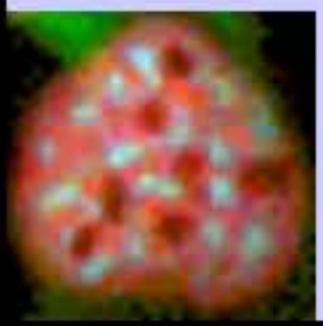


# A visual scripting interface for ImageJ and its usage at the microscopy facility Montpellier RIO Imaging

Volker Baecker and Pierre Travo

19.05.2006

Montpellier RIO Imaging



Cell Image Analyzer

[volker.baecker@mri.cnrs.fr](mailto:volker.baecker@mri.cnrs.fr)



# Overview

A visual scripting interface for ImageJ

- introduction and motivation
- using visual scripting
  - simple applications
  - batch applications
  - interactive applications
- extending the framework
  - adding operations
  - accessing ImageJ methods
- the implementation

... and its usage at the microscopy facility MRI

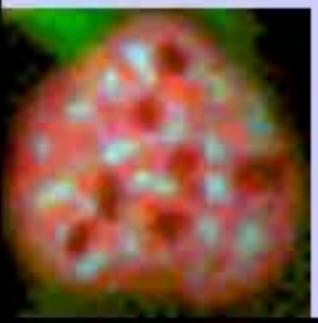
- DNA combing application
- measuring intensity ratios
- measuring fluorescent stained proteins
- counting cells and nuclei
- automation of simple tasks
- further project
- conclusions





# Who am I

- Born: 29.08.1970
- Nationality: German (living in France since Nov. 2003)
- 2000  
Master thesis in computer science at the University of Dortmund:  
“A development environment for cellular automata with fuzzy rules”
- 2000 – 2003  
Software developer and consultant for object oriented systems  
George Heeg eK
- Nov. 2003 – Feb. 2004  
Centre de Recherches de Biochimie Macromoléculaire,  
Structural Bioinformatics and Molecular Modelling, Andrey Kajava
- From Feb. 2004  
Software development at the Microscopy Facility: Montpellier RIO Imaging



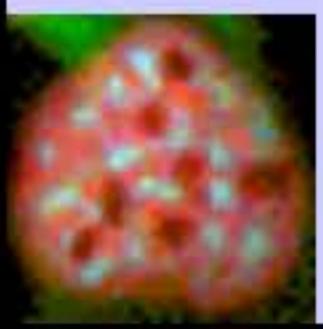
**Responsable**

PierreTravo, IRCE CNRS

# Montpellier RIO Imaging

- regional imaging facility
- 4 sites
- 23 microscopes
- 420 users
- 25413 hours in 2005
- 3M images in 2005
- promote the usage of microscopy
- participate in the development of microscopy
- provide training

<b>MRI-EDU</b> Composition variable Toutes opérations de formation et communication Resp. J. Cau	<b>MRI-DEV</b> Corine Tran-Aupiais IE2 CNRS Optronique Optique adaptative	Olivier Miquel T3 CNRS Systèmes Réseaux Soutien à la plate-forme	Sylvain de Rossi IE2 INSERM Optique et systèmes LASER Soutien à la plate-forme	Volker Bäcker, IE CDD Conception développement MRI Cell Image Analyzer
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Cell Image Analyzer

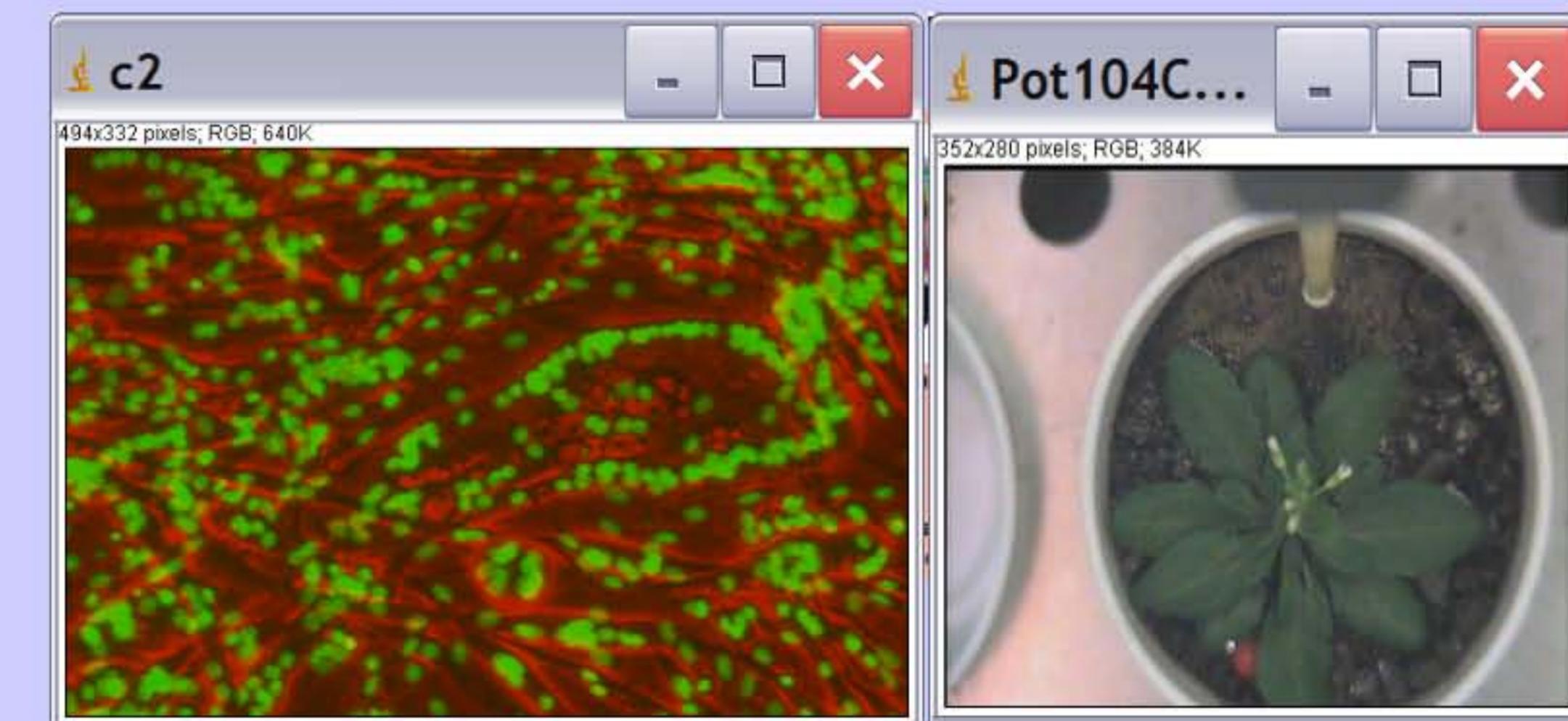
volker.baecker@mri.cnrs.fr

**Responsable**

Pierre Travo, IRCE CNRS

# Montpellier RIO Imaging

- regional imaging facility
  - 4 sites
  - 23 microscopes
  - 420 users
  - 25413 hours in 2005
  - 3M images in 2005
- wide range of mostly biological applications images from sub-cellular to entire organisms



Cell Image Analyzer

volker.baecker@mri.cnrs.fr



# The problem

robotized acquisition,  
time series, volume images

- large amounts of data

manual analysis



- time consuming
- biased results?

analysis is the  
bottleneck

→ automatic analysis  
needed

wide range of

- analysis needs
- image qualities



→ analysis must use a priori knowledge

if automatic analysis not possible

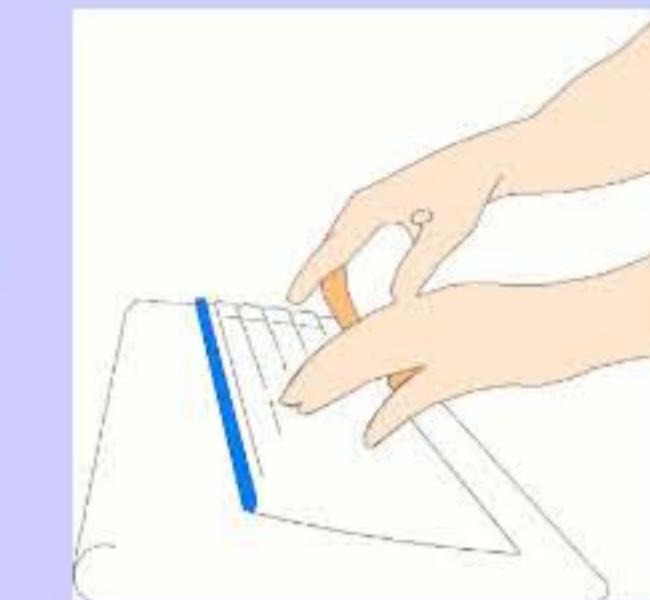
- partial automation can augment efficiency
- let the user only do what the software can't do

→ semi-automatic analysis needed



Cell Image Analyzer

volker.baecker@mri.cnrs.fr



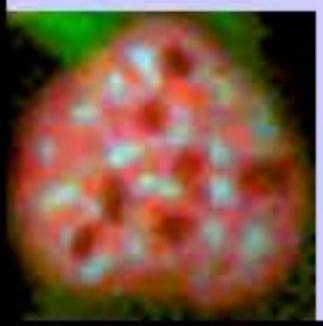
# Problem / Requirements

wanted:

rapid prototyping framework for  
image analysis applications

requirements:

- interactive experimentation to find solutions
- create interactive and batch applications
- build prototype-applications from existing operations rapidly
- extendable - add new operations
- allow to parametrize and run applications
- easy to use for end user



Cell Image Analyzer

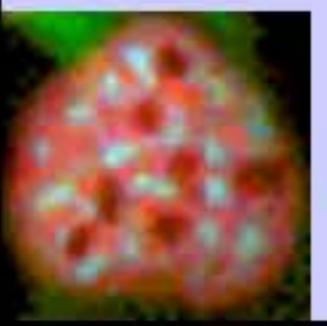
volker.baecker@mri.cnrs.fr

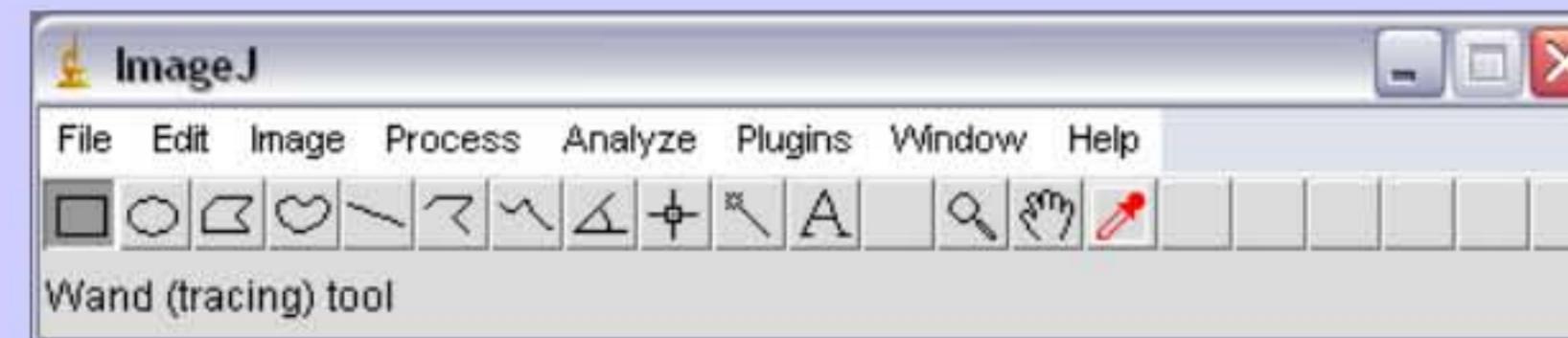


# Process

process:

- use framework
  - to create prototype solutions on demand
  - in close collaboration with biologist
  - extend framework,  
when necessary for a project
    - **only then**
- eventually create full featured application





# ImageJ

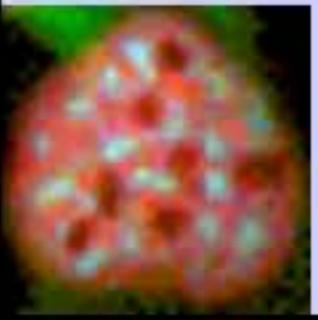
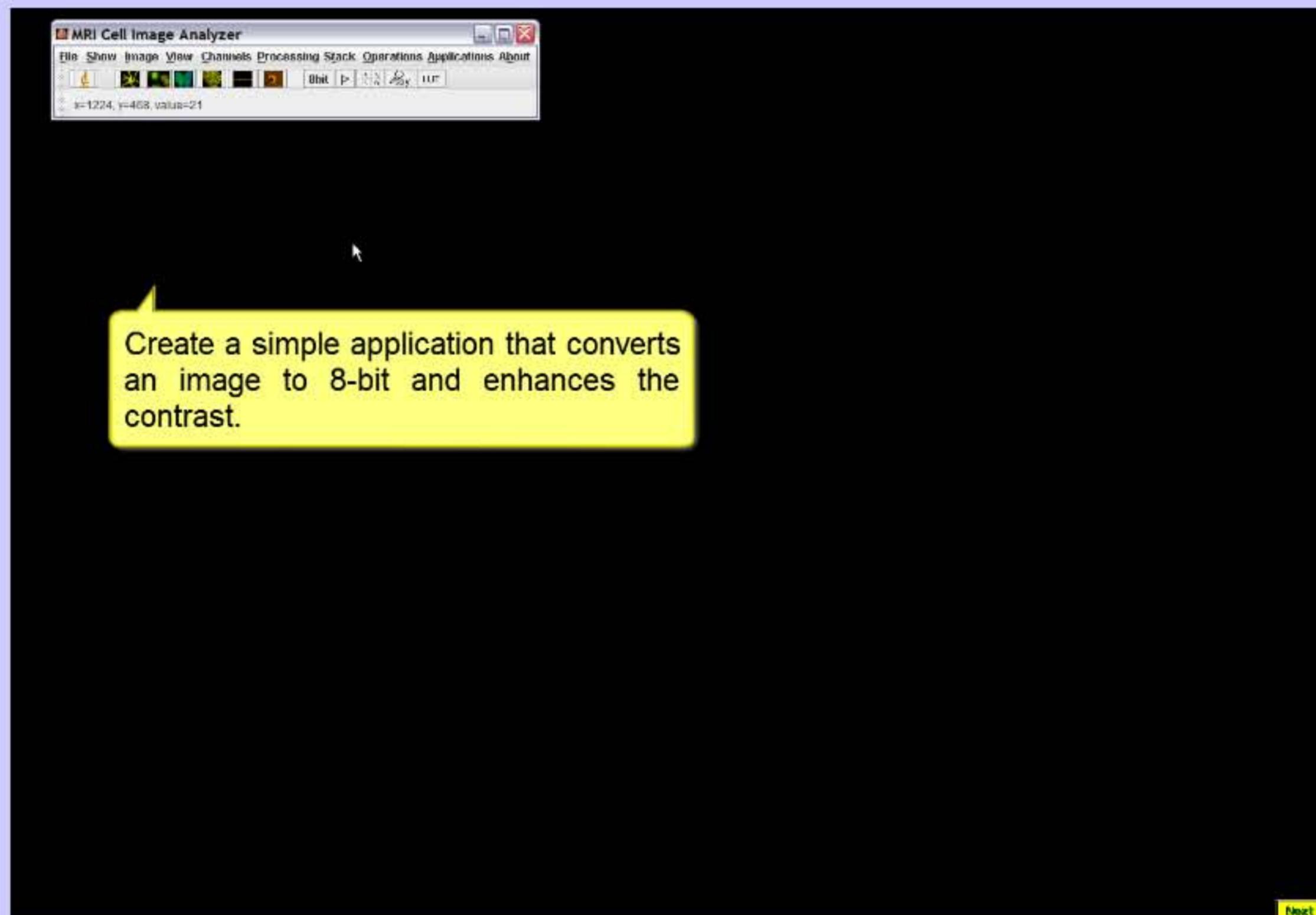
Is ImageJ the desired framework?

- interactive experimentation
  - solid image processing / analysis framework
- create interactive and batch applications
- allow to parametrize and run applications
  - macros
- extendable, configurable
  - plug-ins, source code available, public domain
- build prototype-applications from existing operations rapidly
  - yes, but macro language not understandable for end user
- easy to use
  - yes, but users have to learn command shortcuts or search in menus
- great for image analysis specialist
- some aspects too technical for end user



# Using visual scripting

- create a simple application

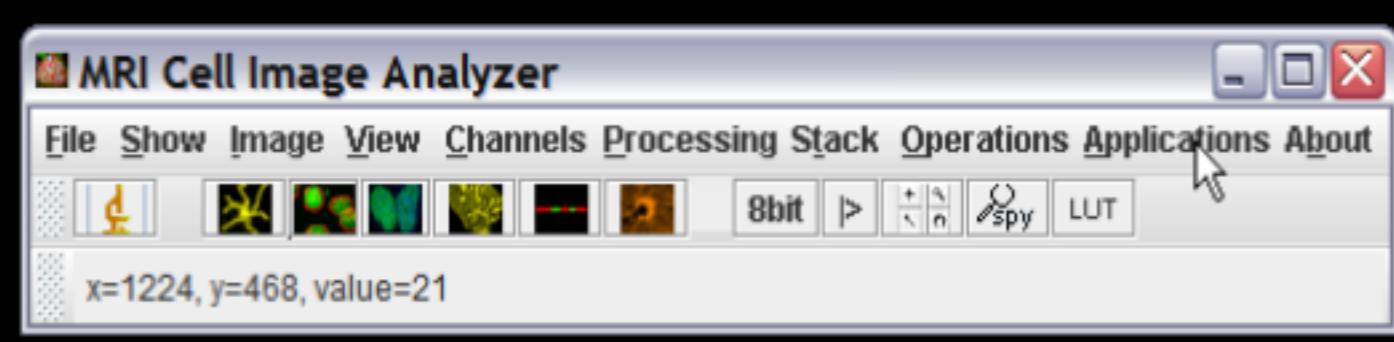


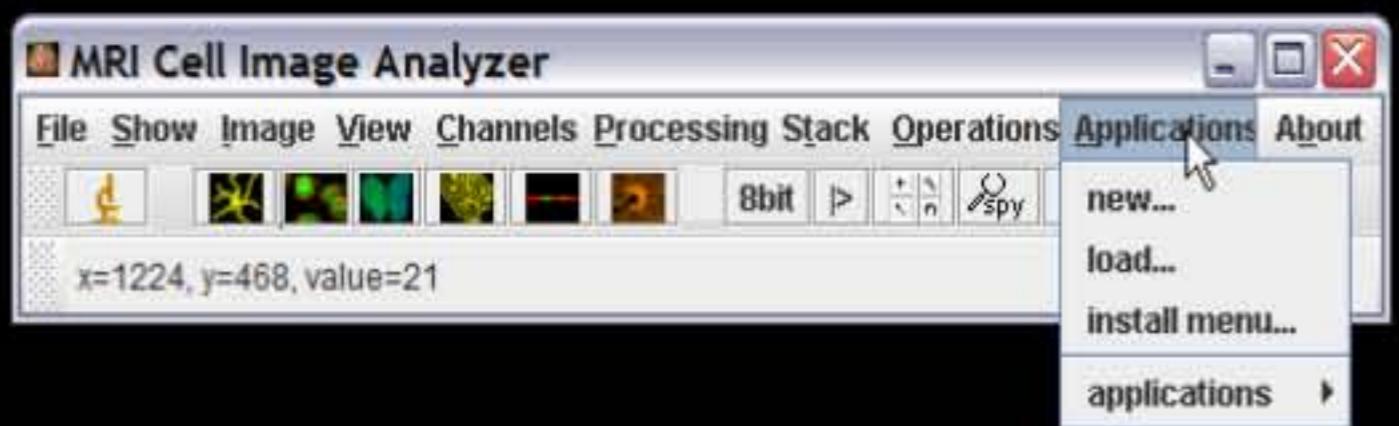
Cell Image Analyzer

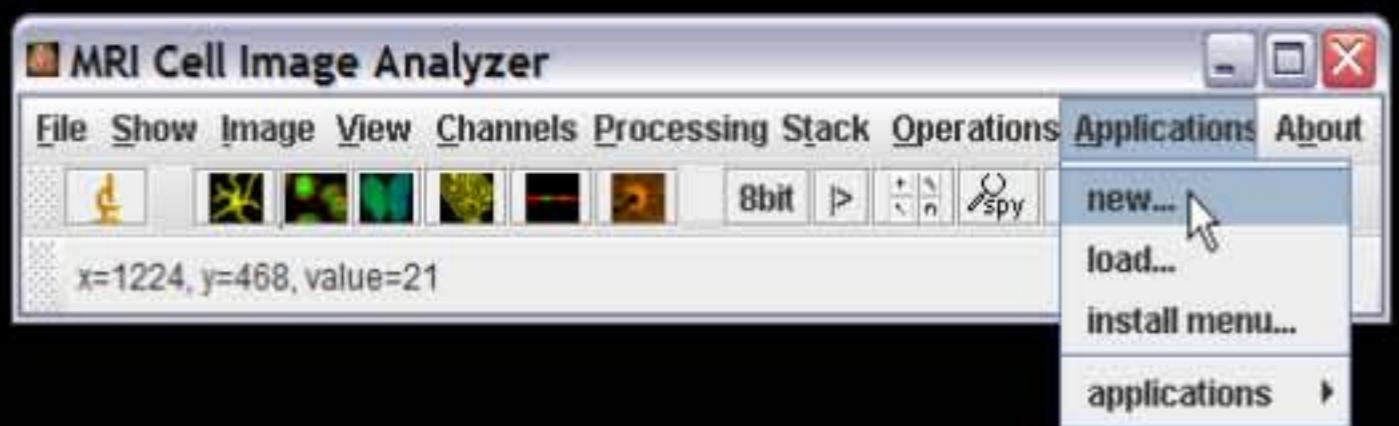
volker.baecker@mri.cnrs.fr



Create a simple application that converts an image to 8-bit and enhances the contrast.







Menu Applications->new...

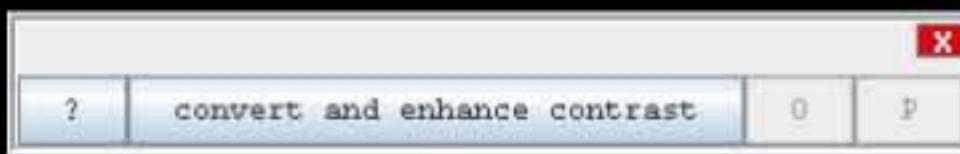


Enter the name of the new application







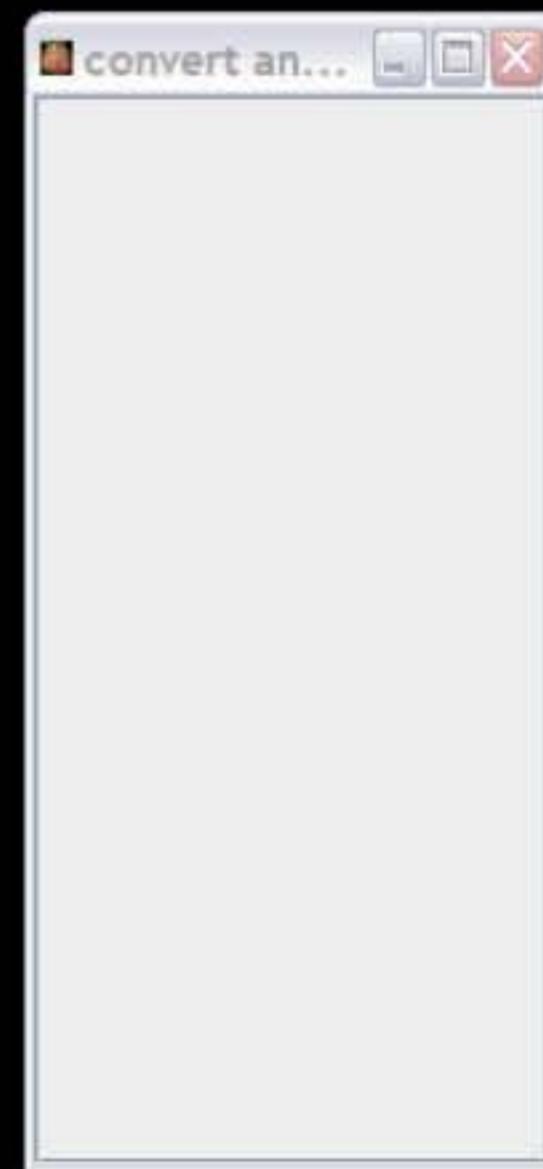
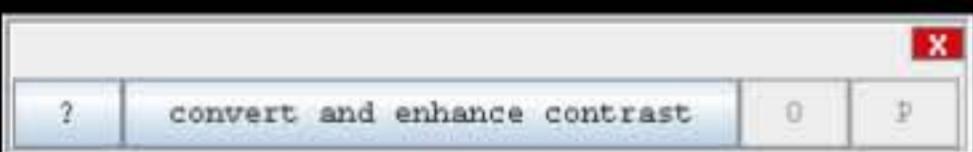


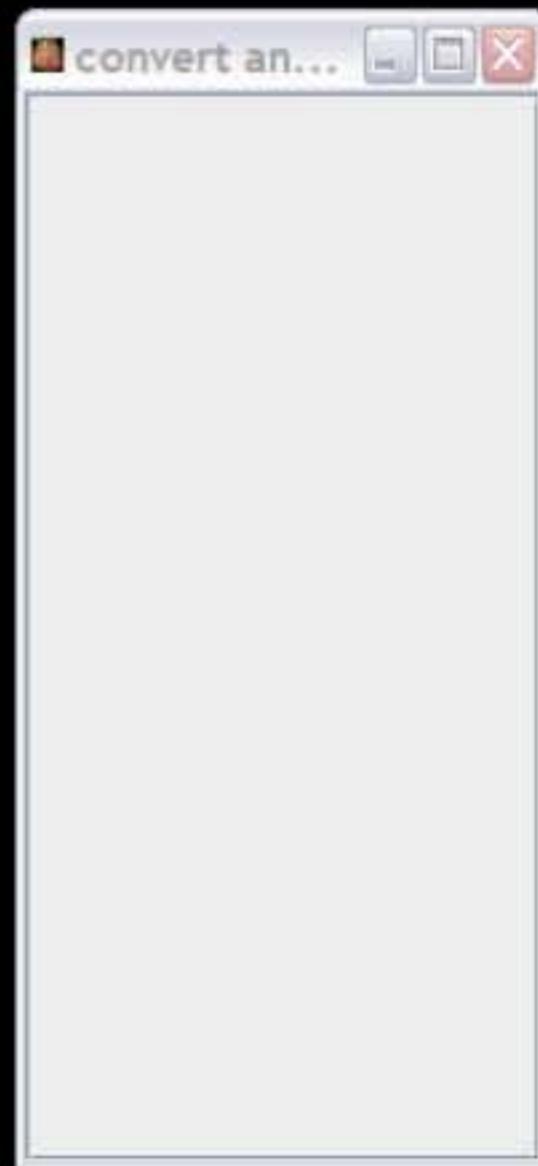
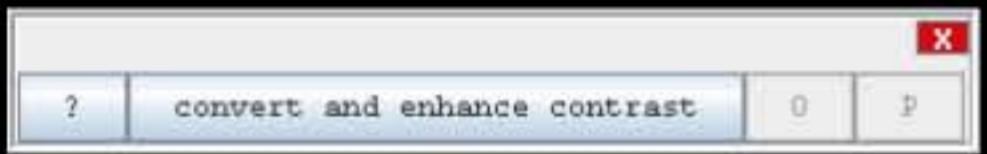
## tile representation with buttons

- help
  - start application

## box representation

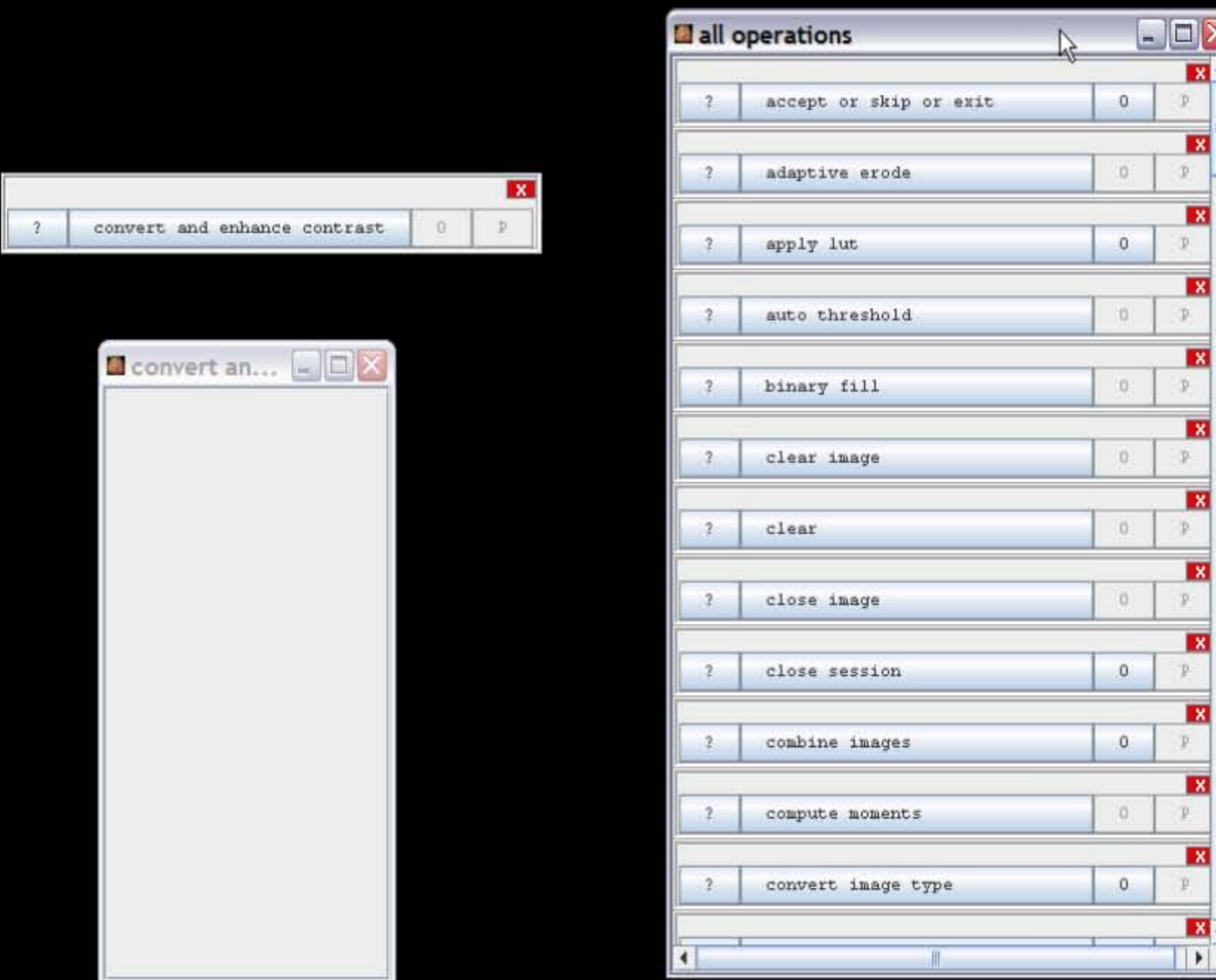
- list of operations (empty)

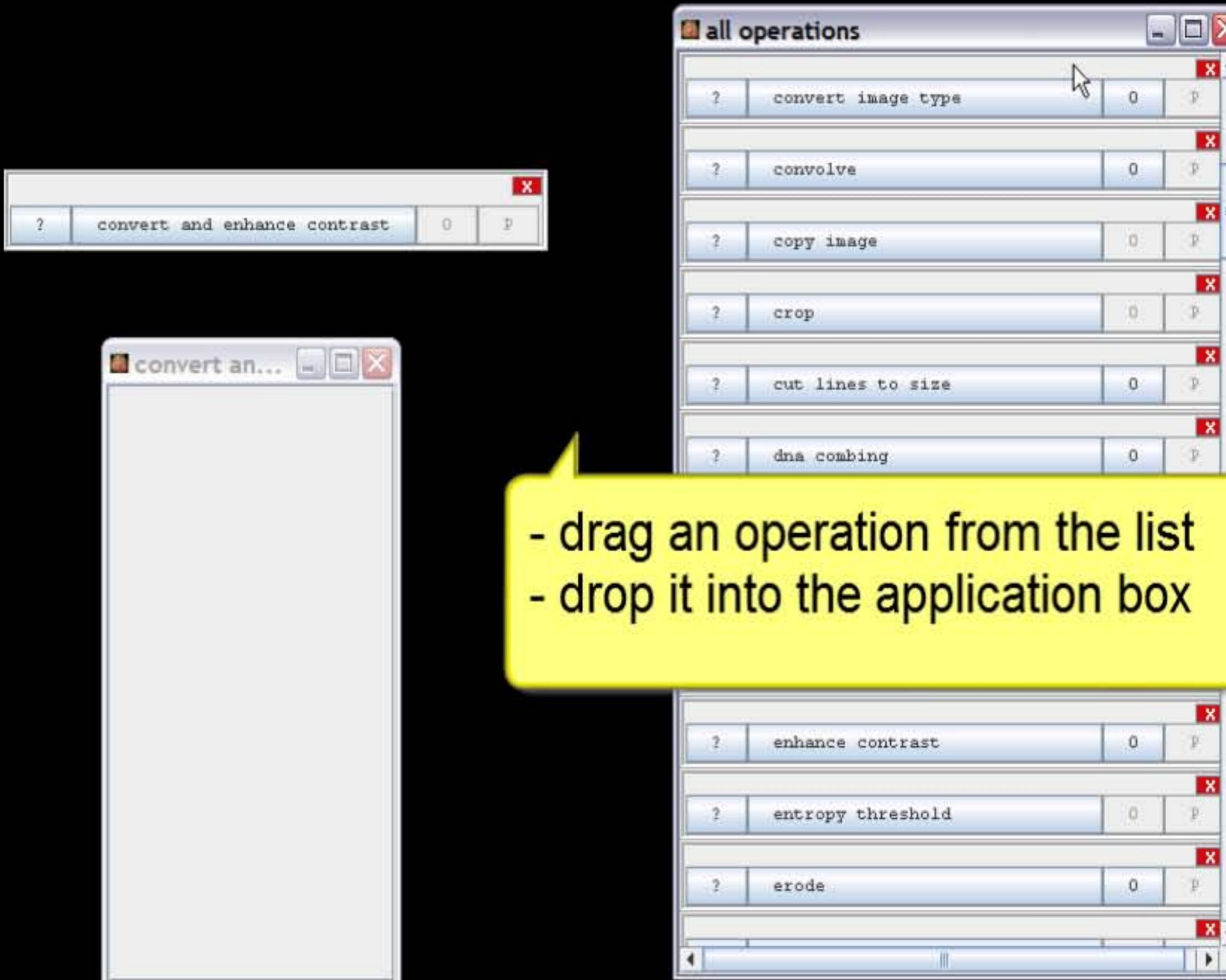


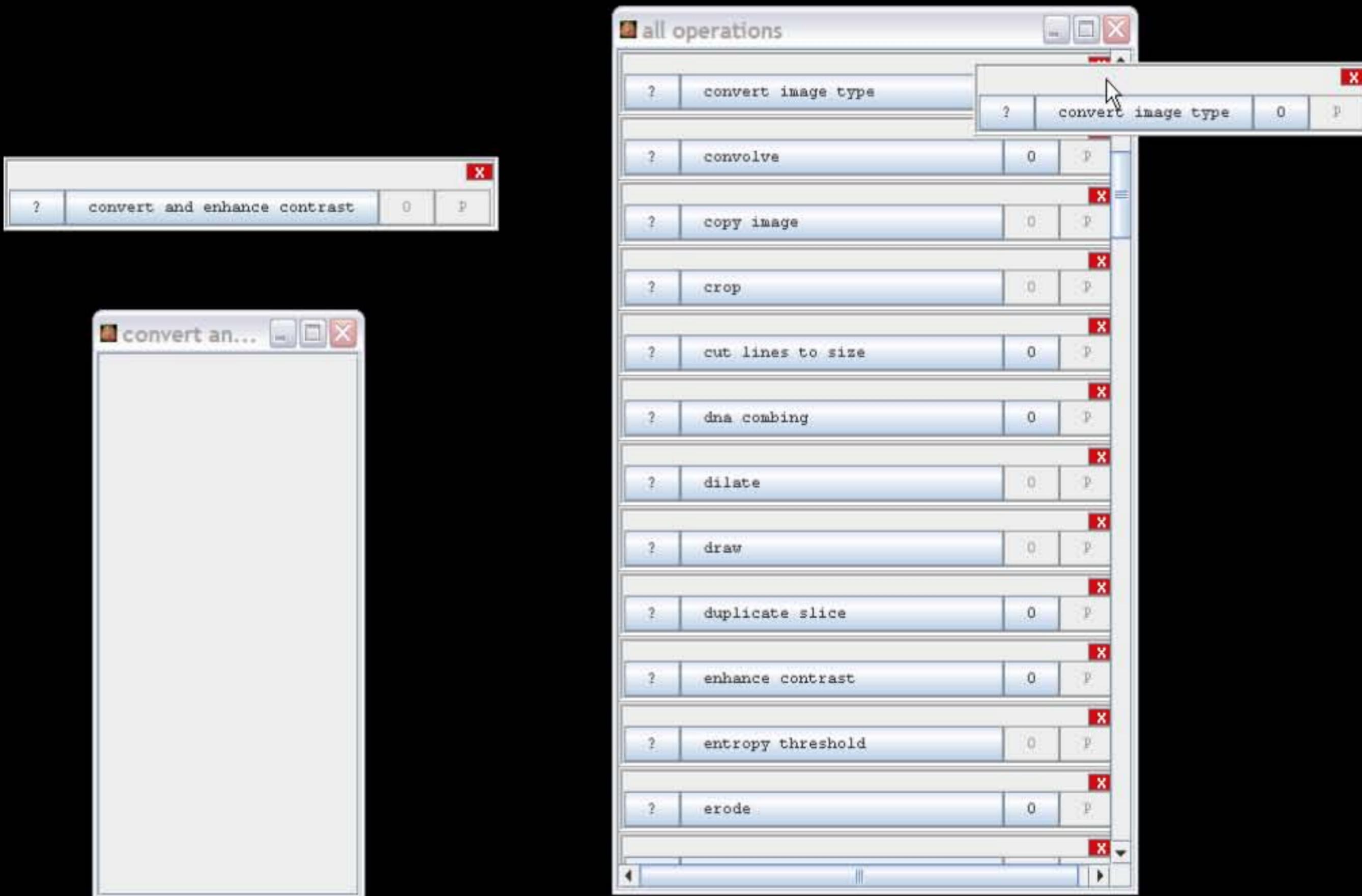


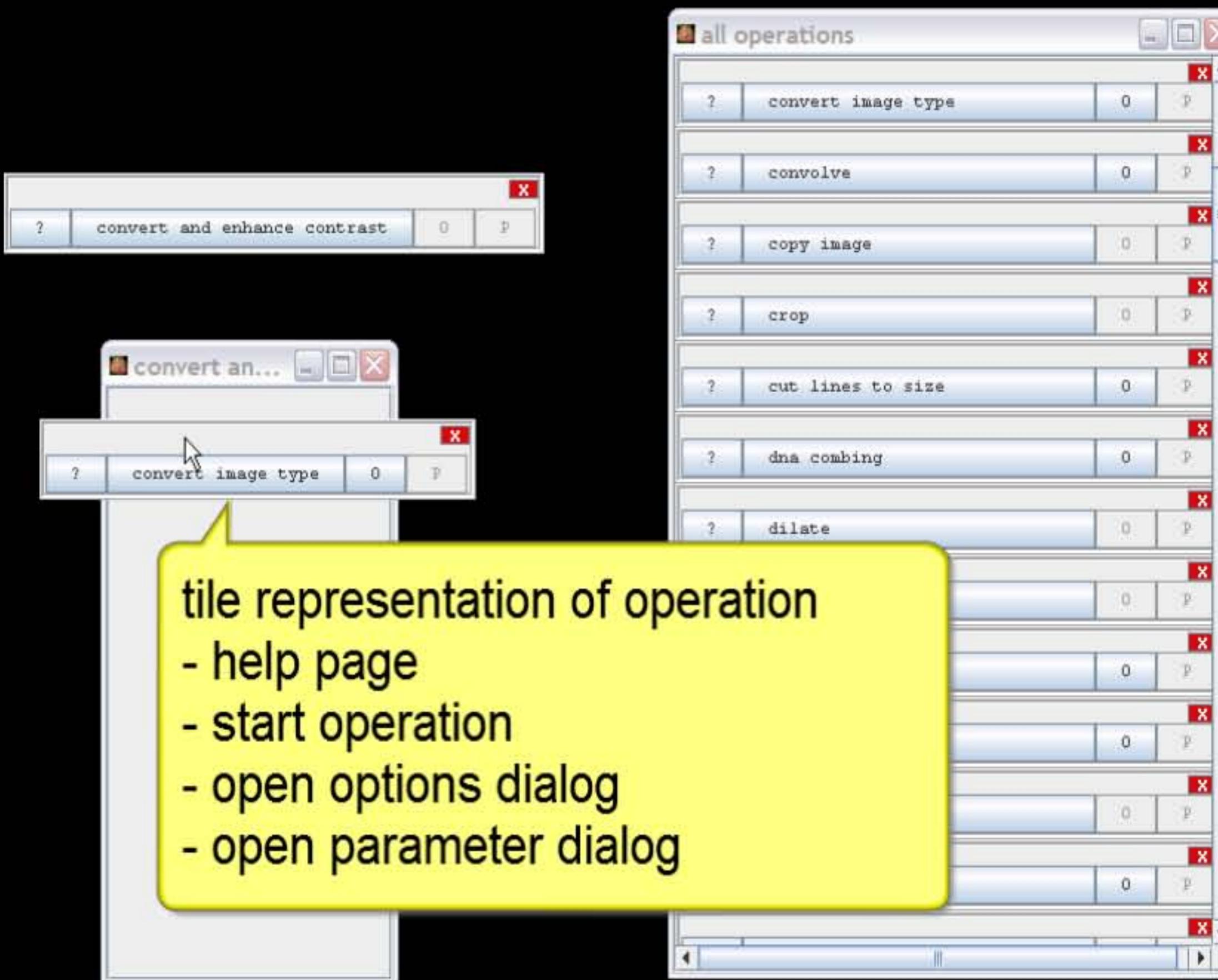


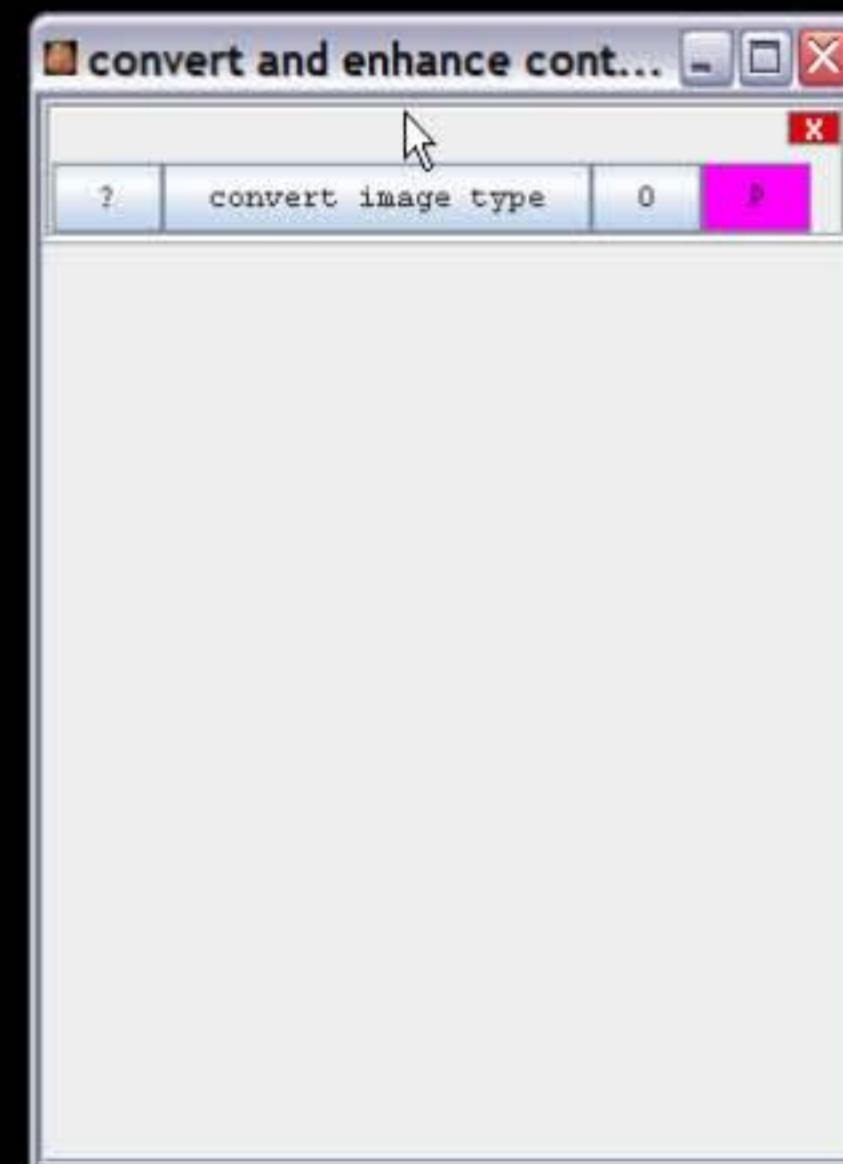
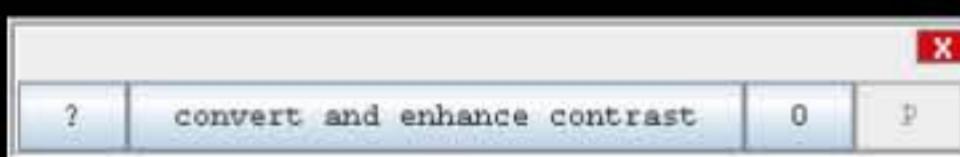
to add operations, open  
- collection of operations  
or  
- list of all operations











all operations			
?	convert image type	0	p
?	convolve	0	p
?	copy image	0	p
?	crop	0	p
?	cut lines to size	0	p
?	dna combing	0	p
?	dilate	0	p
?	draw	0	p
?	duplicate slice	0	p
?	enhance contrast	0	p
?	entropy threshold	0	p
?	erode	0	p



The screenshot shows the 'all operations' dialog box, which lists various image processing operations. A yellow callout points to the help icon in the 'convert and enhance contrast' sub-dialog.

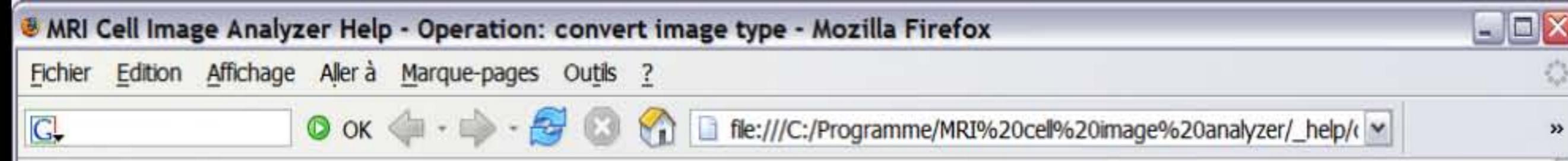
**all operations**

- convert image type
- convolve
- copy image
- crop
- cut lines to size
- dna combing
- dilate
- duplicate slice
- enhance contrast
- entropy threshold
- erode

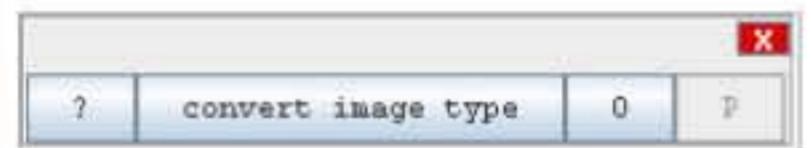
**convert and enhance cont...**

- convert image type

open the operation's help page



# Operation: convert image type



## Author:

The operation uses the Class [Converter](#) from ImageJ.

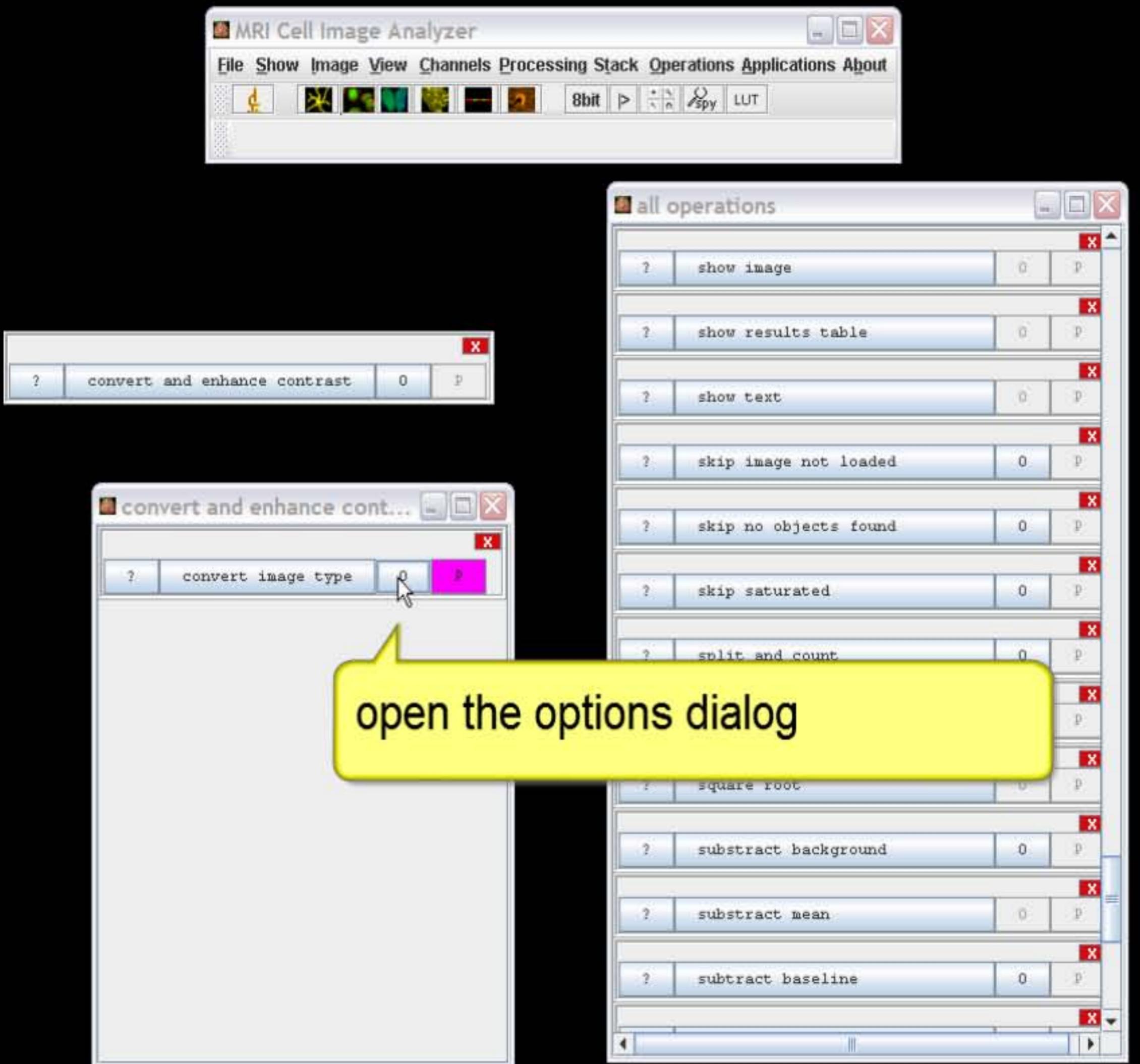
## Description

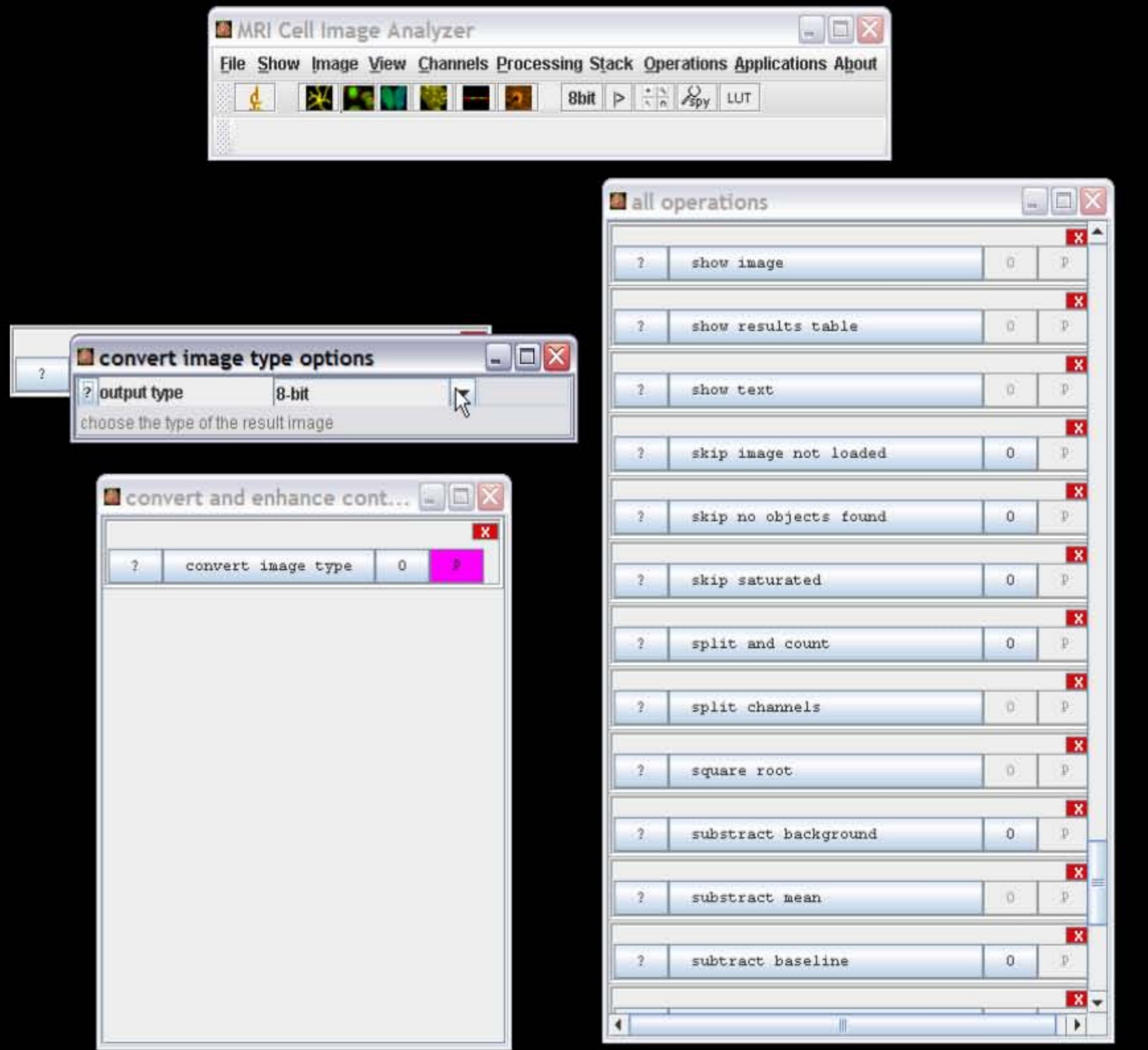
Converts the image type of the input image to the type selected in the operation's options. Depending on the type of the input image not all conversions are possible. See [ImageJ documentation, menu "image"](#) for details.

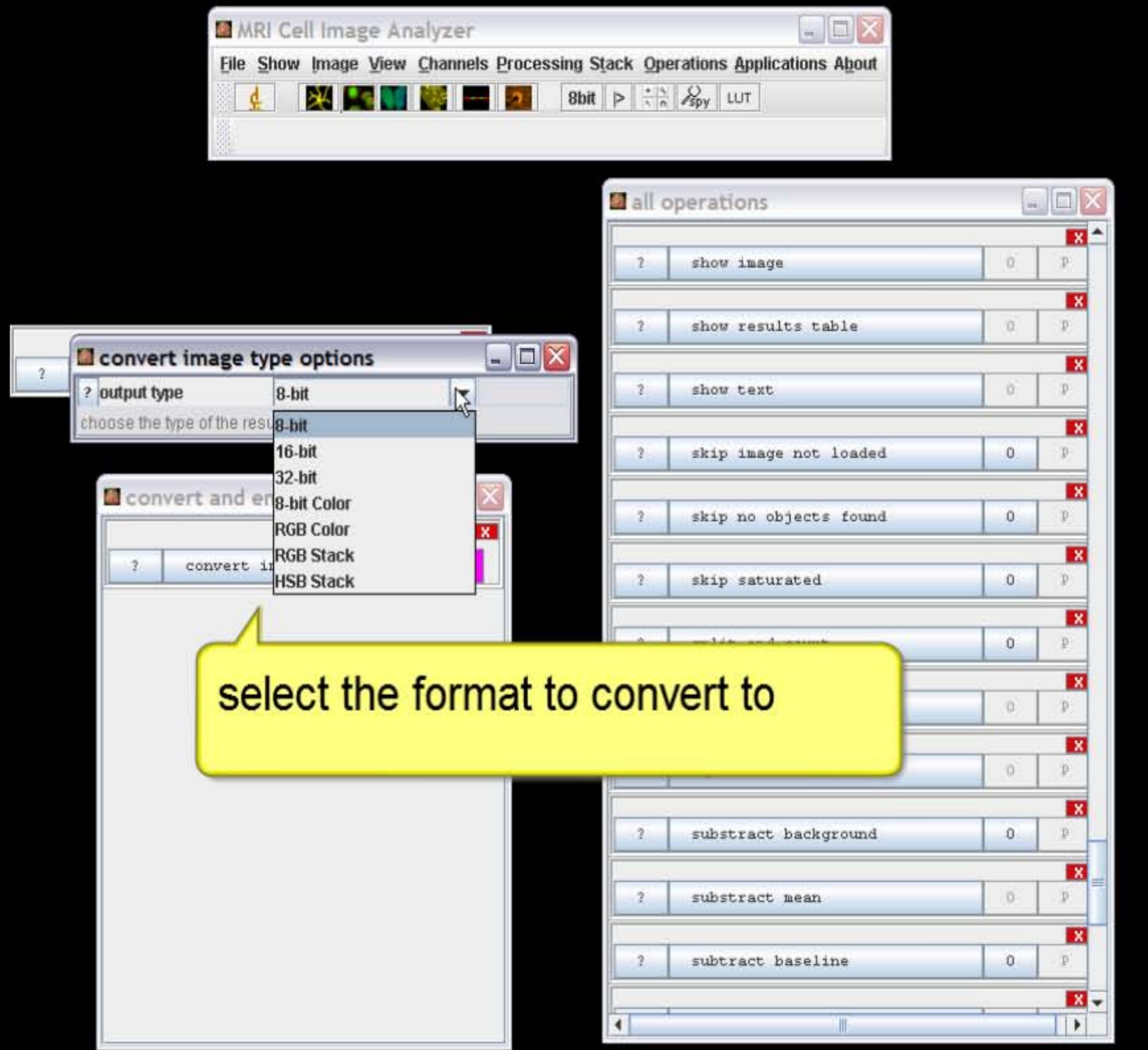
### Supported Conversions:

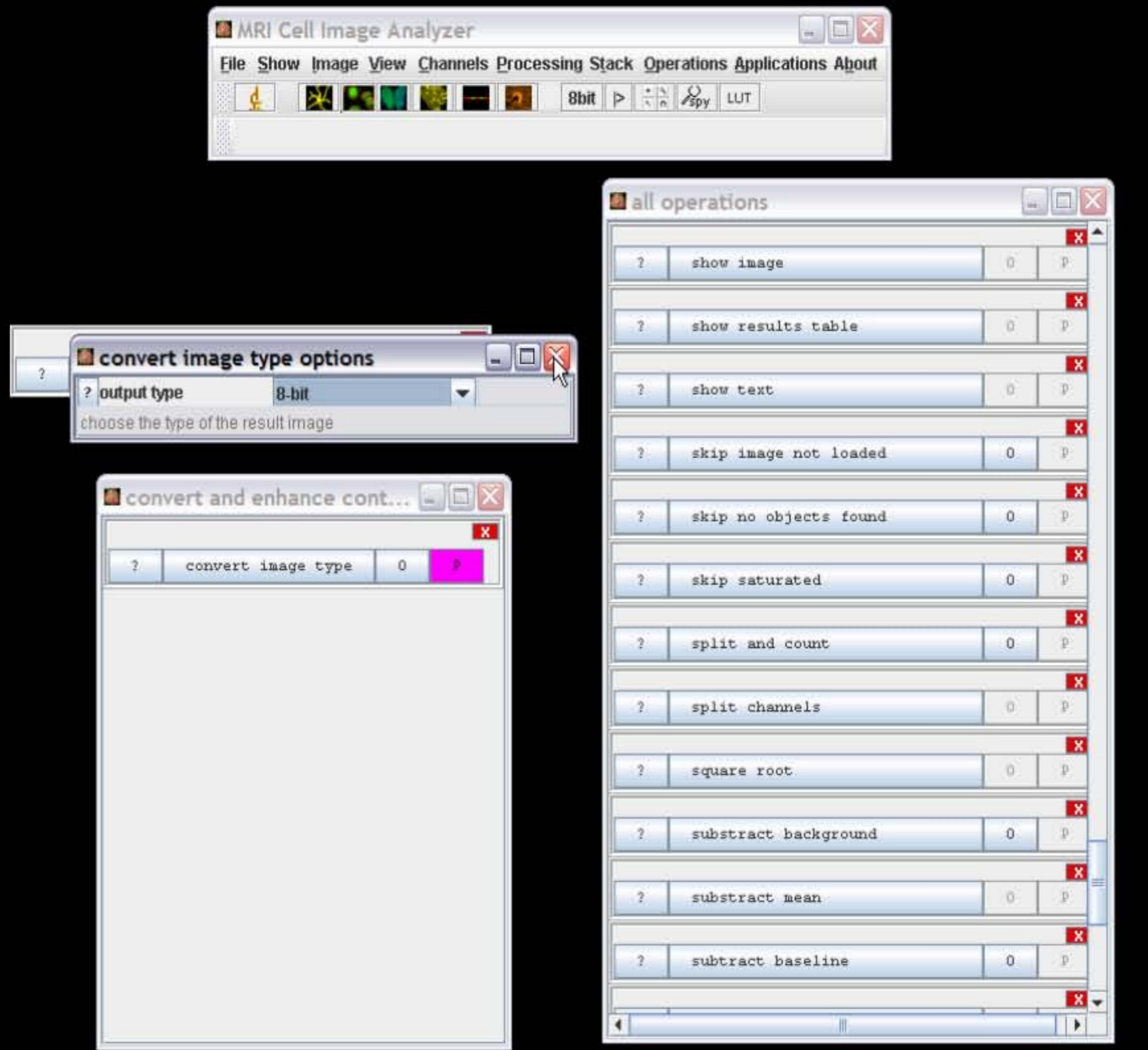
Terminé

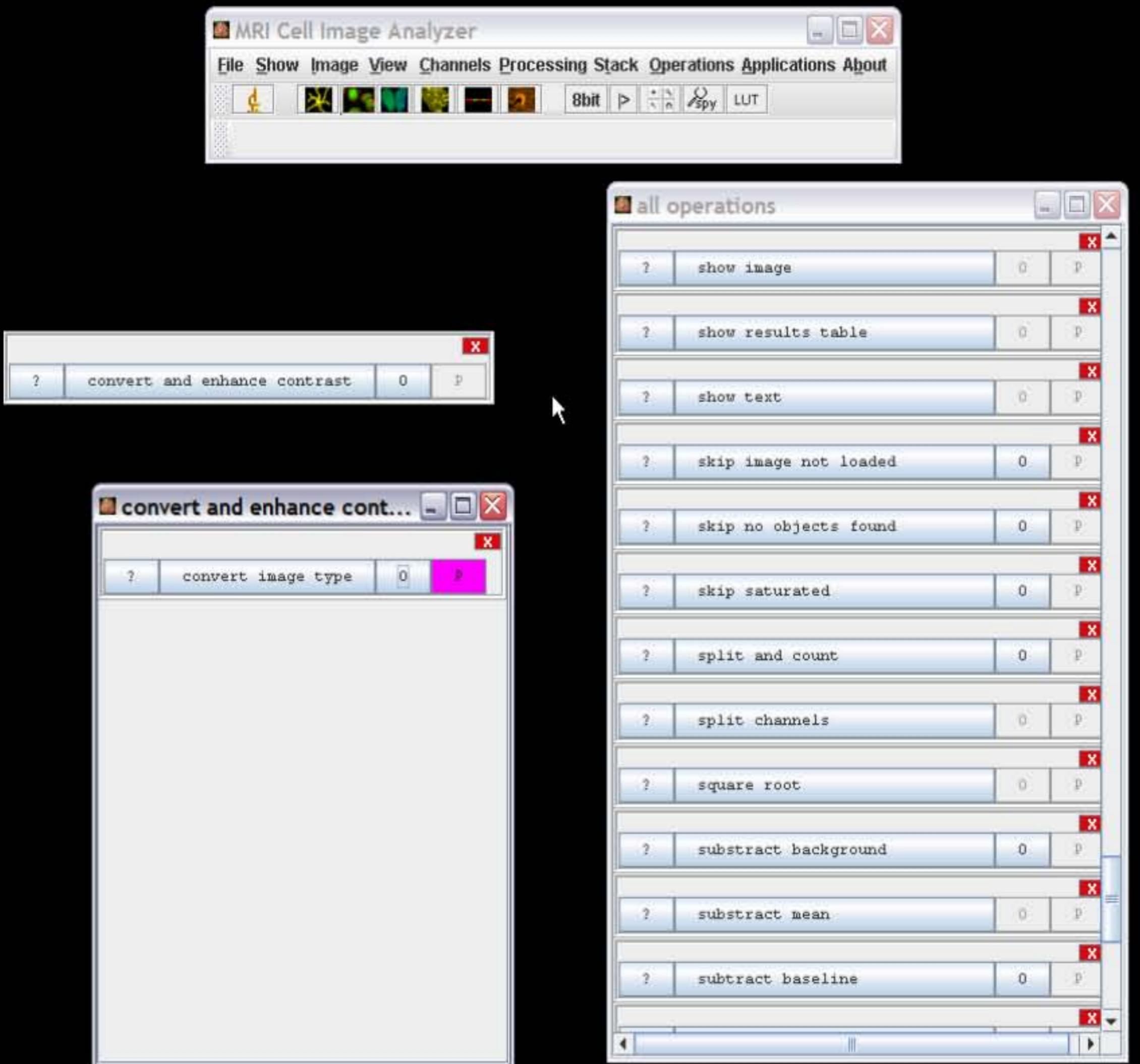


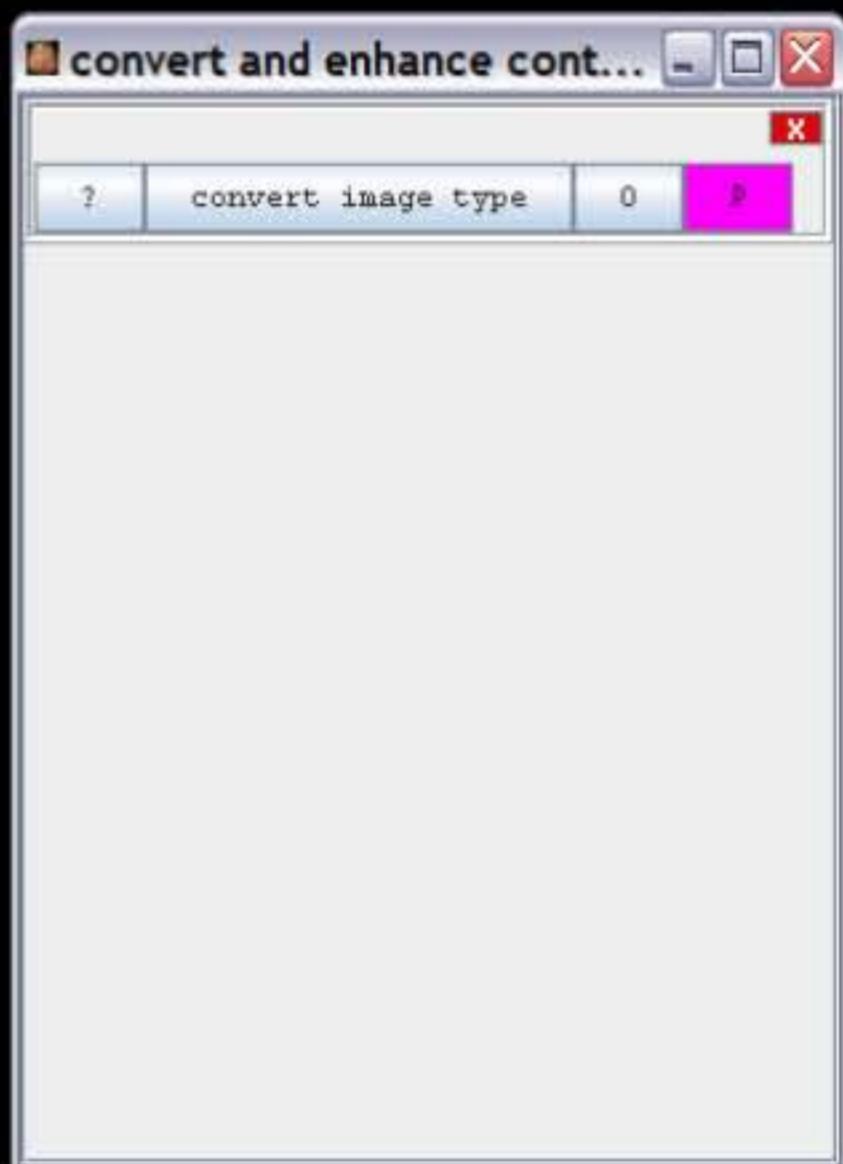
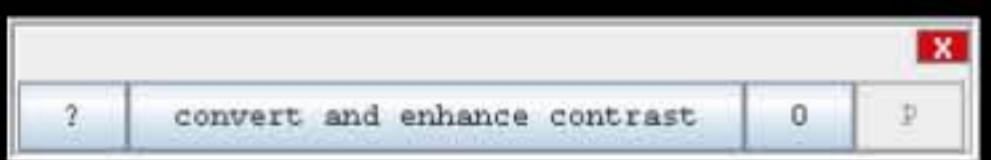






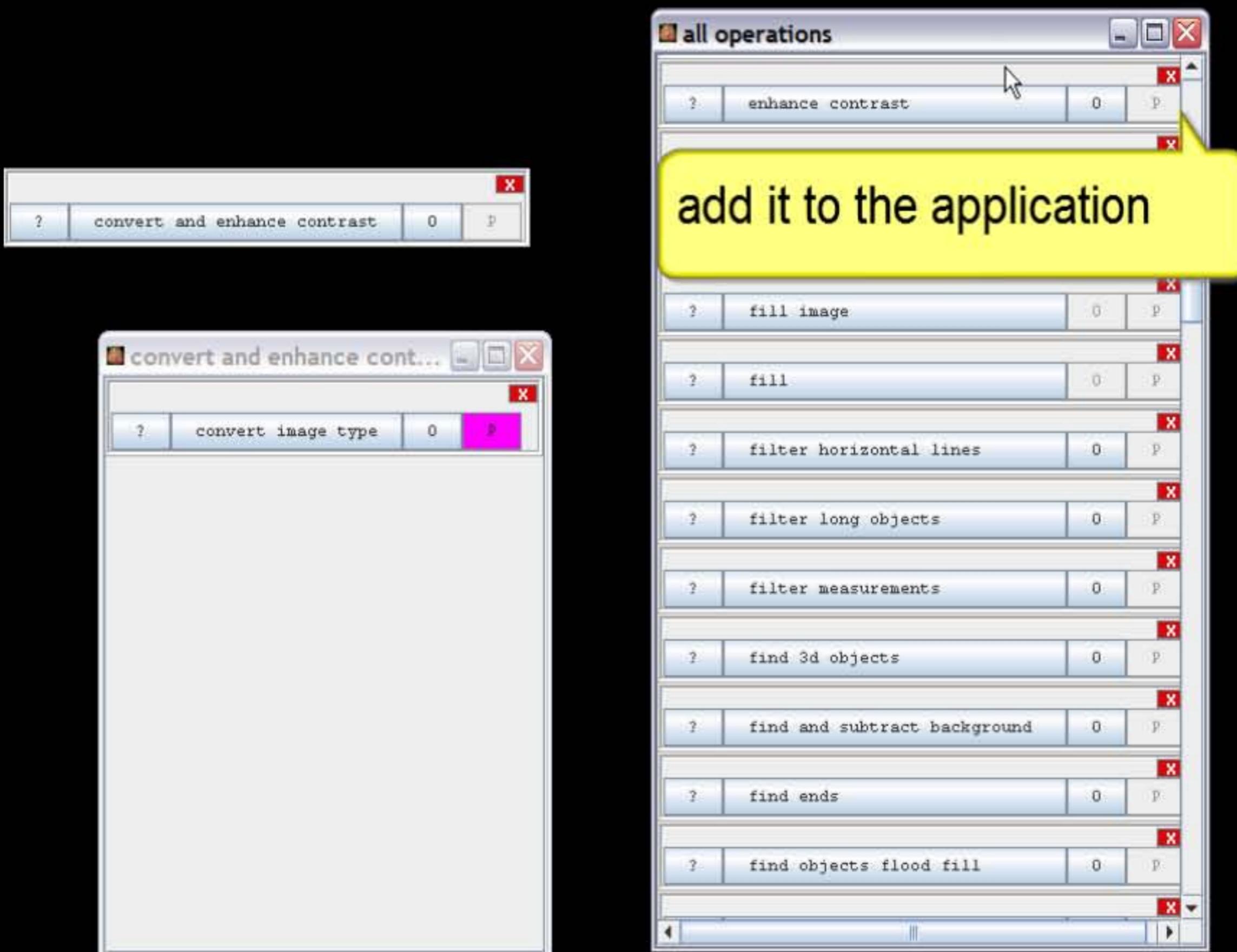


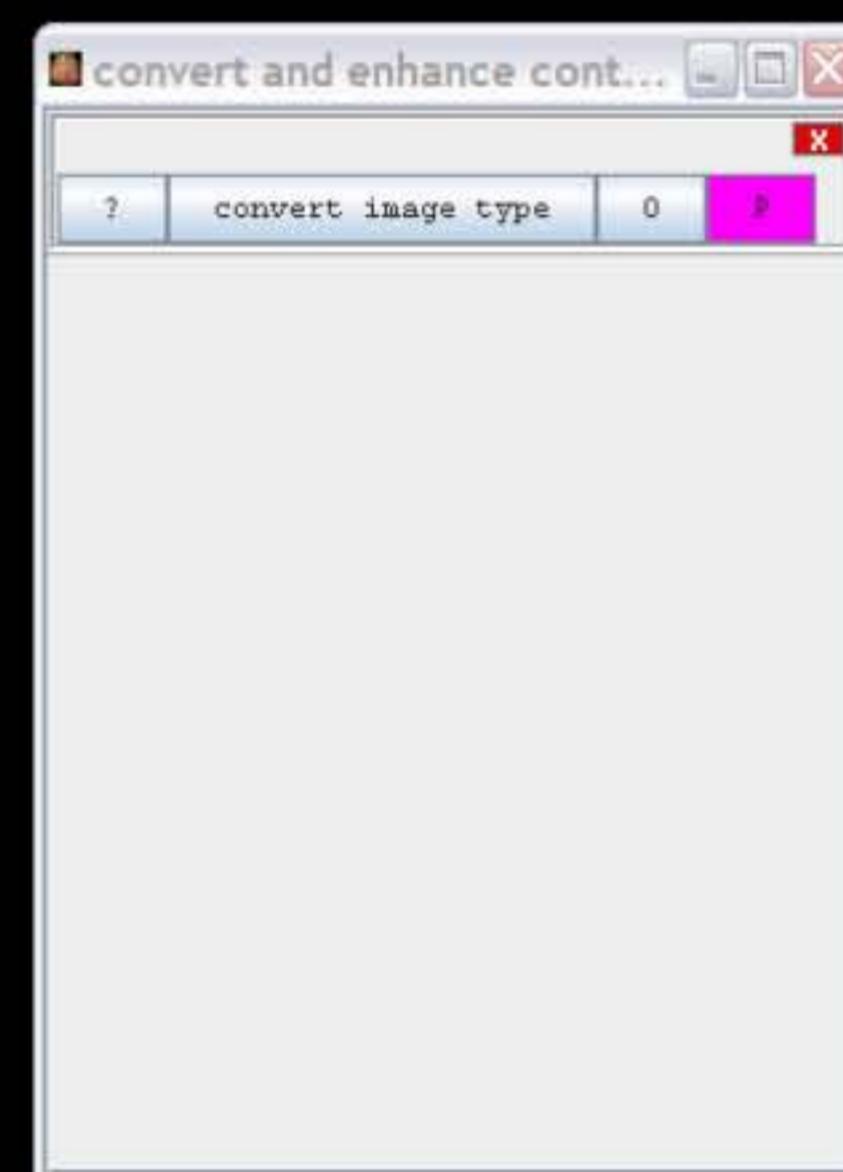
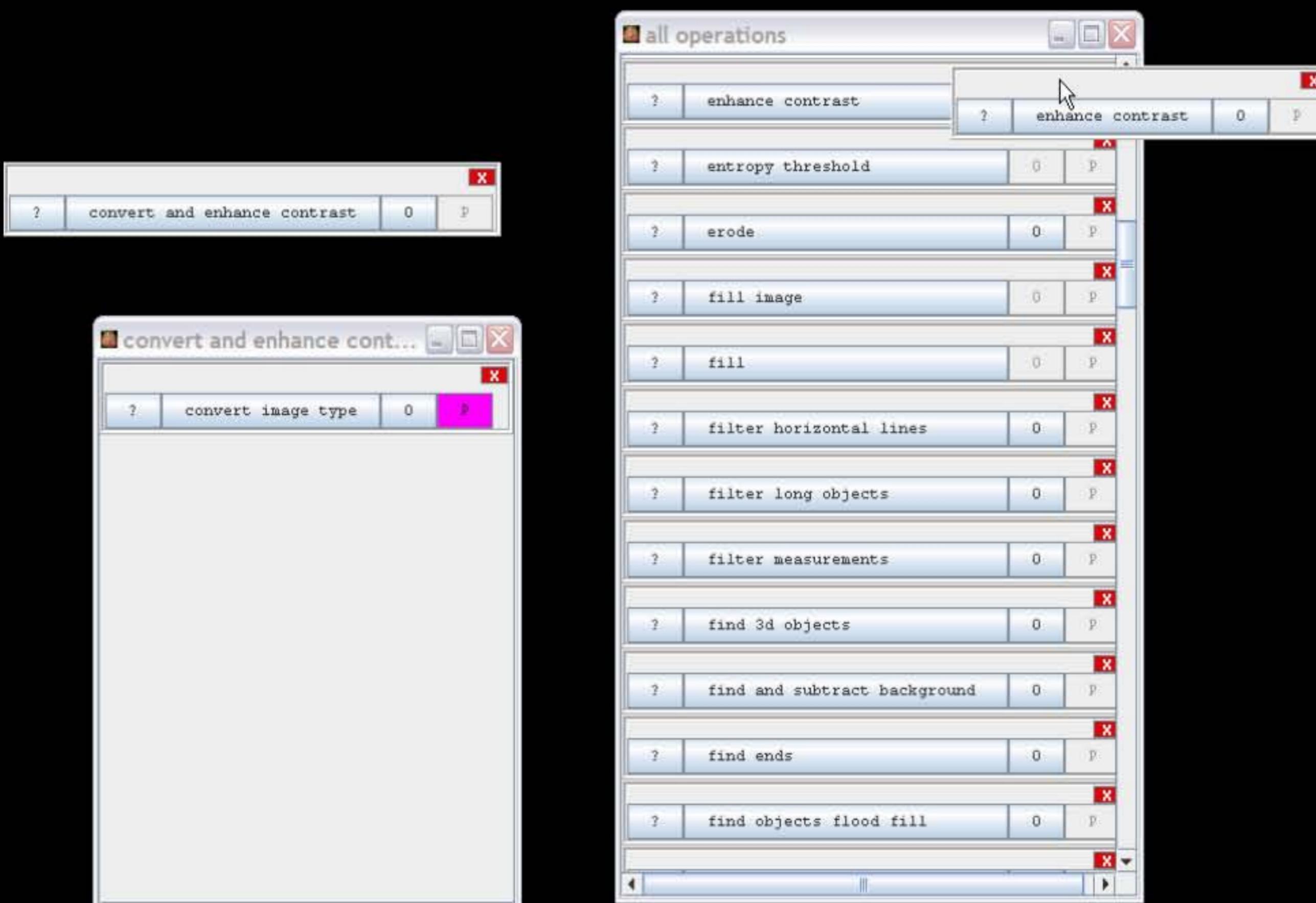


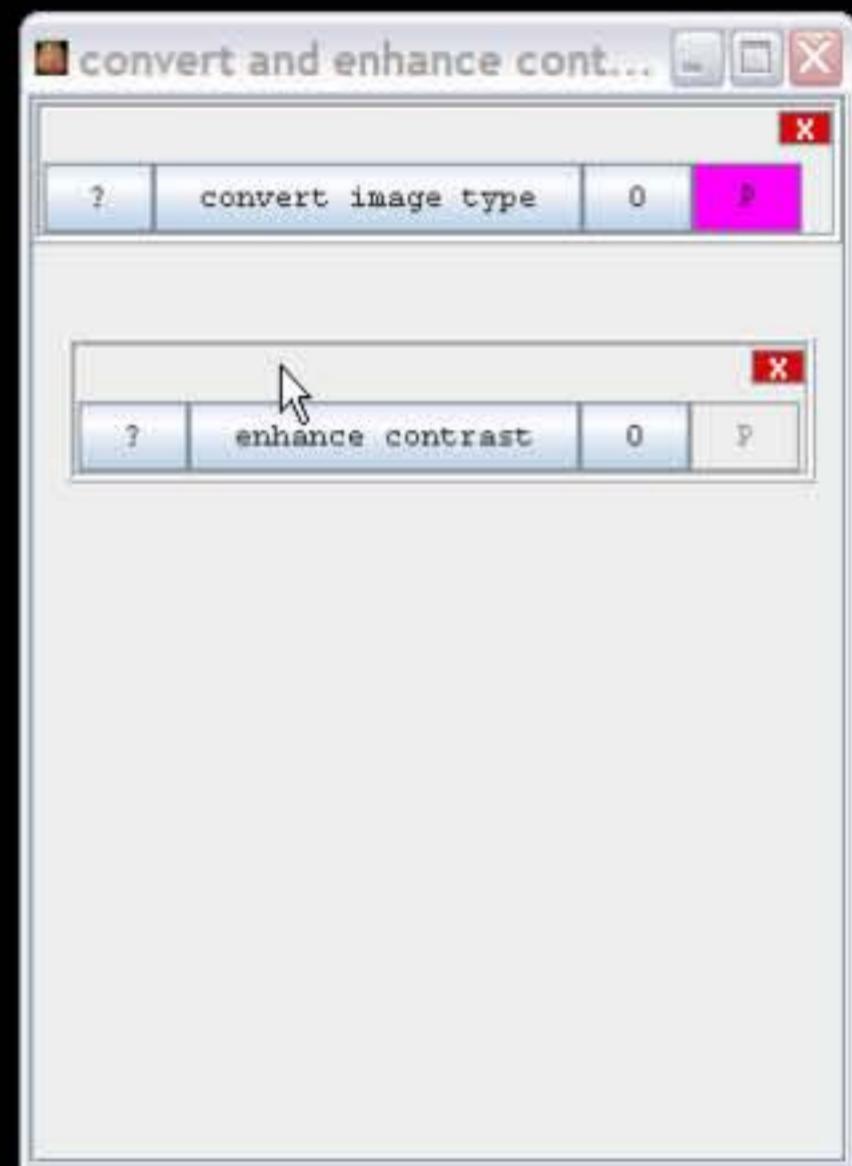


all operations			
?	convert image type	0	p
?	convolve	0	p
?	copy image	0	p
?	dna combing	0	p
?	dilate	0	p
?	draw	0	p
?	duplicate slice	0	p
?	enhance contrast	0	p
?	entropy threshold	0	p
?	erode	0	p

search the next operation









**all operations**

enhance contrast  
entropy threshold  
erode  
fill image  
fill  
filter horizontal lines  
filter long objects  
filter measurements  
find 3d objects  
find and subtract background  
find ends  
find objects flood fill

**convert and enhance cont...**

convert image type  
enhance contrast

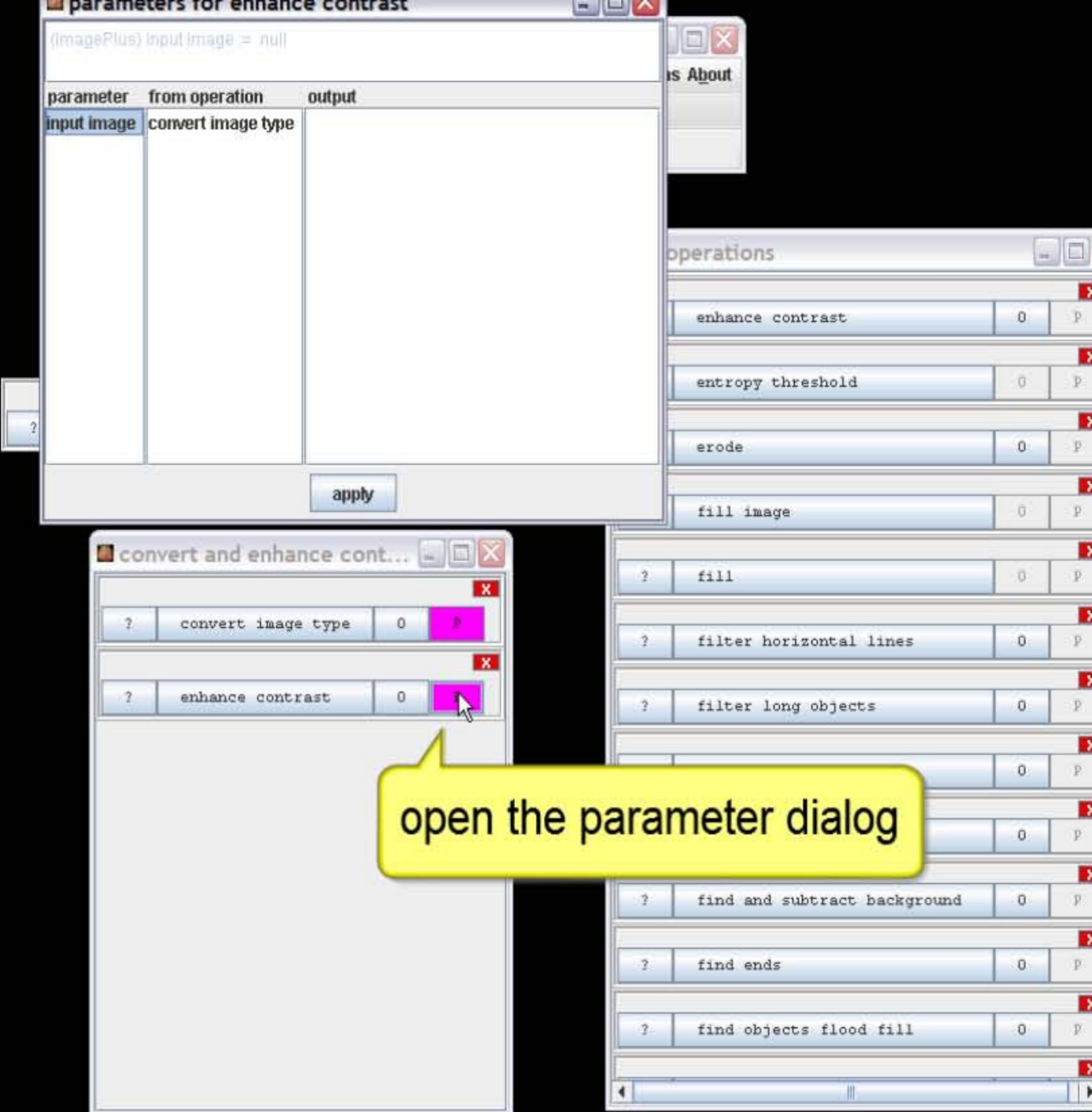


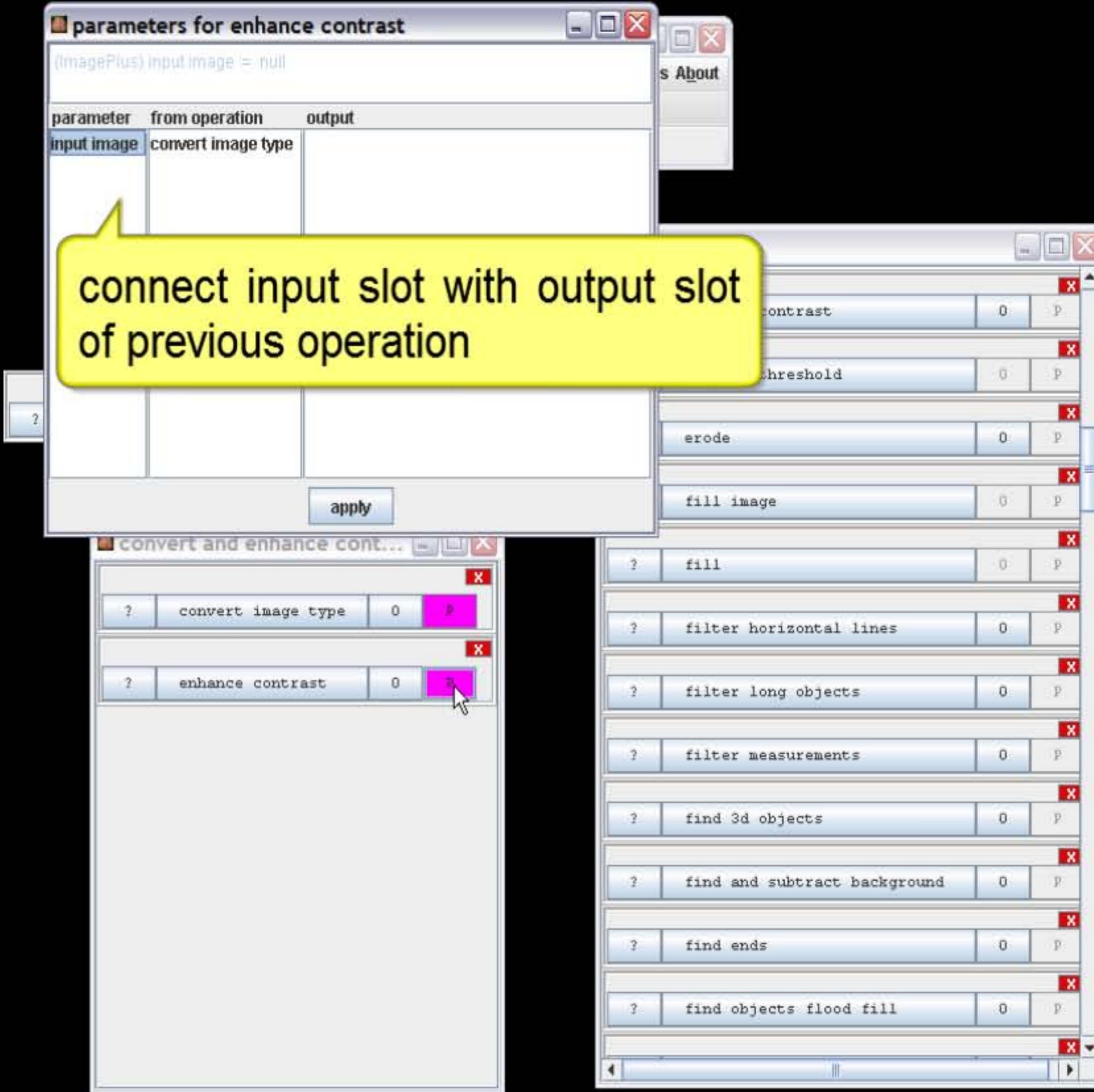
**all operations**

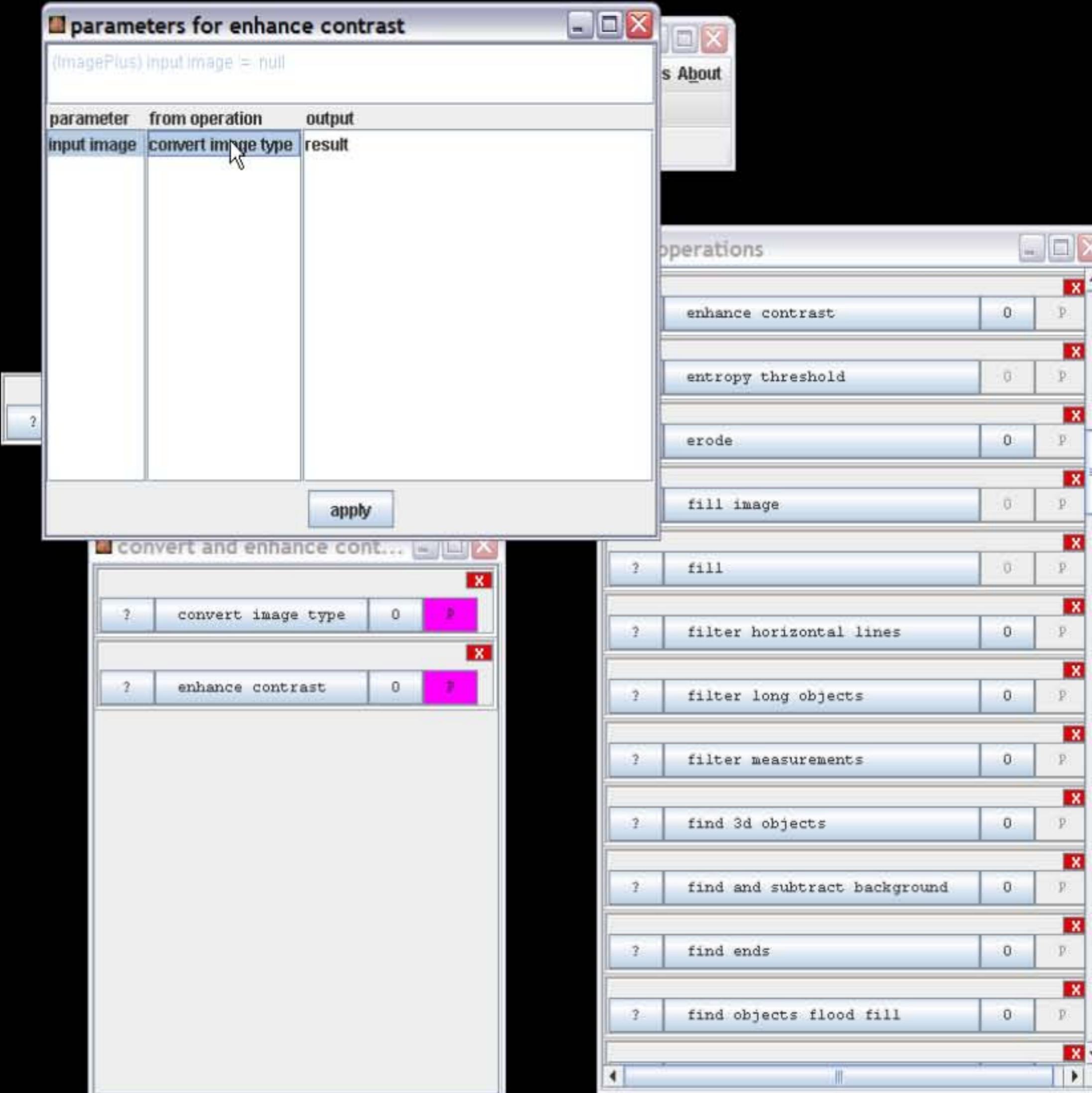
enhance contrast  
entropy threshold  
erode  
fill image  
fill  
filter horizontal lines  
filter long objects  
filter measurements  
find 3d objects  
find and subtract background  
find ends  
find objects flood fill

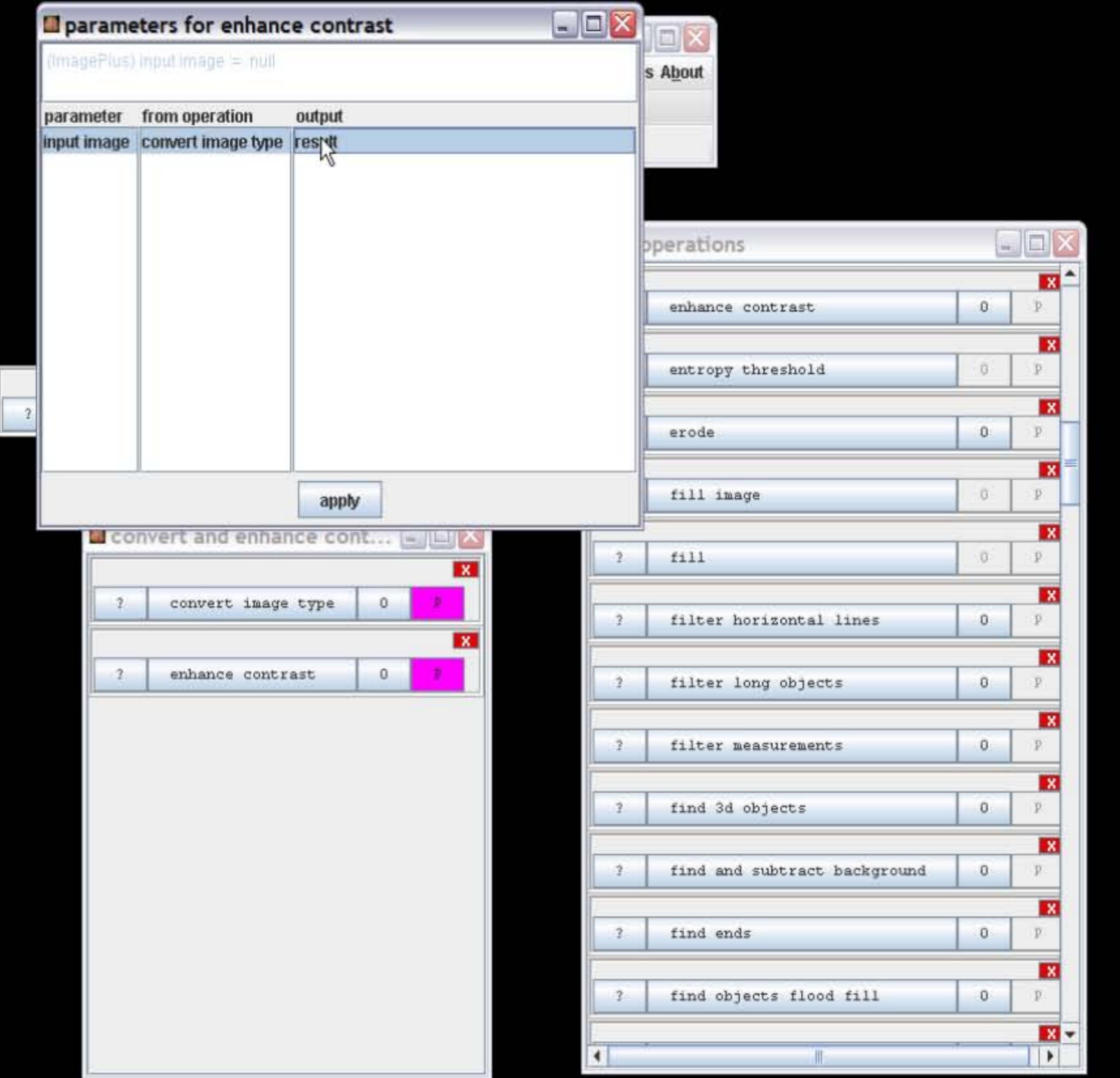
**convert and enhance cont...**

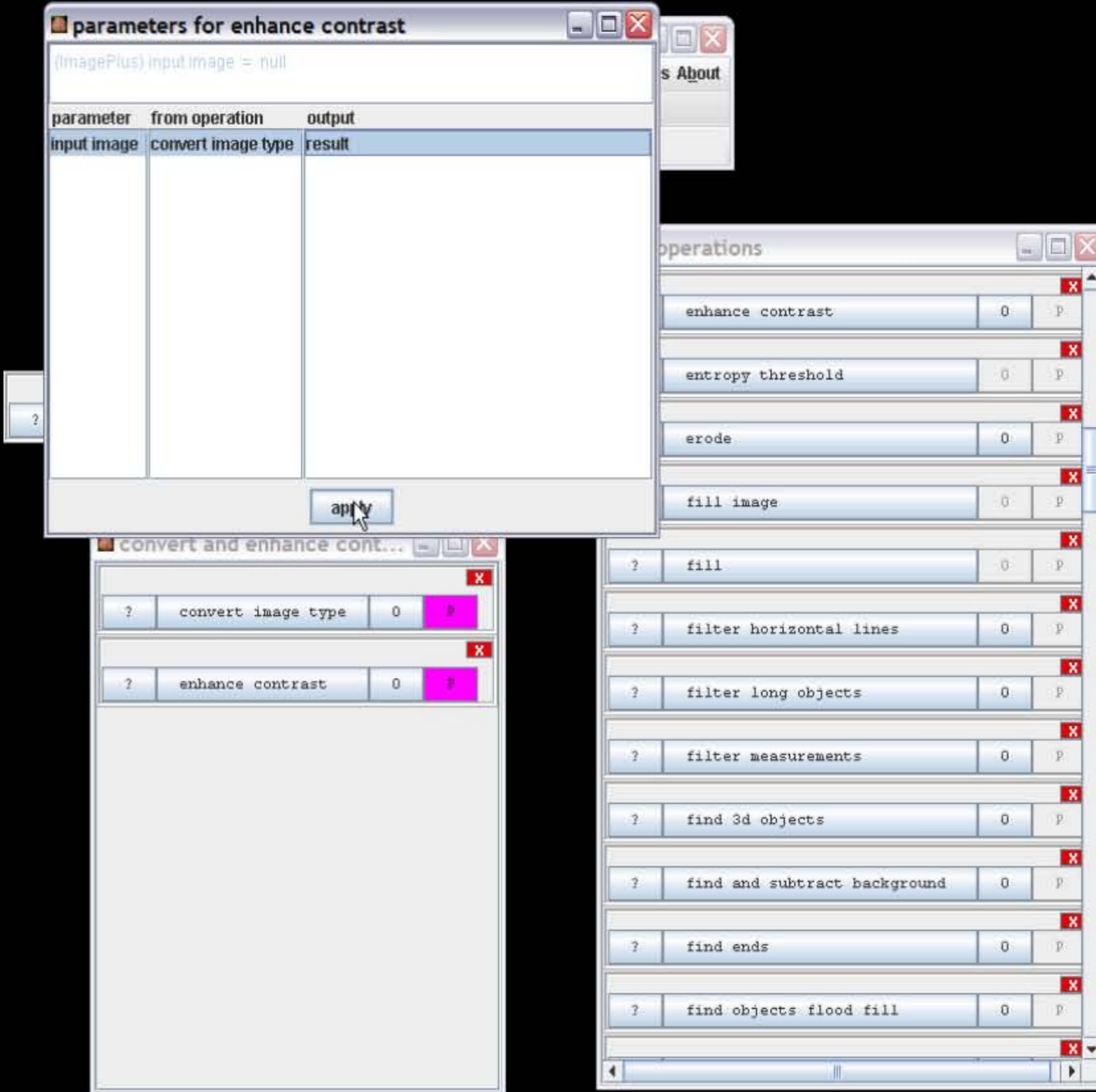
convert image type  
enhance contrast

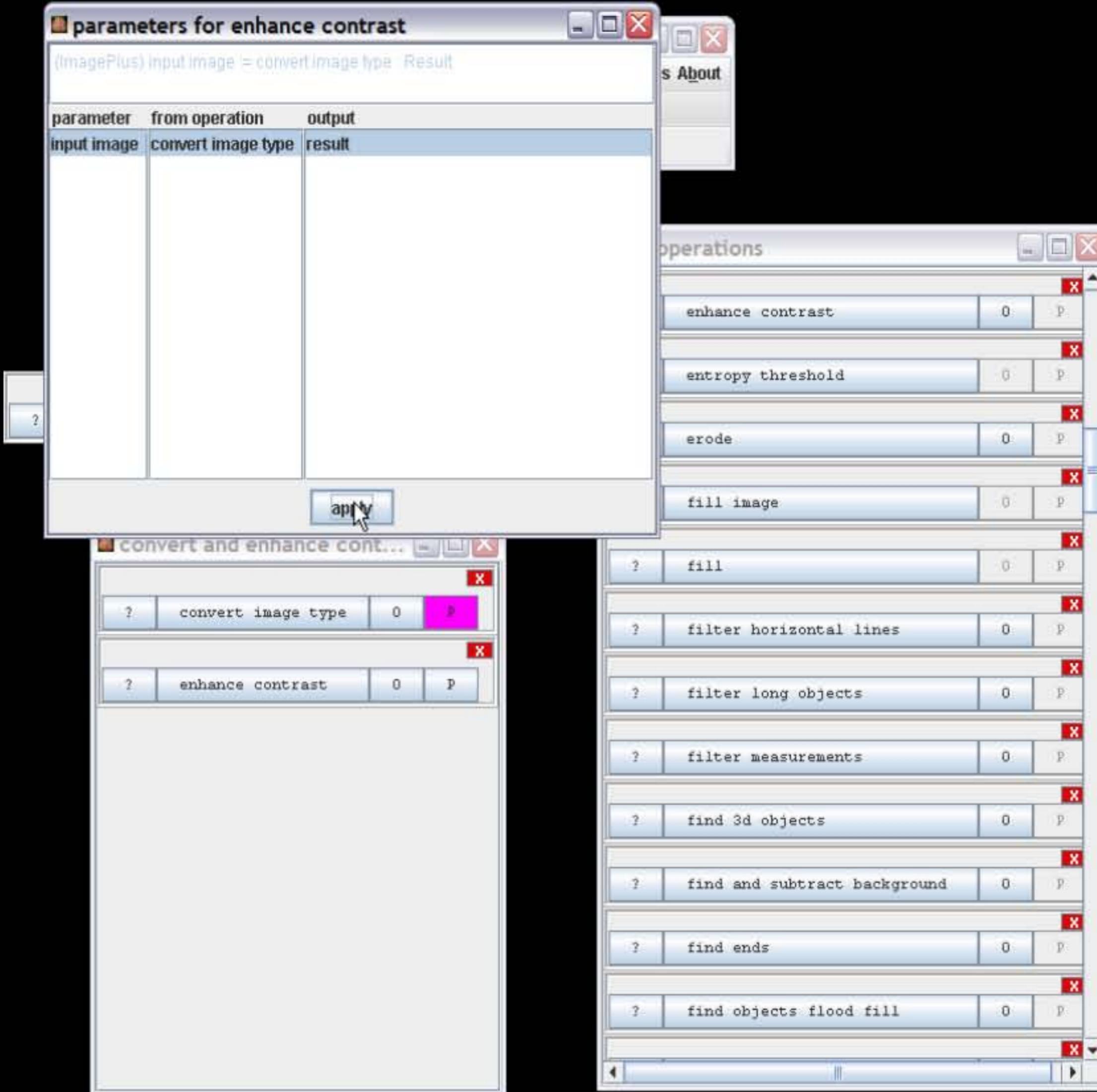


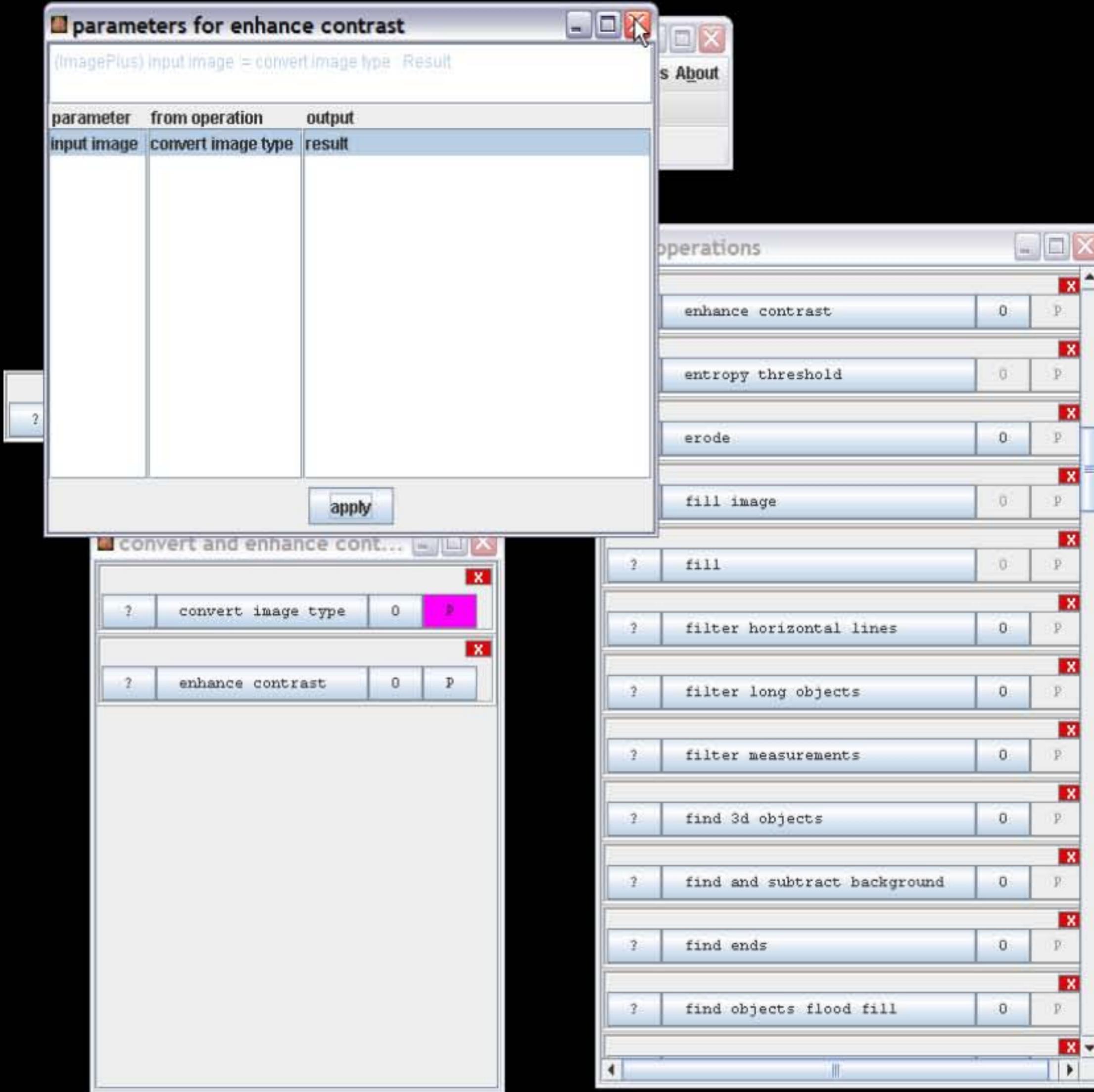


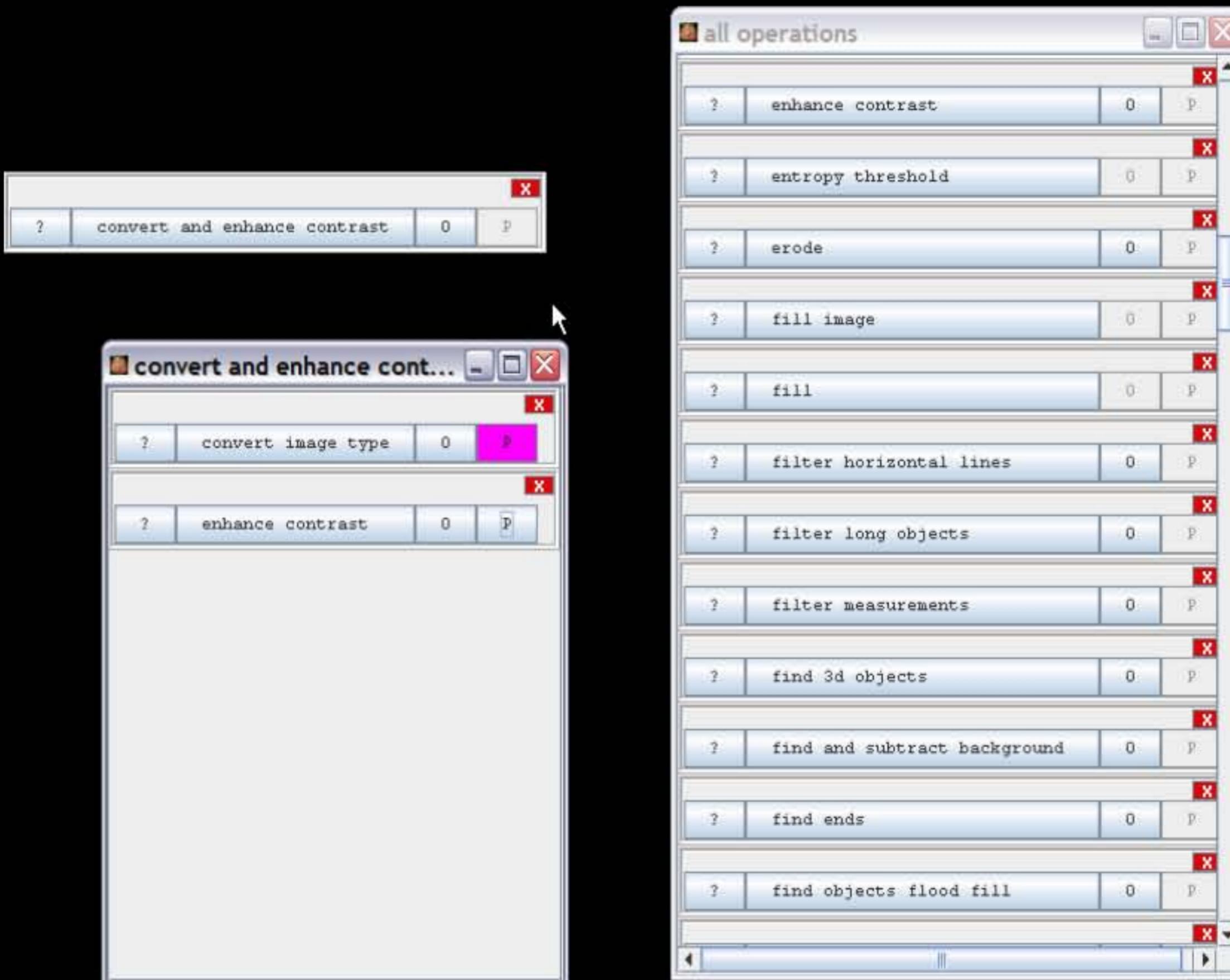












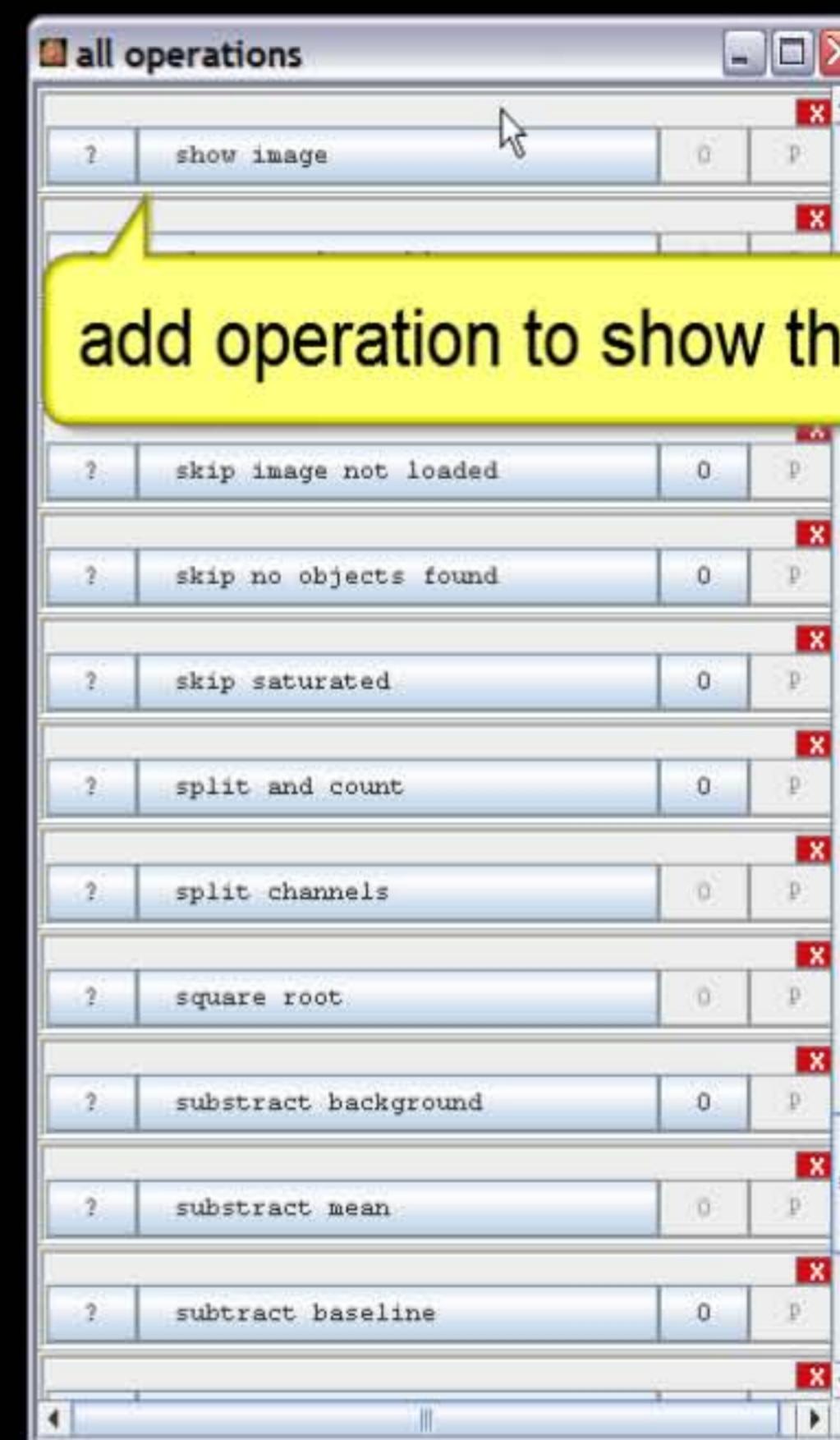
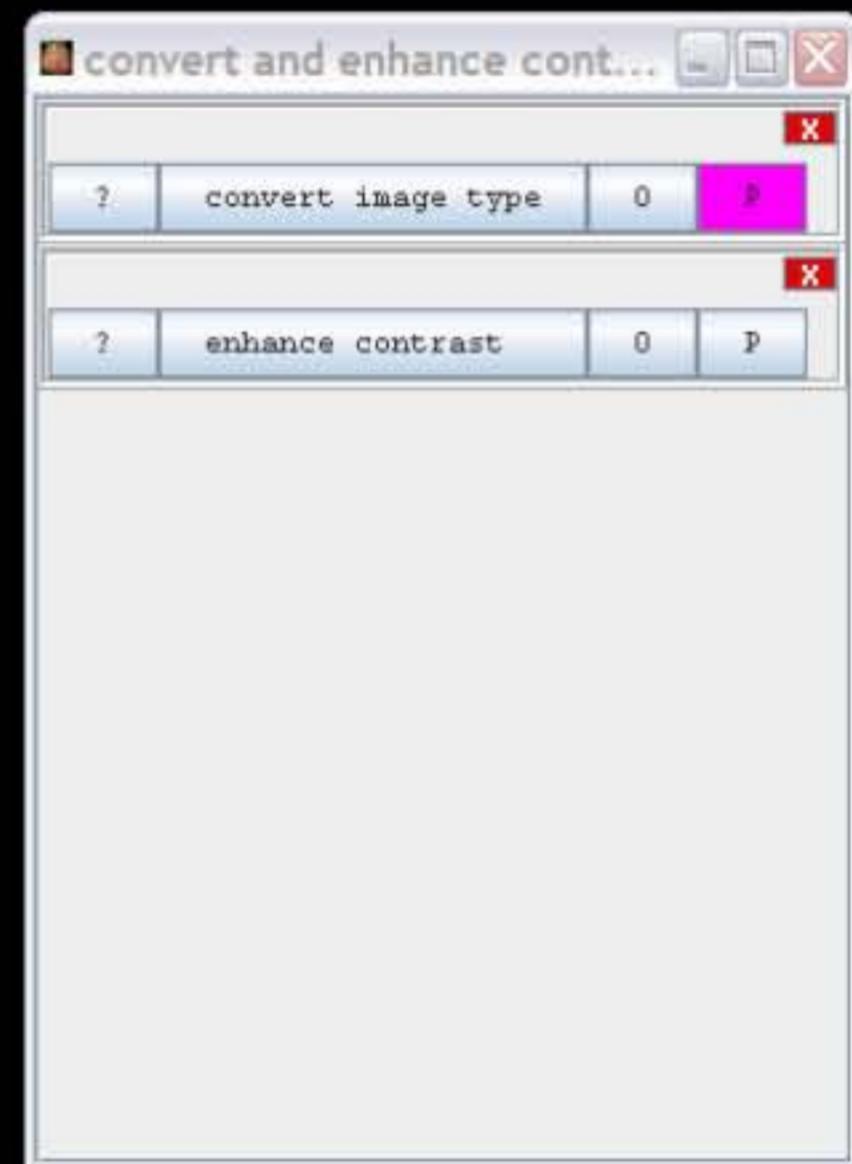
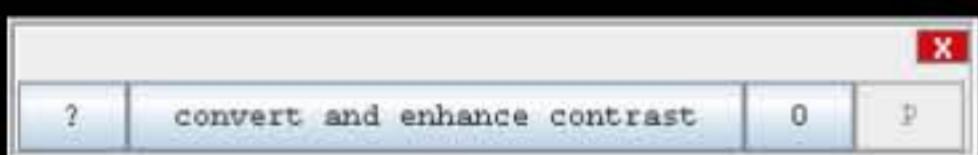


**all operations**

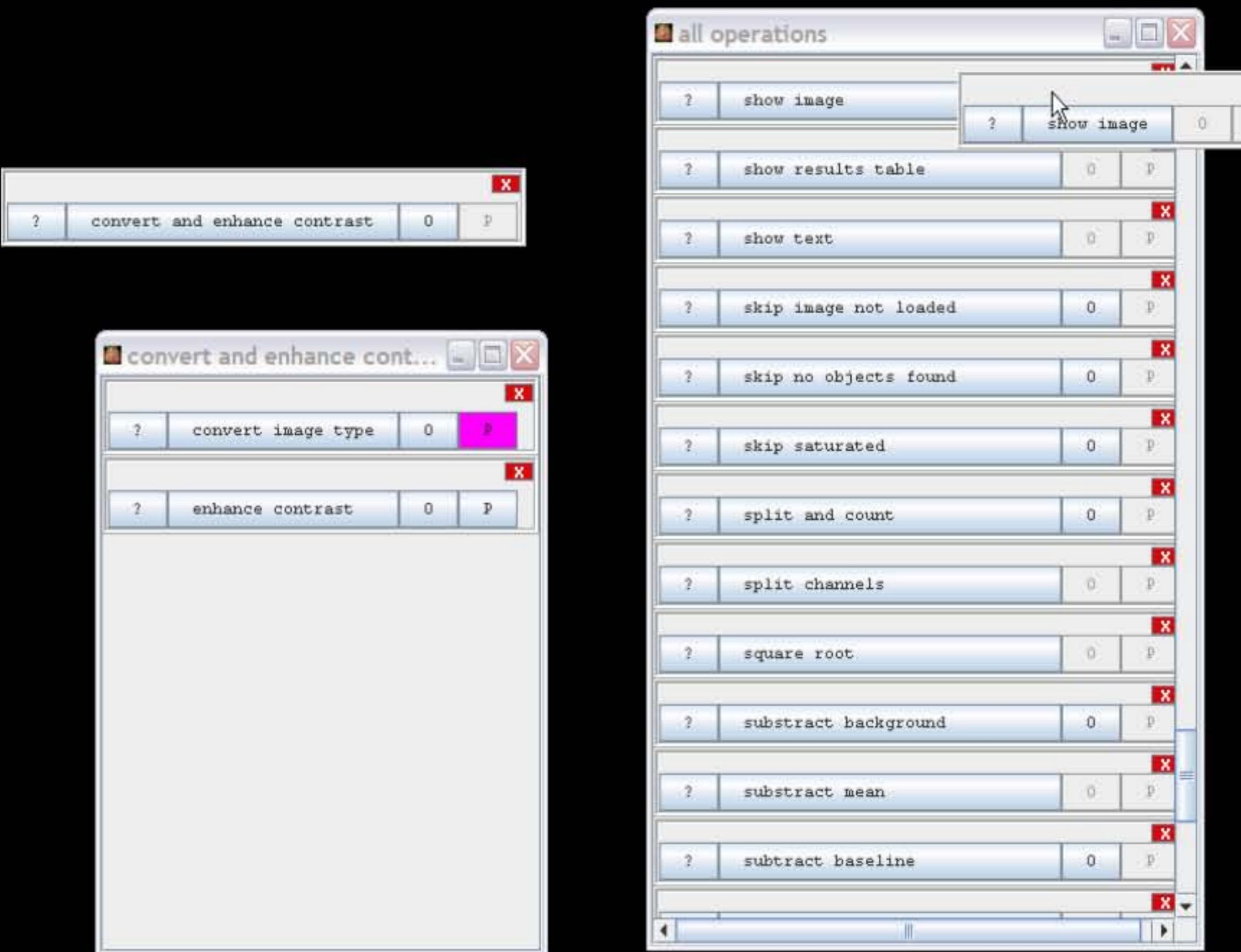
- ? enhance contrast 0 P
- ? entropy threshold 0 P
- ? erode 0 P
- ? fill image 0 P
- ? fill 0 P
- ? filter horizontal lines 0 P
- ? filter long objects 0 P
- ? filter measurements 0 P
- ? find 3d objects 0 P
- ? find and subtract background 0 P
- ? find ends 0 P
- ? find objects flood fill 0 P

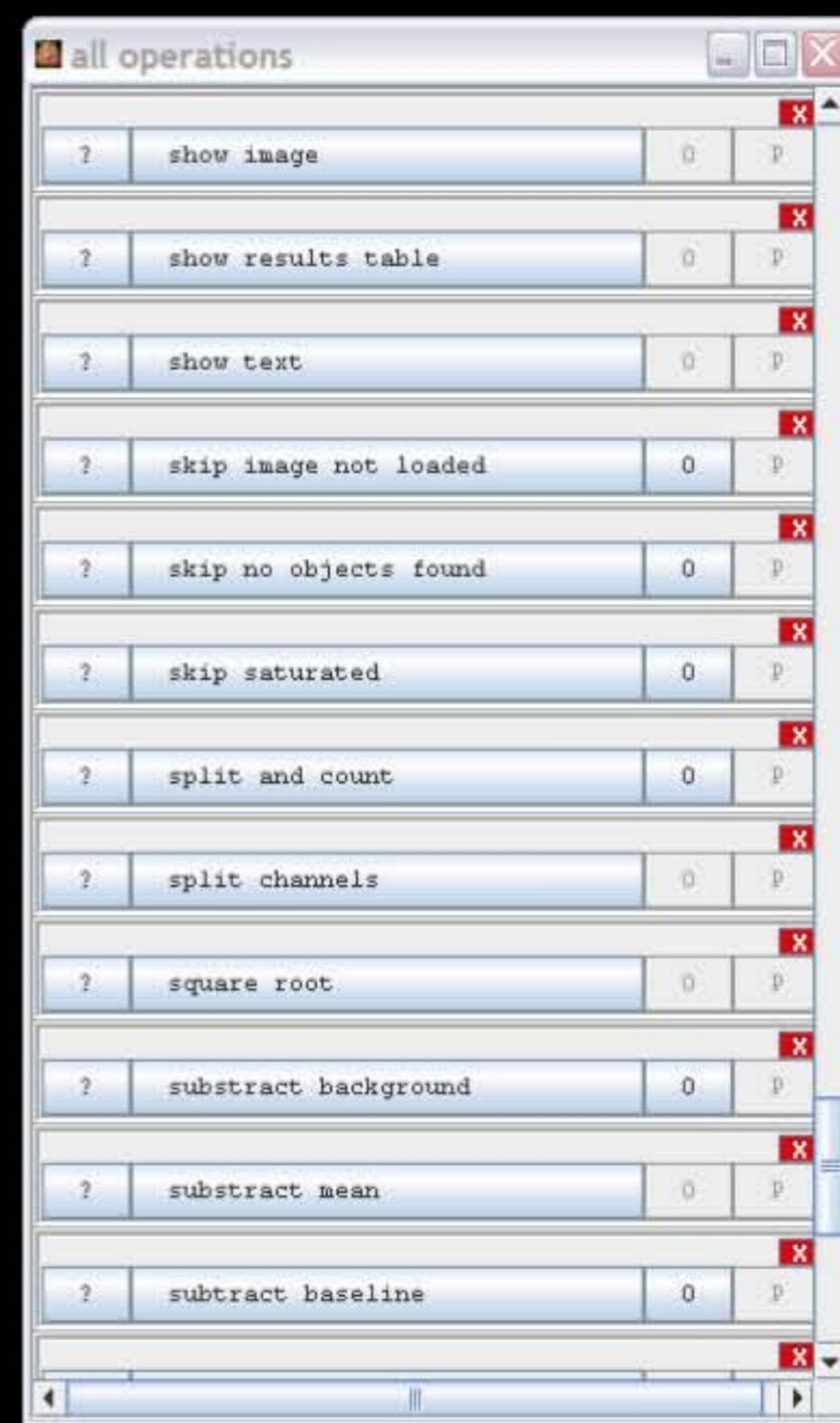
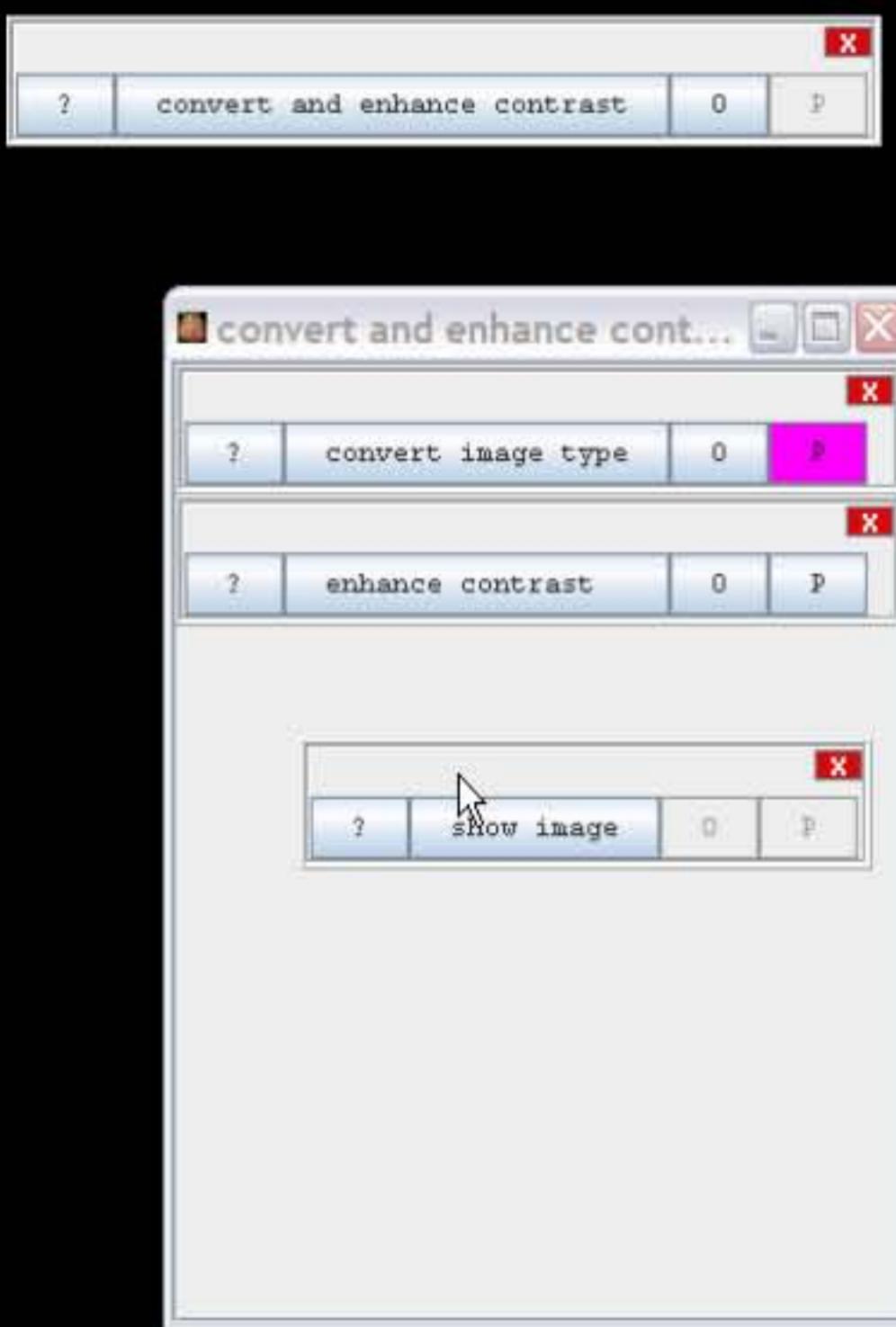
**convert and enhance cont...**

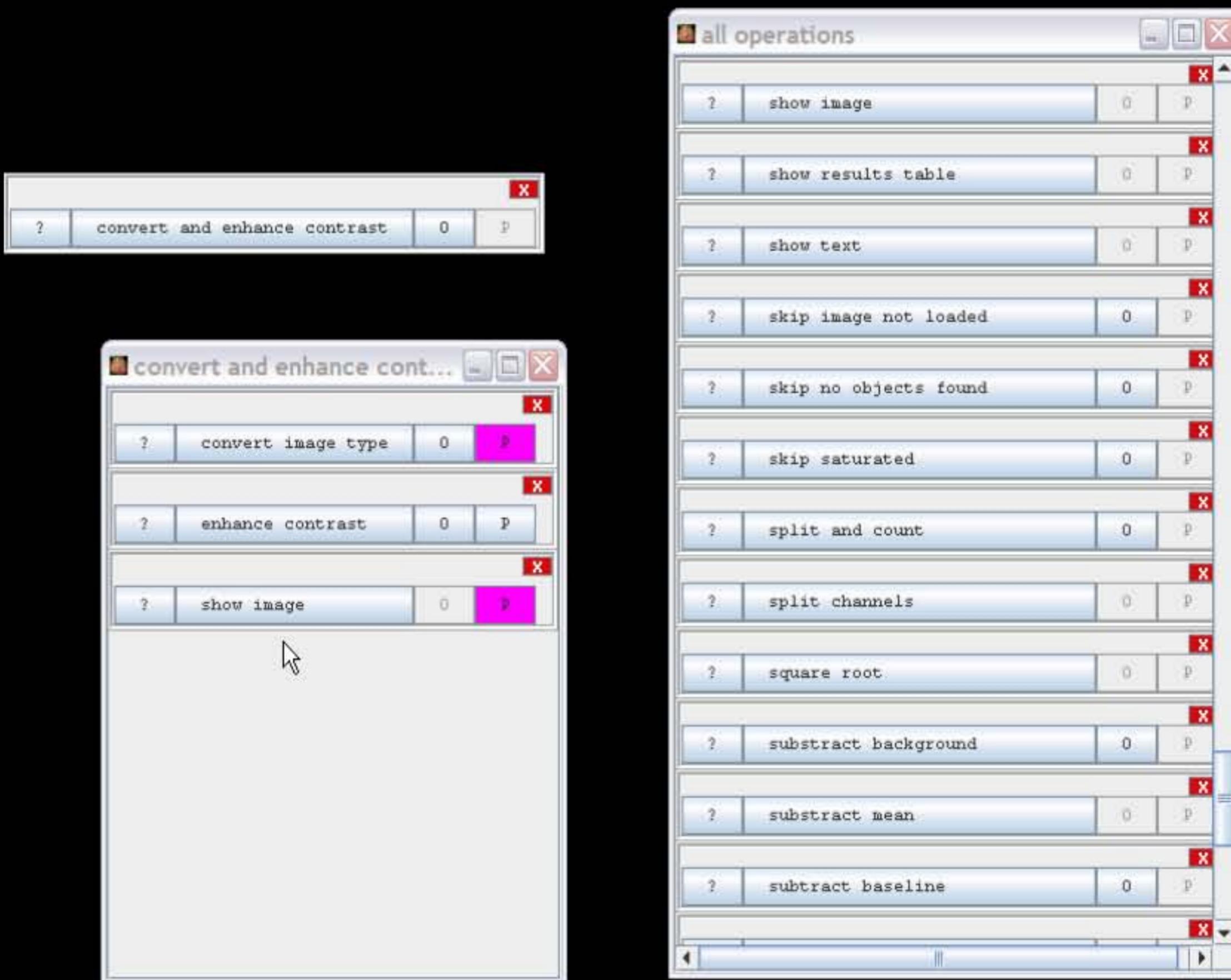
- ? convert image type 0 P
- ? enhance contrast 0 P

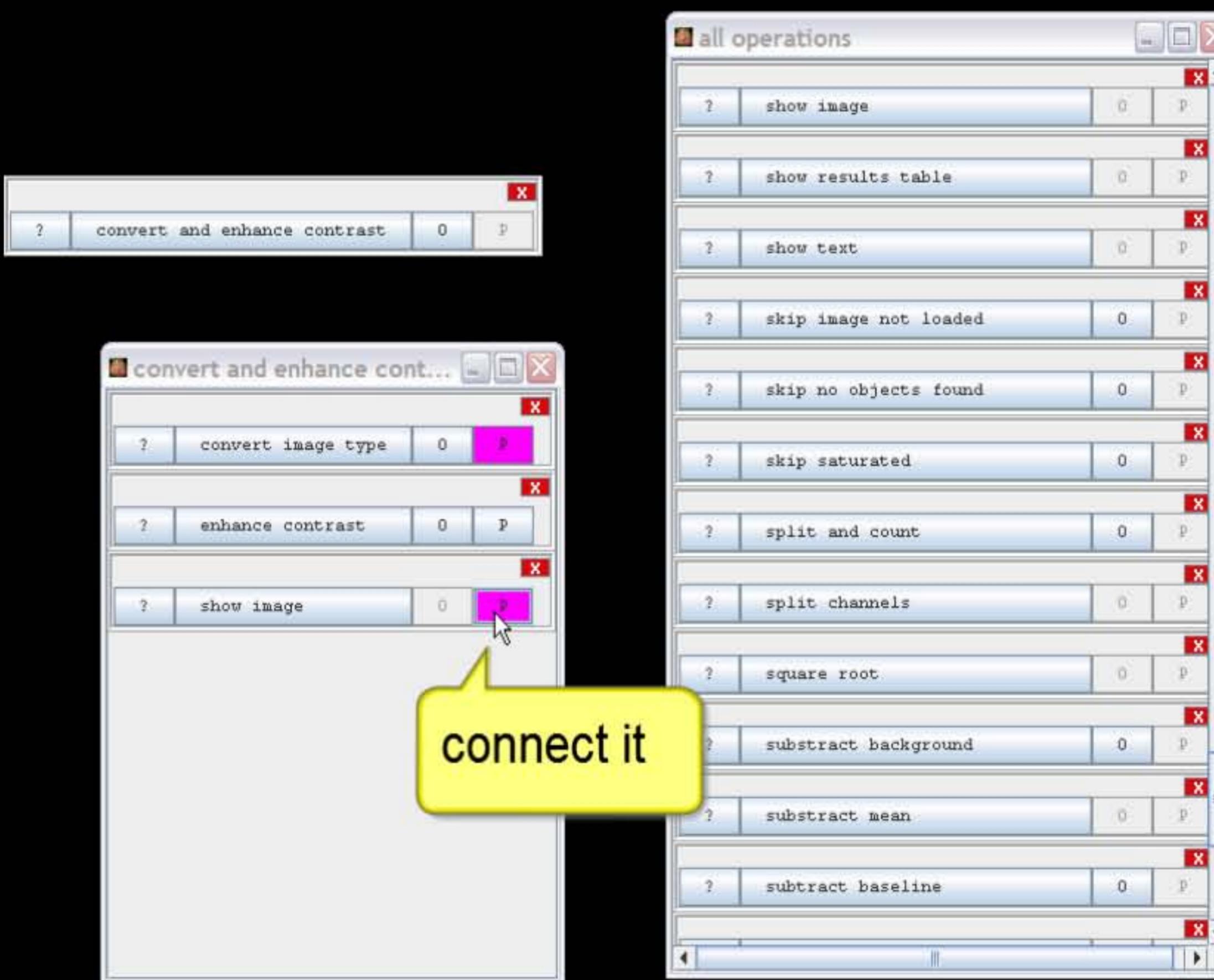


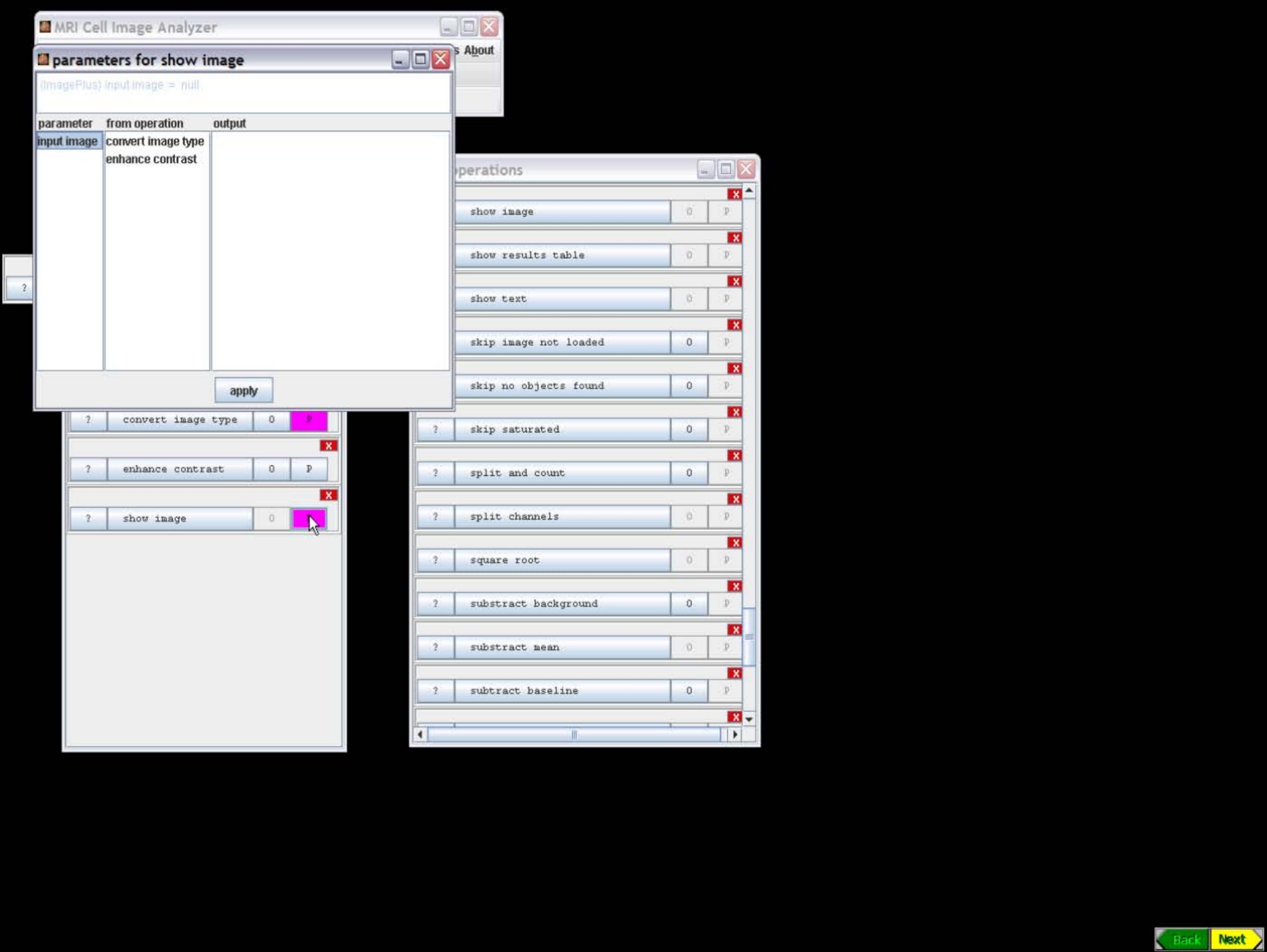
add operation to show the result

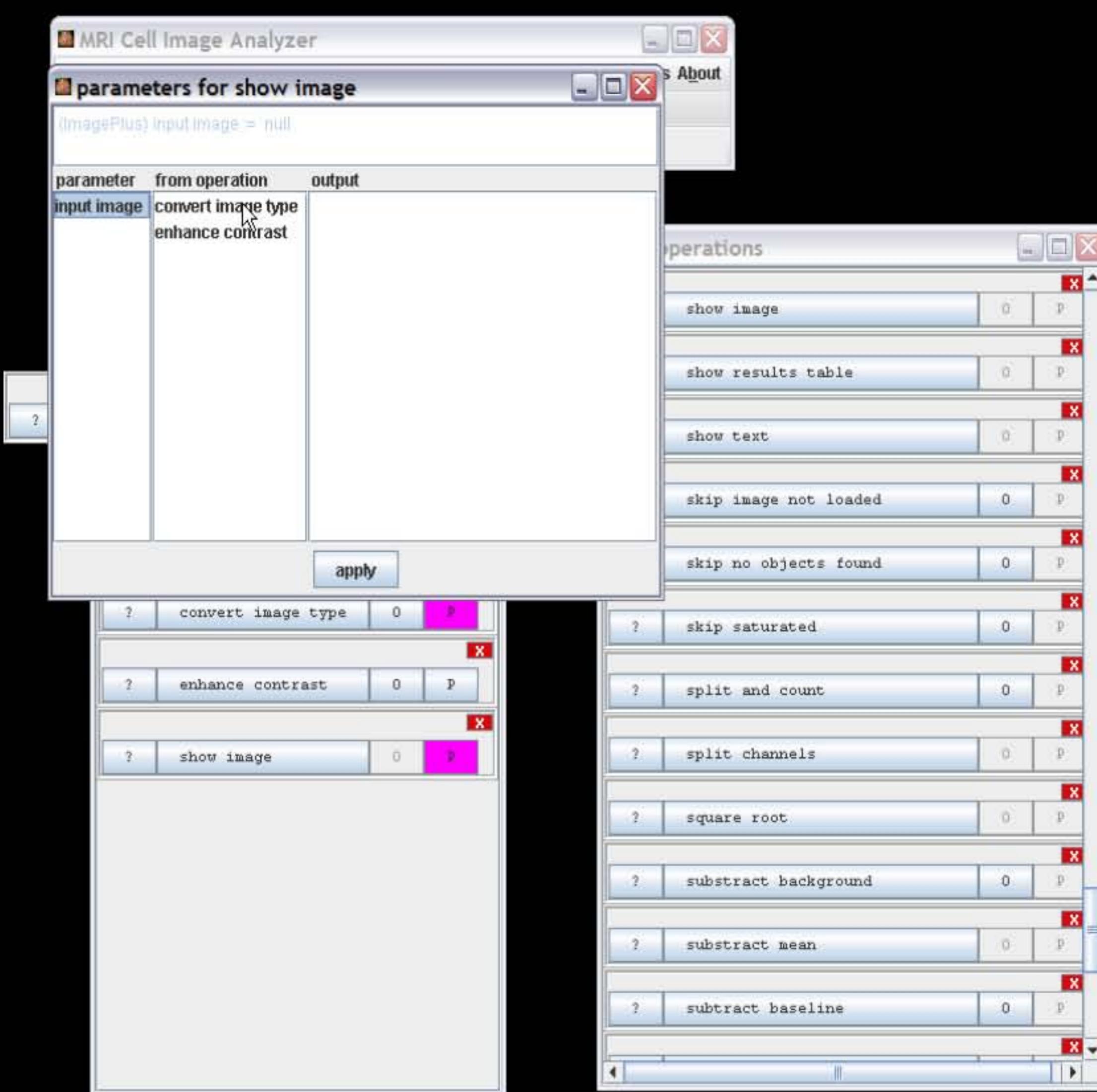


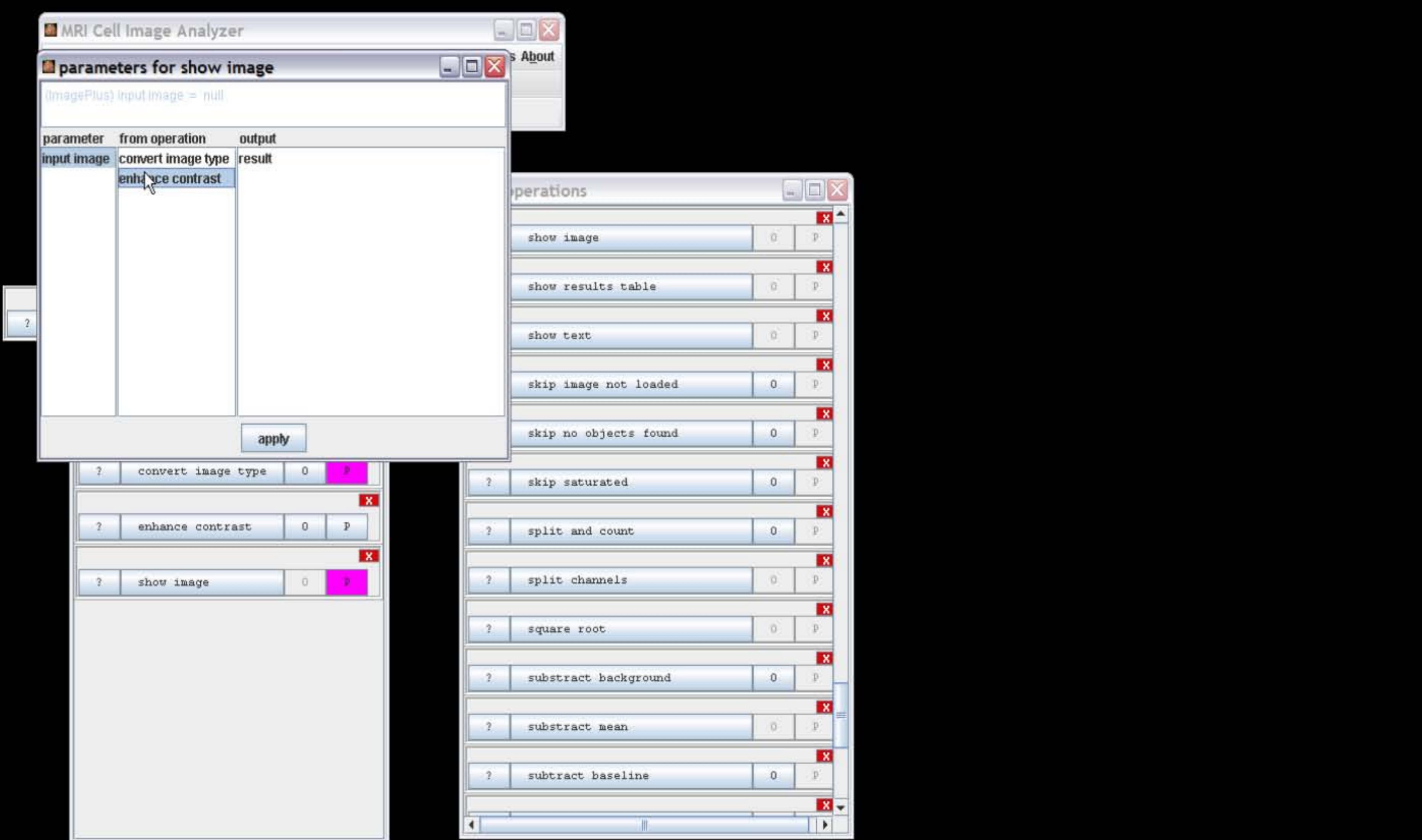


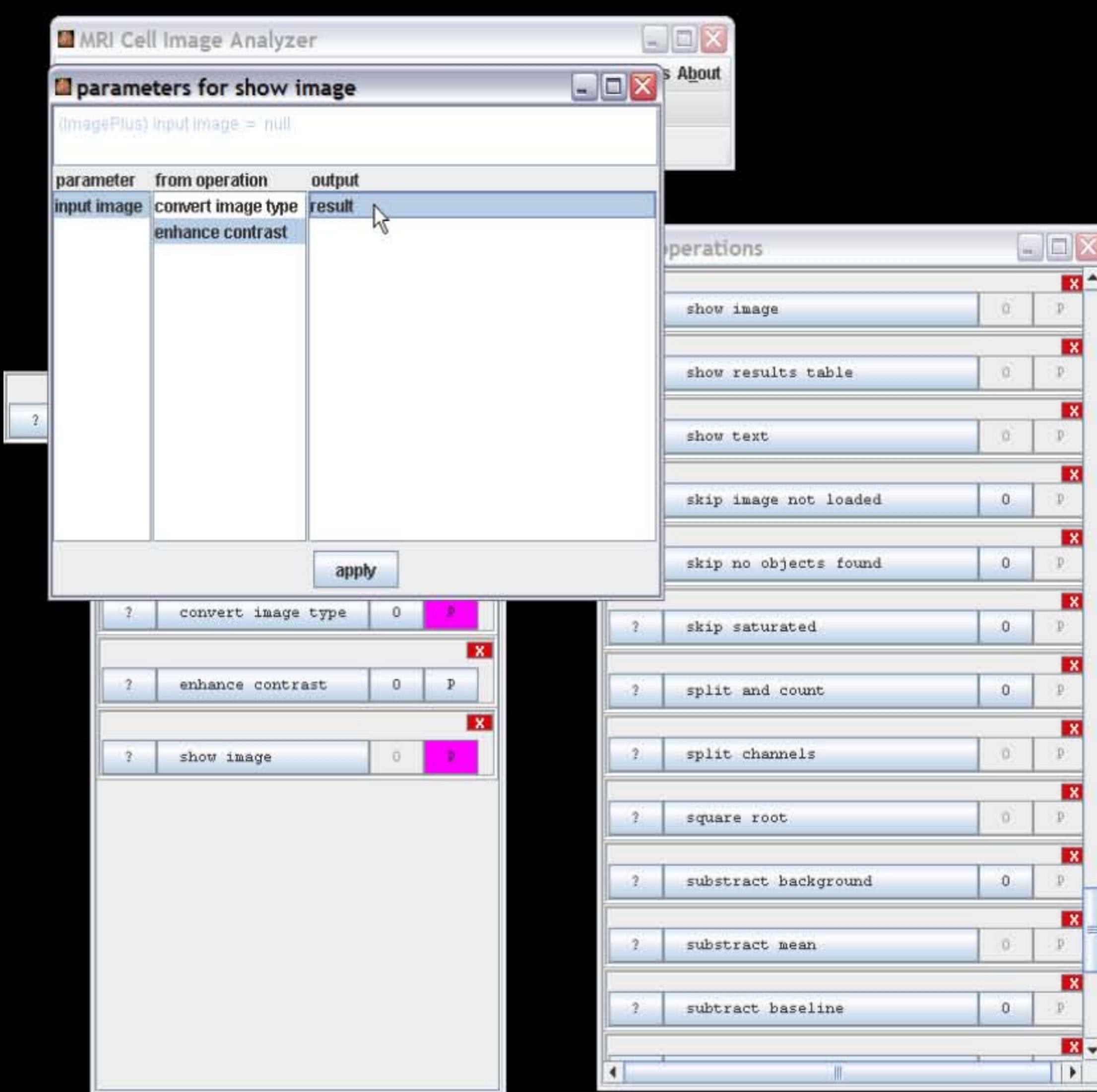


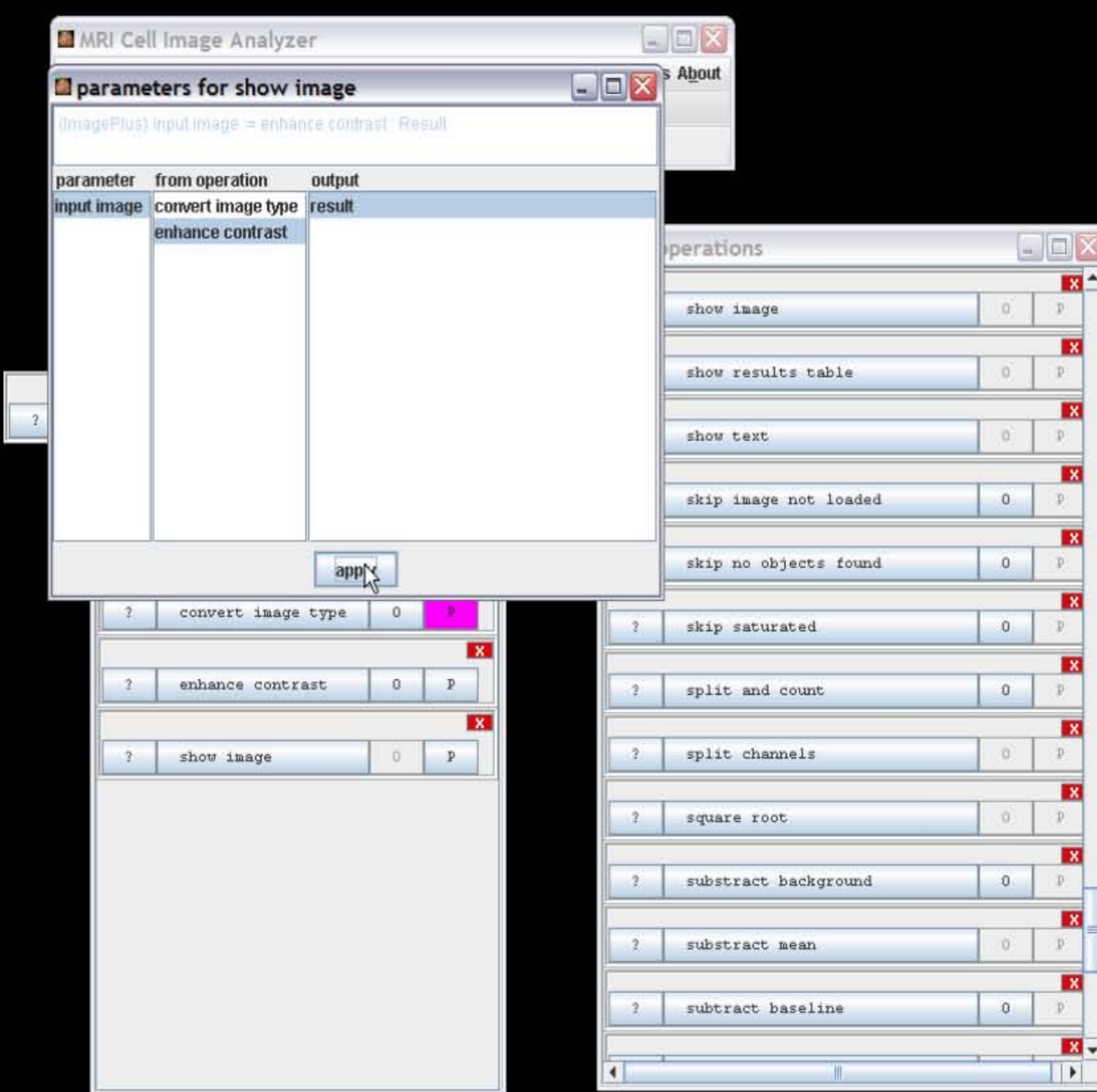


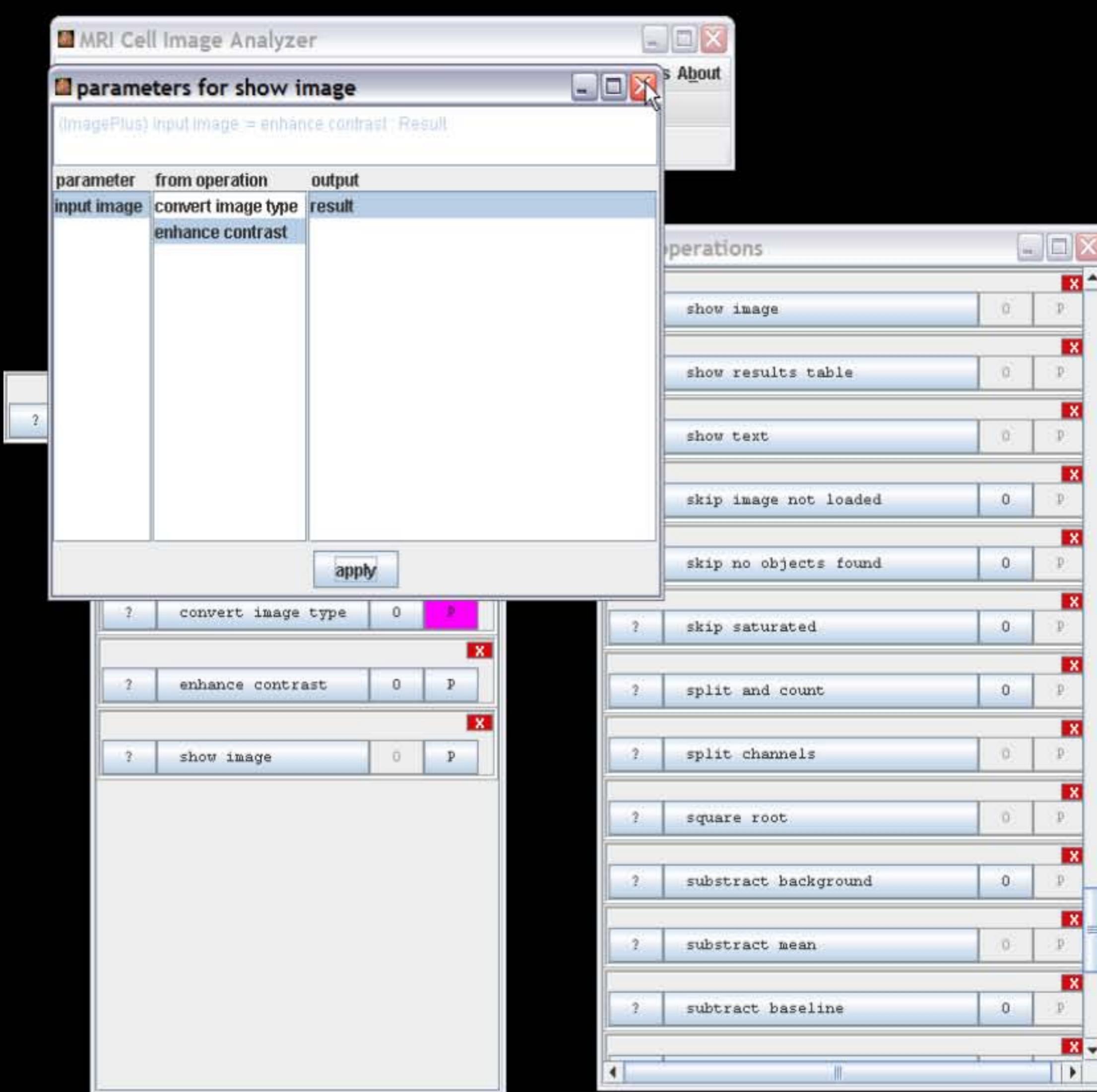














**all operations**

?	show image	0	p
?	show results table	0	p
?	show text	0	p
?	skip image not loaded	0	p
?	skip no objects found	0	p
?	skip saturated	0	p
?	split and count	0	p
?	split channels	0	p
?	square root	0	p
?	subtract background	0	p
?	subtract mean	0	p
?	subtract baseline	0	p

**convert and enhance cont...**

convert image type

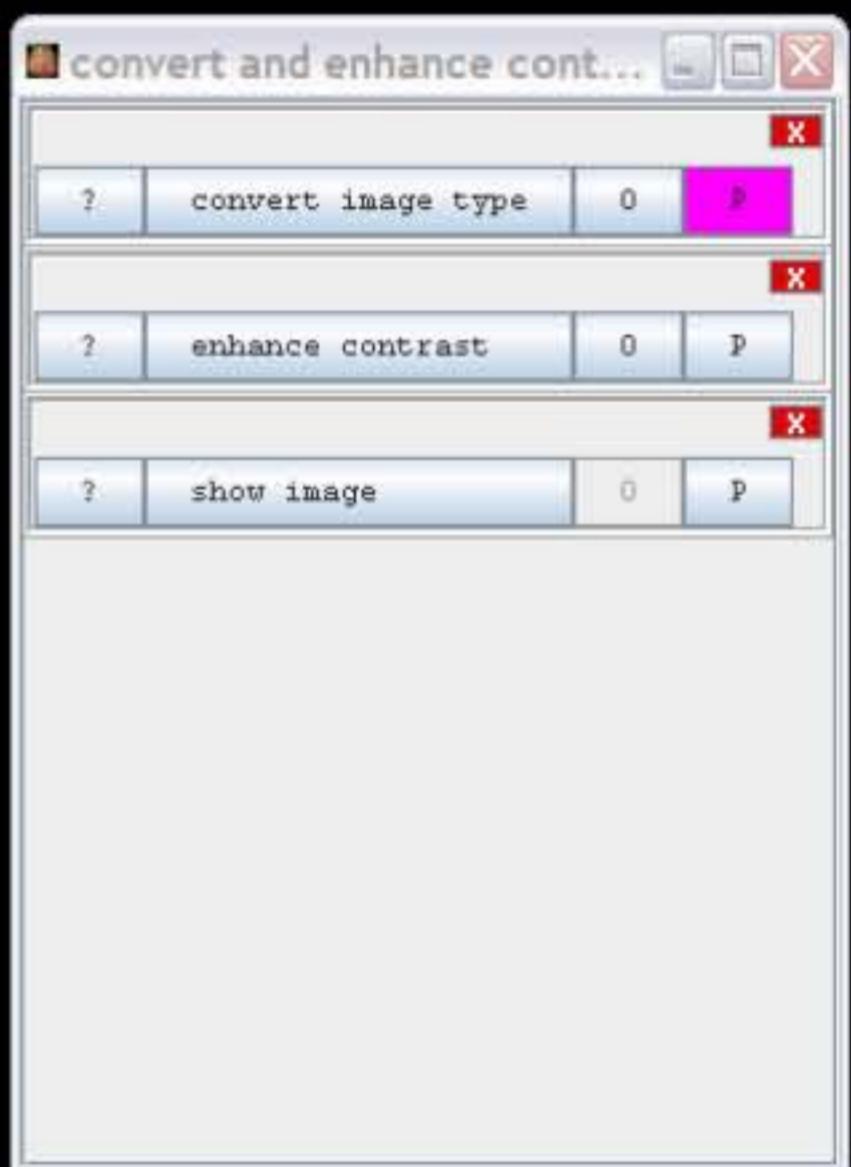
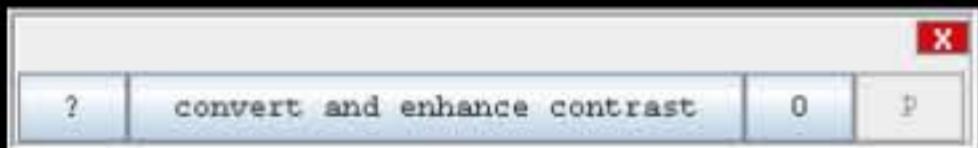
enhance contrast

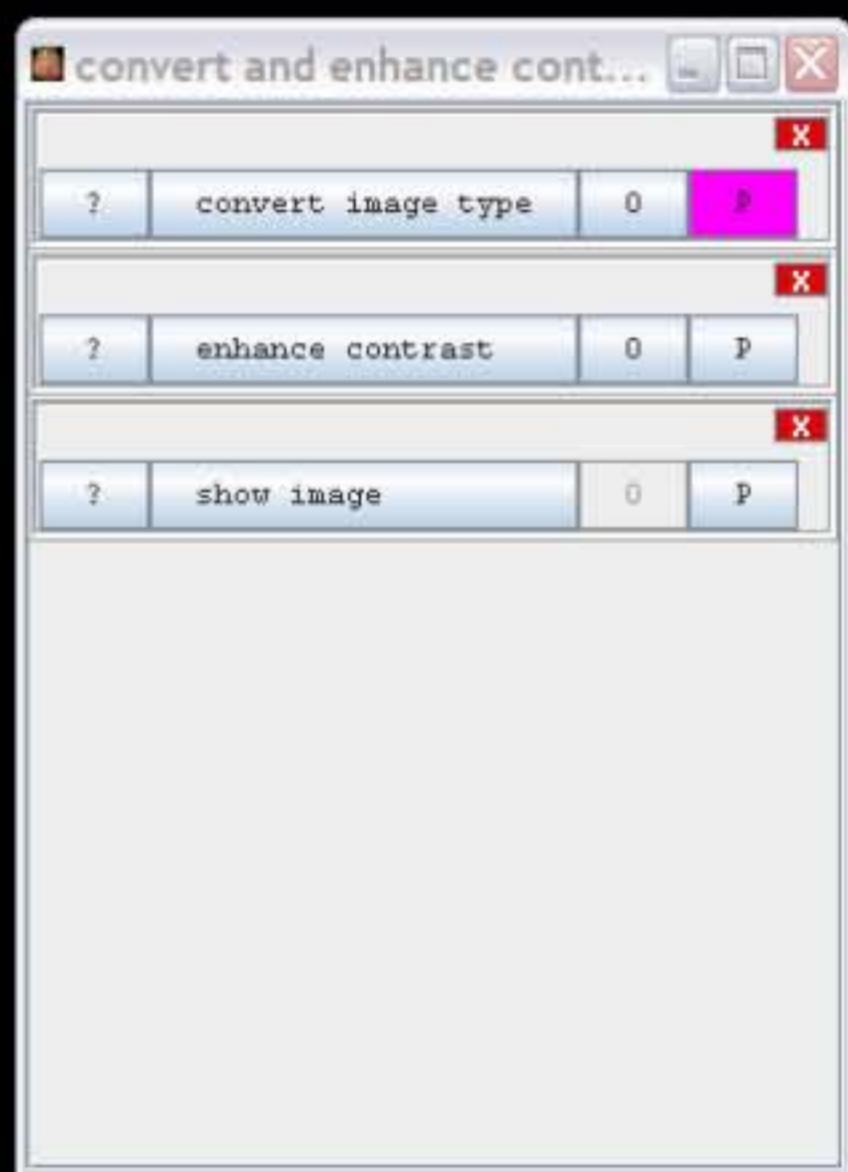
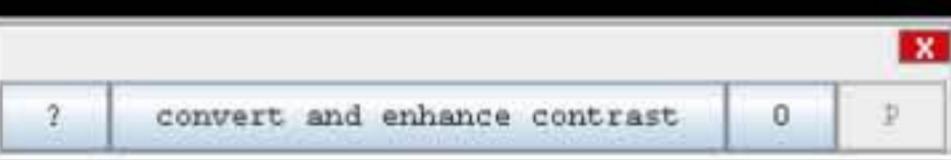
show image

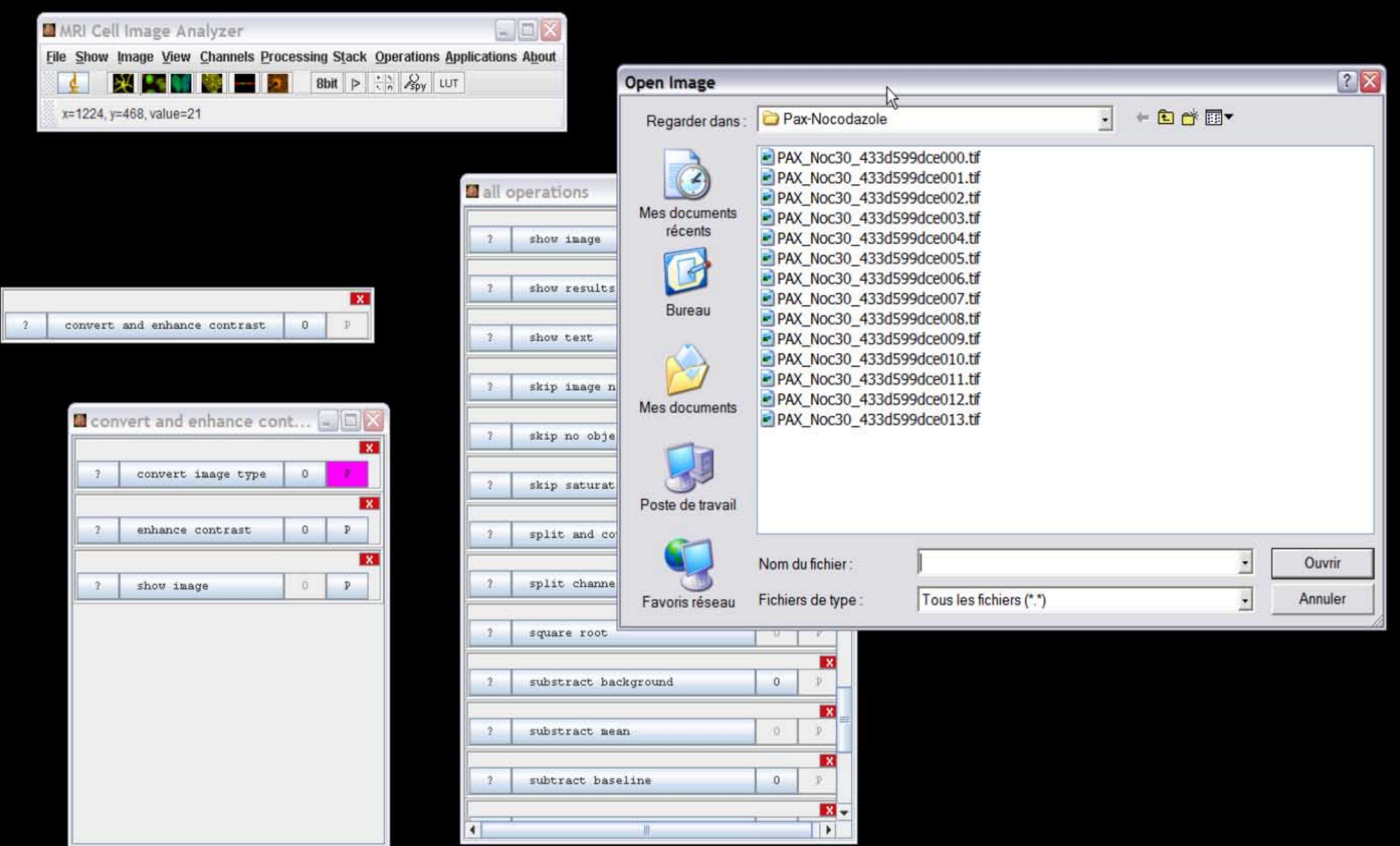
This is a dialog box titled "convert and enhance cont...". It contains three stacked operations: "convert image type" (with a pink highlighted button), "enhance contrast", and "show image". A cursor arrow is pointing towards the bottom right corner of the dialog box.

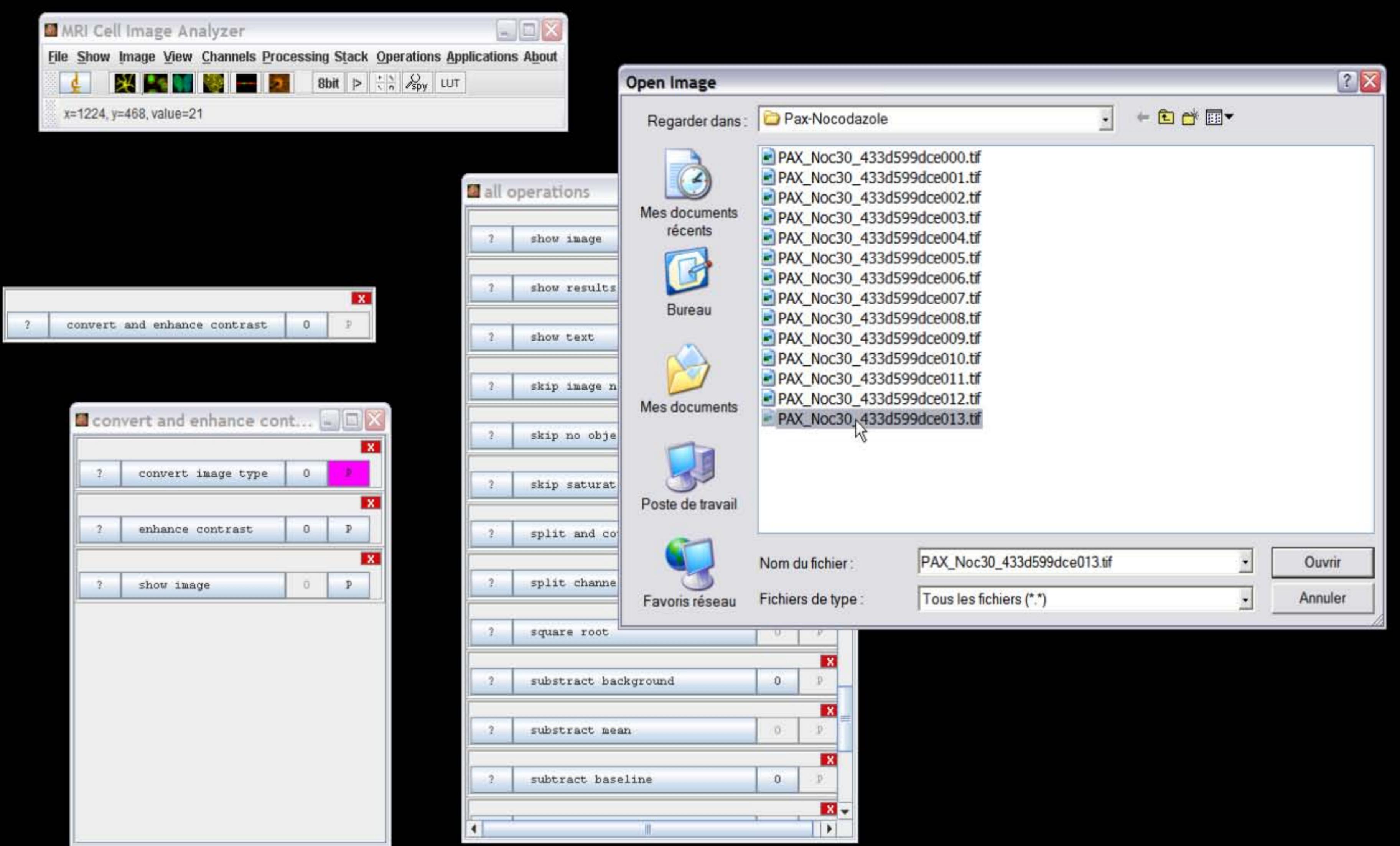


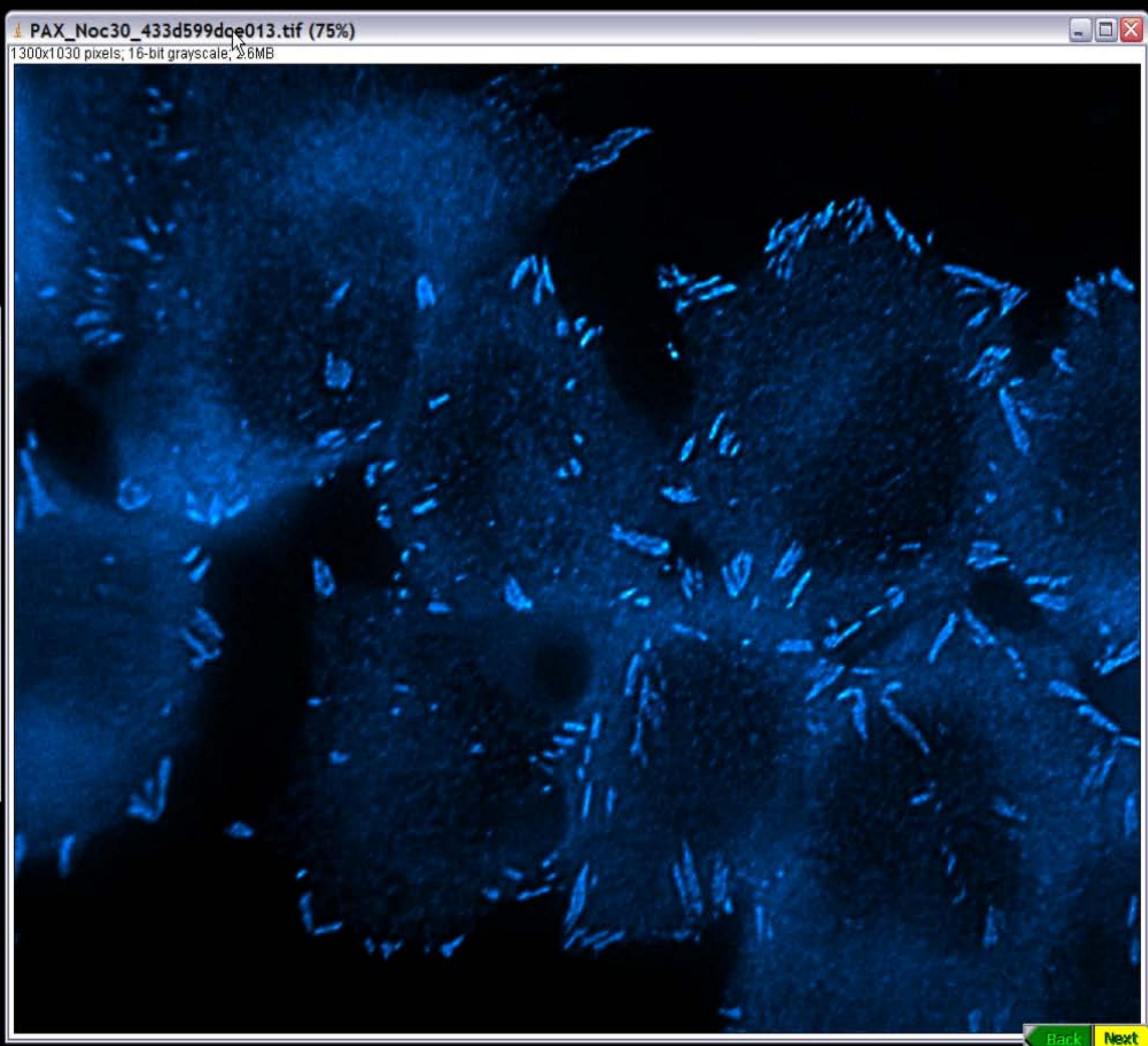
open an image

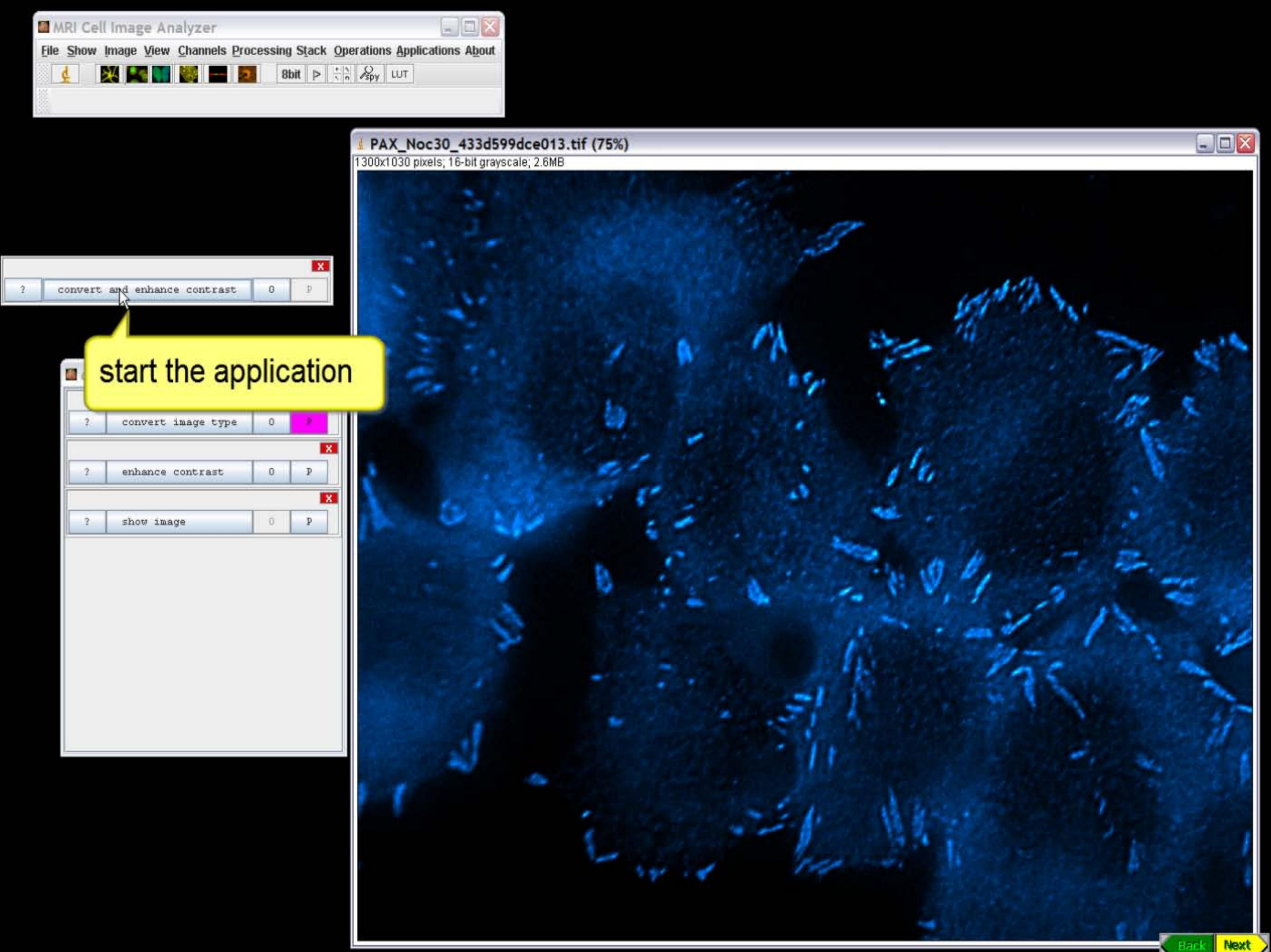


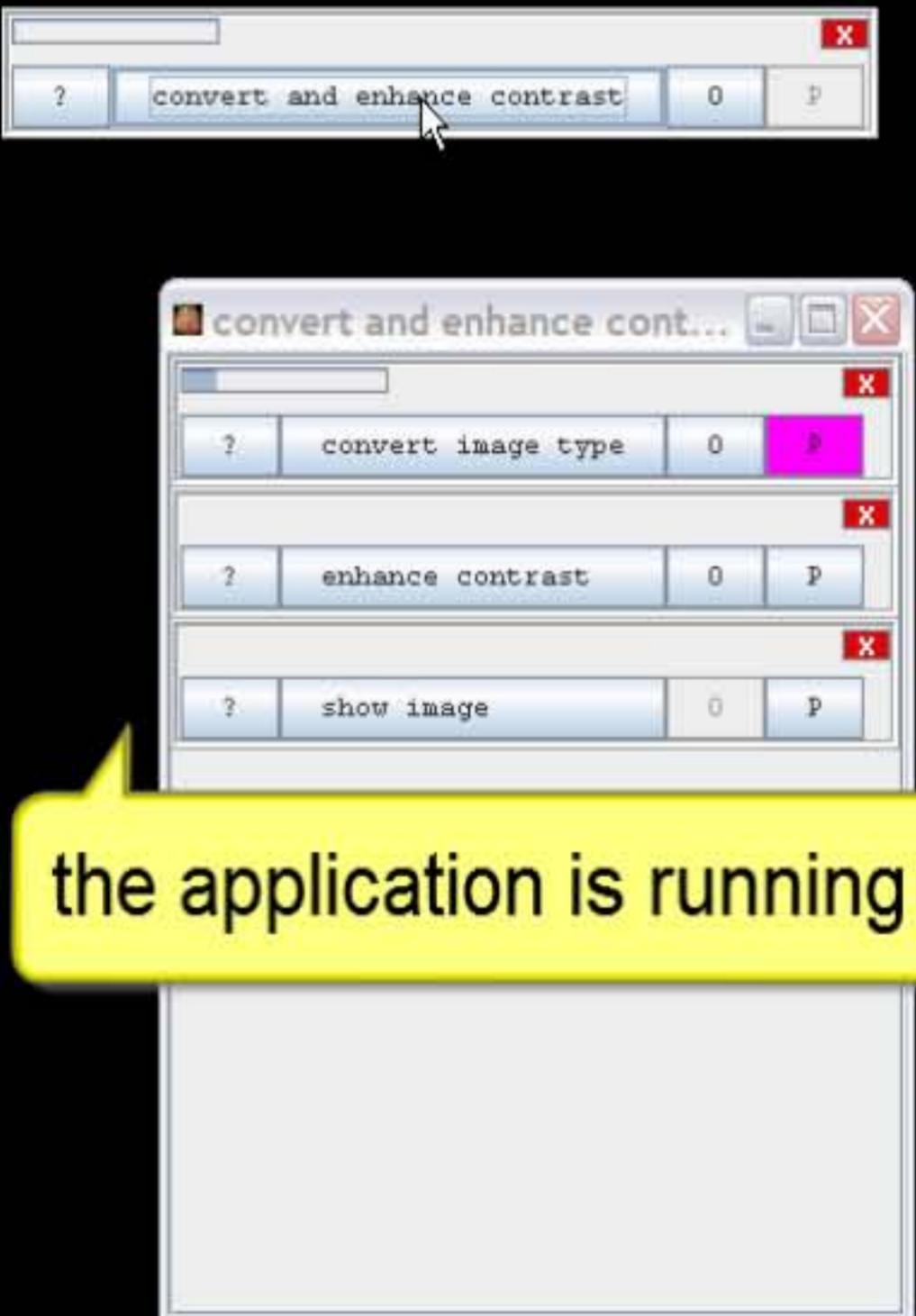
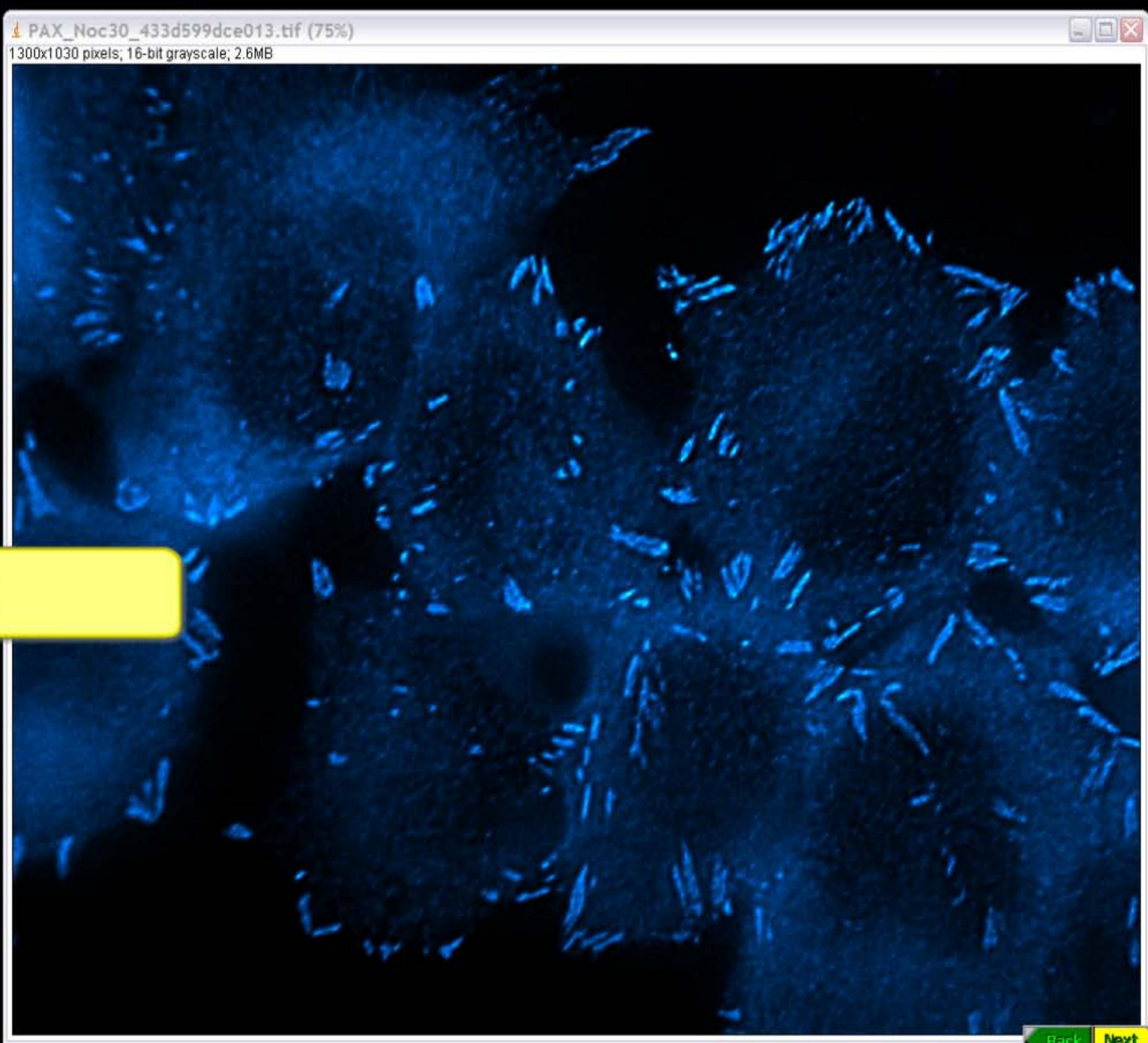








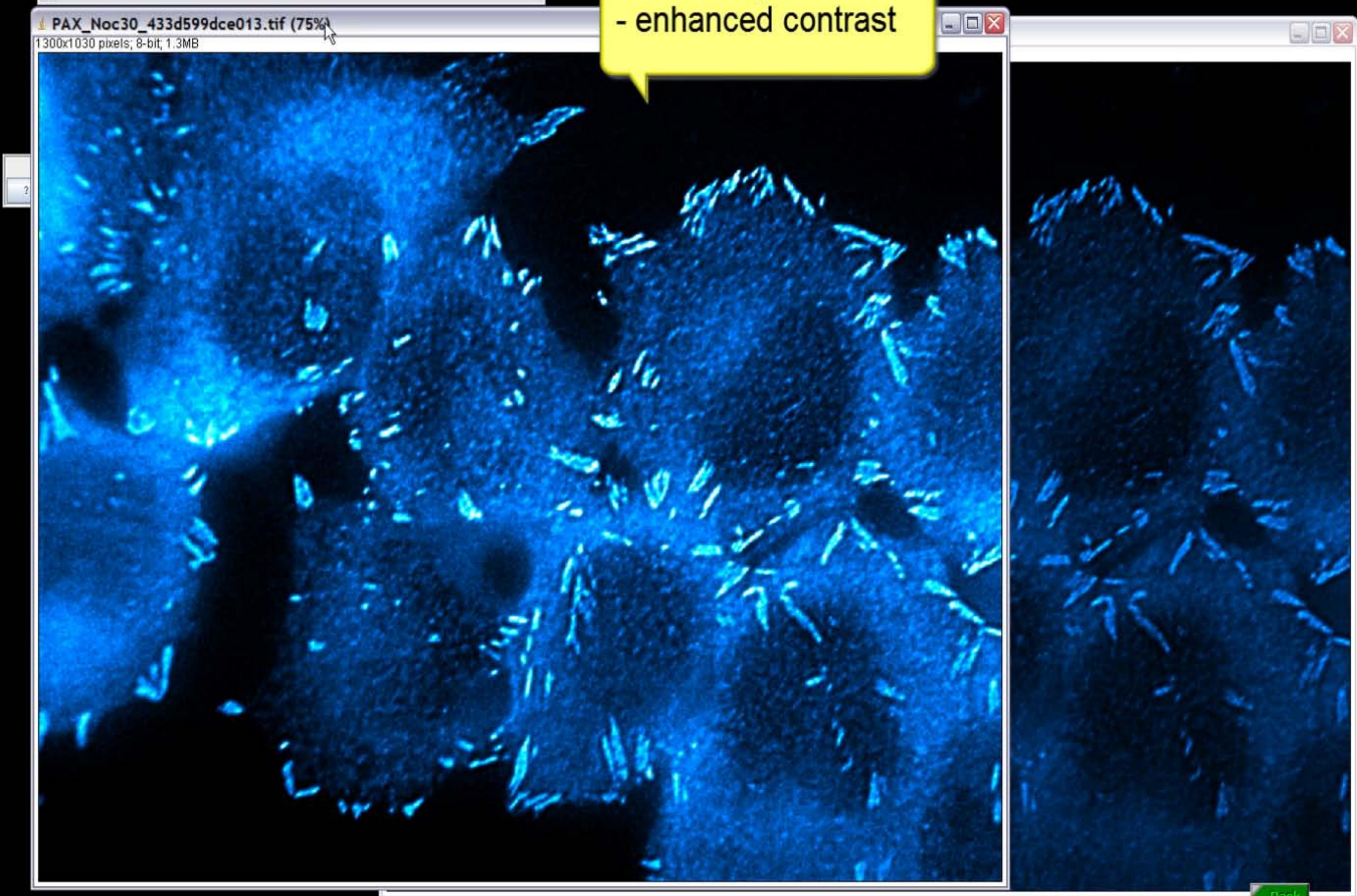




the application is running

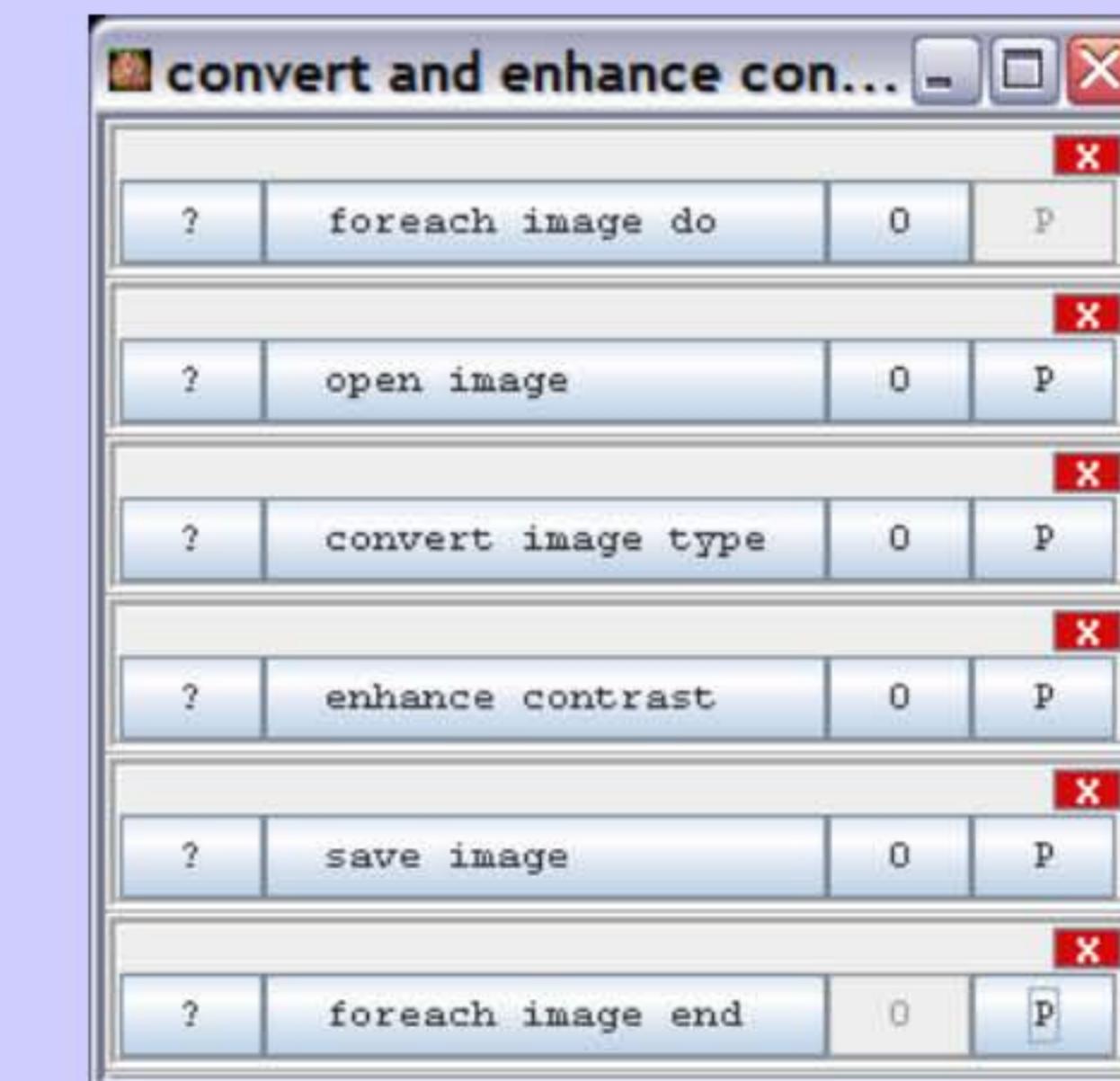
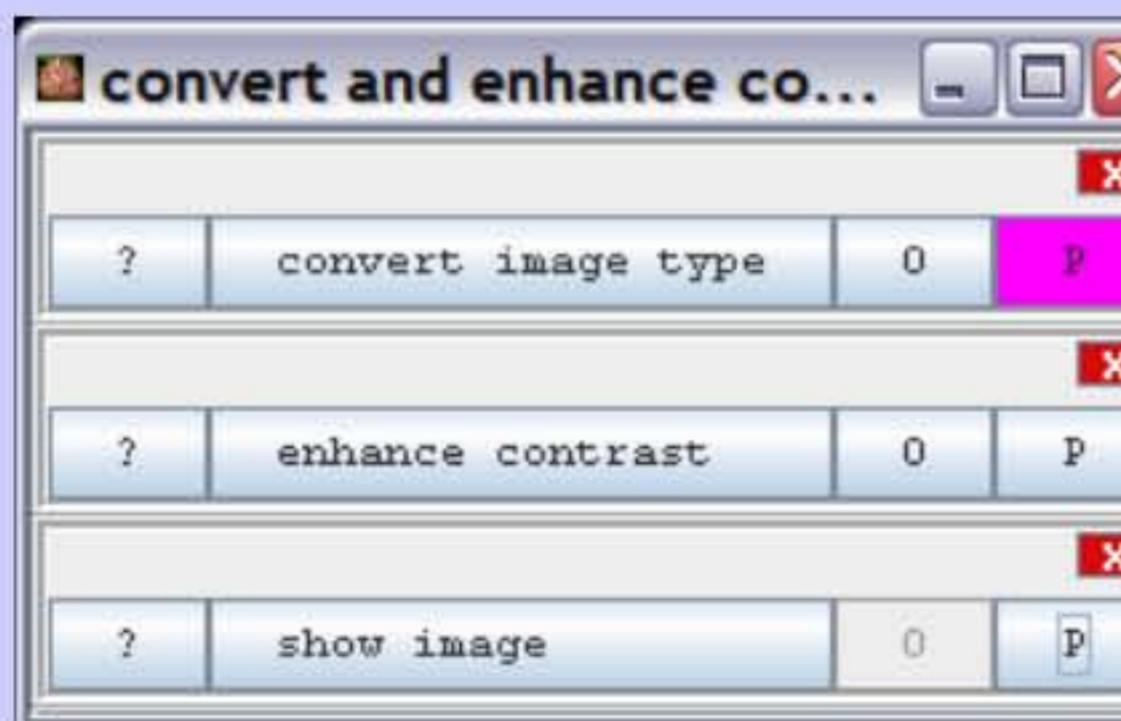


the result  
- 8 bit image  
- enhanced contrast



# Using visual scripting

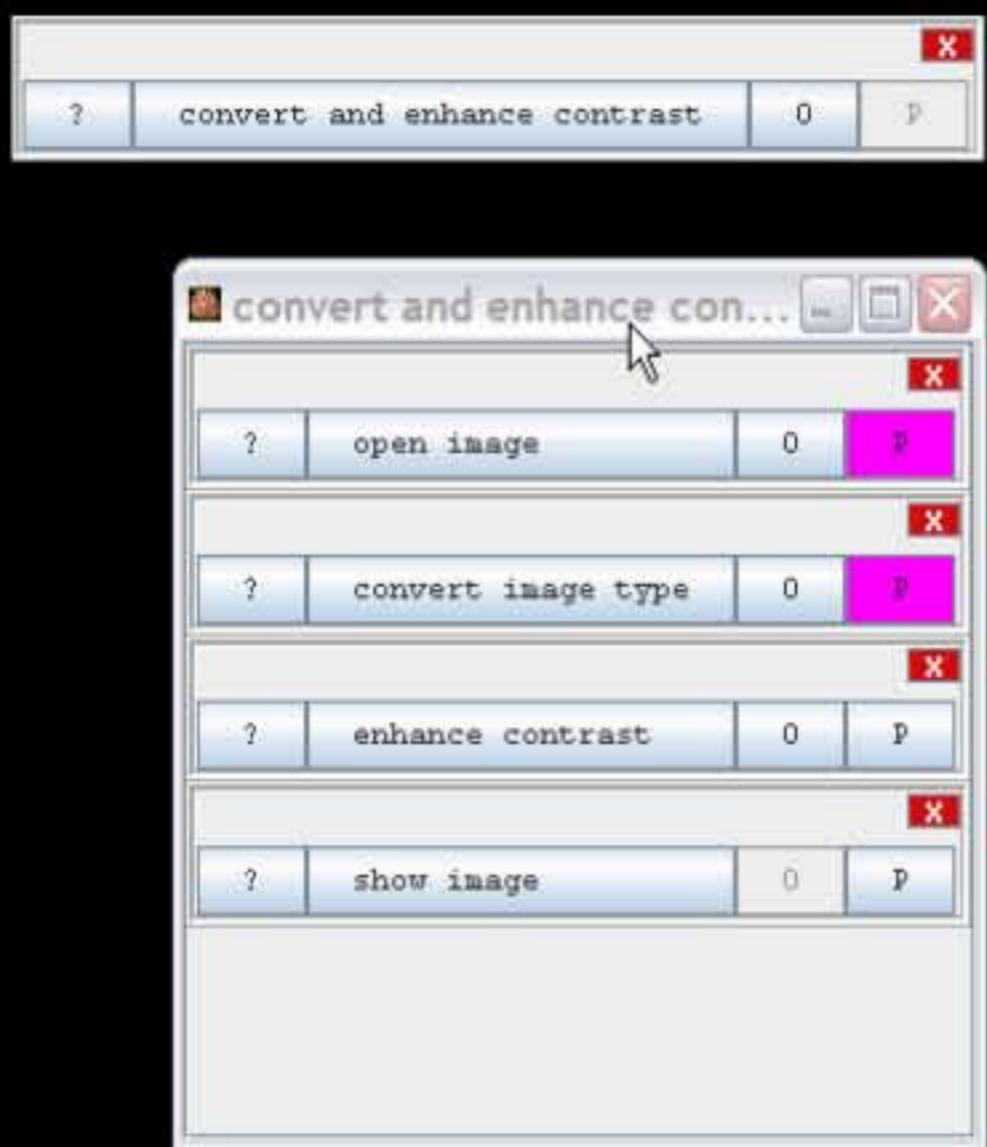
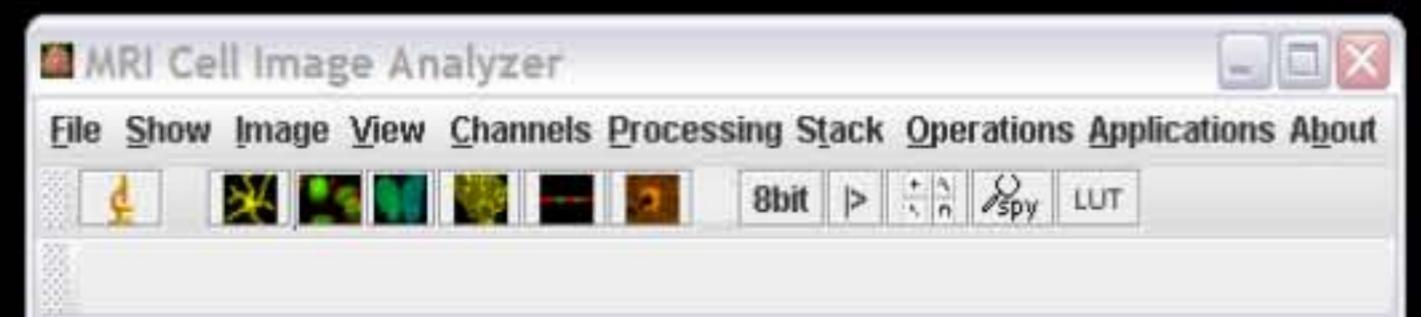
- create a batch application

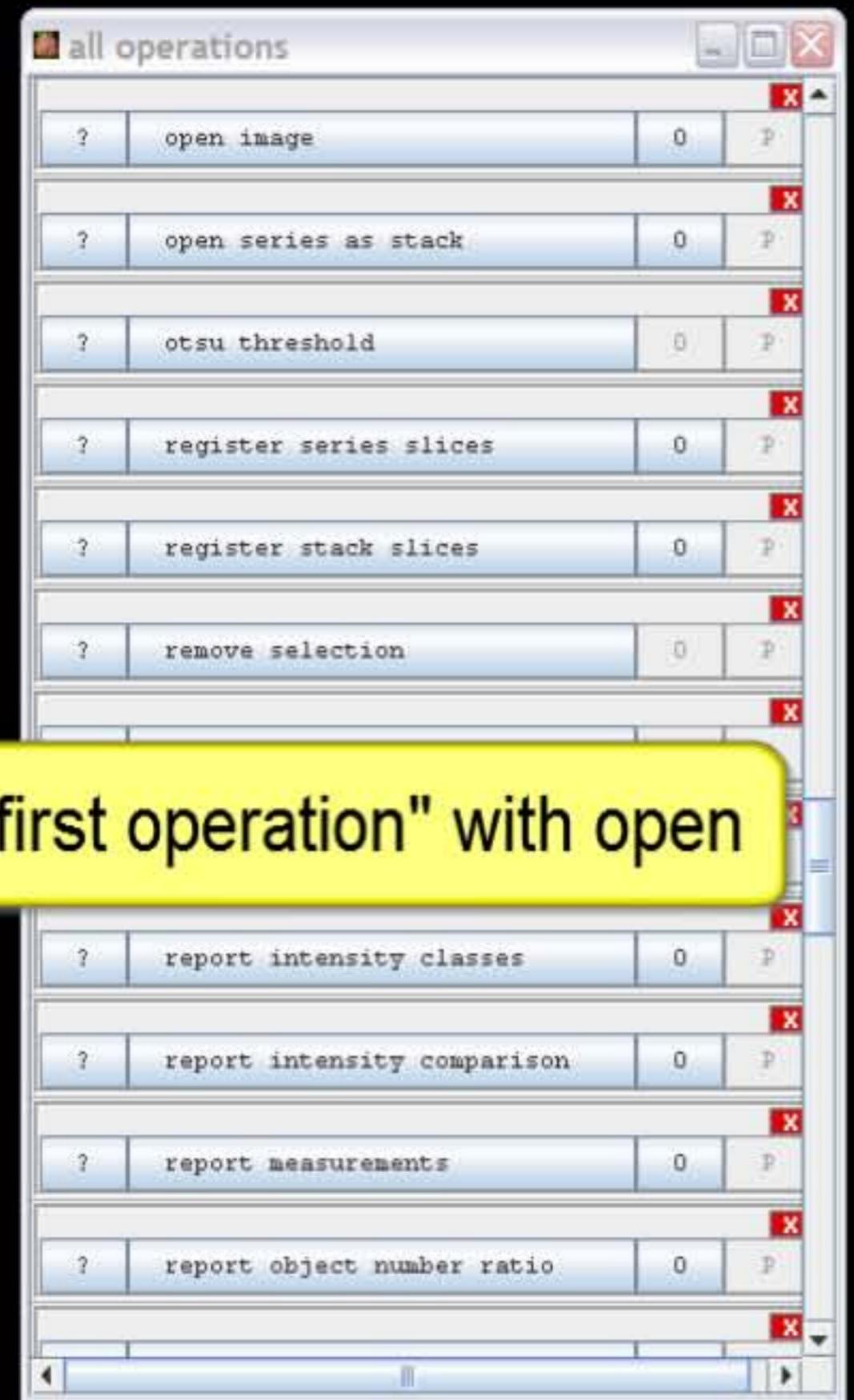
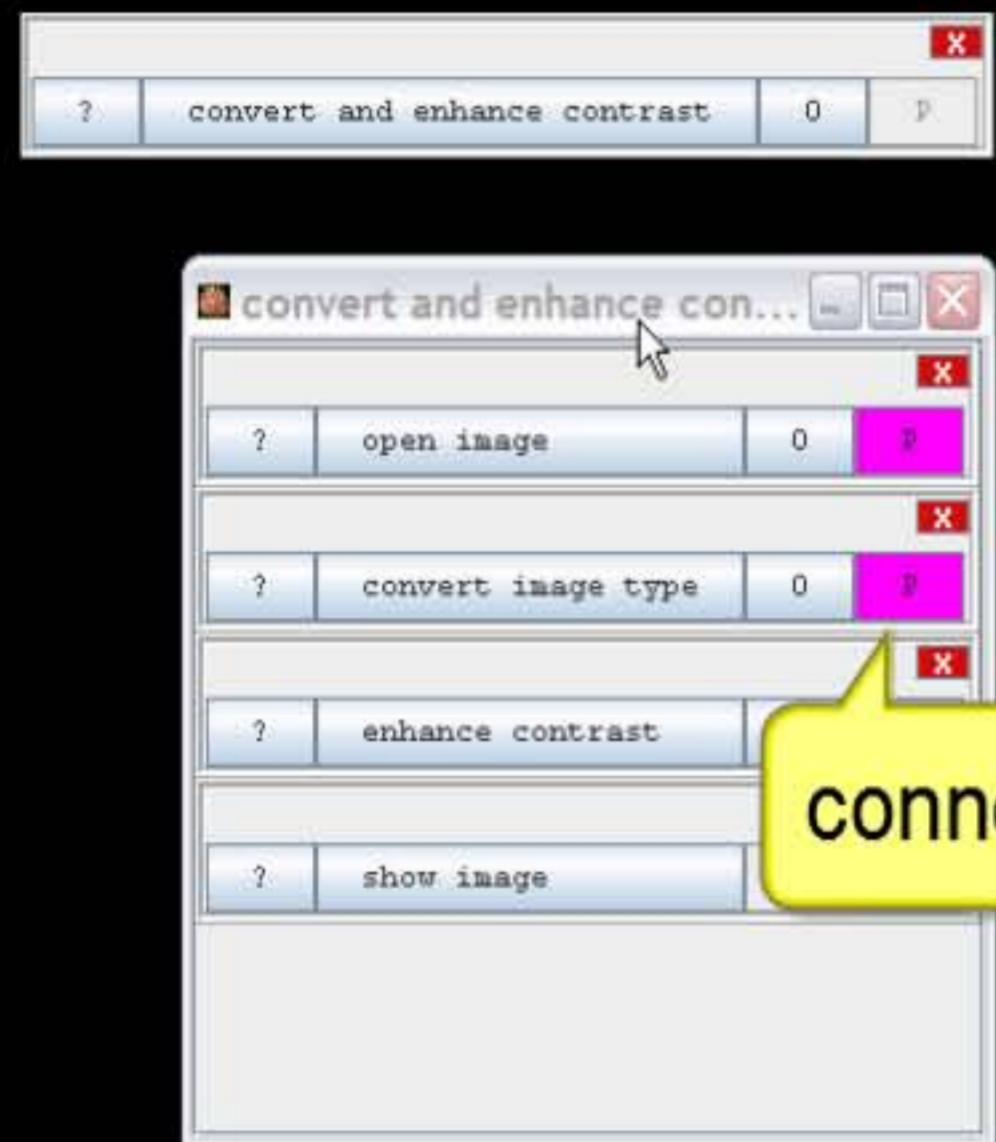




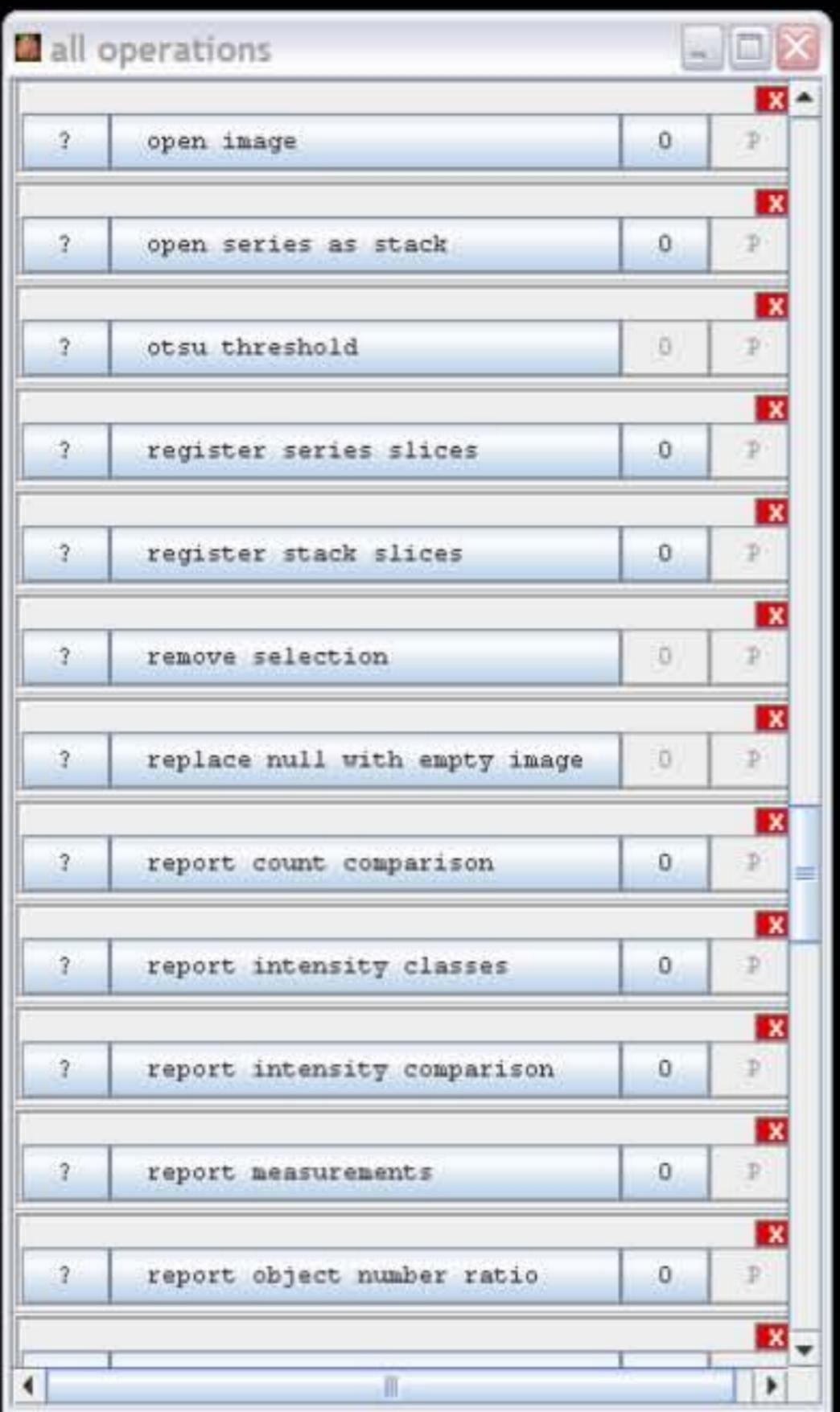
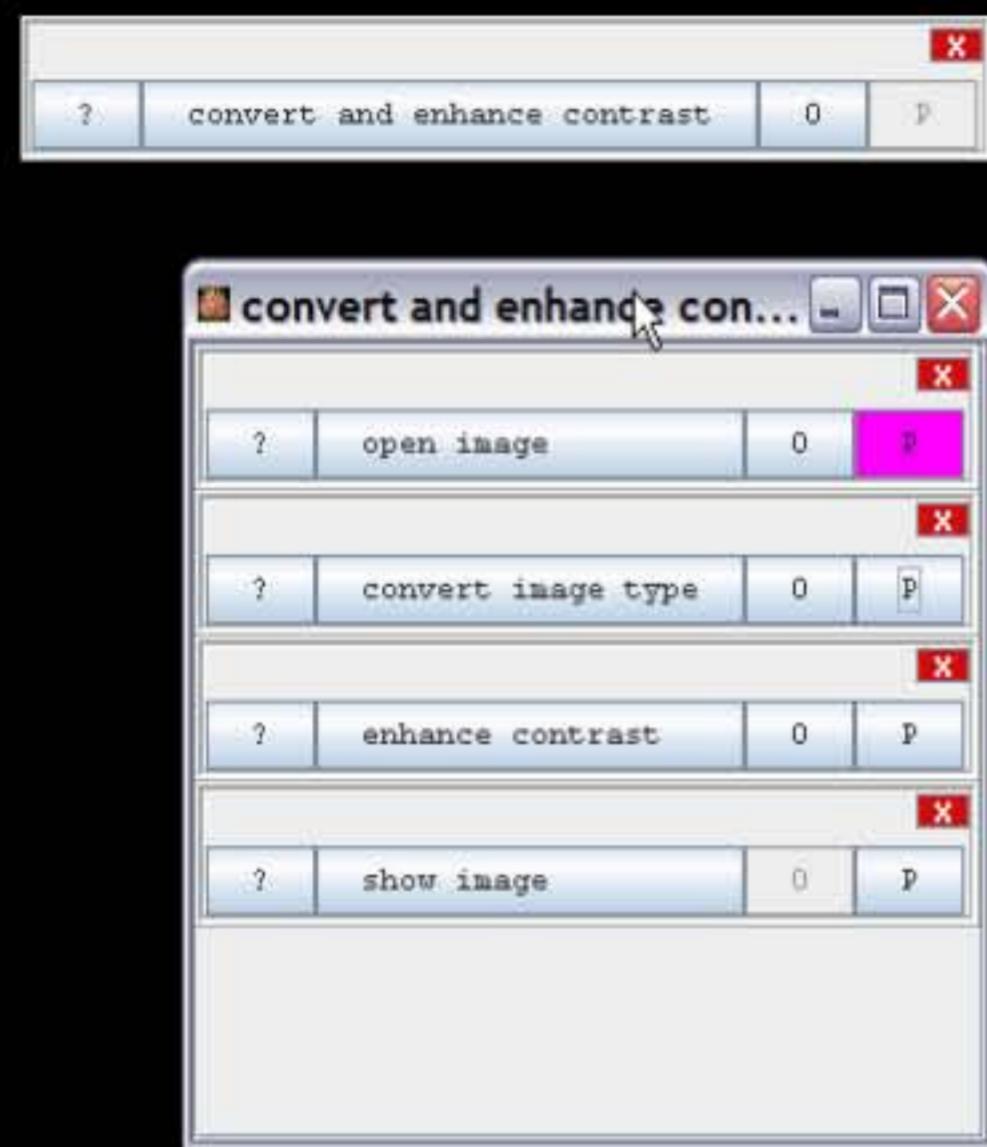
need to open image from disk now

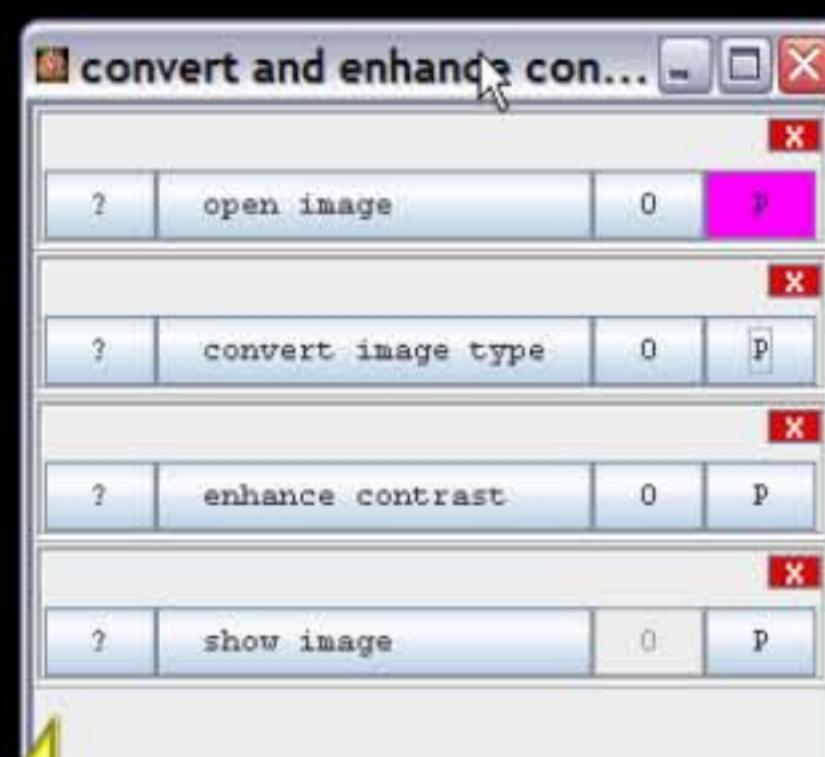
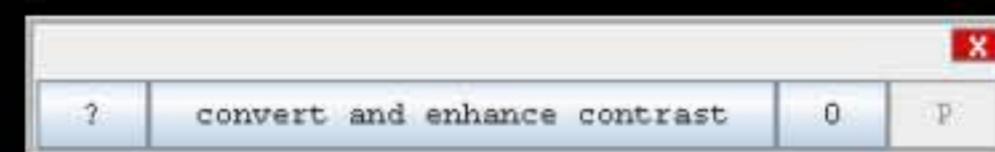


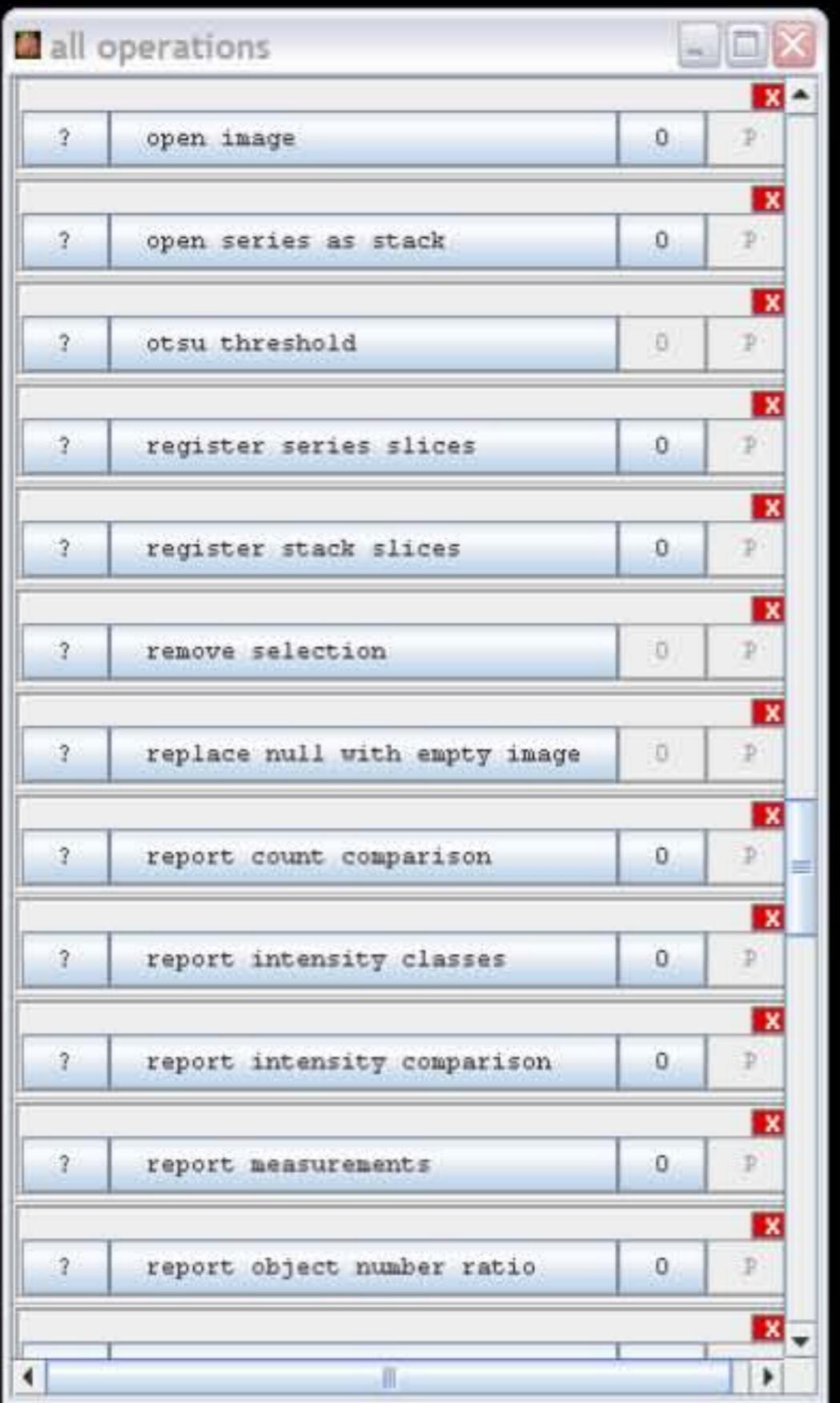
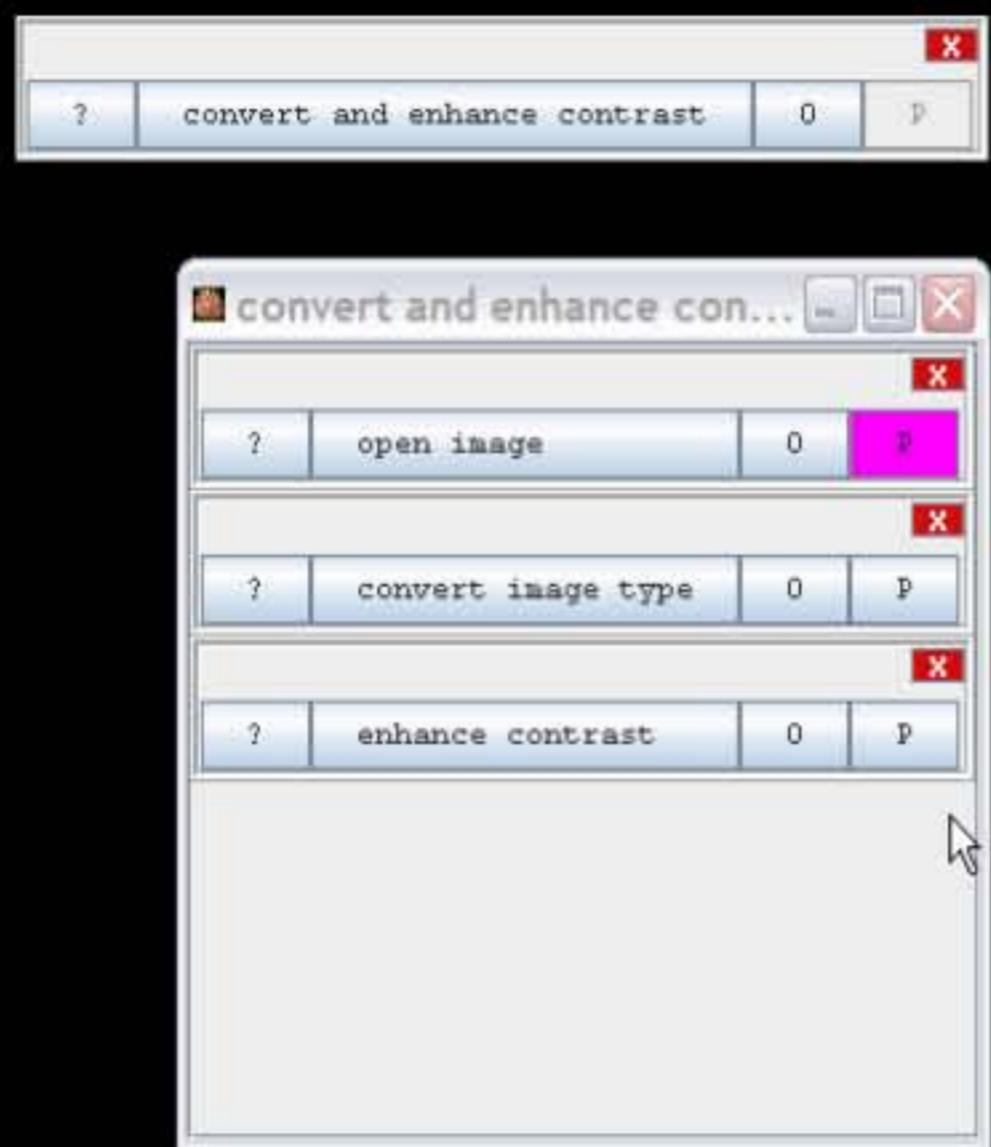


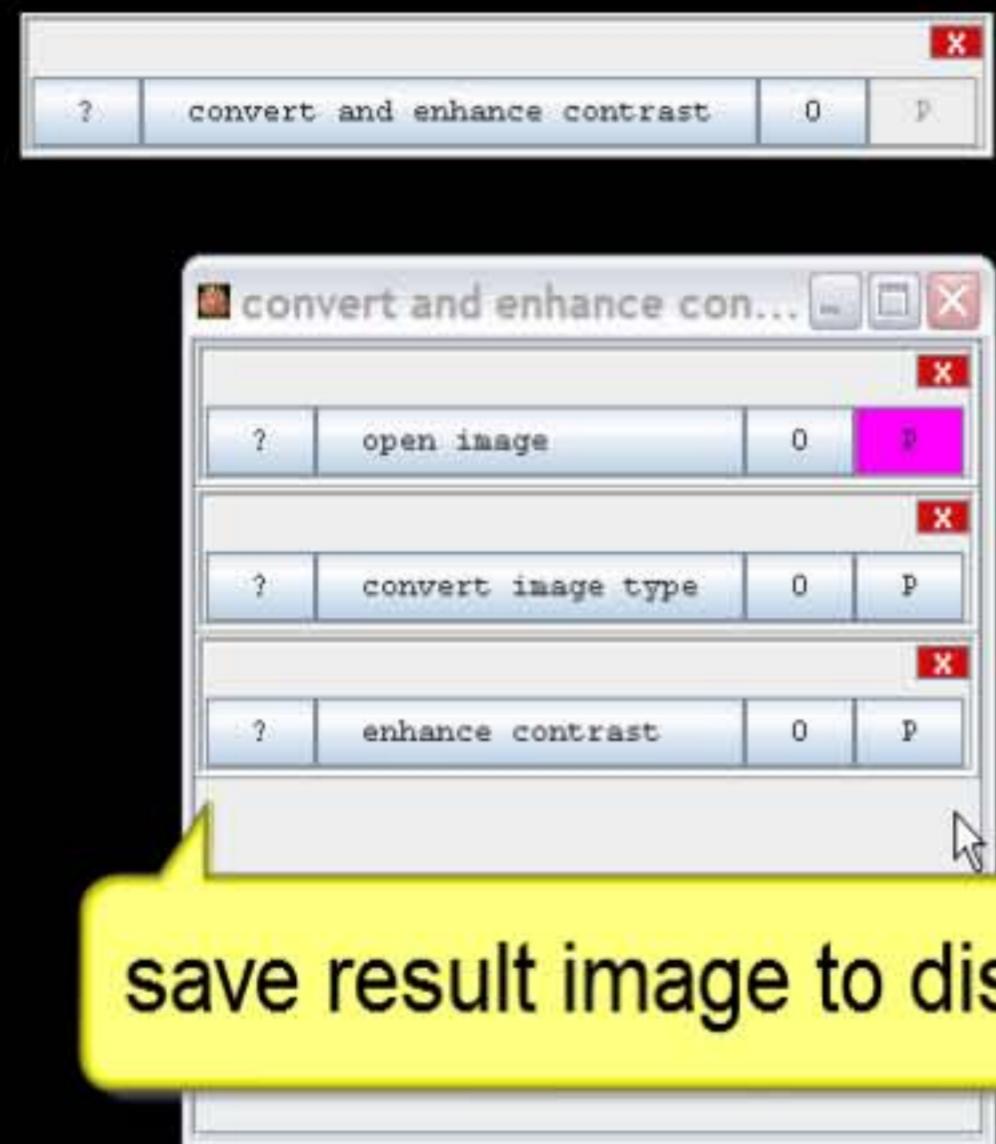


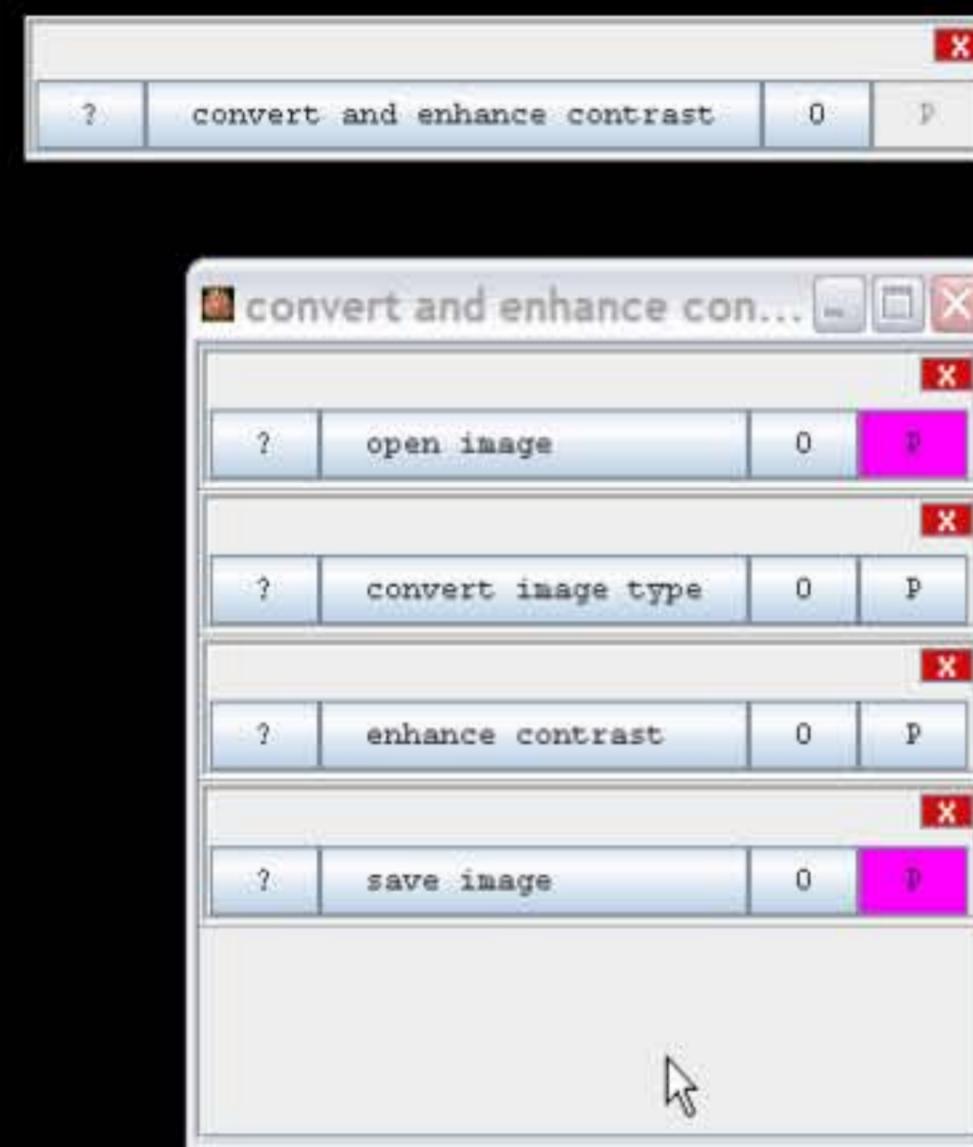
connect "first operation" with open



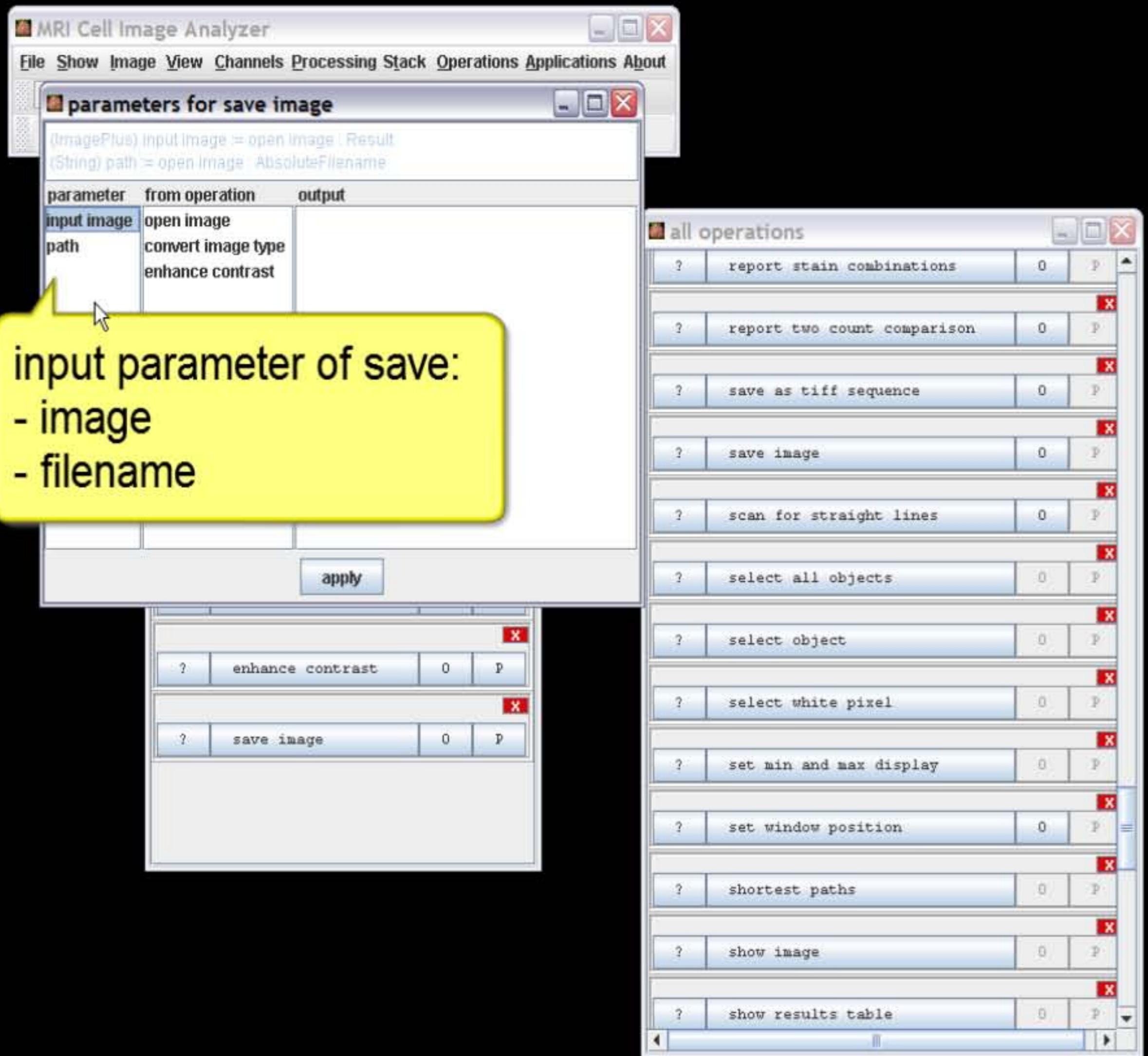


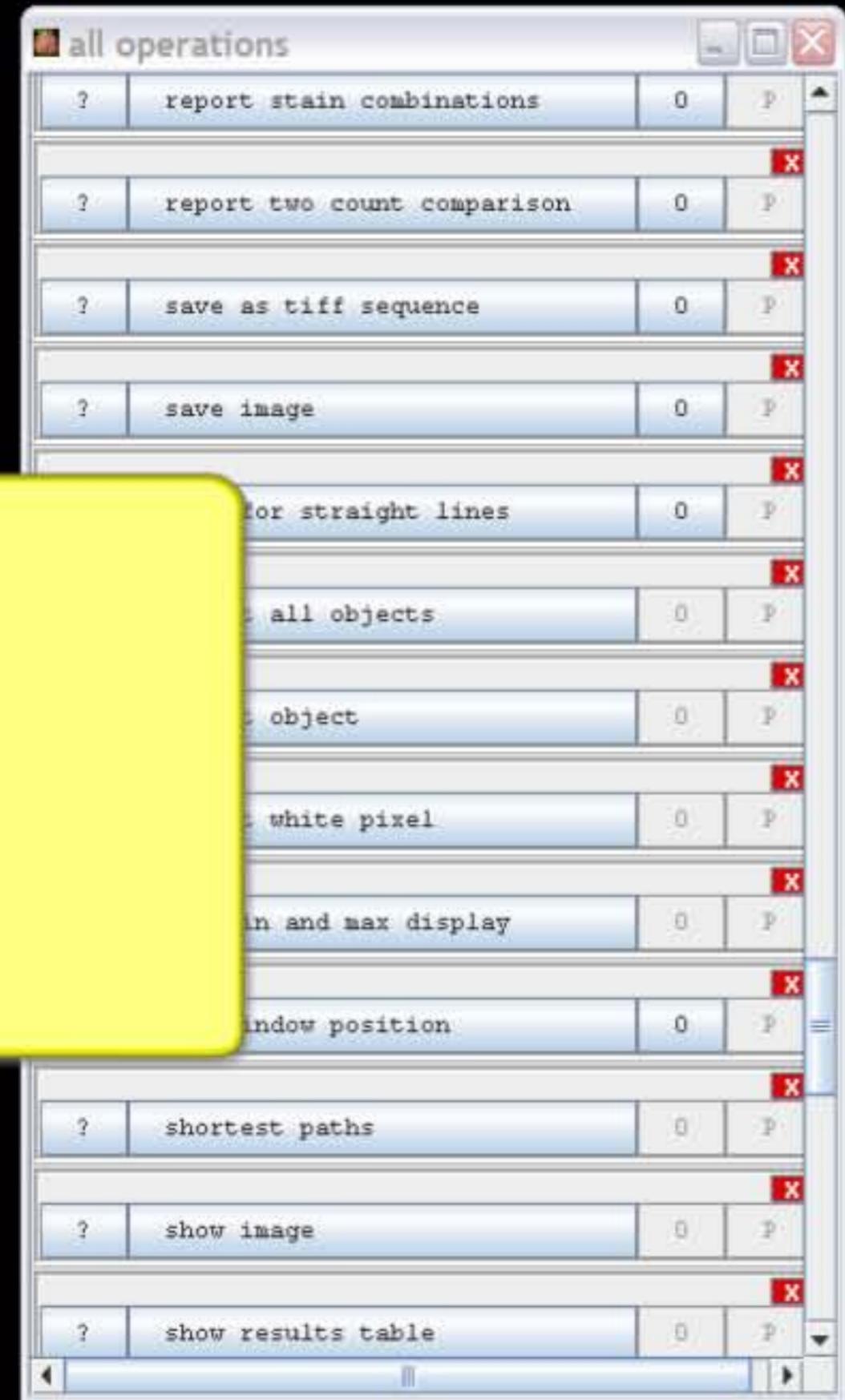






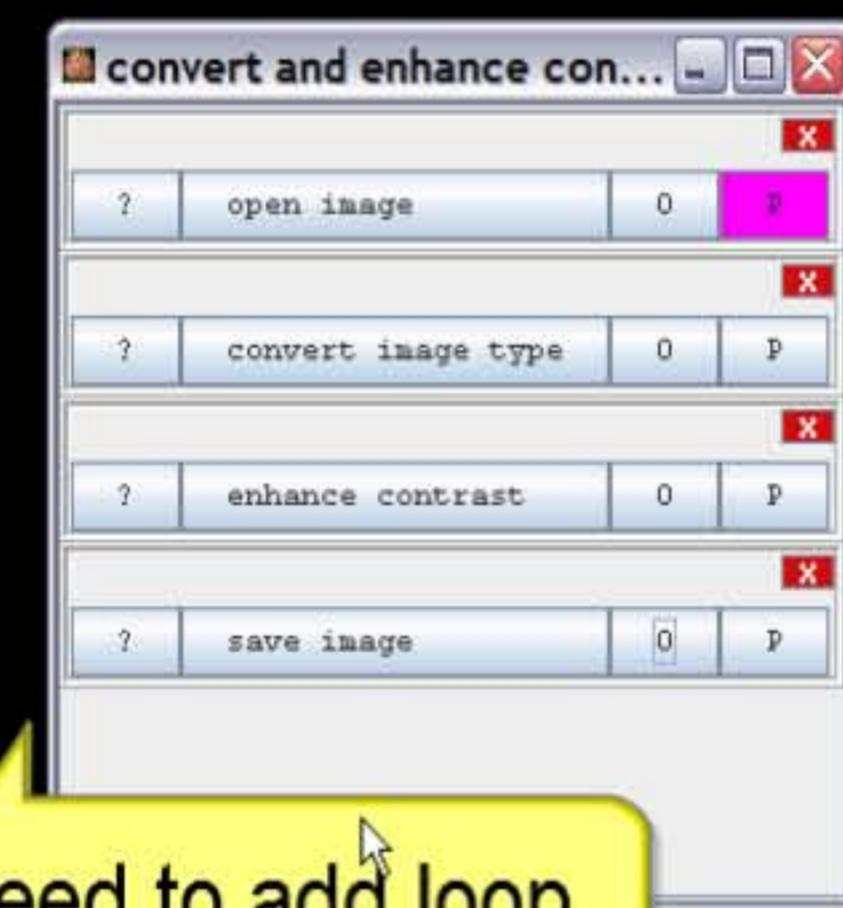
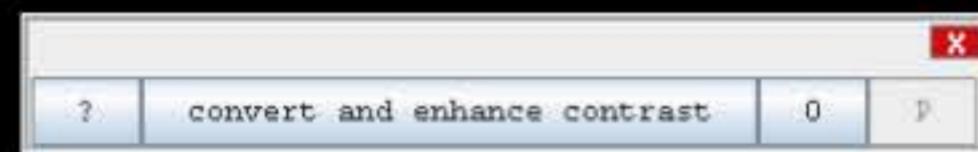
all operations			
?	report stain combinations	0	P
?	report two count comparison	0	P
?	save as tiff sequence	0	P
?	save image	0	P
?	scan for straight lines	0	P
?	select all objects	0	P
?	select object	0	P
?	select white pixel	0	P
?	set min and max display	0	P
?	set window position	0	P
?	shortest paths	0	P
?	show image	0	P
?	show results table	0	P





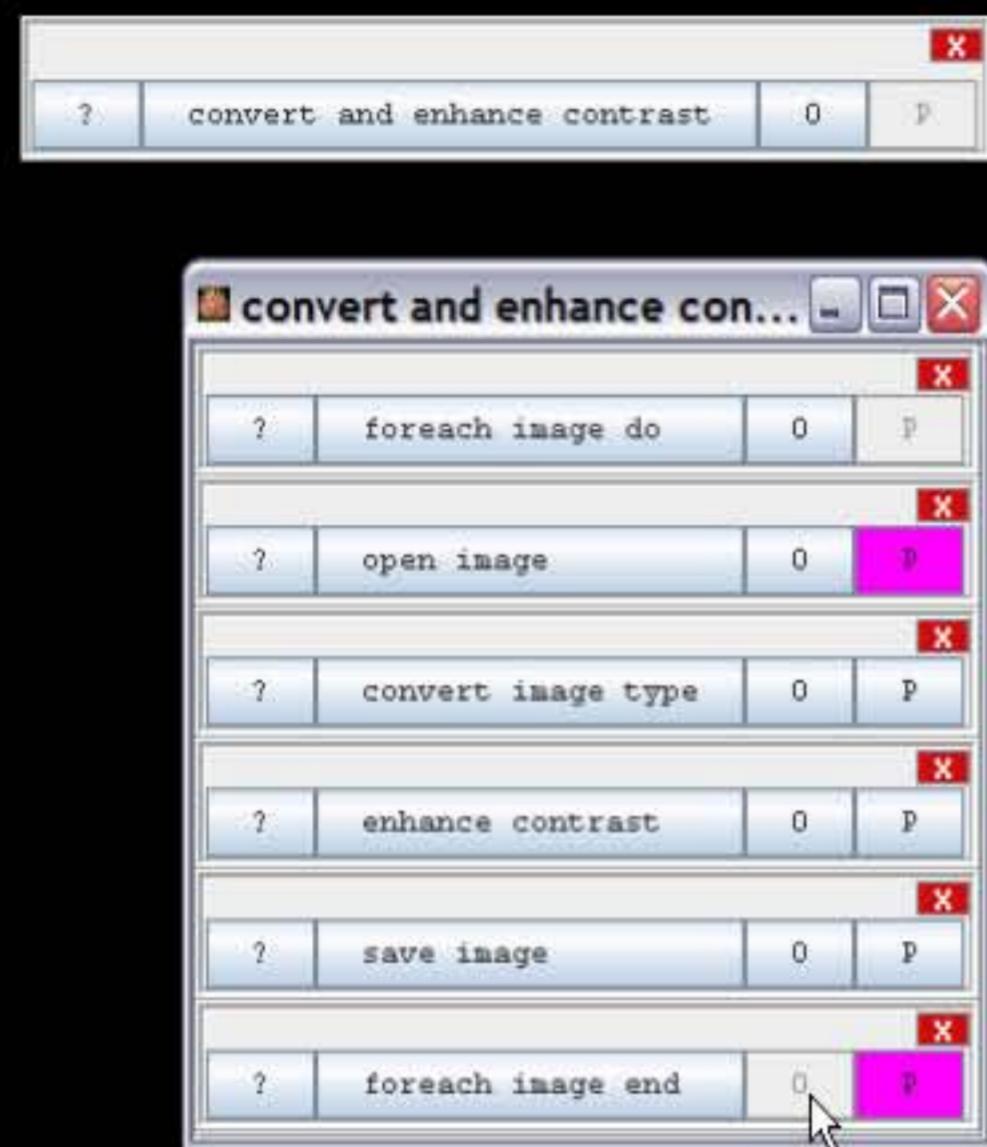
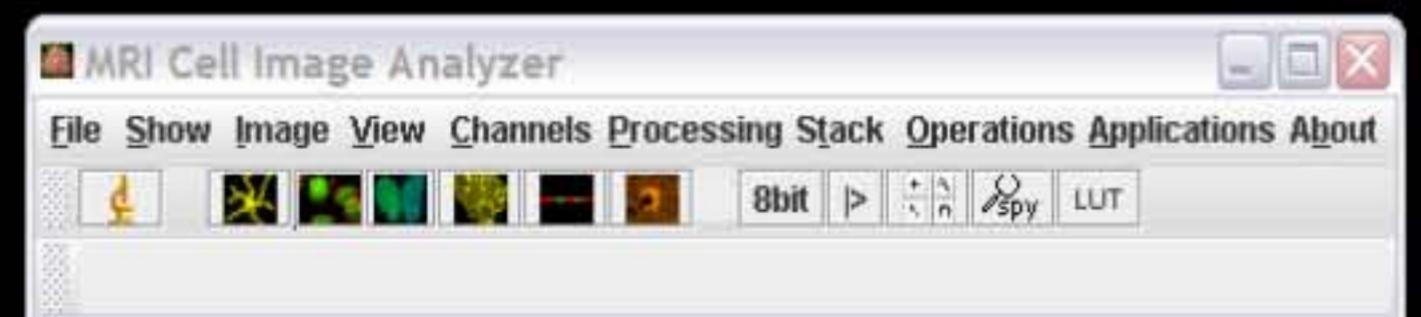
result location:

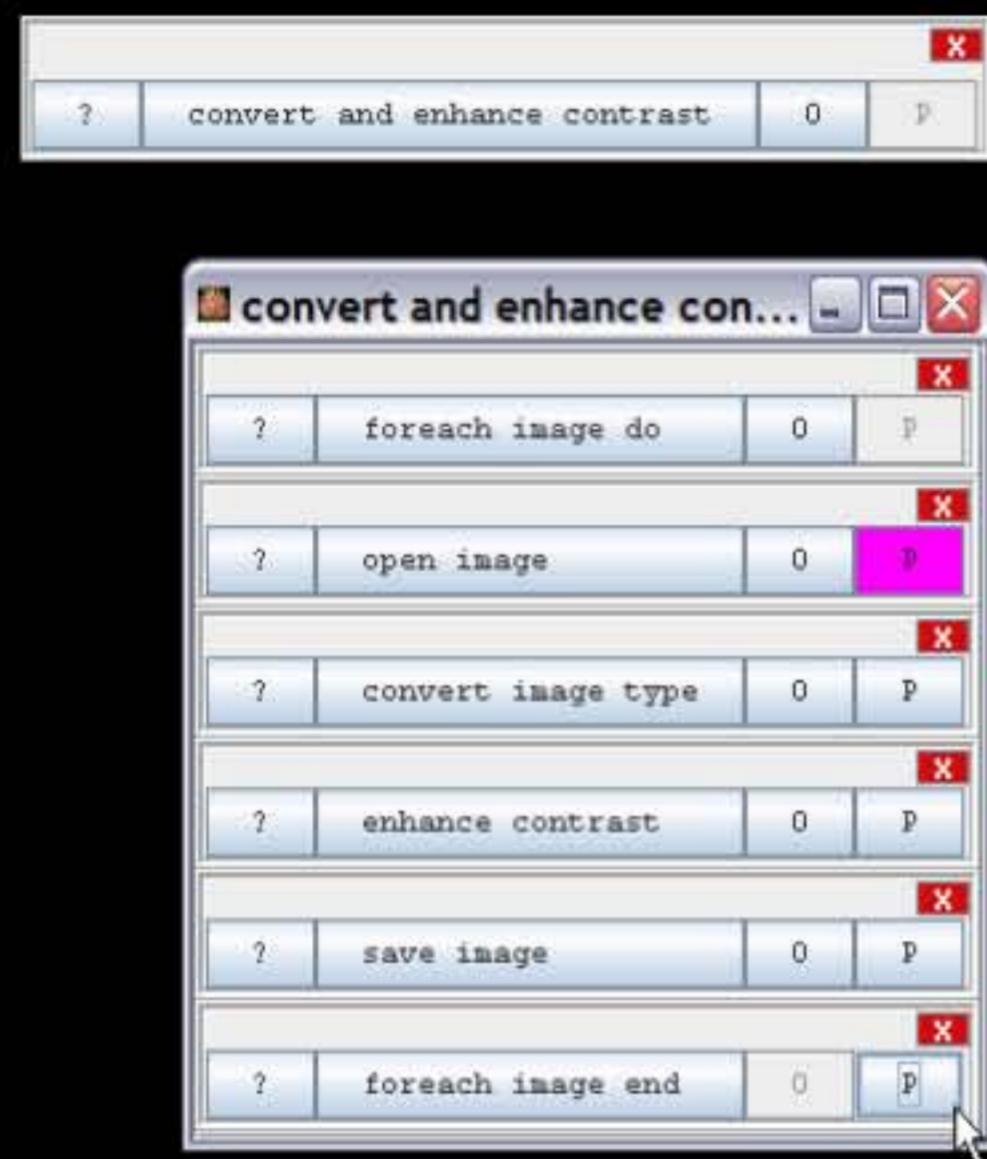
- absolute path
- path relative to input folder
- add string to filename
- add loop index to filename

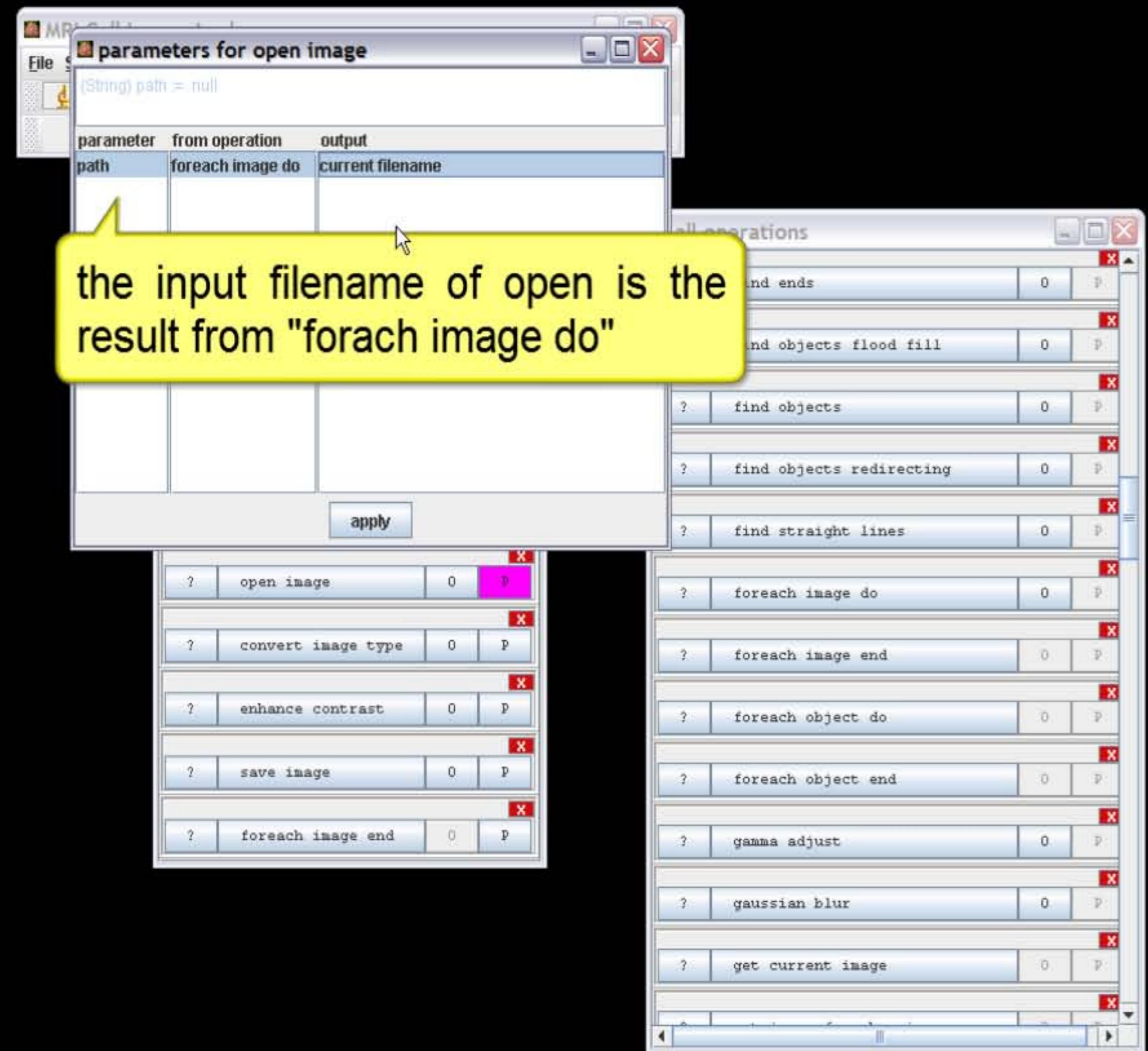


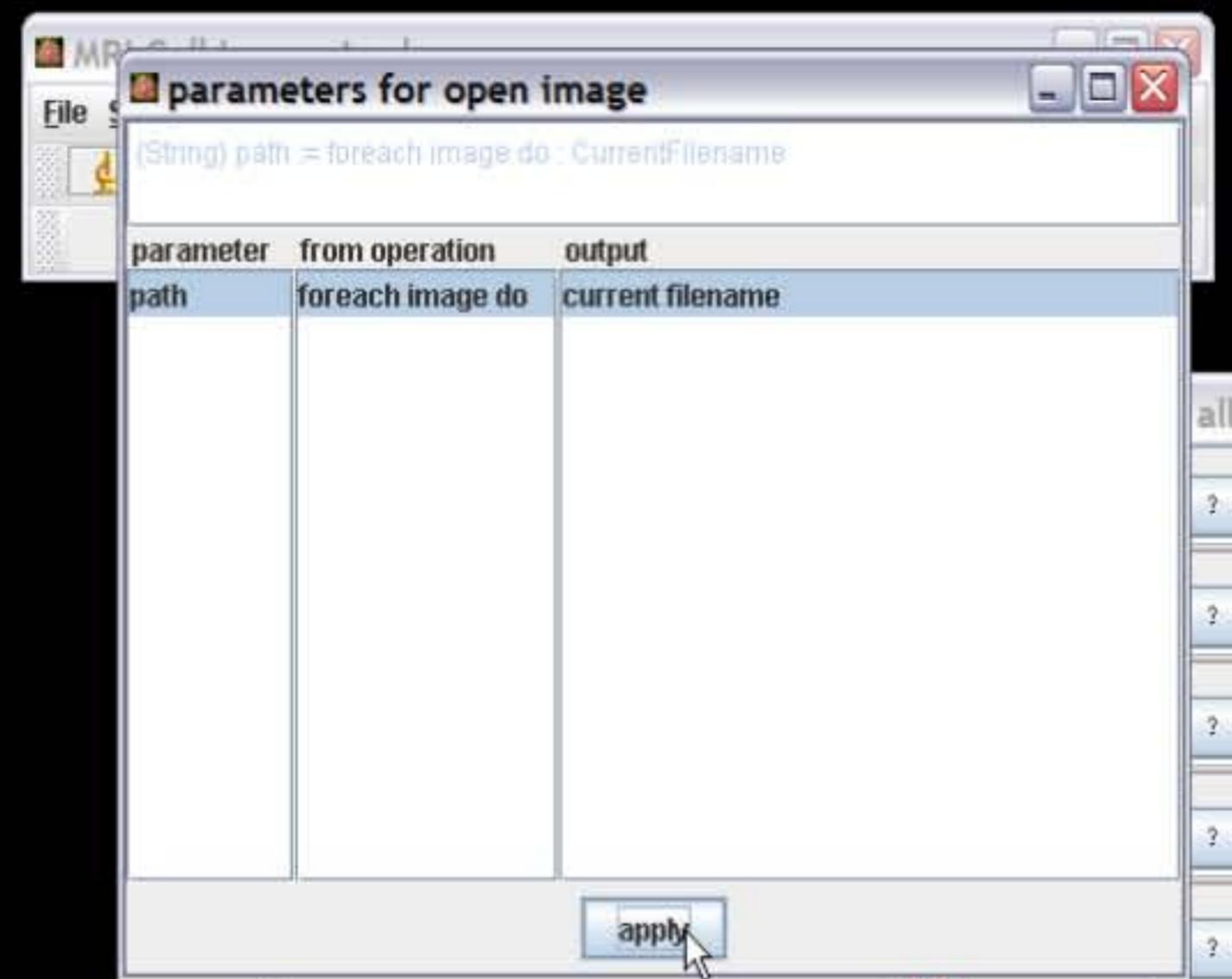
need to add loop







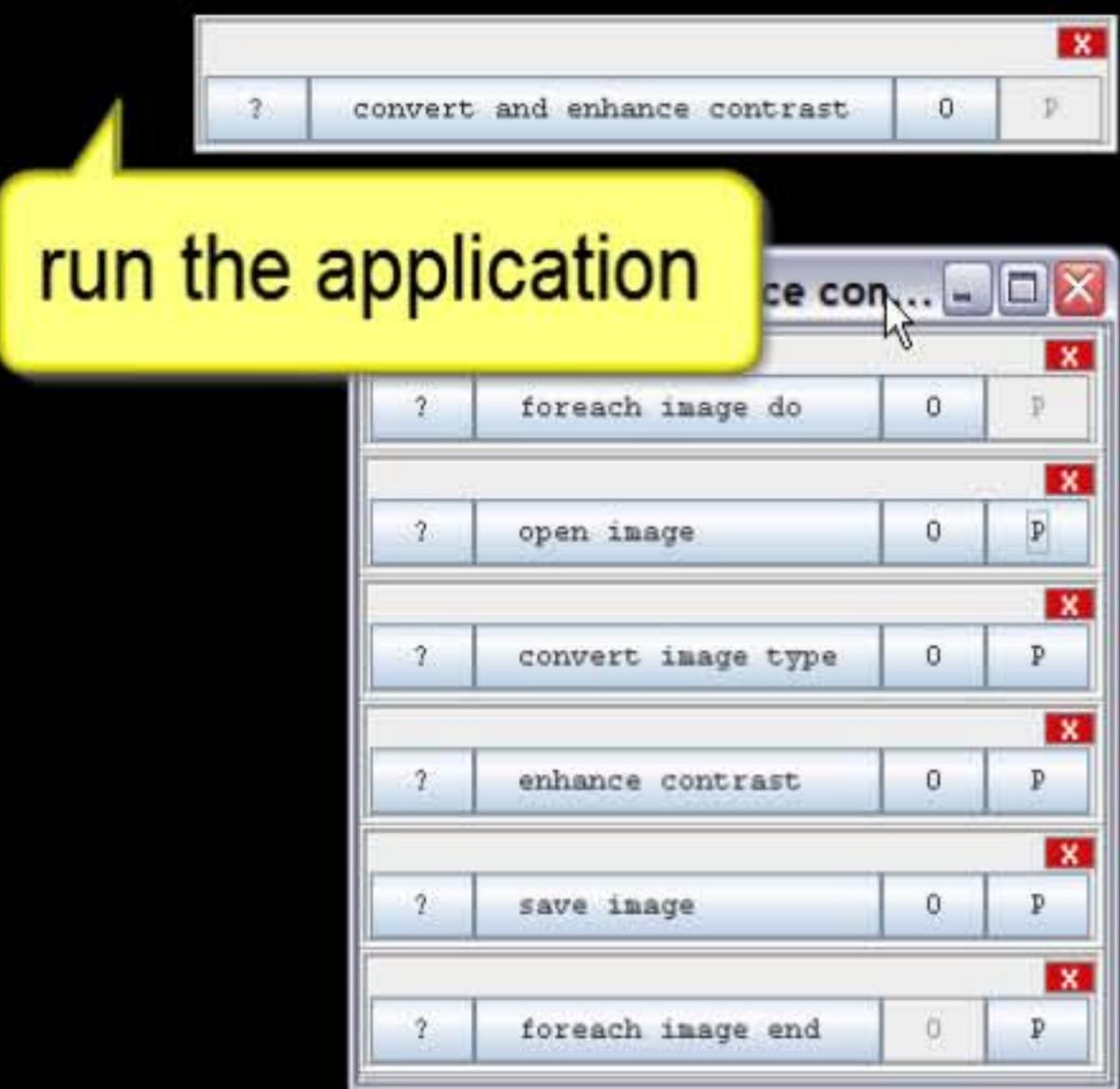


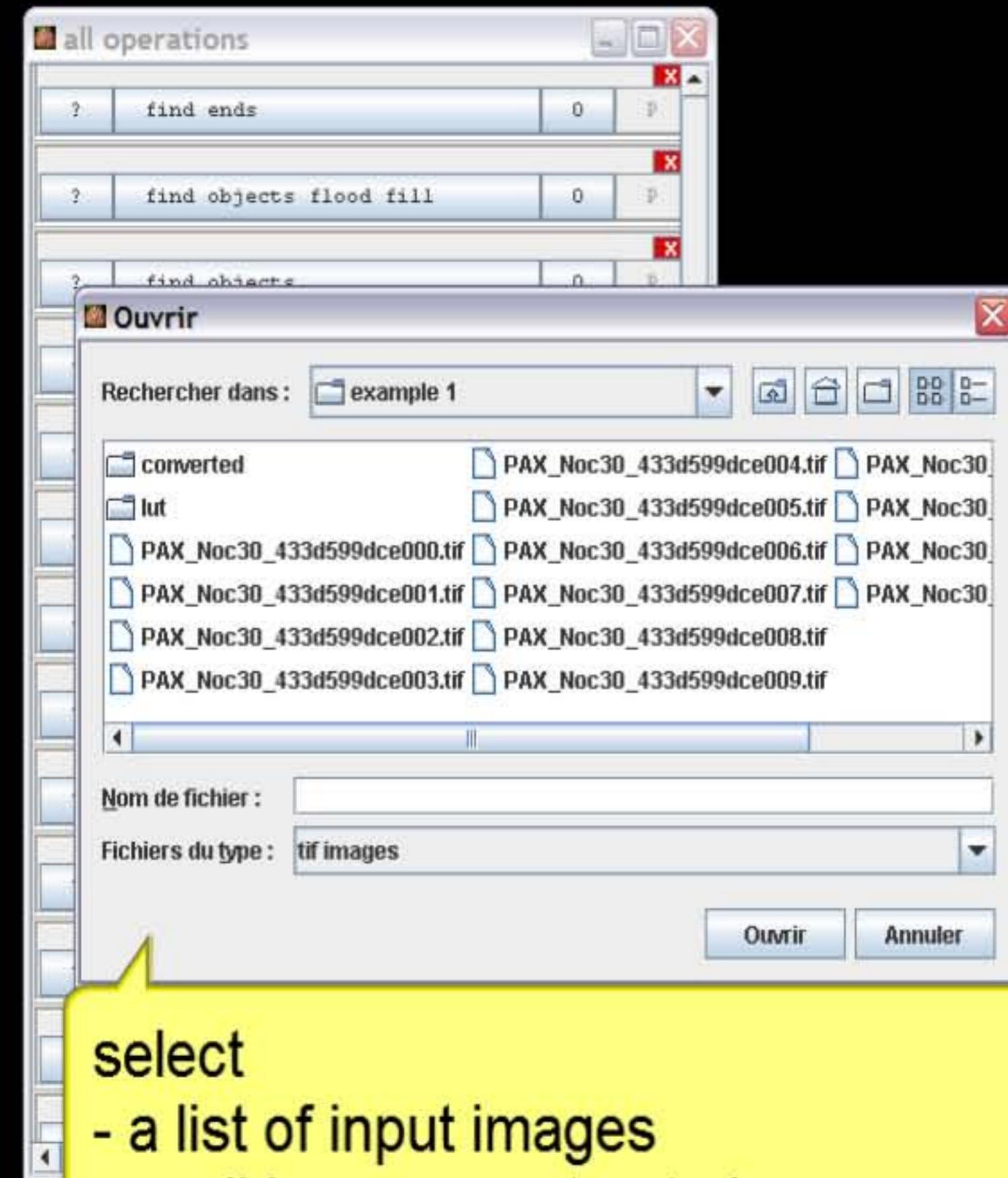


?   open image	0	P
?   convert image type	0	P
?   enhance contrast	0	P
?   save image	0	P
?   foreach image end	0	P

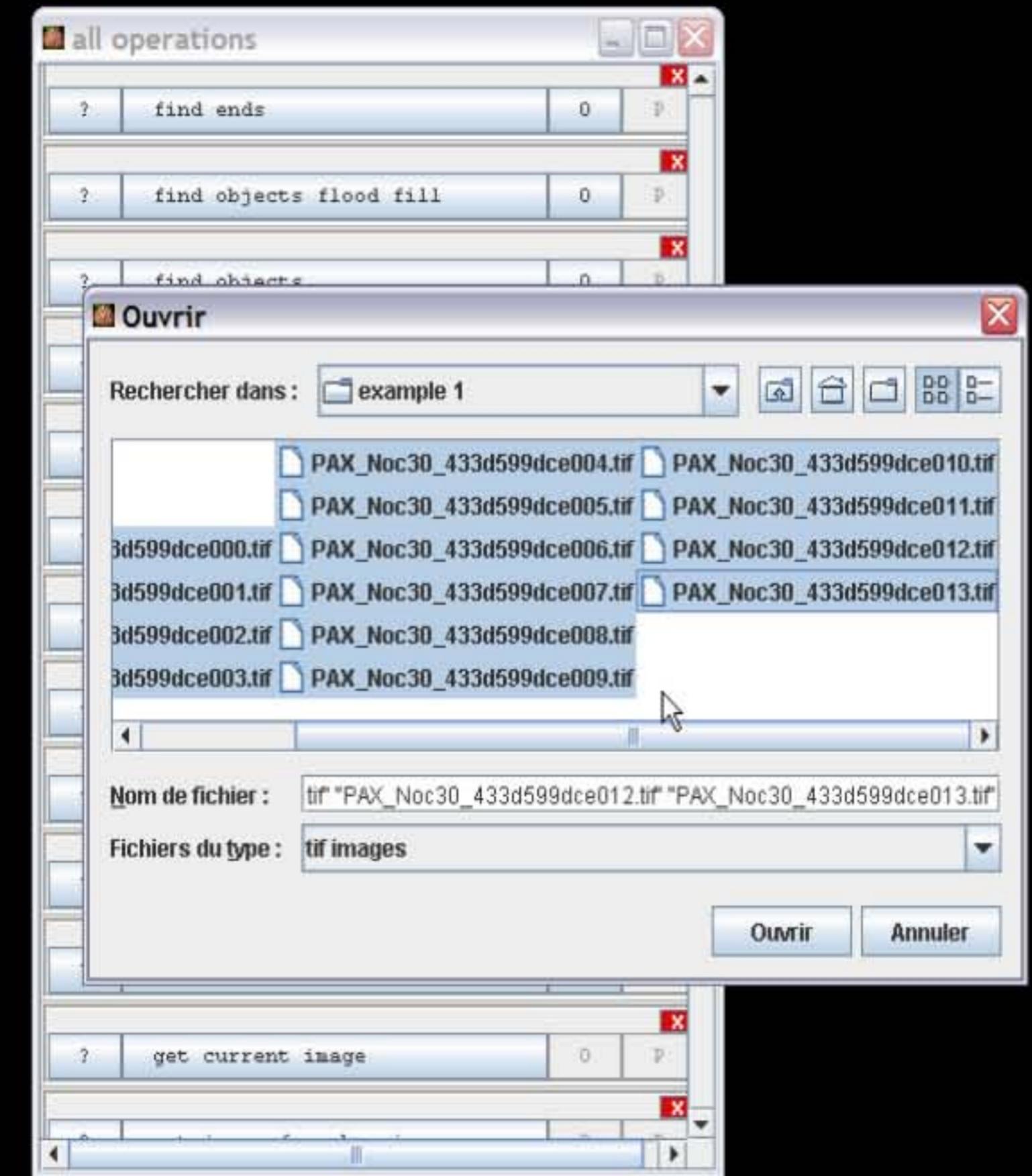
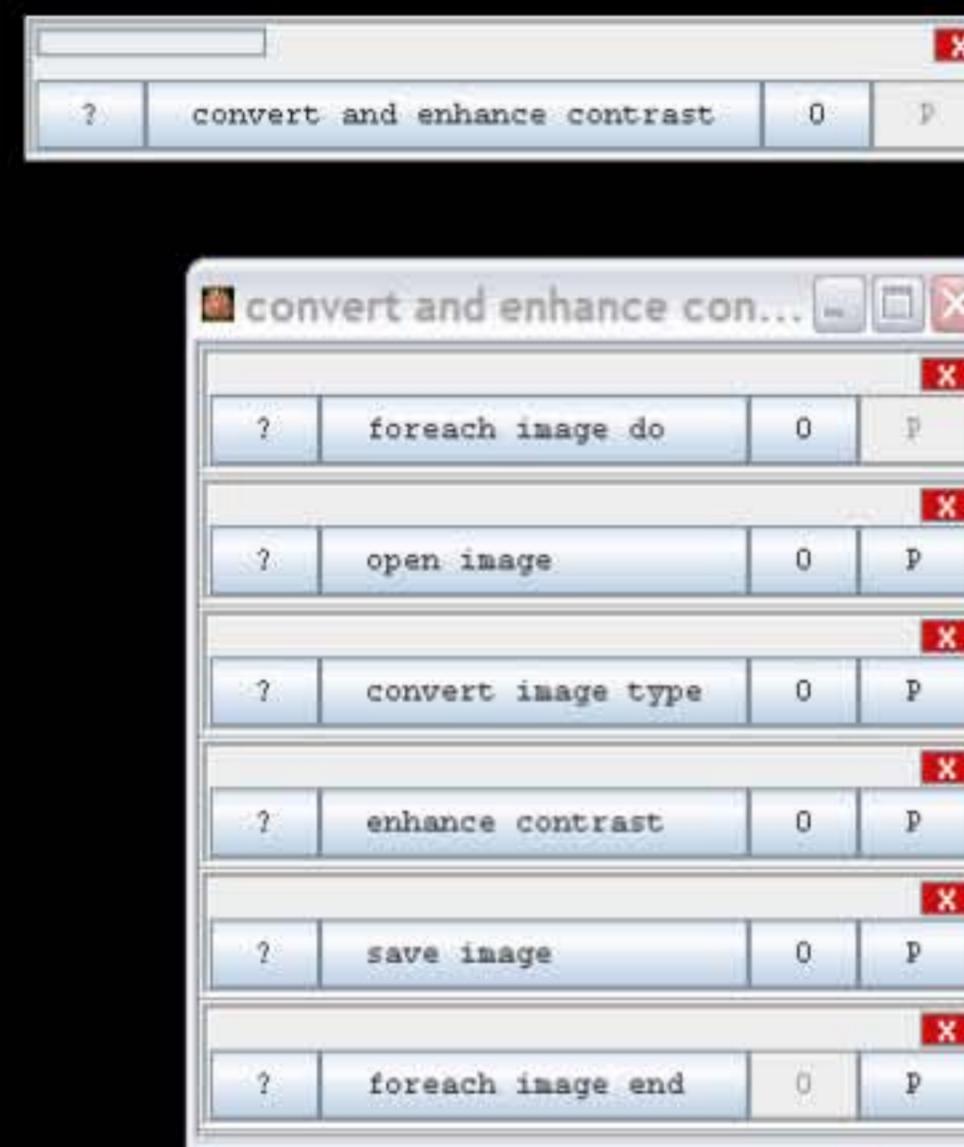
all operations

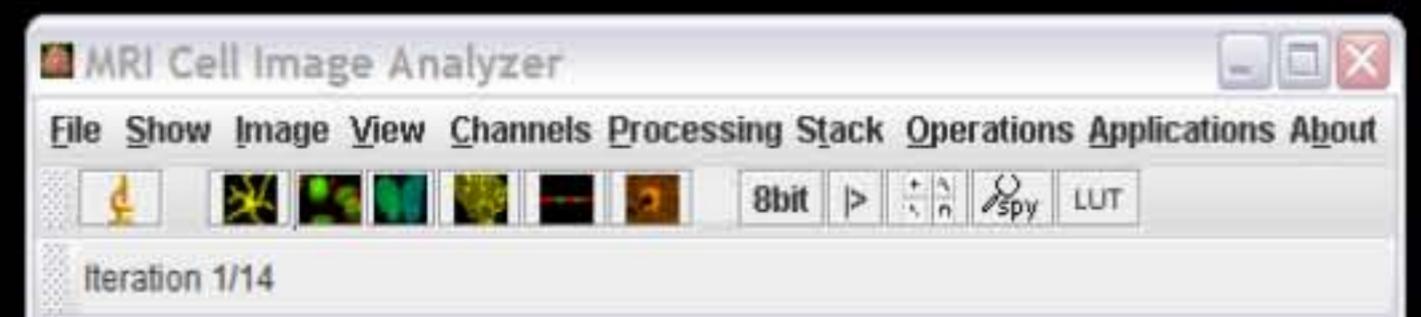
?   find ends	0	P
?   find objects flood fill	0	P
?   find objects	0	P
?   find objects redirecting	0	P
?   find straight lines	0	P
?   foreach image do	0	P
?   foreach image end	0	P
?   foreach object do	0	P
?   foreach object end	0	P
?   gamma adjust	0	P
?   gaussian blur	0	P
?   get current image	0	P





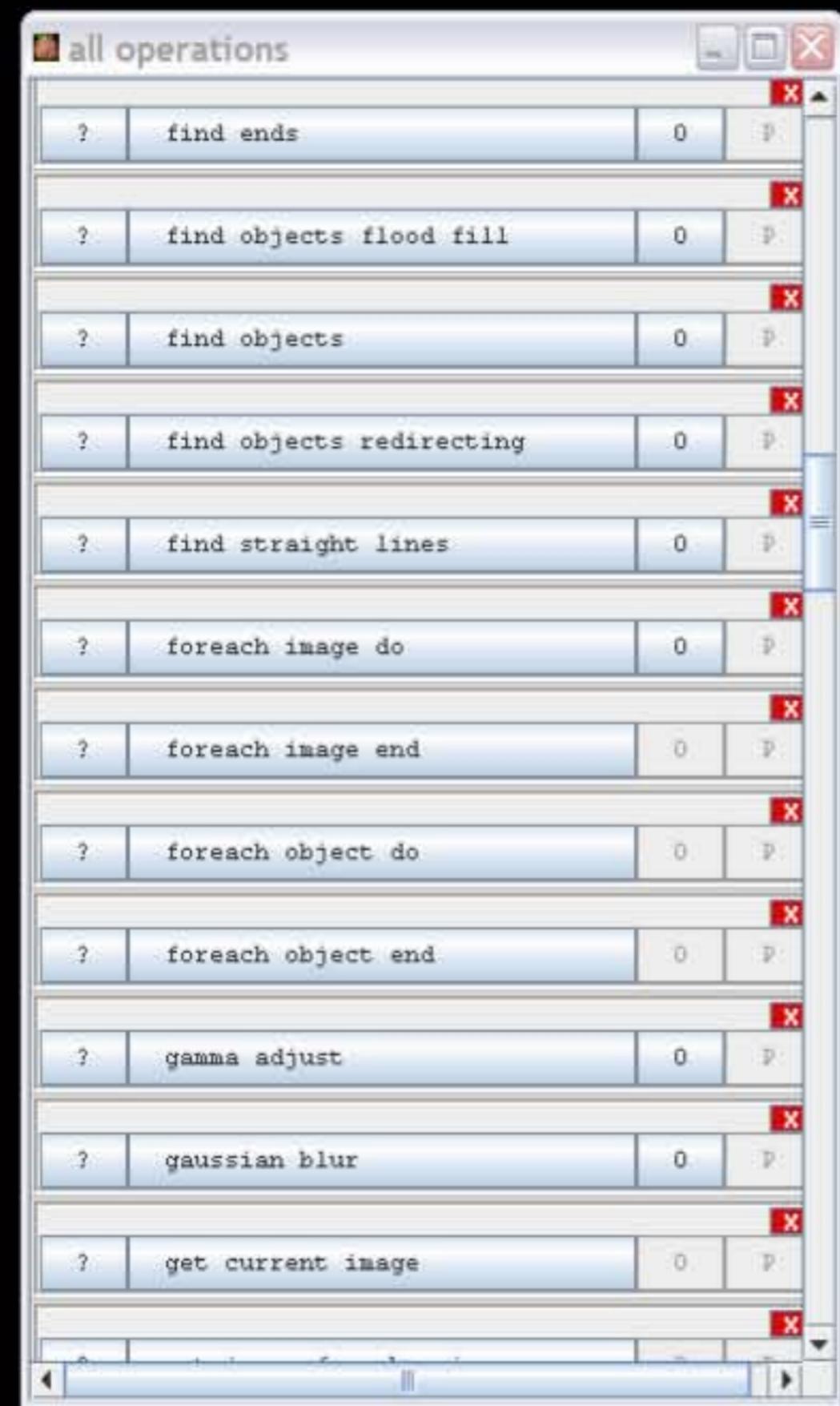
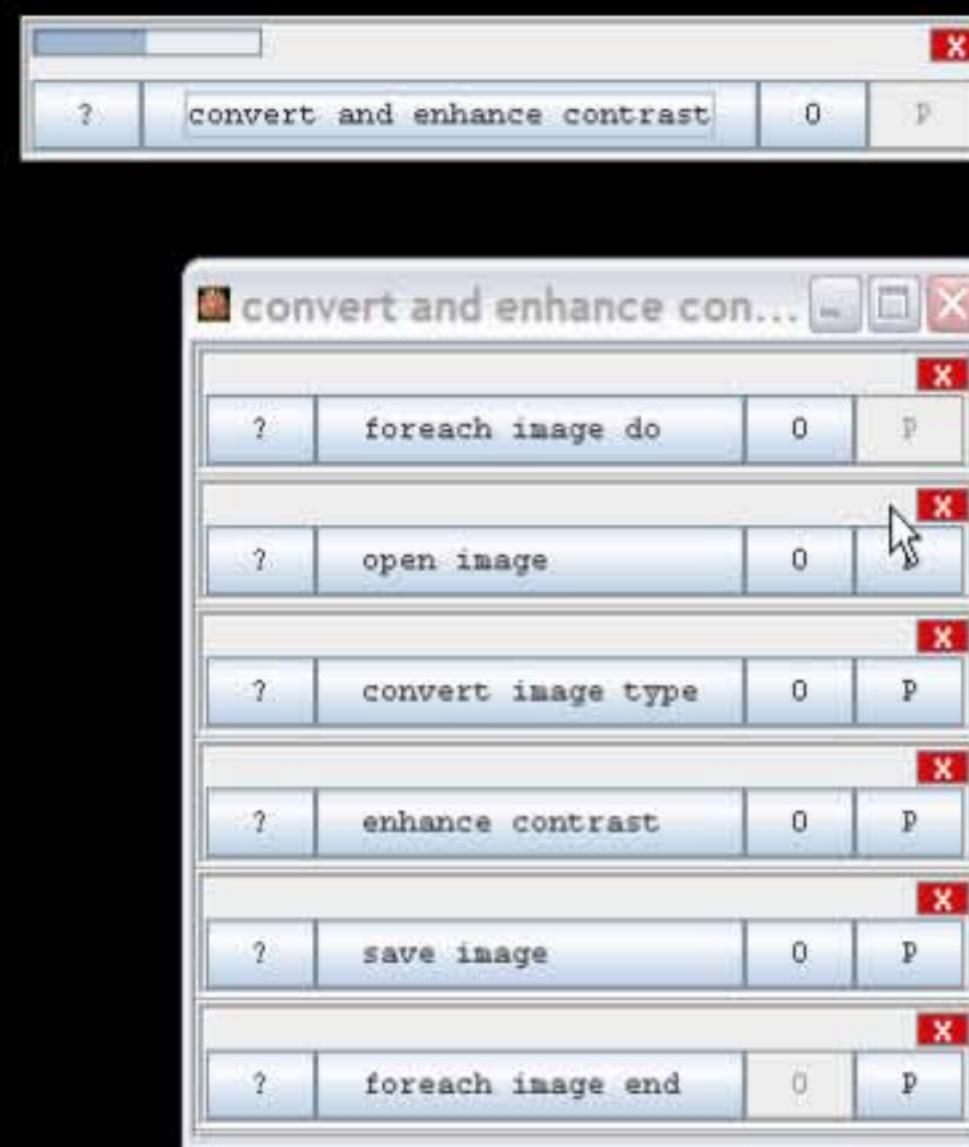
select  
- a list of input images  
  - all images are treated  
- one folder  
  - all images in the folder and in all sub-folders  
    are treated

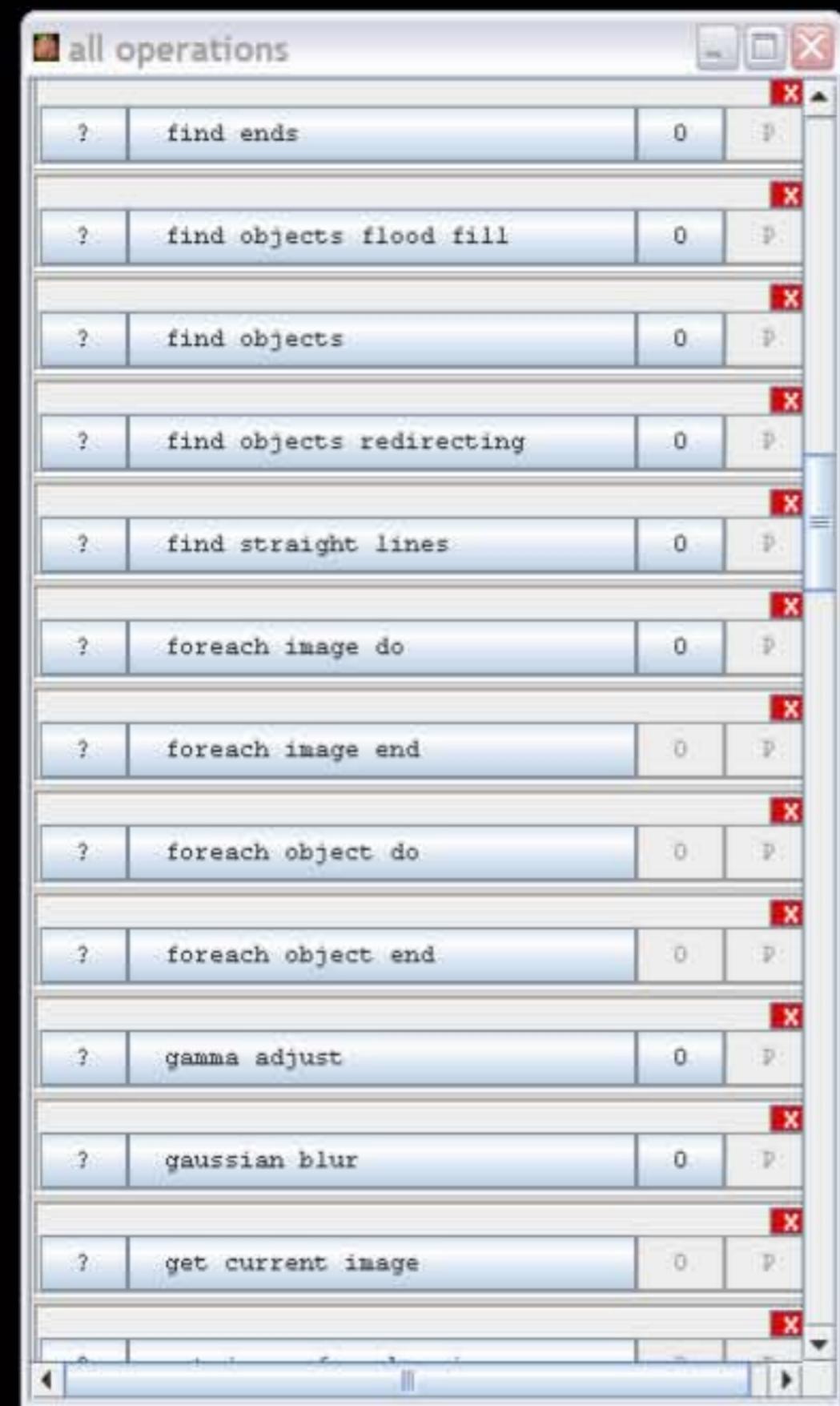
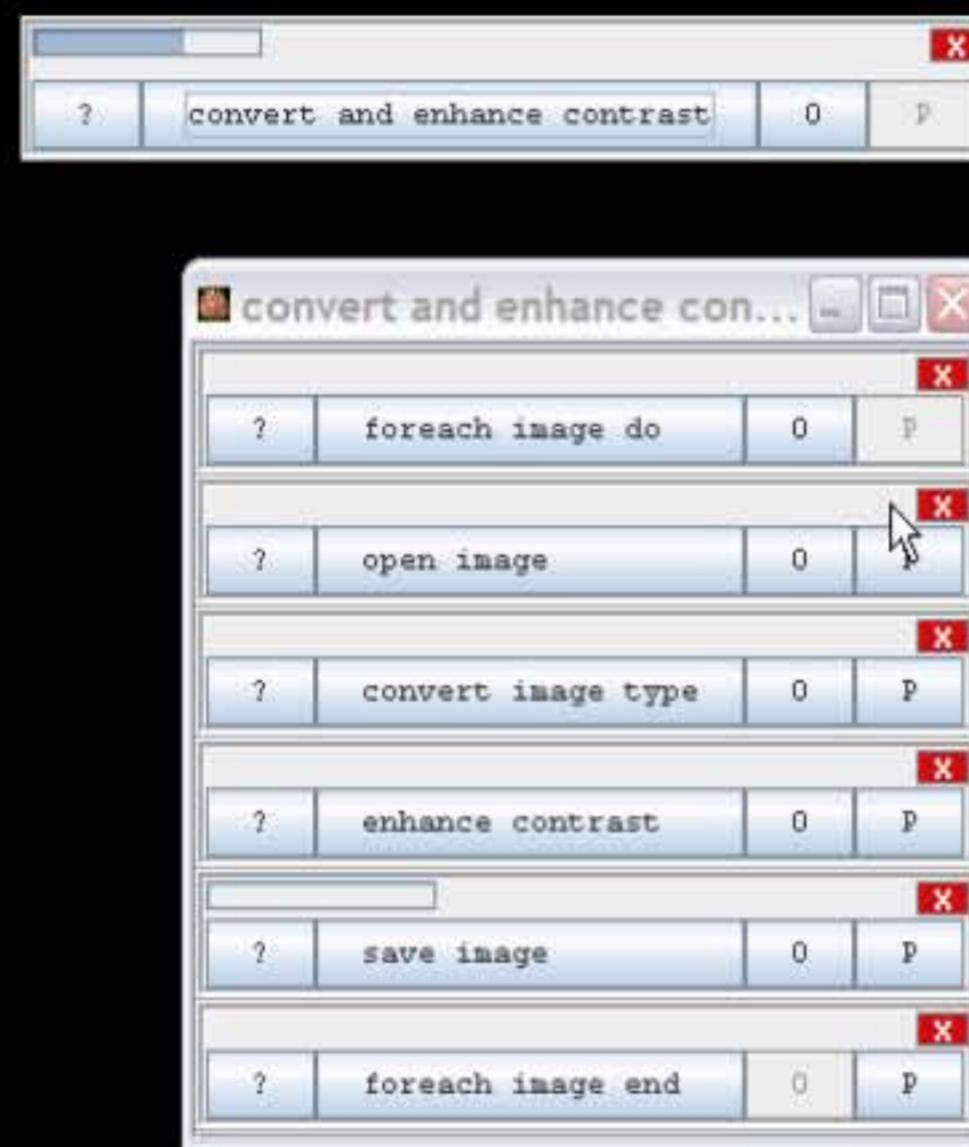




the application is running



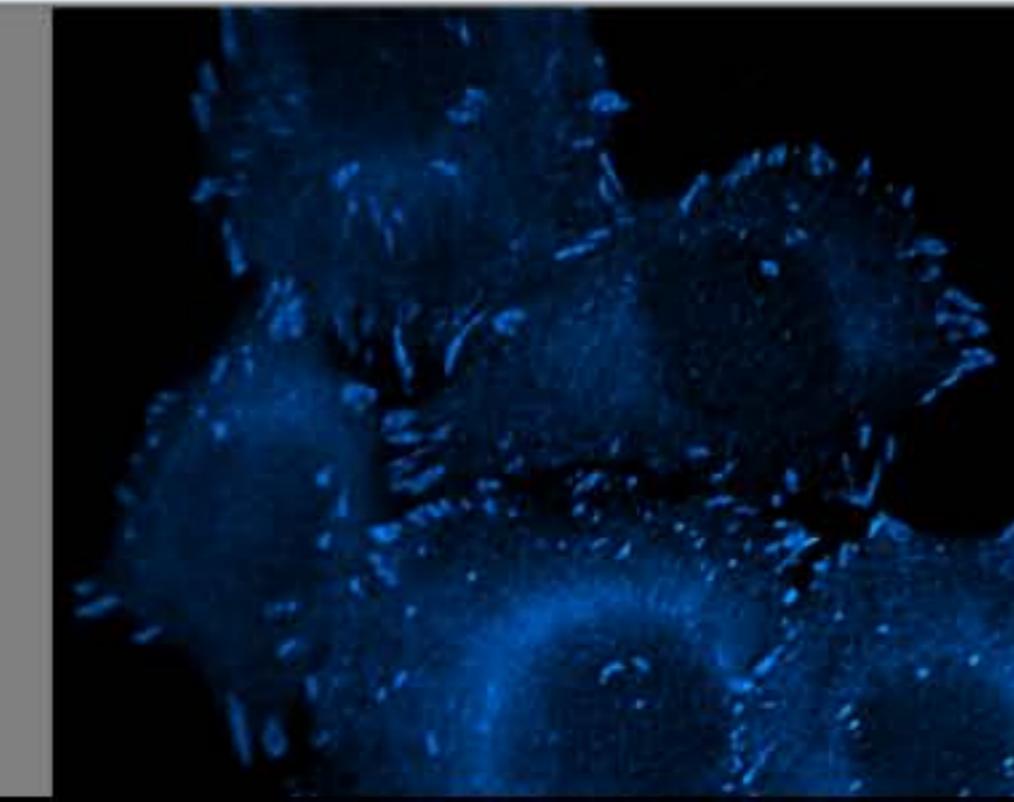
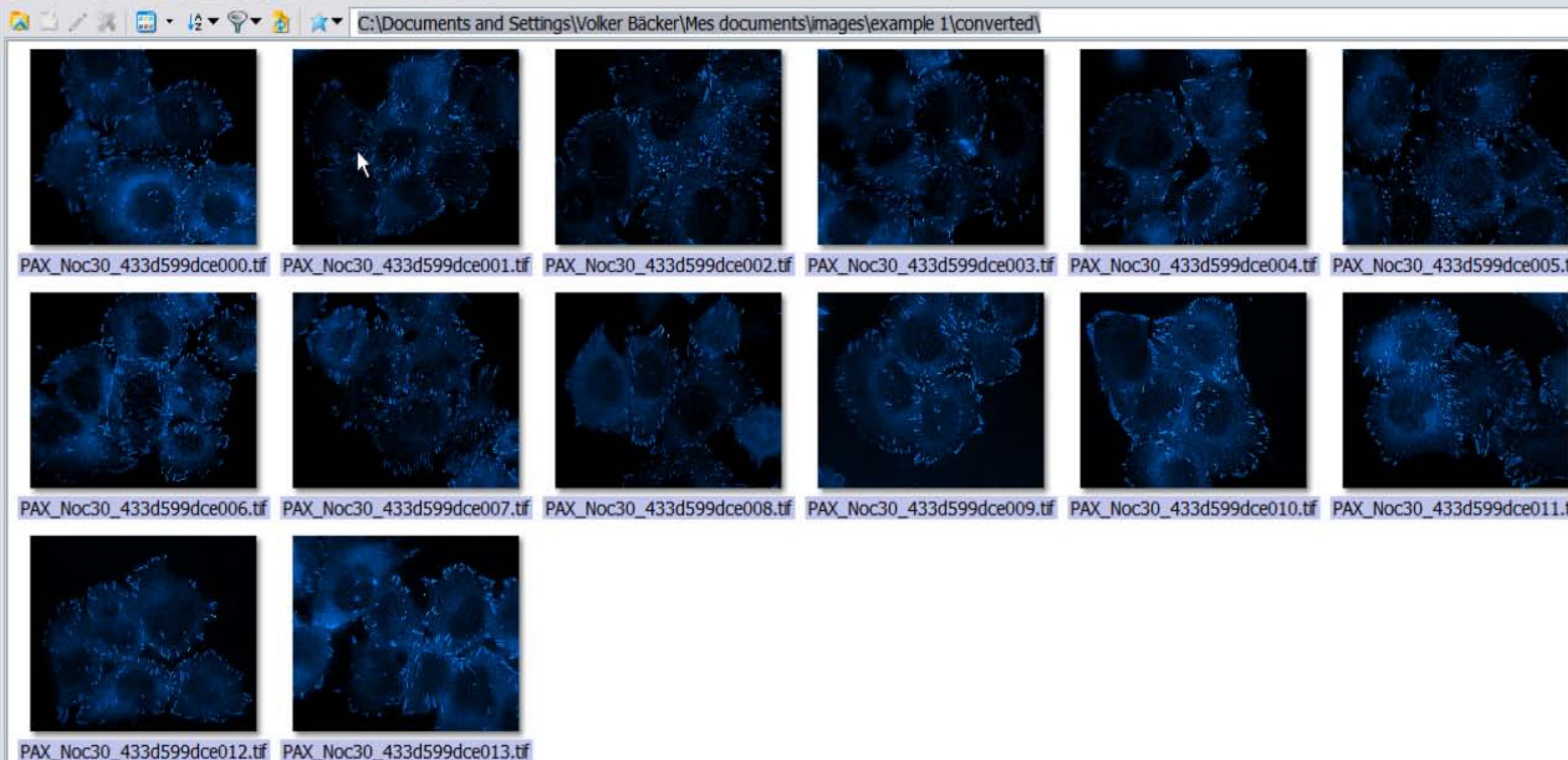


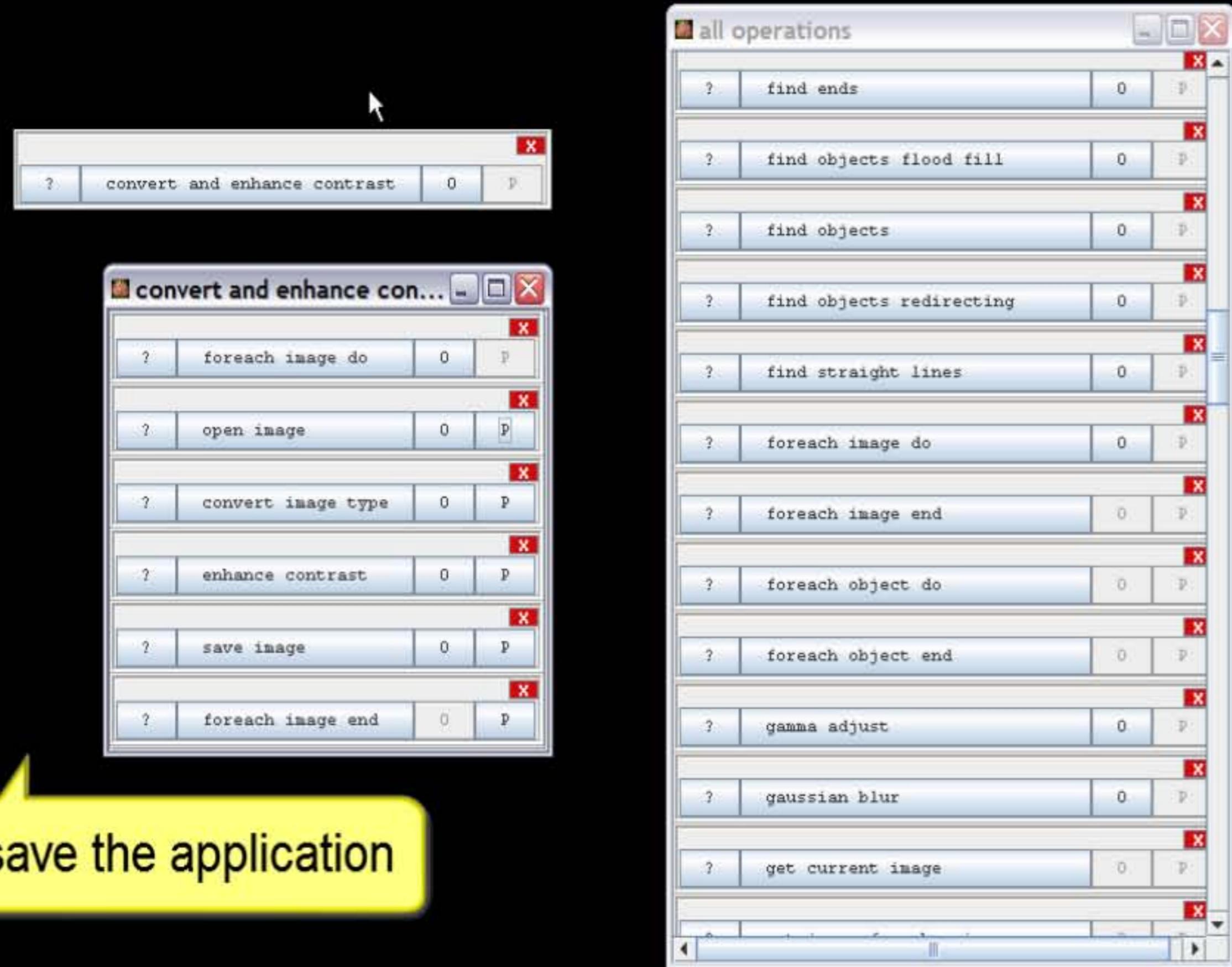
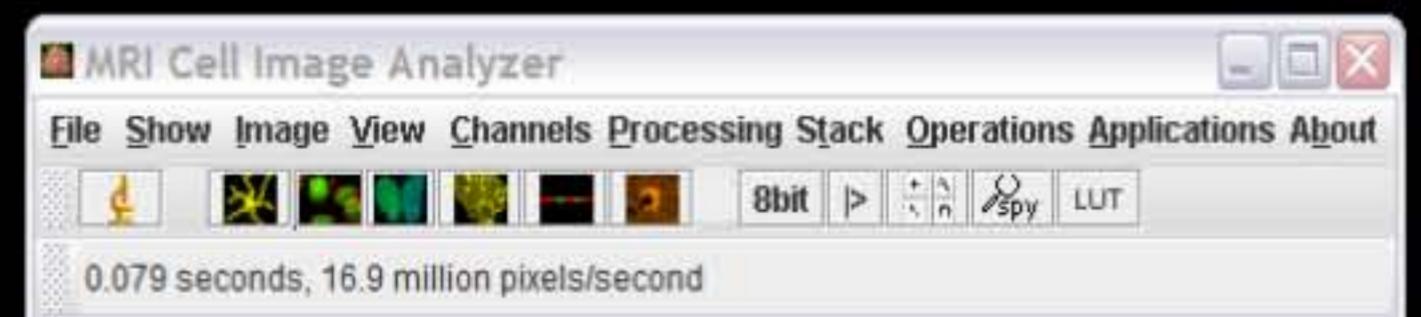


# XnView - [Browser - C:\...\Mes documents\images\example 1\converted]

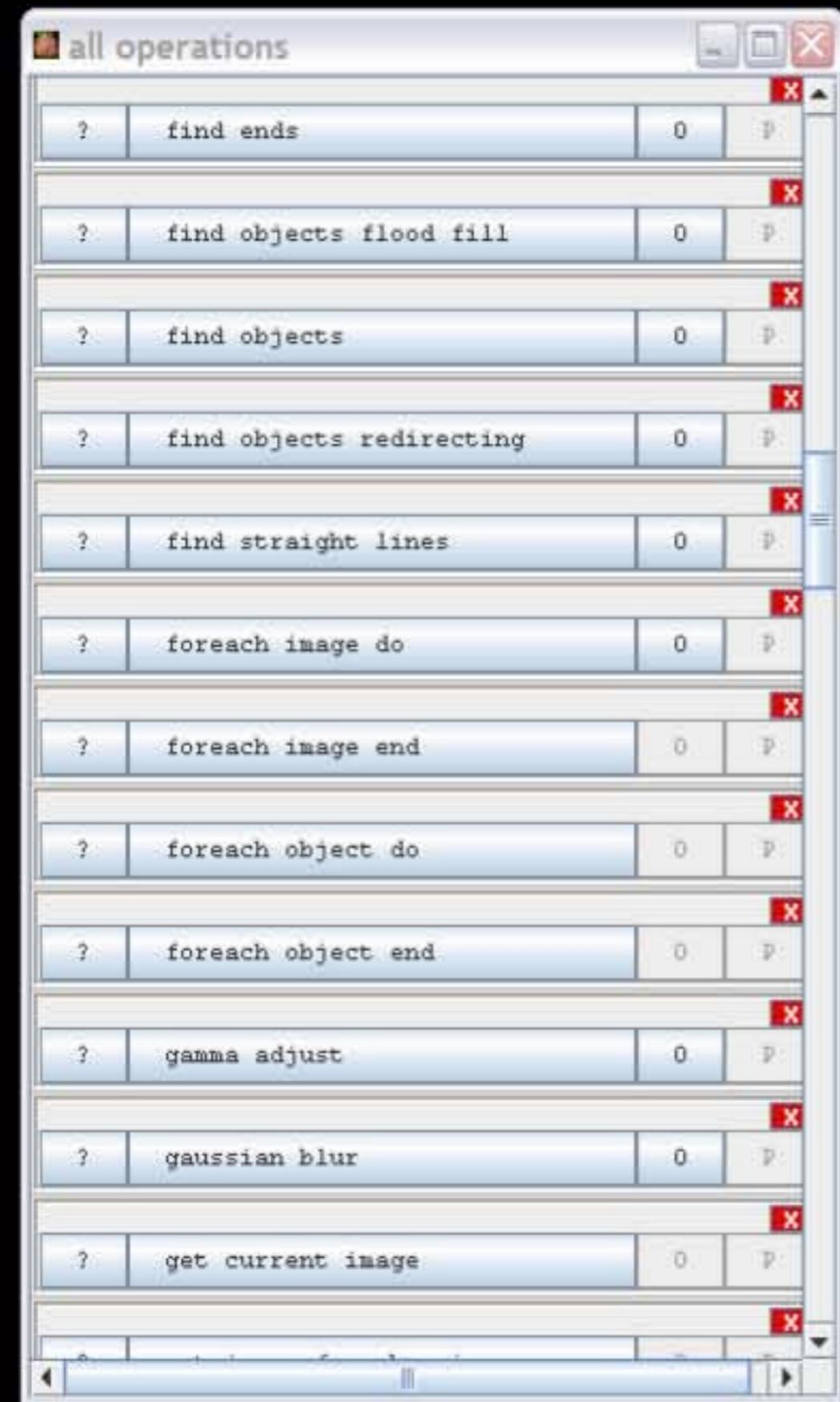
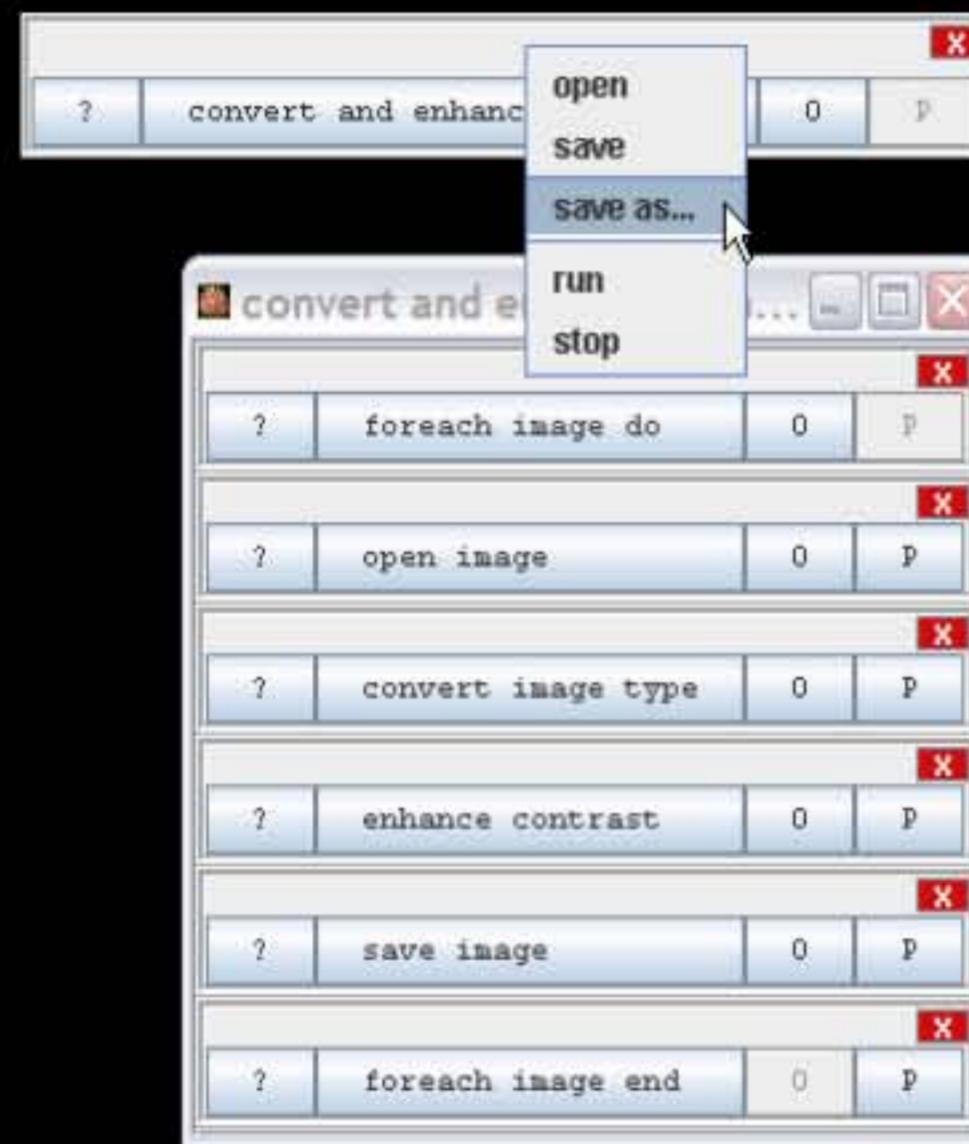
Fichier Édition Affichage Outils Créer Fenêtre Info

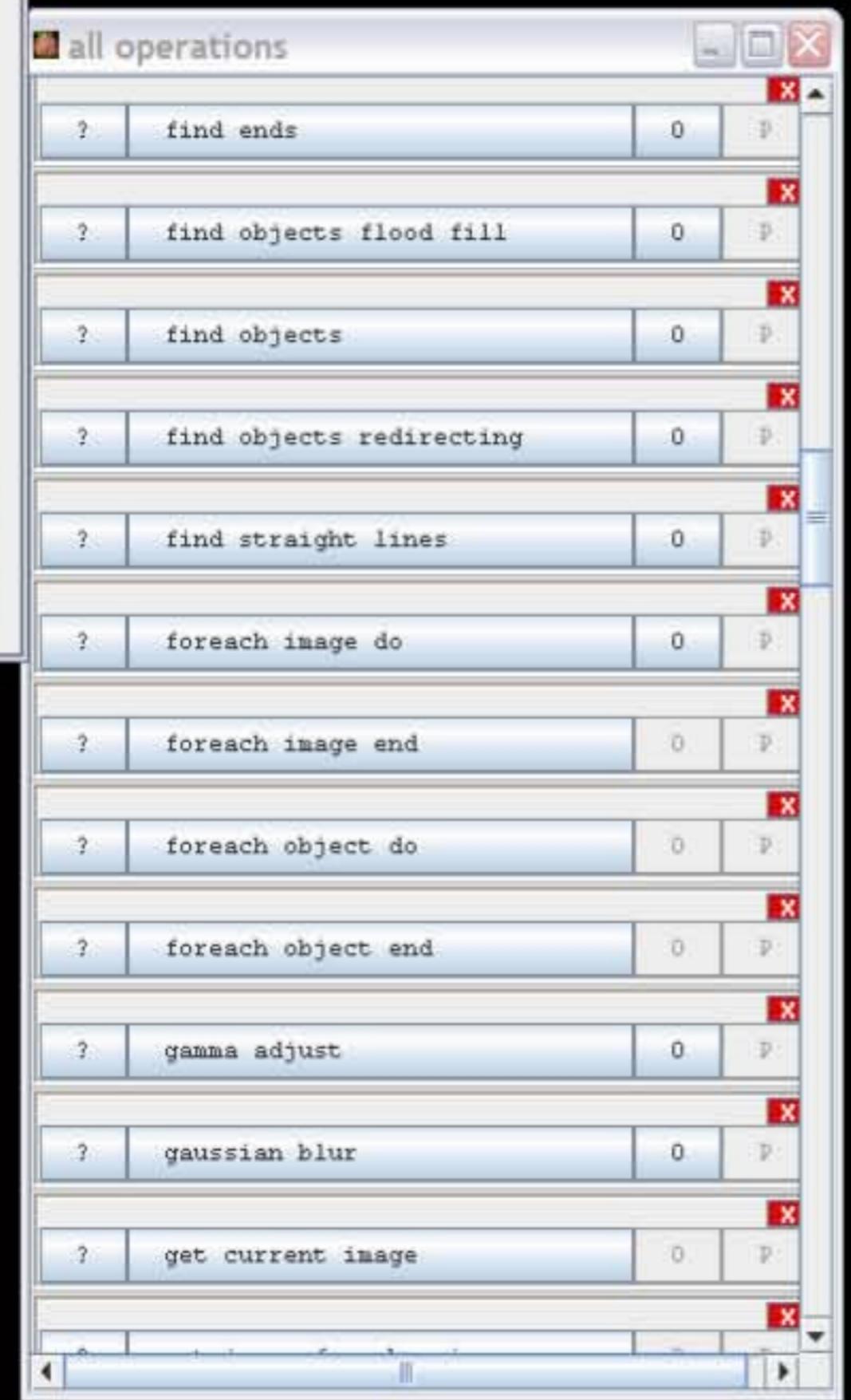
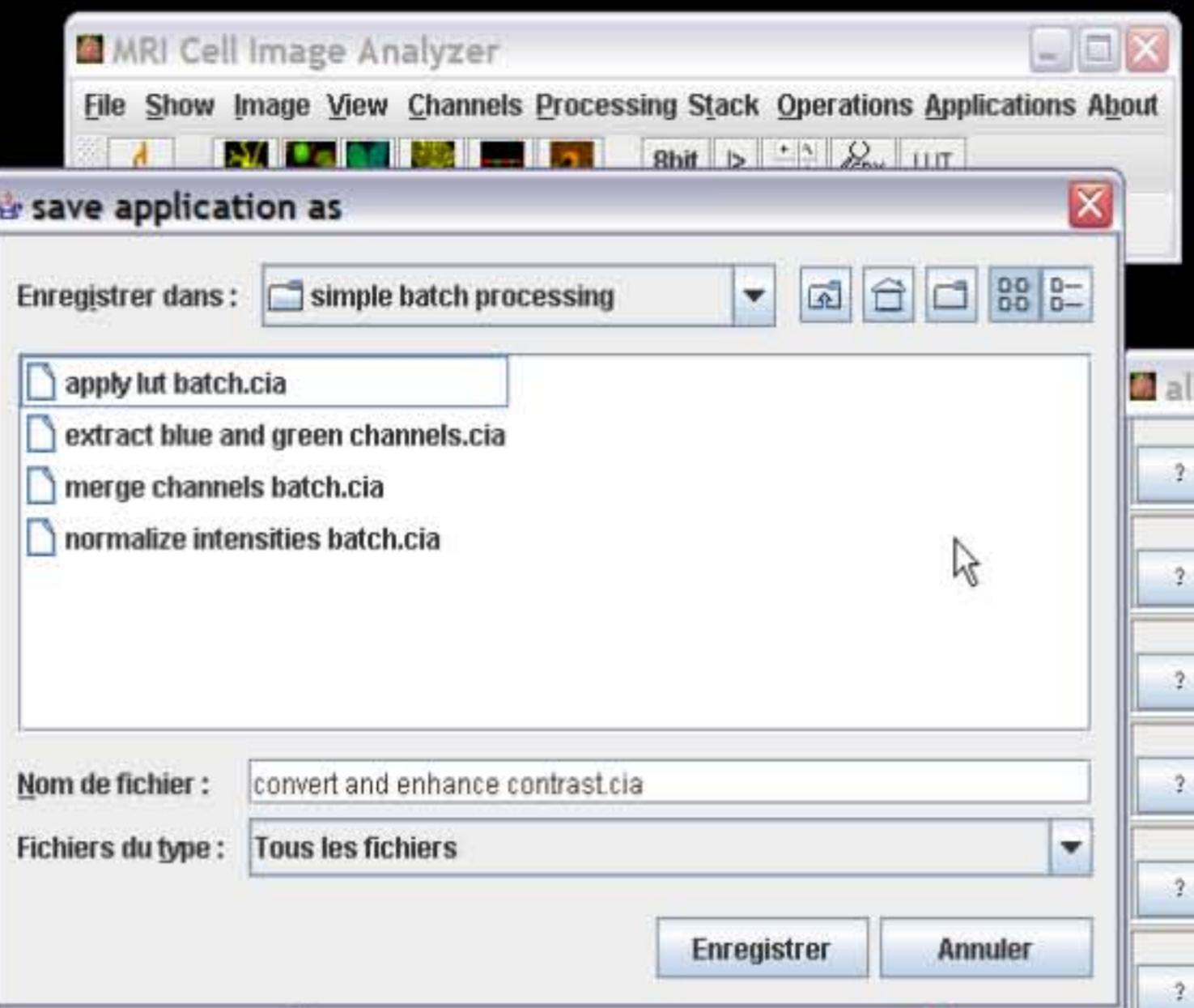
Parcourir

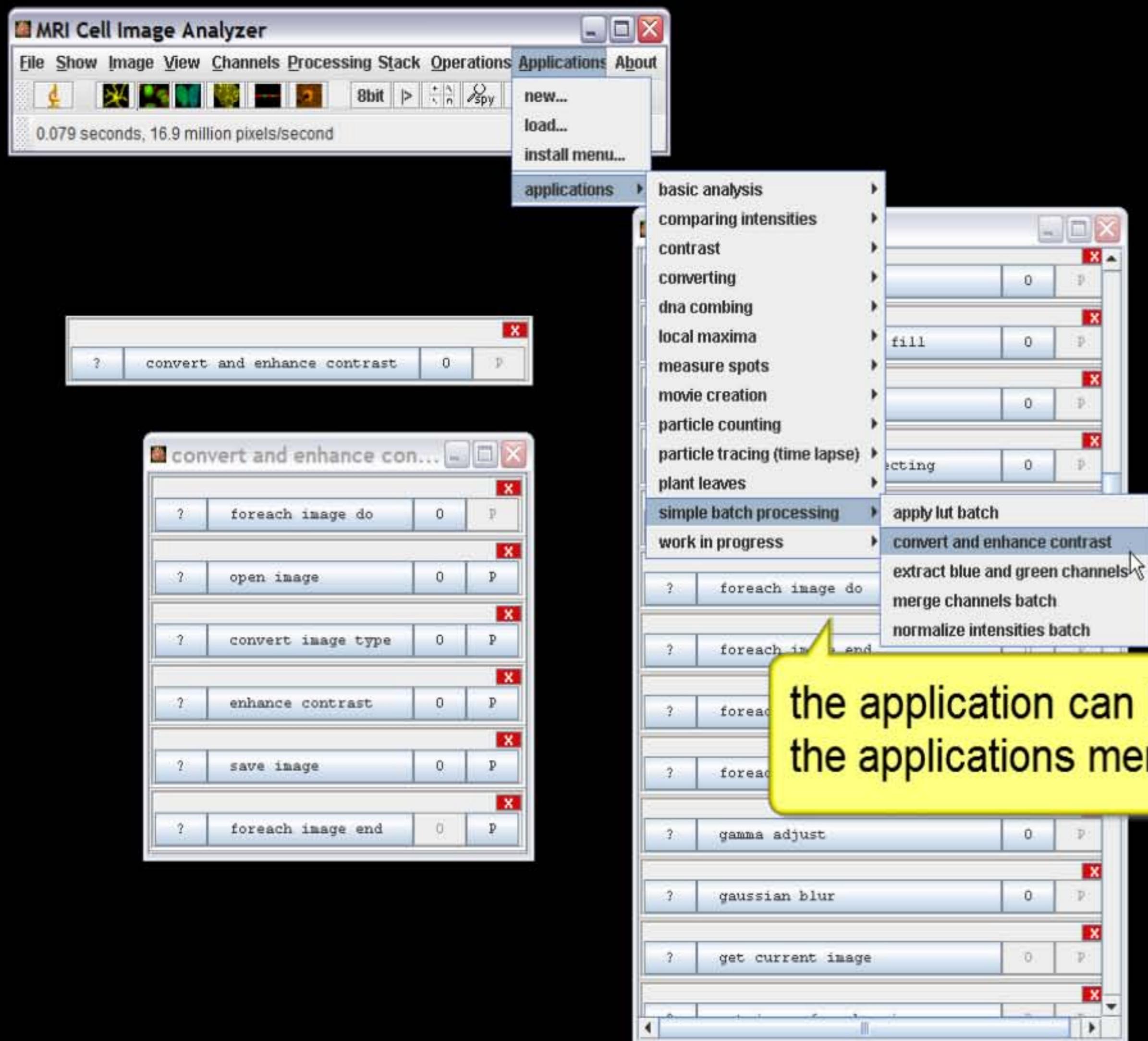




save the application

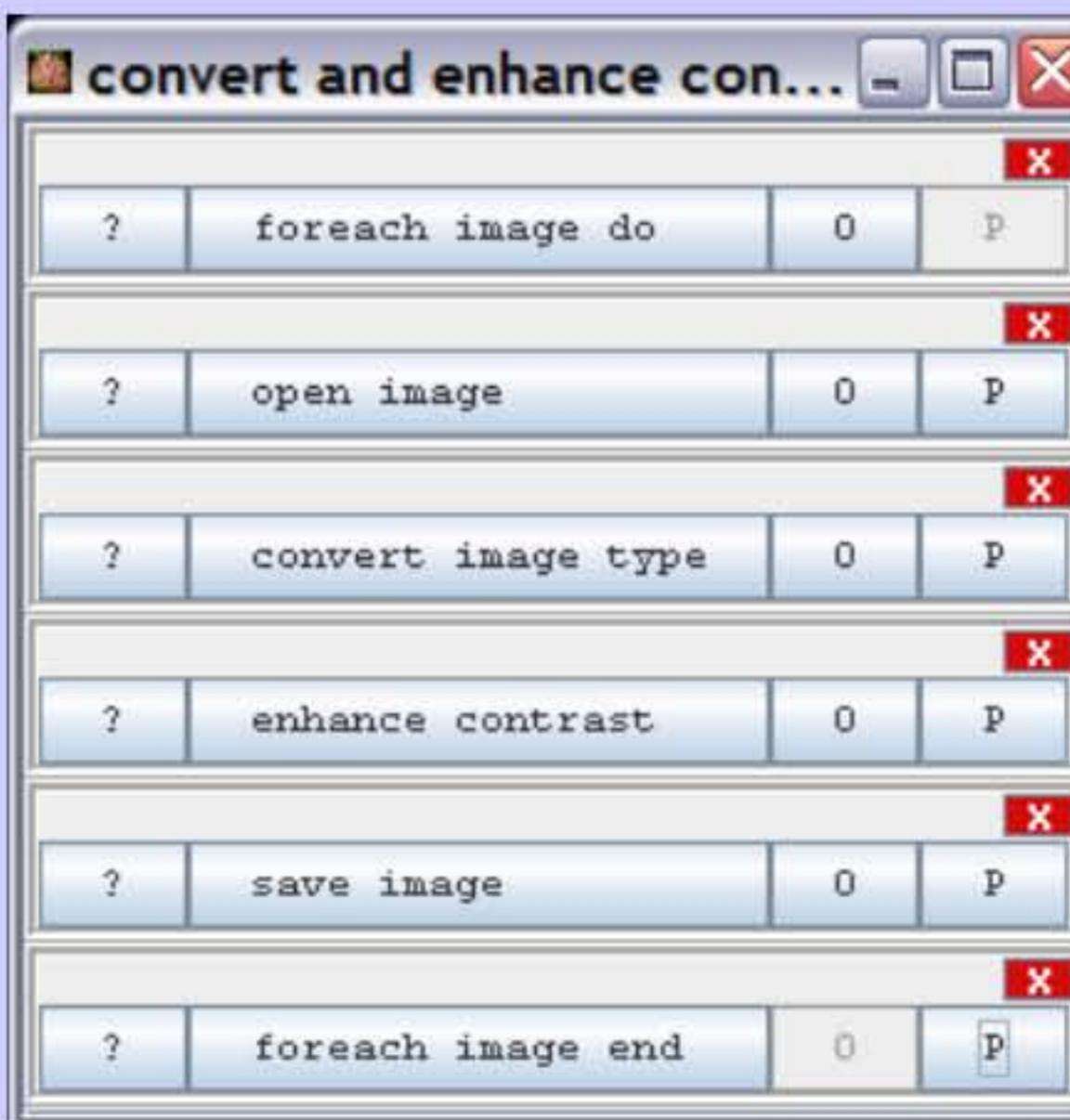






the application can be opened from  
the applications menu

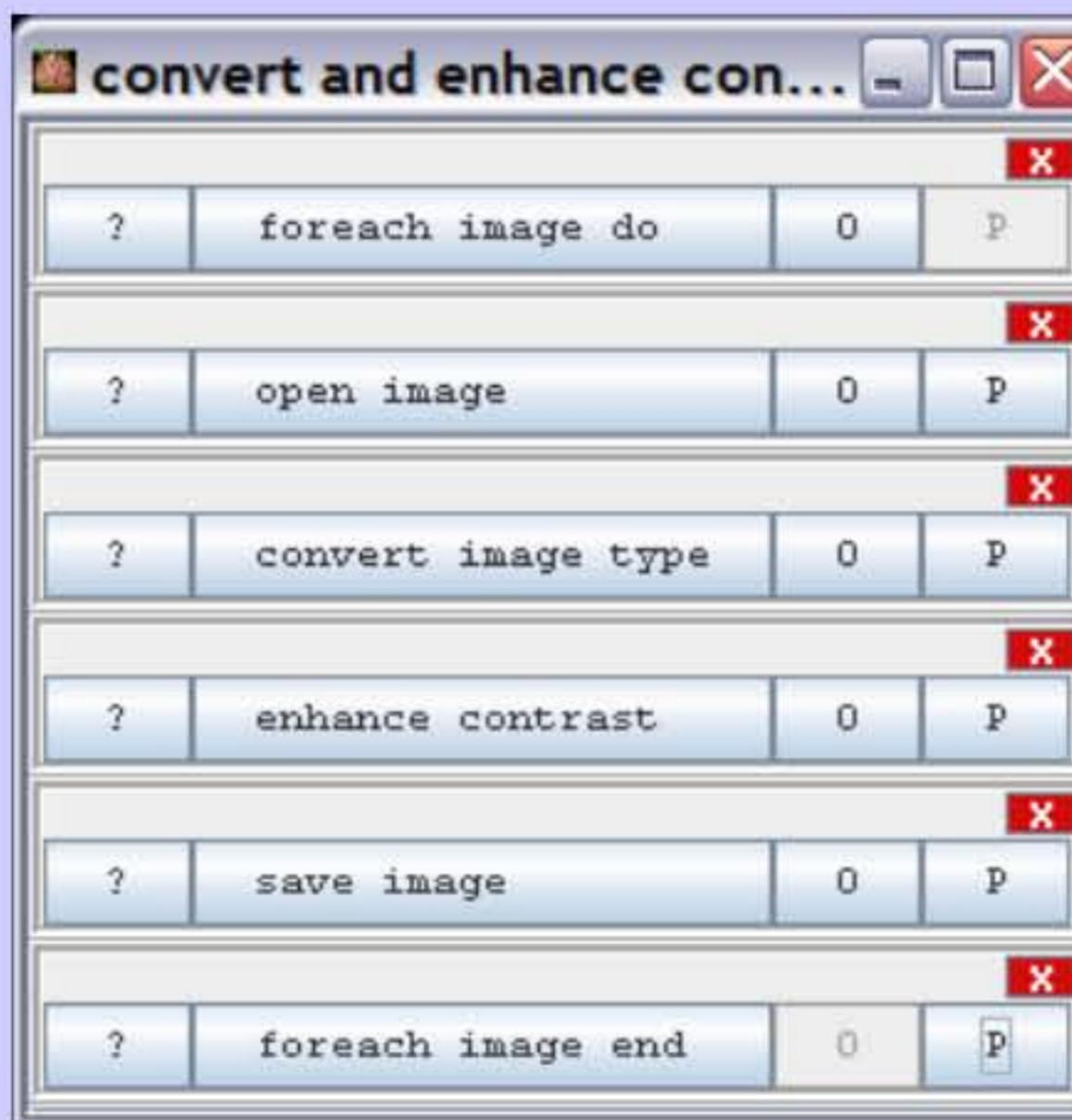
# Comparison visual script / macro



```
dir1 = getDirectory("Choose Source Directory ");
dir2 = getDirectory("Choose Destination Directory ");
list = getFileList(dir1);
Dialog.create("enhance contrast options");
Dialog.addNumber("percent saturated", 0.5);
Dialog.addCheckbox("equalize", false);
Dialog.addCheckbox("normalize", true);
Dialog.addCheckbox("use stack histogram", false);
Dialog.show();
saturated=Dialog.getNumber();
equalize = Dialog.getCheckbox();
normalize = Dialog.getCheckbox();
useStackHistogram = equalize = Dialog.getCheckbox();
setBatchMode(true);
for (i=0; i<list.length; i++) {
    showProgress(i+1, list.length);
    if (endsWith(list[i], ".tif")) {
        open(dir1+list[i]);
        run("8-bit");
        run("Enhance Contrast", "saturated=" + saturated + " normalize");
        saveAs("Tiff", dir2+list[i]);
    }
}
```



# Comparison visual script / macro



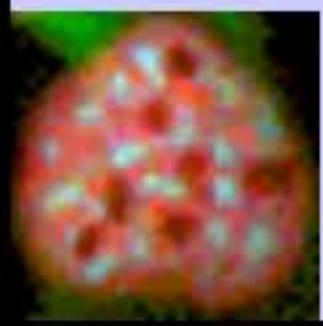
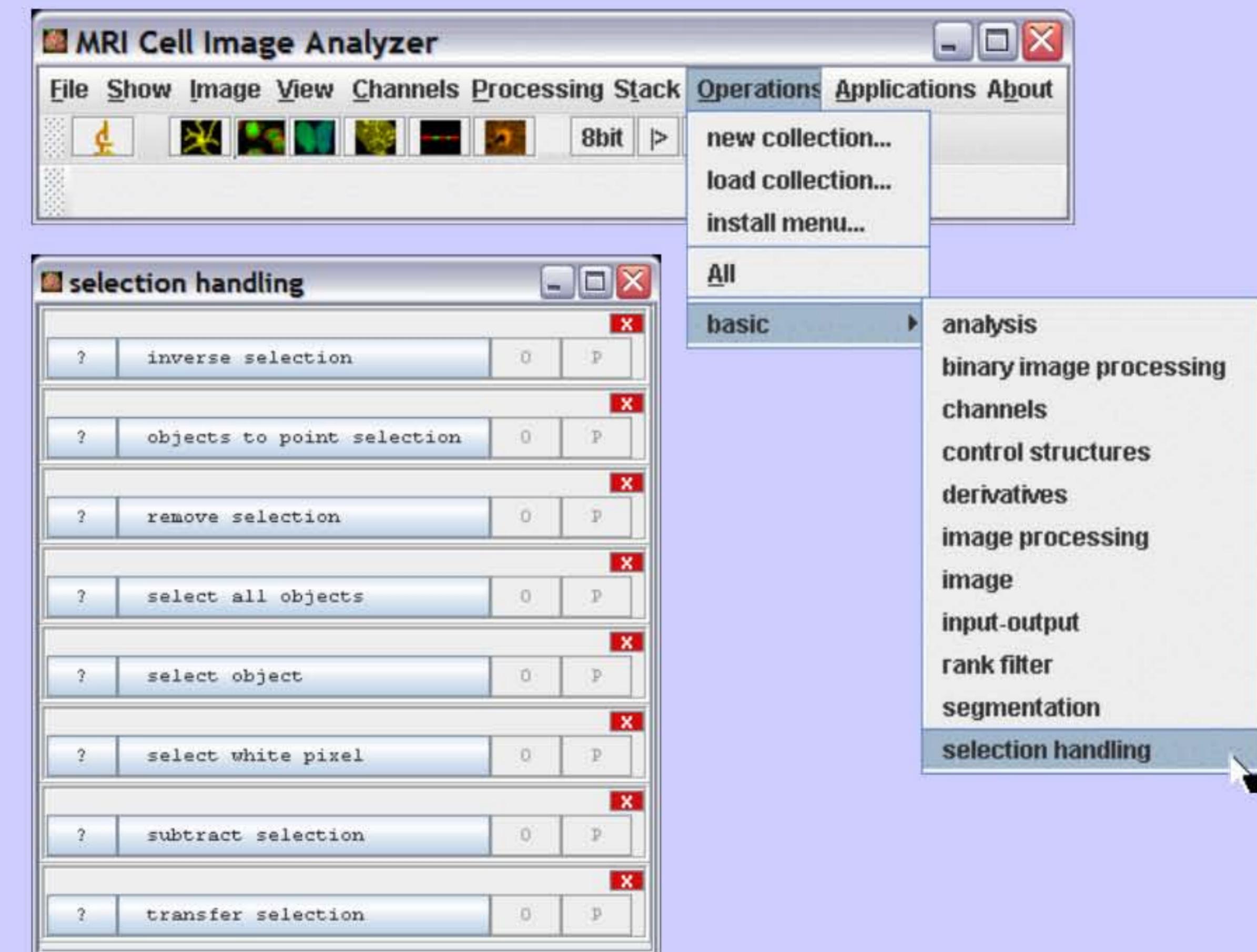
```
dir1 = getDirectory("Choose Source Directory ");
dir2 = getDirectory("Choose Destination Directory ");
list = getFileList(dir1);

setBatchMode(true);
for (i=0; i<list.length; i++) {
    showProgress(i+1, list.length);
    if (endsWith(list[i], ".tif")) {
        open(dir1+list[i]);
        run("8-bit");
        run("Enhance Contrast", "saturated=" + saturated + " normalize");
        saveAs("Tiff", dir2+list[i]);
    }
}
```



# Operation collections

- processing
- analysis
- control structures
- selection handling
- input / output
- reporting



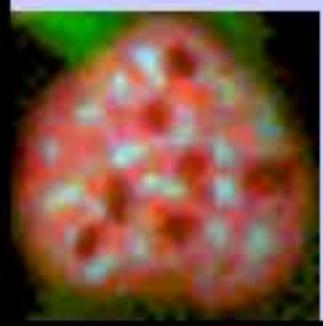
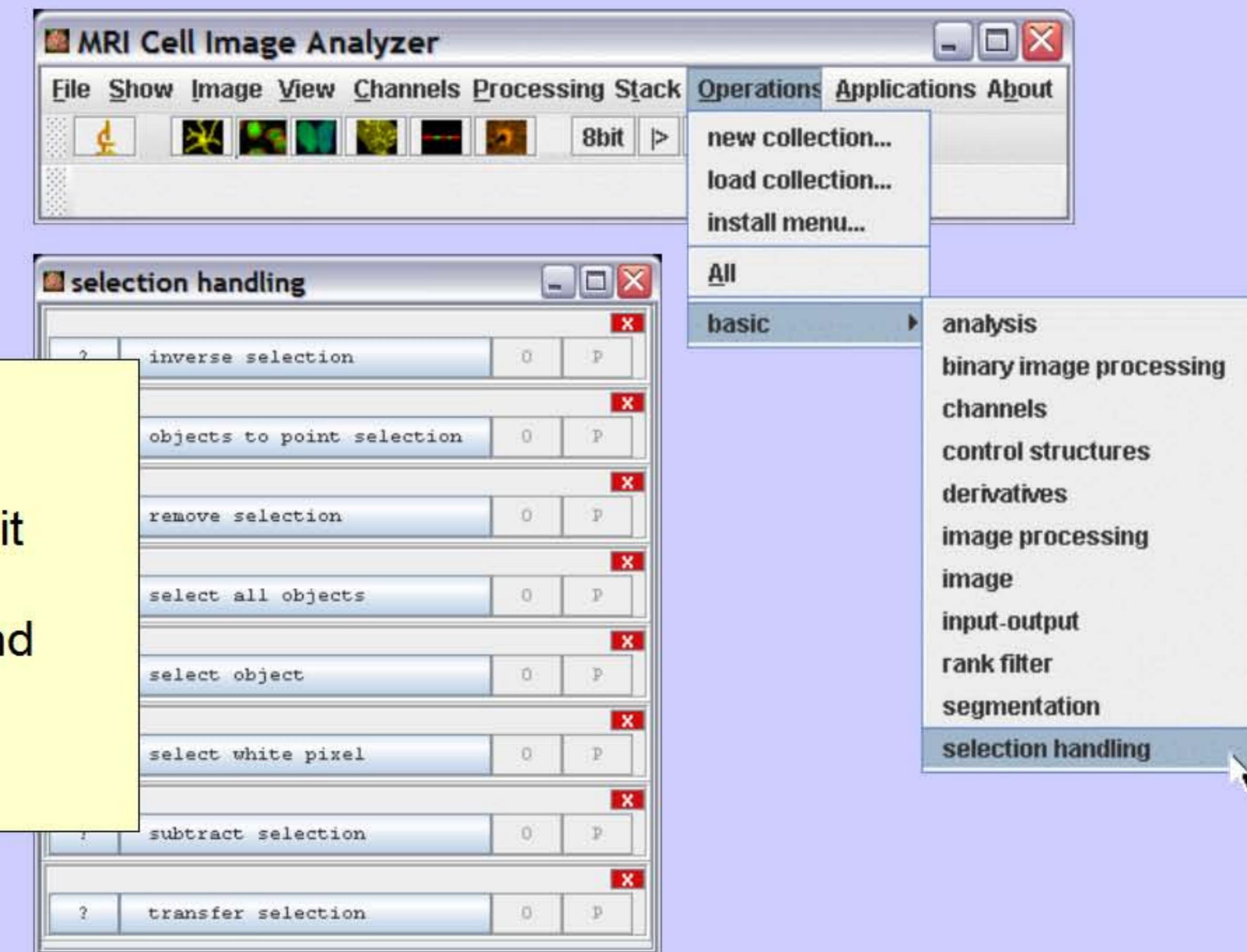
Cell Image Analyzer

volker.baecker@mri.cnrs.fr

# Operation collections

- processing
- analysis
- control structures

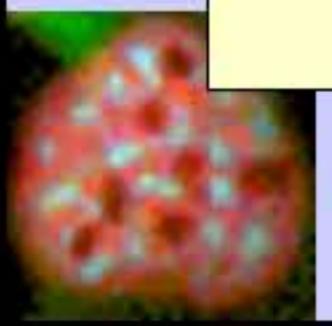
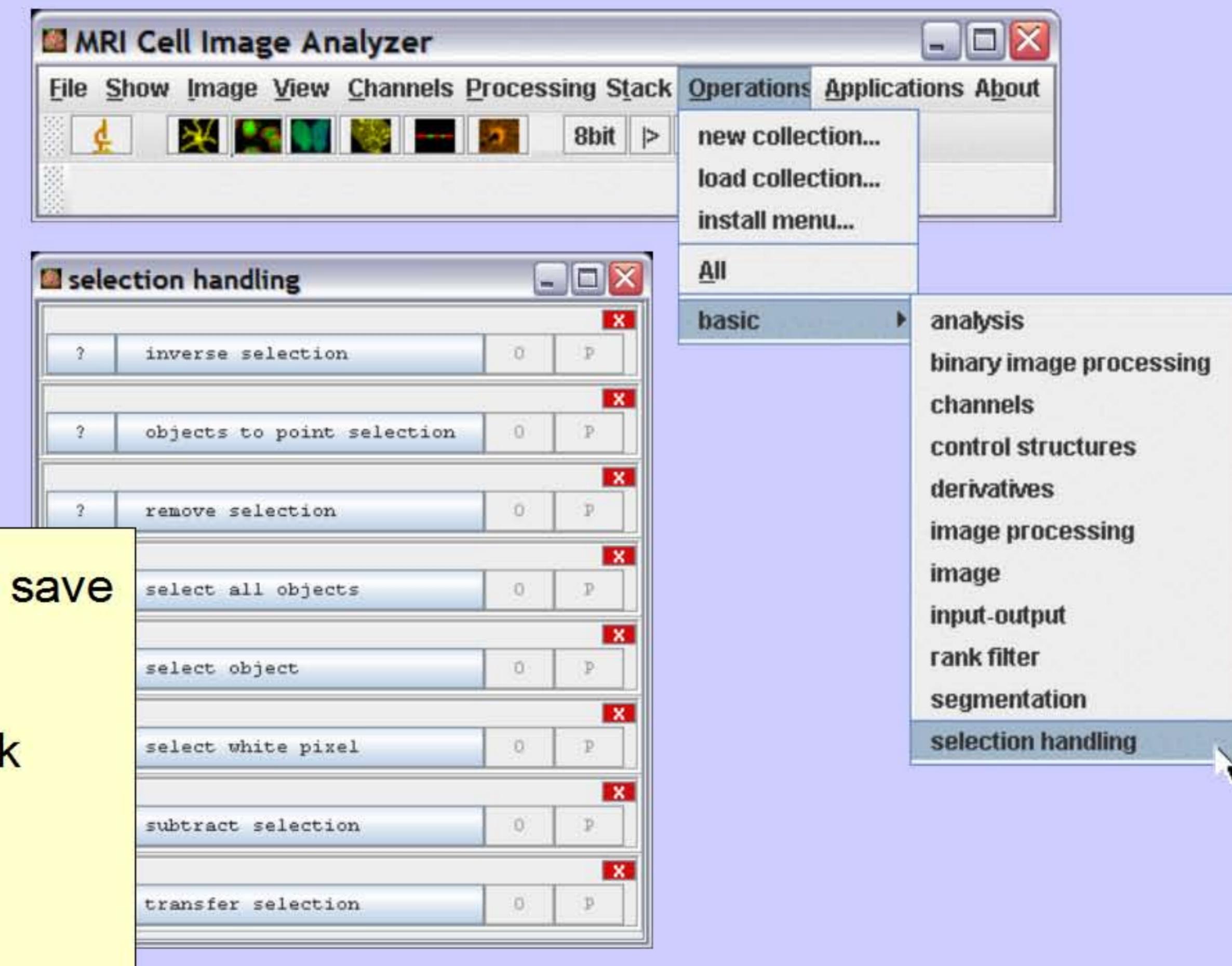
```
foreach image do
foreach object do
accept or skip or exit
wait for user
skip no objects found
skip saturated
...
```



# Operation collections

- processing
- analysis
- control structures
- selection handling
- input / output

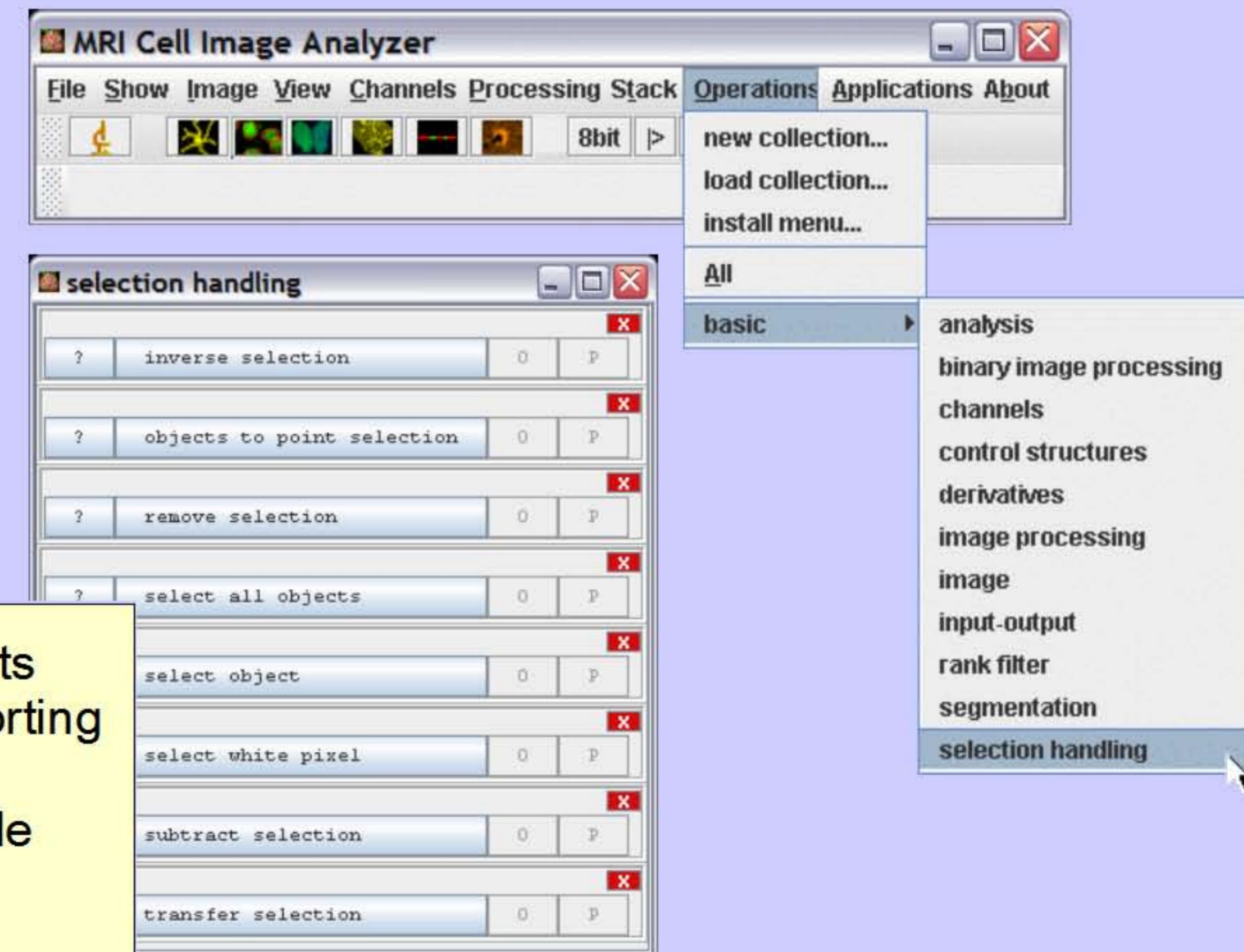
open / show / hide / save  
/ close image  
show results table  
open series as stack  
save as tiff series



# Operation collections

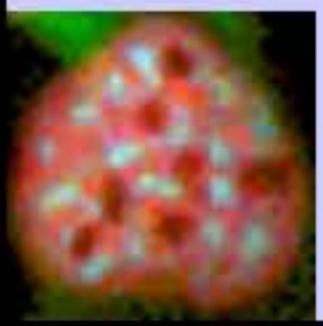
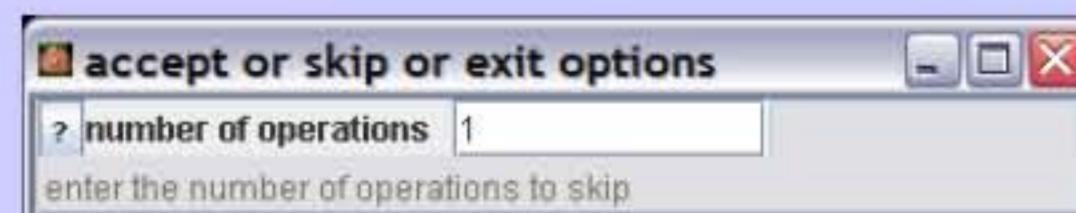
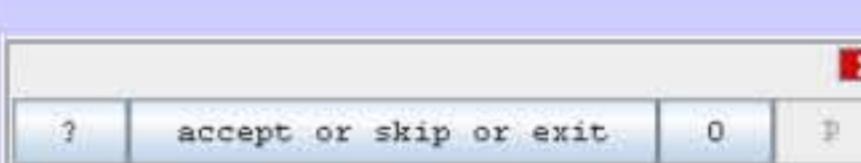
- processing
- analysis
- control structures
- selection handling
- input / output
- reporting

report measurements  
project specific reporting  
operations  
write spreadsheet file

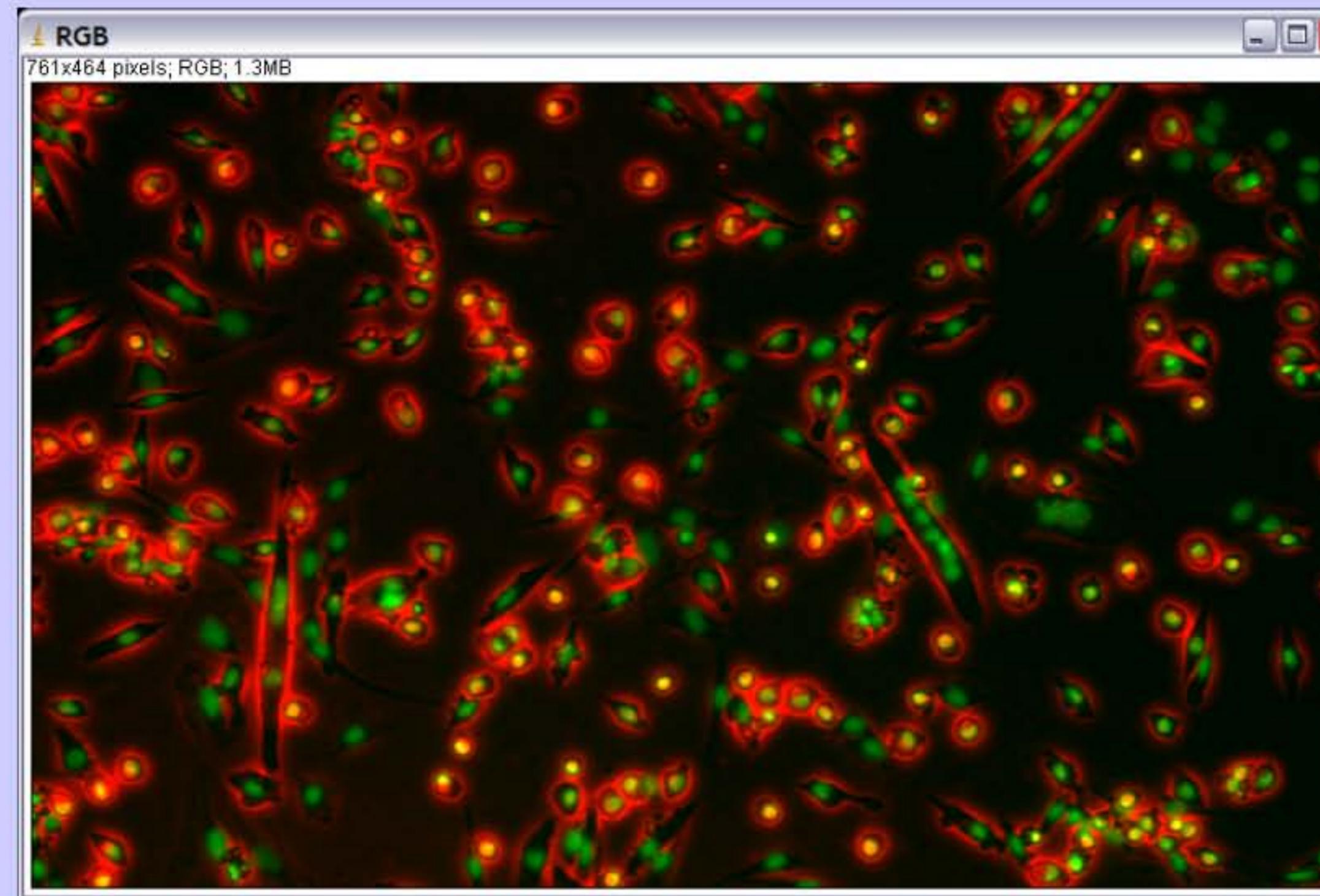


# Interactive applications

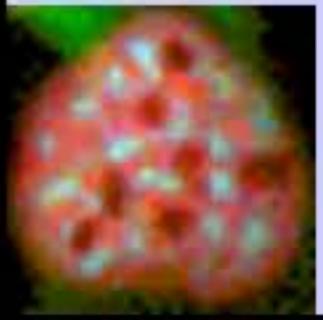
- let the computer do the work when possible
- the user take decisions when necessary
- execution of application stops
- user decides to take result into account
- user corrects automatic result
  - selection
  - mask



# Interactive applications

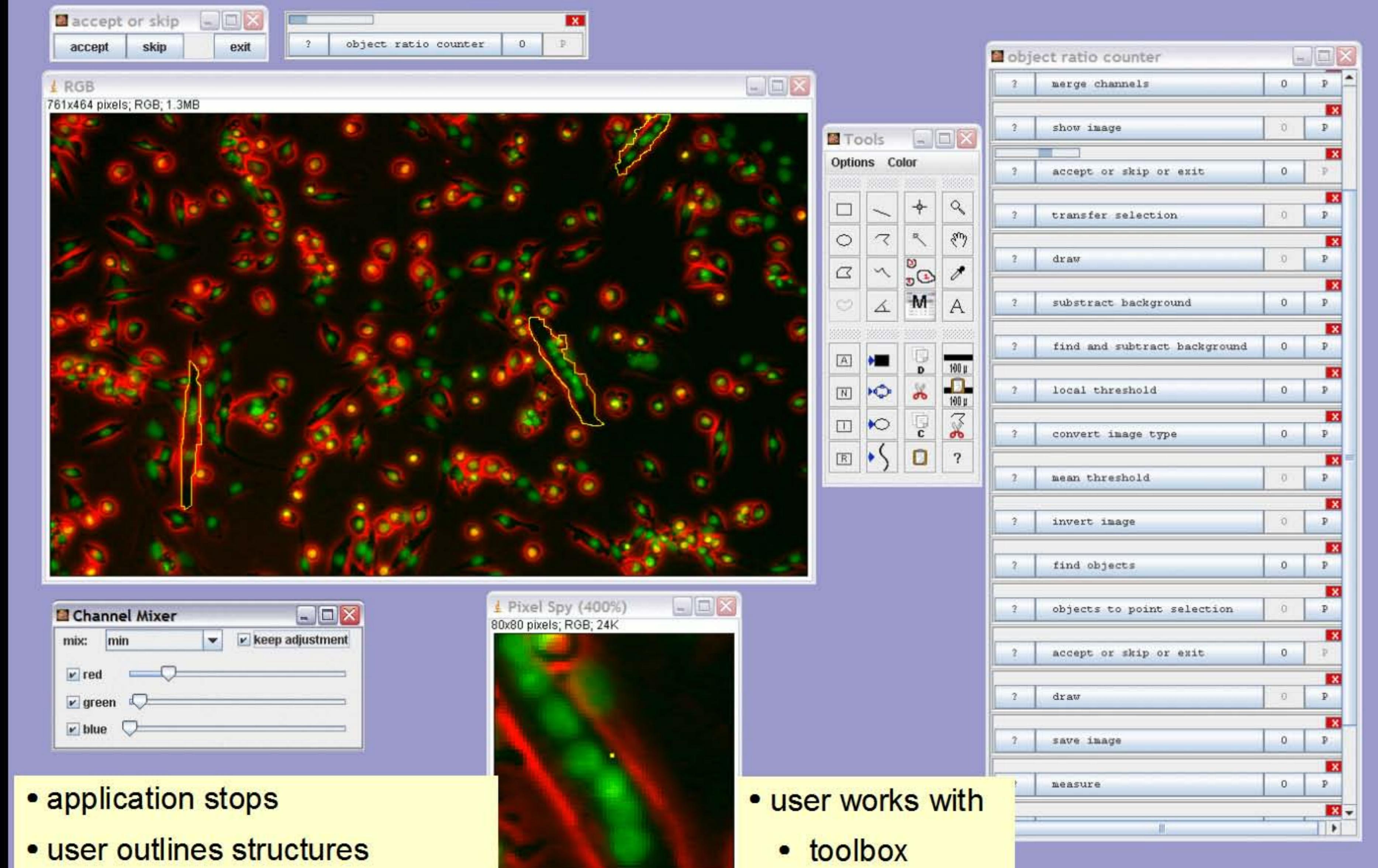


- count nuclei
  - all
  - inside certain structures
- calculate the ratio



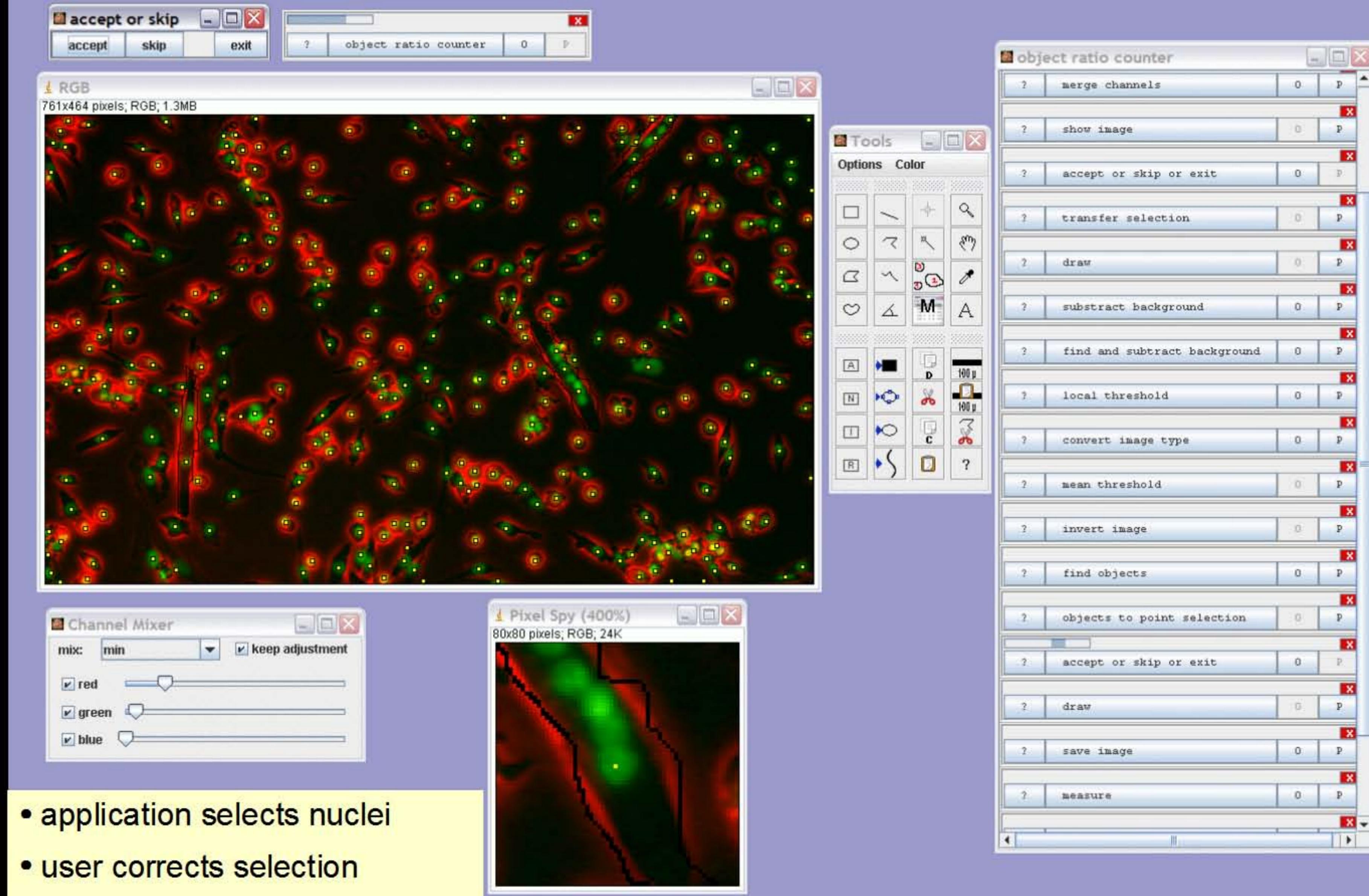
Cell Image Analyzer

[volker.baecker@mri.cnrs.fr](mailto:volker.baecker@mri.cnrs.fr)

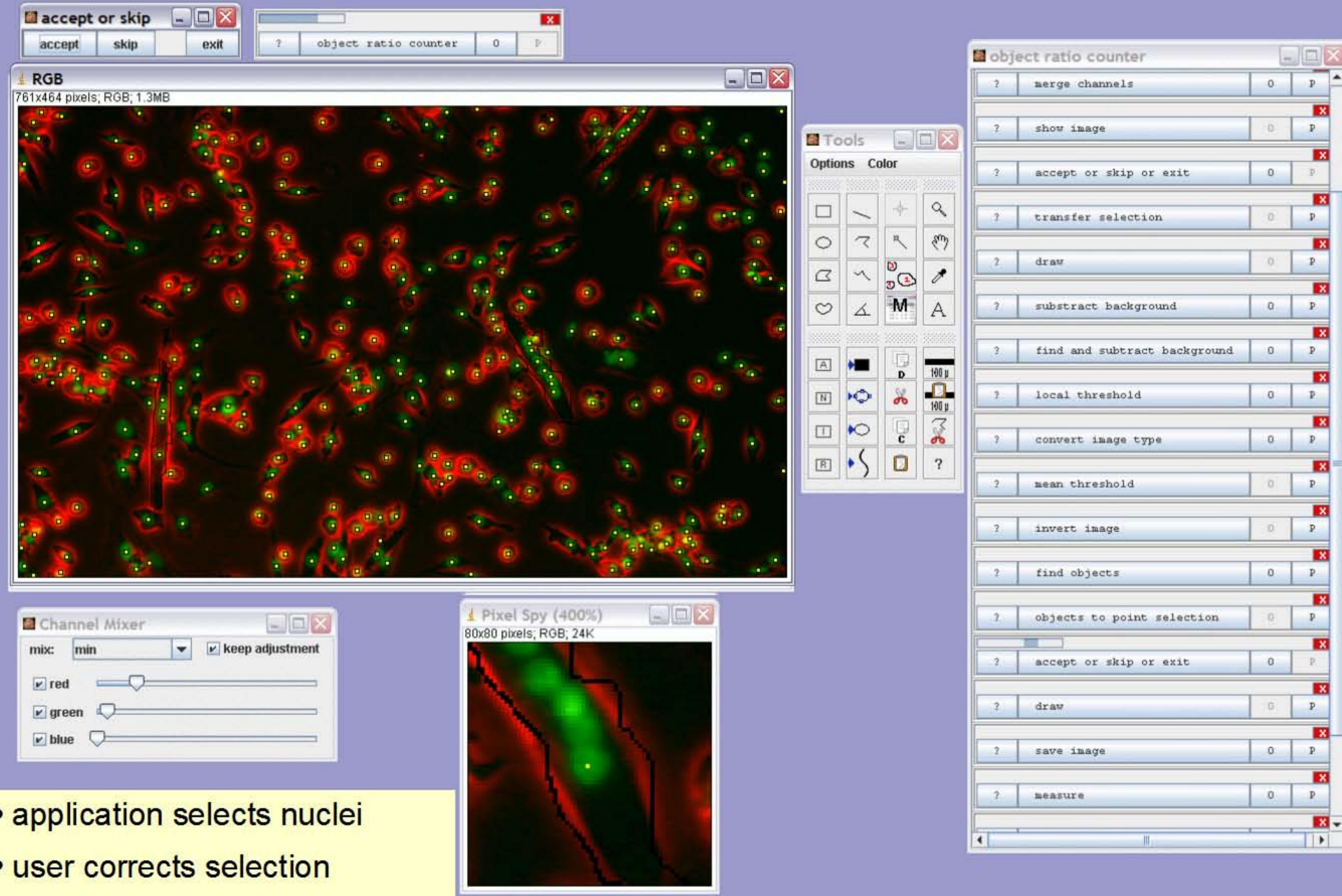


- application stops
- user outlines structures
- user presses accept to continue

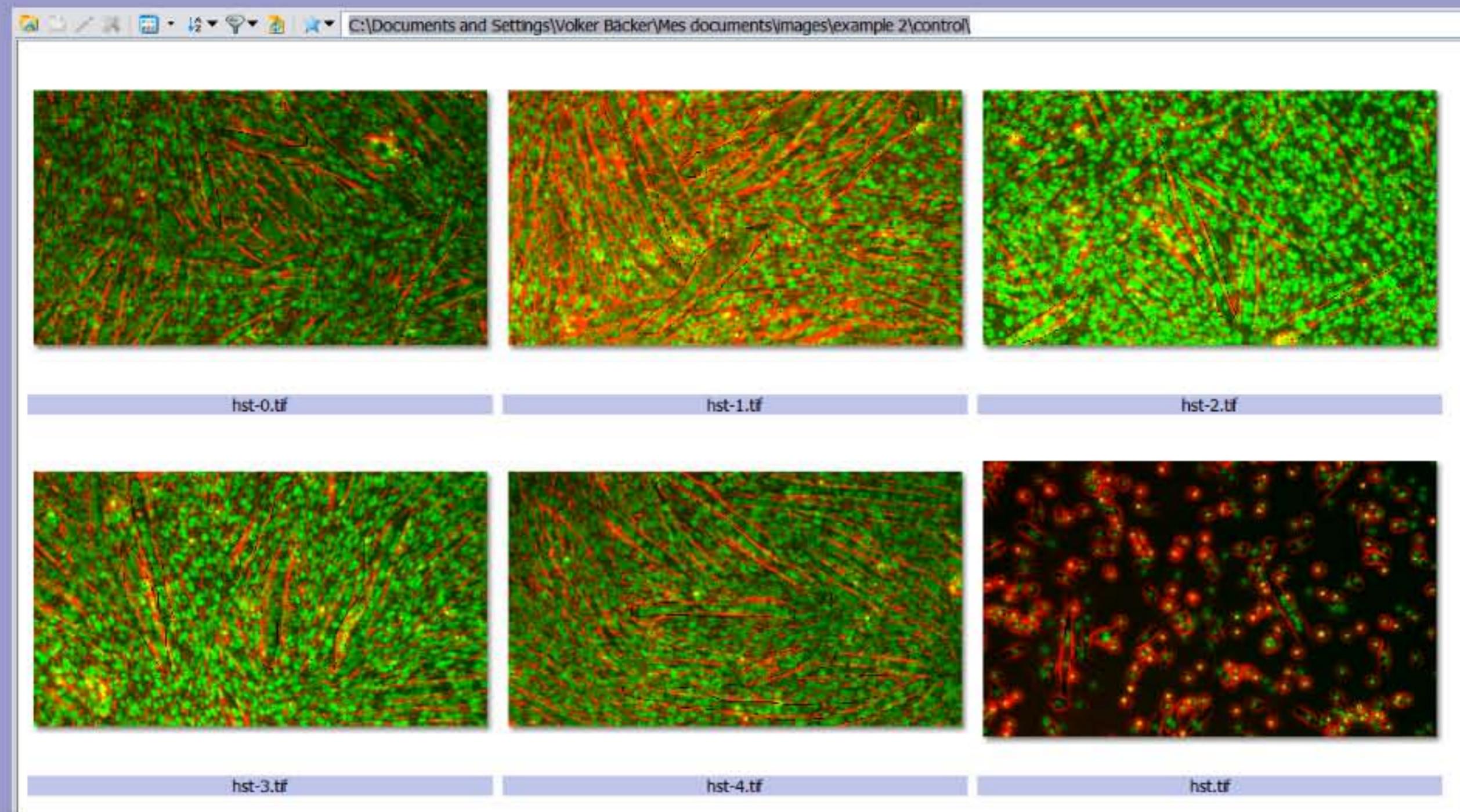
- user works with
  - toolbox
  - channel mixer
  - pixel spy



- application selects nuclei
- user corrects selection
- user presses accept to continue



- application selects nuclei
- user corrects selection
- user presses accept to continue

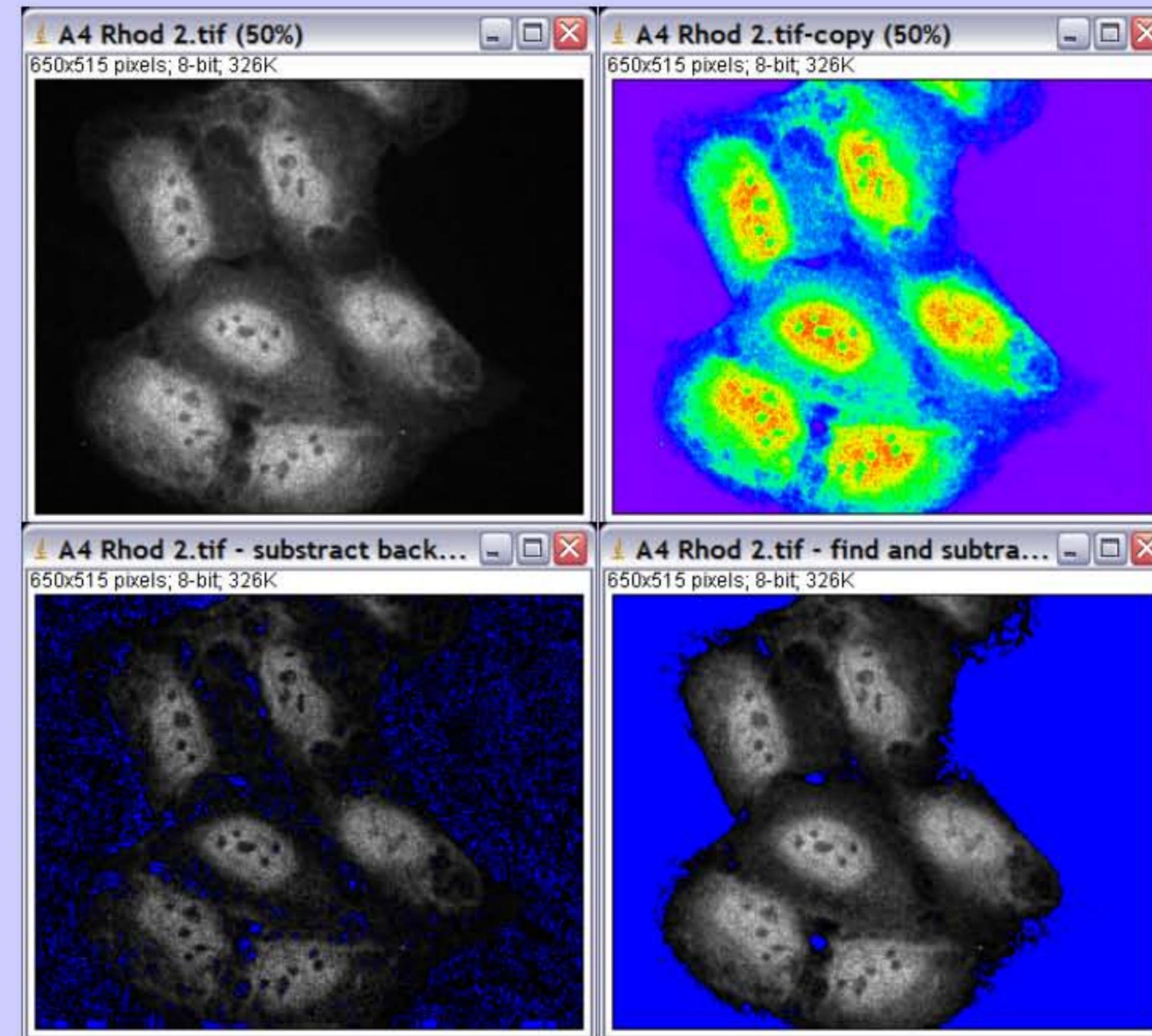


	A	B	C	D	E	F
1	<b>Image</b>	<b>Areas</b>	<b>Objects</b>	<b>Objects inside areas</b>	<b>ratio</b>	<b>folder</b>
2	hst-0.tif	3	891	52	0,06	C:\images\example 2\
3	hst-1.tif	4	918	89	0,1	C:\images\example 2\
4	hst-2.tif	3	942	61	0,06	C:\images\example 2\
5	hst-3.tif	4	899	70	0,08	C:\images\example 2\
6	hst-4.tif	9	966	116	0,12	C:\images\example 2\
7	hst.tif	3	315	17	0,05	C:\images\example 2\

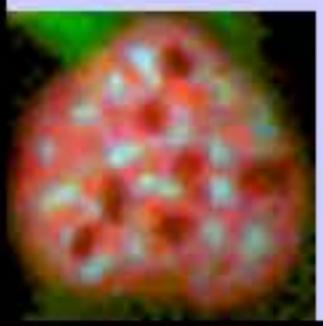
# Further interactive tools - LUT tool



- apply lookup table to
  - active image
  - all open images



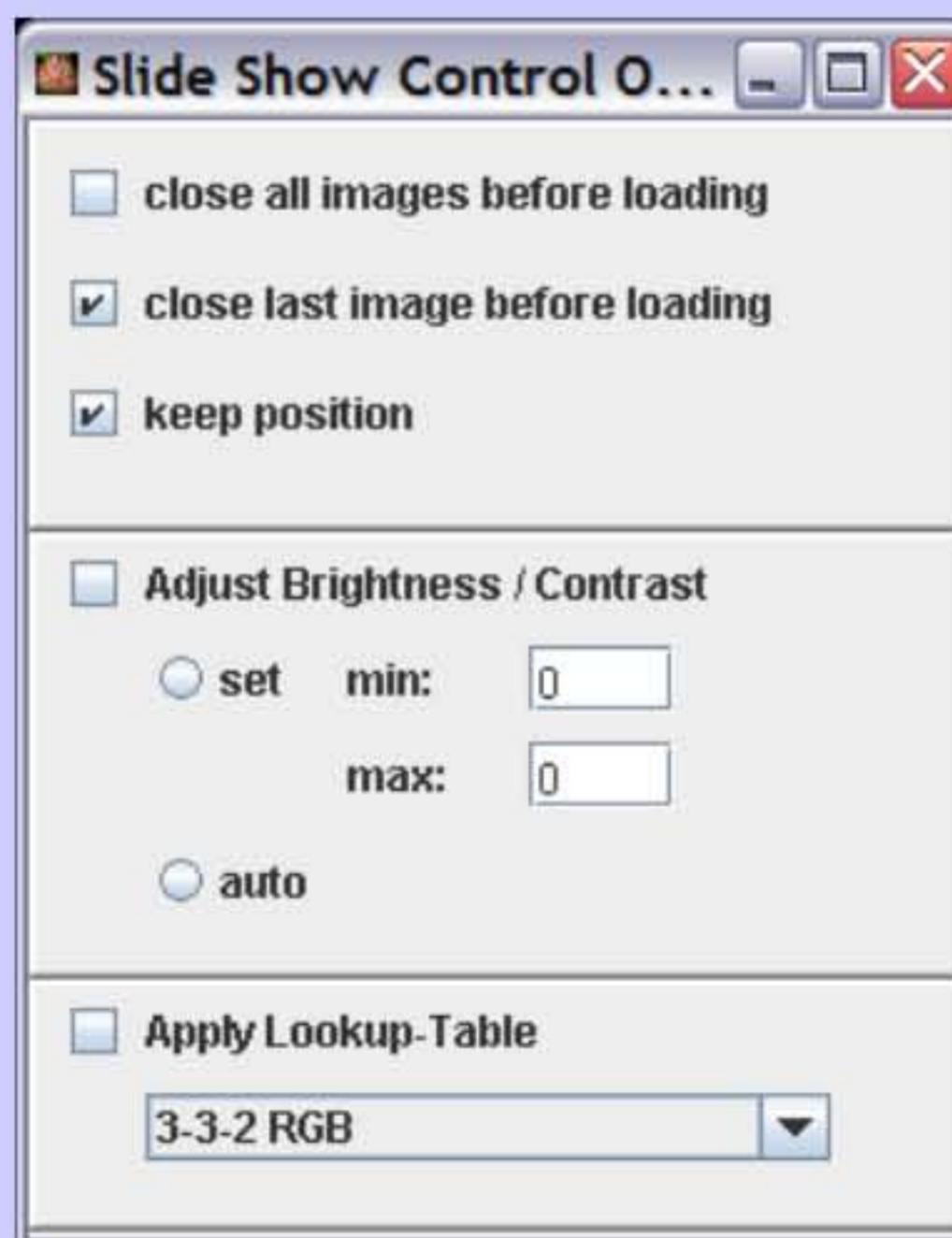
1. gray
2. rainbow smooth
3. hilo after "subtract background"
4. hilo after "find and subtract" background



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# Further interactive tools – slide show control

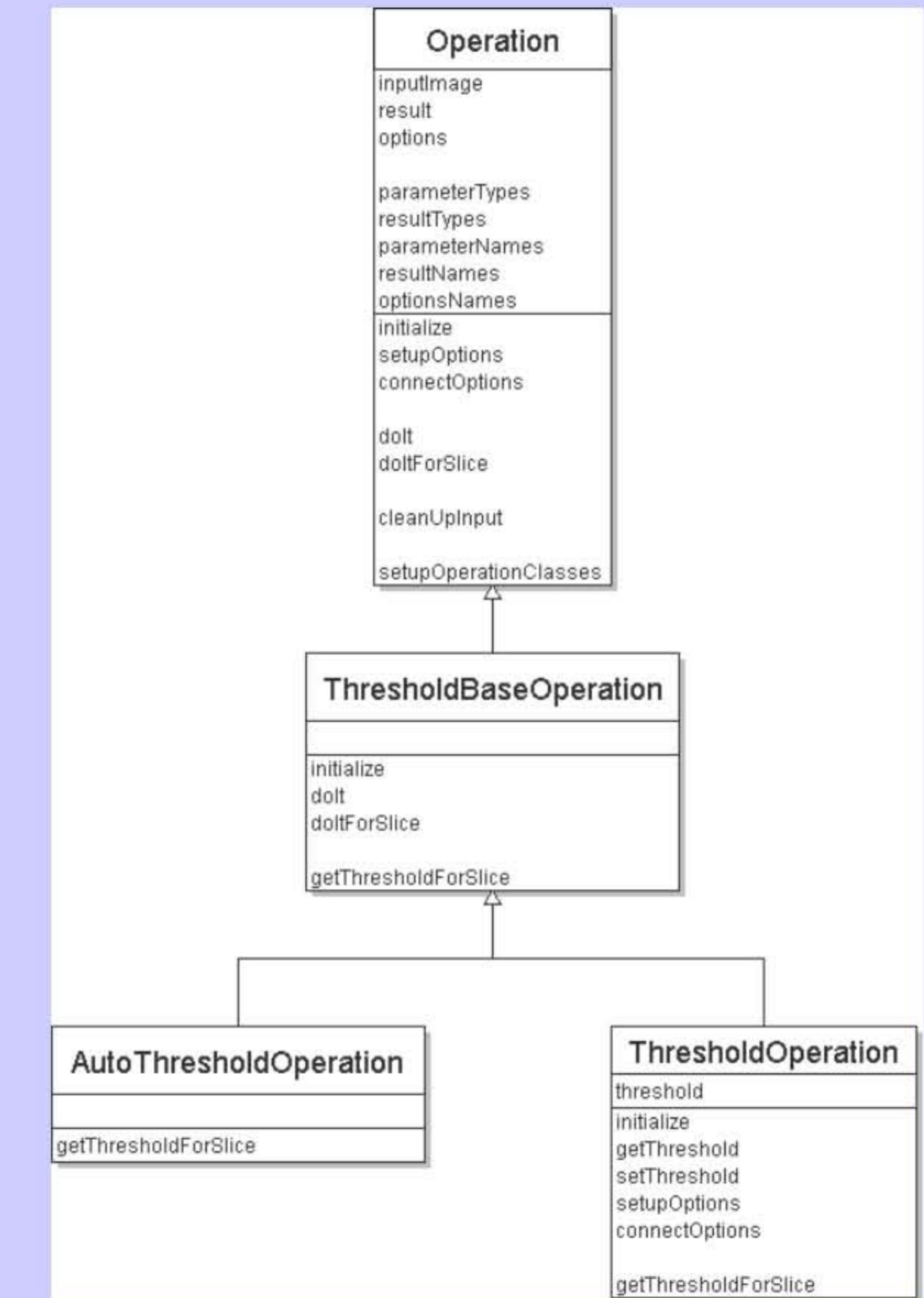


- **navigation**
  - select folder
  - goto first image
  - goto last image
  - goto next image
  - goto last image
  - reload current image
- **when opening next image**
  - close all open images
  - close last image opened with slide show control
  - keep position and zoom
  - adjust brightness/contrast (fix or auto)
  - apply LUT



# Extending the framework

- to add an operation (without options)
  - declare input parameter and result in initialize
  - implement
    - dolt
    - doltForSlice

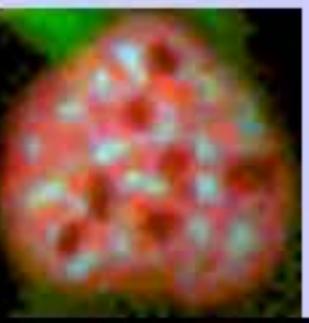


# Extending the framework

```
protected void initialize() throws ClassNotFoundException {
    super.initialize();
    parameterTypes = new Class[1];
    parameterTypes[0] = Class.forName("ij.ImagePlus");
    parameterNames = new String[1];
    parameterNames[0] = "InputImage";
    resultTypes = new Class[1];
    resultTypes[0] = Class.forName("ij.ImagePlus");
    resultNames = new String[1];
    resultNames[0] = "Result";
}

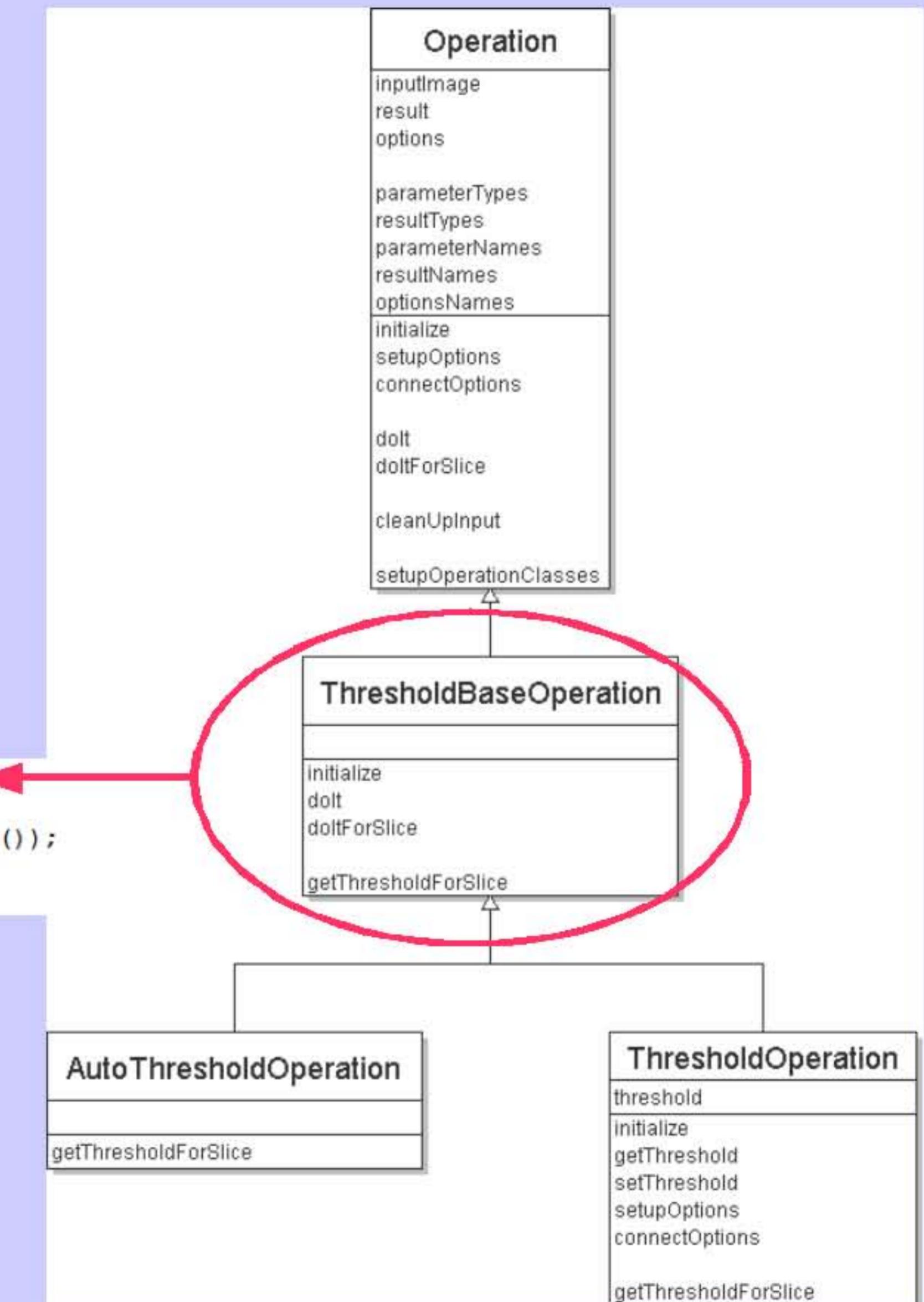
public void doIt() {
    ImagePlus inputImage = this.getInputImage();
    result = this.getCopyOfOrReferenceTo(inputImage, inputImage.getTitle());
    this.processSlices();
}

protected void doItForSlice(int sliceNumber, ImageStack stack) {
    ImageProcessor ip = stack.getProcessor(sliceNumber);
    ip.threshold(this.getThresholdForSlice(sliceNumber));
}
```



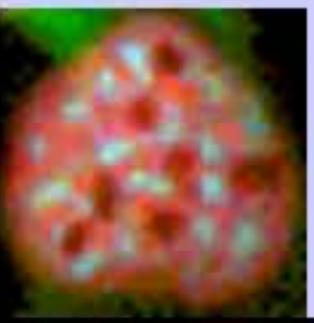
Cell Image Analyzer

volker.baecker@mri.cnrs.fr



# Extending the framework

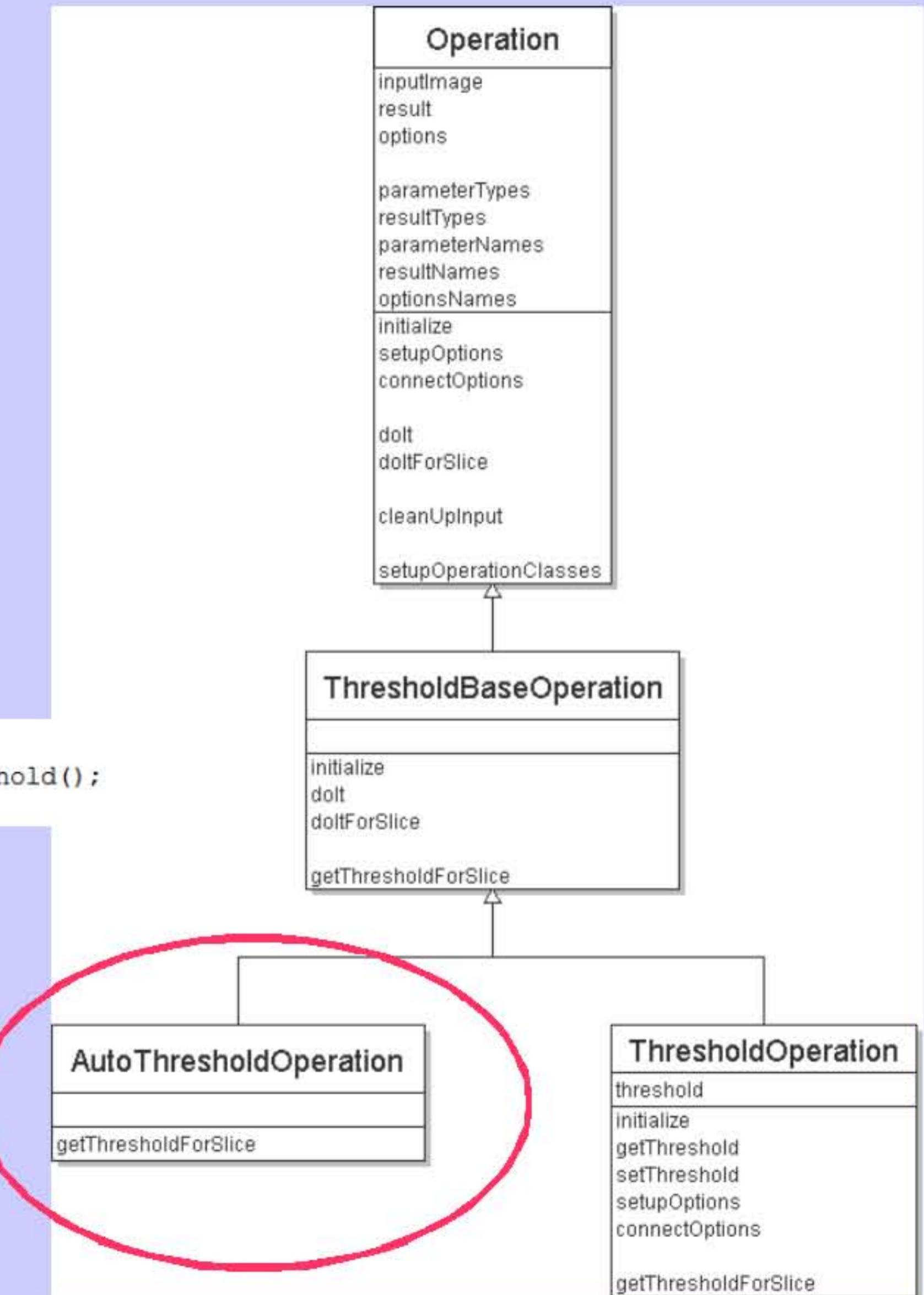
```
public int getThresholdForSlice(int i) {  
    return this.getInputImage().getStack().getProcessor(i).getAutoThreshold();  
}
```



Cell Image Analyzer

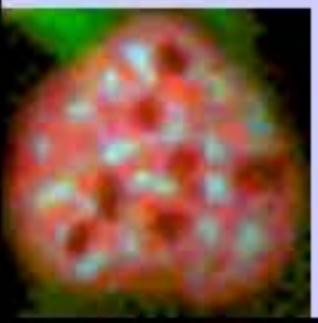
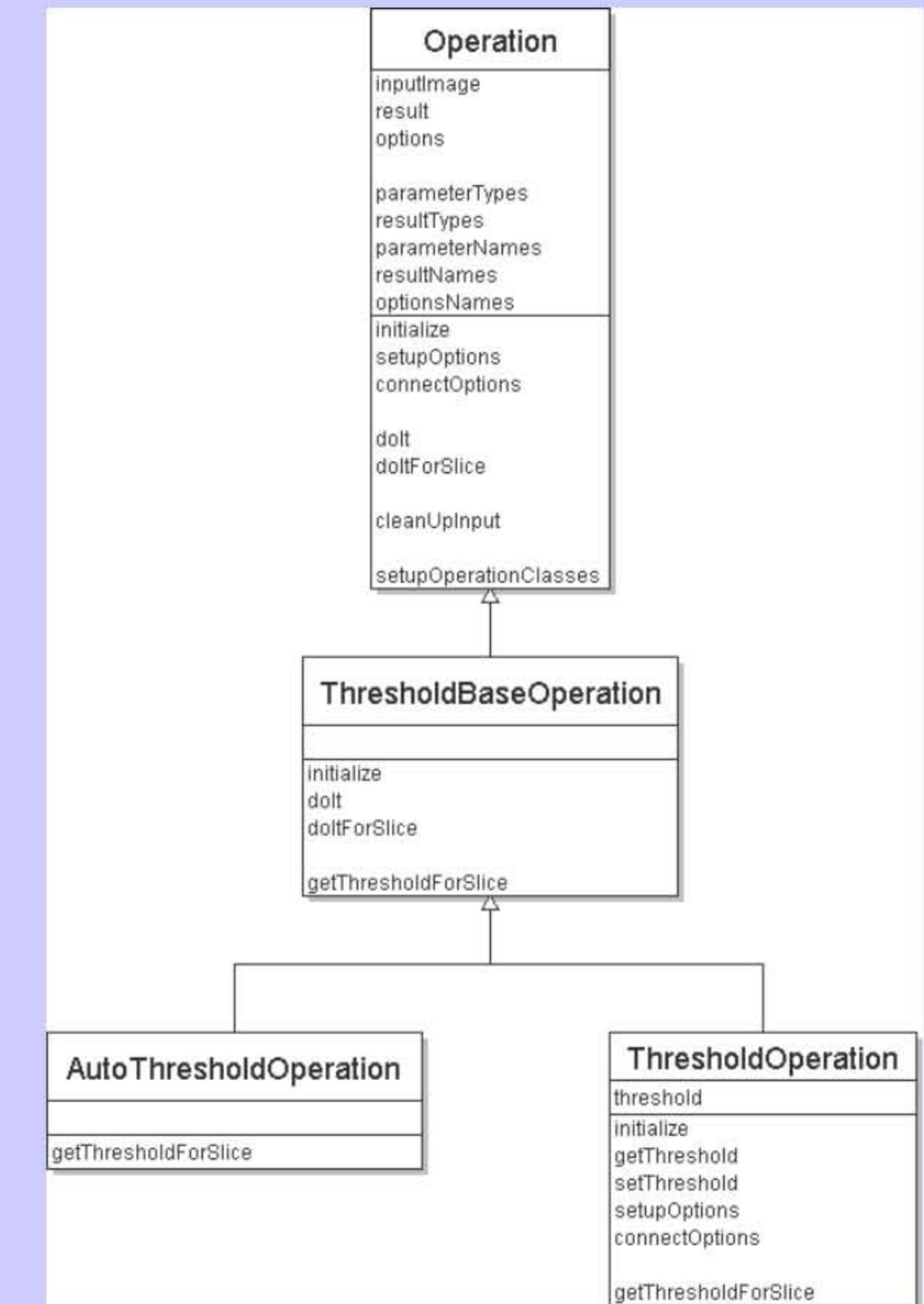
volker.baecker@mri.cnrs.fr

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# Extending the framework

- to add an operation with options
  - declare options in initialize
  - setup options
    - set name, default value, min, max and short help text
  - to facilitate access
    - declare instance variable
    - connectOptions
    - getter / setter



# Extending the framework

```

protected void initialize() throws ClassNotFoundException {
    super.initialize();
    optionsNames = new String[1];
    optionsNames[0] = "threshold";
}

// update options in subclasses

protected void setupOptions() {
    super.setupOptions();
    this.setThreshold(128);
    threshold.setMin(0);
    threshold.setShortHelpText("all intensities above threshold" +
        " will be mapped to 255 and all below to 0");
}

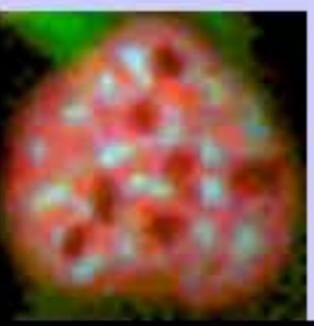
public int getThreshold() {
    return threshold.getIntegerValue();
}

public void setThreshold(int threshold) {
    this.threshold.setValue(new Integer(threshold).toString());
}

• getter / setter

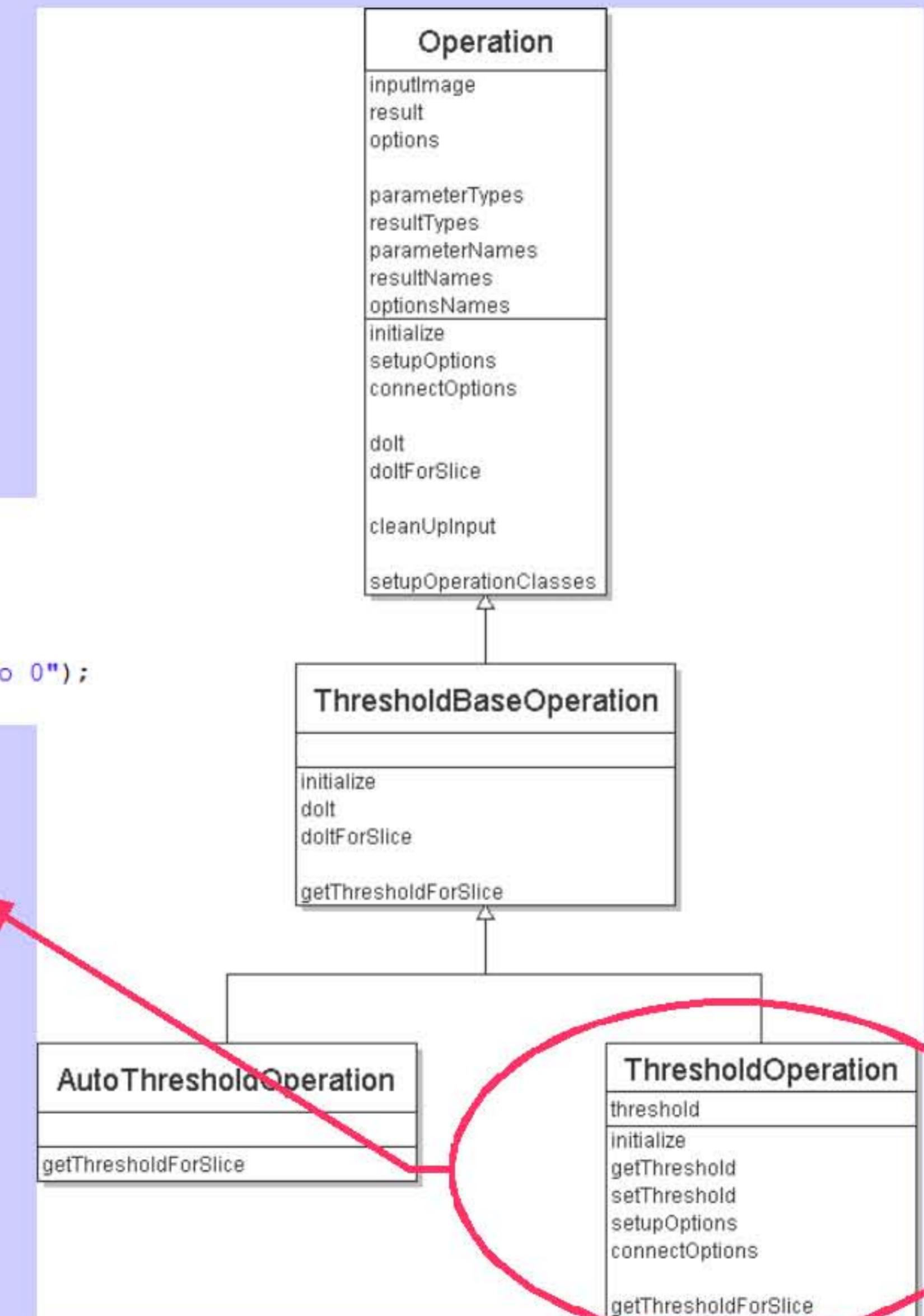
public void connectOptions() {
    this.threshold = (Option) this.options.getOptions().elementAt(0);
}

public int getThresholdForSlice(int i) {
    return this.getThreshold();
}
  
```



Cell Image Analyzer

volker.baecker@mri.cnrs.fr



## Option

gamma adjust options

? gamma 0.5 [0.1, 5.0]  
Enter the value for gamma (intensity(pixel)/255)<sup>gamma</sup>\*255

open image options

? replace string   
enter the part of the filename to be replaced  
? replace with   
enter the substitution for the part to be replaced

report count comparison options

? output path  browse

## BooleanOption

close session options

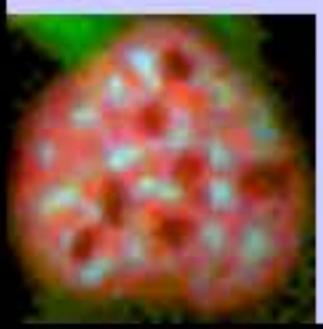
? deactivate   
Check to skip the operation.

## MatrixOption

convolve options

? kernel , -1;-1,-1,-1,-1,-1  
enter a matrix. Use ';' to separate rows and ',' to separate values in

? normalize   
normalize the values to preserve the image brightness



Cell Image Analyzer

## Options

### ChoiceOption

apply lut options

? lookup tables 3-3-2 RGB  
select the lookup table 3-3-2 RGB

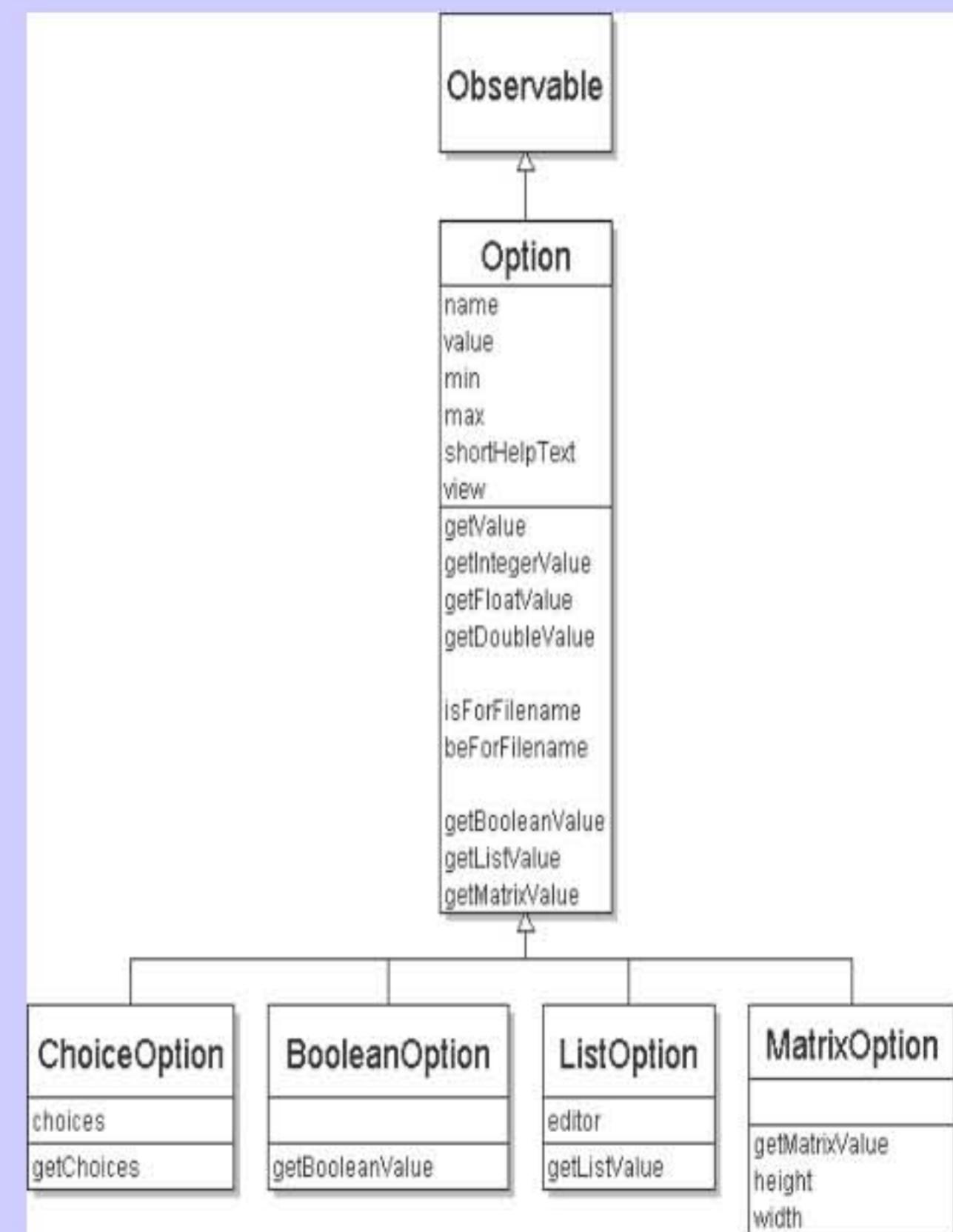
- blue
- brown
- cornflower
- cyan
- cyan hot
- cyan pale
- fire

### ListOption

foreach image do options

? image list   
press edit to select images or a folder

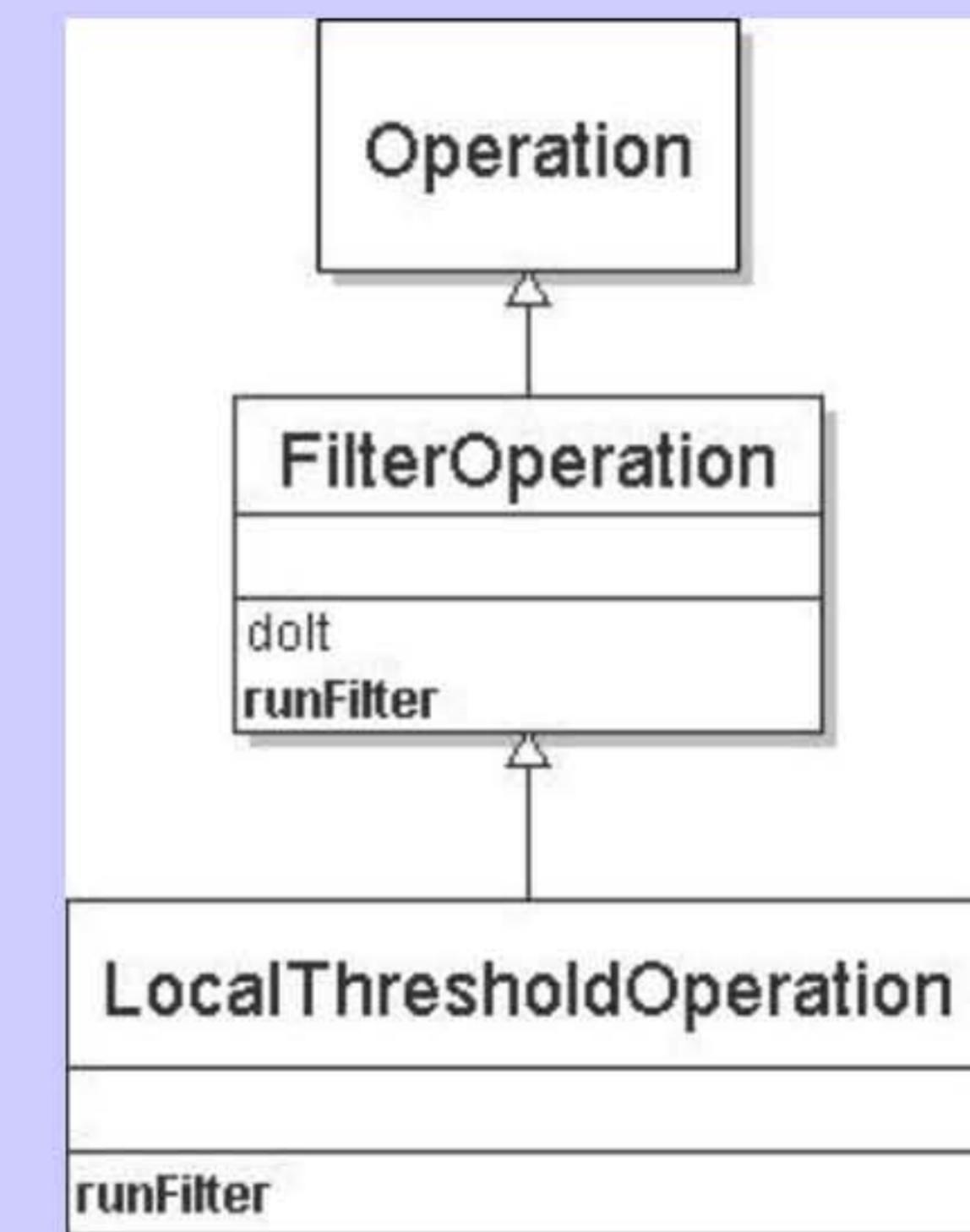
? use sequence opener   
check to use the sequence opener instead of the file dialog.



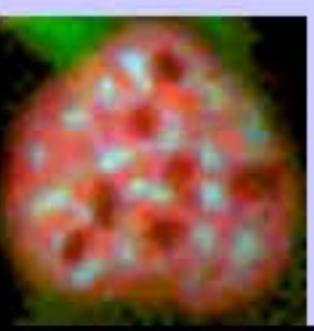
# Accessing ImageJ methods

- simplest method:
- use the ImageJ macros interface
  - IJ.run(...)

```
public void runFilter() {  
    IJ.run("Duplicate...", "title=Original");  
    IJ.run("32-bit");  
    IJ.run("Duplicate...", "title=Filtered");  
    IJ.selectWindow("Filtered");  
    IJ.run(this.getFilter(), "radius=" + this.getFilterRadius());  
    IJ.run("Image Calculator...",  
          "image1=Original operation=Subtract image2=Filtered create");  
    IJ.run("Rename...", "title=Result");  
    IJ.run("8-bit");  
}
```

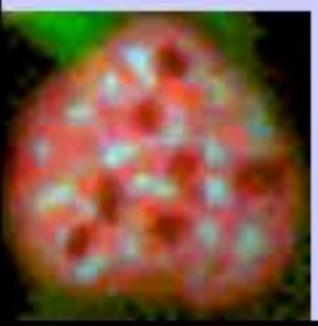


Local threshold macro by R.Couture 11-14-03 Dept. of Radiology Washington University School of Medicine, couture@wuerl.wustl.edu

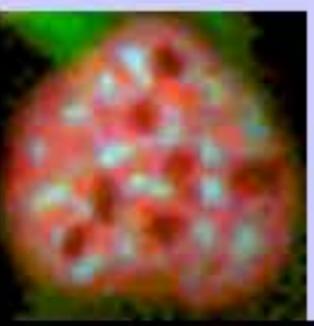
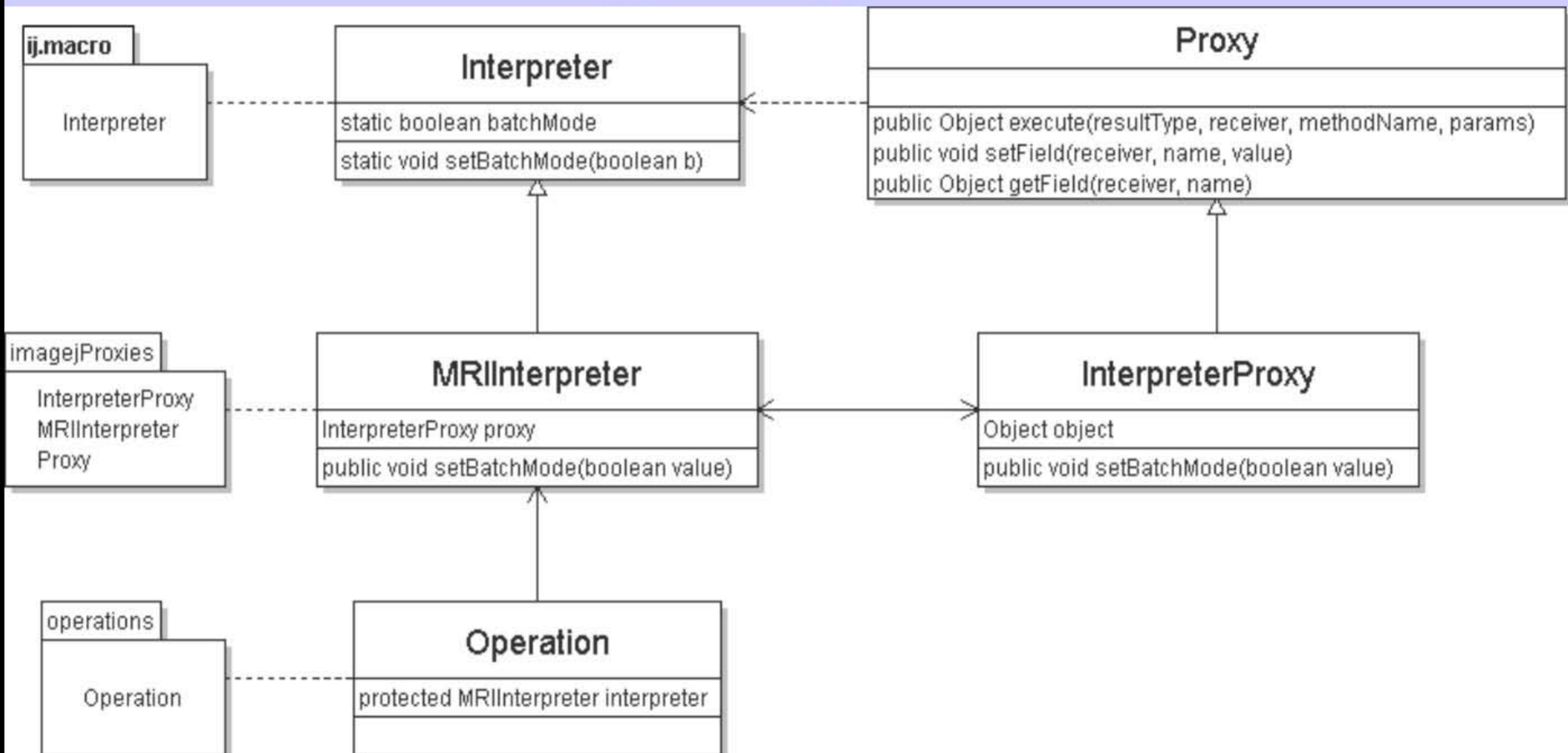


# Accessing ImageJ methods

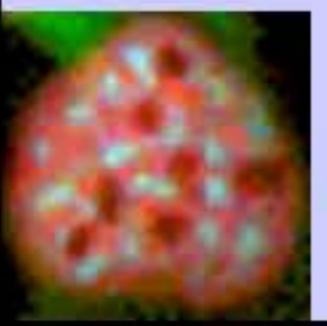
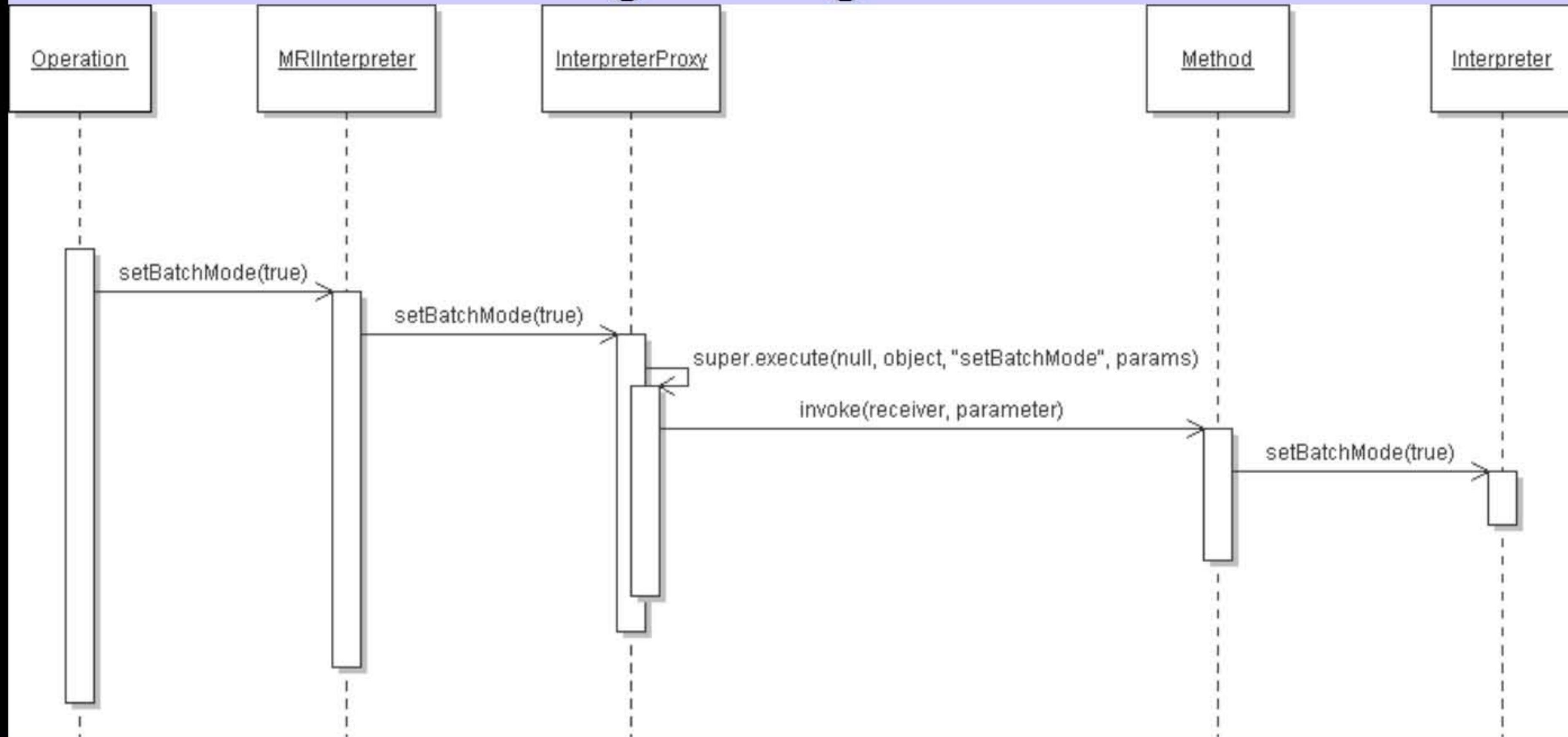
- what if method or data member not accessible
  - access to protected:
    - subclass in own package
  - access to private:
    - use java reflection api
- class Proxy facilitates reflection api usage
  - Object execute(...)
  - void setField(...)
  - Object getField(...)



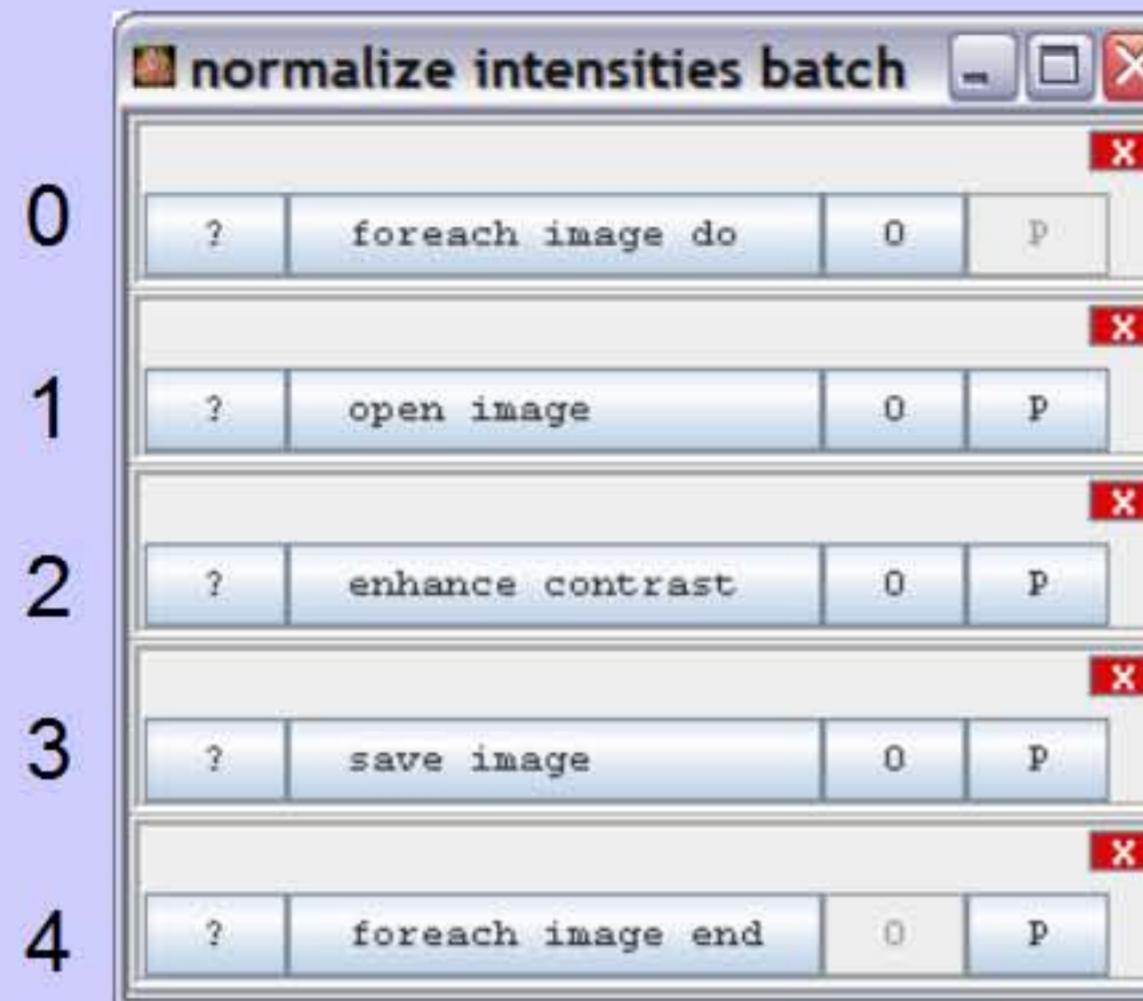
# Accessing ImageJ methods



# Accessing ImageJ methods



# The implementation



input maps:

operation

result nr.

0:

-

-

1:

0

0

2:

1

0

3:

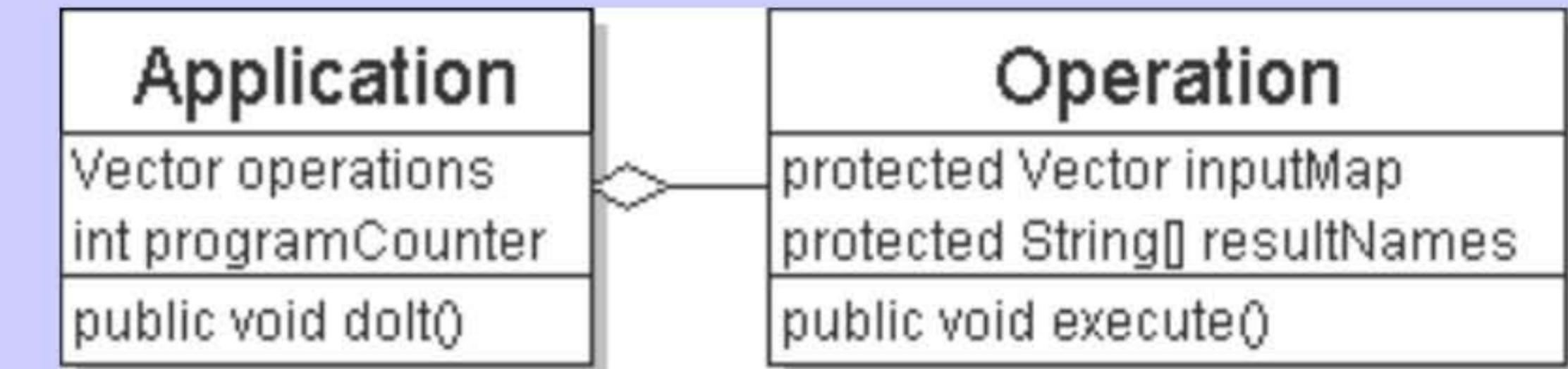
2

0

4:

0

0



- When application is loaded from text file
  - objects are created from names, using reflection
  - parameters of operation are connected to results of preceding operations



# The implementation



Application>>doIt

FOR programCounter = 0 TO numberOfOperations - 1

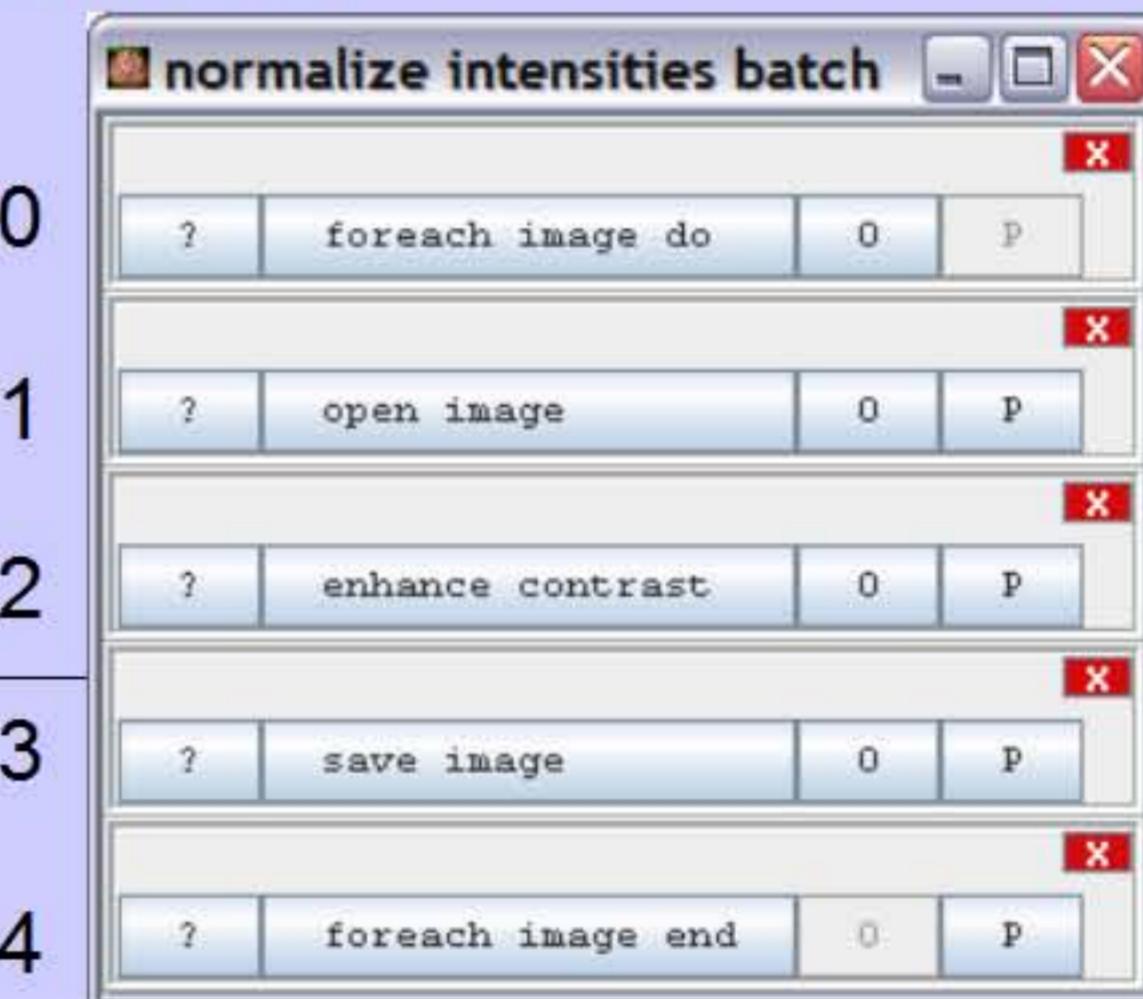
  if (stopped) return

  execute operation

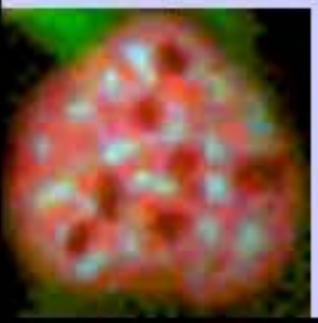
  cleanup preceding results not referenced afterwards

  get next operation

  set parameters of next operation from results of preceding operations, using reflection

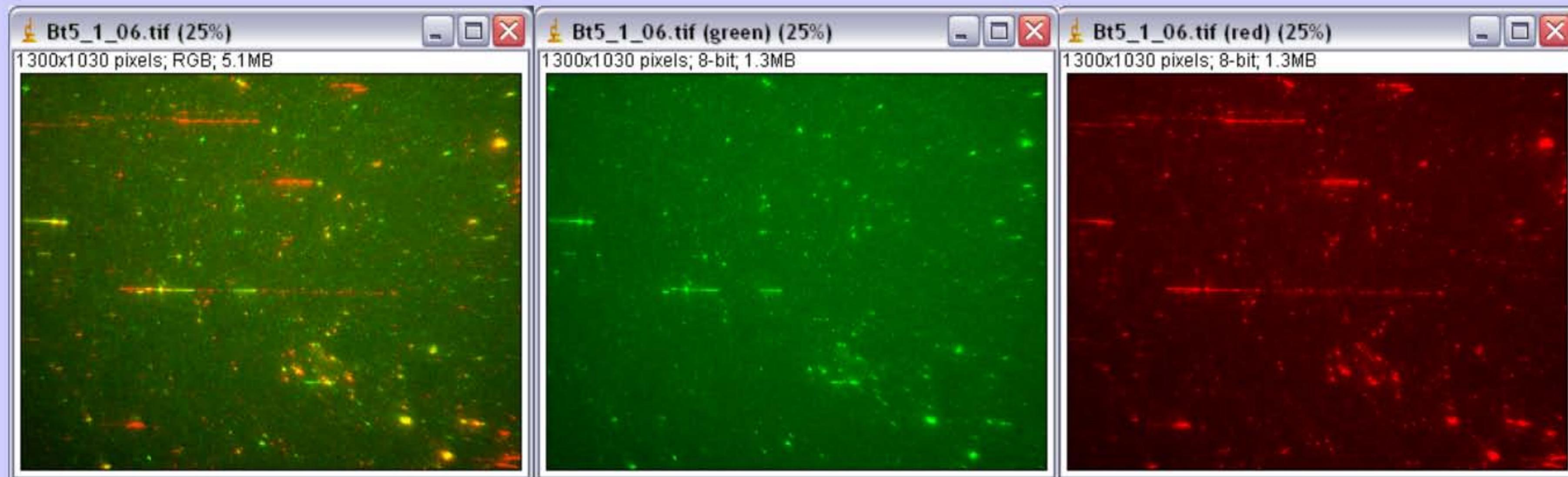


jump and loop operations modify the programCounter





# DNA combing



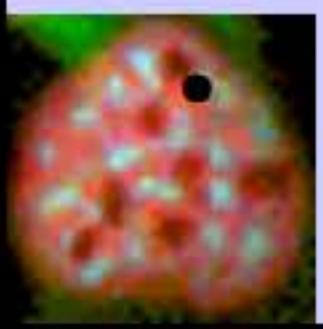
the images:

red: combed DNA

green: sites where replication takes place

the task, measure:

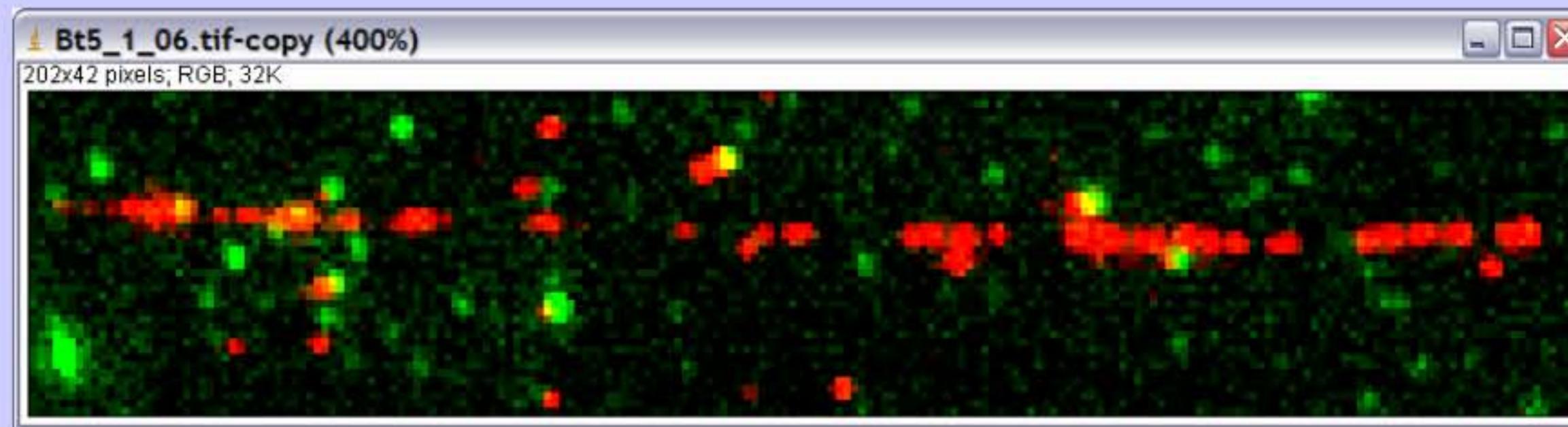
- the lengths of the DNA molecules
- the lengths of the replication sites within each DNA molecule
- the distances between replication sites for each DNA molecule



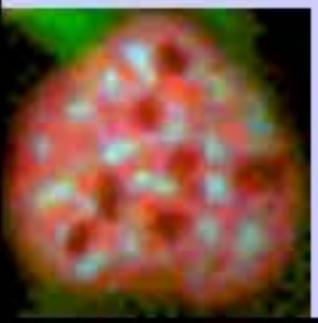
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volker.baecker@mri.cnrs.fr

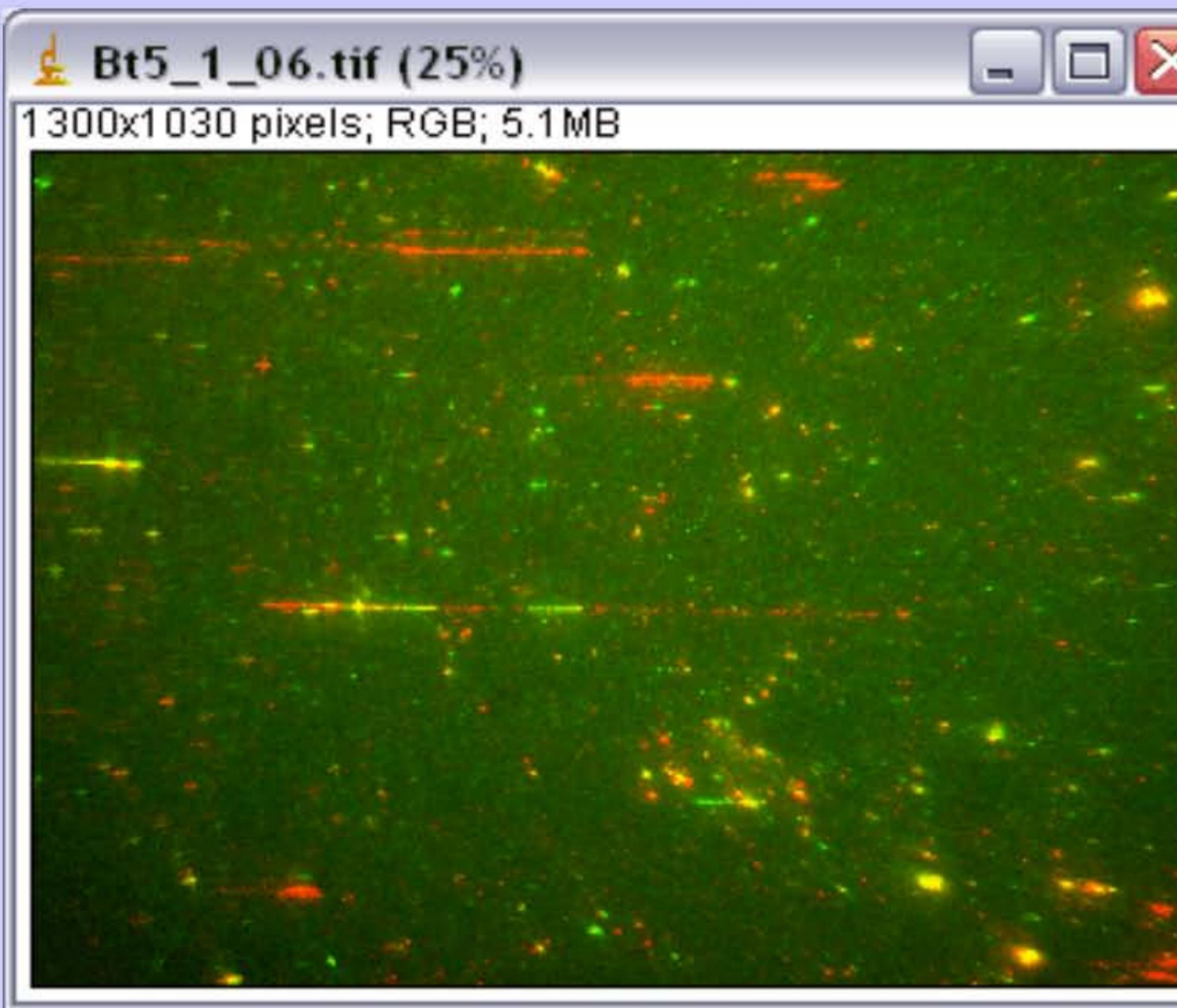
# DNA combing



- difficulties
  - high level of (biochemical) noise
  - stretched out molecules are not straight
  - signal has large gaps

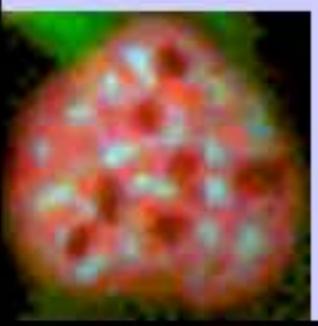


# DNA combing



ImageJ macro titled "dna tracing batch" showing a sequence of operations:

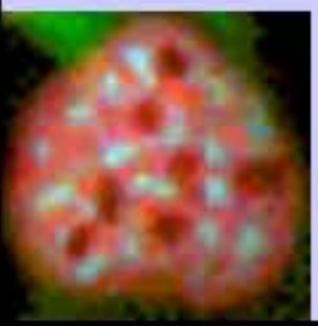
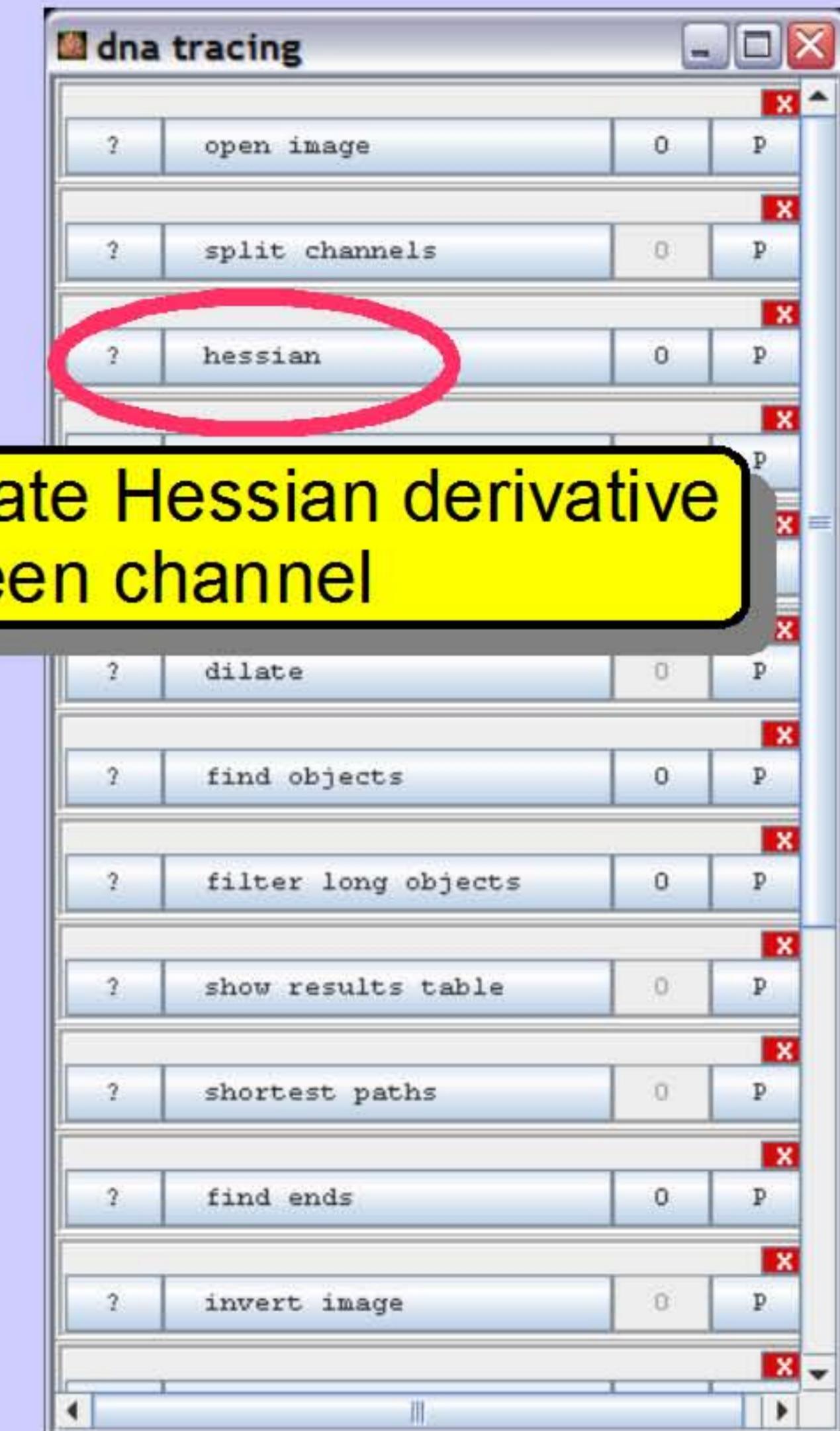
- foreach image do
- open image
- split channels
- hessian
- get image from hessian
- auto threshold
- dilate
- find objects
- filter long objects
- shortest paths
- find ends
- invert image



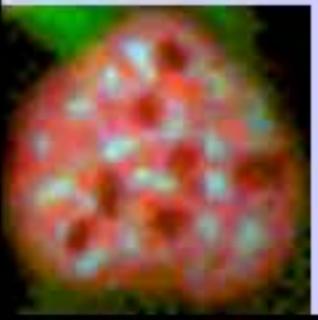
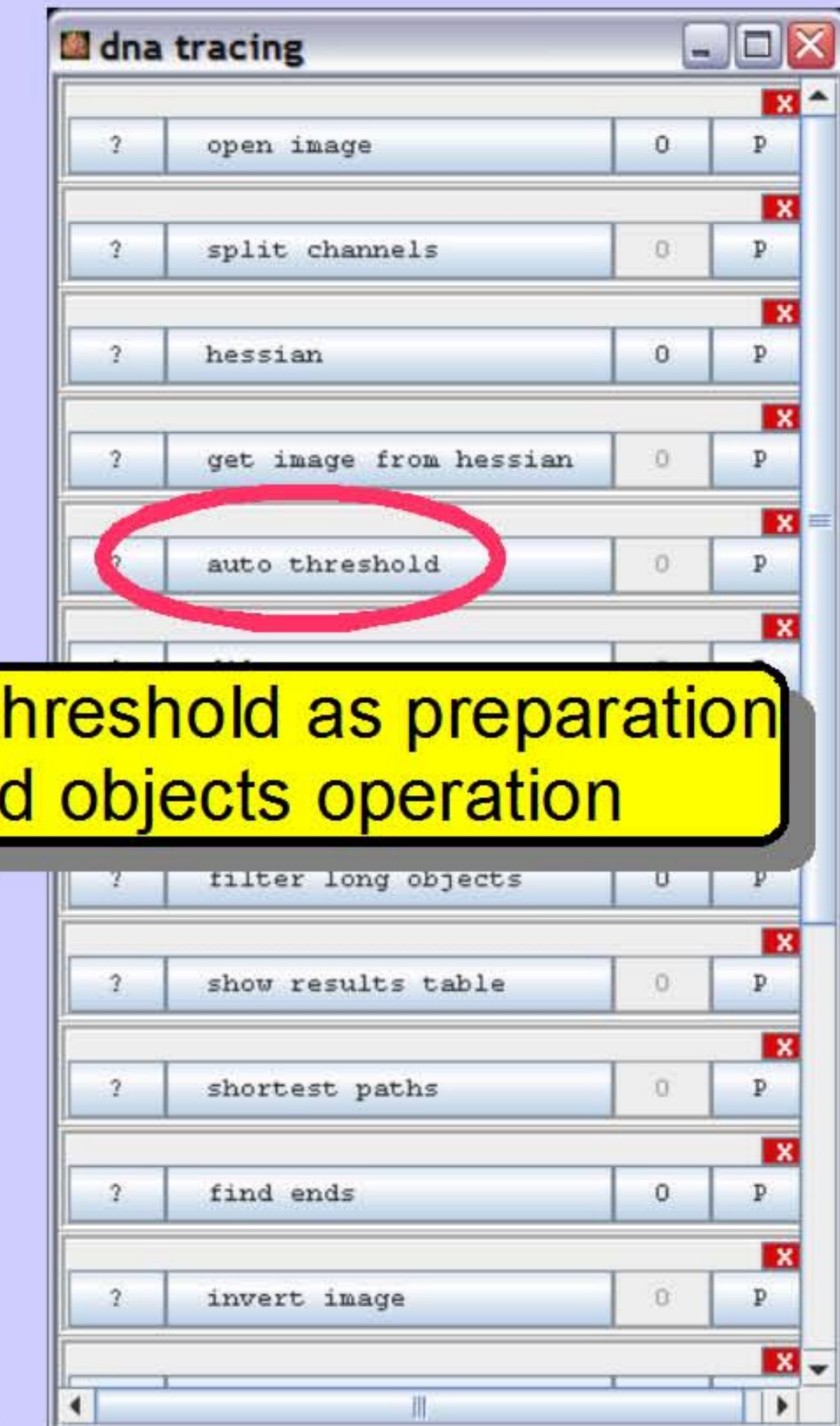
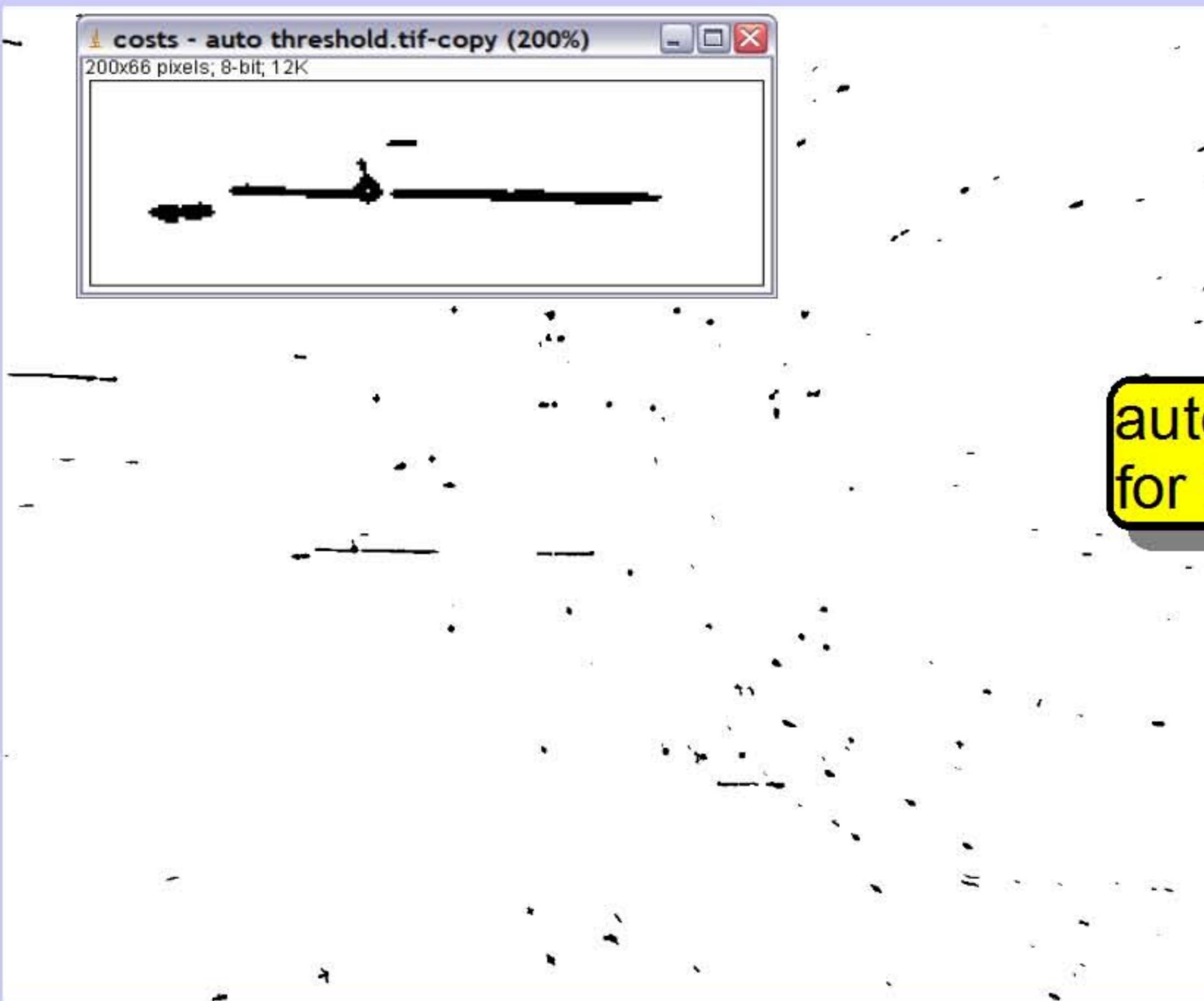
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volker.baecker@mri.cnrs.fr

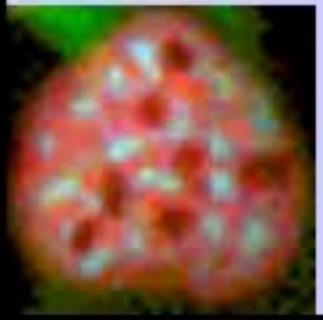
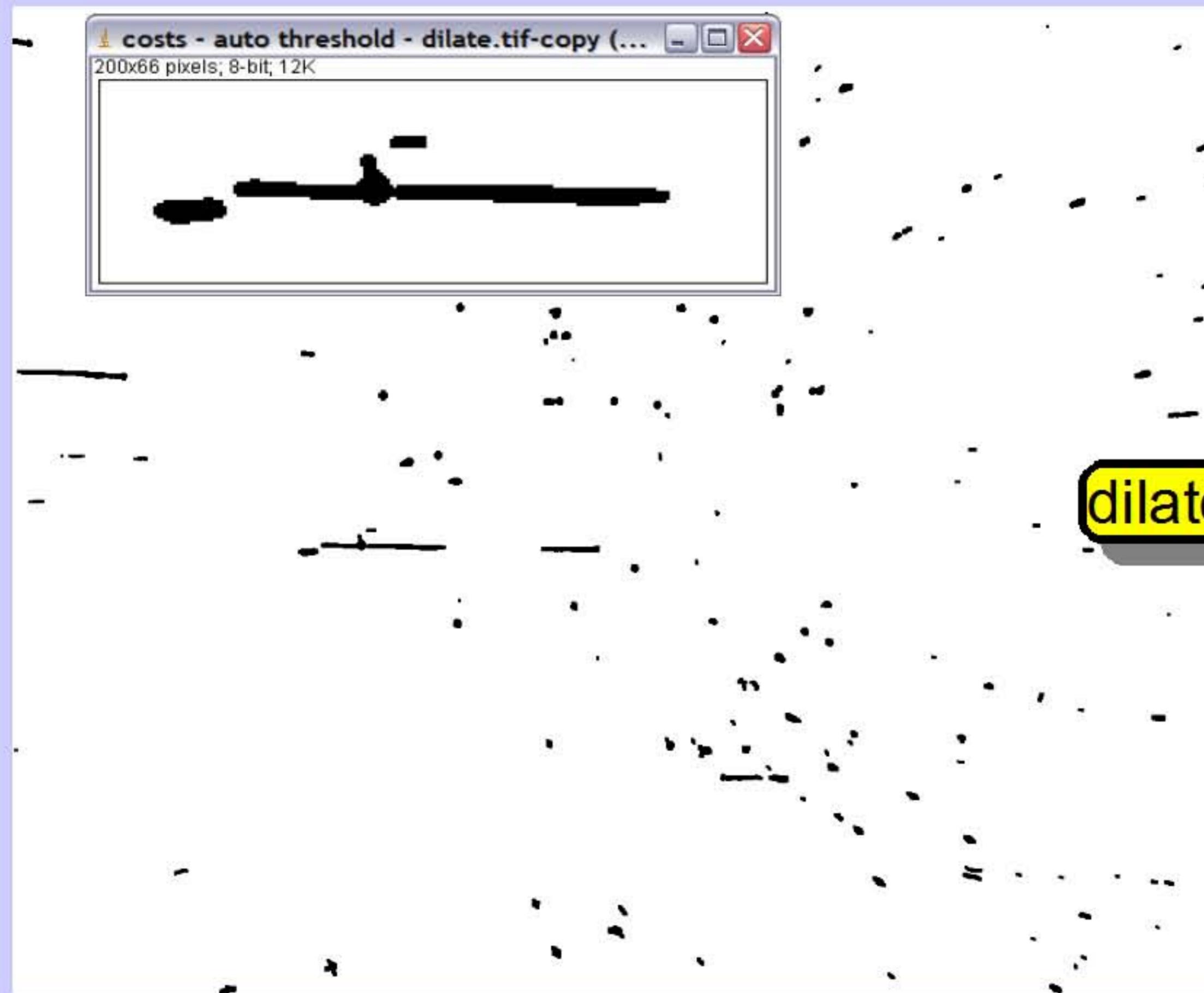
# DNA combing



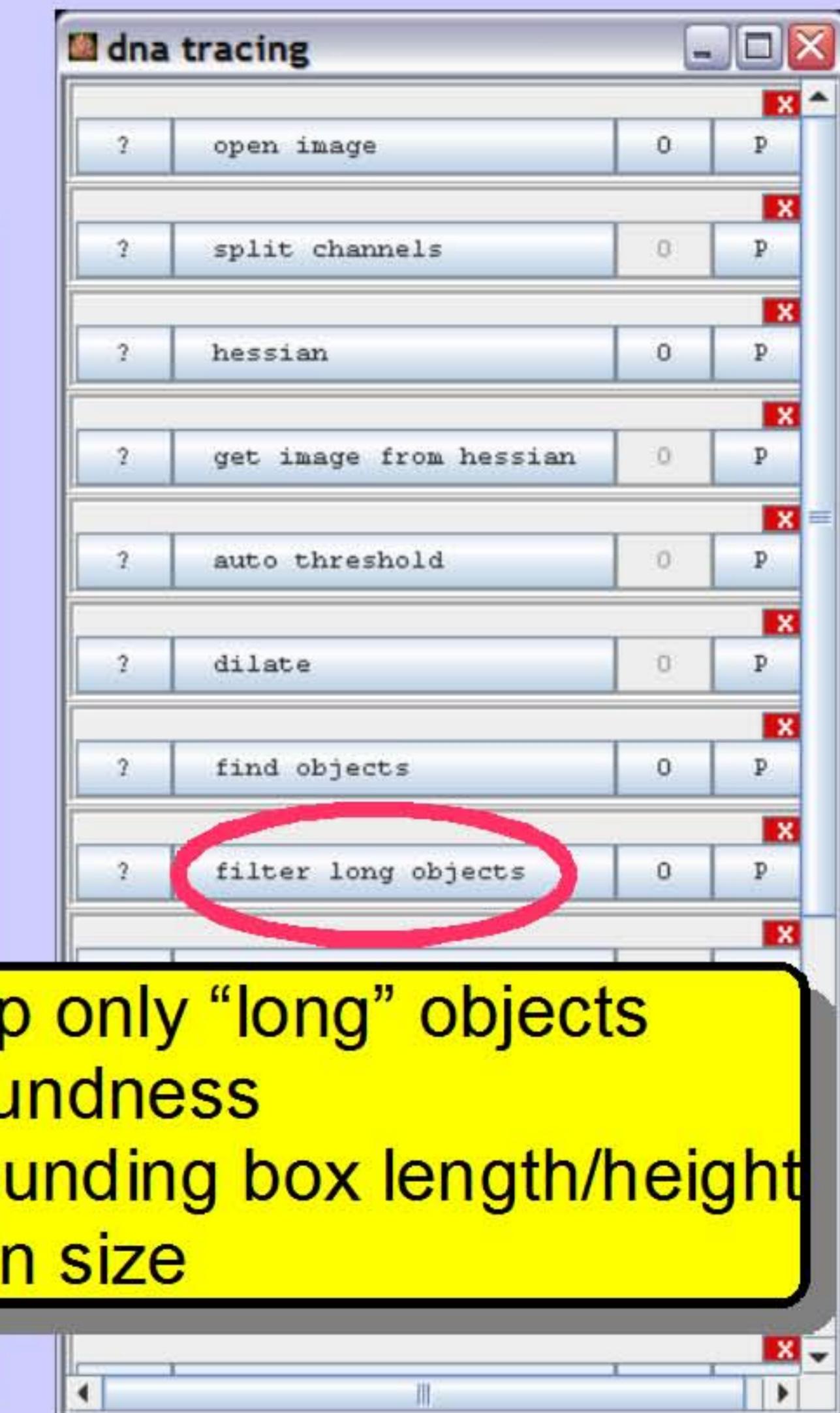
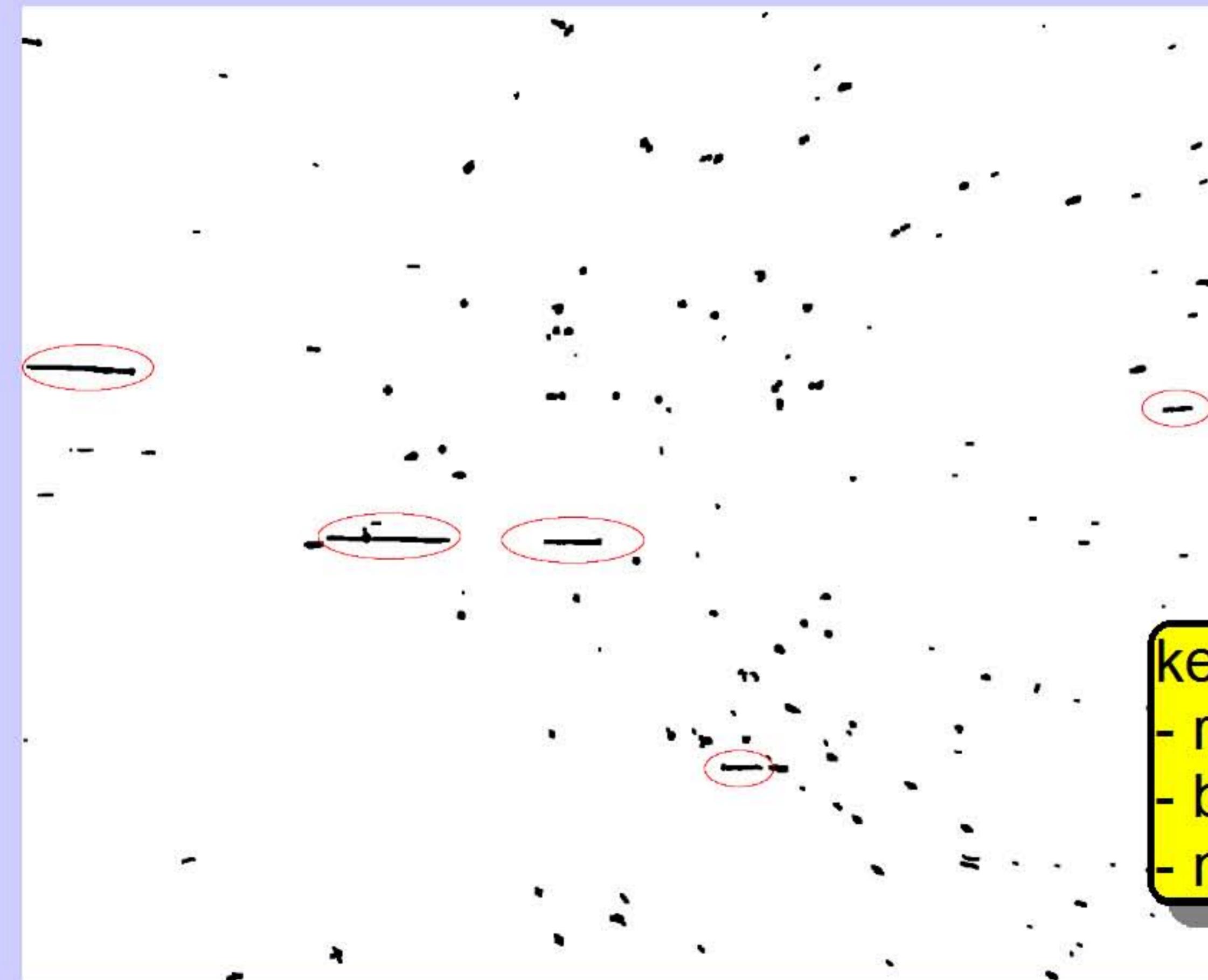
# DNA combing



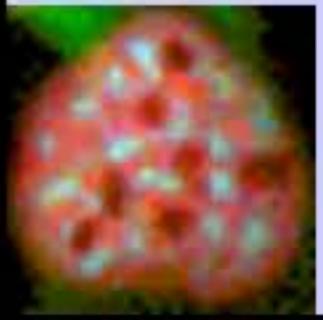
# DNA combing



# DNA combing



keep only “long” objects  
- roundness  
- bounding box length/height  
- min size

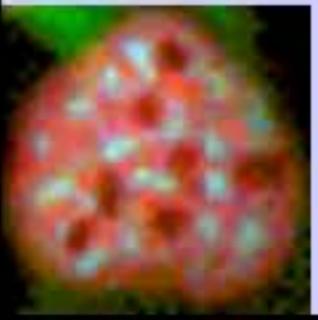
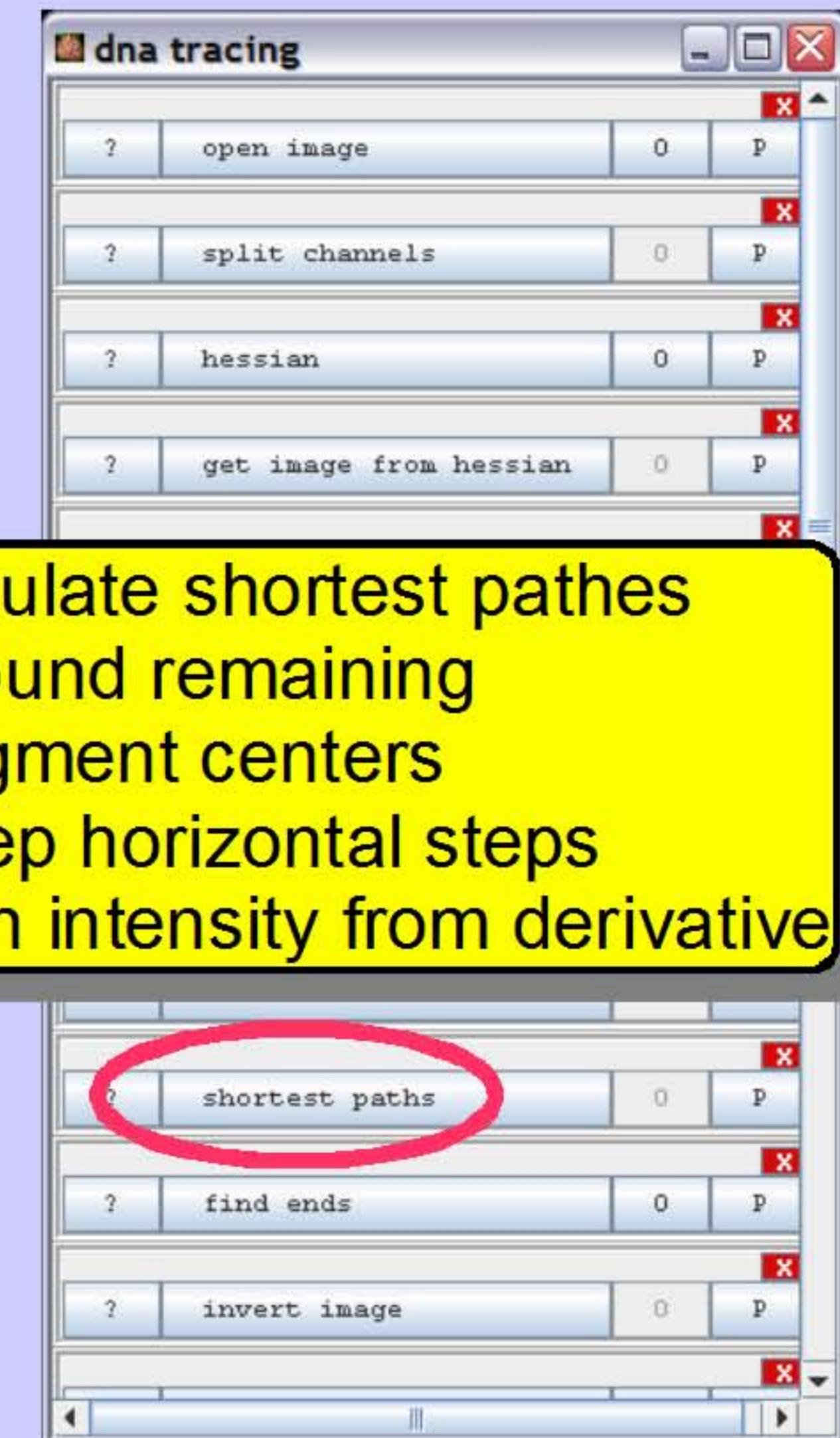


# DNA combing

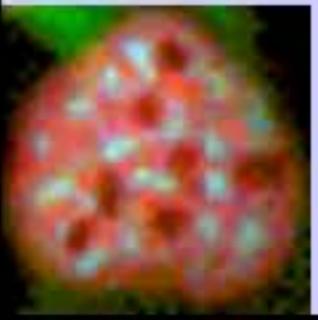
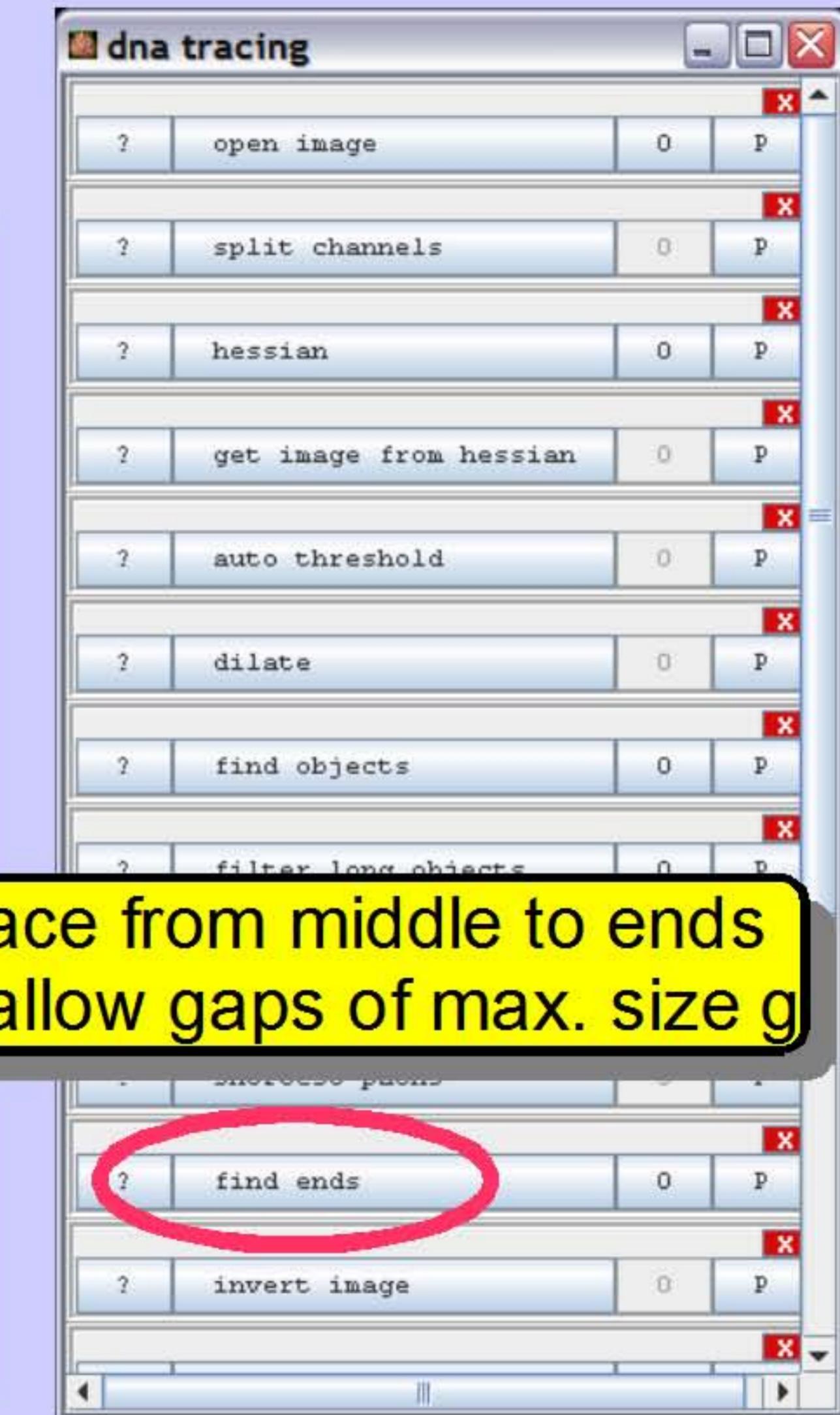


Calculate shortest pathes

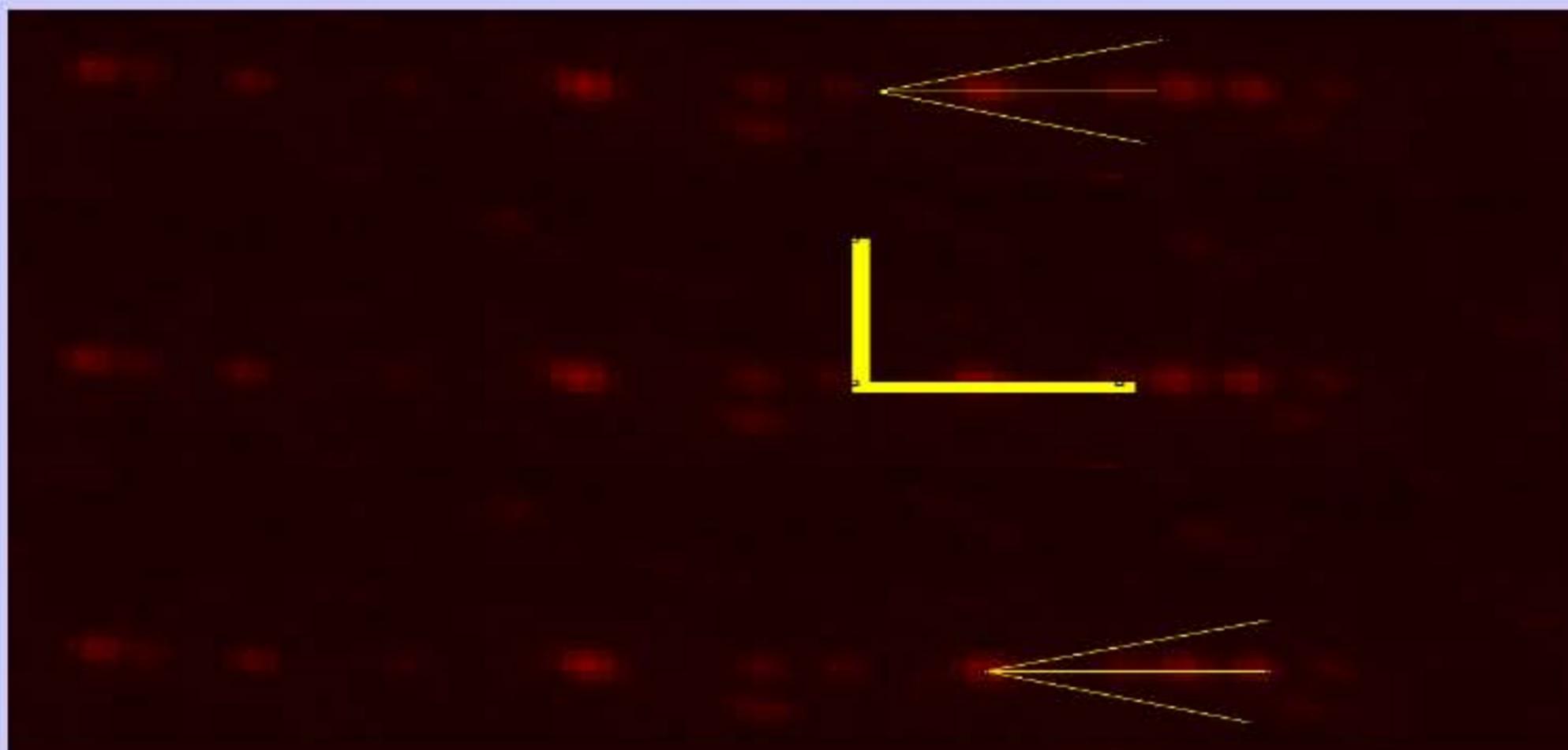
- around remaining segment centers
- keep horizontal steps with intensity from derivative



# DNA combing

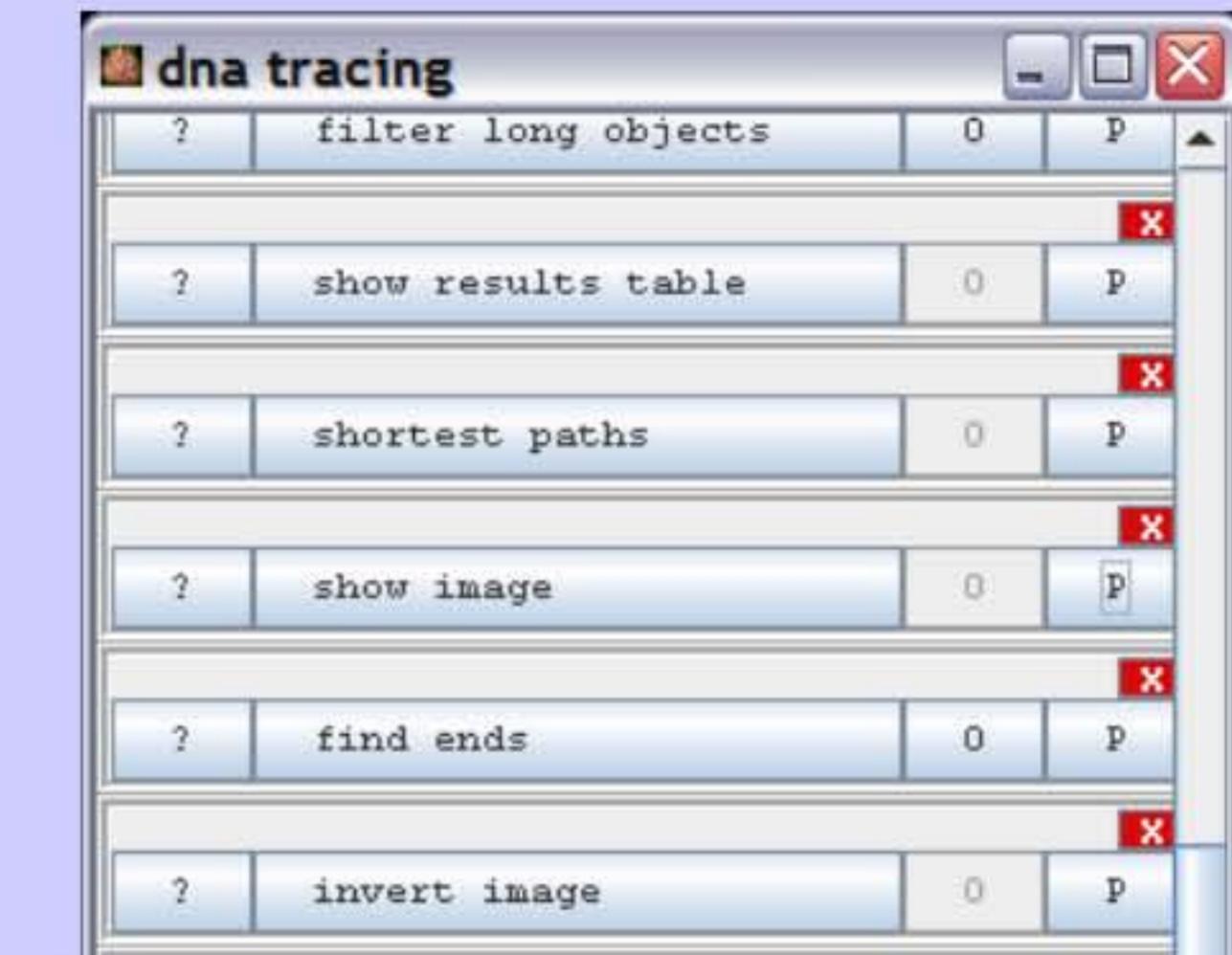


# DNA combing

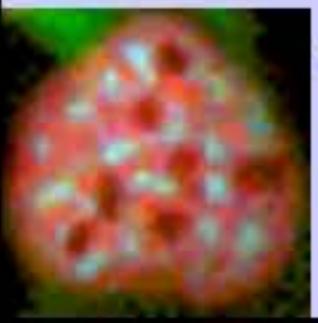
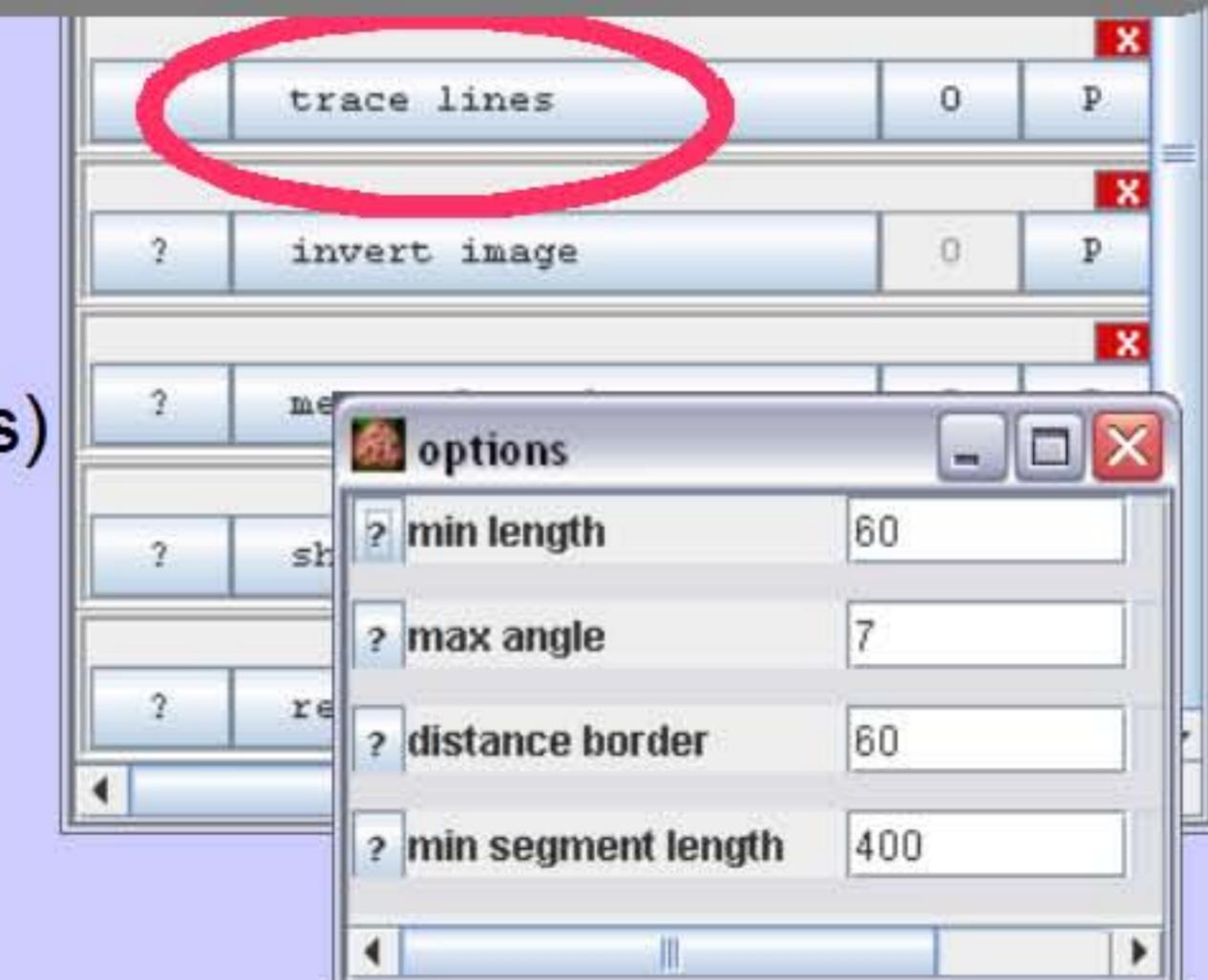


to find start and end of the molecule (red)

- start in the middle of a green segment
- find the best direction to go  
(highest average intensity for a line segment of size s)
- move one pixel in that direction, if intensity in a line segment in that direction is higher than in the perpendicular direction
- else stop



trace lines in red signal  
- from centers of green lines



# DNA combing

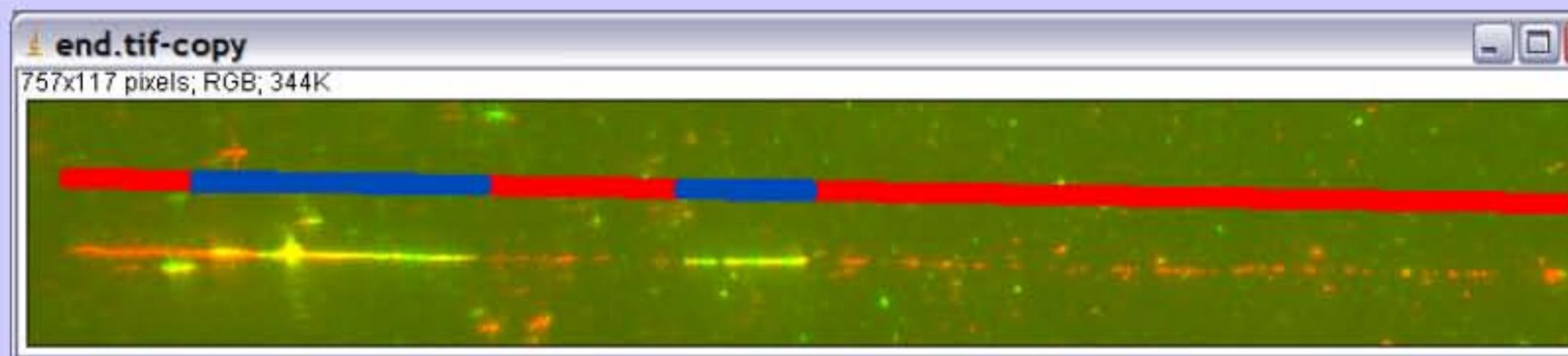
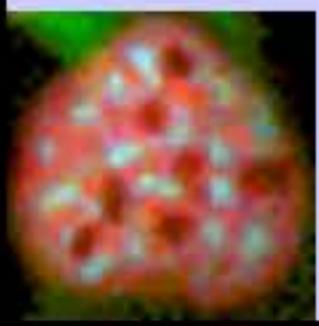


image	na brin	start x	start y	end x	end y	total length	folder
Bt5_1_06.tif	1	254,86	559,48	973,72	570,55	718,95	Z:\baecker\combing\
1		2					
318,0, 560,0, 453,0, 562,0		551,0, 564,0, 610,0, 564,0					
red	green	red	green	red			
63,14	135,01	98,02	59	363,78			
1-2	2-3	3-4	4-5				
195,02							

## Report:

- total length
- length of each segment
- distances between centers of green segments



# DNA combing, manual

use **slide show control** to select image

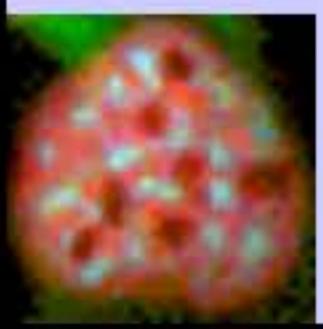
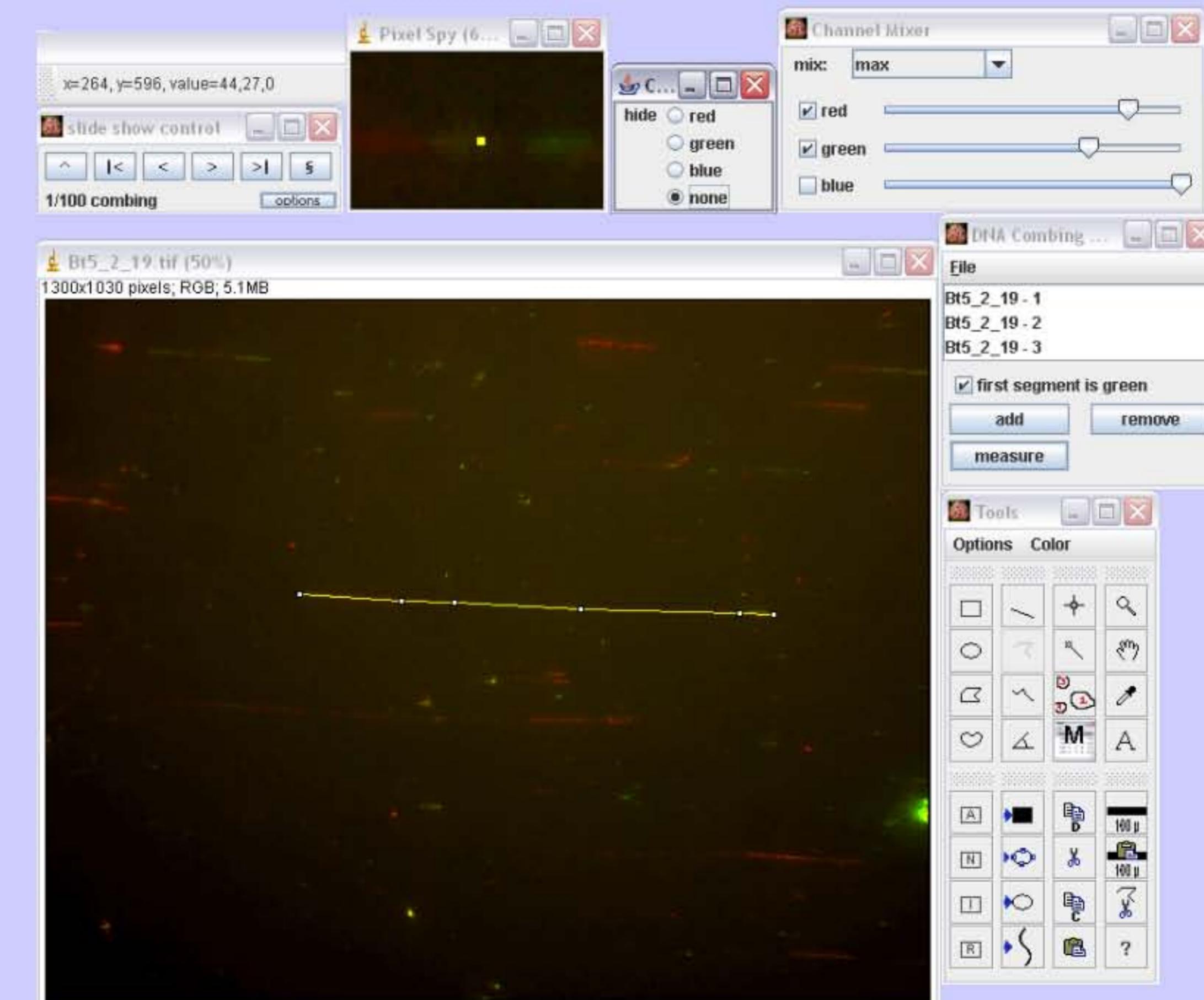
use **channel mixer** to adjust view

use **pixel spy** to see exactly where you set marks

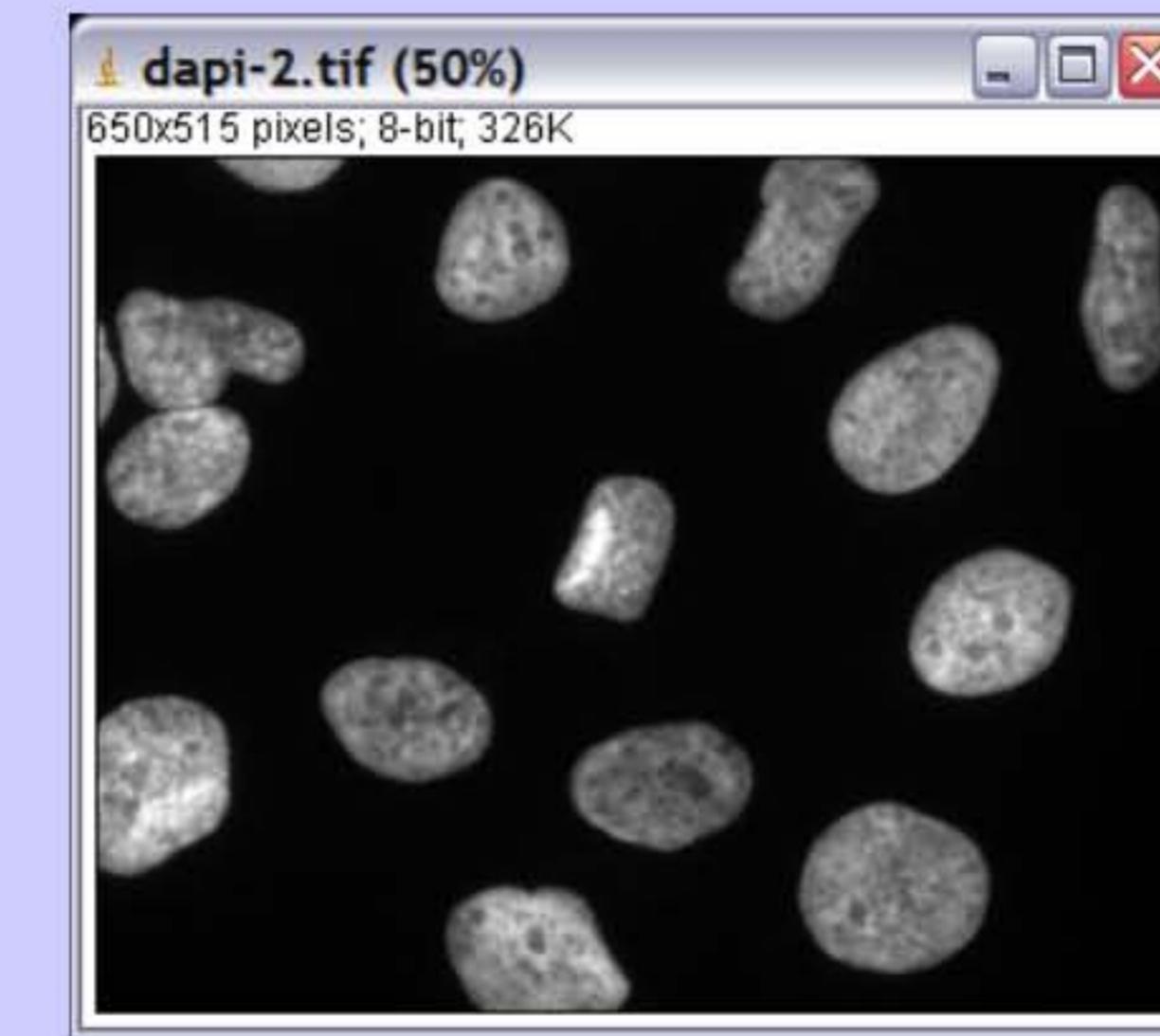
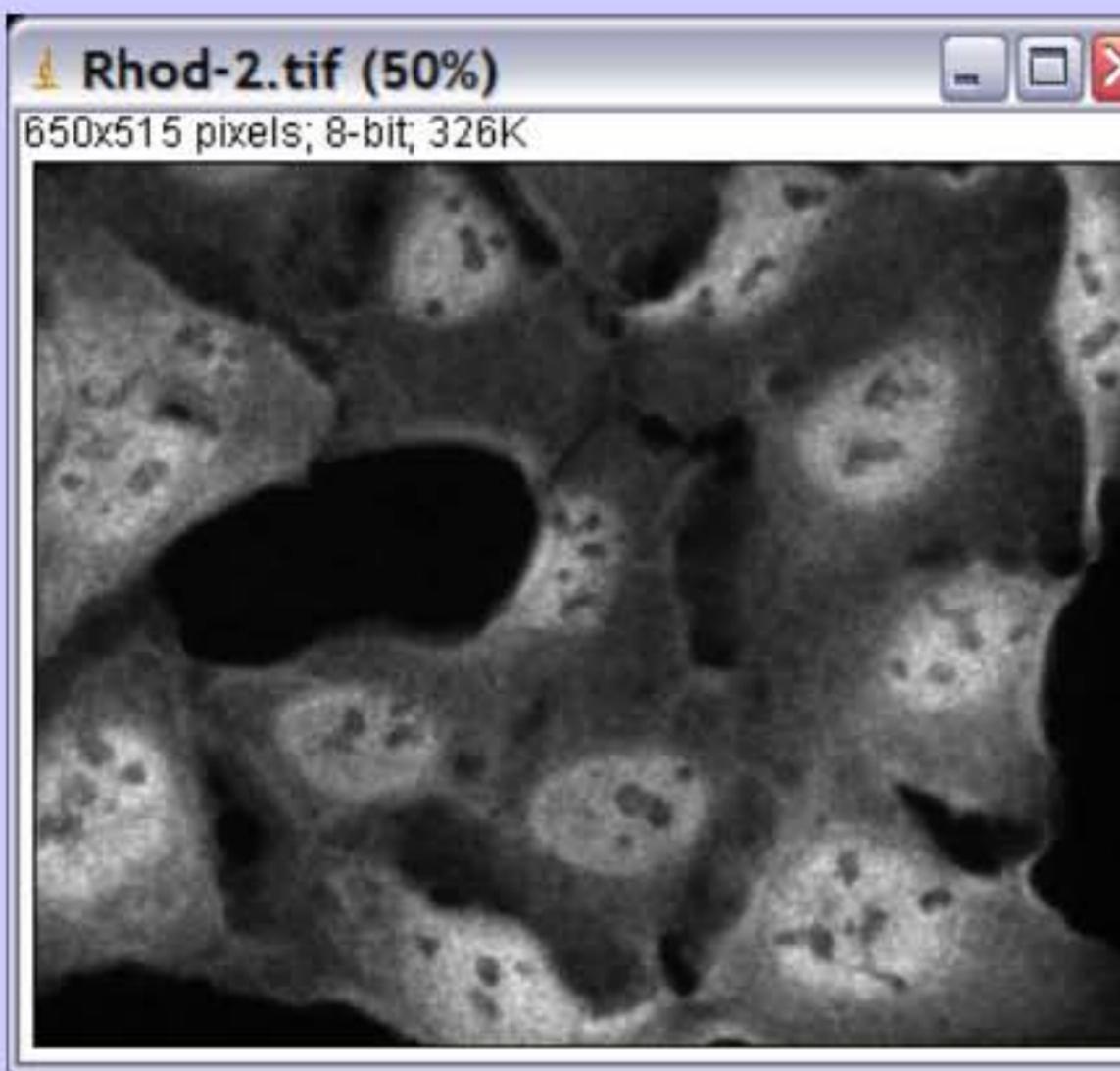
use **Polygon selection tool** to mark red and green segments

use **DNA combing tool** to save / load selections and to create reports

reports have the same format as in the automatic application

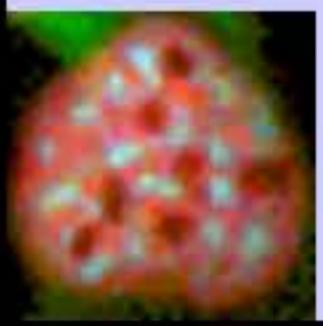


# Measuring intensity ratios



what is the proportion of fluorescence between nuclei and cytoplasm in the first image?

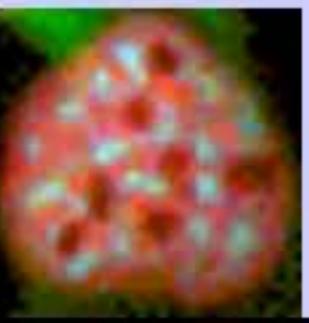
the second image is used to identify the nuclei



# Measuring intensity ratios

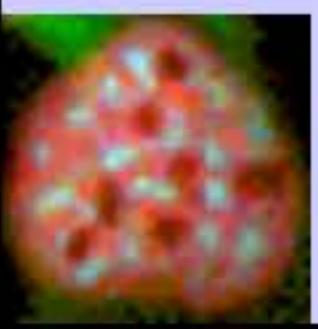
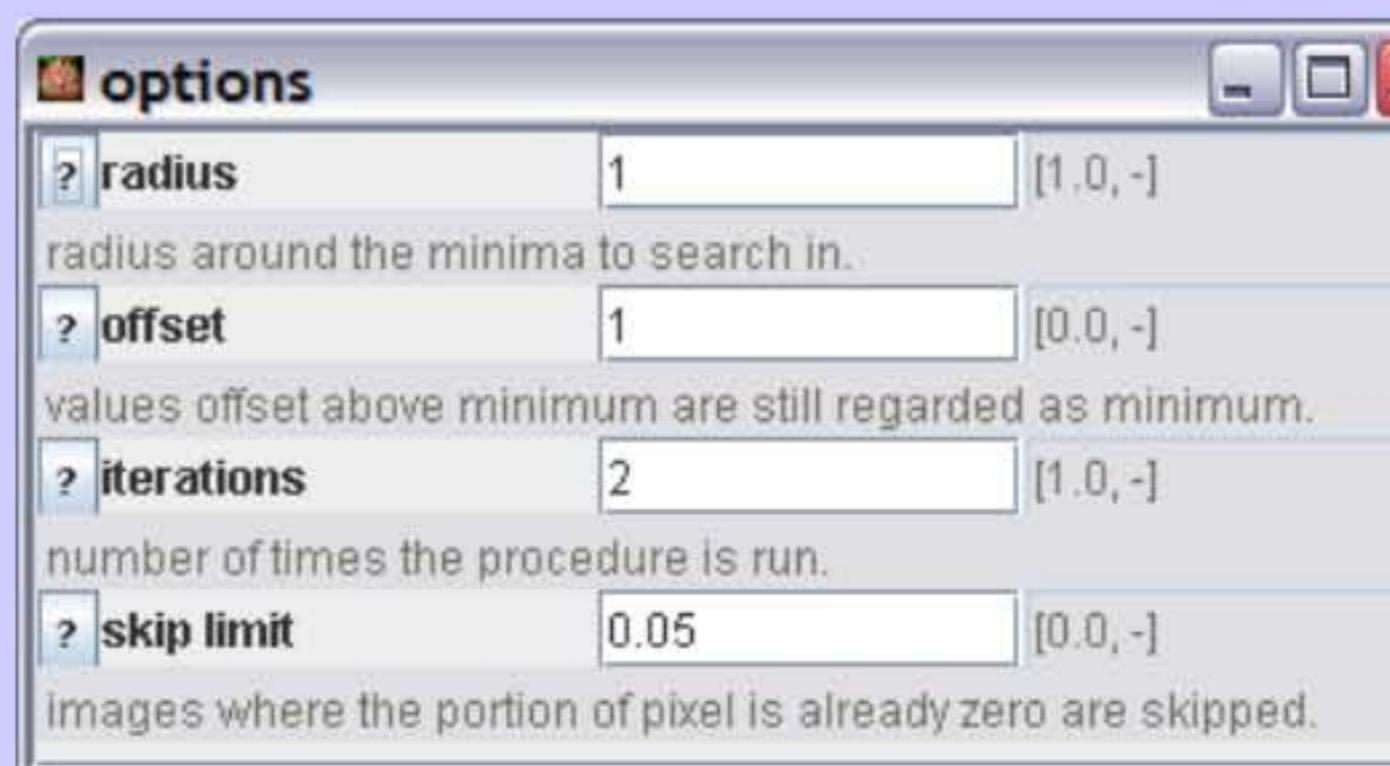
The screenshot shows the Cell Image Analyzer interface. On the left, an 'Ouvrir' (Open) dialog box is displayed, allowing the user to select a folder ('coux') containing 'testdata'. The 'Nom de fichier:' field is set to 'testdata' and the 'Fichiers du type:' dropdown is set to 'tif images'. At the bottom of this dialog are 'Ouvrir' and 'Annuler' buttons. To the right of the dialog is a 'list editor' window titled 'list editor' which lists file paths for various TIF images. The list includes files from multiple sub-folders under 'testdata'. Below the list are buttons for 'add...', 'remove selected', and 'close'. A search bar at the bottom contains the text 'rhod' and a 'select' button.

- click « add » on the list editor and select a folder
  - all images in all sub-folders are added to list
  - use list editor to remove unwanted images



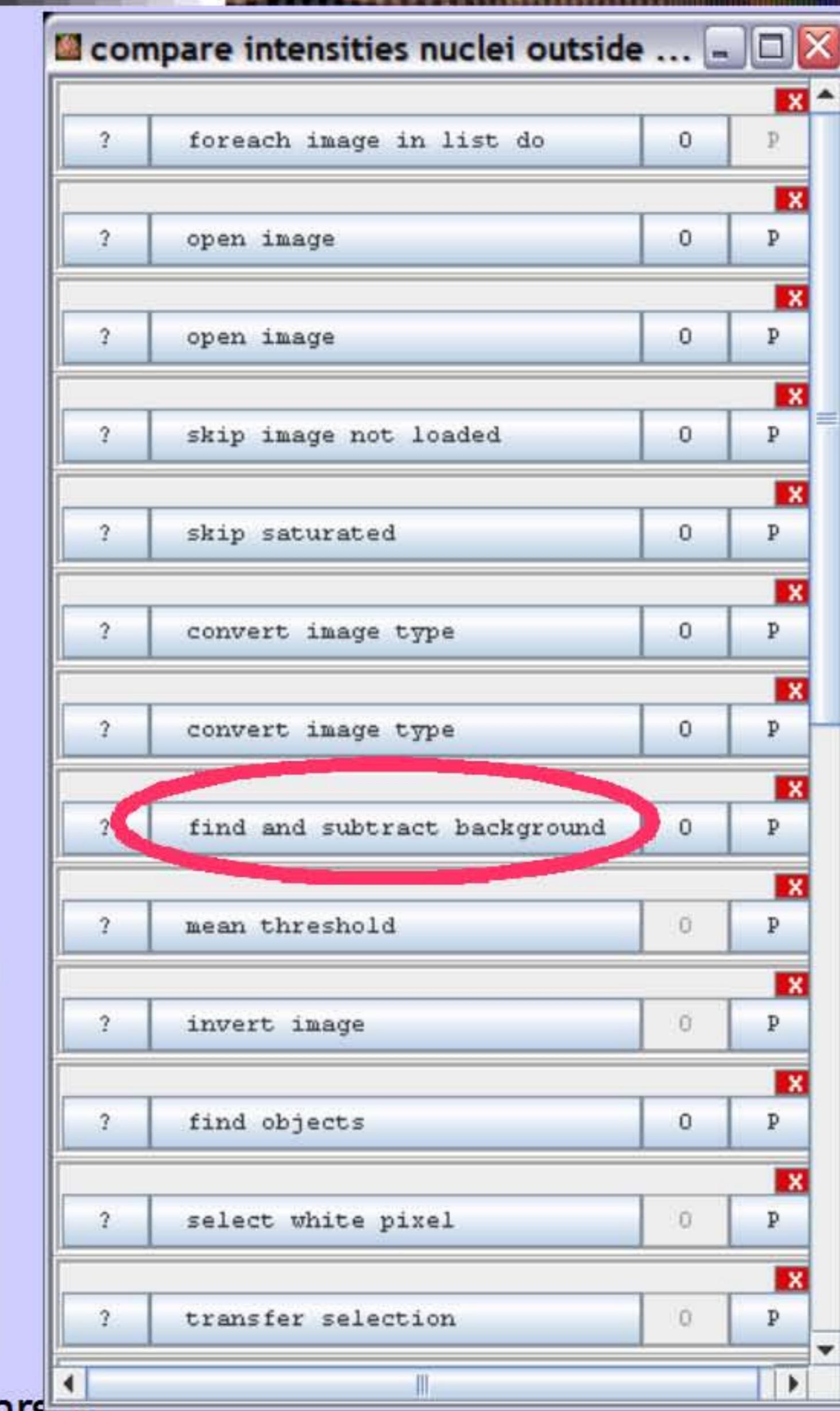
# Measuring intensity ratios

- find and subtract background
  - find pixels P with intensity in  $[min, offset]$
  - Find maximum intensity in area of size radius around pixels in P
  - subtract the max value from the image

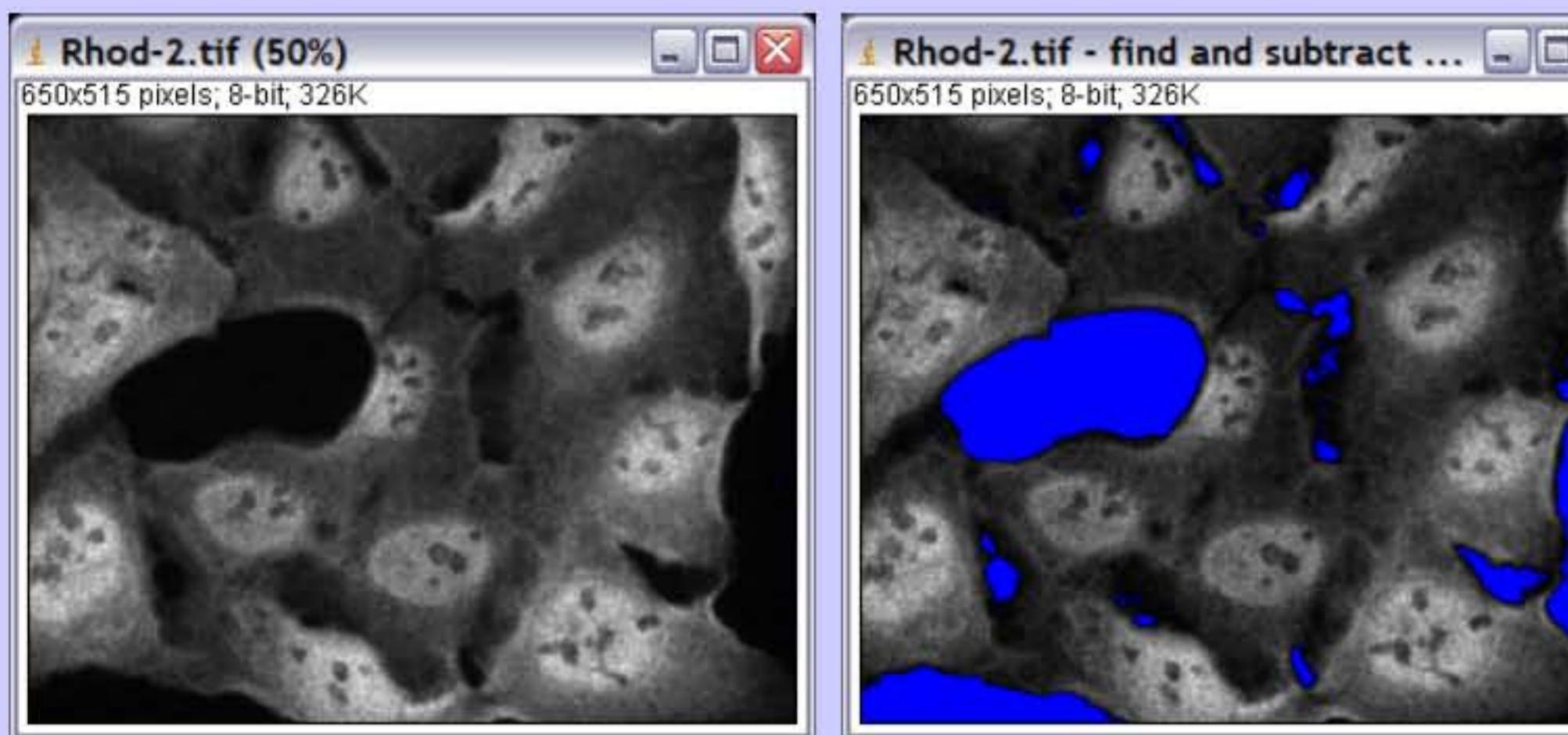


Cell Image Analyzer

volker.baecker@mri.cnrs.fr

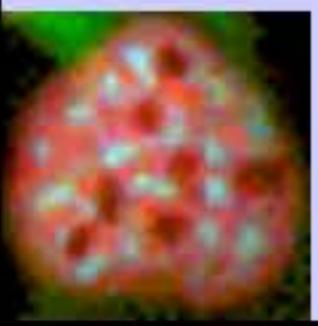


# Measuring intensity ratios



both images with hilo LUT  
after background subtraction

blue = intensity is zero



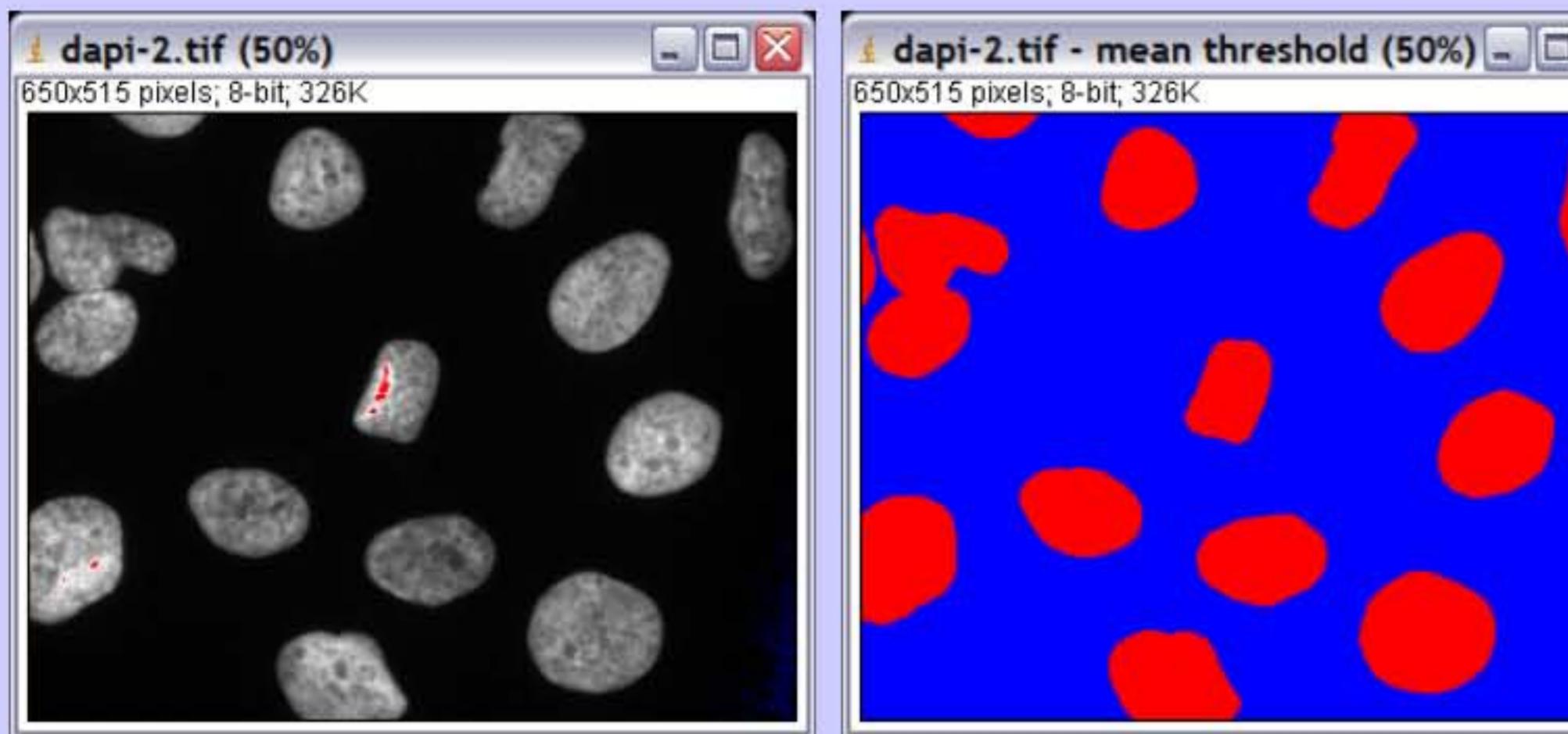
Cell Image Analyzer

volker.baecker@mri.cnrs.fr

compare intensities nuclei outside ...

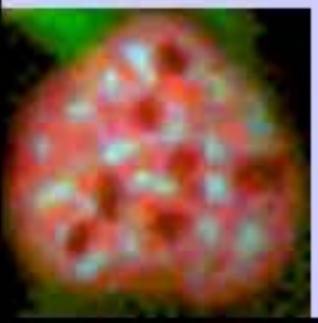
```
? foreach image in list do 0 p
? open image 0 p
? open image 0 p
? skip image not loaded 0 p
? skip saturated 0 p
? convert image type 0 p
? convert image type 0 p
? find and subtract background 0 p
? mean threshold 0 p
? invert image 0 p
? find objects 0 p
? select white pixel 0 p
? transfer selection 0 p
```

# Measuring intensity ratios



to find nuclei

- threshold with mean intensity value



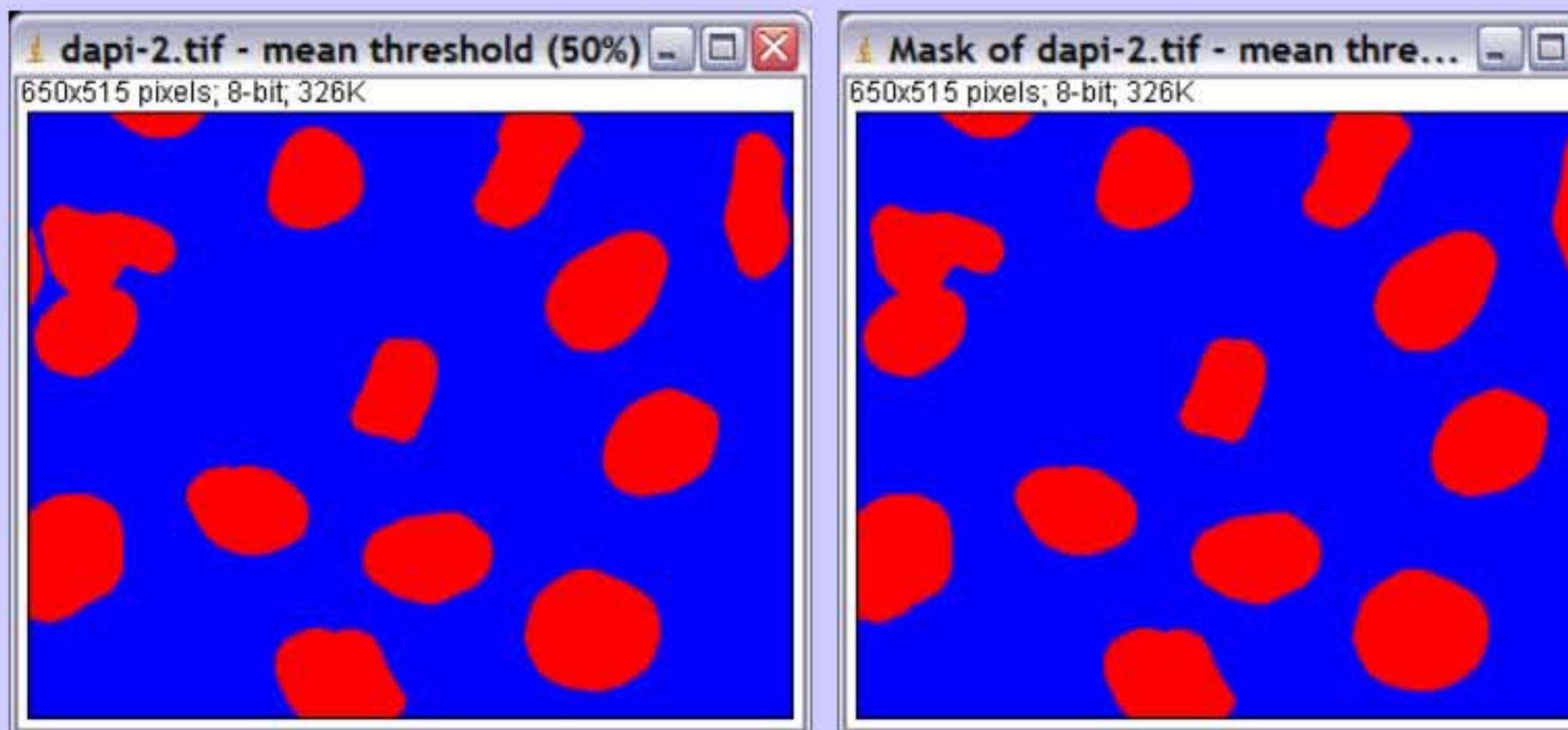
Cell Image Analyzer

volker.baecker@mri.cnrs.fr

compare intensities nuclei outside ...

```
? foreach image in list do 0 p
? open image 0 p
? open image 0 p
? skip image not loaded 0 p
? skip saturated 0 p
? convert image type 0 p
? convert image type 0 p
? find and subtract background 0 p
? mean threshold 0 p
? invert image 0 p
? find objects 0 p
? select white pixel 0 p
? transfer selection 0 p
```

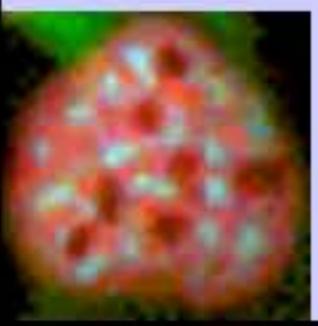
# Measuring intensity ratios



find objects (analyze particles)

- exclude objects smaller min size

gets rid of objects that are not nuclei

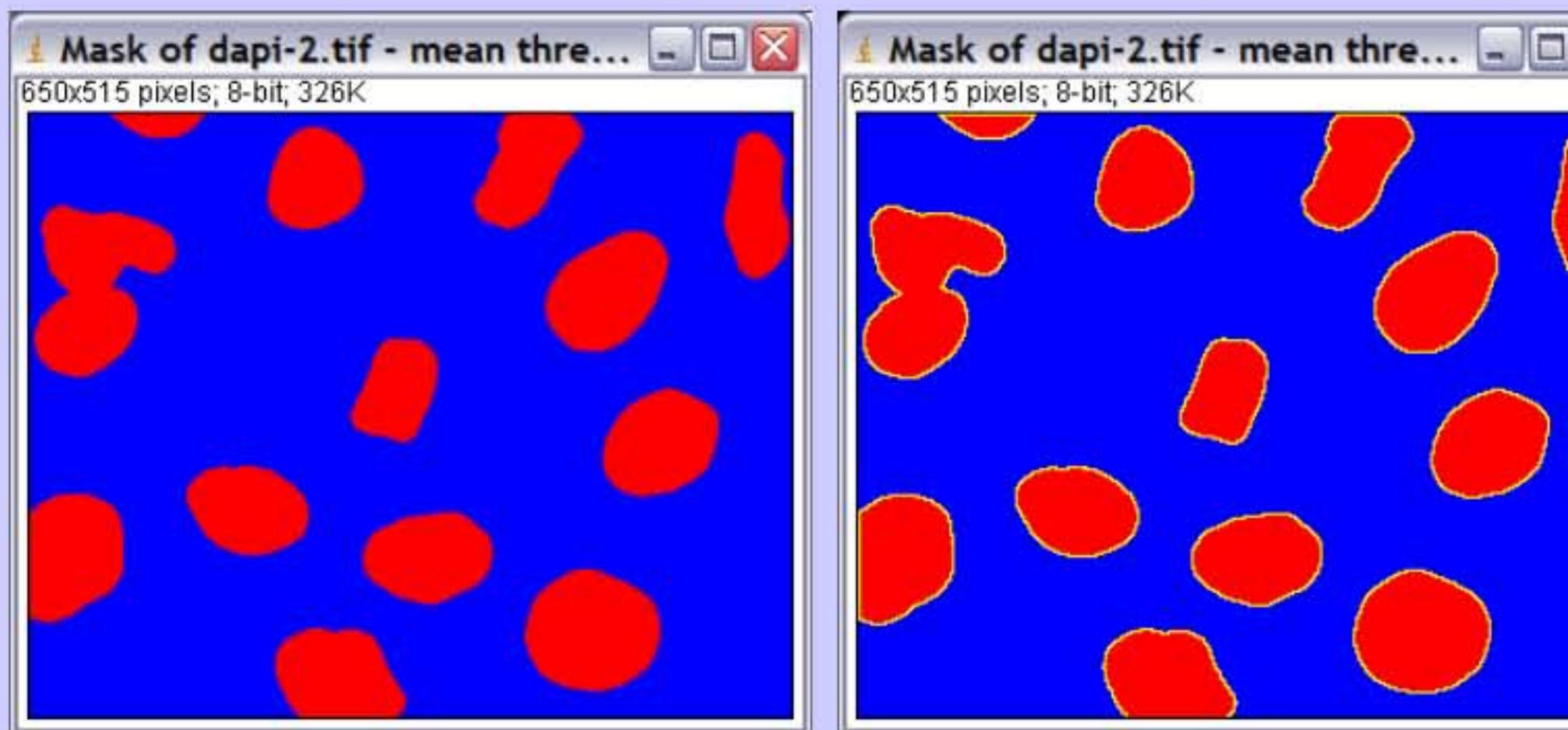


Cell Image Analyzer

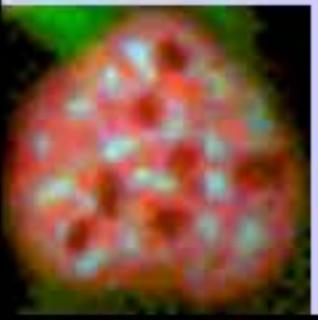
volker.baecker@mri.cnrs.fr

```
? foreach image in list do 0 p
? open image 0 p
? open image 0 p
? skip image not loaded 0 p
? skip saturated 0 p
? convert image type 0 p
? convert image type 0 p
? find and subtract background 0 p
? mean threshold 0 p
? invert image 0 p
? find objects 0 p
? select white pixel 0 p
? transfer selection 0 p
```

# Measuring intensity ratios



create selection (roi) from mask



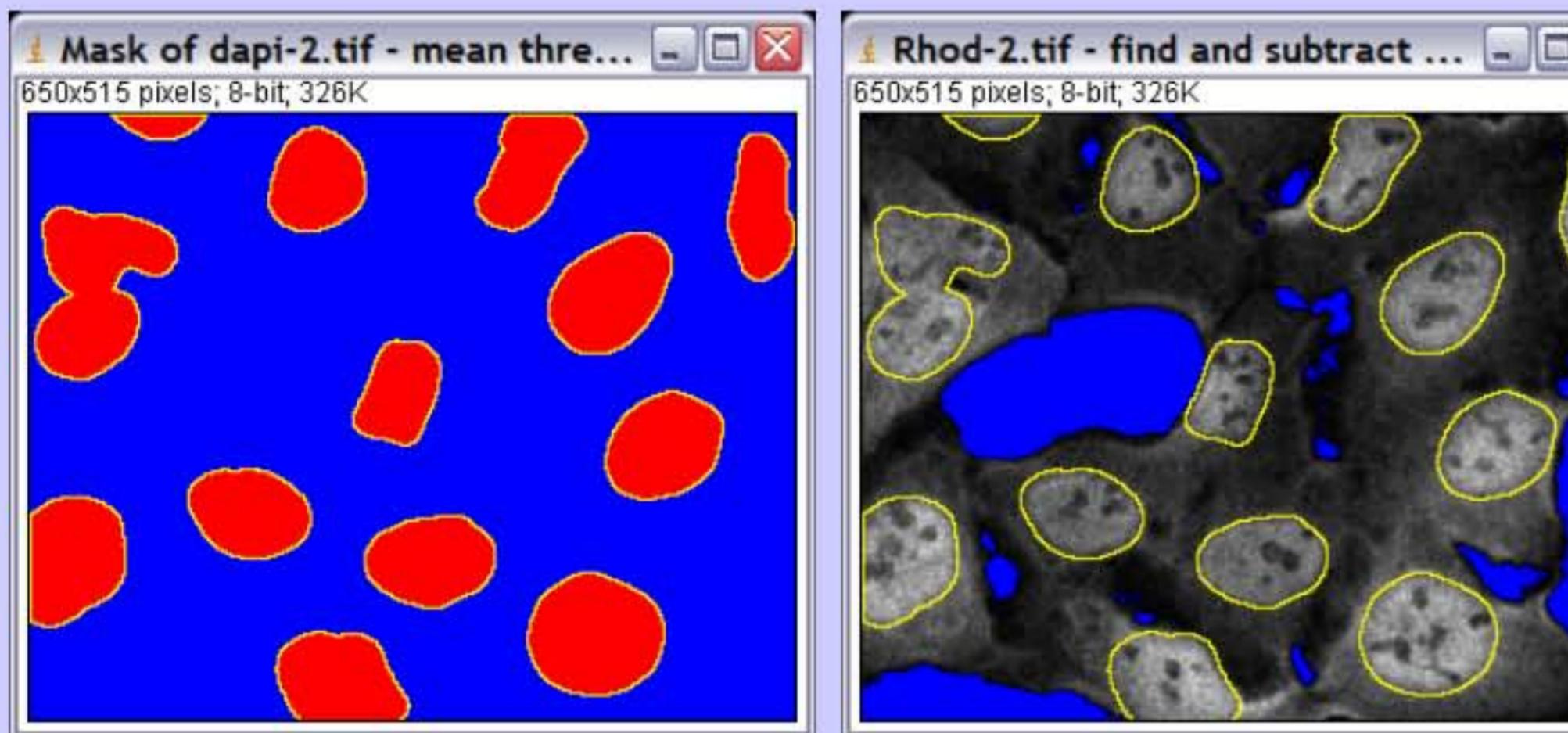
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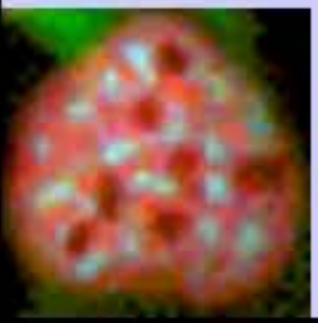
compare intensities nuclei outside ...

```
? foreach image in list do 0 p
? open image 0 p
? open image 0 p
? skip image not loaded 0 p
? skip saturated 0 p
? convert image type 0 p
? convert image type 0 p
? find and subtract background 0 p
? mean threshold 0 p
? invert image 0 p
? find objects 0 p
? select white pixel 0 p
? transfer selection 0 p
```

# Measuring intensity ratios



transfer selection to background corrected input image

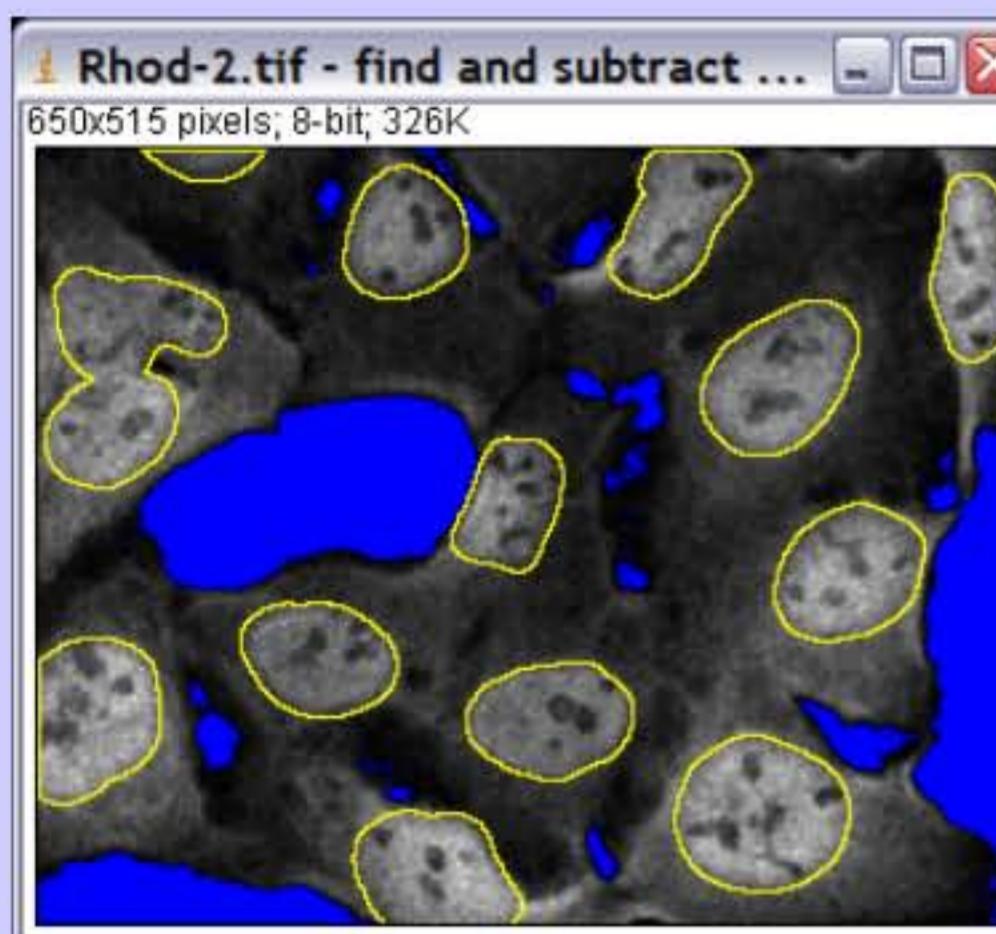


Cell Image Analyzer

volker.baecker@mri.cnrs.fr

```
? foreach image in list do 0 p
? open image 0 p
? open image 0 p
? skip image not loaded 0 p
? skip saturated 0 p
? convert image type 0 p
? convert image type 0 p
? find and subtract background 0 p
? mean threshold 0 p
? invert image 0 p
? find objects 0 p
? select white pixel 0 p
? transfer selection 0 p
```

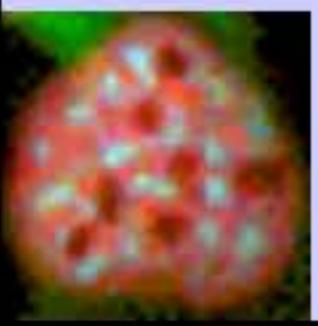
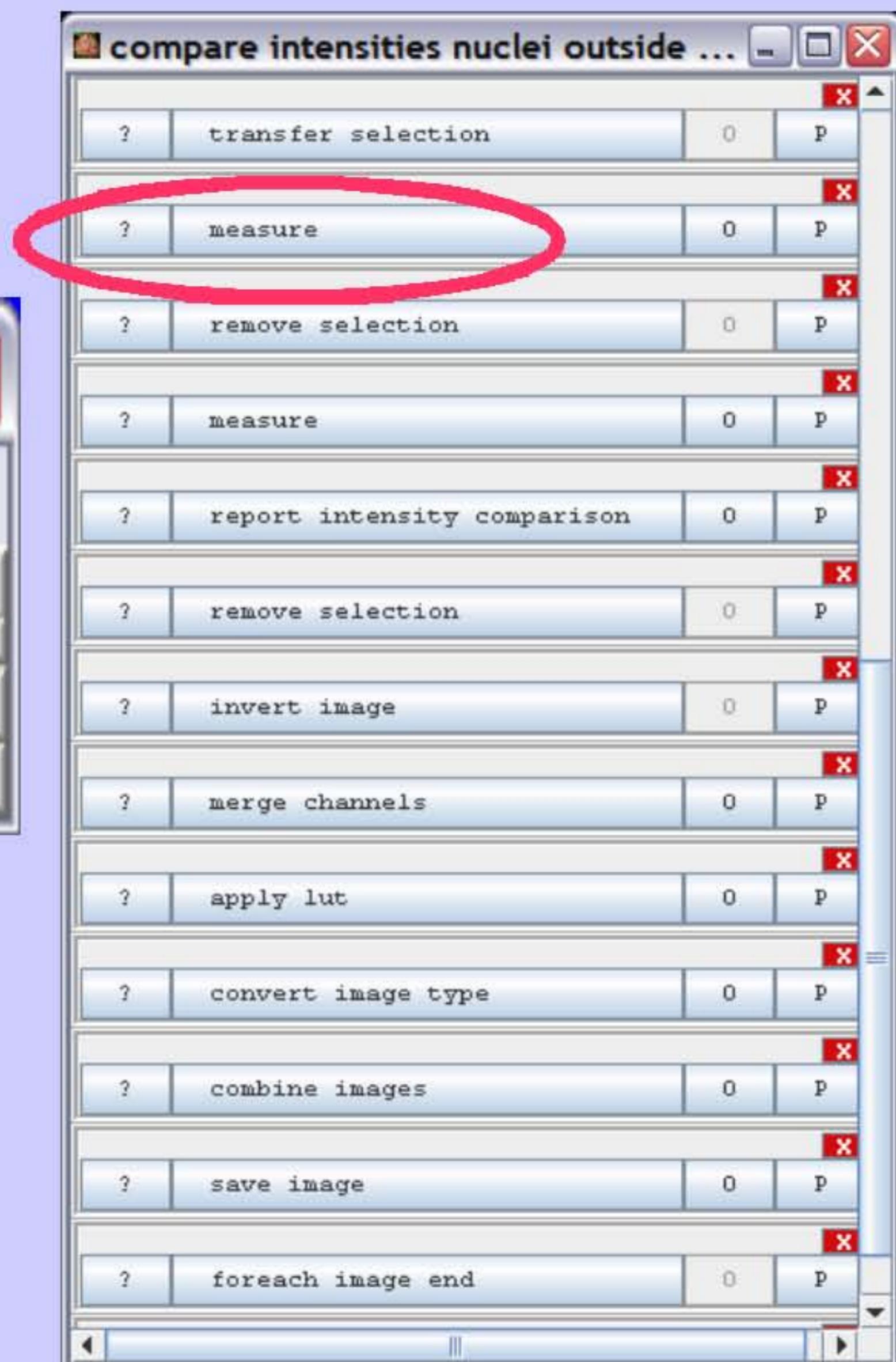
# Measuring intensity ratios



Results	
File	Edit
Area	IntDen
1	84203 9347903

## measure

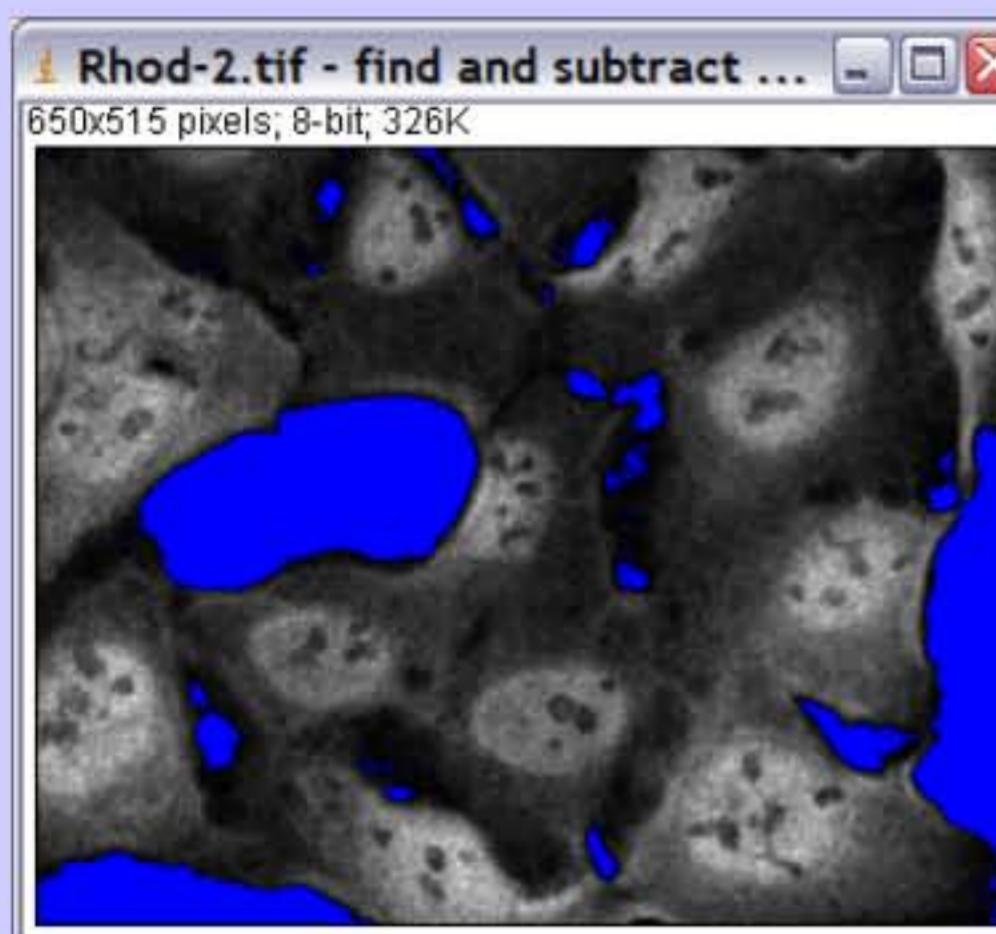
- area
- total intensity of nuclei



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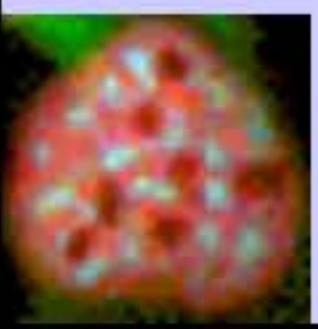
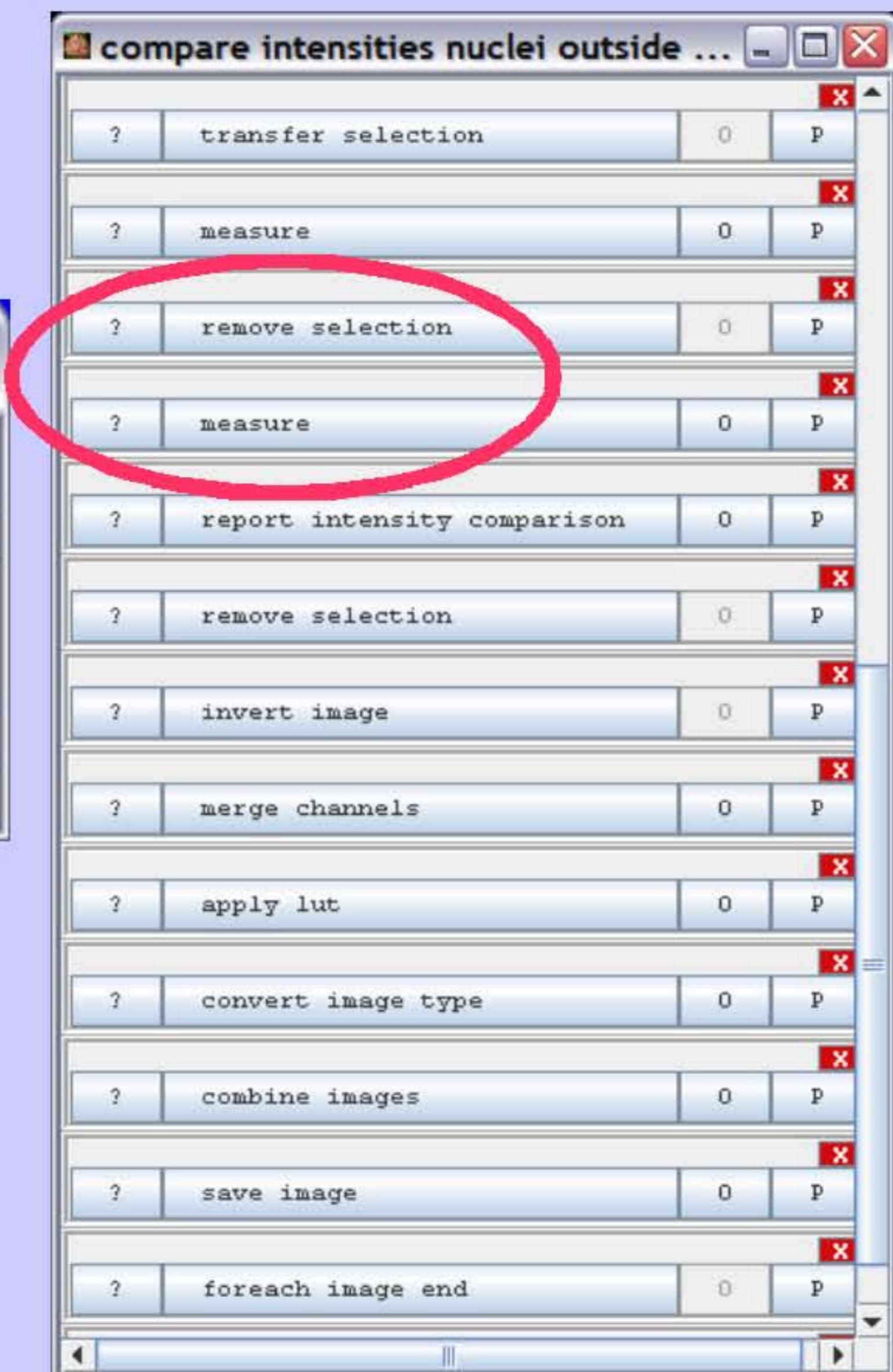
volker.baecker@mri.cnrs.fr

# Measuring intensity ratios



	Area	IntDen
1	84203	9347903
2	334750	18258131

remove selection  
measure area and intensity of the  
whole image



# Measuring intensity ratios

calculate percentage of intensity

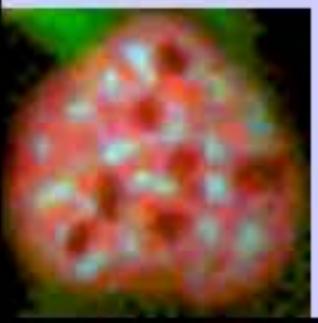
- in nuclei
- outside nuclei

$$p1 = d1 / d2$$

$$p2 = (d2 - d1) / d2$$

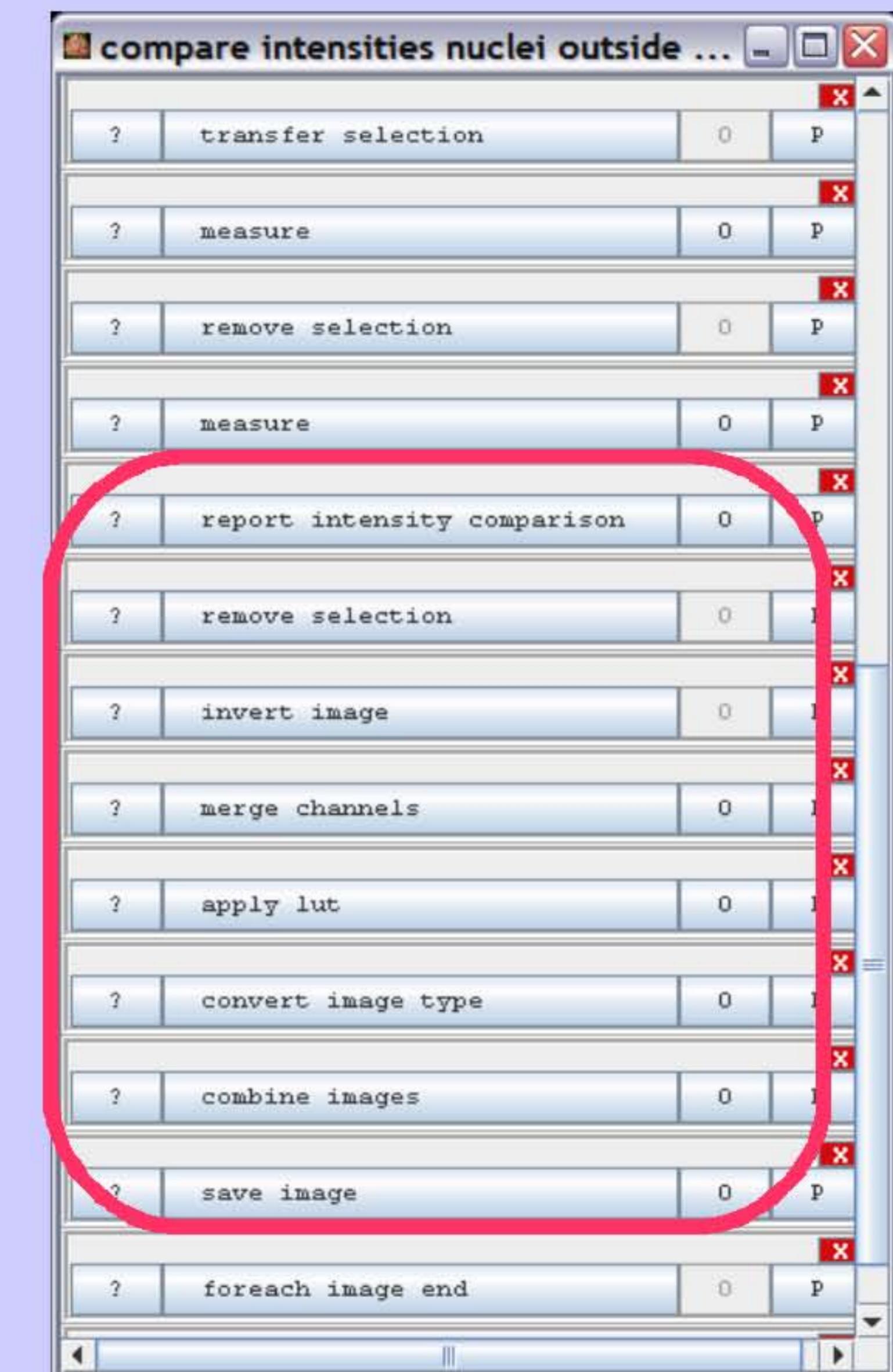
Results

	Area	IntDen
1	84203	9347903
2	334750	18258131



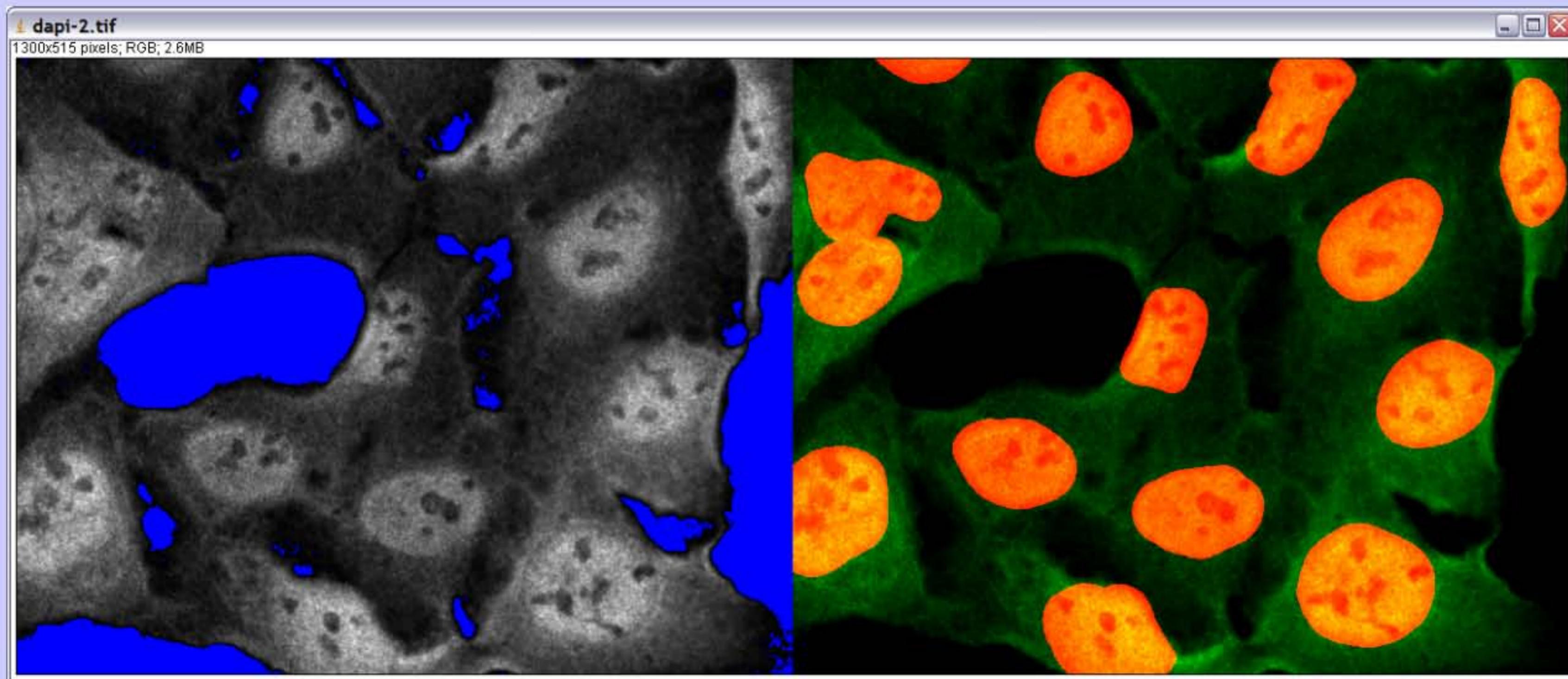
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volker.baecker@mri.cnrs.fr



# Measuring intensity ratios

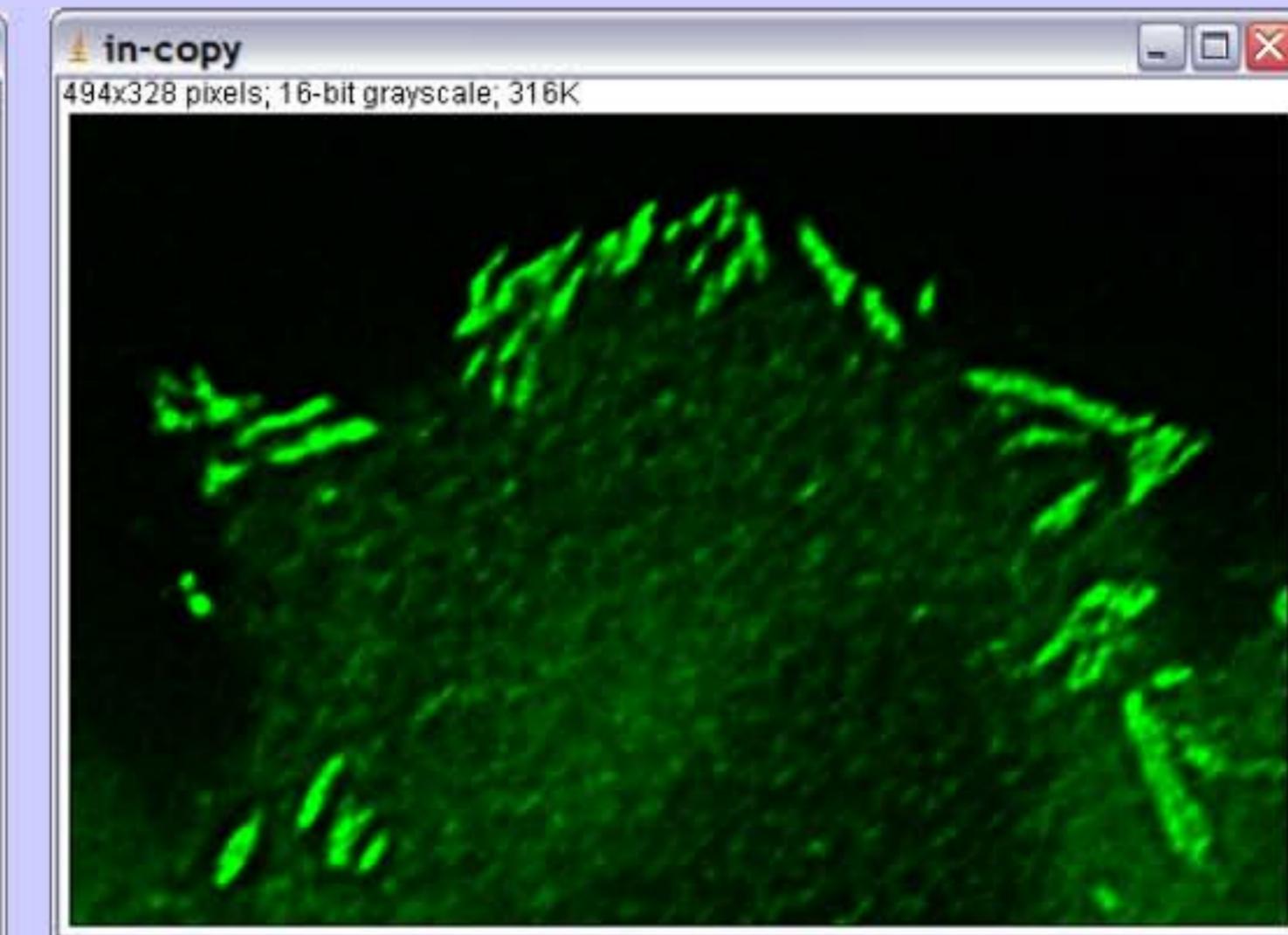
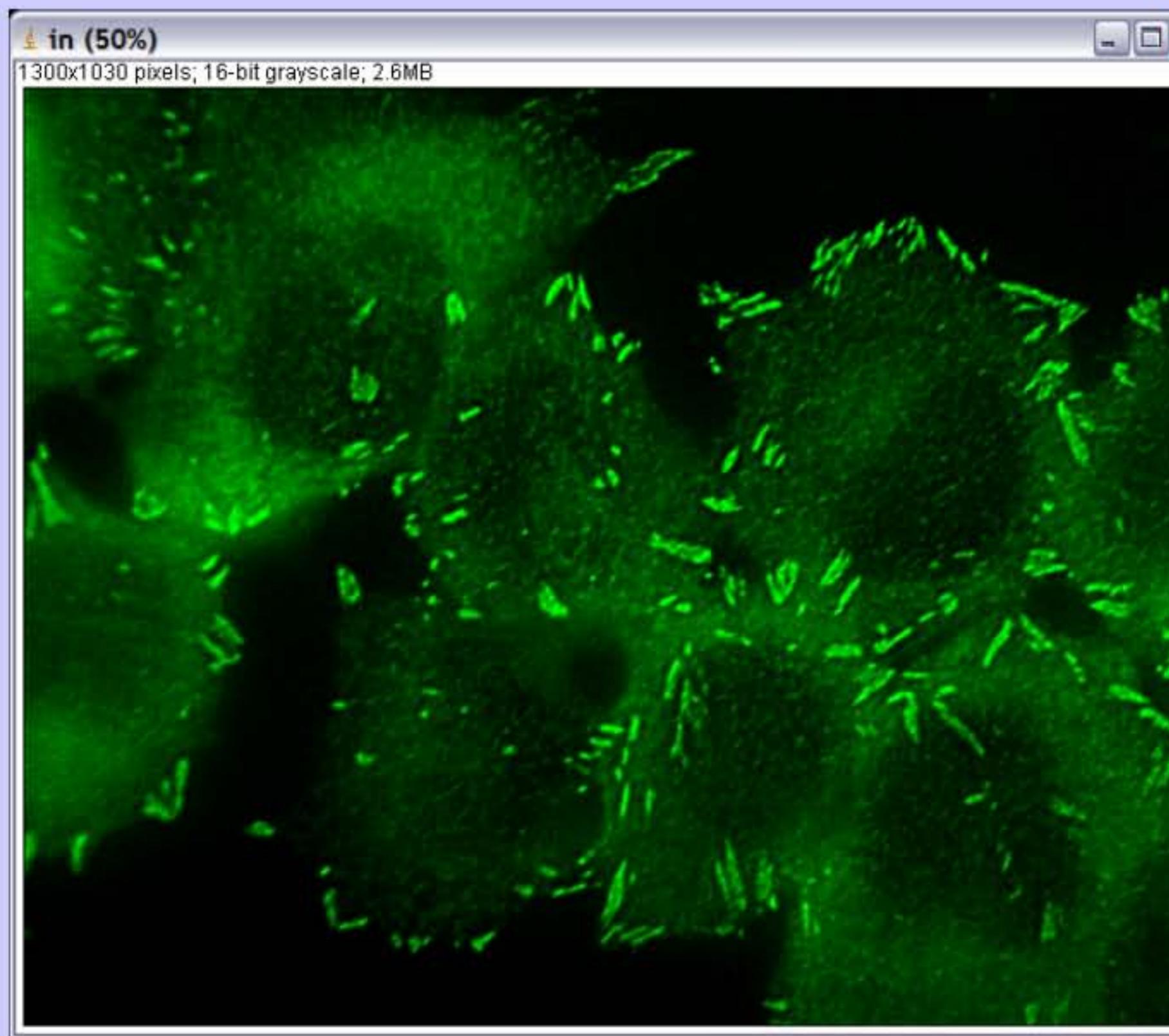
image	icn factor	percent nuclei	percent cytoplasm	av.	
dapi-2.tif	1,05	0,51		0,49	report to spreadsheet-file save control images



Cell Image Analyzer

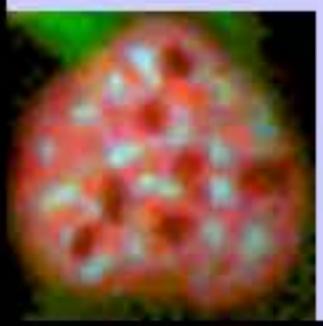
volker.baecker@mri.cnrs.fr

# Measuring stained proteins

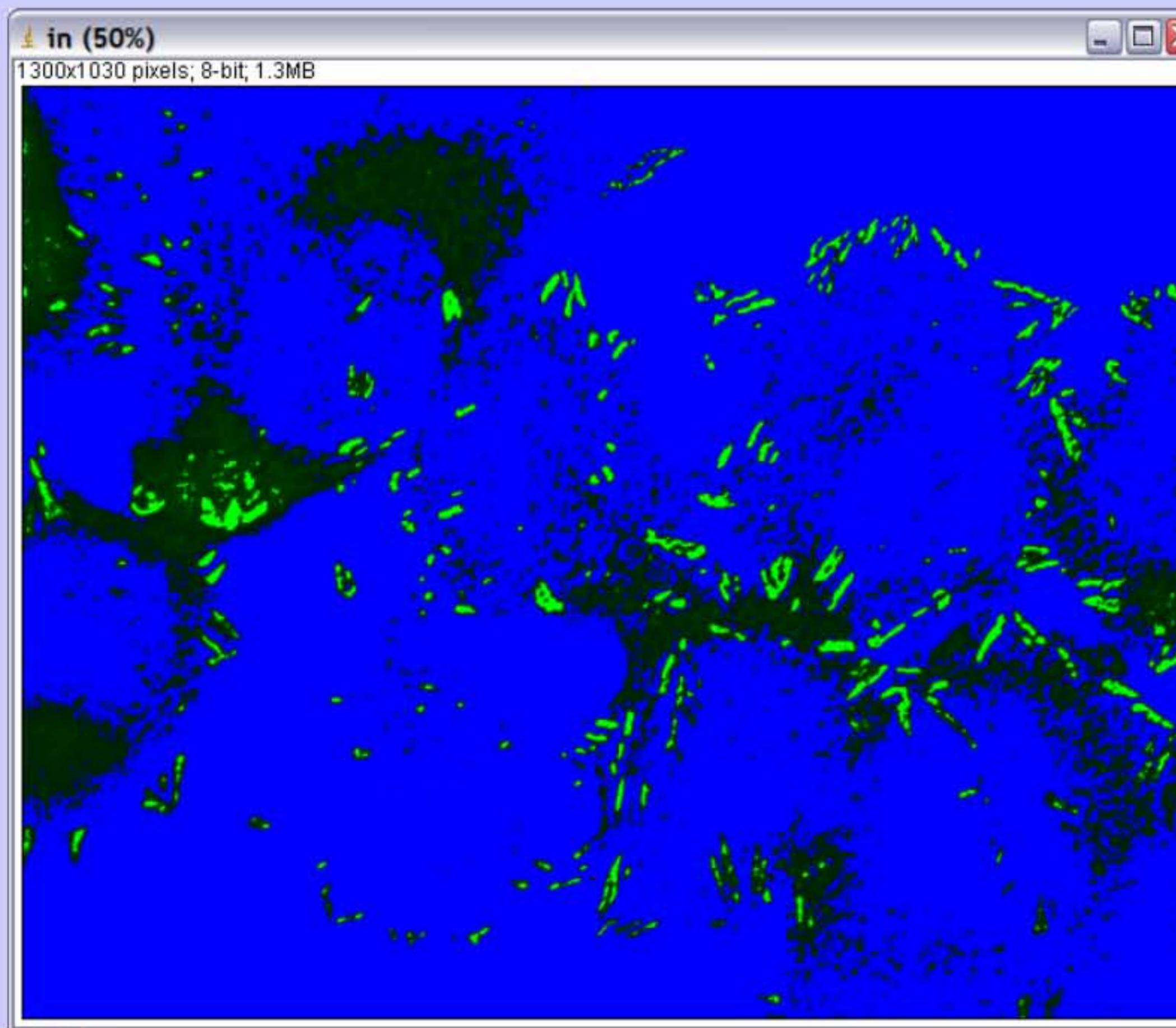


task:

- count plaques
- measure size of plaques



# Measuring stained proteins



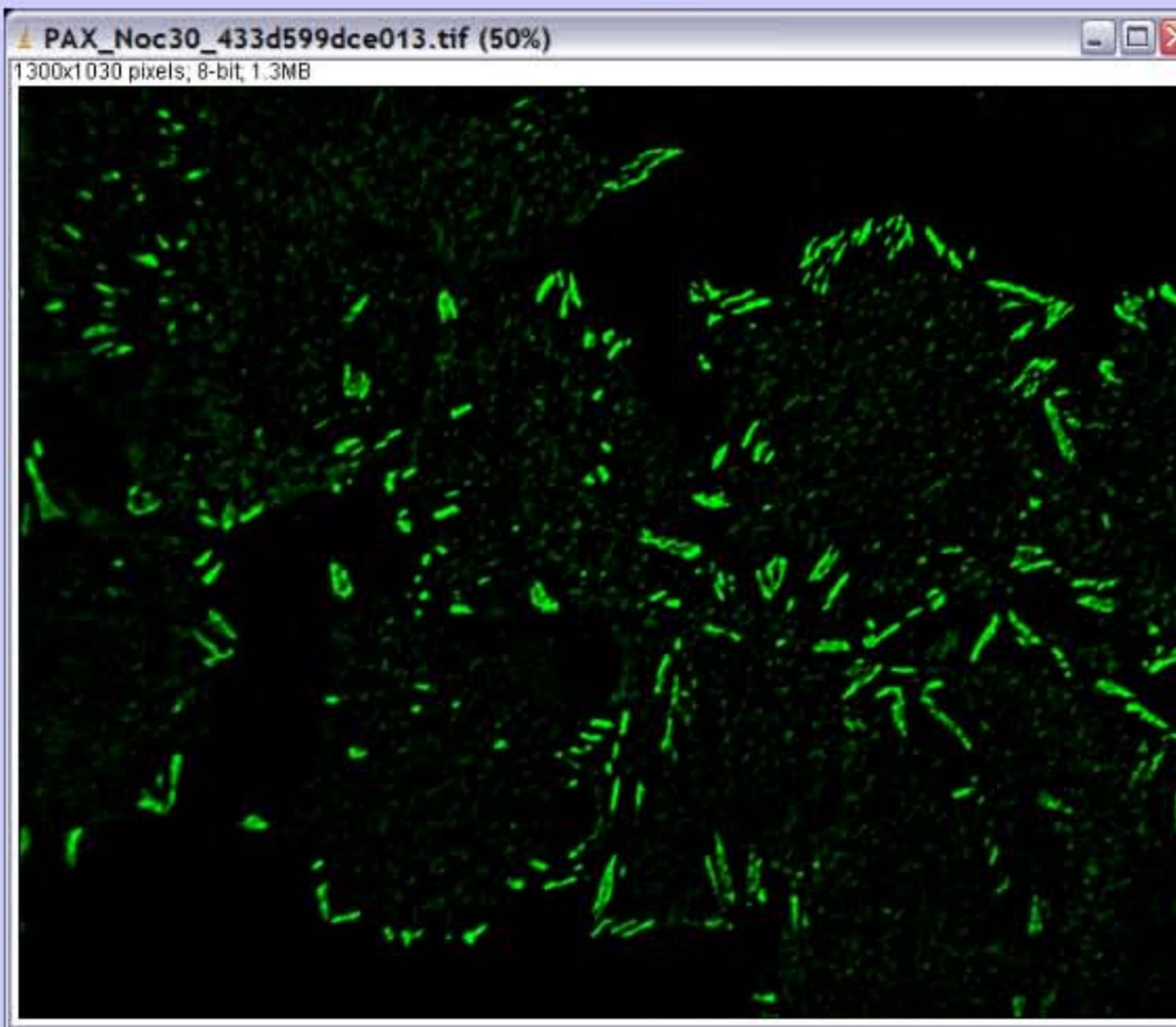
Cell Image Analyzer

volker.baecker@mri.cnrs.fr

problem:

- same intensities in plaques and cytoplasm
- simple threshold doesn't separate plaques from background

# Measuring stained proteins

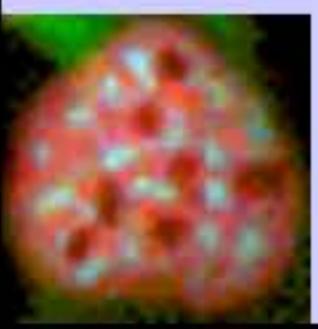


measure spots batch

```
? foreach image do 0 p
? open image 0 p
? convert color to grayscale 0 p
? gaussian blur 0 p
? image calculation 0 p
? auto threshold 0 p
? invert image 0 p
? dilate 0 p
? find objects 0 p
? save image 0 p
? report measurements 0 p
? foreach image end 0 p
```

The "gaussian blur" step in the script is highlighted with a red oval.

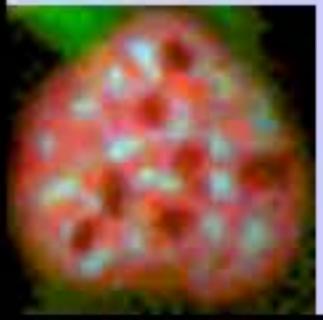
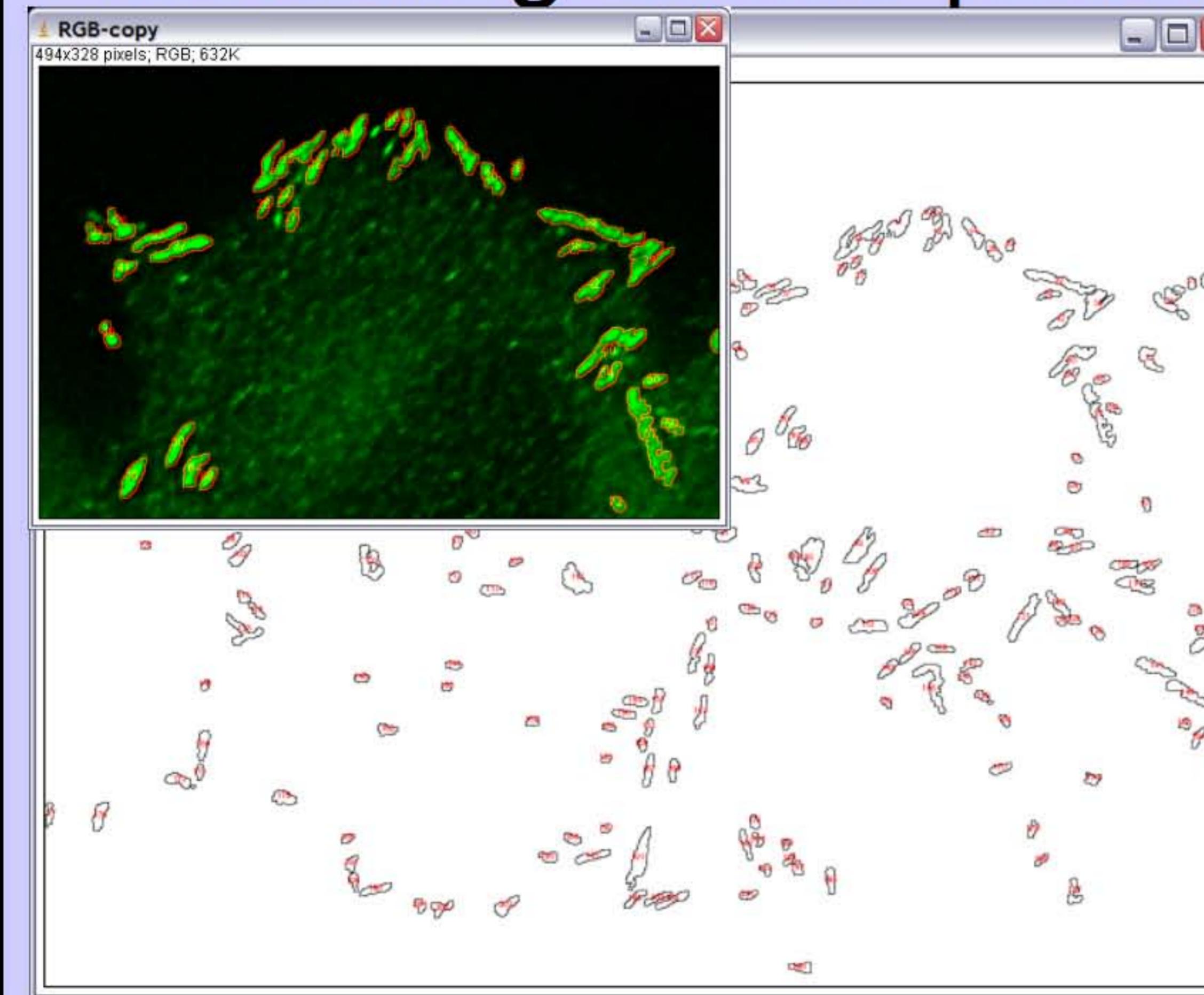
- subtract a blurred version of the image from the original
- only small, isolated dots of the background remain



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volker.baecker@mri.cnrs.fr

# Measuring stained proteins



Cell Image Analyzer

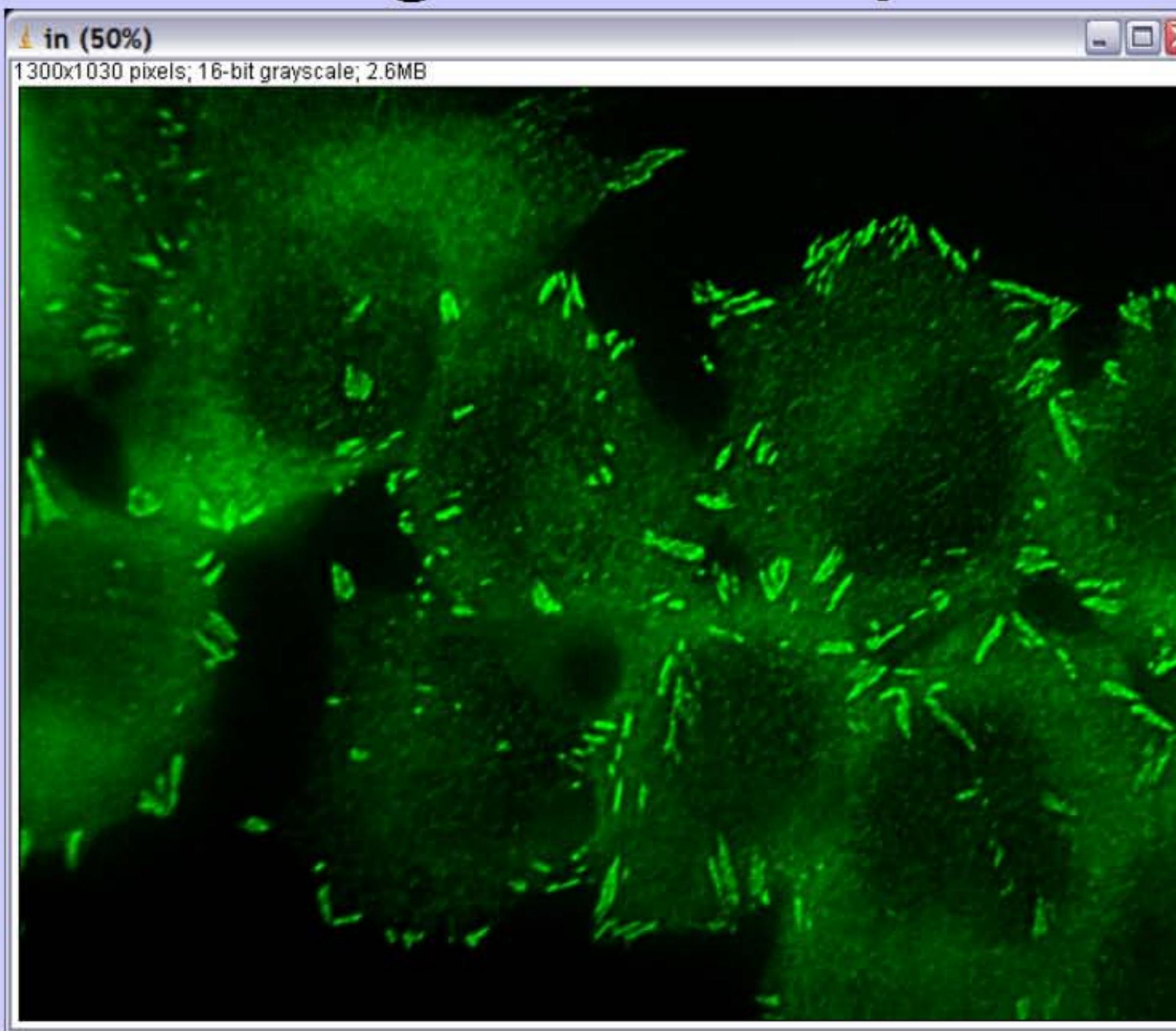
volker.baecker@mri.cnrs.fr

measure spots batch

```
? foreach image do 0 p
? open image 0 p
? convert image type 0 p
? gaussian blur 0 p
? image calculation 0 p
? auto threshold 0 p
? invert image 0 p
? dilate 0 p
? find objects 0 p
? save image 0 p
? report measurements 0 p
? foreach image end 0 p
```

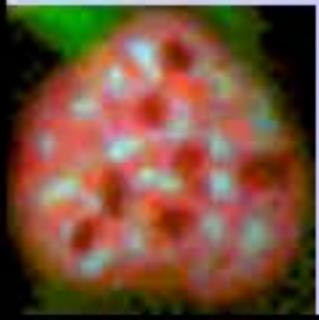
A screenshot of the ImageJ macro editor titled "measure spots batch". The macro consists of a series of ImageJ commands. A red circle highlights the "find objects" command, which is part of the "foreach image do" loop. The "find objects" command is used to detect objects in each image and generate a binary mask for further processing.

# Measuring stained proteins



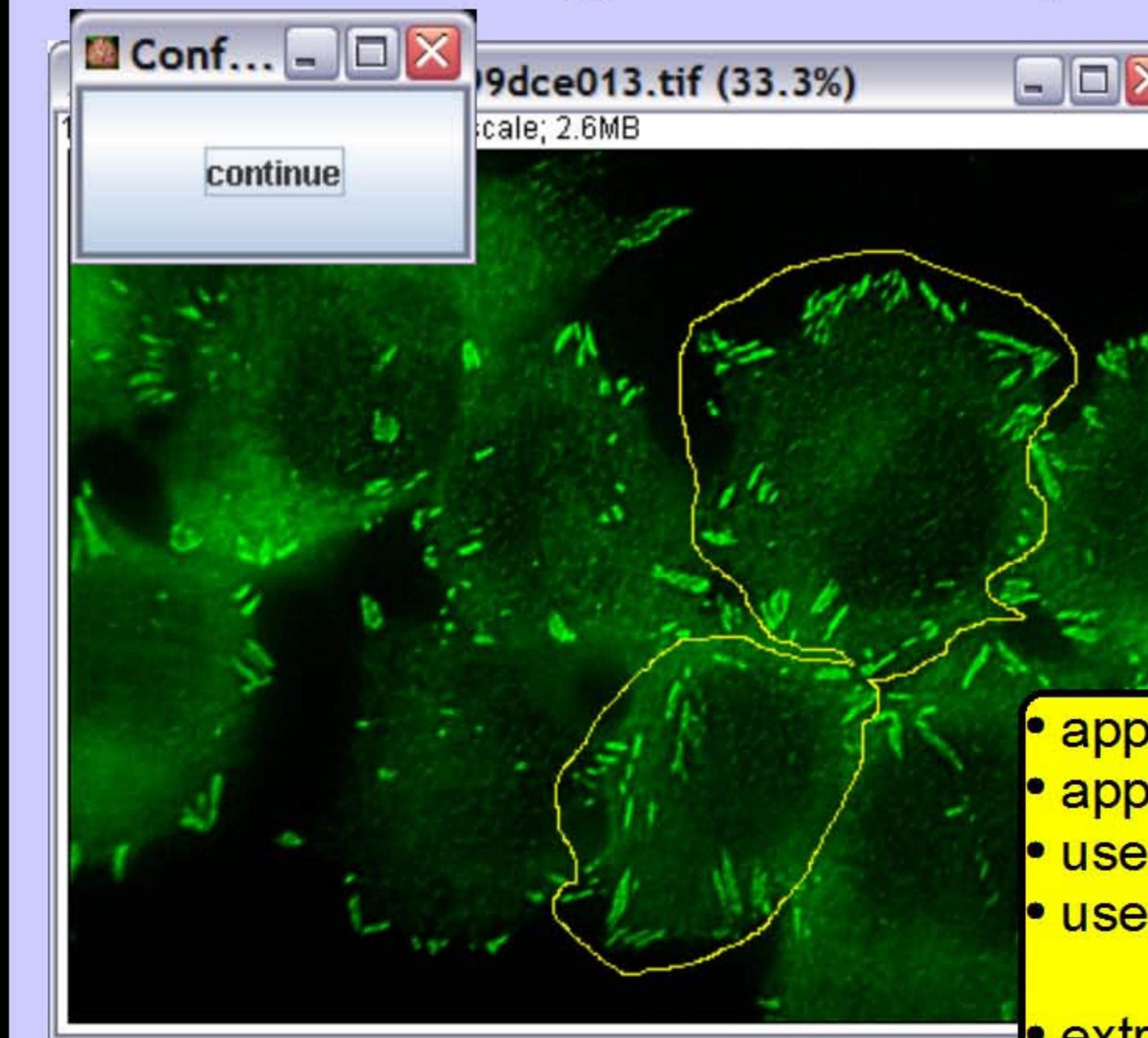
new requirement:

- count and measure plaques only for some selected cells





# Measuring stained proteins

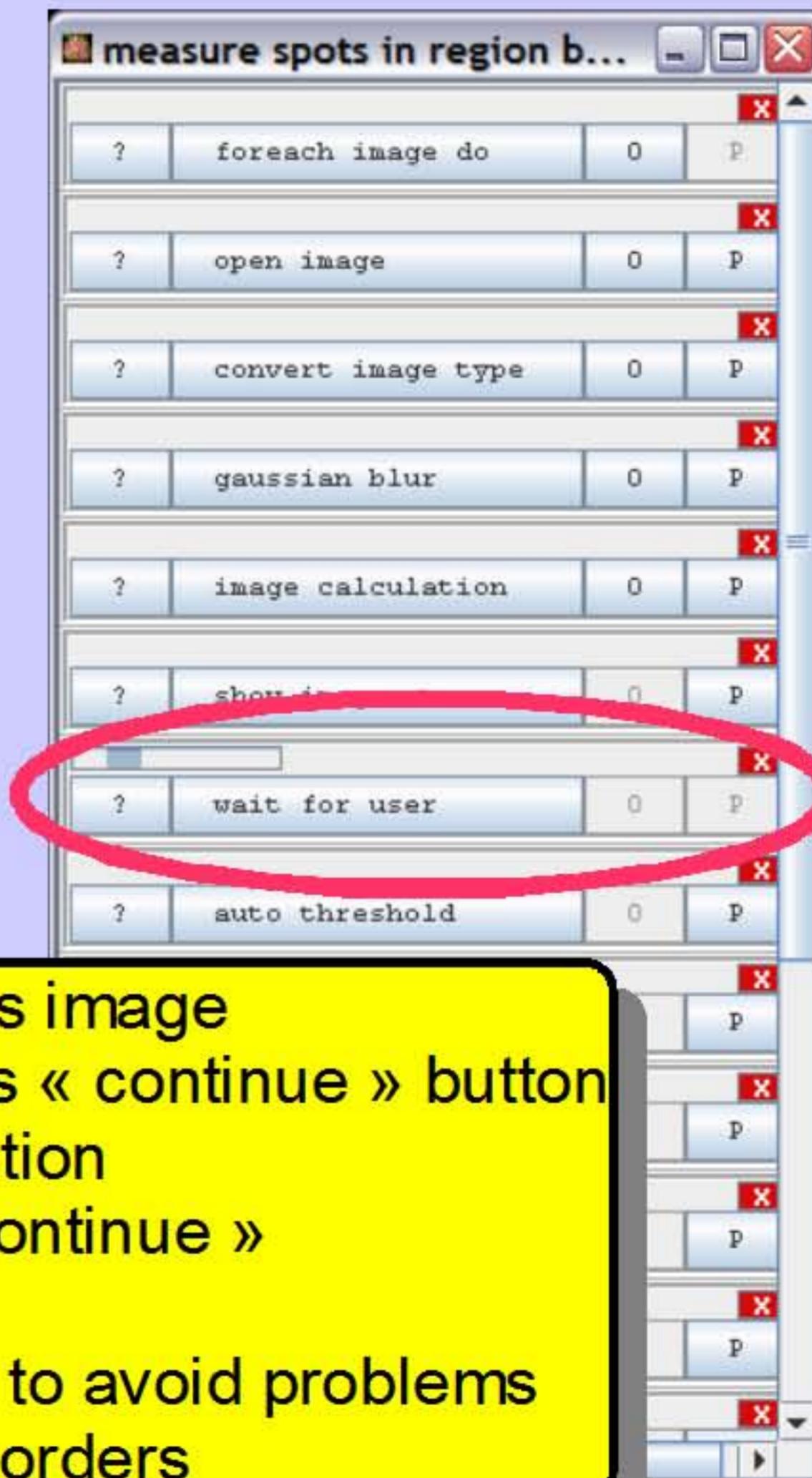
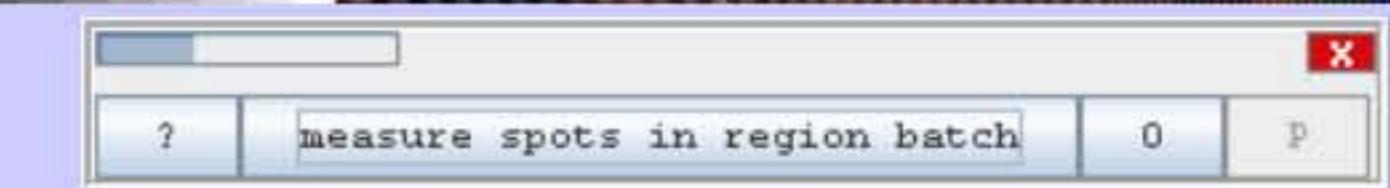


- application shows image
- application opens « continue » button
- user draws selection
- user presses « continue »
- extra processing to avoid problems at the selection borders

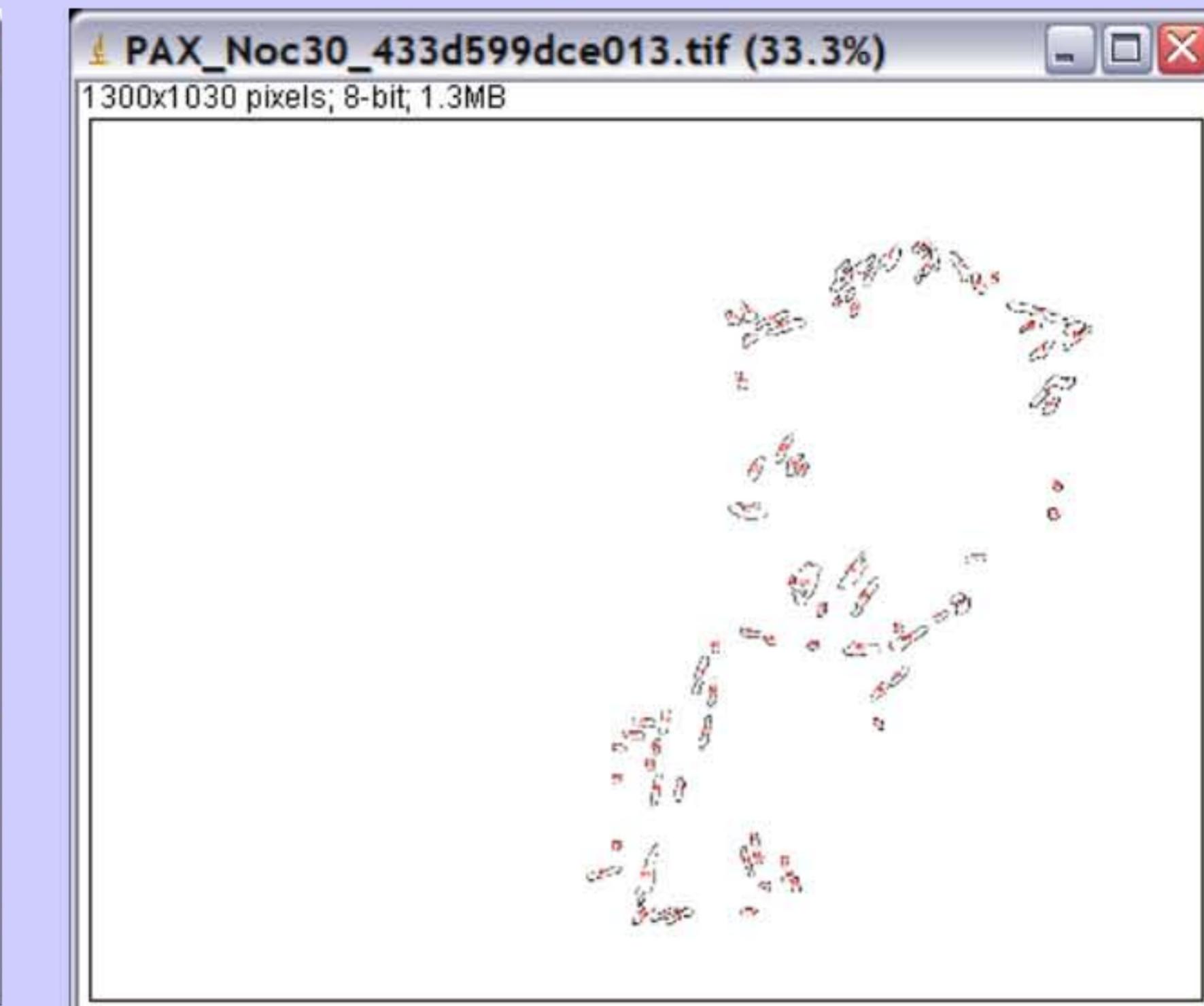
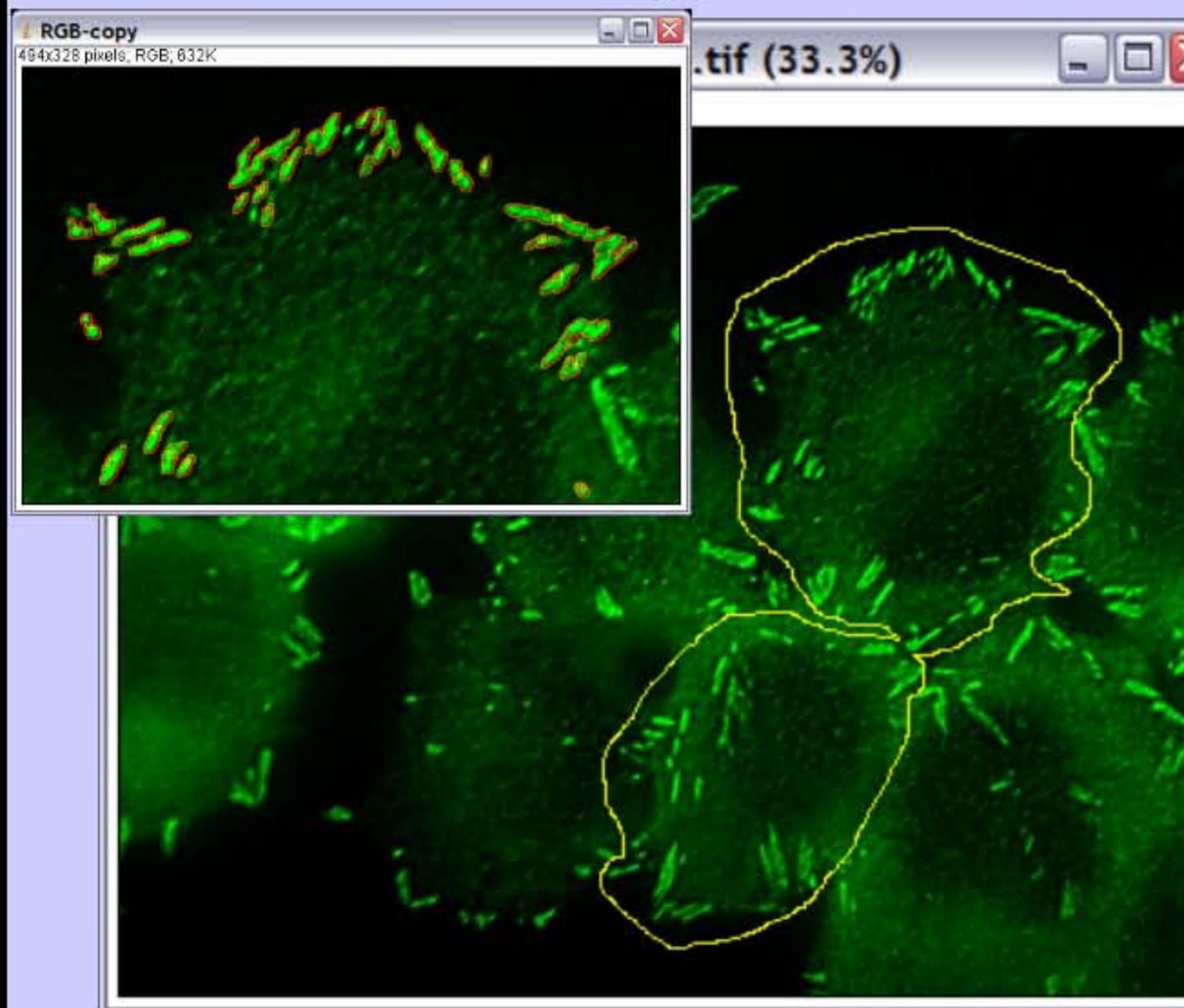


Cell Image Analyzer

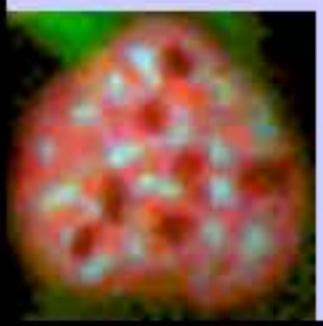
volker.baecker@mri.cnrs.fr



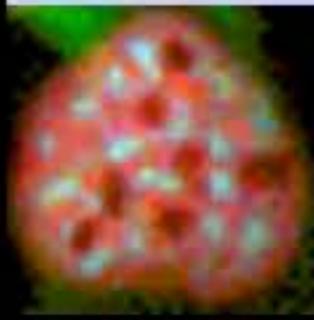
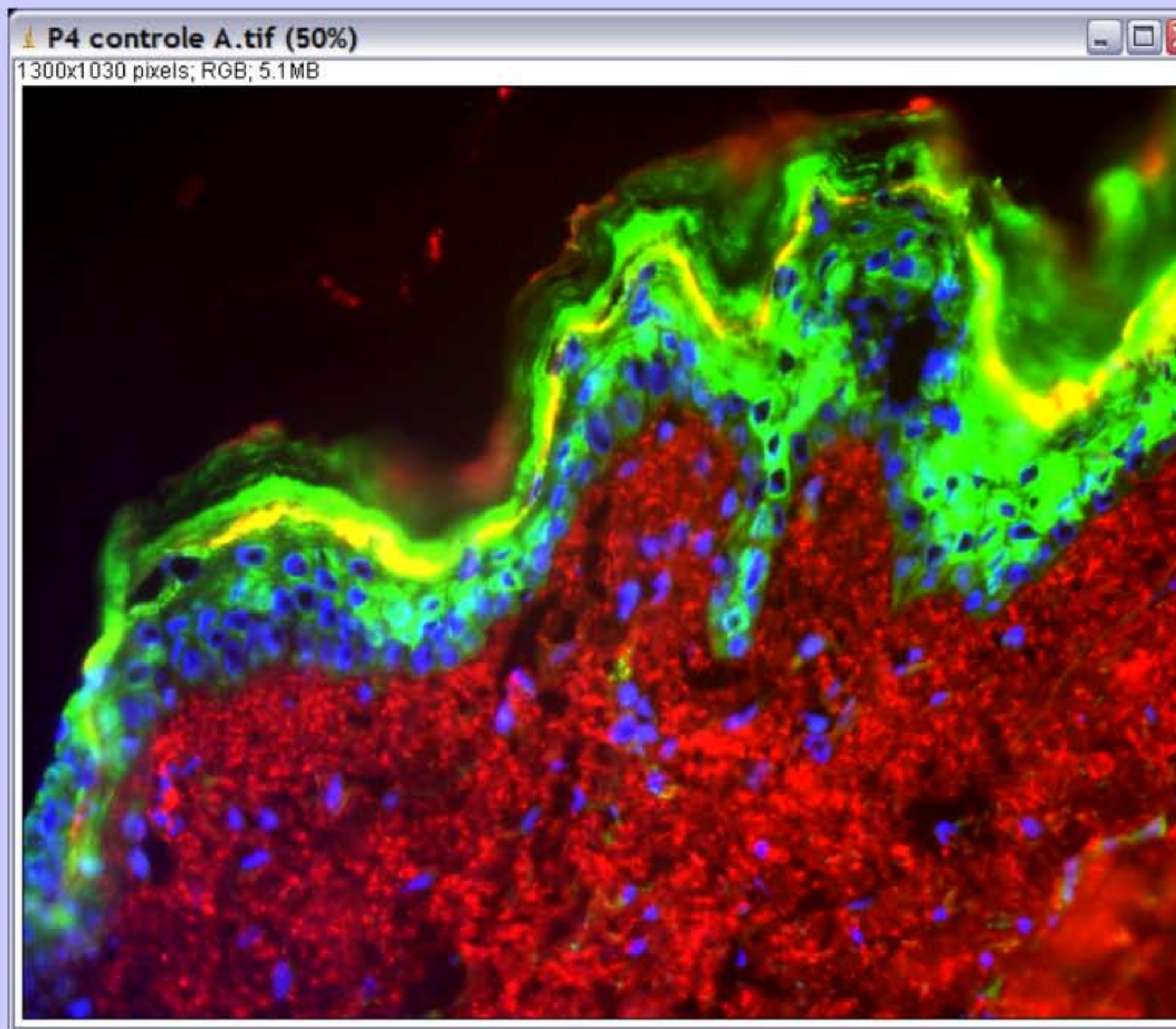
# Measuring stained proteins



only the plaques within the selection are taken into account



# Counting nuclei



Cell Image Analyzer

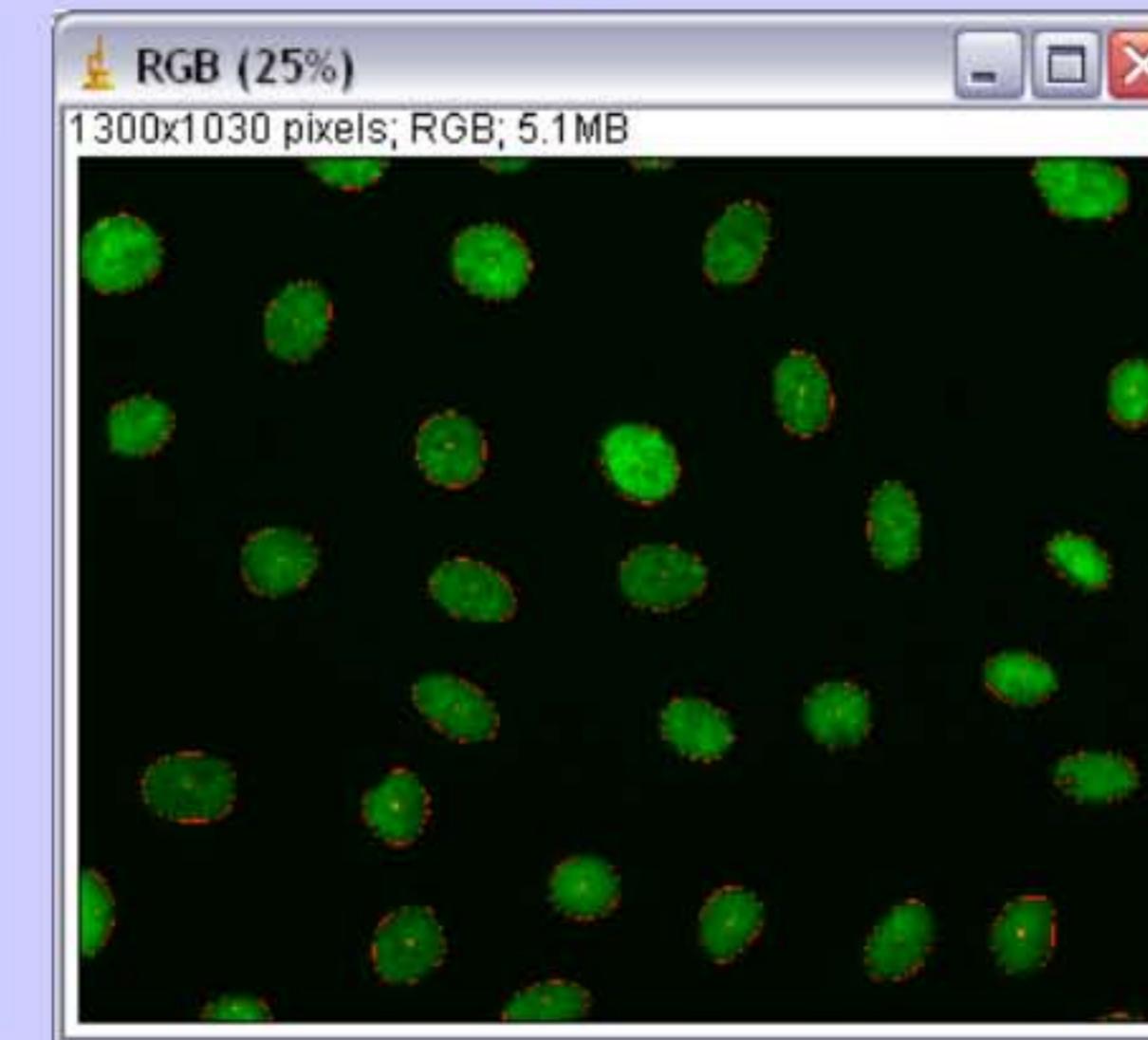
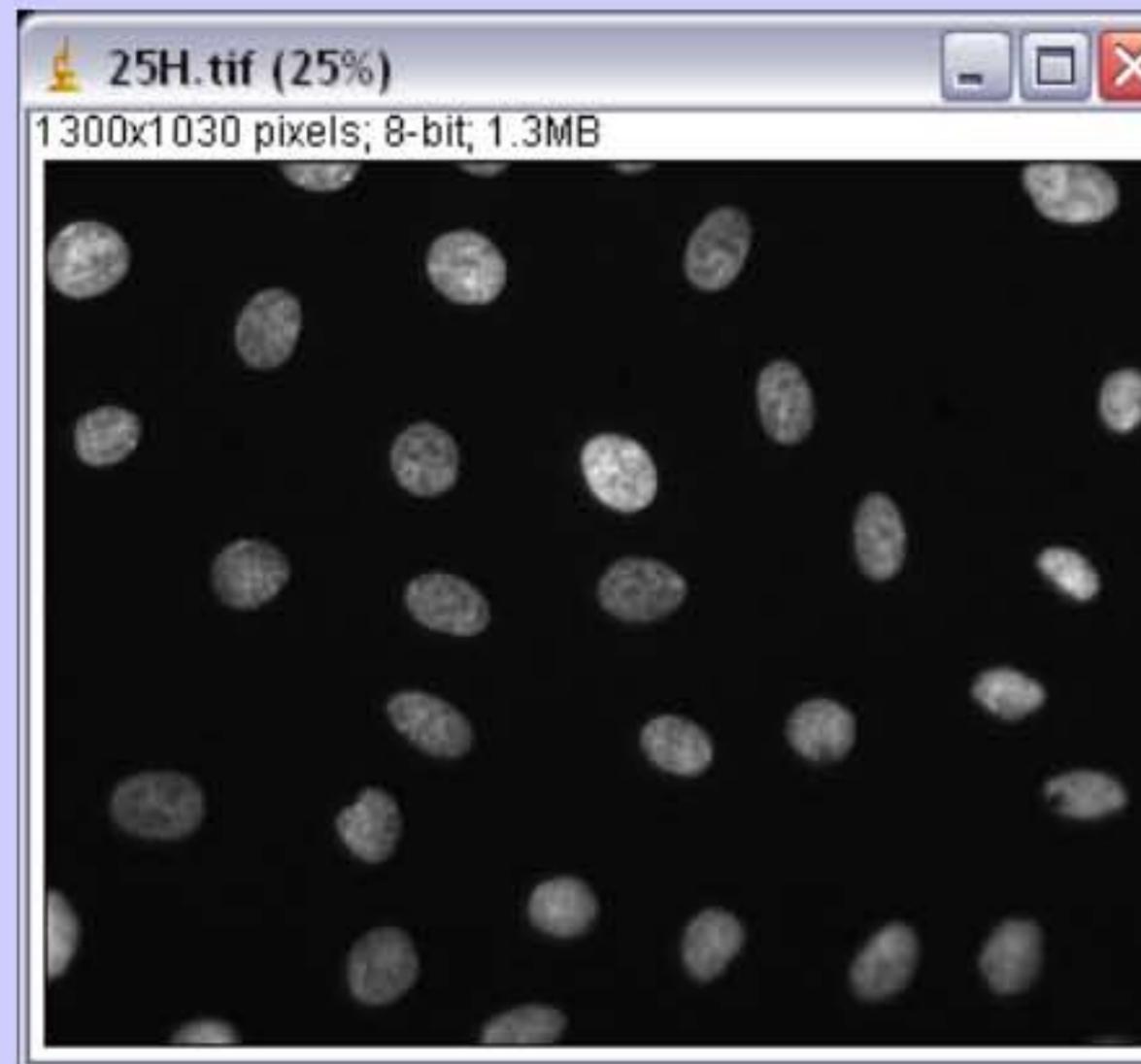
volker.baecker@mri.cnrs.fr

## applications

- count cells or nuclei
- count stain combinations
  - blue only, red and blue,

...

# Counting nuclei



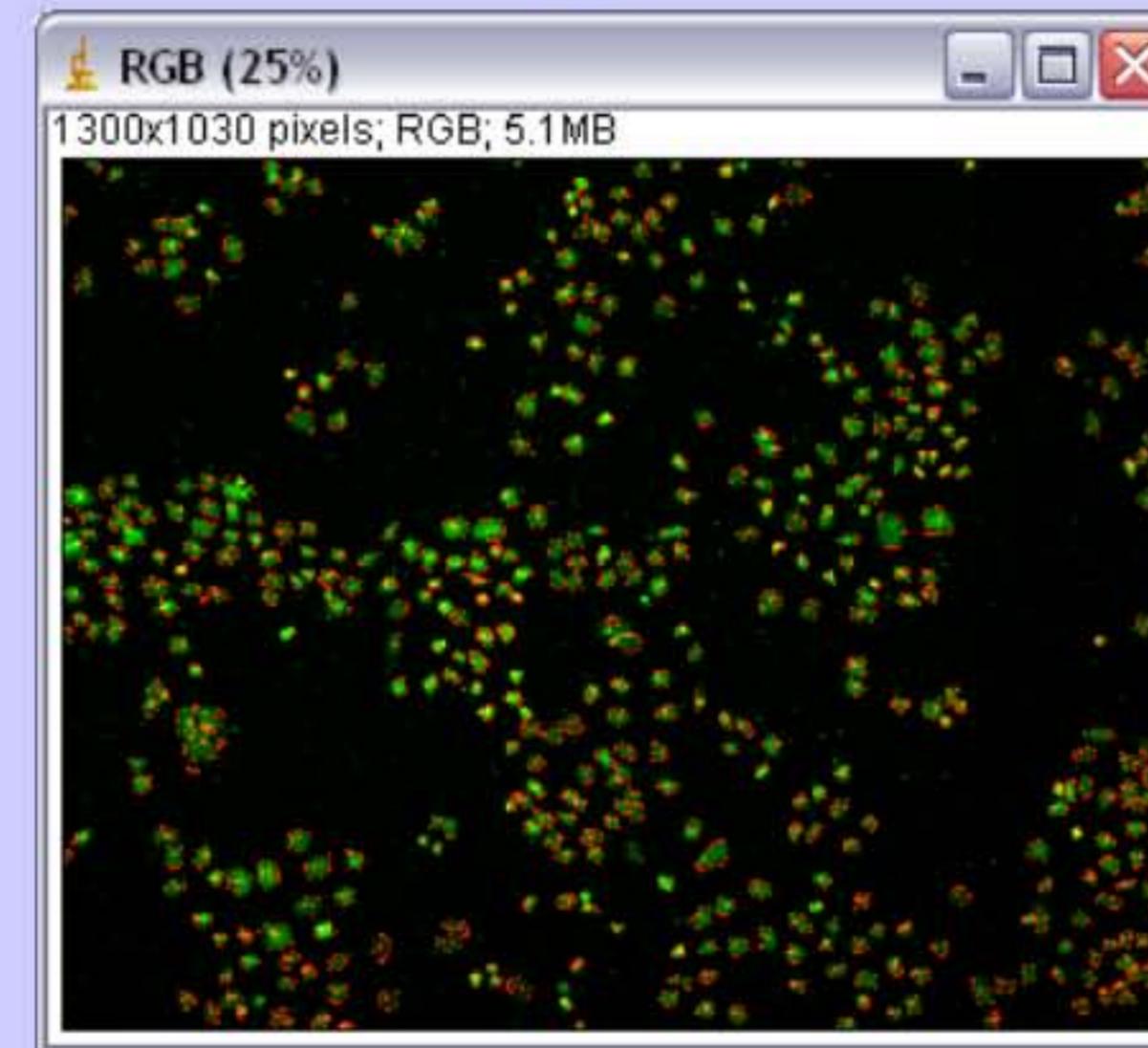
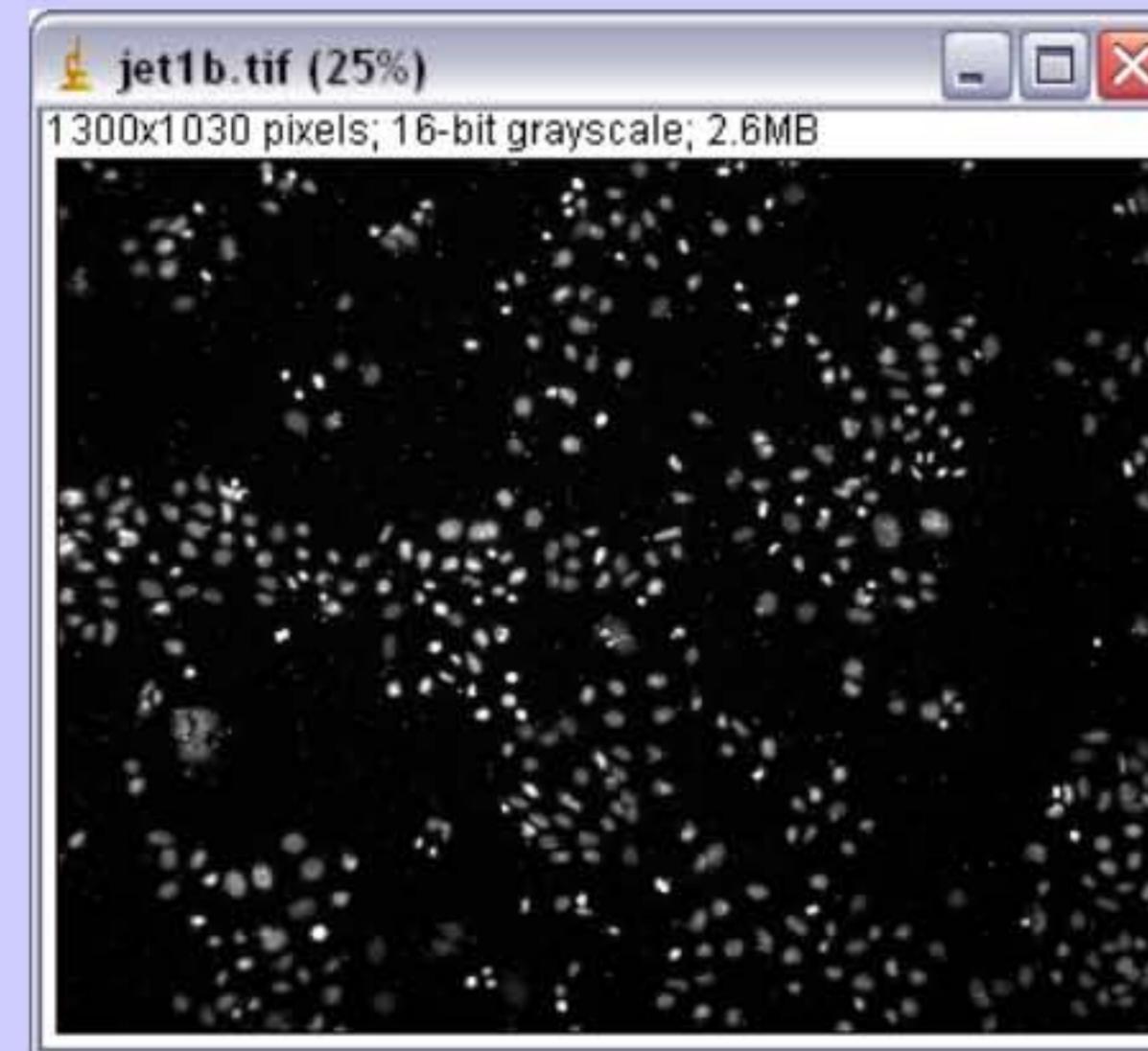
How many cells  
are there?

image	number of objects	folder
25H.tif	34	E:\besnard\
jet1b.tif	495	E:\etienne\delepine\

- watershed
- derivative
- local threshold
- full automatic
- interactive



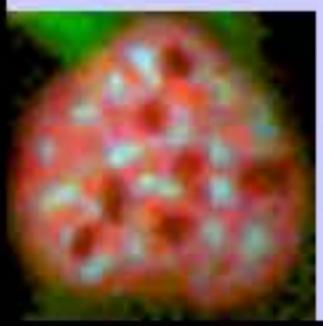
# Counting nuclei



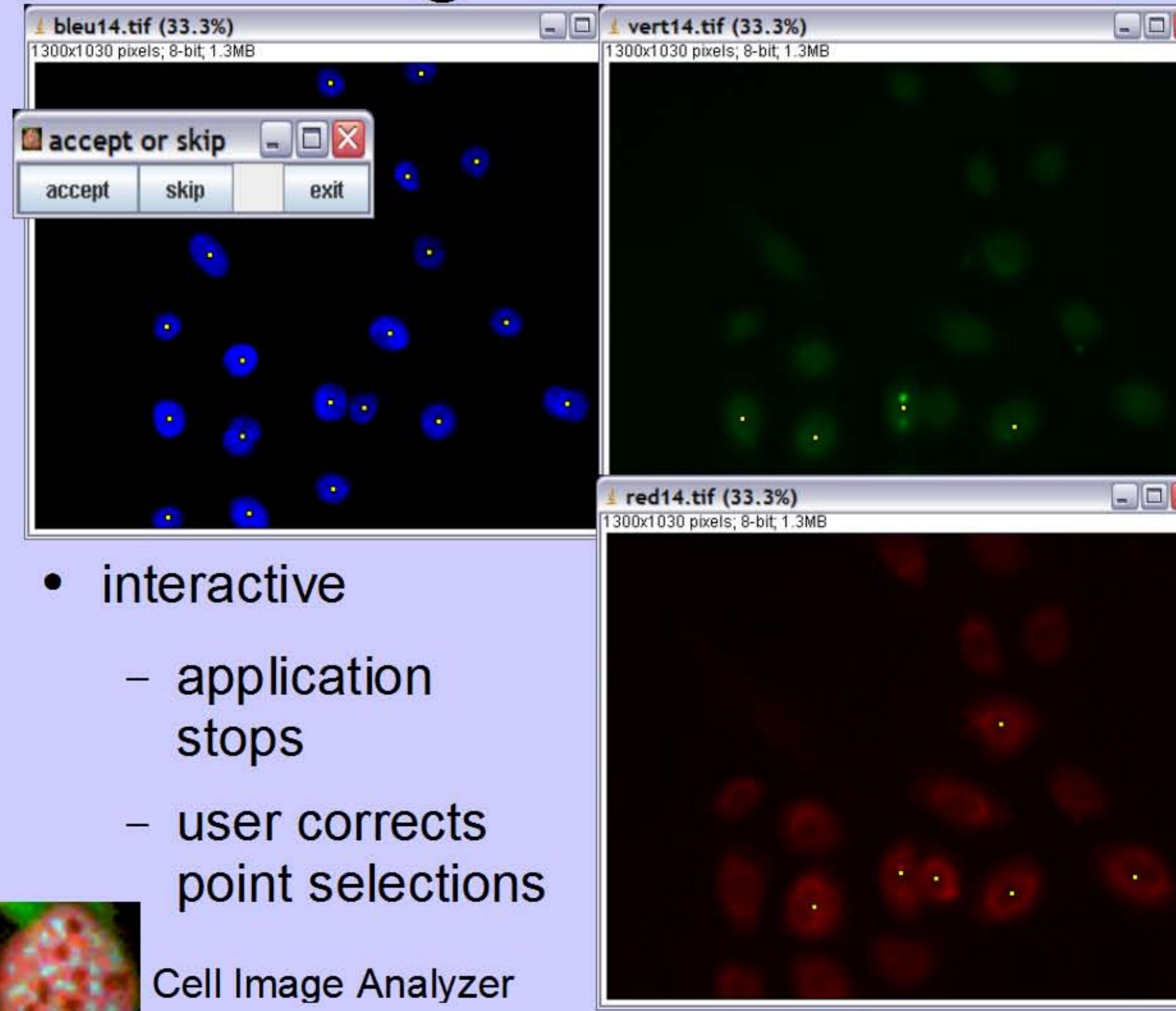
How many cells  
are there?

image	number of objects	folder
25H.tif	34	E:\besnard\
jet1b.tif	495	E:\etienne delepine\

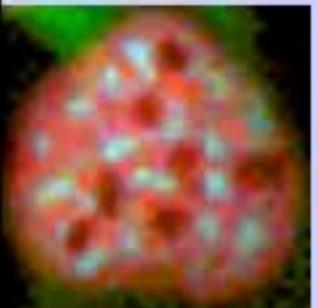
- watershed
- derivative
- local threshold
- full automatic
- interactive



# Counting nuclei



- interactive
  - application stops
  - user corrects point selections



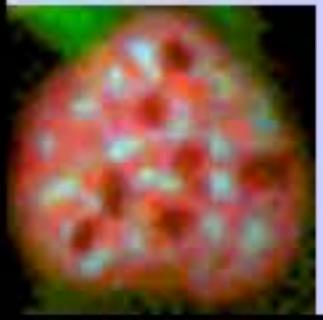
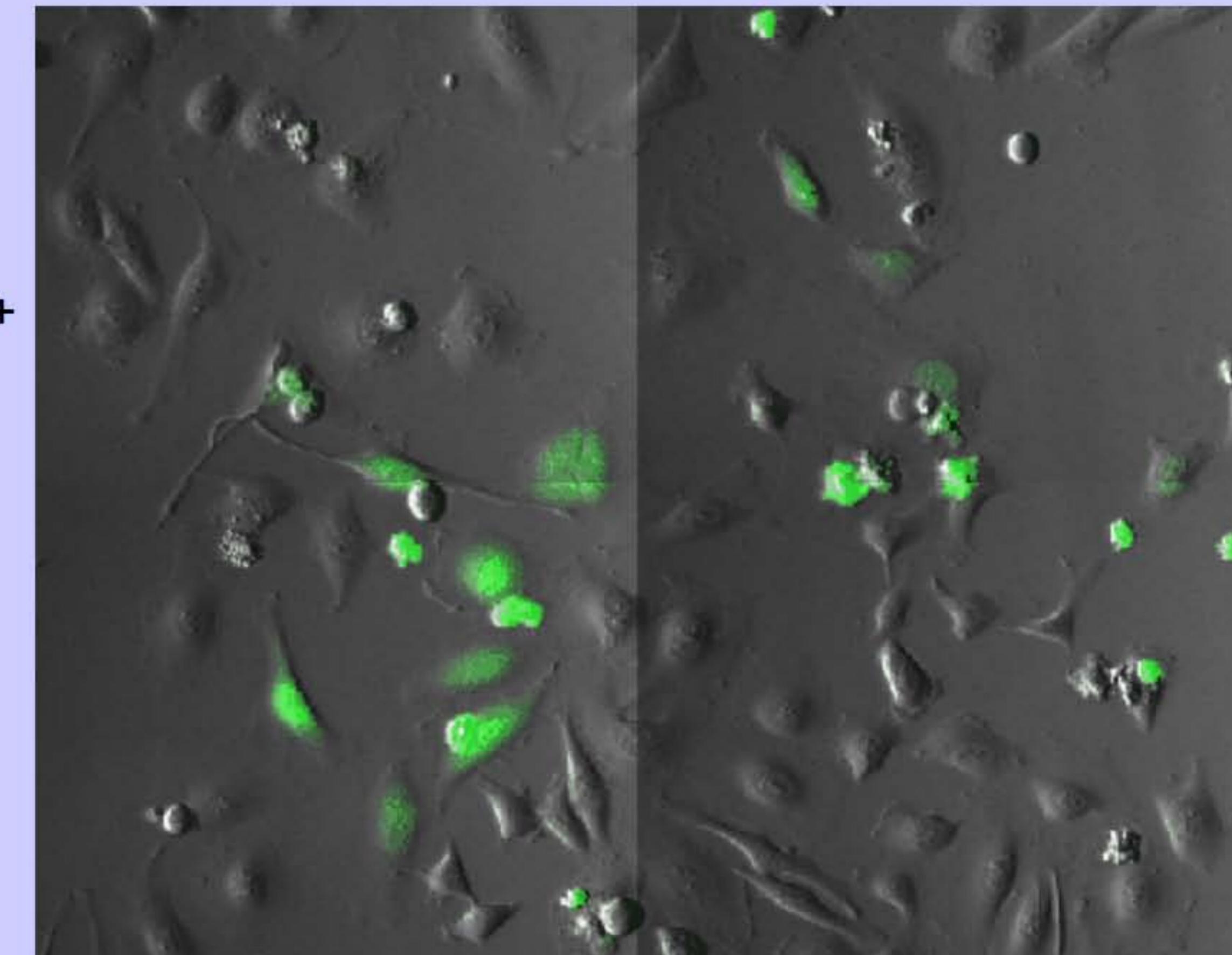
Cell Image Analyzer

The screenshot shows the ImageJ macro editor window titled "count stain combinations". It contains a vertical stack of processing steps:

- ? count stain combinations 0 P
- ? foreach image do 0 P
- ? open image 0 P
- ? find and subtract background 0 P
- ? convert image type 0 P
- ? open image 0 P
- ? convert image type 0 P
- ? open image 0 P
- ? convert image type 0 P
- ? hessian 0 P
- ? get image from hessian 0 P
- ? mean threshold 0 P
- ? find objects 0 P

# Automation of simple tasks

- batch type conversions
- creating compressed movies from large data sets
  - use virtual stack opener + QuickTime Stack Writer plugin
- creating overlay of fluorescence and phase contrast image series
- ...



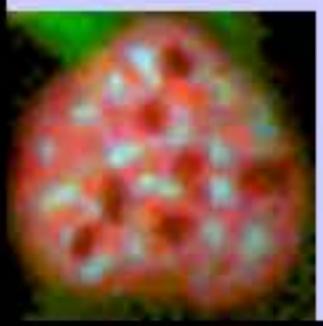
Cell Image Analyzer

volker.baecker@mri.cnrs.fr

# Further projects and projects in work



- measuring growth of plant surface (first version deployed)
- measuring growth of plant roots
- 3d modelling from histological sections
  - mouse
  - palm tree meristem



Cell Image Analyzer

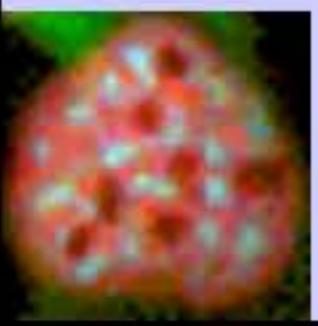
volker.baecker@mri.cnrs.fr

# Conclusions

MRI Cell Image Analyzer

ImageJ + visual scripting

- rapidly
  - create image analysis applications
  - automate image analysis tasks
    - batch applications
    - semi-automatic applications
- interface application developer - scientist
  - easy to use by non computer experts
- the framework helps create new operations at the programming level
- all ImageJ methods can be accessed with the help of proxies
- used at Montpellier RIO Imaging
  - to create image analysis applications on demand
  - in close collaboration with the biologists
- made it possible to provide solutions that could not be obtained with standard image analysis packages
- outlook:
  - allow hierarchical applications (the use of applications in applications)
  - allow to work seamlessly with very big data sets (elaborate the virtual stack concept)



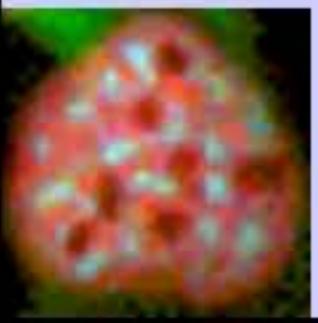


# The last slide

- Thanks to
  - Wayne Rasband
  - all ImageJ plugin and macro authors
  - the ImageJ community
  - The ImageJ conference - organisation
  - Montpellier RIO Imaging
  - the research groups that participated in developing image analysis applications

Thank you, for your attention!

? Questions ?





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