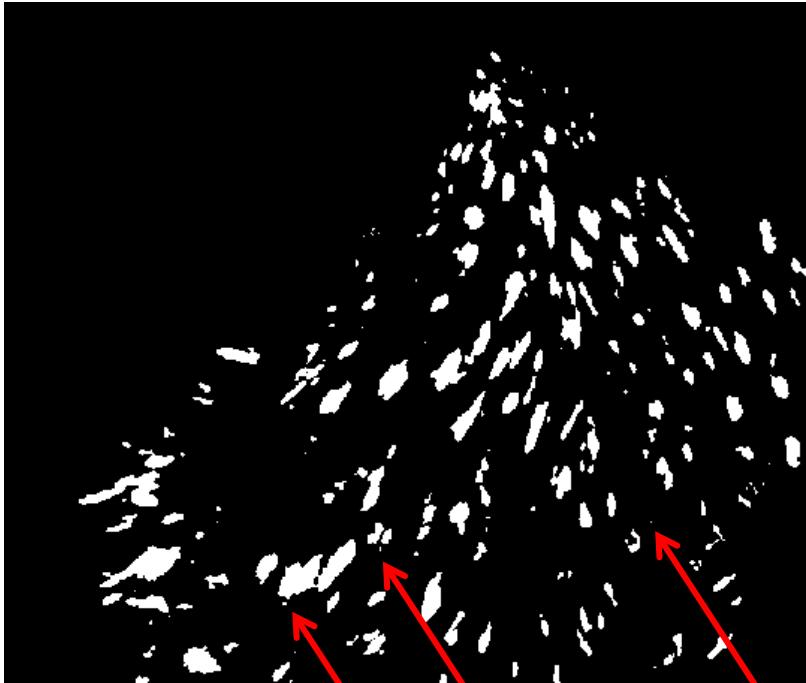
Filter out regions both smaller and larger than the limits

Filter out only the regions smaller than the limits

Fill holes in regions if the hole size is smaller than the limits

Mask Refinement

Before size filtering



Examples of regions removed

After filtering out regions smaller than 15 pixels



Mask Refinement

Morphological Operations can be performed on the mask

http://en.wikipedia.org/wiki/Mathematical_morphology

1. Choose the operation

Option: Entire Image

Grow (Dilate)

Grow (Dilate)

Shrink (Erode)

Smooth&grow (Close)

Smooth&shrink (Open)

Thin

Before

Grow (Dilate)

Morphological Operation on Mask

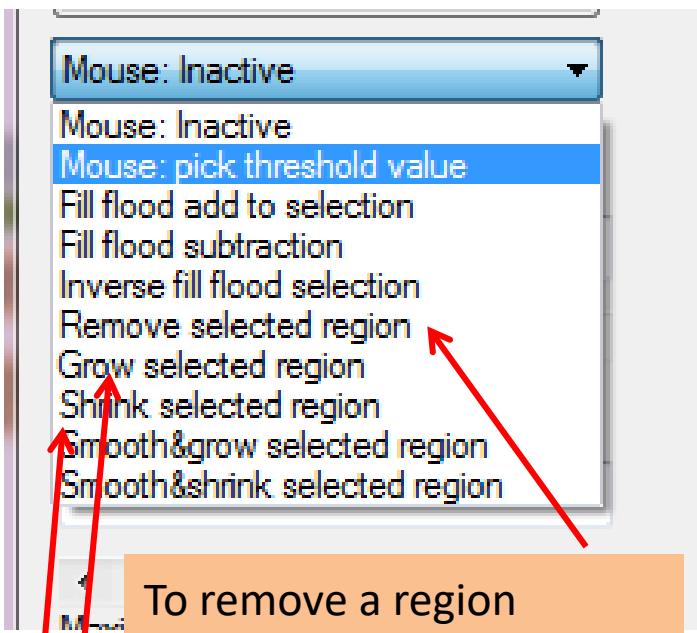
2. Click to perform morphological operation

After Grow operation (dilate)



Mask Refinement

The FA mask can also be modified interactively by many mouse-based options

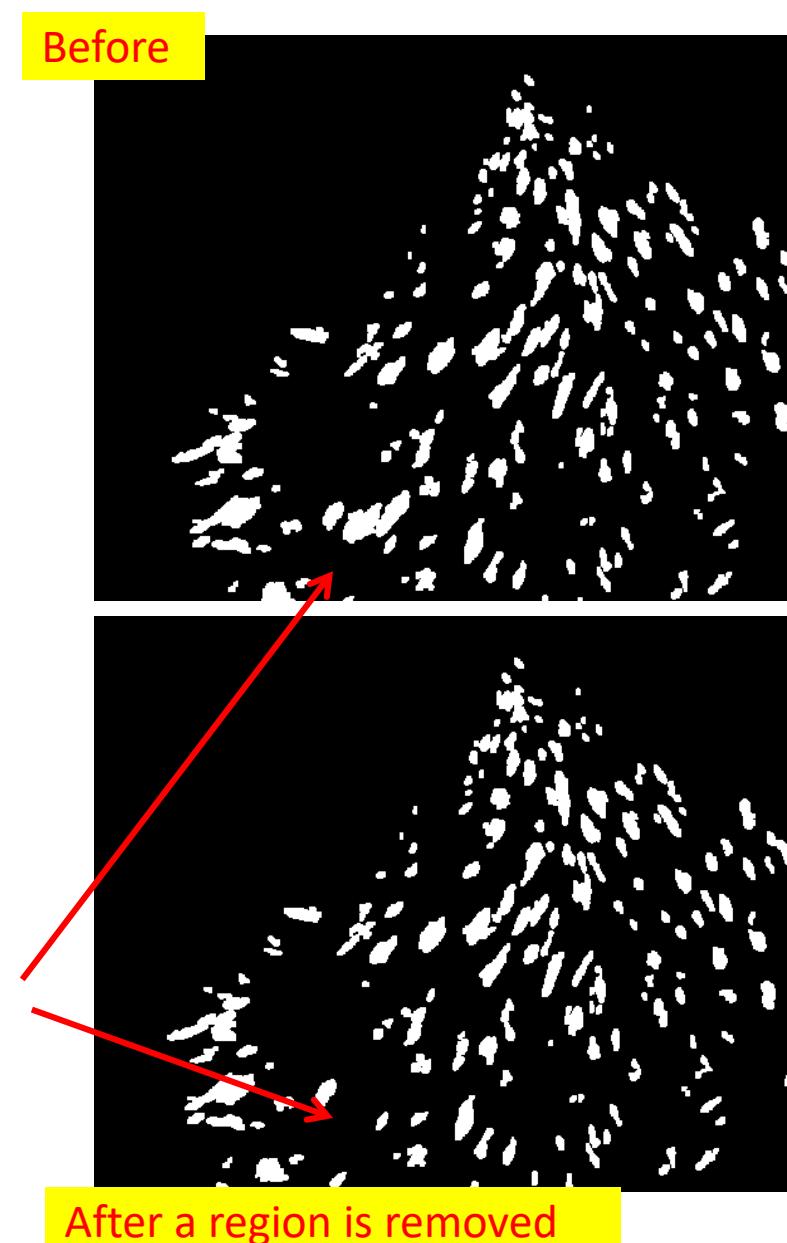


To remove a region

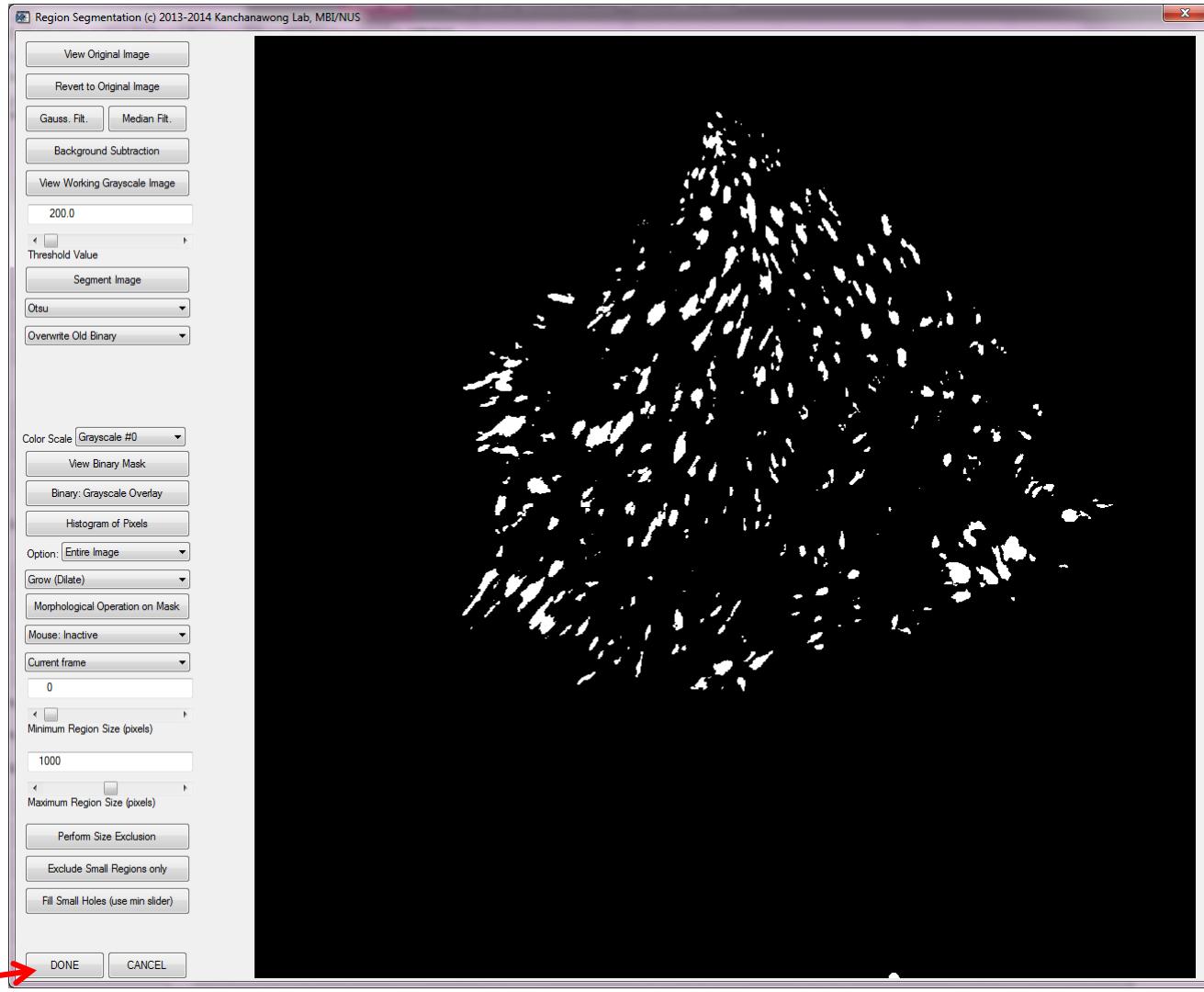
To grow a region

To shrink a region

And so on



Segmentation of Binary Mask



Once satisfied, click DONE to exit the window. Make sure to save the file as
***morph.sav** for example: **20140401_A_B_C_morph.sav**

Segmentation of Binary Mask

The **FA binary mask** and the Overlay can be checked in the main window as well

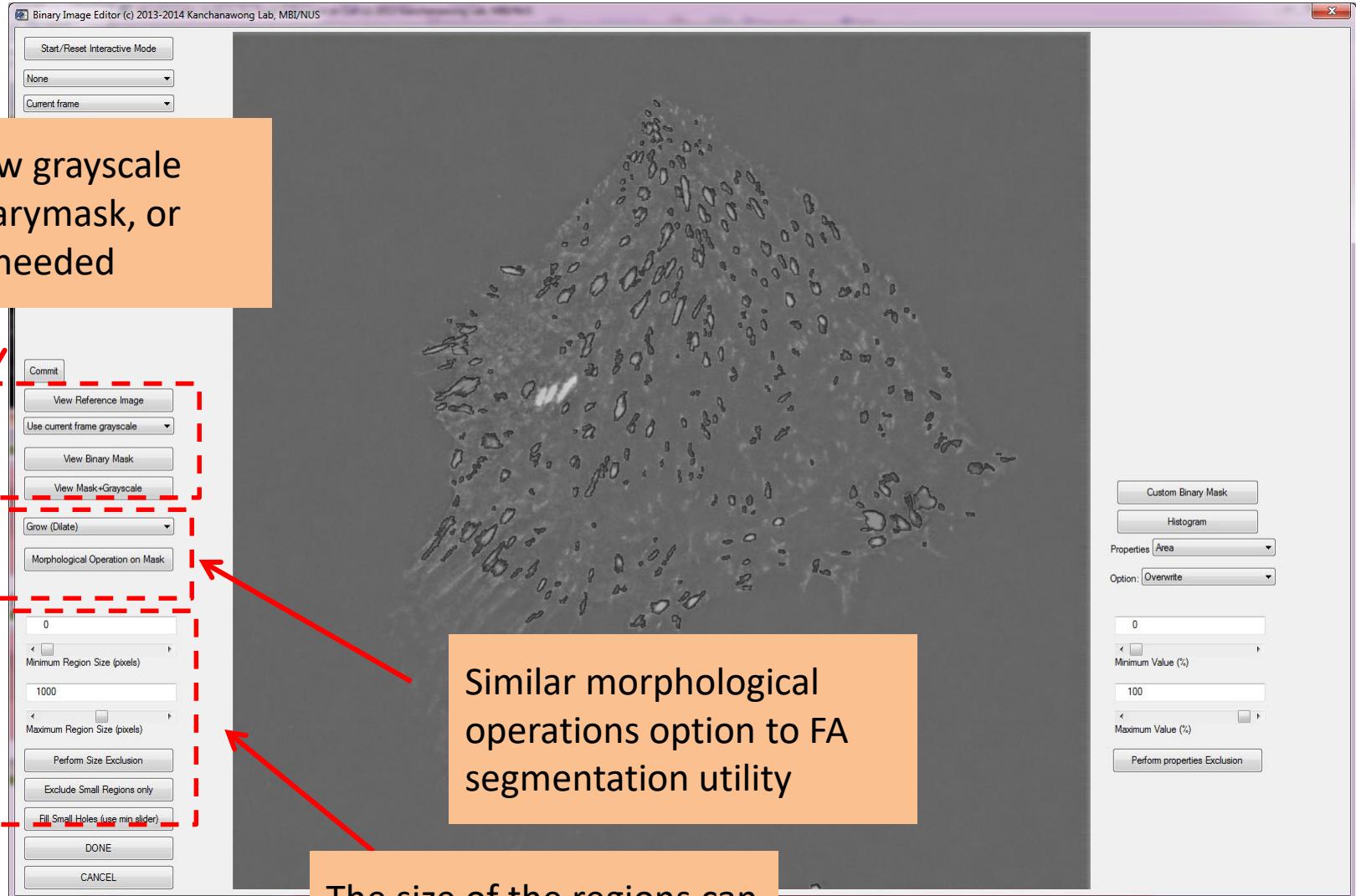


Binary Mask Editing Utility

Manual/interactive refinement of FA mask can be done by the editing utility



Binary Mask Editing Utility

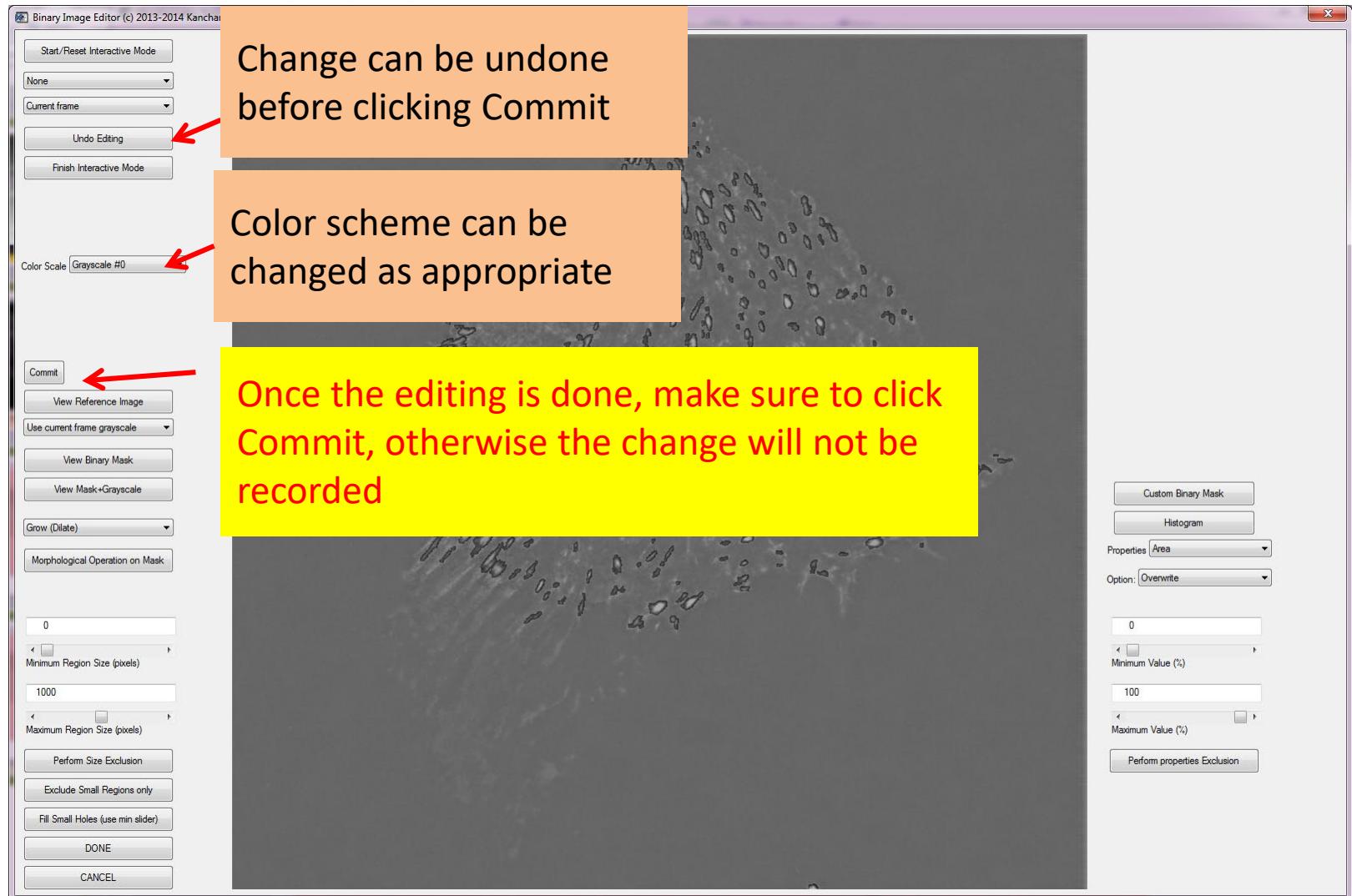


Click to view grayscale image, binarymask, or overlay as needed

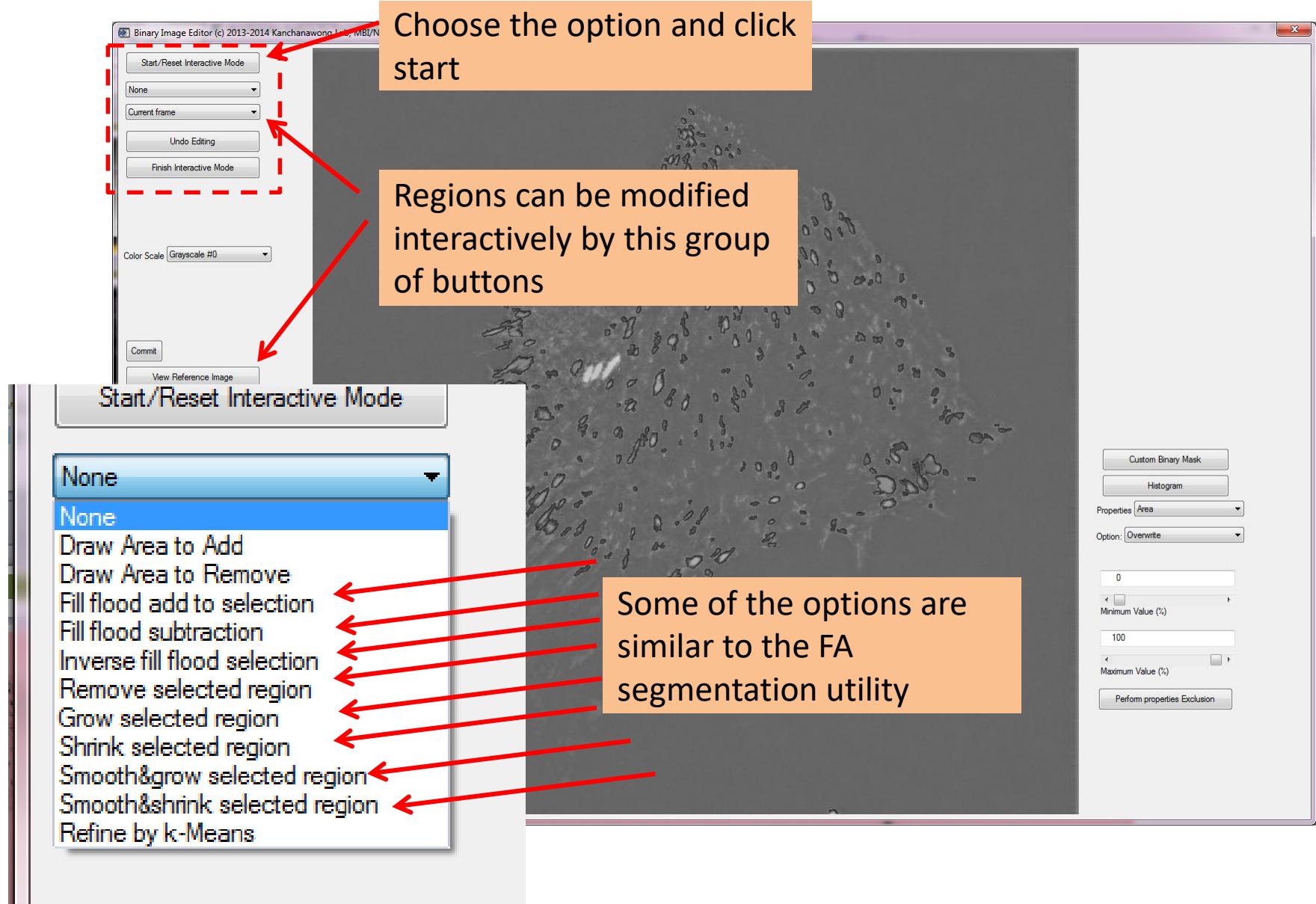
Similar morphological operations option to FA segmentation utility

The size of the regions can be filtered similarly to the FA segmentation utility

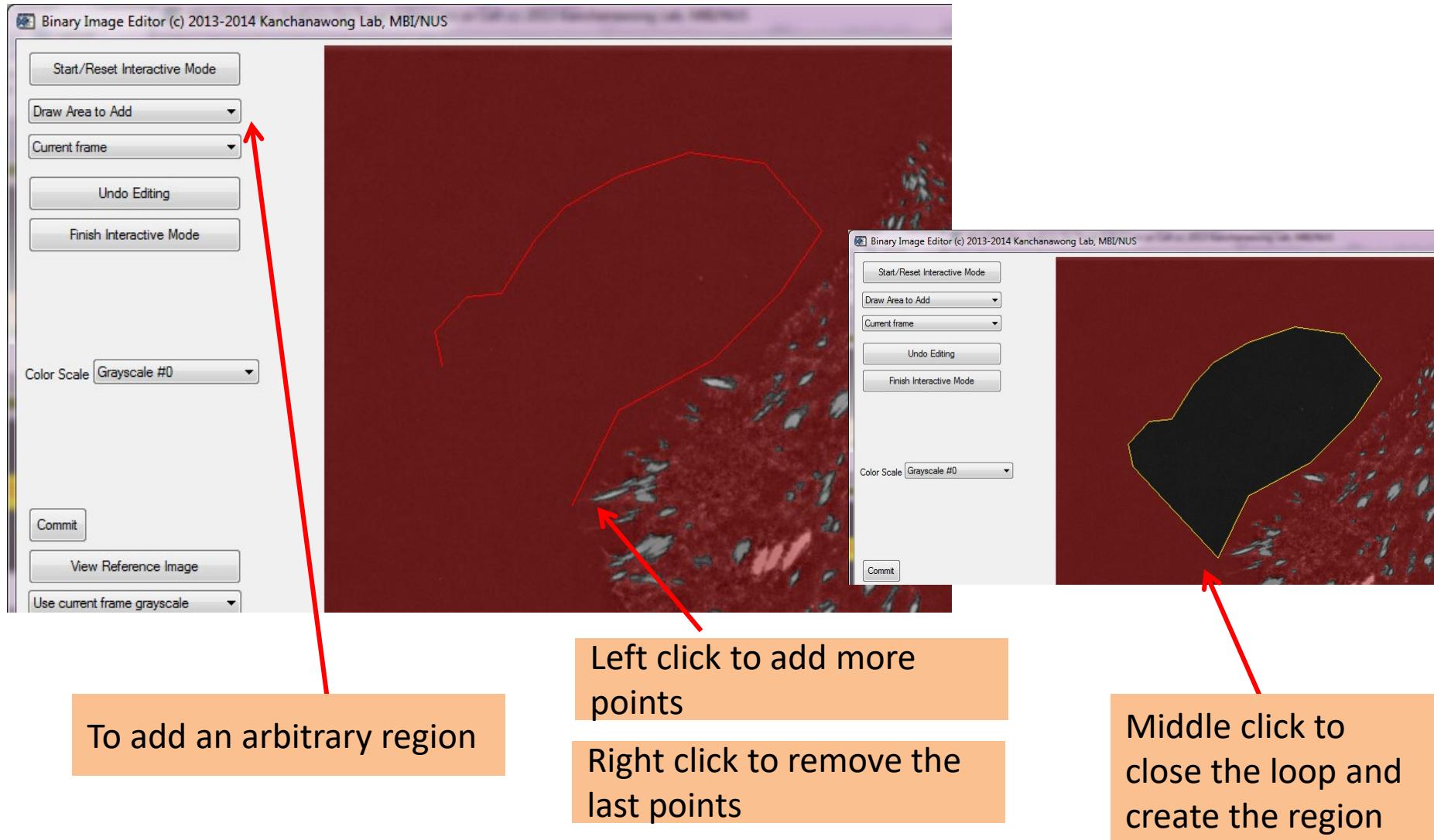
Binary Mask Editing Utility



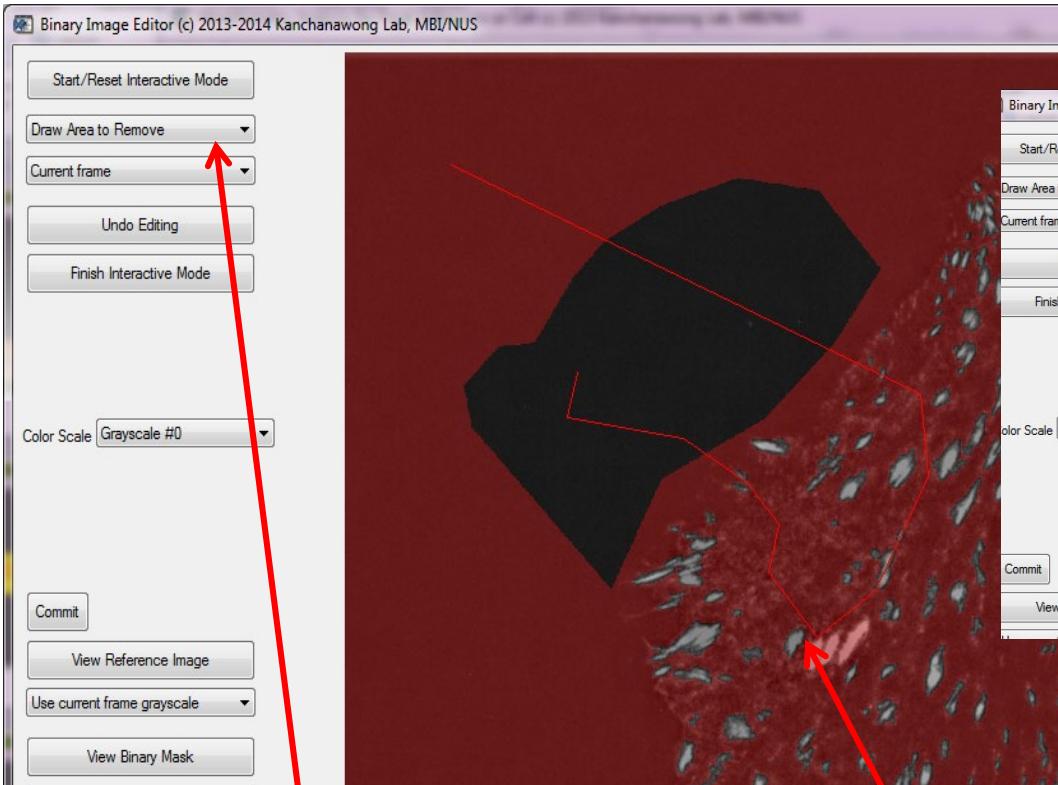
Binary Mask Editing Utility



Binary Mask Editing Utility



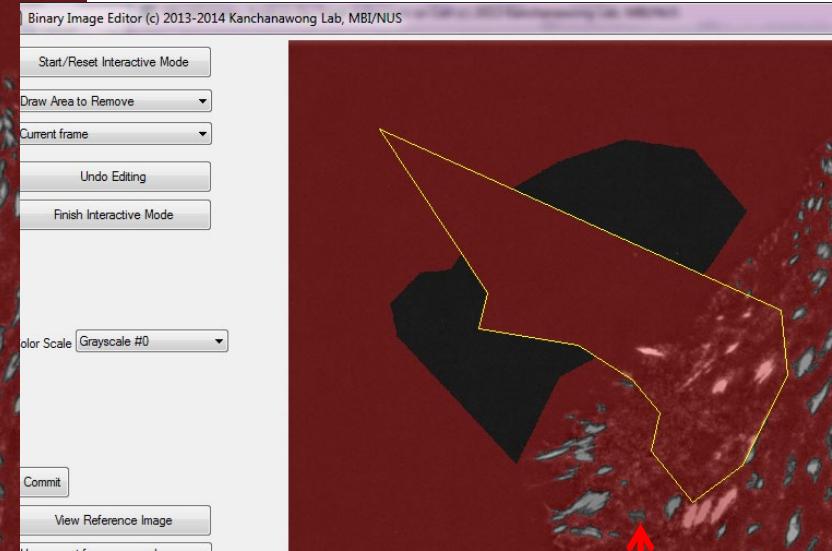
Binary Mask Editing Utility



To remove an arbitrary region

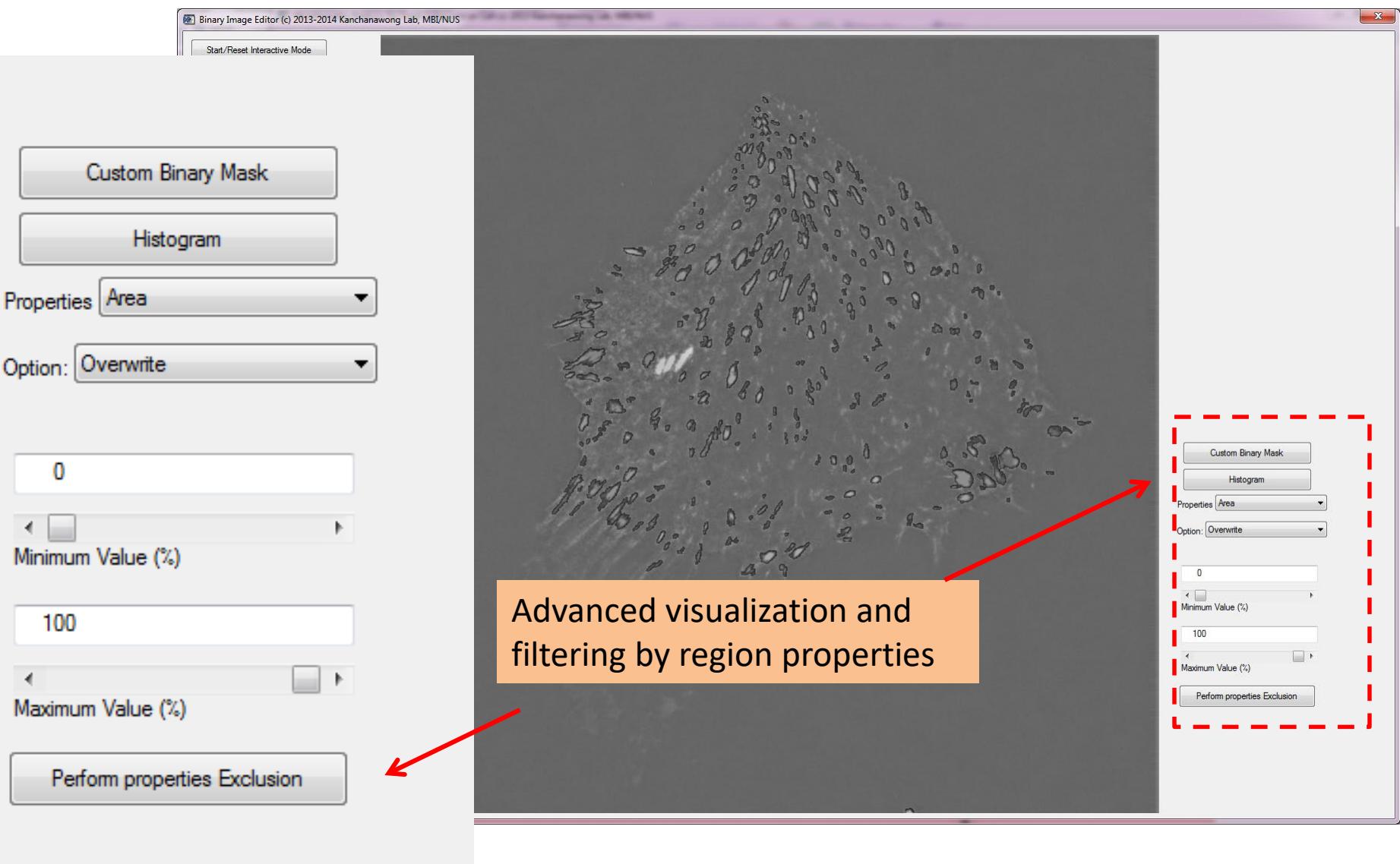
Left click to add more points

Right click to remove the last points



Middle click to close the loop and create the region

Binary Mask Editing Utility



Binary Mask Editing Utility

In this example, regions are color-coded by color/rainbow scale

Each region can be colored according the their properties
(Use color menu to choose the color scheme)

FA properties

Custom Binary Mask

Histogram

Properties: Area

Option: Overwrite

Minimum Value (%)

Maximum Value (%)

Perform properties Ex

Properties: Area

Area

Axial Ratio

Density

Length

Total Intensity

Perimeter

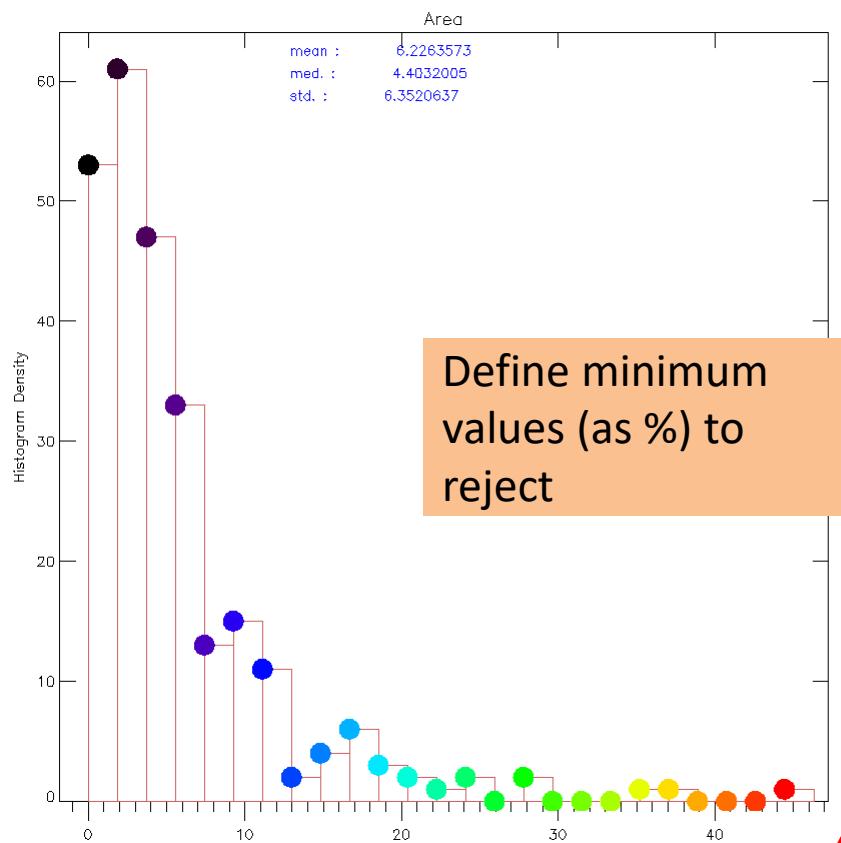
Dist. to Edge (COM)

Dist to Edge (Avg)

Orientation

Minimum Value (%)

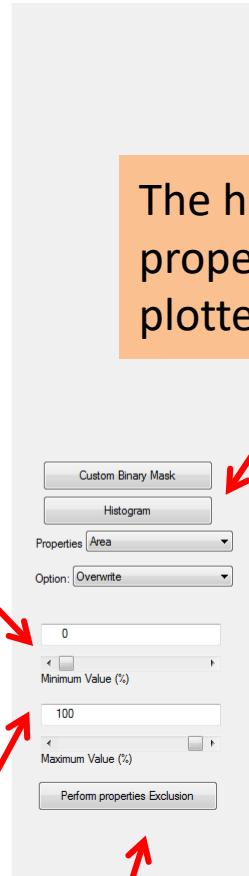
Binary Mask Editing Utility



Define minimum values (as %) to reject

Define maximum values (as %) to reject

Click to filter OUT



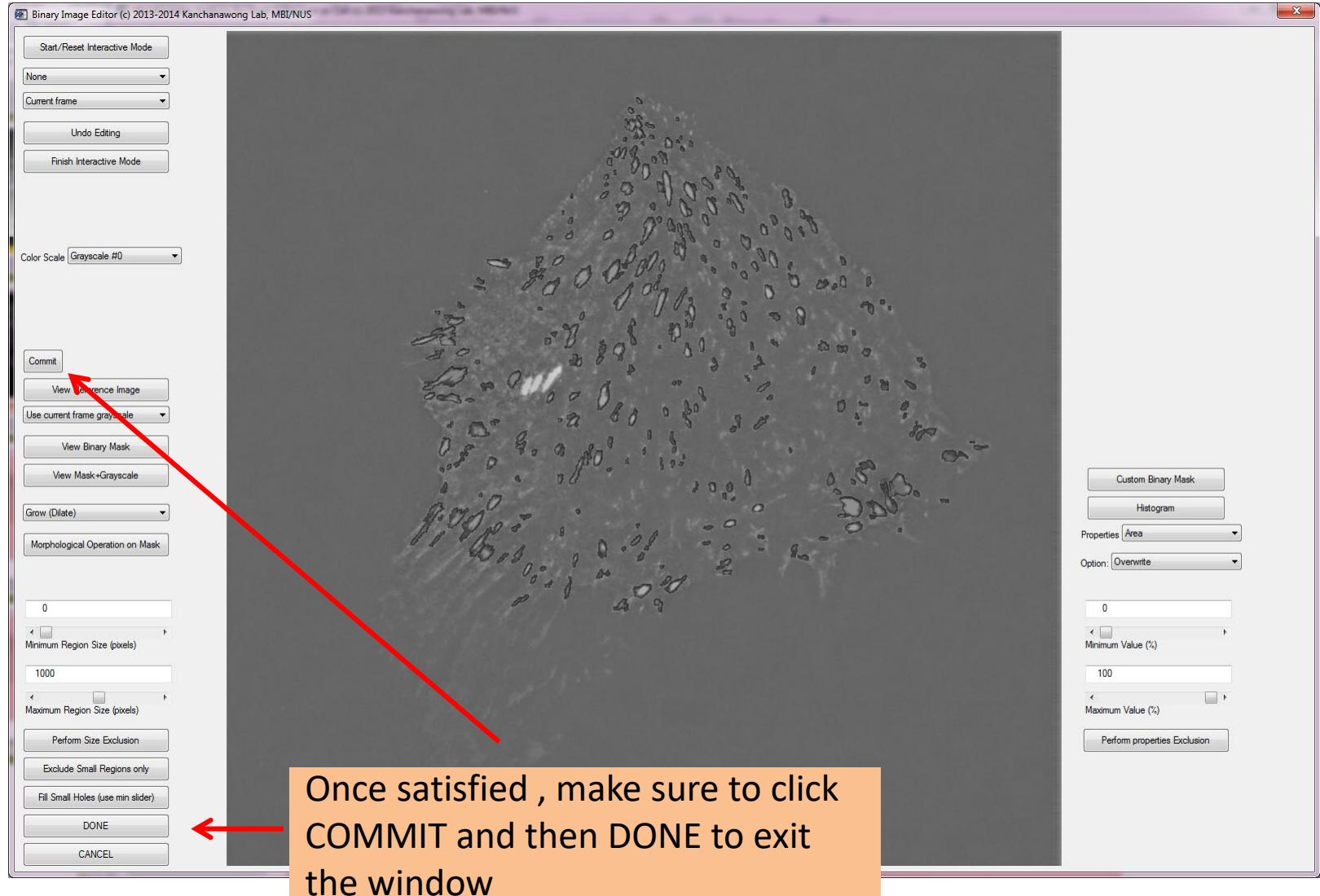
The histogram of the region properties distribution can be plotted

The region can be filtered OUT based on the selected properties

Example



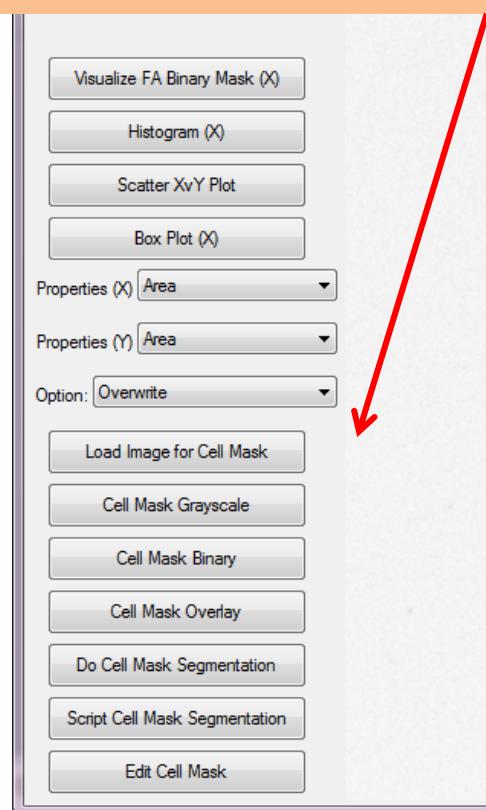
Binary Mask Editing Utility



Cell Mask

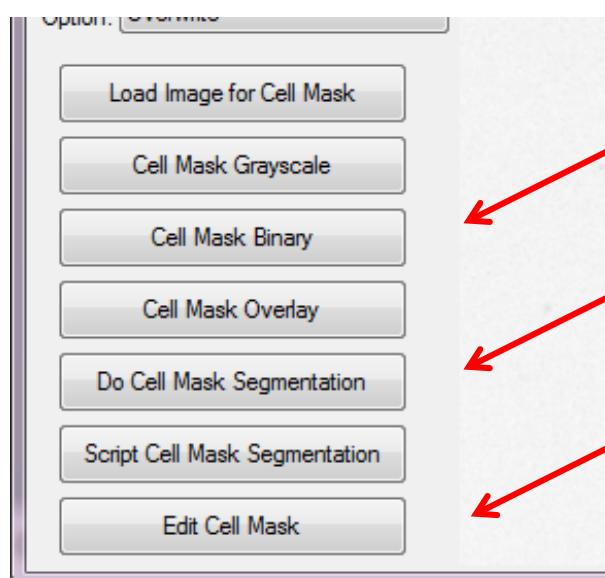
Cell Mask can be defined in a similar manner from a grayscale image

To load a separate grayscale image for cell mask segmentation



To use the same image for both FA mask and Cell mask

Cell Mask

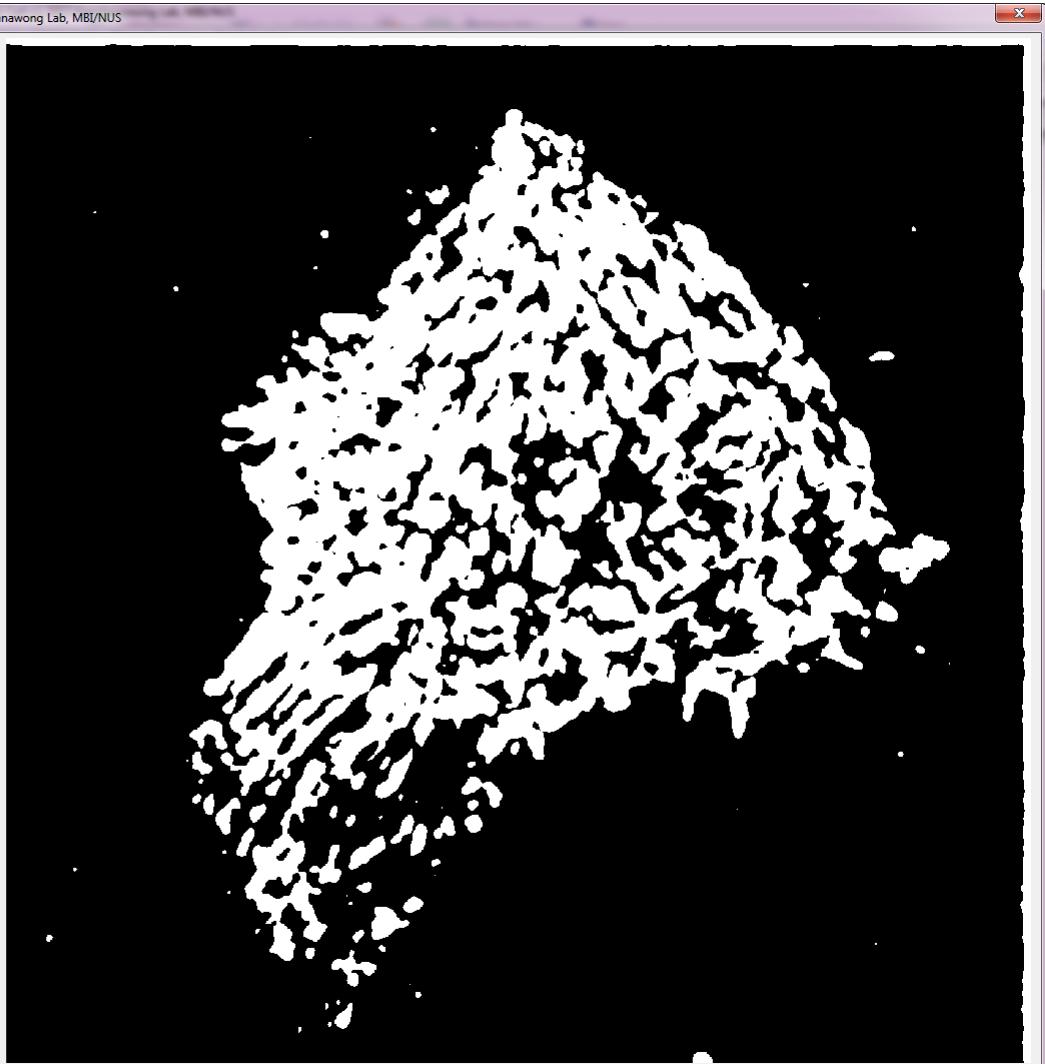
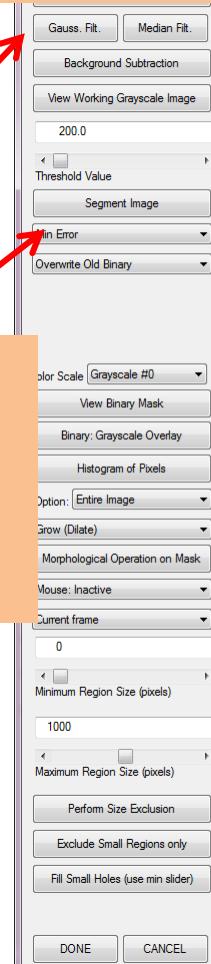


Display, Segmentation, and Editing functions are similar

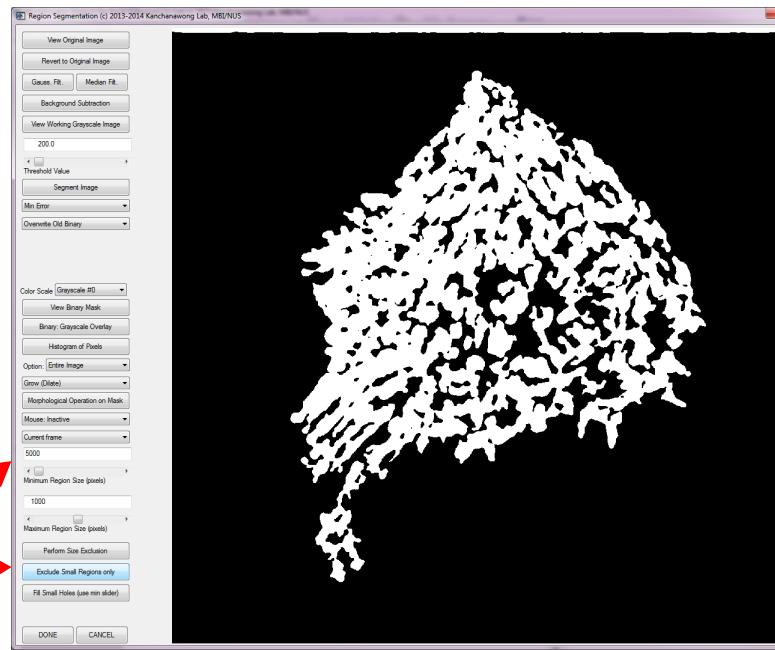
Cell Mask

For cell mask segmentation using FA image, Background subtraction is not necessary

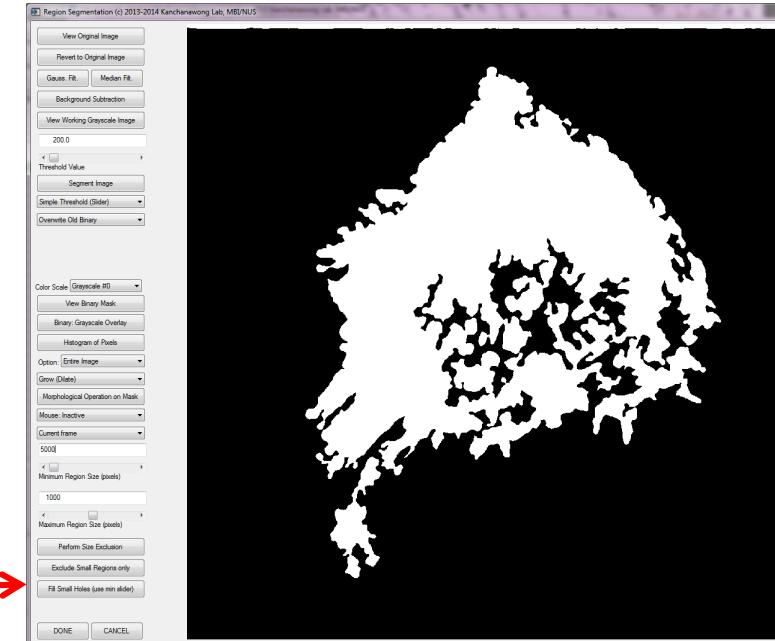
In this example, the image is blurred several times, then segmented by min error



Cell Mask

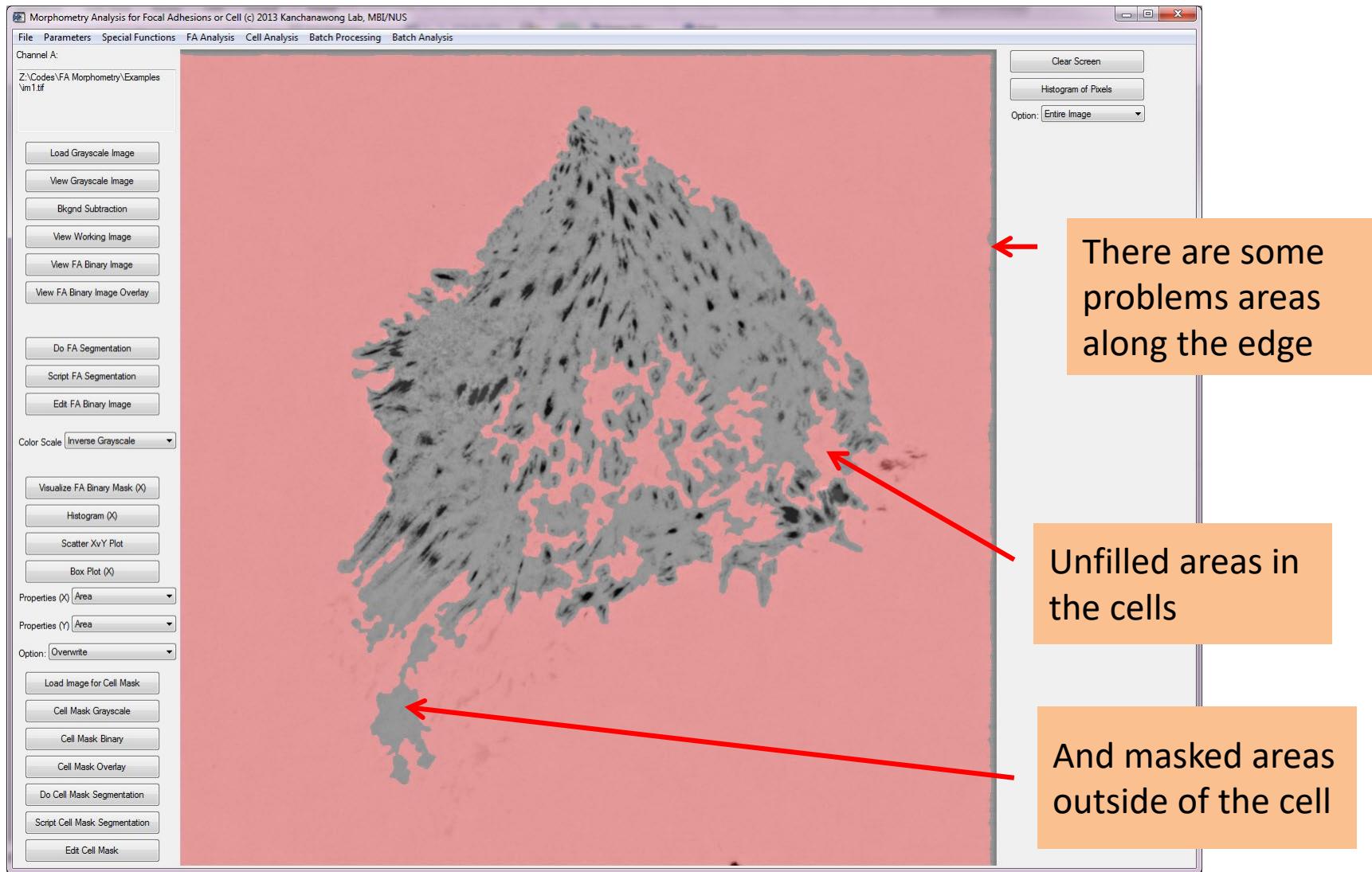


Region smaller
than 5000 pixels
are rejected

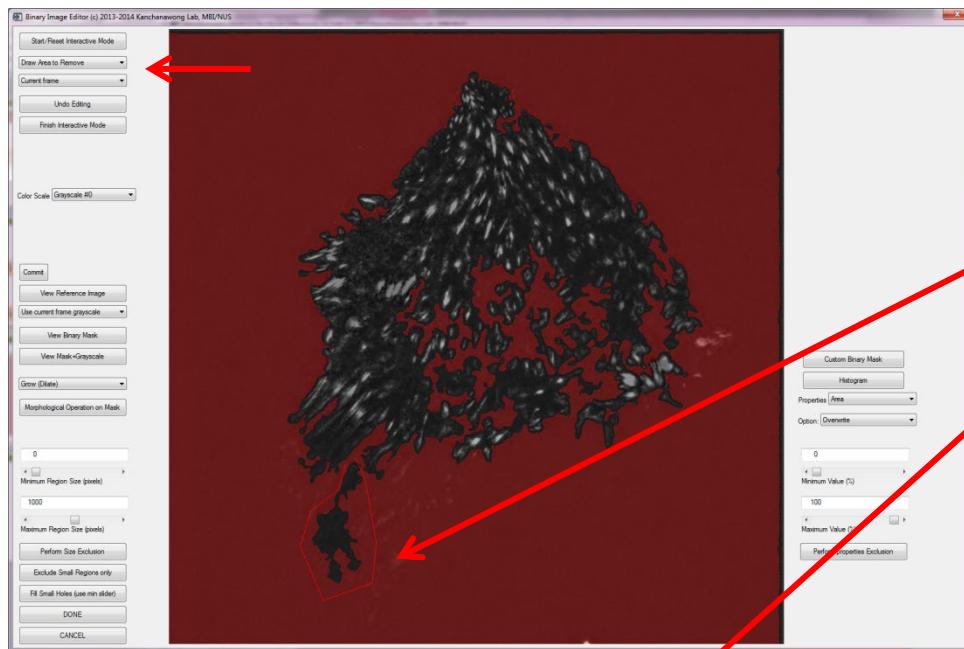


Holes smaller
than 5000 pixels
are filled

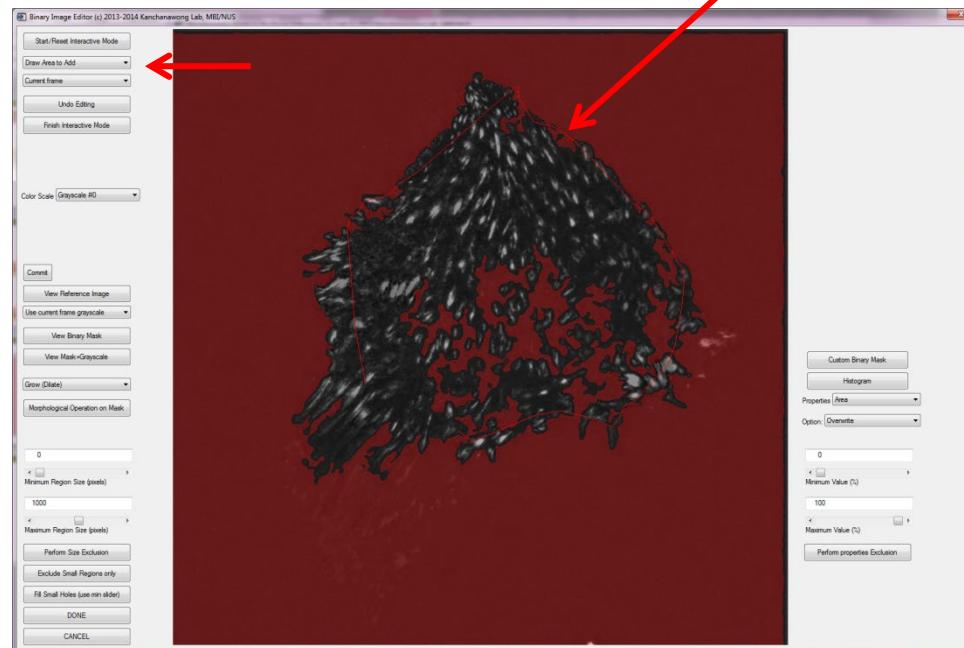
Cell Mask



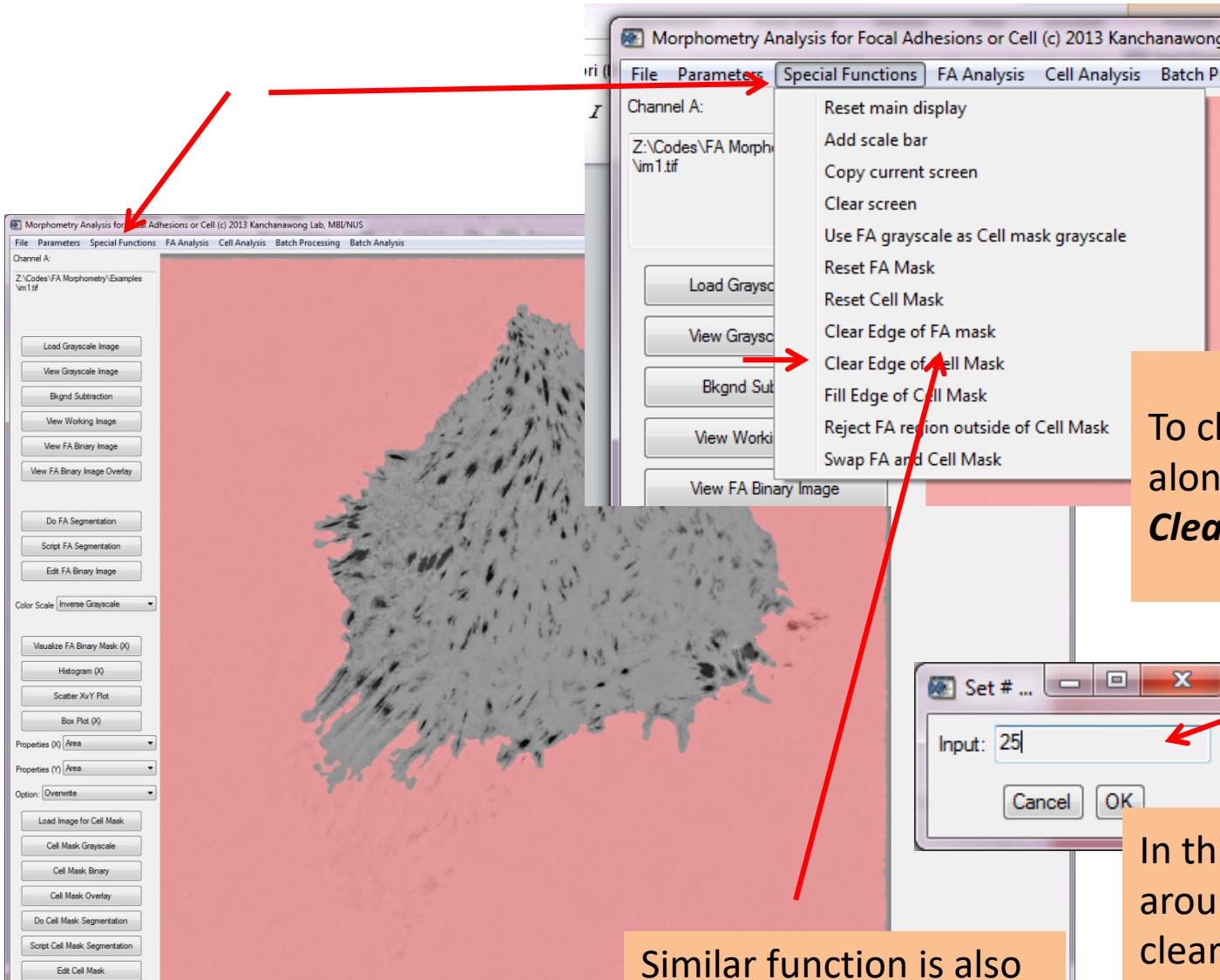
Cell Mask



The unwanted area and the holes can be corrected by Edit Cell Mask utility



Cell Mask

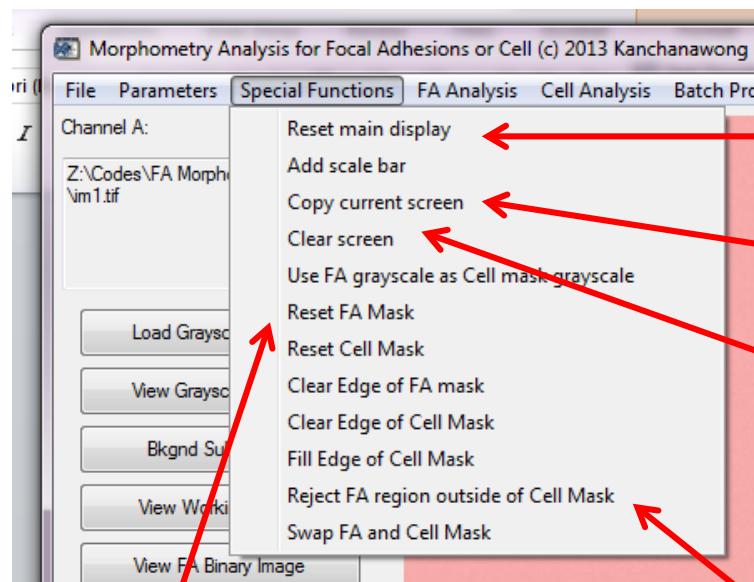


To clear unwanted area along the edge, choose
Clear Edge of Cell Mask

Similar function is also available for FA mask

In this example, 25 pixels around the edge will be cleared

Special Functions



Other Special functions

If strange looking windows pop-up, reset it here.

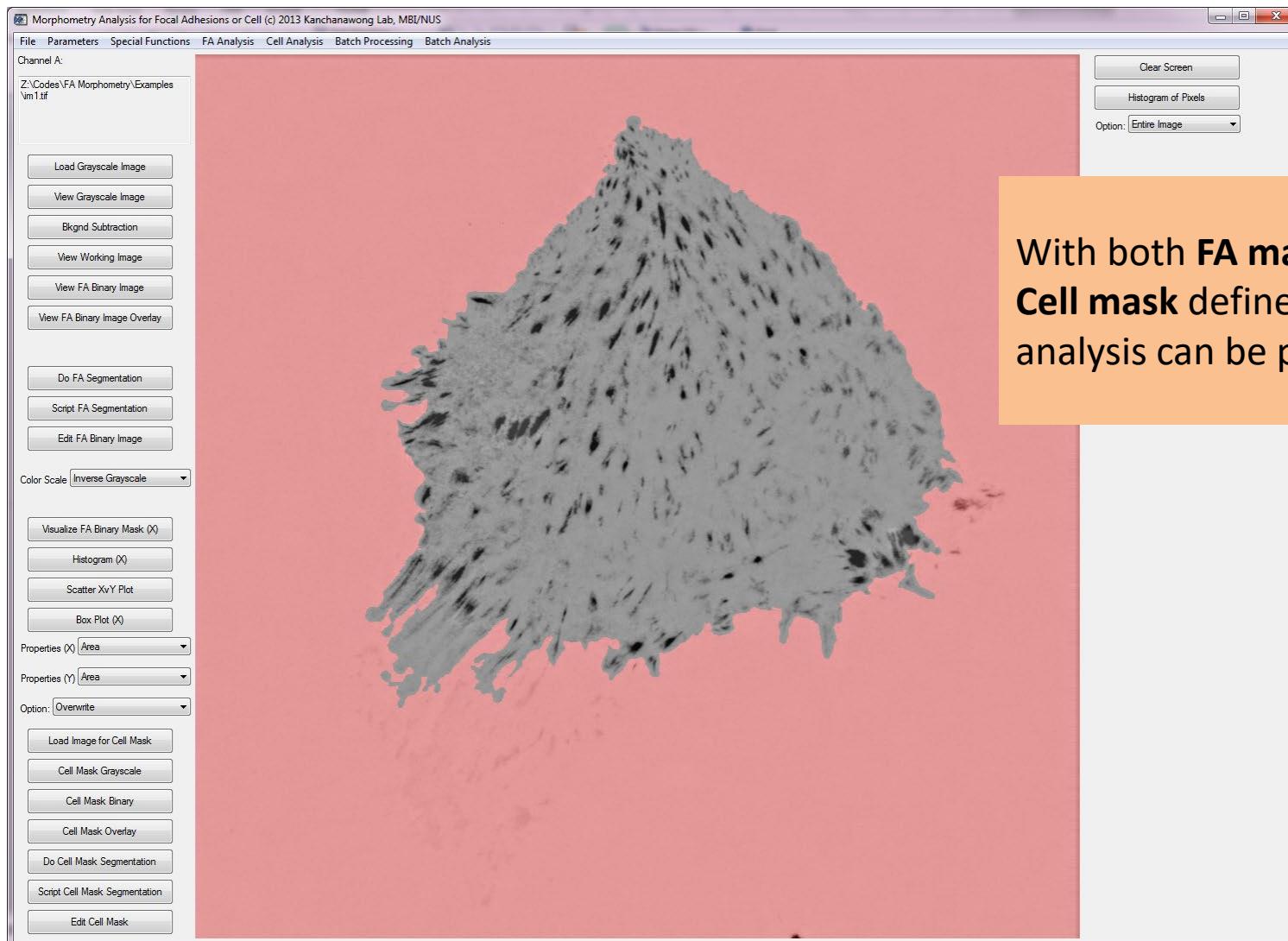
Show image of current screen in a new window

Clear the main window

Delete FA or Cell mask

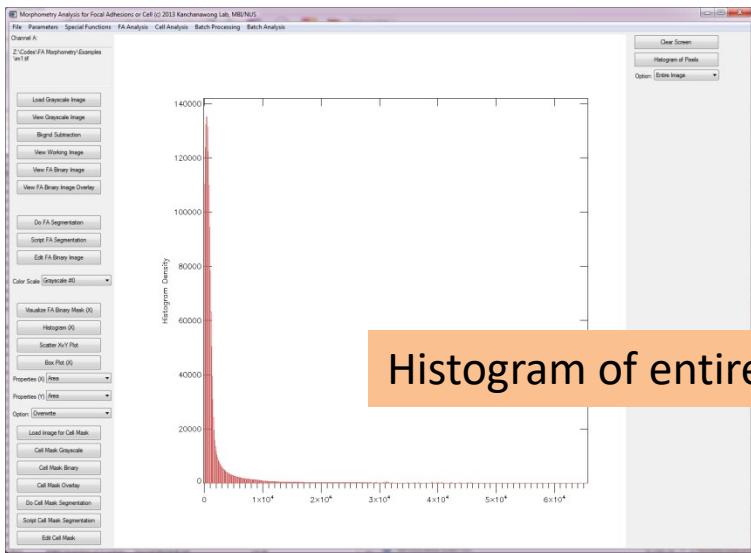
Remove FA region not within Cell mask

Analysis

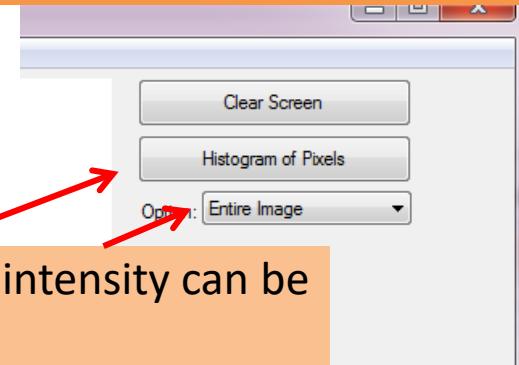


With both **FA mask** and
Cell mask defined, more
analysis can be performed

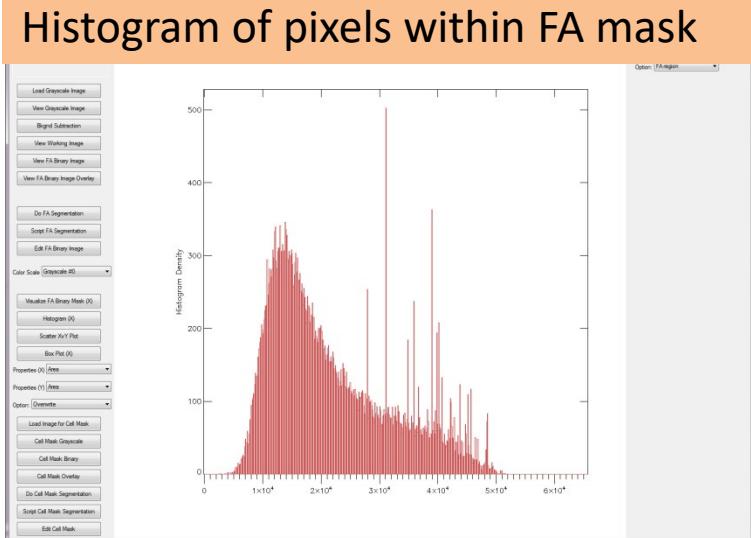
Analysis



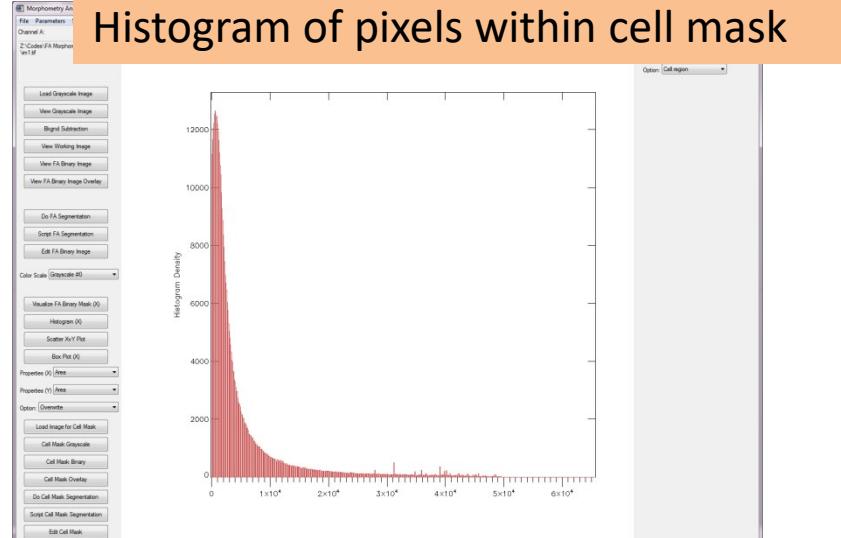
Histogram of entire image



Histogram of pixel intensity can be plotted here



Histogram of pixels within FA mask



Histogram of pixels within cell mask

Analysis

Adhesions or Cell (c) 2013 Kanchanawong Lab, MBI/NUS

FA Analysis Cell Analysis Batch Processing Batch Analysis

View Overlay with Indices

View Overlay with Best Fit Ellipses

Histogram: Area, Axial Ratio, Long Axis, Density

Histogram: all properties (3x3)

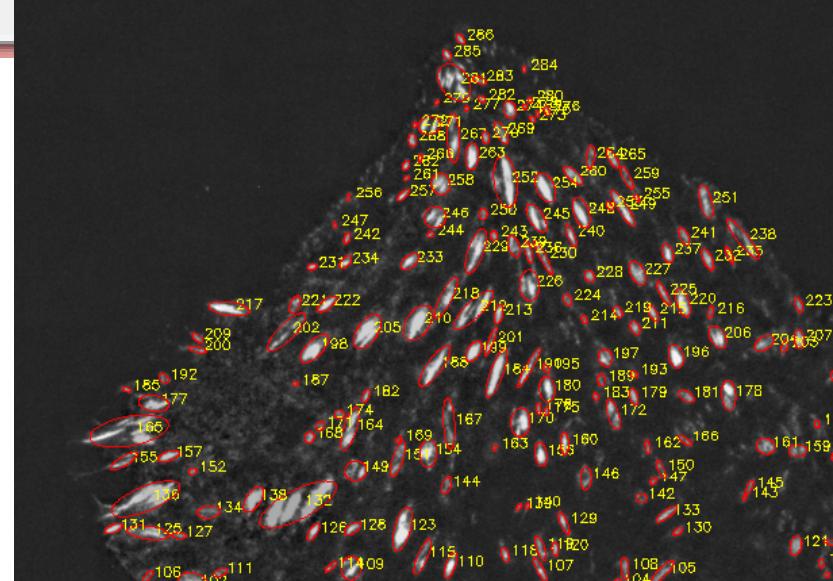
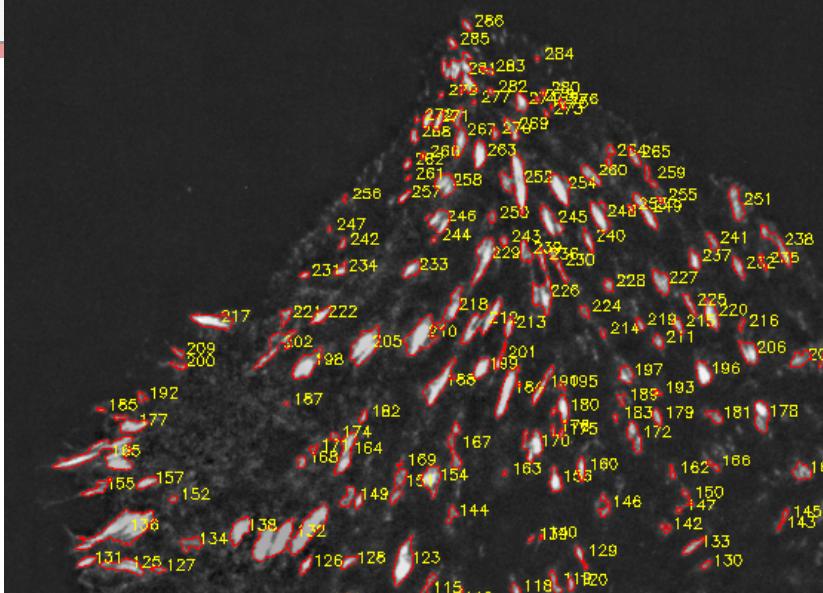
Boxplot: Area, Axial Ratio, Long Axis, Density

Boxplot: all properties (3x3)

Bar Graph (Area): nascent(<0.25) - mid-sized - large(>3)

For visualization of the FA mask

For checking the quality of the mask/ the ellipse is used to calculate length and axial ratio



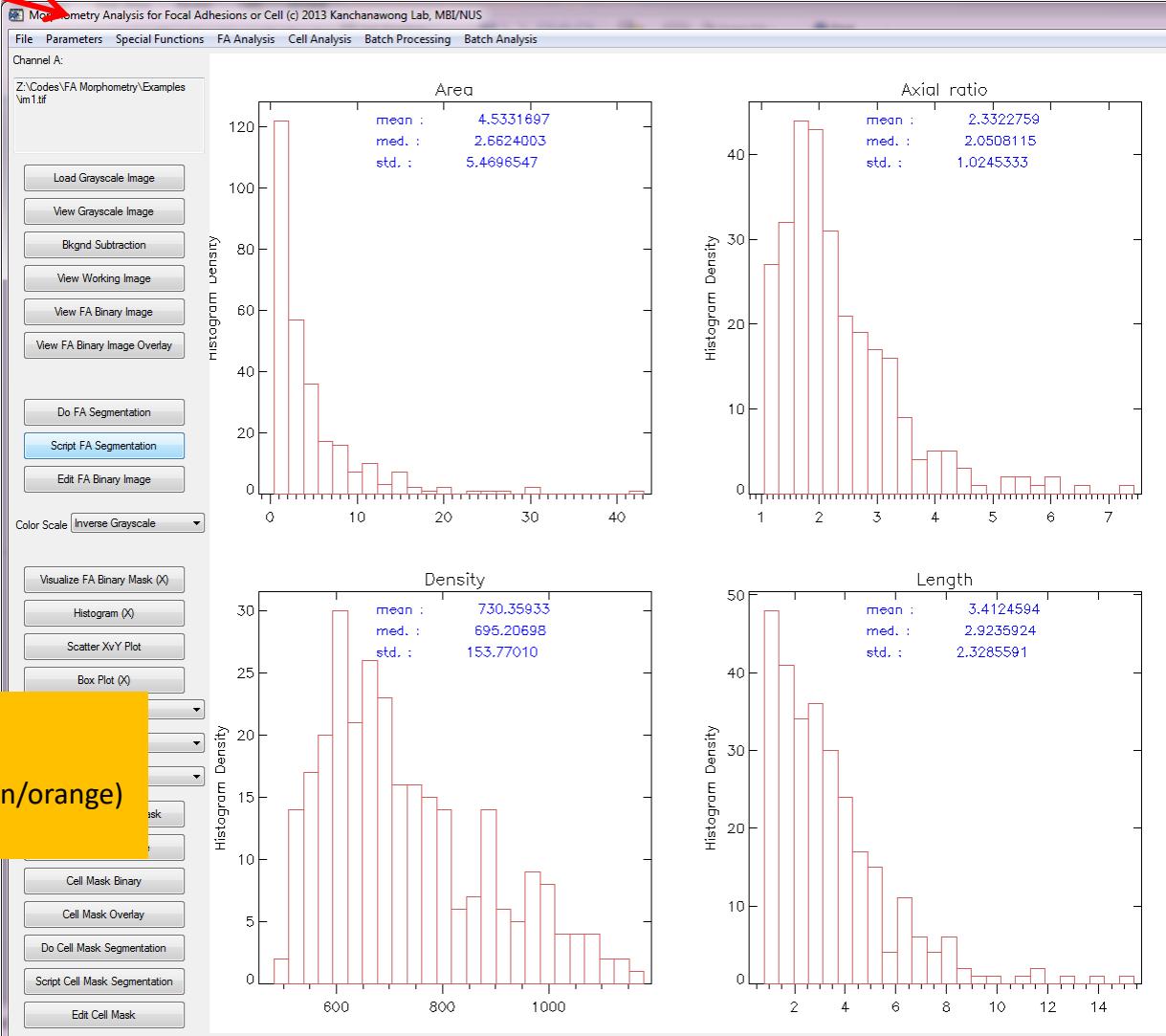
Analysis

Focal Adhesions or Cell (c) 2013 Kanchanawong Lab, MBI/NUS

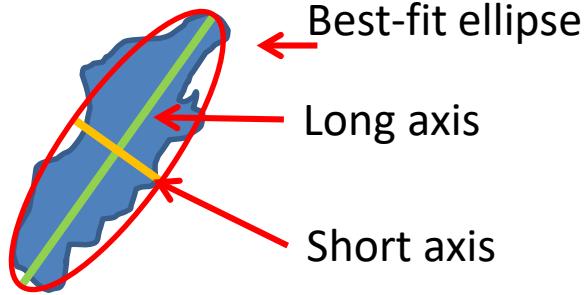
FA Analysis Cell Analysis Batch Processing Batch Analysis

- View Overlay with Indices
- View Overlay with Best Fit Ellipses
- Histogram: Area, Axial Ratio, Long Axis, Density
- Histogram: all properties (3x3)
- Boxplot: Area, Axial Ratio, Long Axis, Density
- Boxplot: all properties (3x3)
- Bar Graph (Area): nascent(<0.25) - mid-sized - large(>3)
- Bar Graph (Area): (0.1) - (0.1-0.25) - (0.25-1) - (1-4) - (>4)
- Rose plot: FA Orientation

Histogram of the FA properties



definition



Area: # of pixels x pixel size

Length: long axis of best-fit ellipse (green line)

Axial ratio: length of long axis / short axis (green/orange)

Density: Summed of all pixel values in FA/ Area

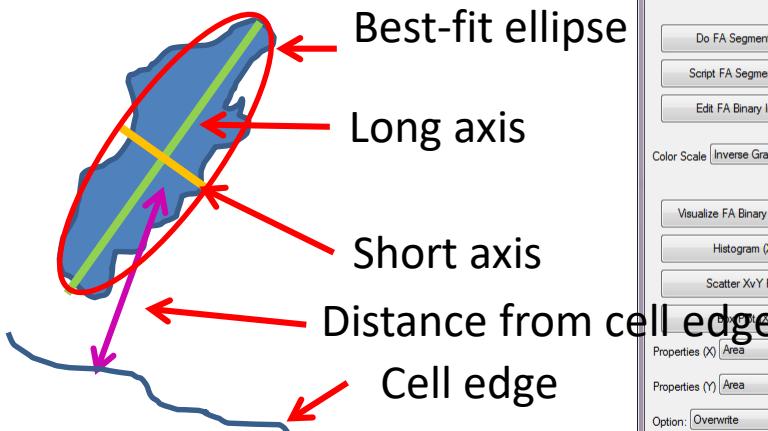
Analysis

Focal Adhesions or Cell (c) 2013 Kanchanawong Lab, MBI/NUS

FA Analysis Cell Analysis Batch Processing Batch Analysis

- [View Overlay with Indices](#)
- [View Overlay with Best Fit Ellipses](#)
- [Histogram: Area, Axial Ratio, Long Axis, Density](#)
- [Histogram: all properties \(3x3\)](#)
- [Boxplot: Area, Axial Ratio, Long Axis, Density](#)
- [Boxplot: all properties \(3x3\)](#)
- [Bar Graph \(Area\): nascent\(<0.25\) - mid-sized - large\(>3\)](#)
- [Bar Graph \(Area\): \(0.1\) - \(0.1-0.25\) - \(0.25-1\) - \(1-4\) - \(>4\)](#)
- [Rose plot: FA Orientation](#)

definition



Perimeter length: Length of the edge of FA
smooth FA mask: small perimeter length/area
Rough FA mask: large perimeter length/area

Orientation: Angle of long axis (currently in absolute terms)
 Will implement angle relative to cell edge if needed.

Morphometry Analysis for Focal Adhesions or Cell (c) 2013 Kanchanawong Lab, MBI/NUS

File Parameters Special Functions FA Analysis Cell Analysis Batch Processing Batch Analysis

Channel A:

Z:\Codes\FA Morphometry\Examples\Vm1.tif

Load Grayscale Image

View Grayscale Image

Bkgnd Subtraction

View Working Image

View FA Binary Image

View FA Binary Image Overlay

Do FA Segmentation

Script FA Segmentation

Edit FA Binary Image

Color Scale Inverse Grayscale

Visualize FA Binary Mask (X)

Histogram (X)

Scatter XvY Plot

Properties (X) Area

Properties (Y) Area

Option: Overwrite

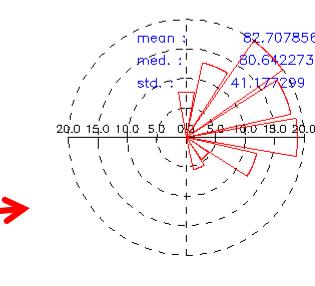
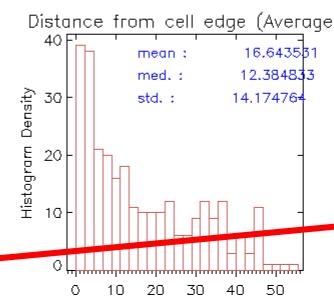
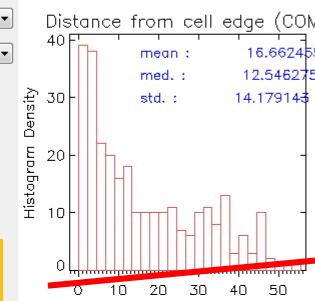
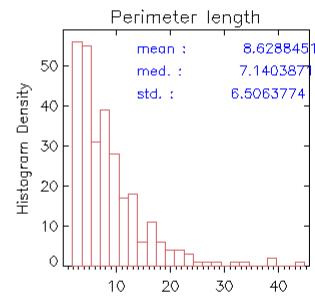
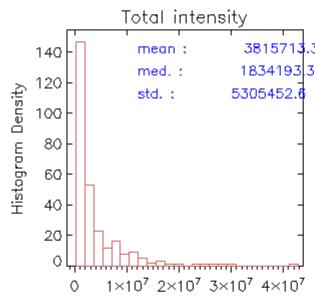
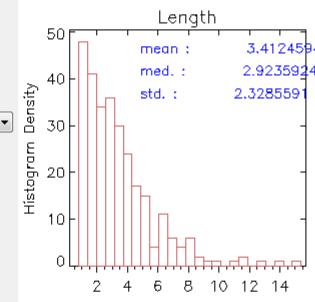
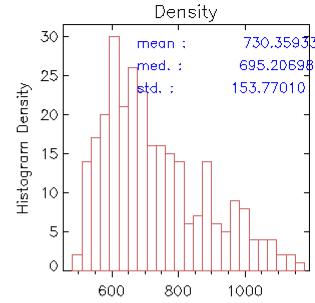
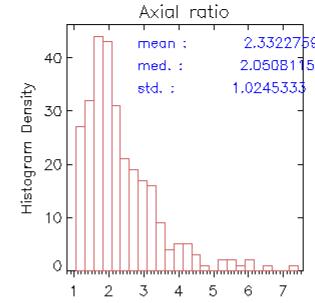
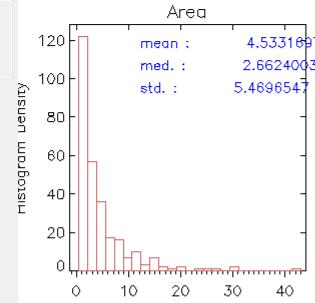
Load Image for Cell Mask

Cell Mask Grayscale

Cell Mask Binary

Cell Mask Overlay

Do Cell Mask Segmentation



Analysis

Thesions or Cell (c) 2013 Kanchanawong Lab, MBI/NUS

FA Analysis Cell Analysis Batch Processing Batch Analysis

View Overlay with Indices

View Overlay with Best Fit Ellipses

Histogram: Area, Axial Ratio, Long Axis, Density

Histogram: all properties (3x3)

Boxplot: Area, Axial Ratio, Long Axis, Density

Boxplot: all properties (3x3)

Bar Graph (Area): nascent(<0.25) - mid-sized - large(>3)

Bar Graph (Area): (0.1) - (0.1-0.25) - (0.25-1) - (1-4) - (>4)

Rose plot: FA Orientation

Bknd Subtraction

View Working Image

View FA Binary Image

View FA Binary Image Overlay

Do FA Segmentation

Script FA Segmentation

Edit FA Binary Image

Color Scale Inverse Grayscale

Visualize FA Binary Mask (X)

Histogram (X)

Scatter XvY Plot

Box Plot (X)

Properties (X) Area

Properties (Y) Area

Option: Overwrite

Load Image for Cell Mask

Cell Mask Grayscale

Cell Mask Binary

Cell Mask Overlay

Do Cell Mask Segmentation

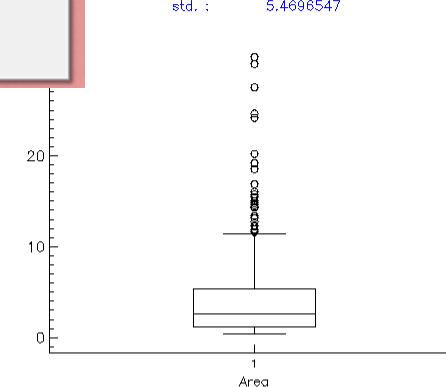
Script Cell Mask Segmentation

Edit Cell Mask

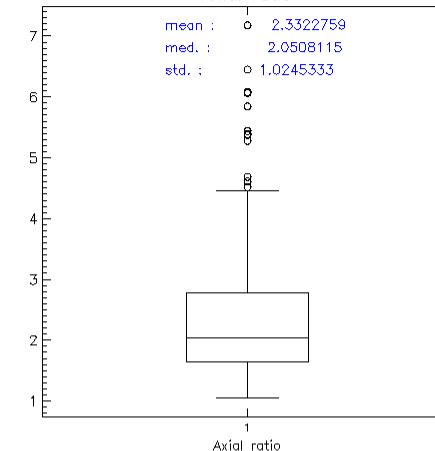
Distribution of Properties shown as box plot

© 2013 Kanchanawong Lab, MBI/NUS
Cell Analysis Batch Processing Batch Analysis

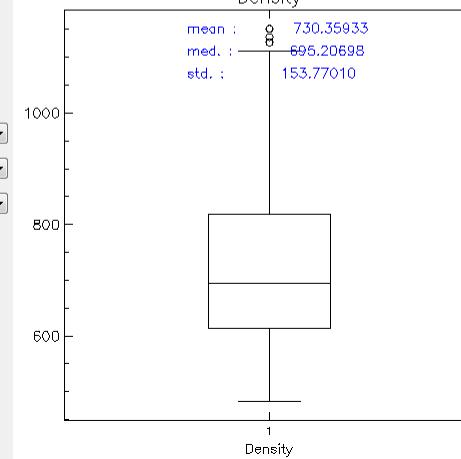
Area
mean : 4.5331897
med. : 2.6624003
std. : 5.4696547



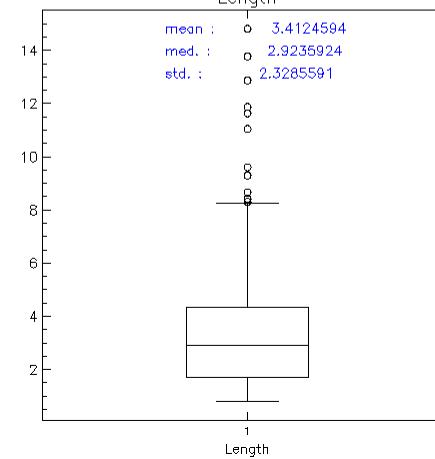
Axial ratio
mean : 2.3322759
med. : 2.0508115
std. : 1.0245333



Density
mean : 730.35933
med. : 695.20698
std. : 153.77010



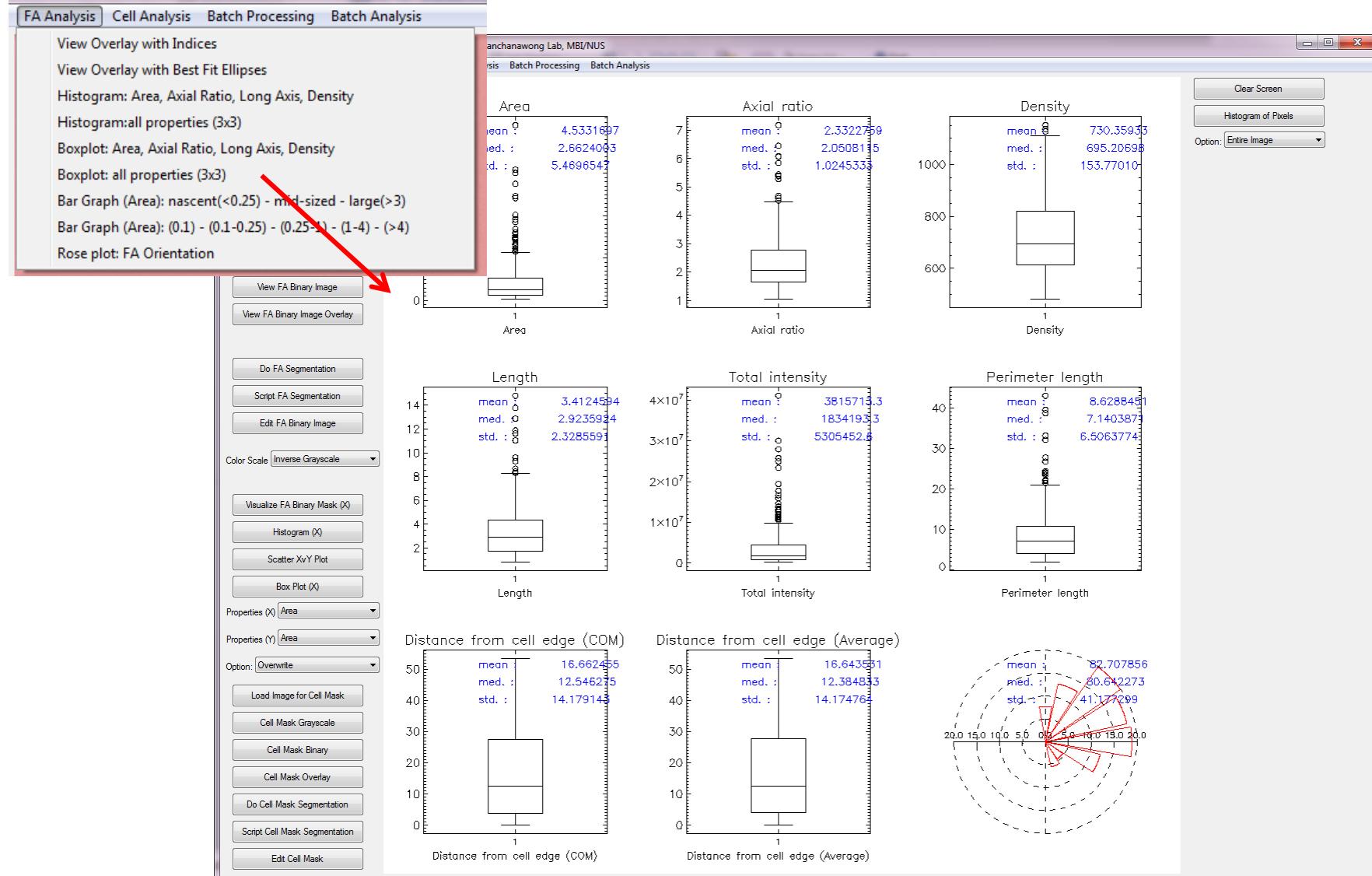
Length
mean : 3.4124594
med. : 2.9235924
std. : 2.3285591



Clear Screen
Histogram of Pixels
Option: Entire Image

Analysis

Thesions or Cell (c) 2013 Kanchanawong Lab, MBI/NUS



Analysis

Adhesions or Cell (c) 2013 Kanchanawong Lab, MBI/NUS

FA Analysis Cell Analysis Batch Processing Batch Analysis

View Overlay with Indices

View Overlay with Best Fit Ellipses

Histogram: Area, Axial Ratio, Long Axis, Density

Histogram: all properties (3x3)

Boxplot: Area, Axial Ratio, Long Axis, Density

Boxplot: all properties (3x3)

Bar Graph (Area): nascent(<0.25) - mid-sized - large(>3)

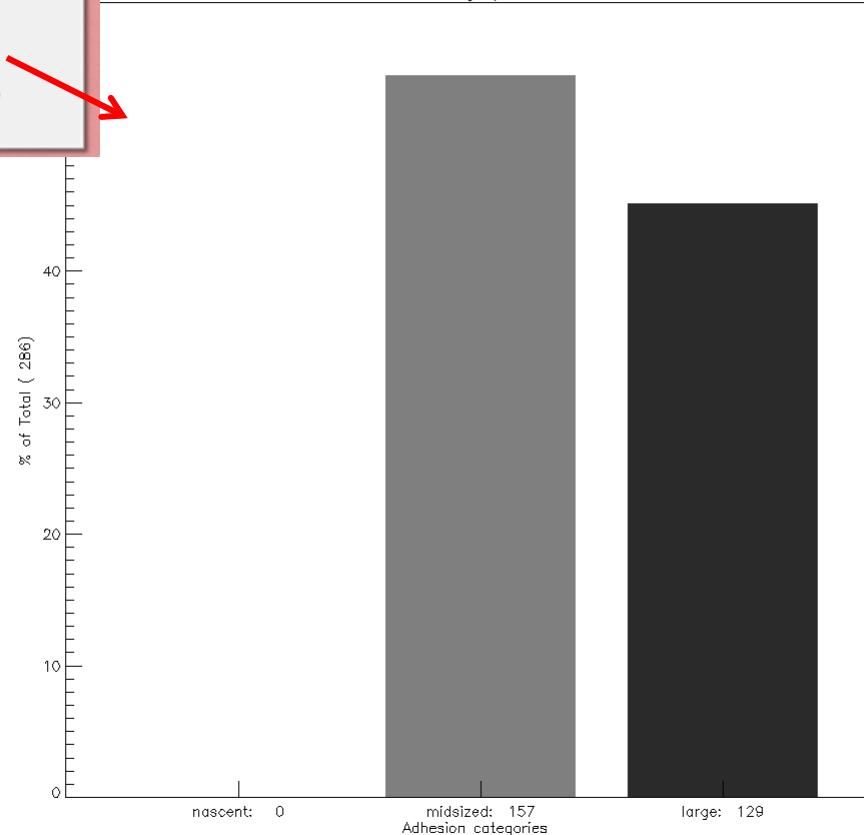
Bar Graph (Area): (0.1) - (0.1-0.25) - (0.25-1) - (1-4) - (>4)

Rose plot: FA Orientation

Kanchanawong Lab, MBI/NUS
Batch Processing Batch Analysis

Categorization of FA by size (3 bins)

Clear Screen
Histogram of Pixels
Option: Entire Image



View FA Binary Image
View FA Binary Image Overlay

Do FA Segmentation
Script FA Segmentation
Edit FA Binary Image

Color Scale: Inverse Grayscale

Visualize FA Binary Mask (X)
Histogram (X)
Scatter XvY Plot
Box Plot (X)

Properties (X): Area
Properties (Y): Area
Option: Overwrite

Load Image for Cell Mask
Cell Mask Grayscale
Cell Mask: Binary
Cell Mask Overlay
Do Cell Mask Segmentation
Script Cell Mask Segmentation
Edit Cell Mask

Analysis

Adhesions or Cell (c) 2013 Kanchanawong Lab, MBI/NUS

FA Analysis Cell Analysis Batch Processing Batch Analysis

- View Overlay with Indices
- View Overlay with Best Fit Ellipses
- Histogram: Area, Axial Ratio, Long Axis, Density
- Histogram: all properties (3x3)
- Boxplot: Area, Axial Ratio, Long Axis, Density
- Boxplot: all properties (3x3)
- Bar Graph (Area): nascent(<0.25) - mid-sized - large(>3)
- Bar Graph (Area): (0.1) - (0.1-0.25) - (0.25-1) - (1-4) - (>4)
- Rose plot: FA Orientation

Bkgnd Subtraction
View Working Image
View FA Binary Image
View FA Binary Image Overlay

Do FA Segmentation
Script FA Segmentation
Edit FA Binary Image

Color Scale Inverse Grayscale

Visualize FA Binary Mask (X)

Histogram (X)

Scatter XvY Plot

Box Plot (X)

Properties (X) Area

Properties (Y) Area

Option: Overwrite

Load Image for Cell Mask

Cell Mask Grayscale

Cell Mask Binary

Cell Mask Overlay

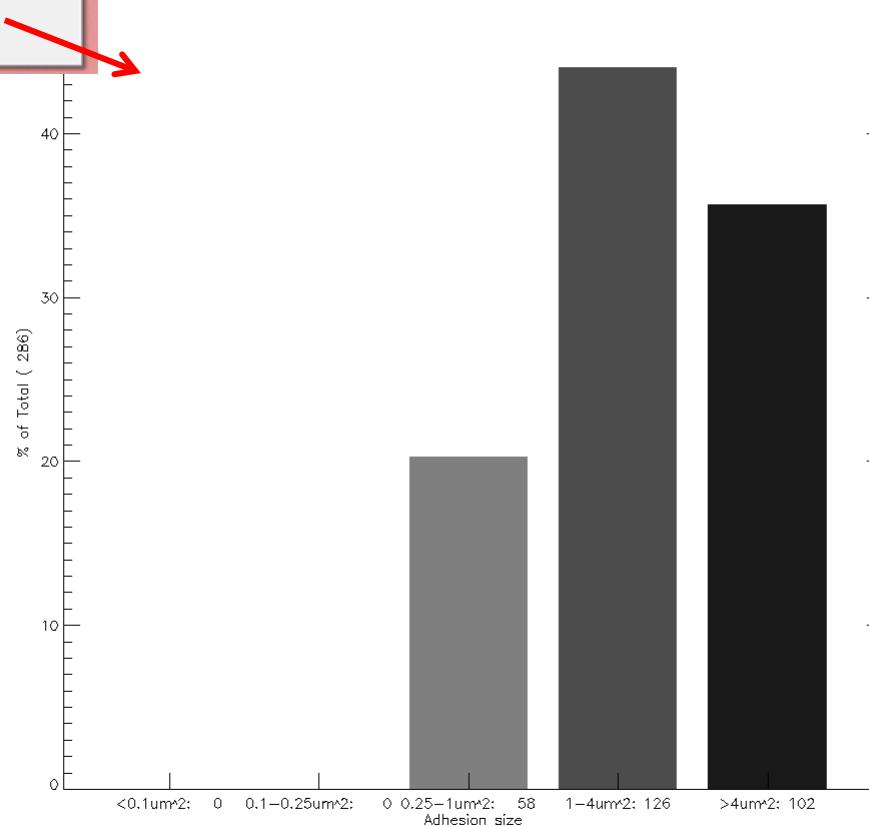
Do Cell Mask Segmentation

Script Cell Mask Segmentation

Edit Cell Mask

Categorization of FA by size (5 bins)

Adhesion size distribution



Clear Screen
Histogram of Pixels
Option Entire Image

Analysis

Thesions or Cell (c) 2013 Kanchanawong Lab, MBI/NUS

FA Analysis Cell Analysis Batch Processing Batch Analysis

- View Overlay with Indices
- View Overlay with Best Fit Ellipses
- Histogram: Area, Axial Ratio, Long Axis, Density
- Histogram: all properties (3x3)
- Boxplot: Area, Axial Ratio, Long Axis, Density
- Boxplot: all properties (3x3)
- Bar Graph (Area): nascent(<0.25) - mid-sized - large(>3)
- Bar Graph (Area): (0.1) - (0.1-0.25) - (0.25-1) - (1-4) - (>4)
- Rose plot: FA Orientation

View Grayscale Image

Bknd Subtraction

View Working Image

View FA Binary Image

View FA Binary Image Overlay

Do FA Segmentation

Script FA Segmentation

Edit FA Binary Image

Color Scale Inverse Grayscale

Visualize FA Binary Mask (X)

Histogram (X)

Scatter XvY Plot

Box Plot (X)

Properties (X) Area

Properties (Y) Area

Option: Overwrite

Load Image for Cell Mask

Cell Mask Grayscale

Cell Mask Binary

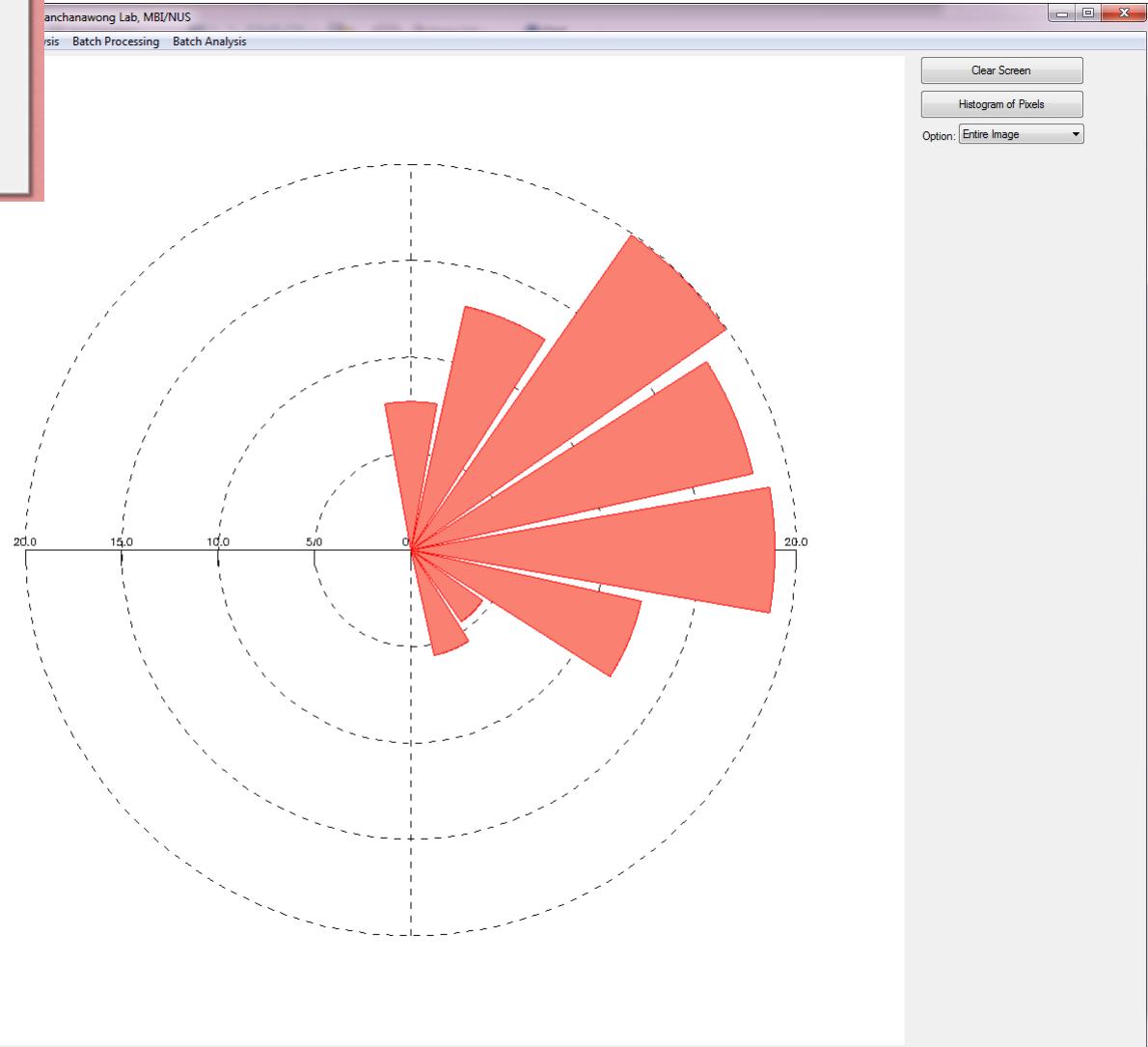
Cell Mask Overlay

Do Cell Mask Segmentation

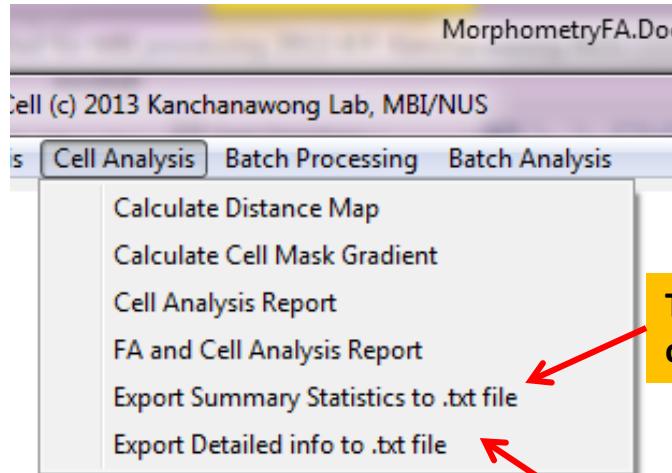
Script Cell Mask Segmentation

Edit Cell Mask

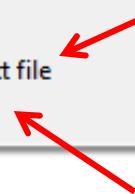
Distribution of FA orientation



Analysis



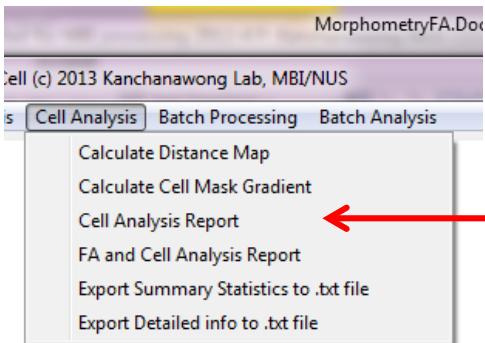
To export the summary statistics to .txt file (for opening in Excel or other graphing program)



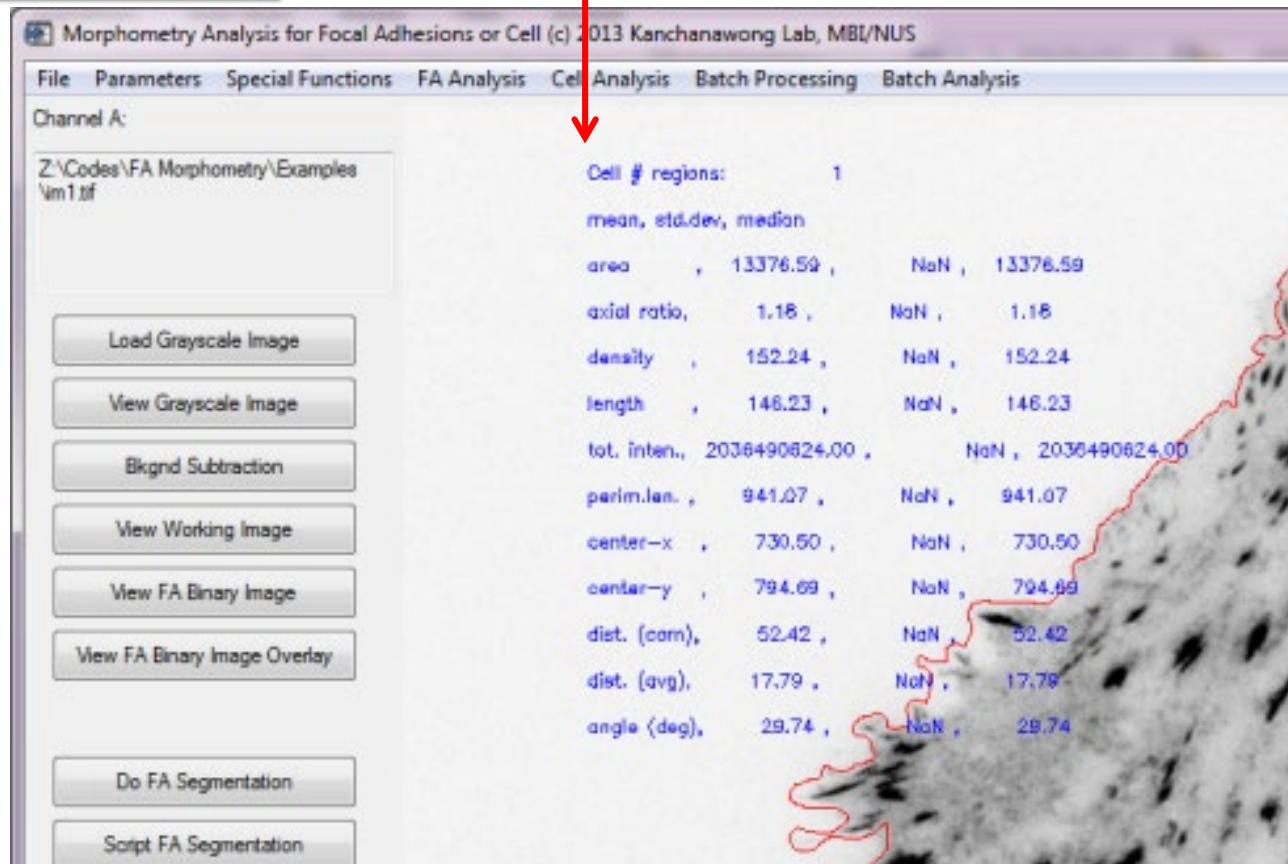
To export the detailed properties of every FA region to .txt file (for opening in Excel or other graphing program)



Analysis



To view properties of Cell mask, e.g. Cell Area, Cell axial ratio etc.



Batch Mode

Acquire images on the microscope,
make sure to note **objective**,
magnification & **camera pixel size**



Batch mode

Organize the images (single
channel) into folder:
e.g. One condition per folder



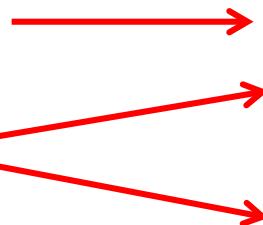
Create **FA mask** or **Cell mask** or
both, either **manually** or by using a
script



Save in ***morph.sav** file



Calculate statistics, analyze FA or
cell properties or create
visualization

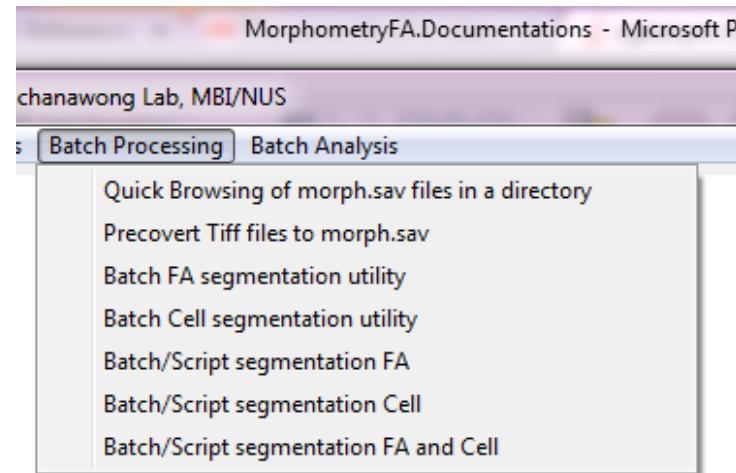


Batch Mode

Organize the images (single channel) into folder:
e.g. One condition per folder

Then

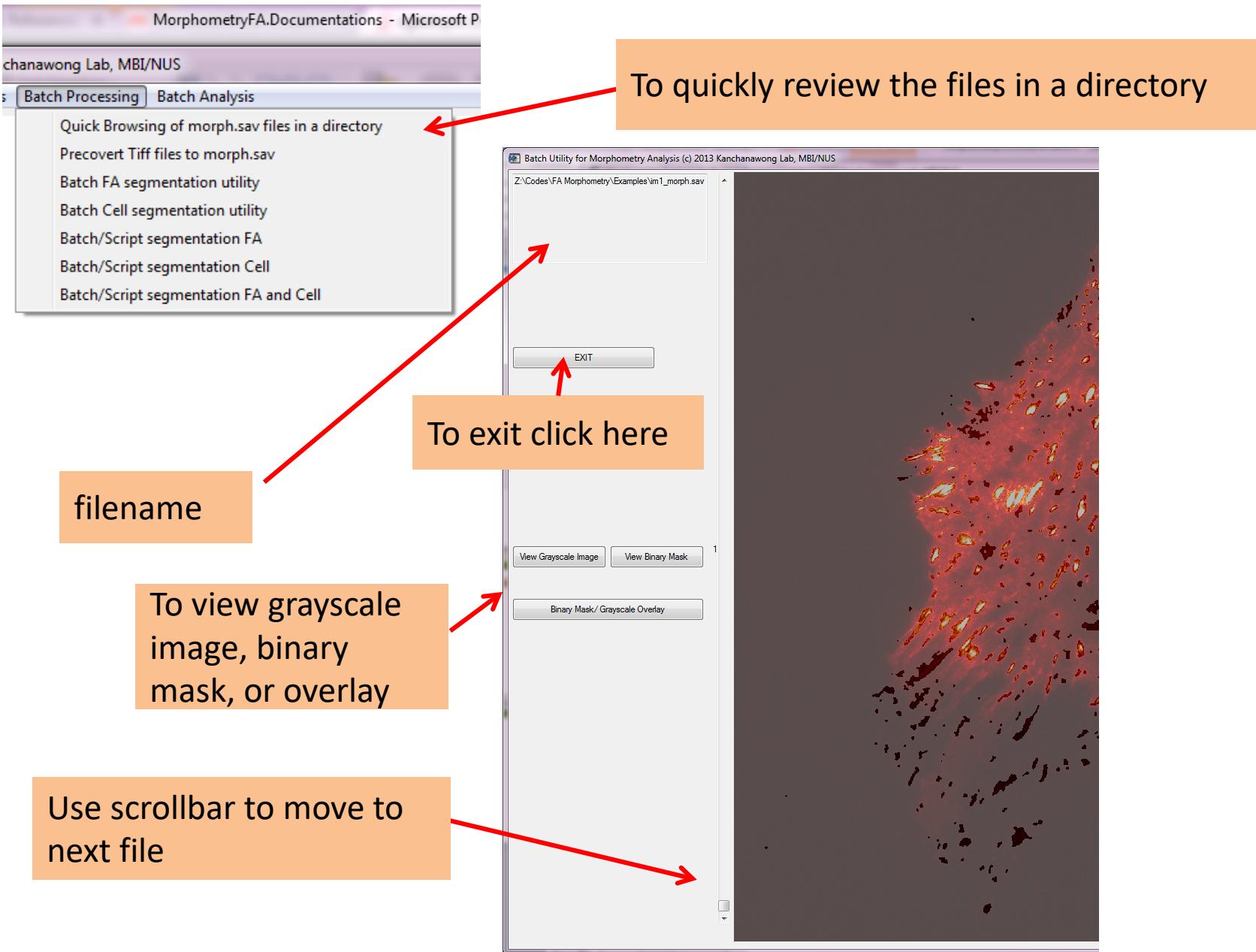
This will look at all .tif files in the folder and create *morph.sav file with the same prefix



For example:

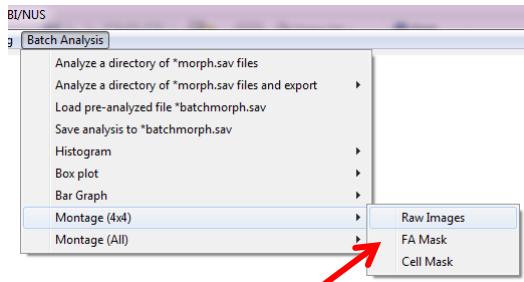
ABC_1.tif → ABC_1_morph.sav
DEF_2.tif → DEF_2_morph.sav
GHI_3.tif → HGI_3_morph.sav

Batch Mode

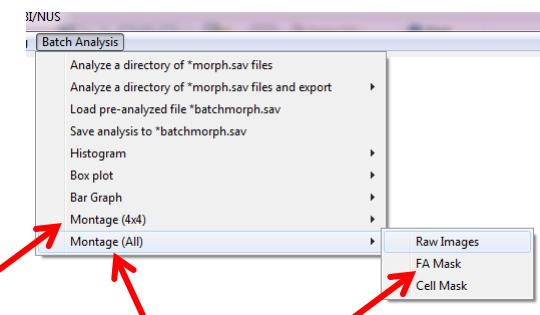
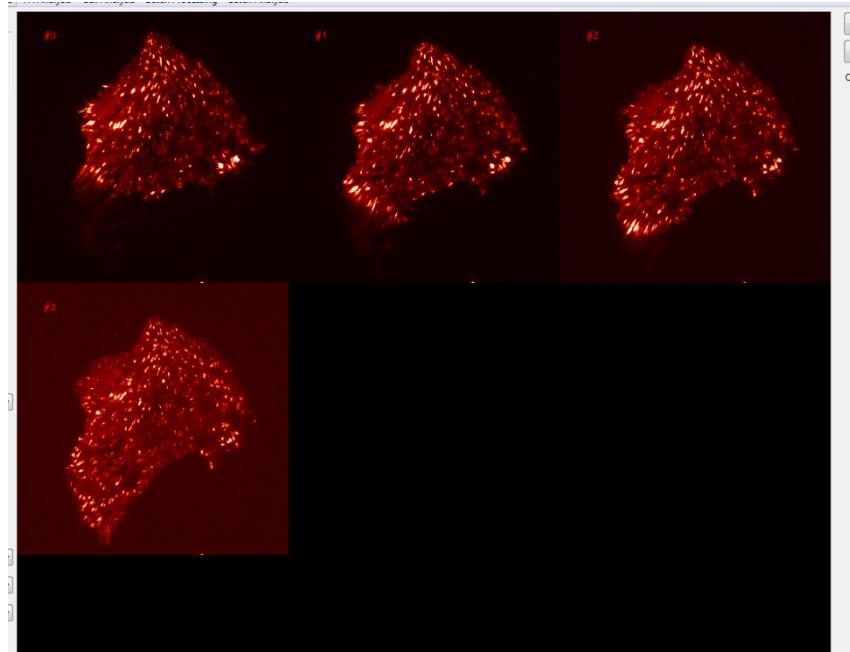


Batch Mode

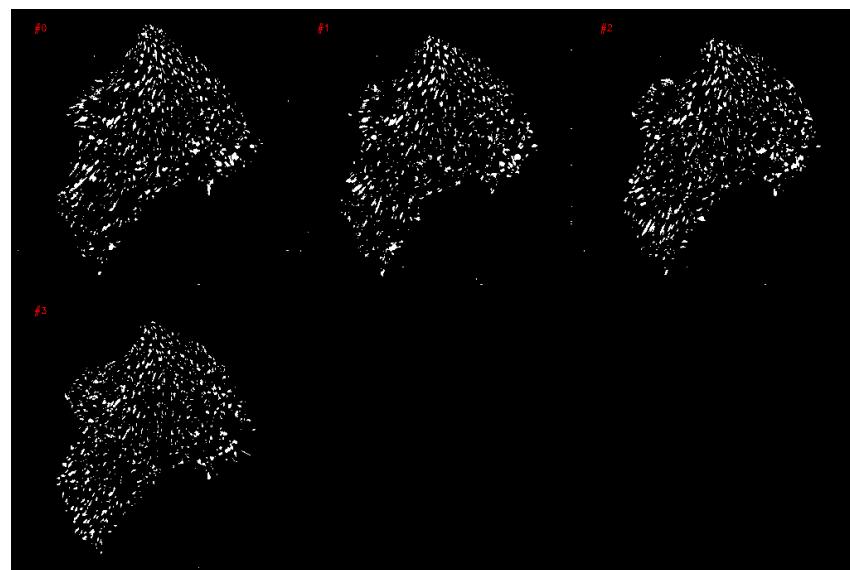
Another method for quick review is to see the image side by side as montage



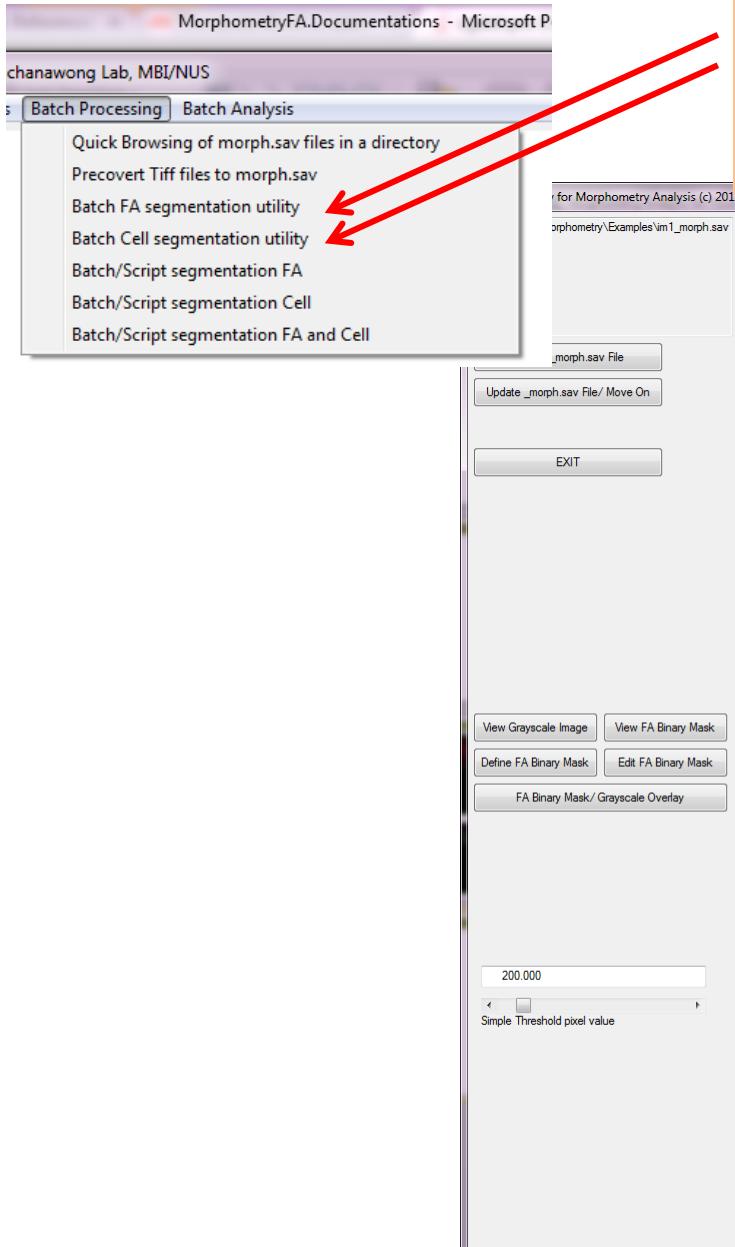
Either Raw image,
FA mask, or cell
mask can be
chosen



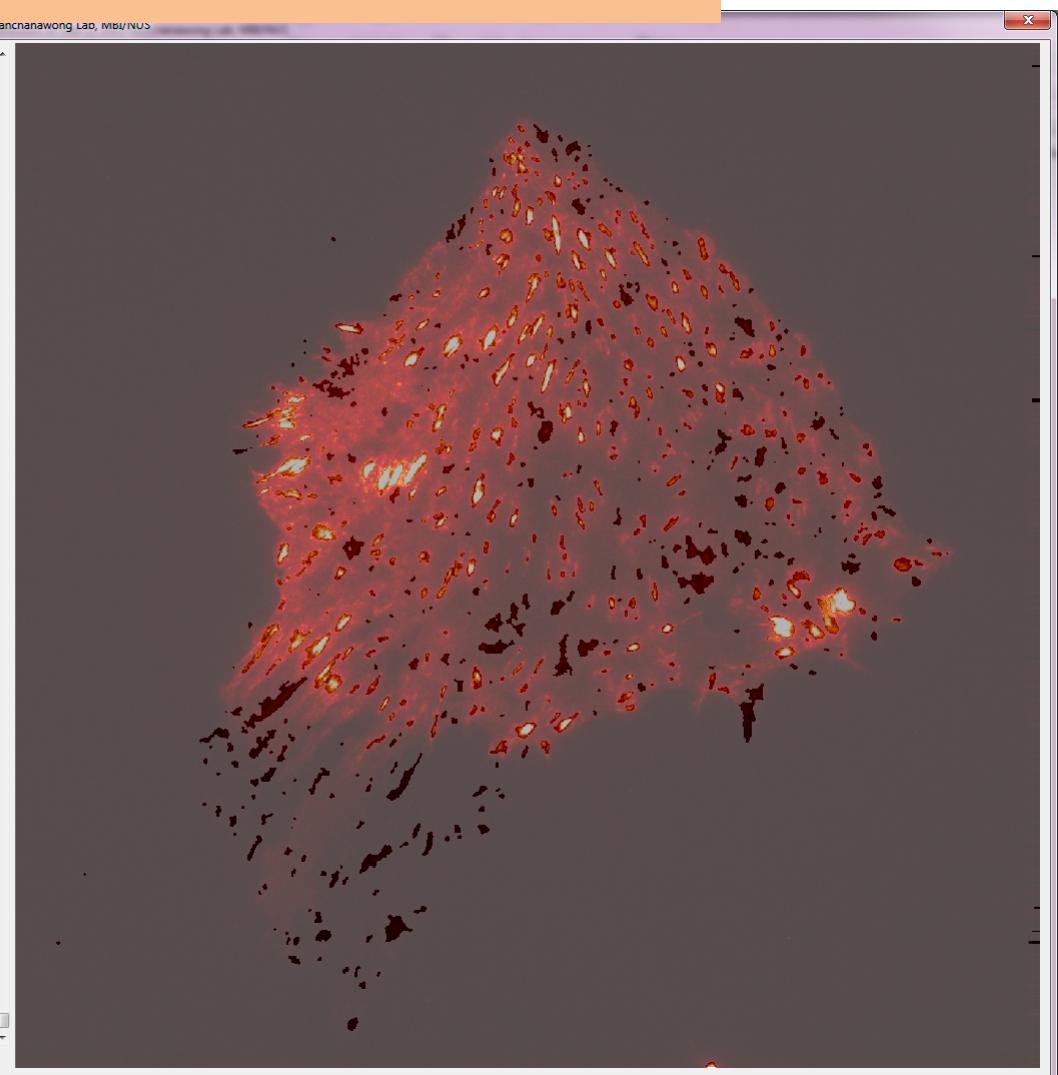
4x4 option shows 16
files at a time. All
options show all files
in one screen



Batch Mode

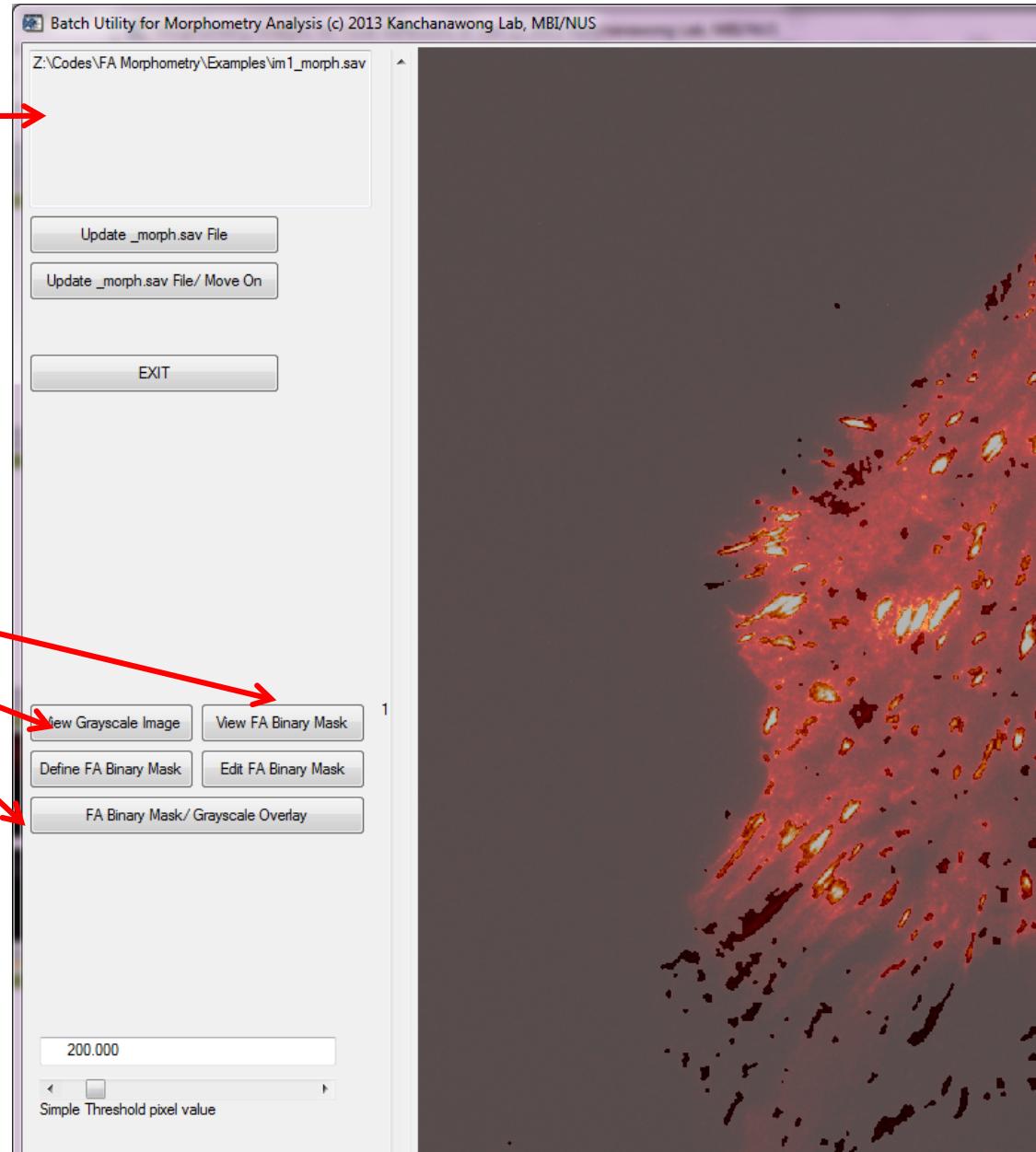


FA mask or Cell mask can be segmented one by one using the Batch Segmentation Utility



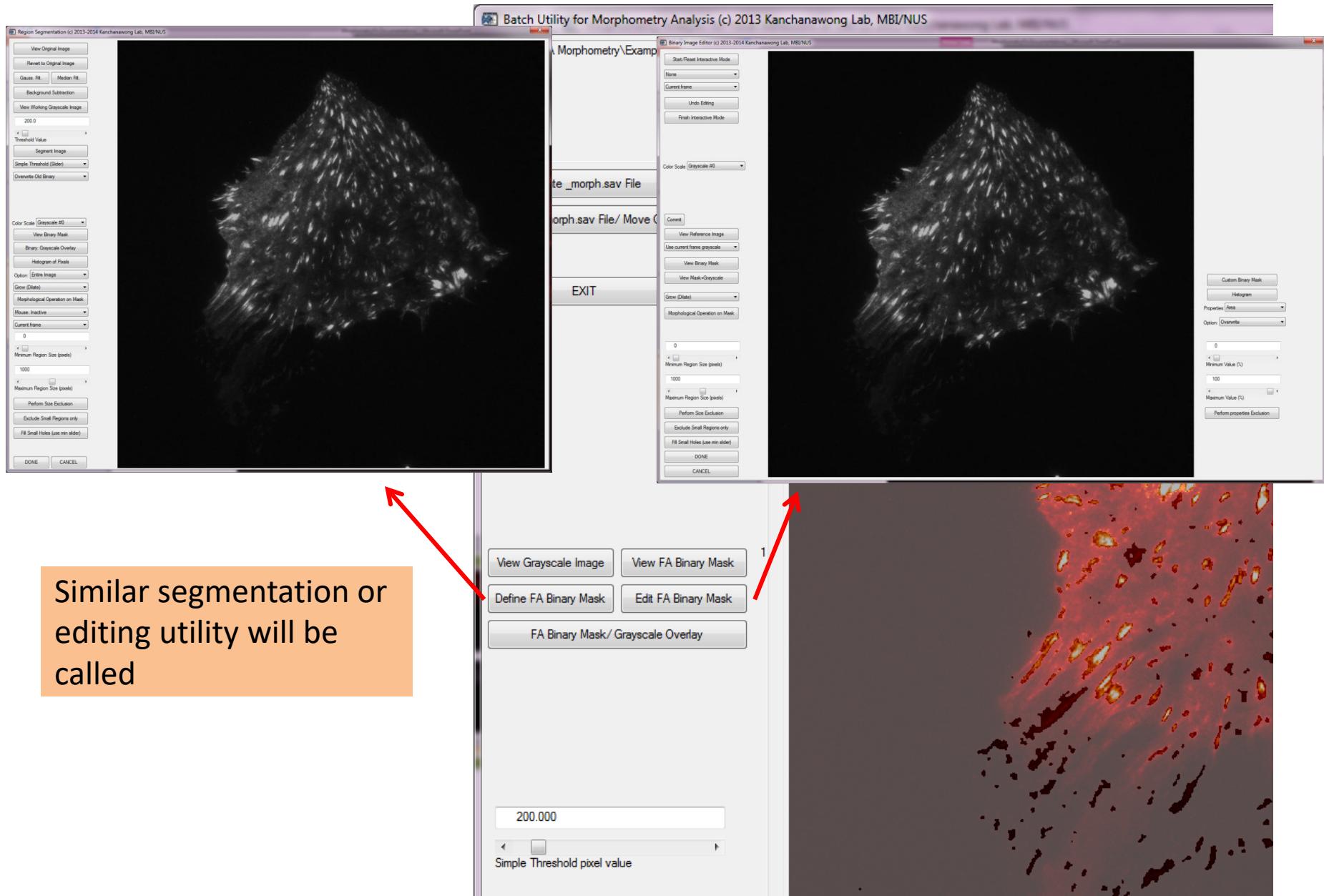
Batch Mode

Current File being displayed



To view grayscale image, binary mask, or overlay

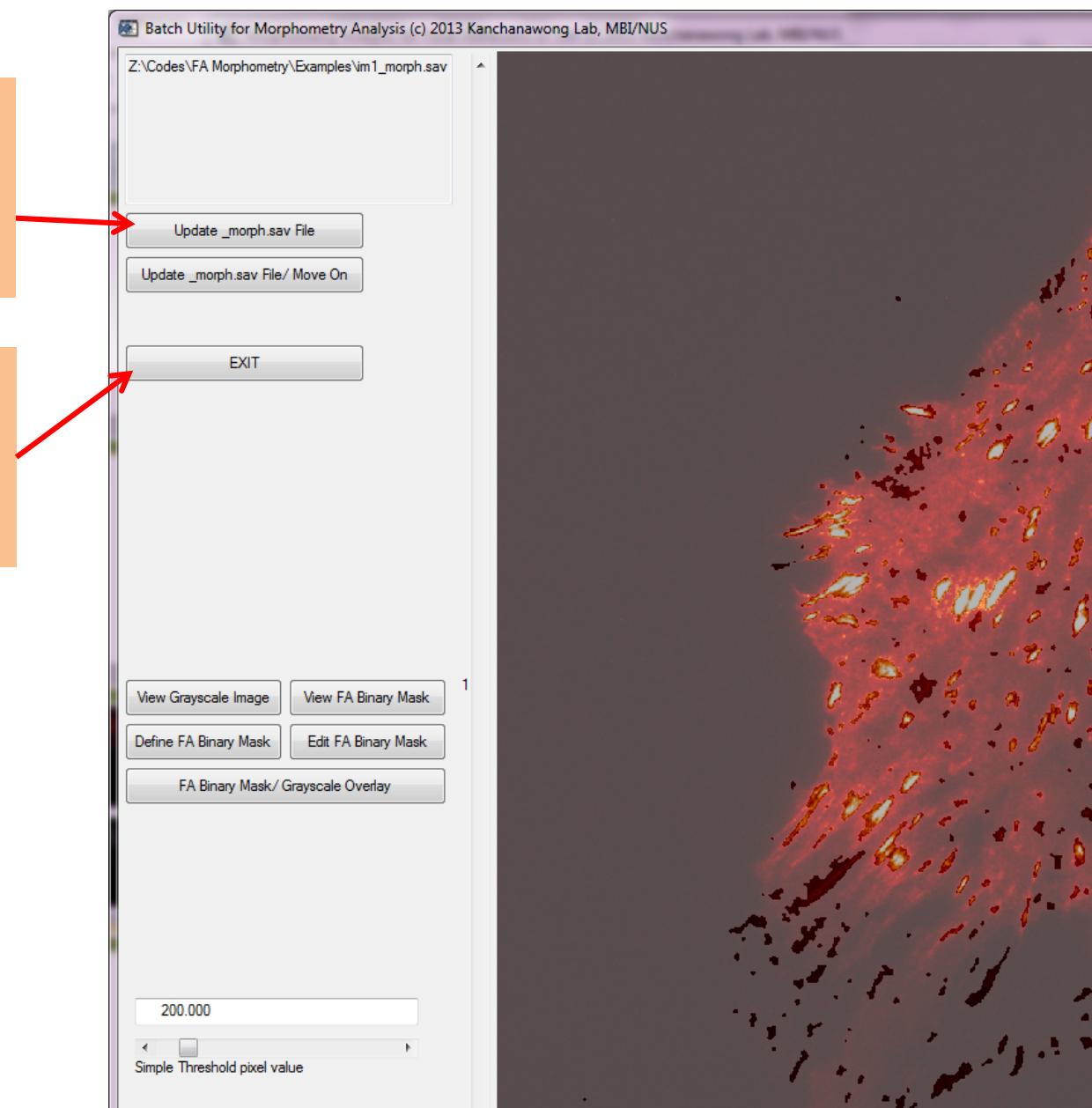
Batch Mode



Batch Mode

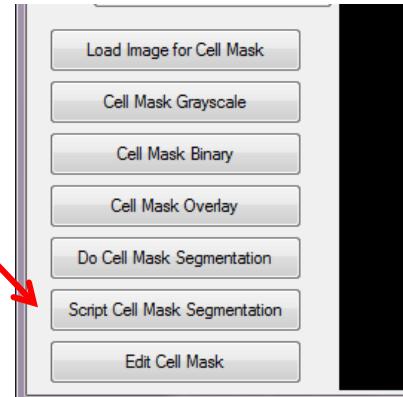
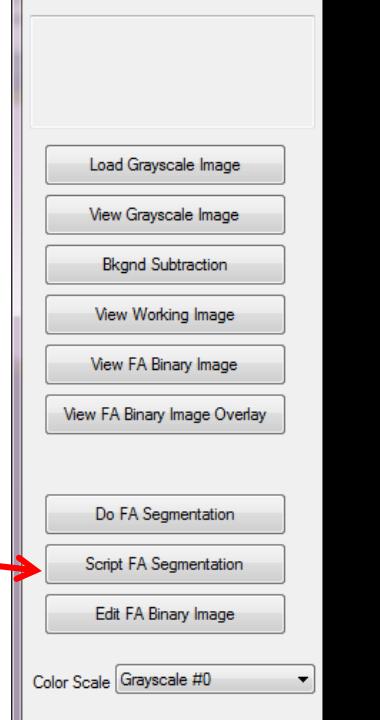
Once the mask is created,
make sure to save it. (i.e.
**Do not scroll to other file
before saving)**

To save and automatically
scroll to the next file

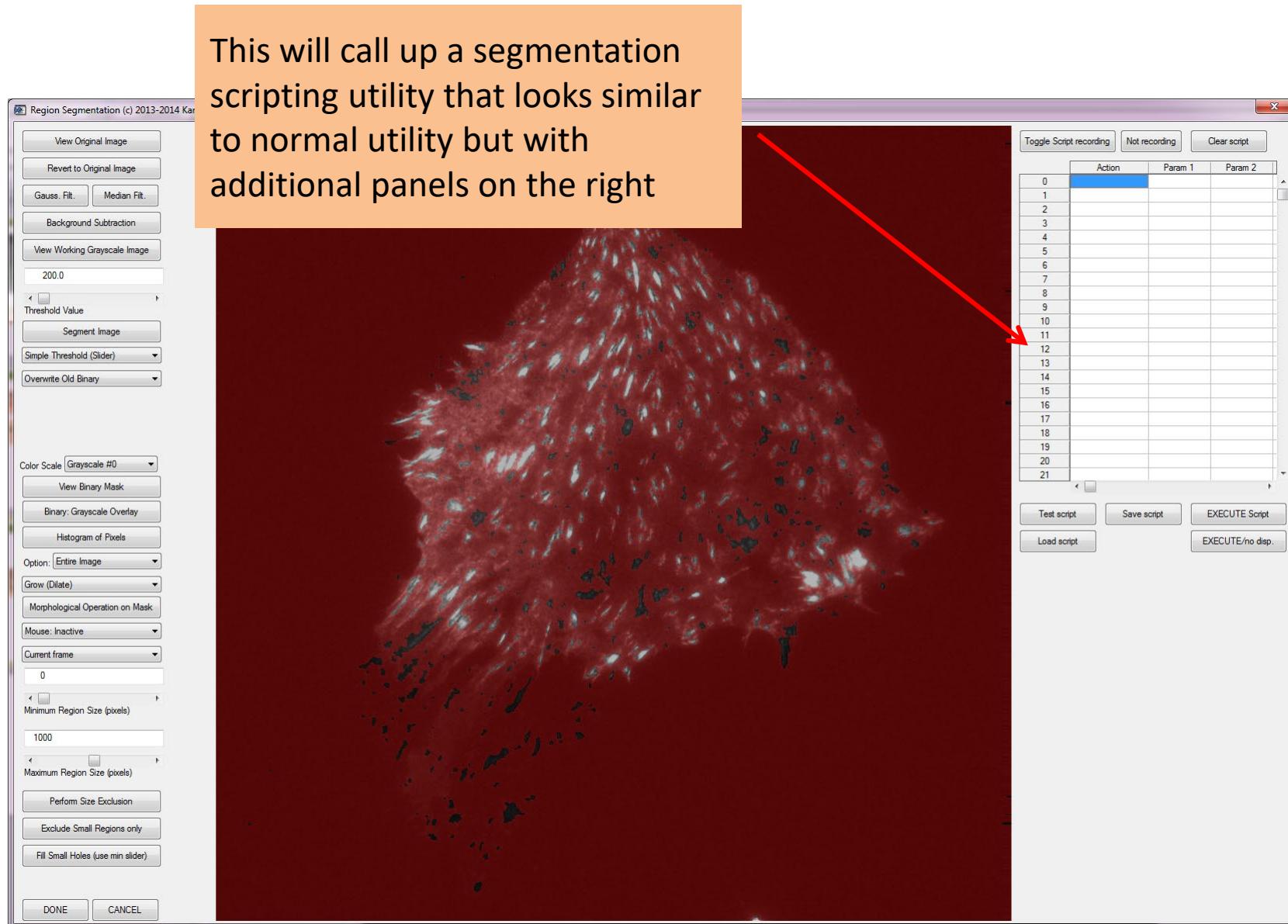


Batch Mode

To speed up processing of large number of files, the script for FA or cell segmentation can be created

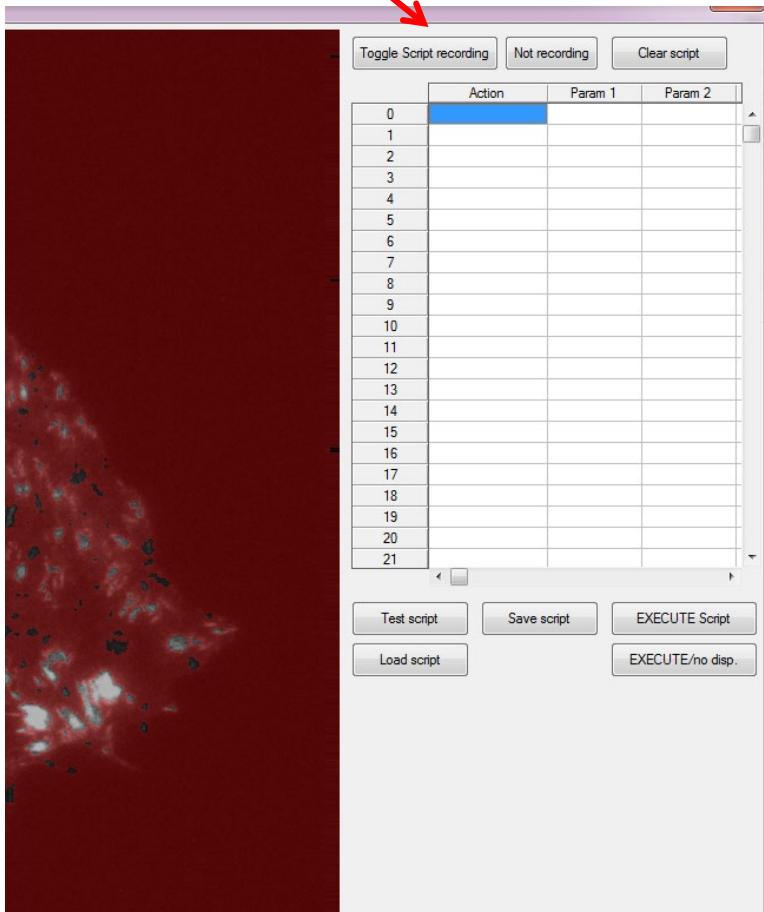


Batch Mode

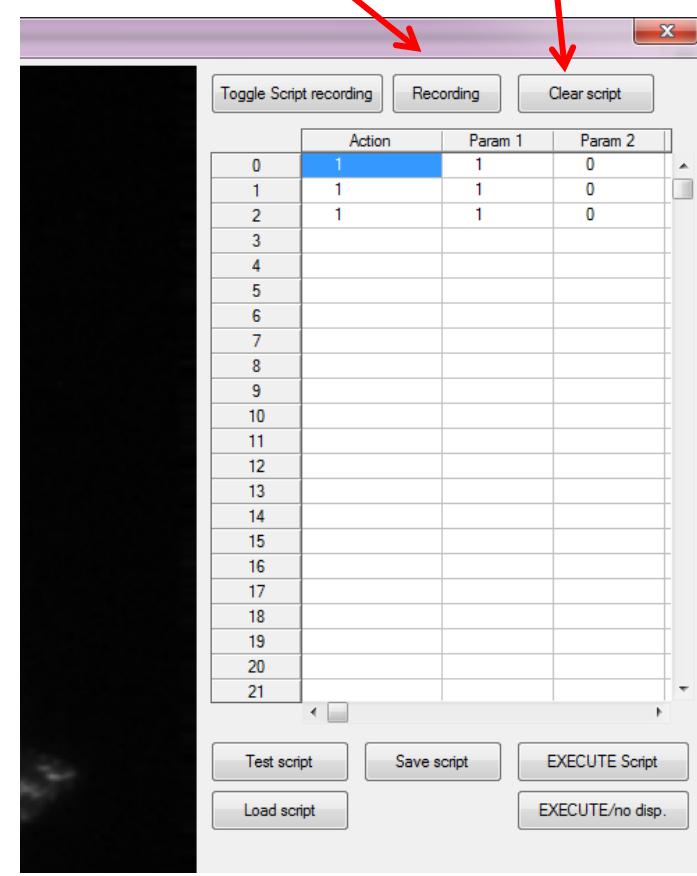


Batch Mode

Click here to toggle
between recording and
not recording

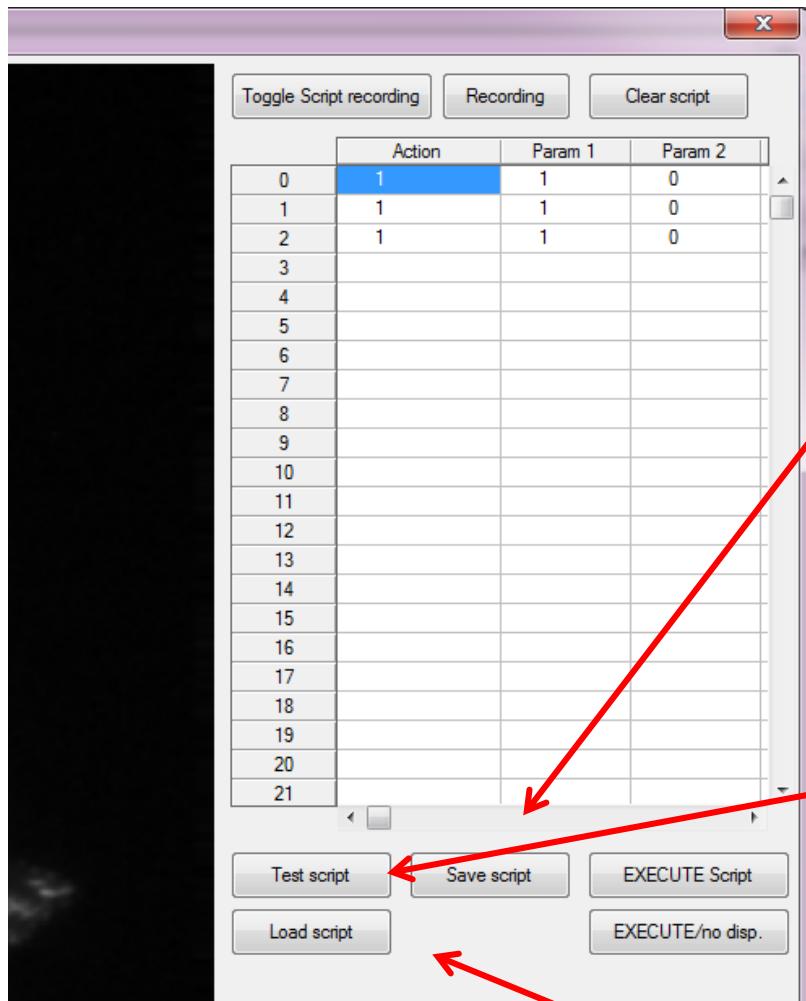


In recording mode,
each step will be
recorded



To clear the
script

Batch Mode

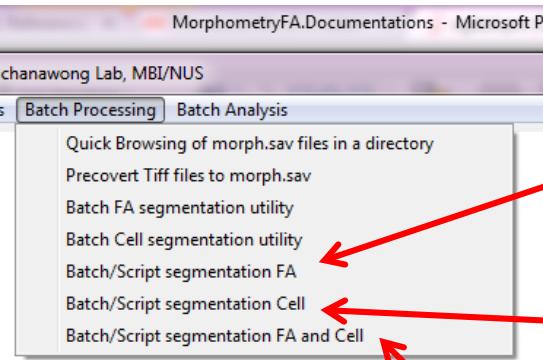


Once the desired outcome
is obtained, the script can
be saved as ***script.sav**

Click here to test the script
on the image

Click here to load previous
save script

Batch Mode



With the scripts file saved, the script can be applied to all files in a folder.

To segment for **FA mask** for all files in a folder

To segment for **cell mask** for all files in a folder

To segment for both **FA** and **cell mask** for all files in a folder

This can take several minutes or longer depending on the number of files

IMPORTANT. Note that the script is unlikely to be perfect. Make sure to manually inspect for qualities of the mask, and to remove artifacts such as areas around the edge etc. , using the tools described earlier before proceeding to further analysis.

Batch Mode

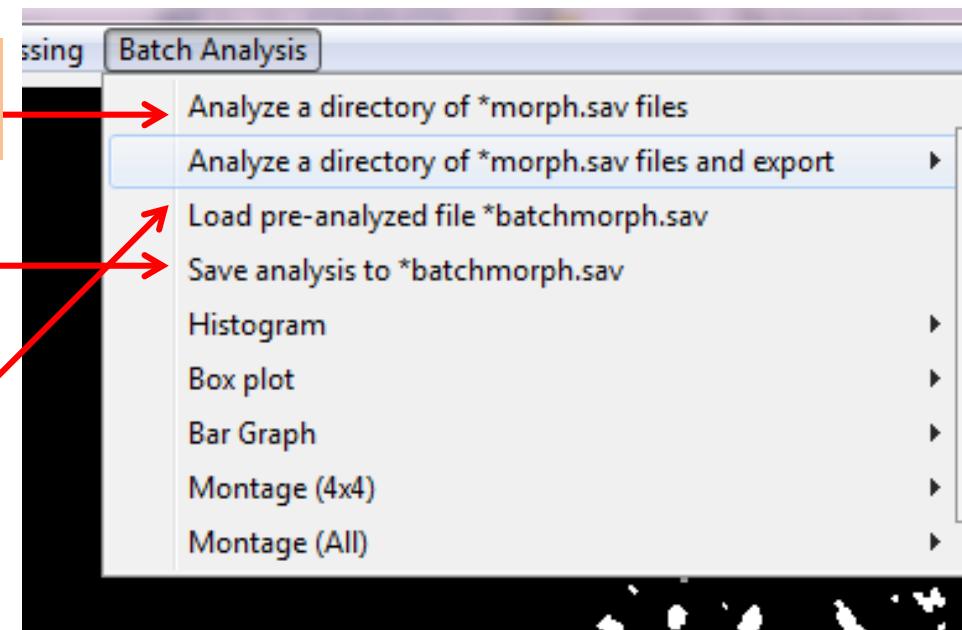
Once the proper mask has been defined, all the *morph.sav files in a folder can be analyzed as a batch.

There are multiple output option for the analysis

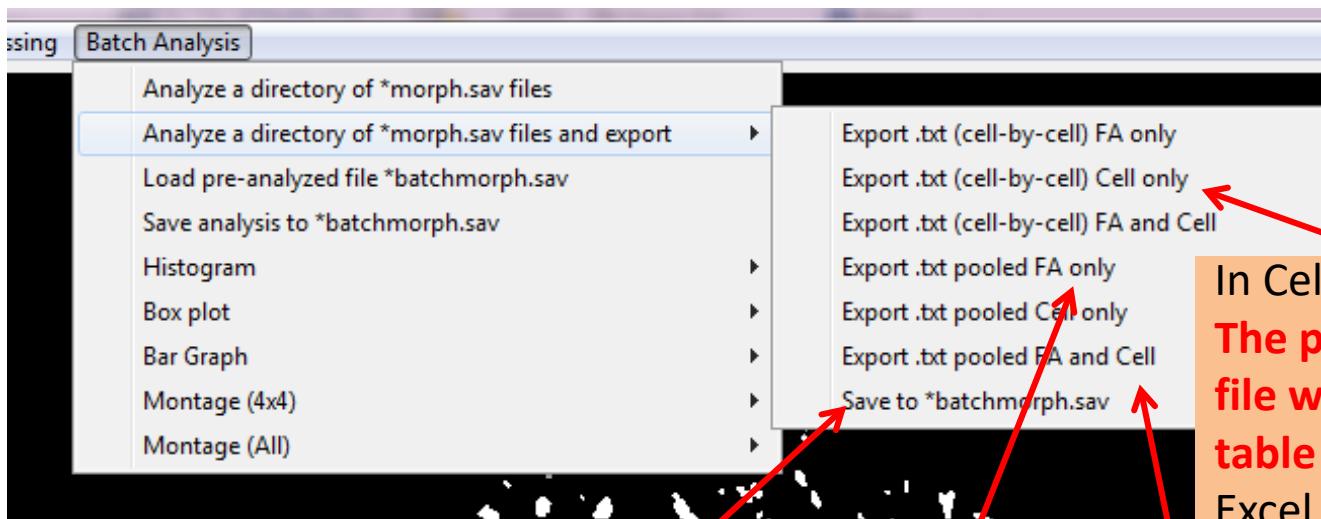
Analyze the batch and keep results in memory

Save the analysis results in memory to a file
(*batchmorph.sav)

Load previously saved analysis results (*batchmorph.sav) to memory



Batch Mode



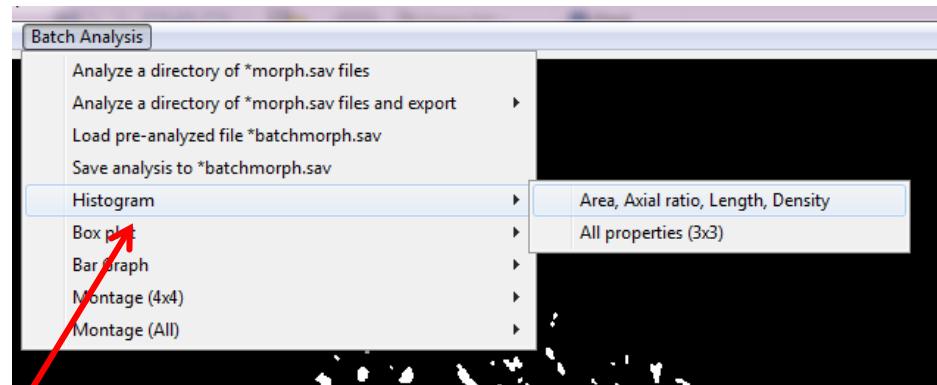
Analyze and save results in
(*batchmorph.sav) file

In pooled mode,
**The properties will be pooled
together in one table**
and exported as .txt file for Excel
or other graphing program

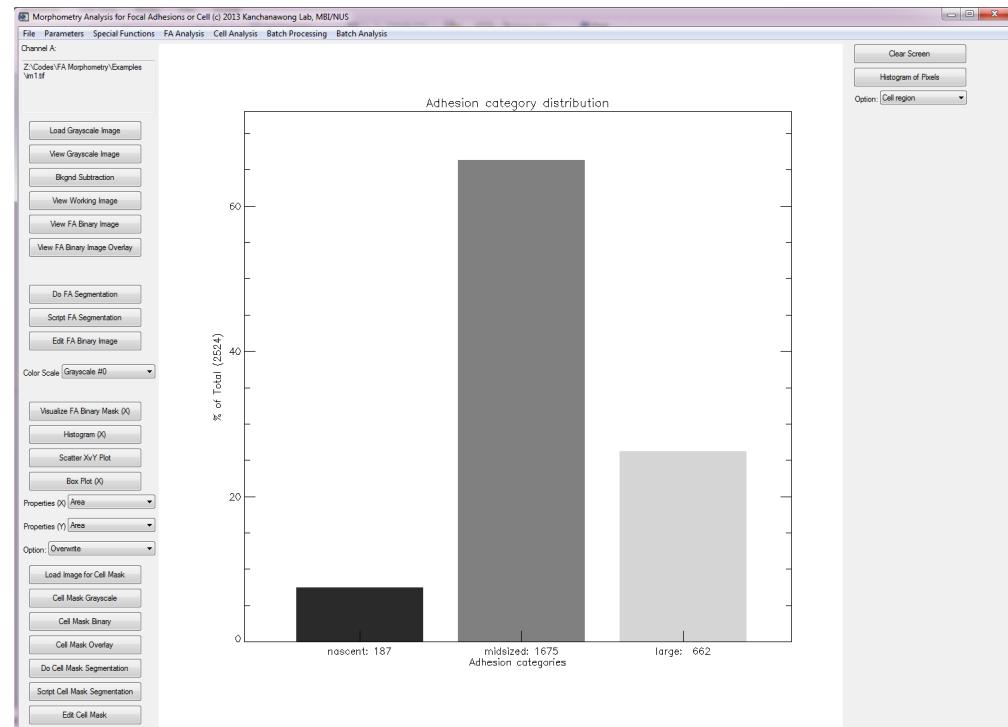
In Cell-by-cell mode,
**The properties belonging to each
file will be listed in separate
table** and exported as .txt file for
Excel or other graphing program

There's the option of FA only, Cell
only or FA and Cell, in case where
only one type of mask or both
types of masks are defined.

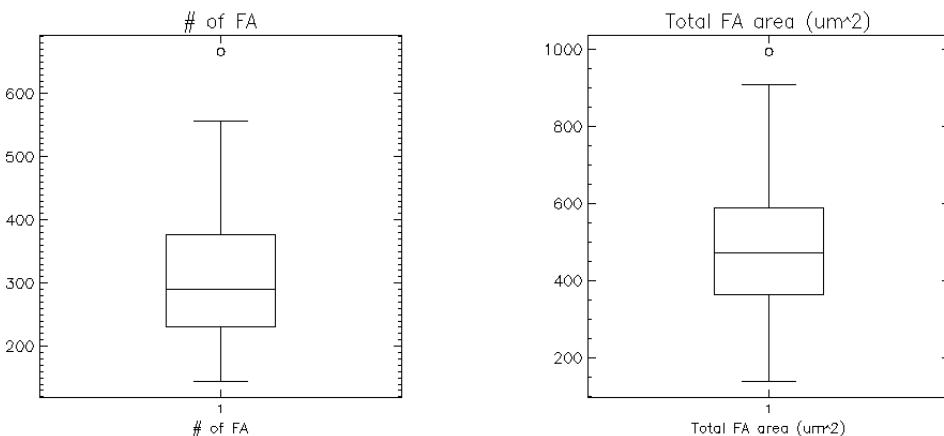
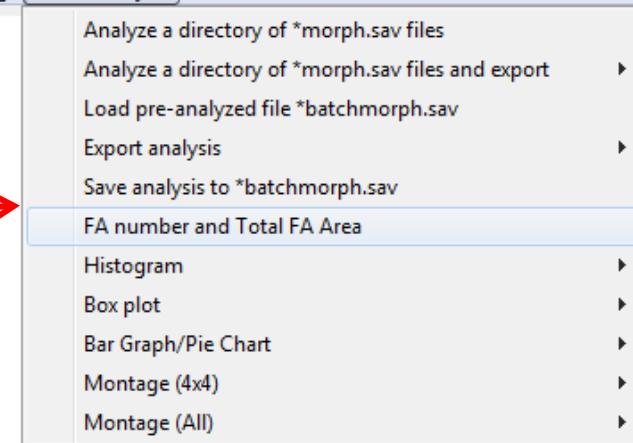
Batch Mode



Similar types of histogram, boxplot or bar graphs can be created for the pooled data set



To view number of FA per file (in this case presumably each file should have only one cell being segmented). And total FA area per file (i.e. cell)



#FA total:10704.000

mean : 324.36364

med. : 291.00000

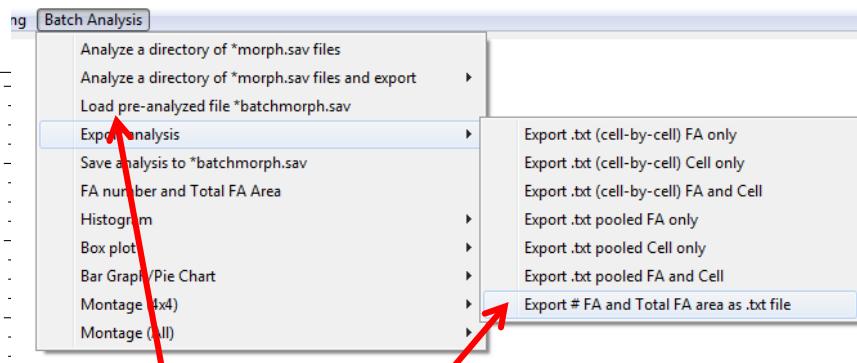
std. : 132.73112

Total Area:33

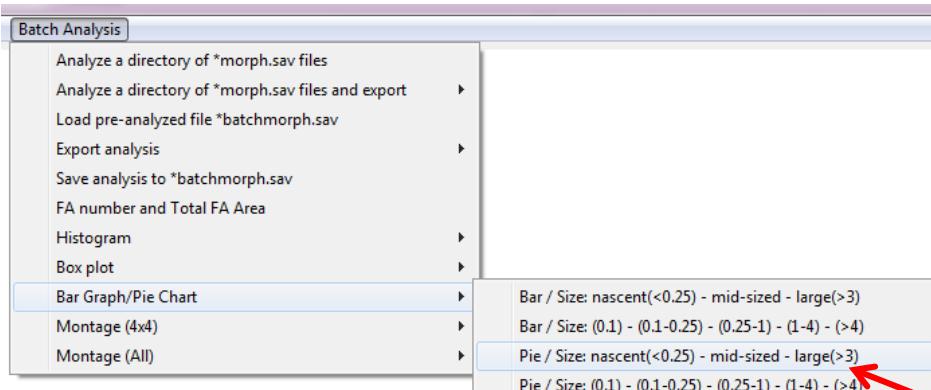
mean : 486.35740

med. : 471.03903

std. : 207.09533

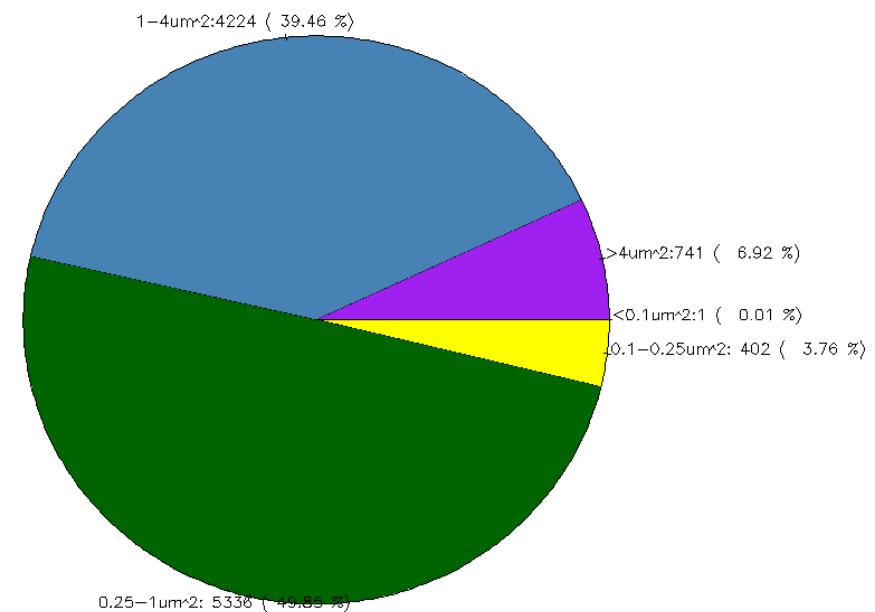
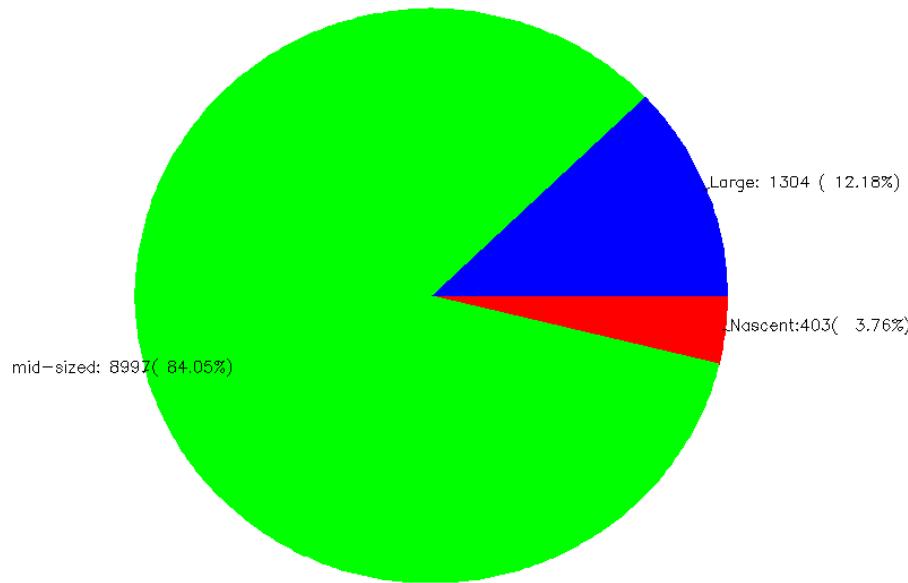


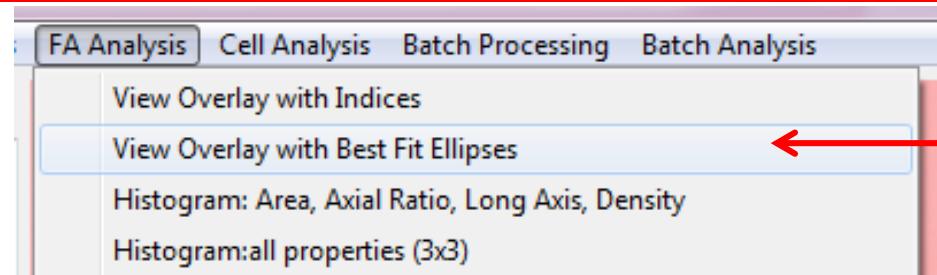
To export this, do the batch analysis or load the saved analysis file and export as .txt through the menu



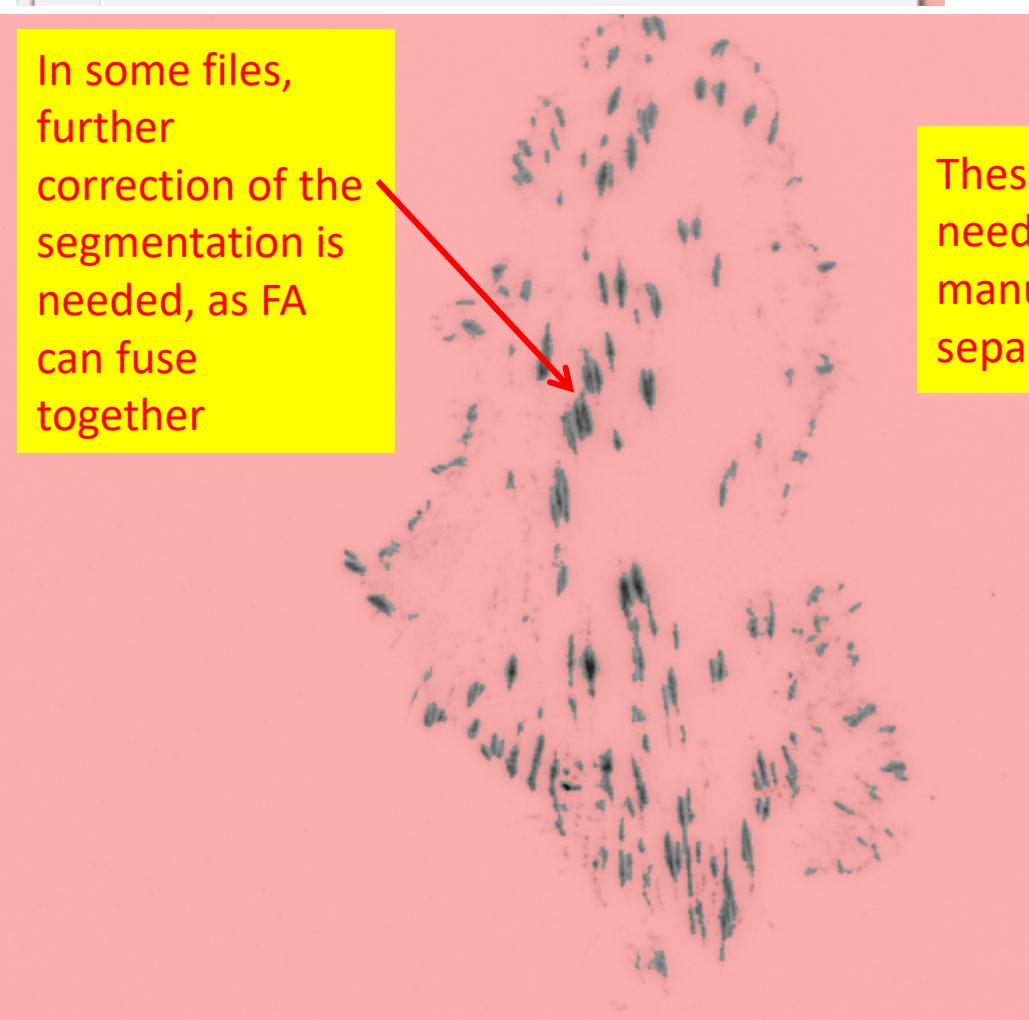
Bar / Size: nascent(<0.25) - mid-sized - large(>3)
Bar / Size: (0.1) - (0.1-0.25) - (0.25-1) - (1-4) - (>4)
Pie / Size: nascent(<0.25) - mid-sized - large(>3)
Pie / Size: (0.1) - (0.1-0.25) - (0.25-1) - (1-4) - (>4)

FA category can also be shown as
Pie Chart instead of Bar graph.



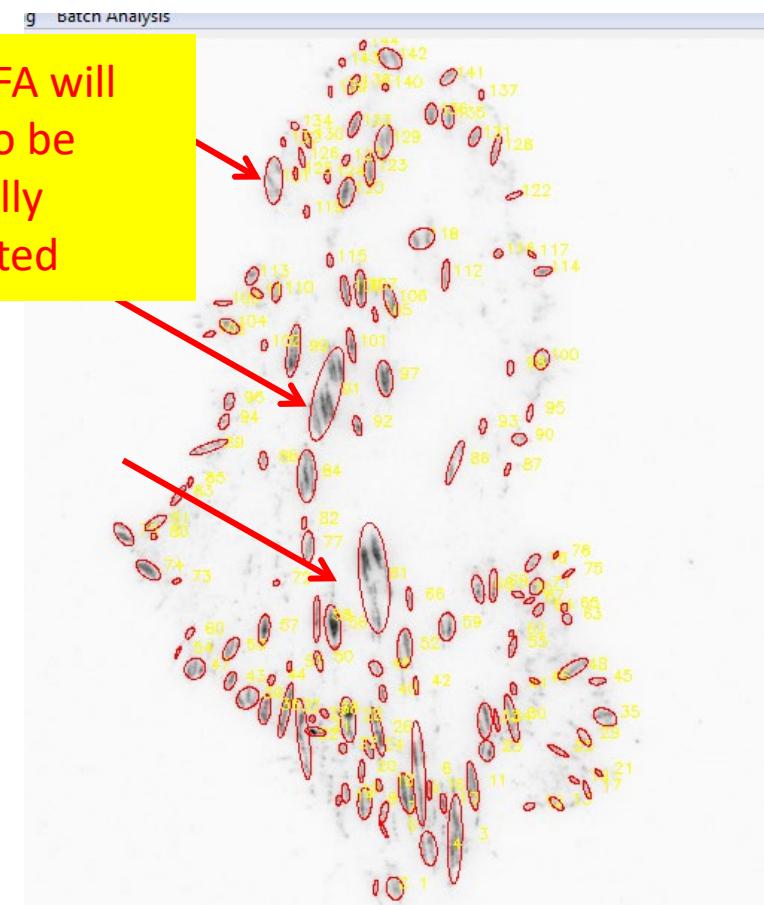


This can be checked by using the Best Fit ellipse overlay

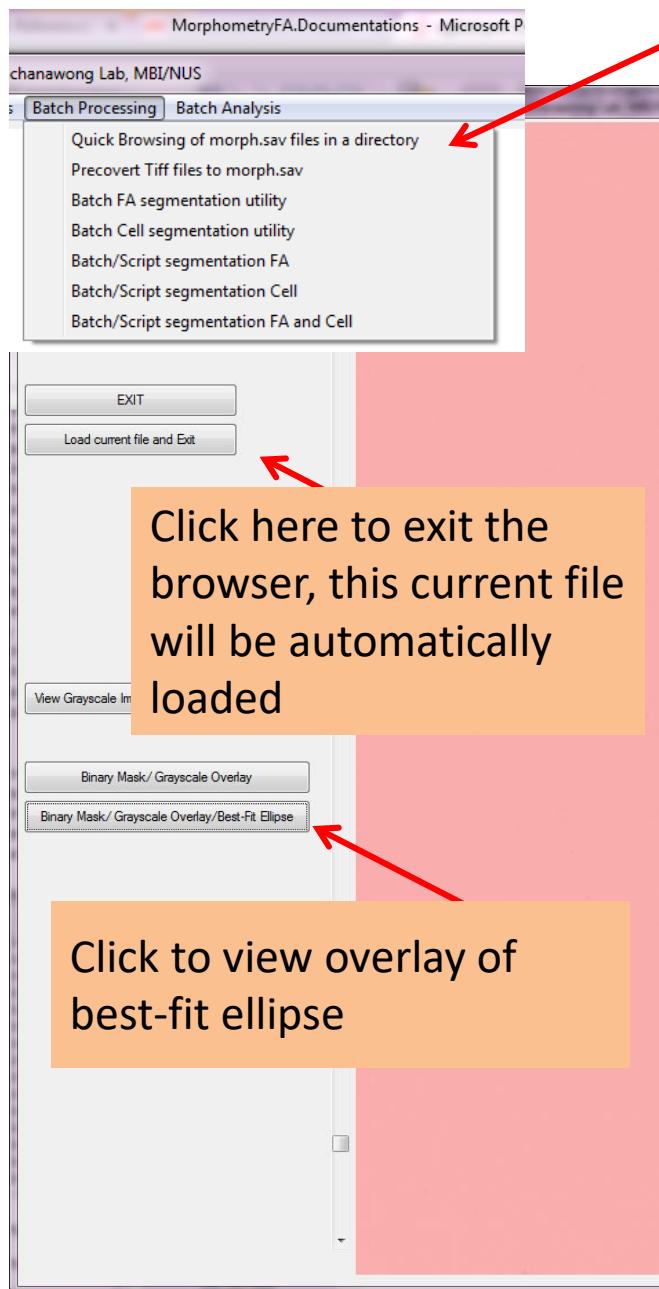


In some files, further correction of the segmentation is needed, as FA can fuse together

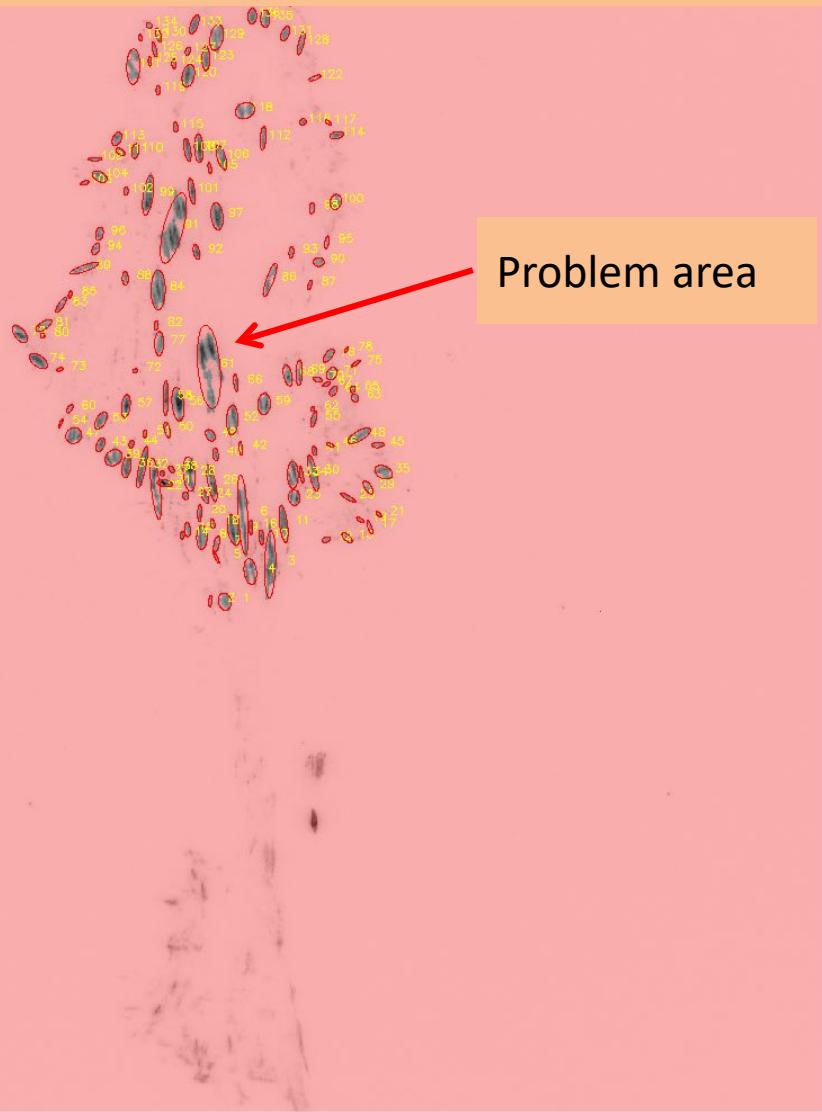
These FA will need to be manually separated



Batch Mode: Update 8/4/2014



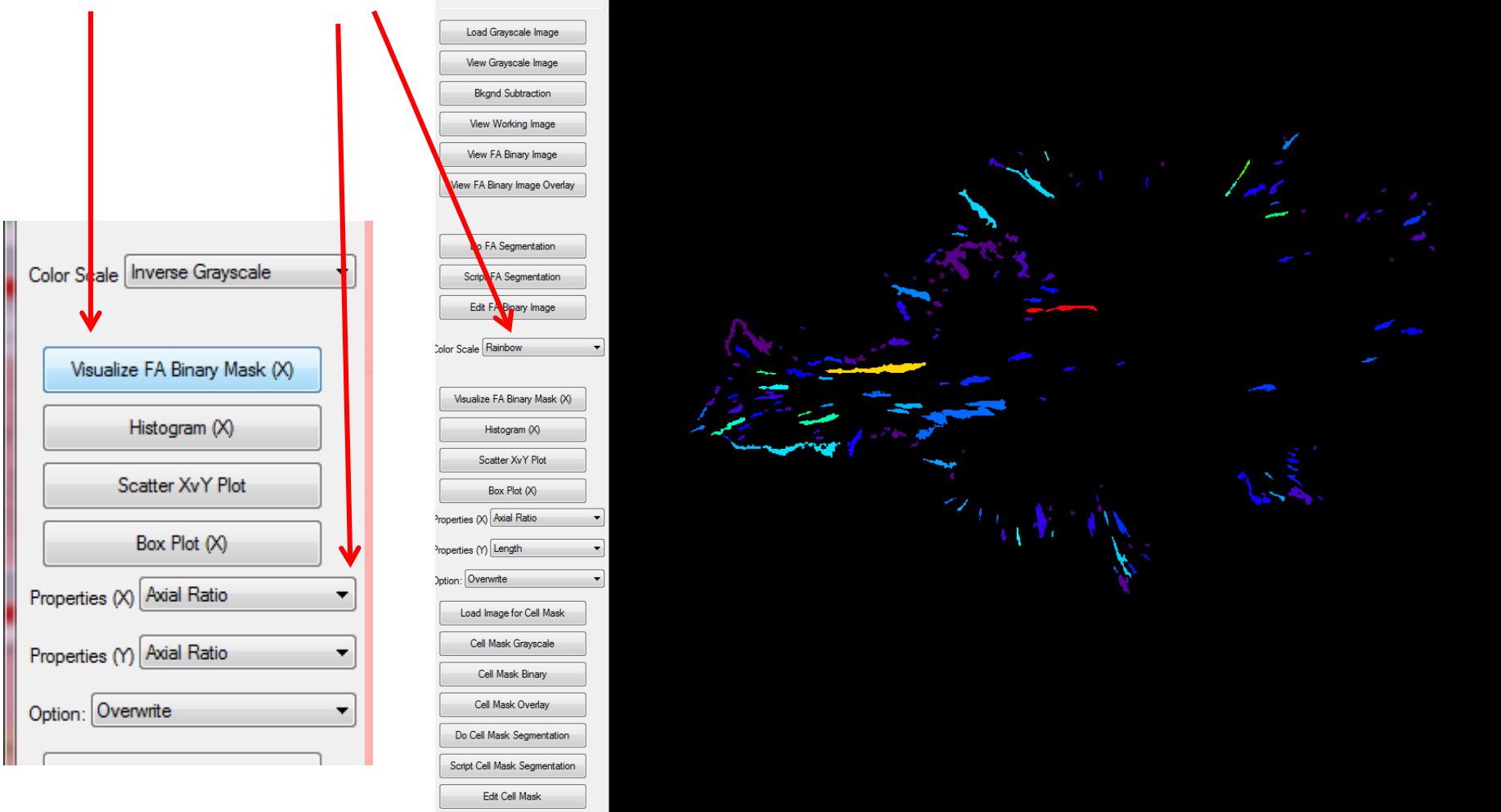
The updated Quick Browser tool have features to help facilitate this



Click here to exit the browser, this current file will be automatically loaded

Click to view overlay of best-fit ellipse

To visualize the FA mask by properties such as area, axial ratio



To view a scatter plot
between a pair of
properties

Visualize FA Binary Mask (X)

Histogram (X)

Scatter XvY Plot

Box Plot (X)

Properties (X) Axial Ratio

Properties (Y) Length

Option: Overwrite

