

Introduction to Bioimage Analysis

Micron Advanced Microscopy Course

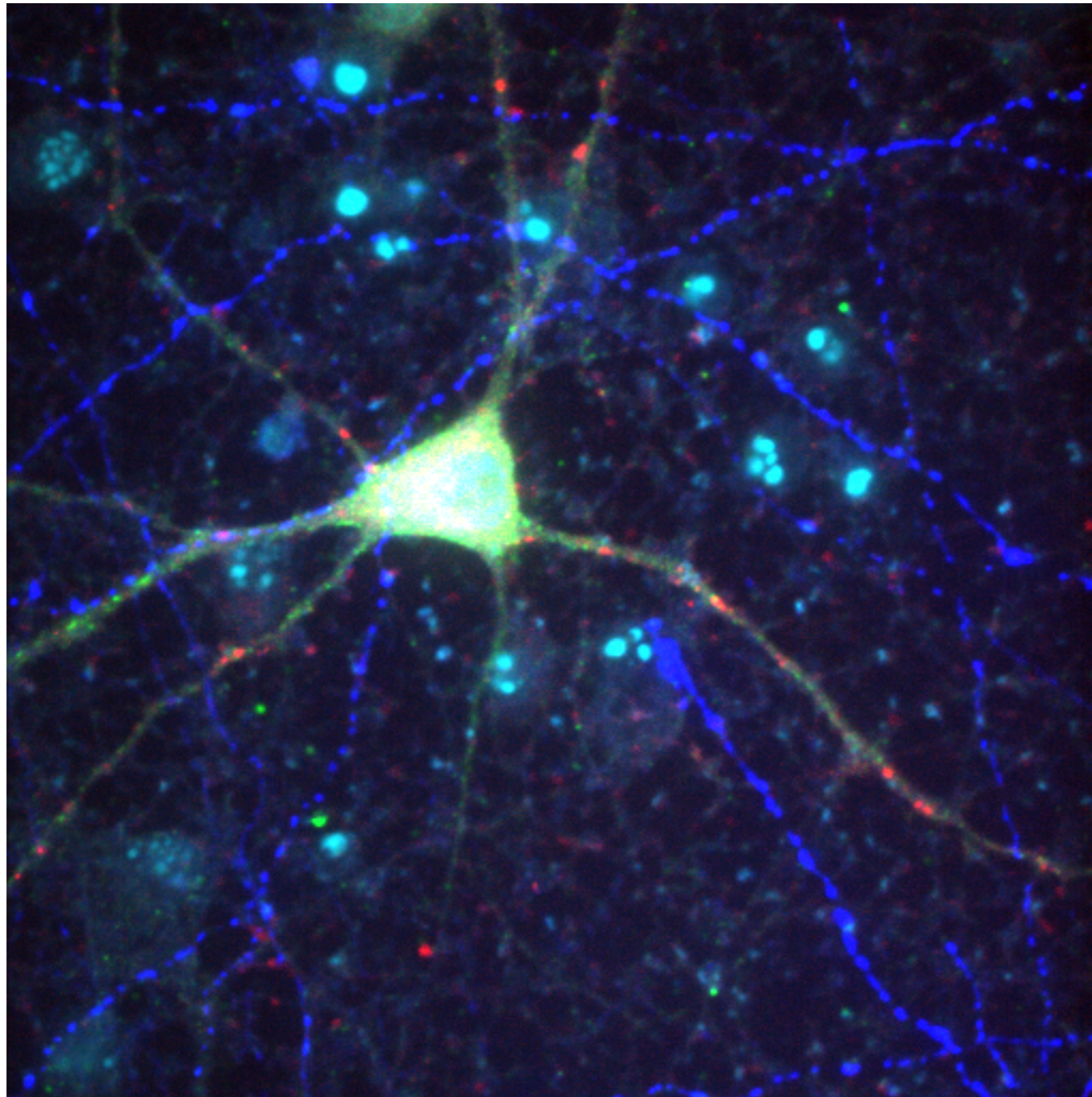
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Molecular Medicine (WIMM)
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University of Oxford, UK.

Ulrike.Schulze@rdm.ox.ac.uk

What is Image Analysis?



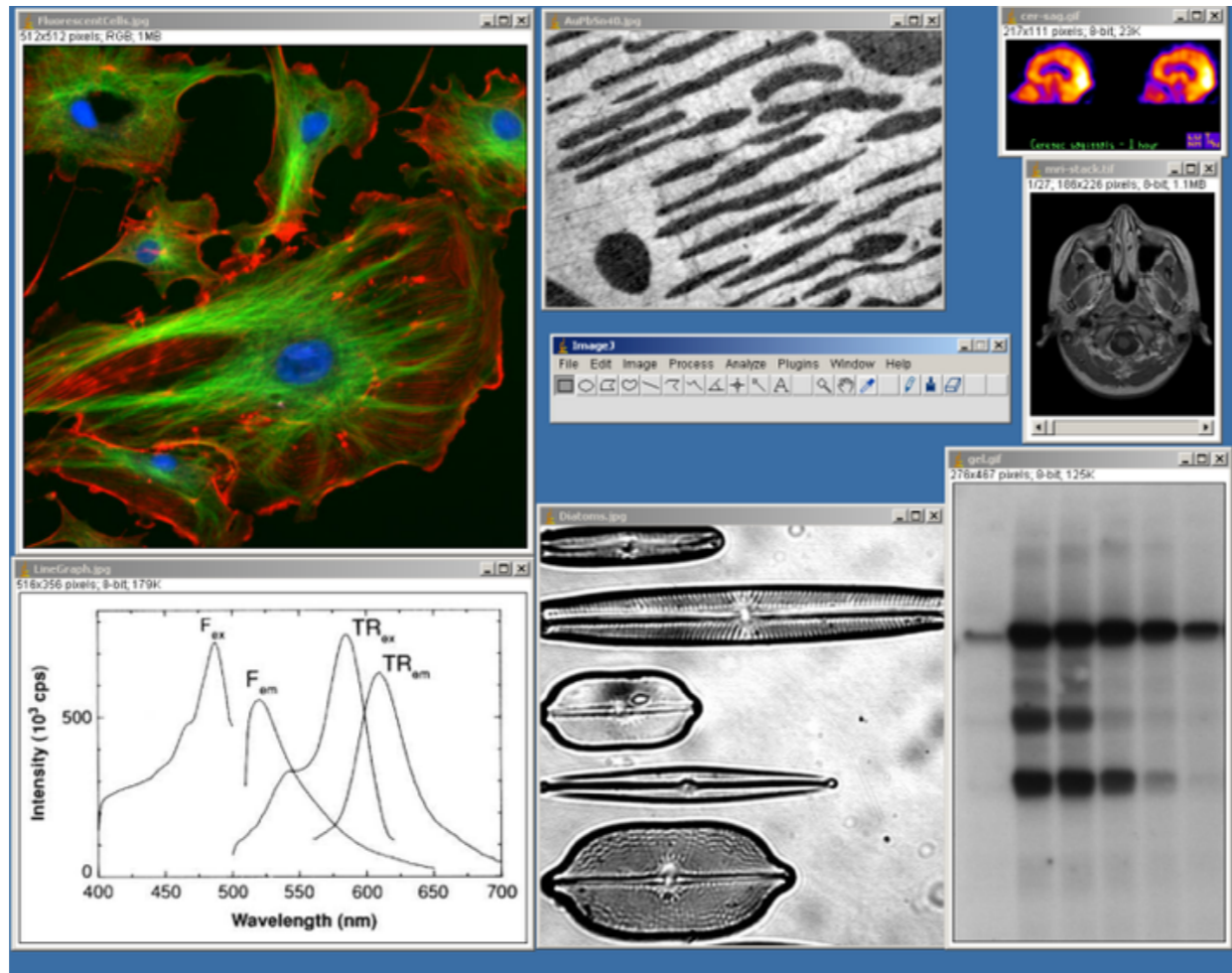
- precise
- unbiased
- reproducible

Available Image processing and Analysis Software

Zen LE software Image-Pro Drishti
Volocity ImageJ Oko-Vision
CellProfiler Clemex Vision PE
Fiji IN Cell Investigator Nikon Z-C1
Omero MetaMorph Image Surfer
Matlab Photoshop ImageTool Imaris
Mathematica MCID ImageTrak
Icy Image Metrology MIATool
SimpleWare ParaView Reconstruct
SoftWoRx FLIMfit Leica LAS Sinema
AutoQuant MeVisLab VIAS Reconstruct
BioImage XD Voxx2

medicine
microscopy
remote sensing
astronomy
materials science
machine vision
security
robotics
geology
optical character recognition
assay micro-plate reading
metallography
defence
filtering

General analysis software: Fiji/ImageJ



- Originally created by Wayne Rasband at the NIH in 1997 as ImageJ.
- Free and easy to get running on all systems.


























Source: Source: <http://fiji.sc/Fiji>

Installation of FIJI

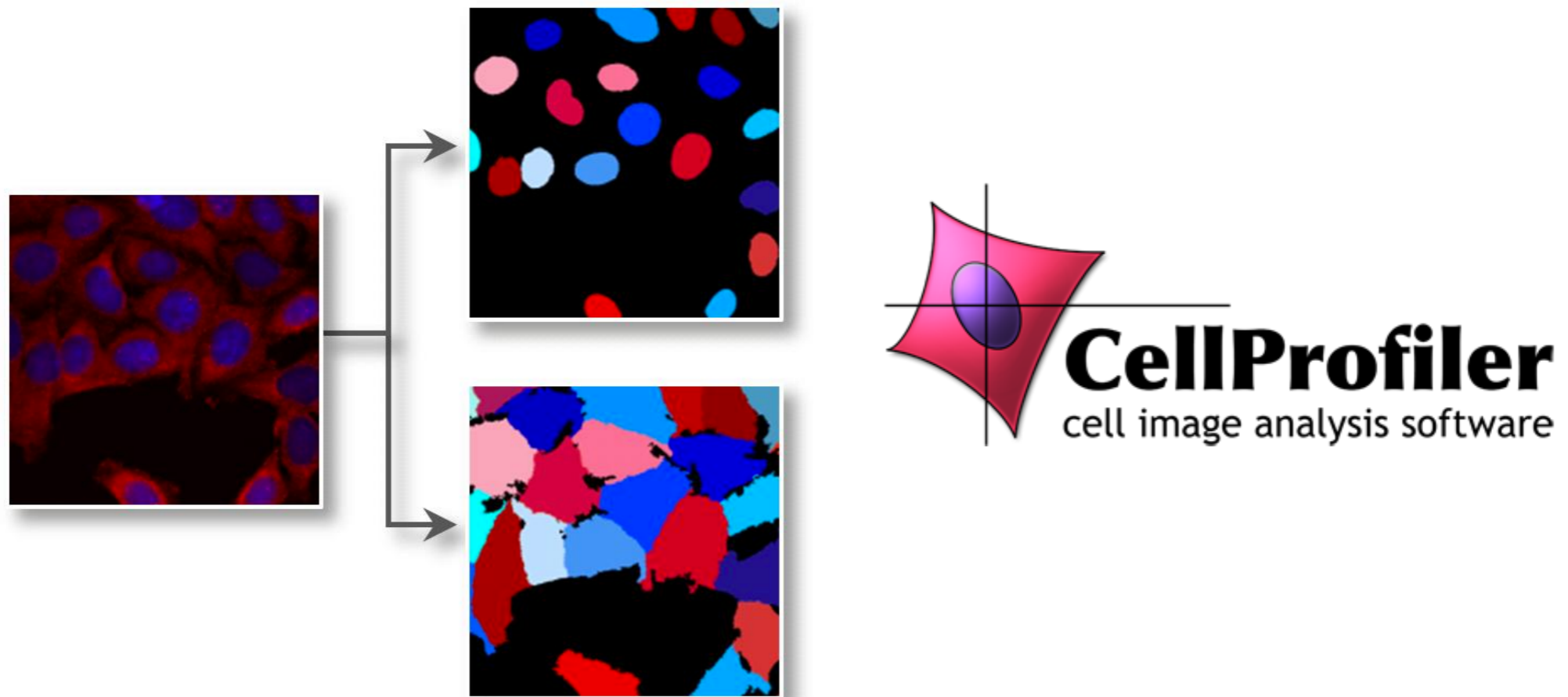
Get it from: <https://imagej.net/Fiji/Downloads>

- Doesn't need installation - just unzip/uncompress and run.
- Don't save it in "Program Files"!
- Updated regularly
- Use lifeline versions if needed to avoid updating issues



Date	Downloads						Description
	64-bit	32-bit	macOS	64-bit	32-bit	no-JRE	
2017 May 30							The final version of Fiji using Java 6, for all platforms.
2015 December 22							Just prior to starting the transition to Java 8 .
2014 November 25							Just prior to a big update to facilitate reproducible builds .
2014 June 02							Just prior to some big changes to ImageJ2 under the hood .
2013 July 15							Just prior to extensive changes reconciling Fiji with ImageJ2 .

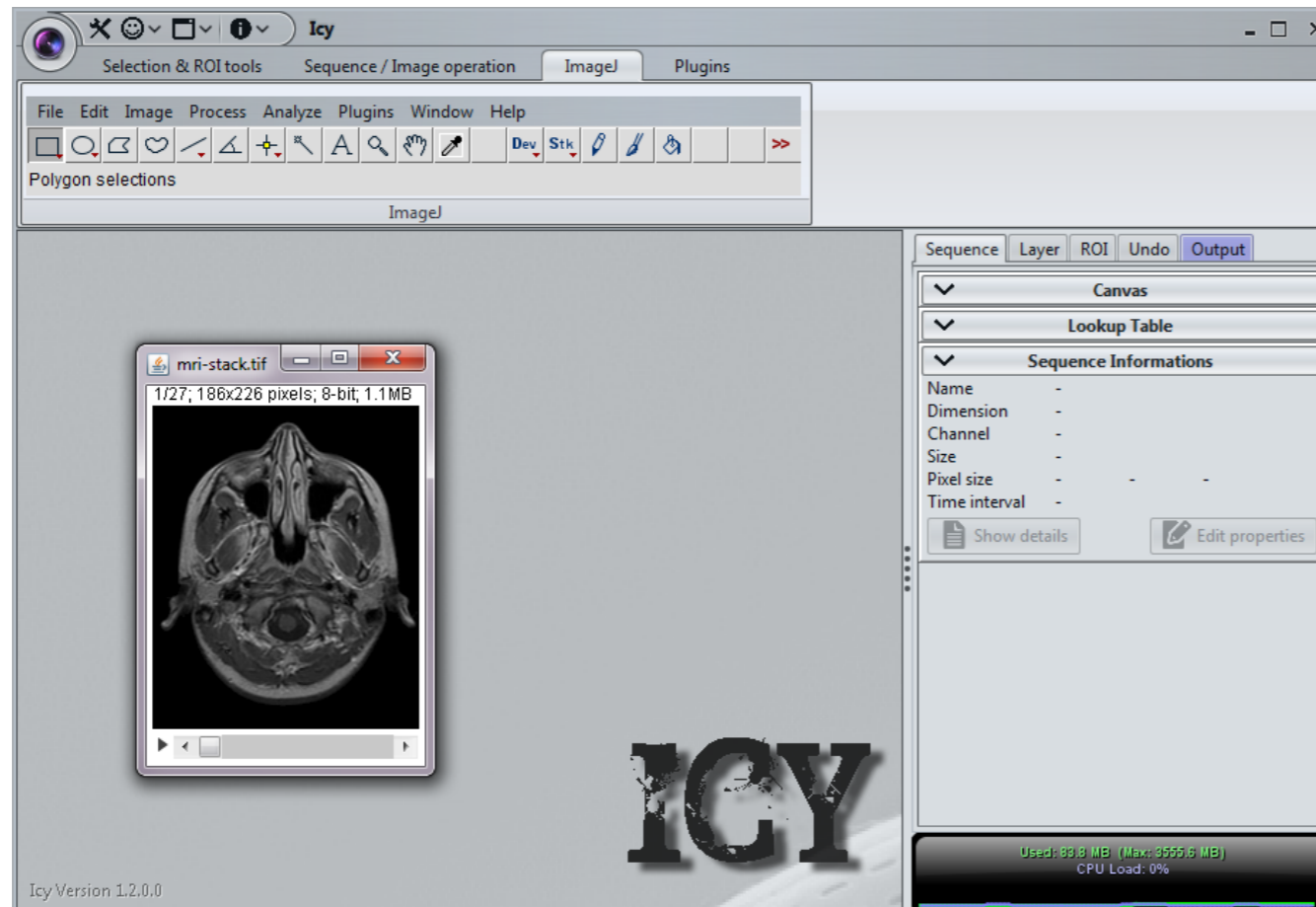
General analysis software: Cell Profiler



- CellProfiler is free open-source software designed to enable biologists without training in computer vision or programming to quantitatively measure phenotypes from thousands of images automatically.

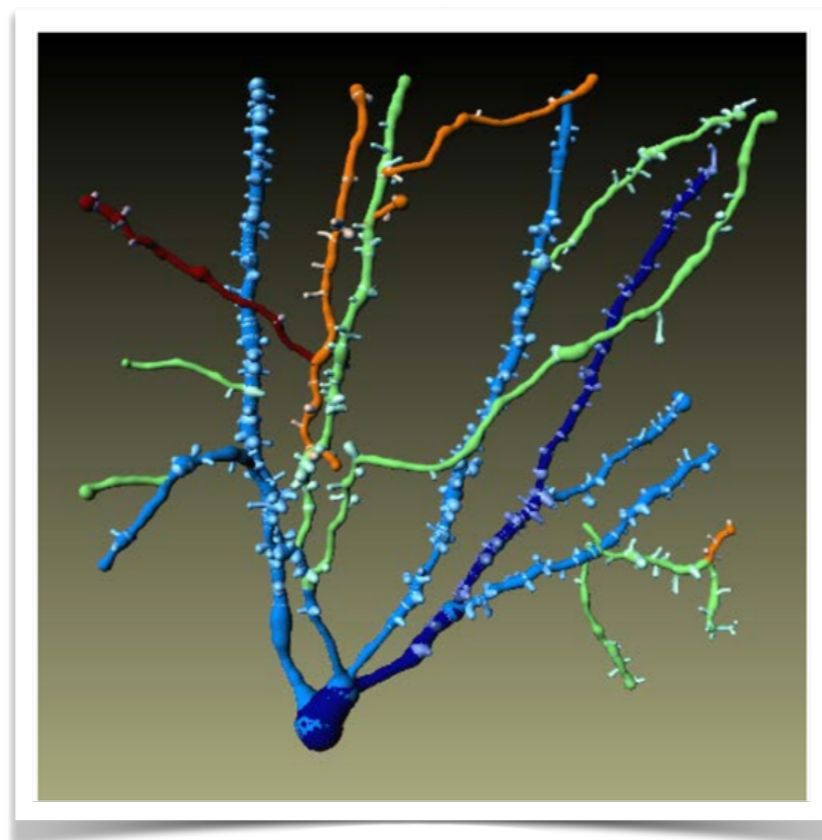
Source: <http://www.cellprofiler.org/> started by Anne E. Carpenter and Thouis Jones

General analysis software: Icy



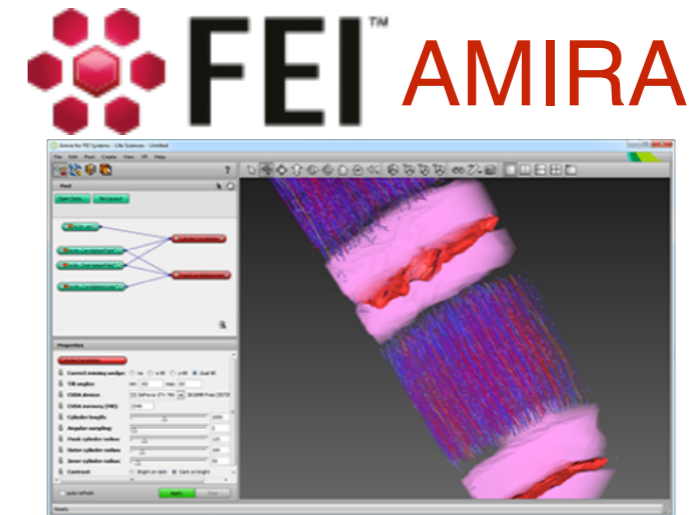
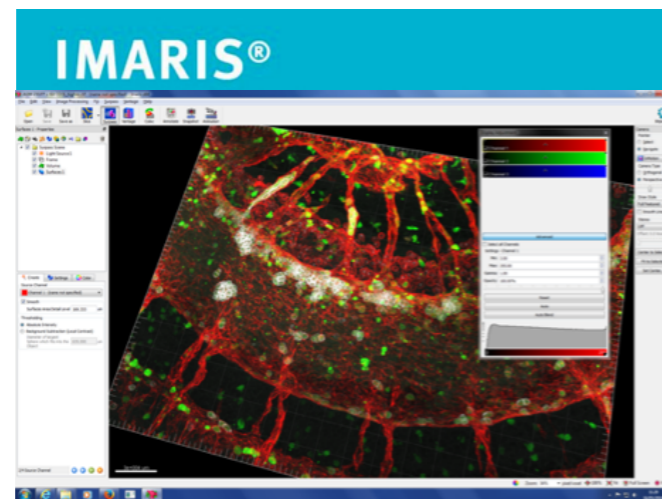
- Icy has been created by the Quantitative Image Analysis Unit at Institut Pasteur. Free and easy to get running on all systems.

Source: <http://www.bioimageanalysis.org/>



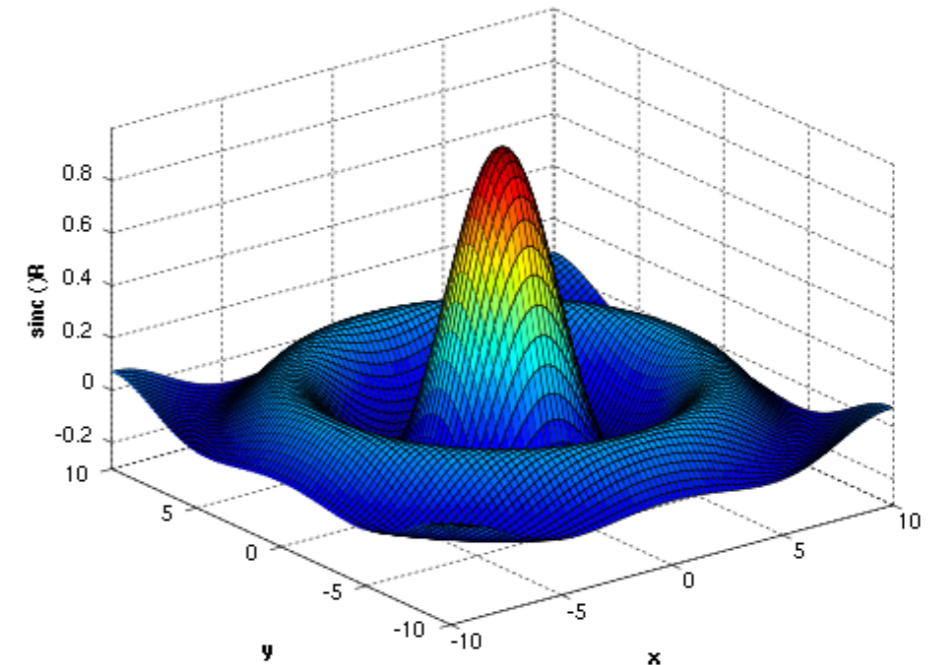
3D
datasets

3D Software



- Volume Visualisation
- Automatic and manual identification of objects in 3D
- Tracking and Colocalisation in 3D
- generally expensive

Matlab and Python



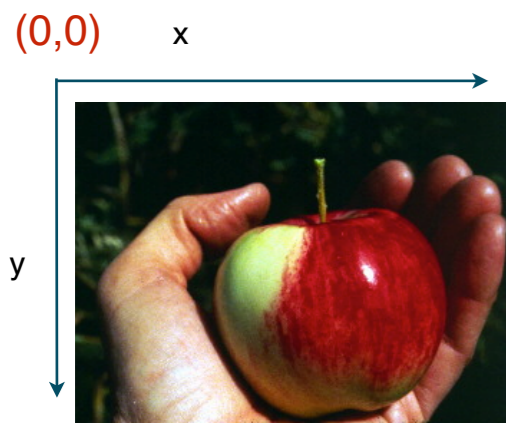
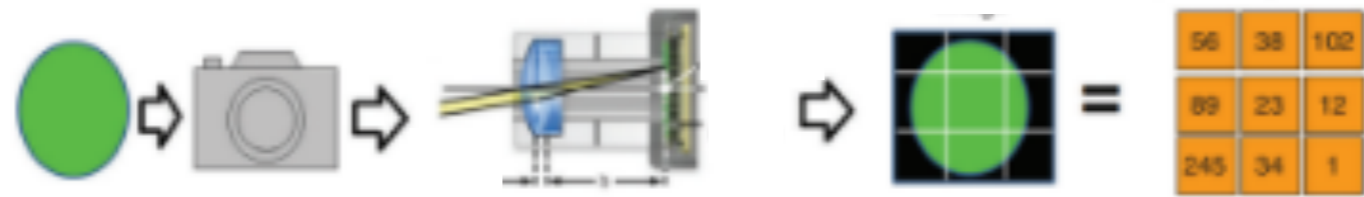
Matlab is popular tool for technical computing. Integrated programming environment. Images are imported as arrays of numbers.

Python is free and very versatile scripting language growing in popularity.

Matlab and python has many tools used for segmentation and analysis of data.

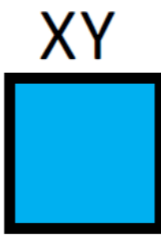
Both include visualisation tools for end-2-end analysis.

Pixel size

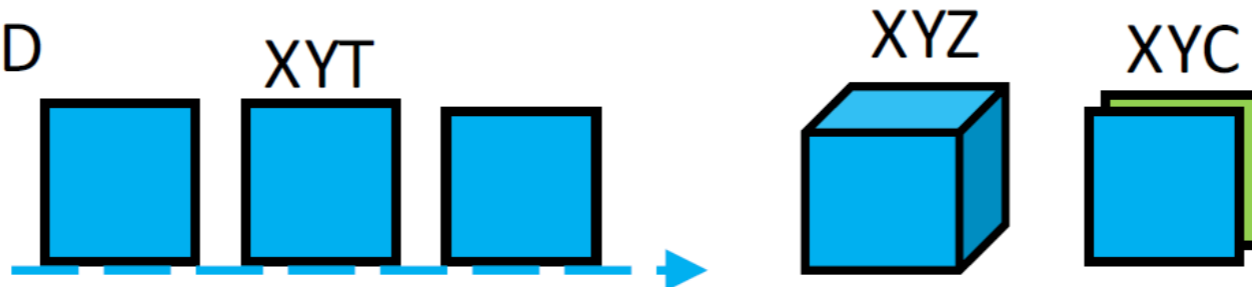


Multiple Dimensions

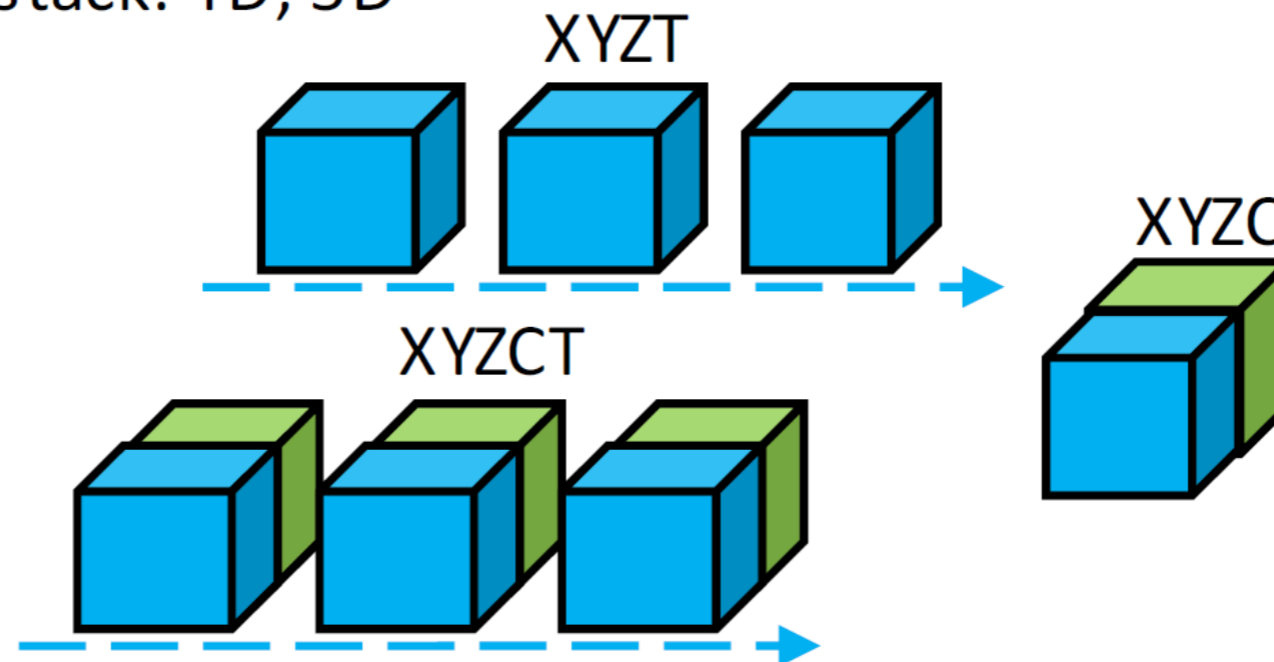
- Image: 2D



- Stack: 3D



- Hyperstack: 4D, 5D



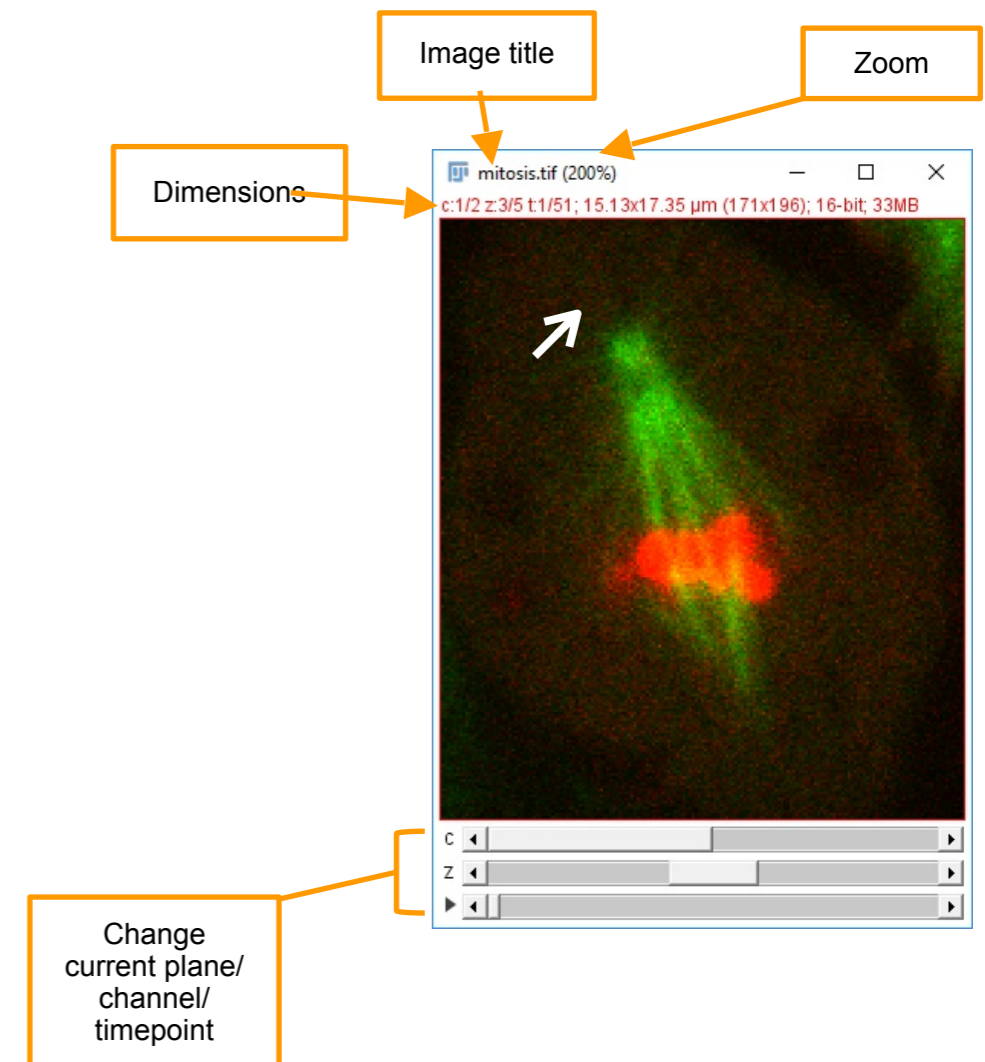


Opening an Image with FIJI



How to interpret an image in ImageJ

- Image Title
 - Includes extension of the file
- Image zoom
- Dimensions and other info
 - Number of channels (c); number of Z planes (z); number of Timepoints (t); size (scaled);
 - size (pixels, x & y); Bit depth; image size
- Dimension sliders



Accessing metadata with FIJI



The screenshot displays the Fiji software interface with several windows open. The main window shows the toolbar and a search bar. A window titled "OME Metadata - AT1_Brd4_Airyscan_i1-Airyscan Processing-07.czi" shows XML data. A "Bio-Formats Import Options" dialog is open, with the "Metadata viewing" section circled in red. This section includes checkboxes for "Display metadata" and "Display OME-XML metadata", both of which are checked. Other sections include "Stack viewing", "Dataset organization", "Memory management", and "Split into separate windows". An "Information" window is also open, displaying the text: "Display metadata - Reads metadata that may be contained within the file format and displays it. You can save it as a text file or copy it from the File and Edit menus specific to the 'Original Metadata' window. Readability depends upon the manner in which metadata is formatted in the data source. The metadata can also be displayed by pressing 'i' (Image > Show Info) when the imported image is active." A "Original Metadata" window is open, showing a table of key-value pairs.

Key	Value
BitsPerPixel	16
DimensionOrder	XYCZT
IsInterleaved	false
IsRGB	false
LittleEndian	true
PixelType	uint16
Series 0 Name	AT1_Brd4_Airyscan_i1 #1
SizeC	4
SizeT	1
SizeX	1572
SizeY	1572
SizeZ	77
Appliance Data ShuttleAndFindData Calibration Marker FocusPosition #1	0
Appliance Data ShuttleAndFindData Calibration Marker FocusPosition #2	0
Appliance Data ShuttleAndFindData Calibration Marker FocusPosition #3	0
Appliance Data ShuttleAndFindData Calibration Marker Id #1	Marker:1
Appliance Data ShuttleAndFindData Calibration Marker Id #2	Marker:2
Appliance Data ShuttleAndFindData Calibration Marker Id #3	Marker:3
Appliance Data ShuttleAndFindData Calibration Marker StageXPosition #1	0
Appliance Data ShuttleAndFindData Calibration Marker StageXPosition #2	0
Appliance Data ShuttleAndFindData Calibration Marker StageXPosition #3	0
Appliance Data ShuttleAndFindData Calibration Marker StageYPosition #1	0
Appliance Data ShuttleAndFindData Calibration Marker StageYPosition #2	0
Appliance Data ShuttleAndFindData Calibration Marker StageYPosition #3	0
Appliance Data ShuttleAndFindData Calibration MicroscopeType #1	LM

Metadata can be found when you import images to Fiji.

Metadata can be found through the image-> show info option also.

Image File Formats

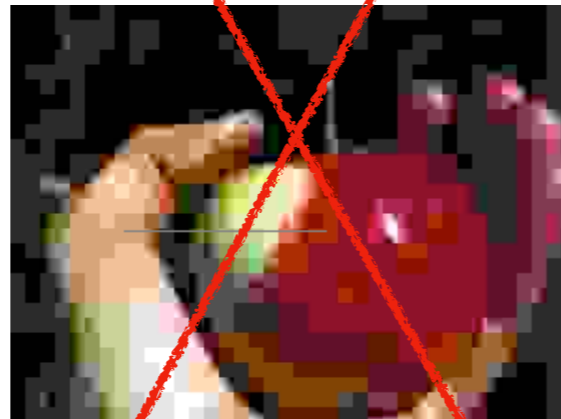
Lossless compression:

TIFF,
Raw



~~Lossy - compression:~~

~~JPEG, JPEG 2000,
TIFF, BMP, PNG,
Movie formats~~



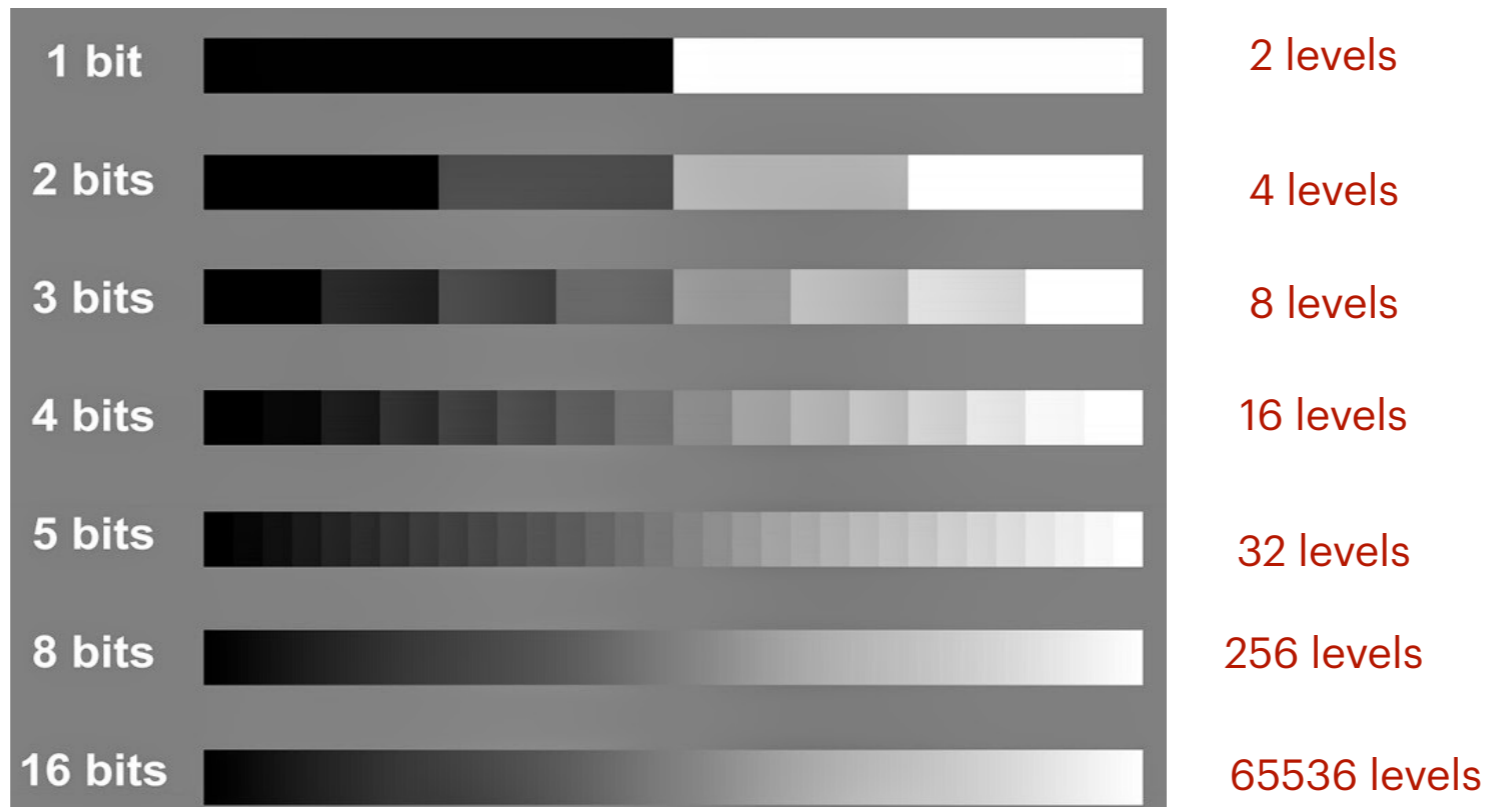
Proprietary microscopy files:

Format	Extensions
3i SlideBook	.sld
Andor Bio-Imaging Division (ABD) TIFF	.tif
AIM	.aim
Alicona 3D	.al3d
Amersham Biosciences Gel	.gel
Amira Mesh	.am, .amiramesh, .grey, .hx, .labels
Amnis FlowSight	.cif
Analyze 7.5	.img, .hdr
Andor SIF	.sif
Animated PNG	.png
Aperio AFI	.afi, .svs
Aperio SVS TIFF	.svs
Applied Precision CellWorX	.htd, .pnl
AVI (Audio Video Interleave)	.avi
Axon Raw Format	.arf
BD Pathway	.exp, .tif
Becker & Hickl SPC FIFO	.spc
Becker & Hickl SPCImage	.sdt
Bio-Rad Gel	.1sc
Bio-Rad PIC	.pic, .raw, .xml
Bio-Rad SCN	.scn
Bitplane Imaris	.ims
Bruker MRI	
Burleigh	.img
Canon DNG	.cr2, .crw
CellH5	.ch5
Cellomics	.c01, .dib
cellSens VSI	.vsi
CellVoyager	.xml, .tif
DeltaVision	.dv, .r3d
DICOM	.dcm, .dicom
ECAT7	.v

Grayscale

8-bit, 16-bit, 32 bit

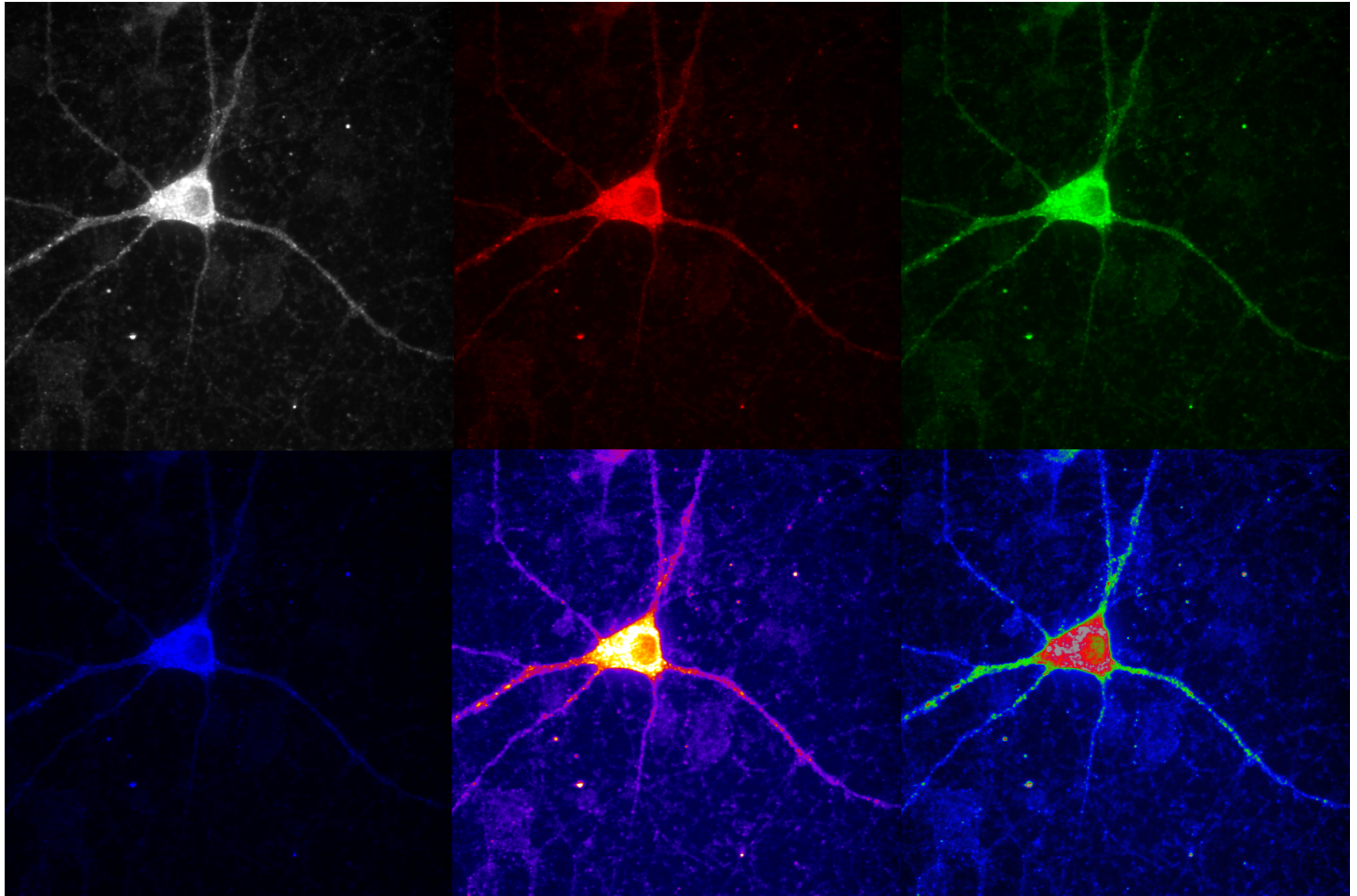
Attention when
converting between
different bit-depth!



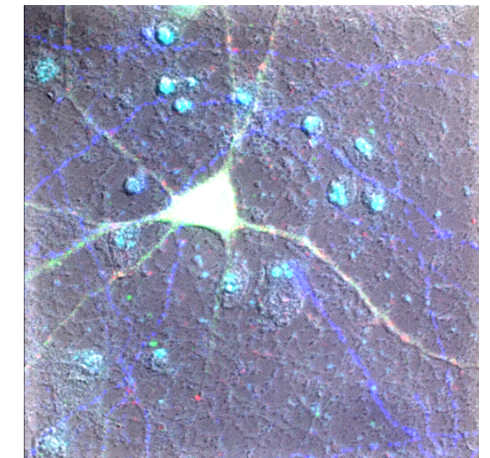
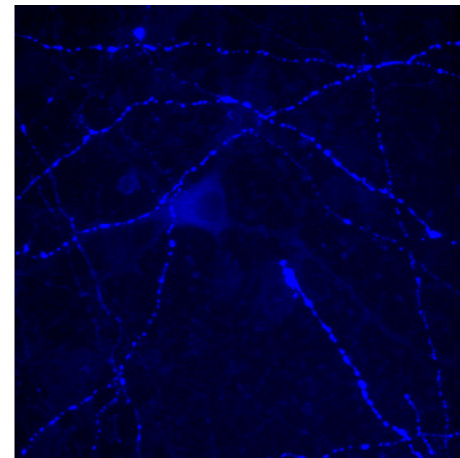
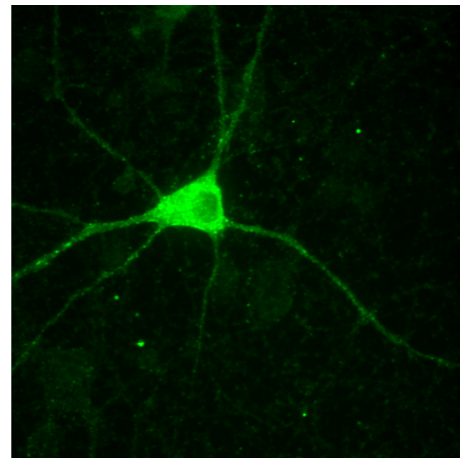
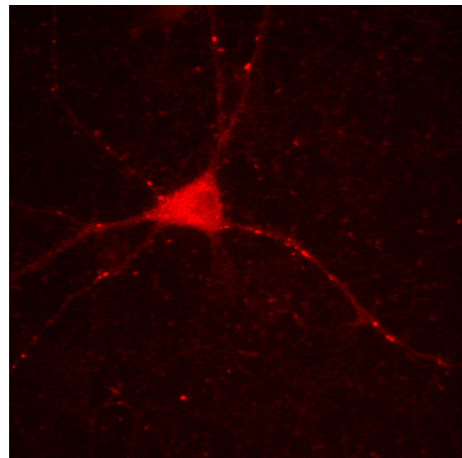
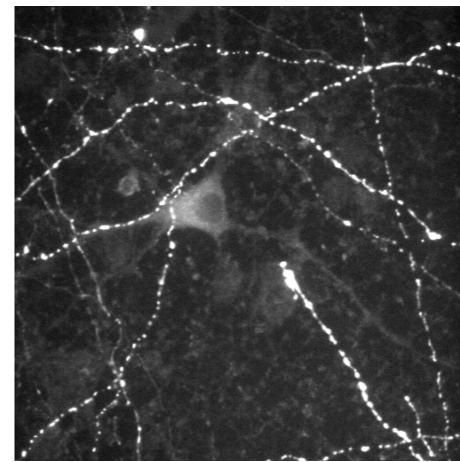
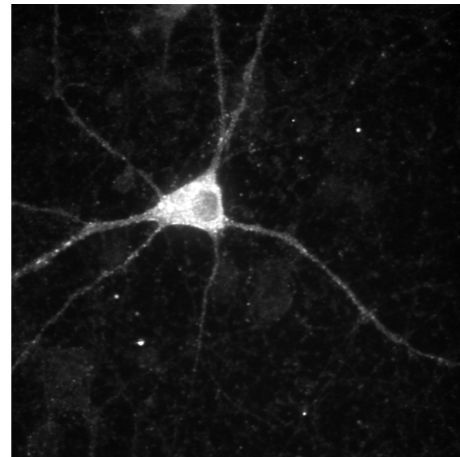
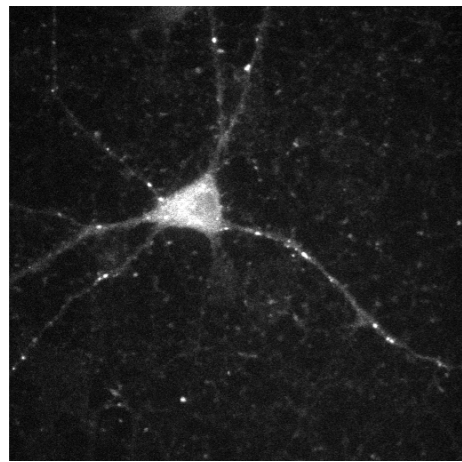
32-bit images:

- Can be positive/negative
- represent floating point numbers
- Useful for image maths

Look up tables

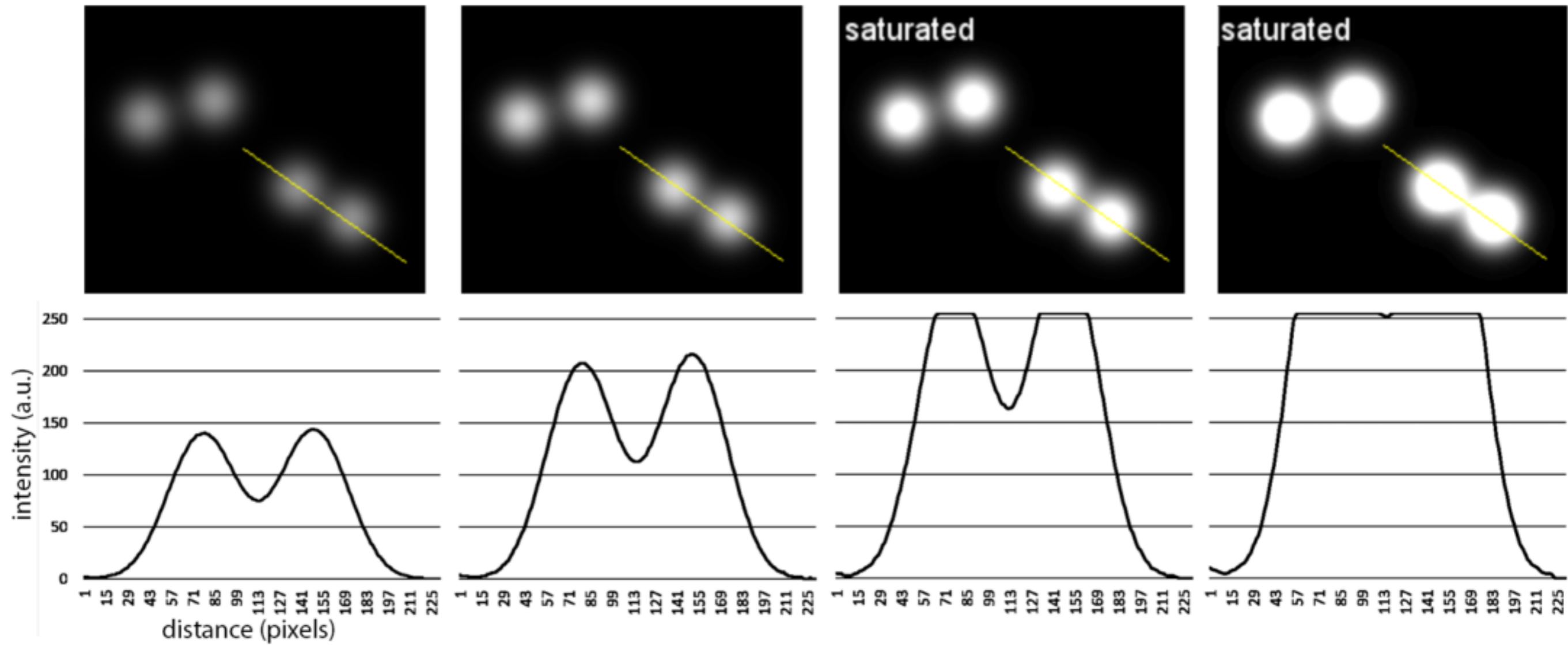


RGB Images

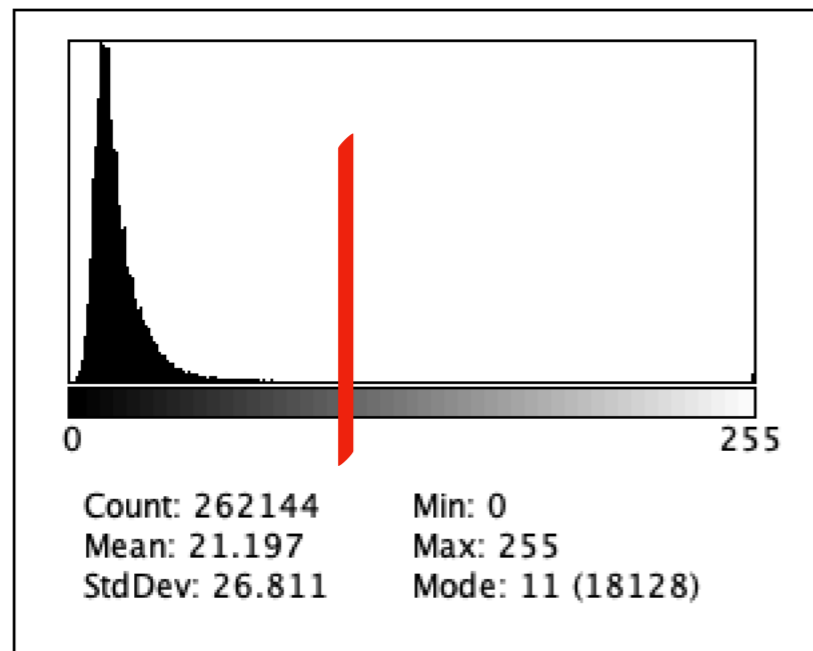
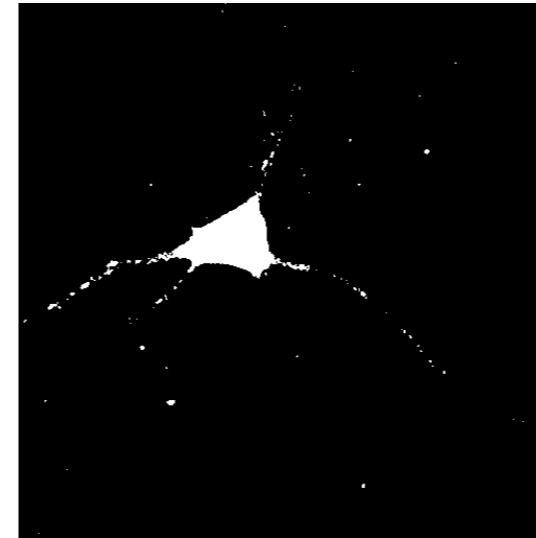
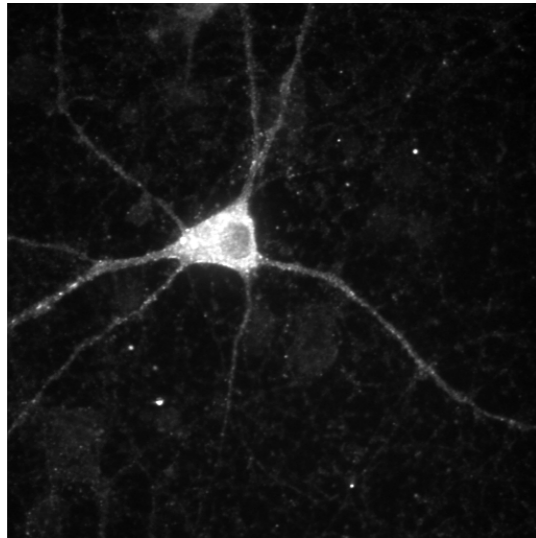


					165	187	209	58	7	
					14	125	233	201	98	159
253	144	120	251	41	147	204				
67	100	32	241	23	165	30				
209	118	124	27	59	201	79				
210	236	105	169	19	218	156				
35	178	199	197	4	14	218				
115	104	34	111	19	196					
32	69	231	203	74						

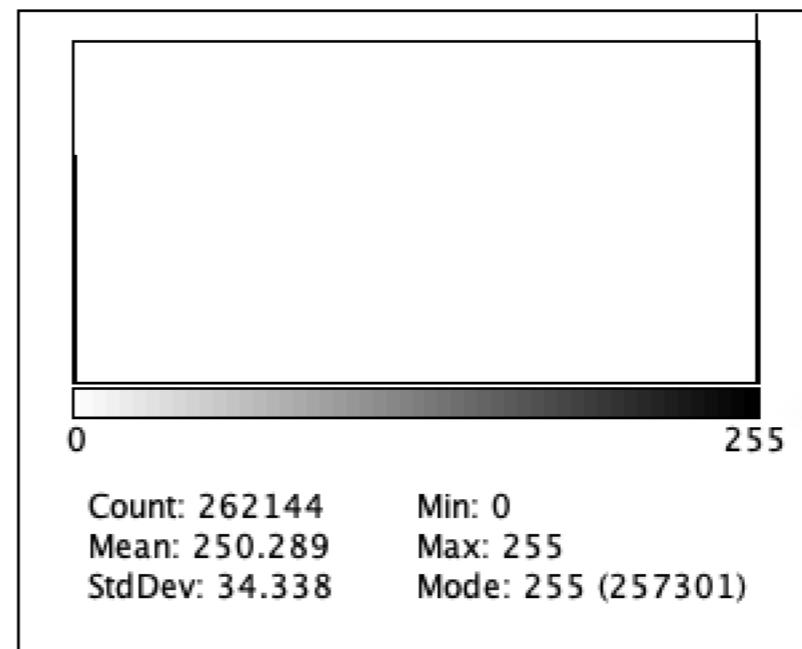
Dead Pixels and Saturated Pixels



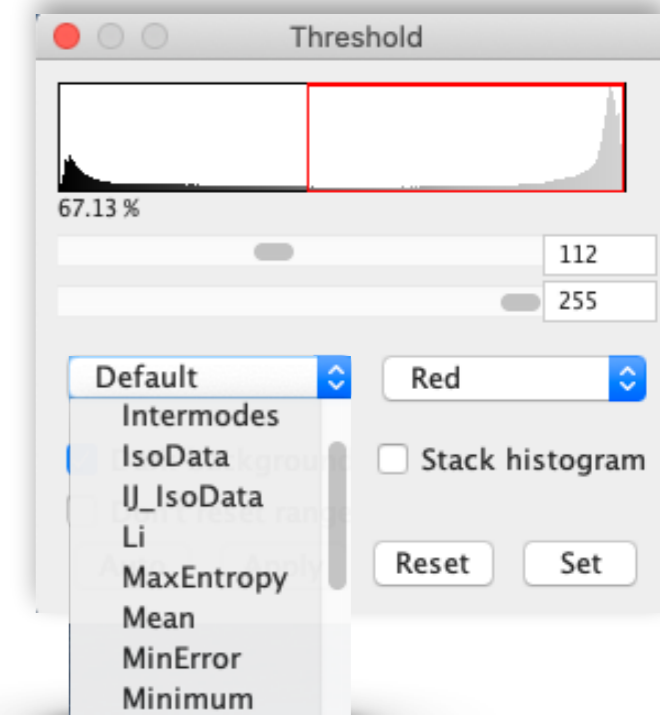
Segmentation - thresholding



List Copy Log Live 50/400



List Copy Log Live



Make Binary
Convert to Mask

Erode
Dilate
Open
Close-

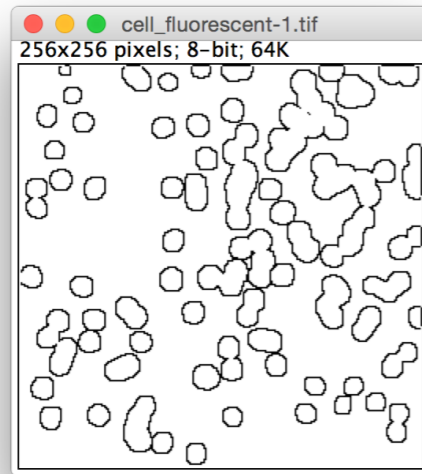
Outline
Fill Holes
Skeletonize

Distance Map
Ultimate Points
Watershed
Voronoi

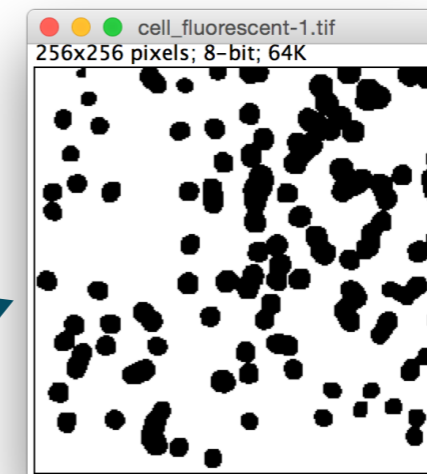
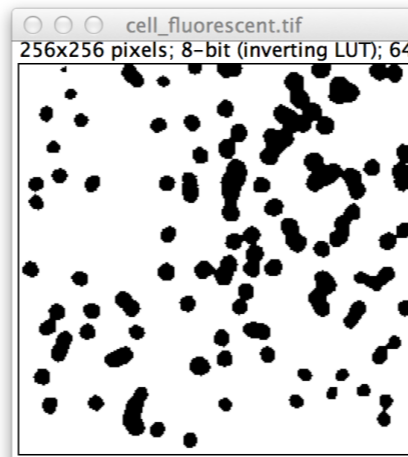
Options...

Morphological operators

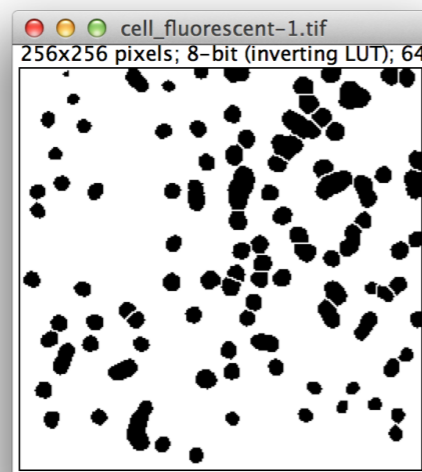
Discrete morphological operators



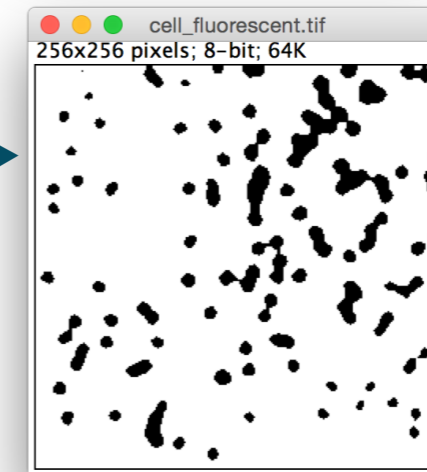
Outline: Find outline



Dilation: Enlarge blobs

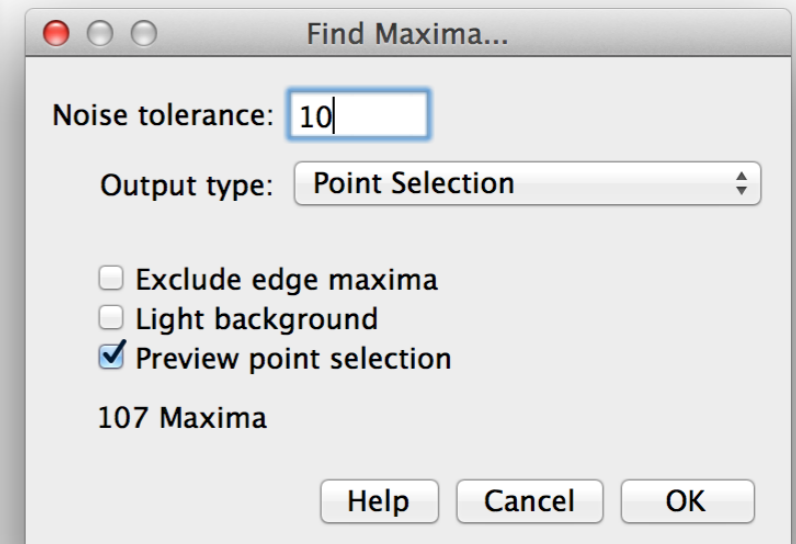
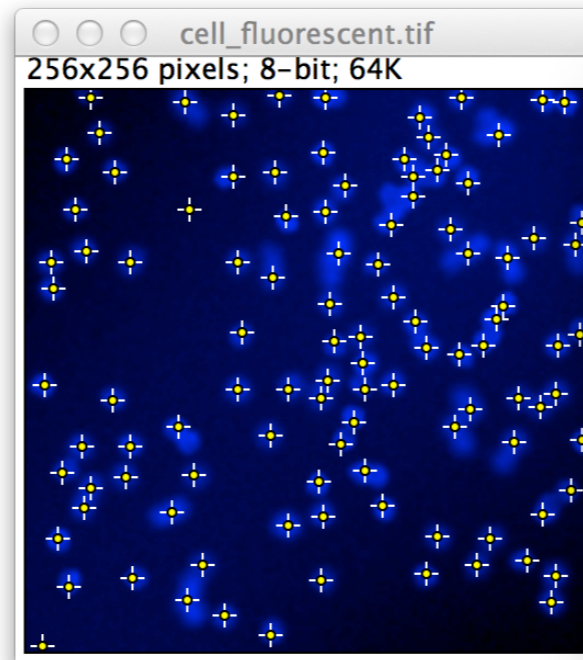
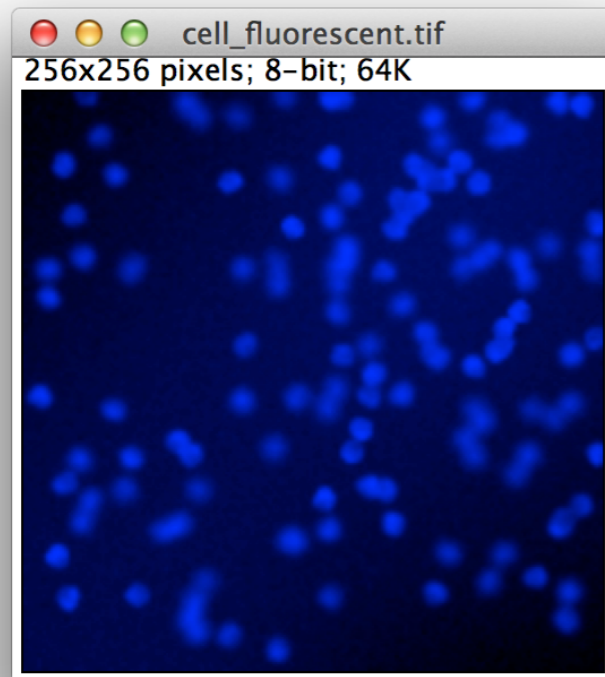


Watershed: Splits blobs

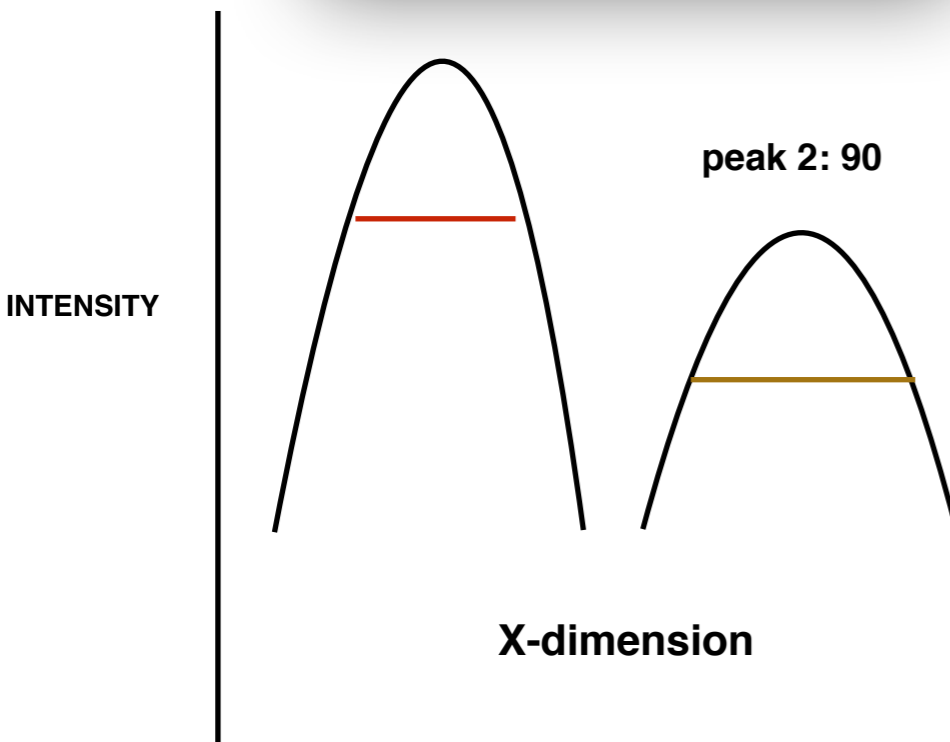


Erosion: Shrink blobs

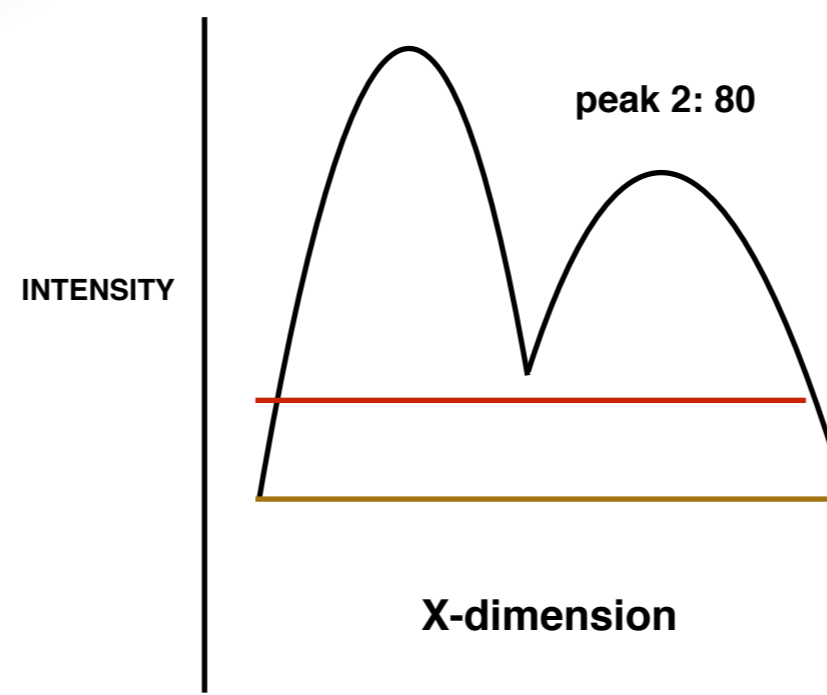
2d peak finding: Process -> Find Maxima



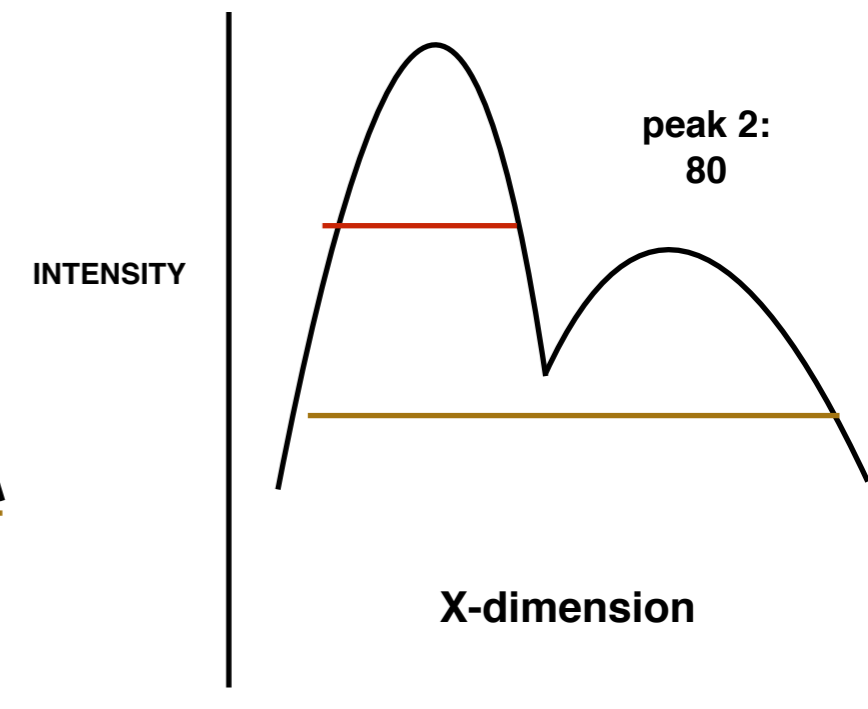
peak 1, intensity=100



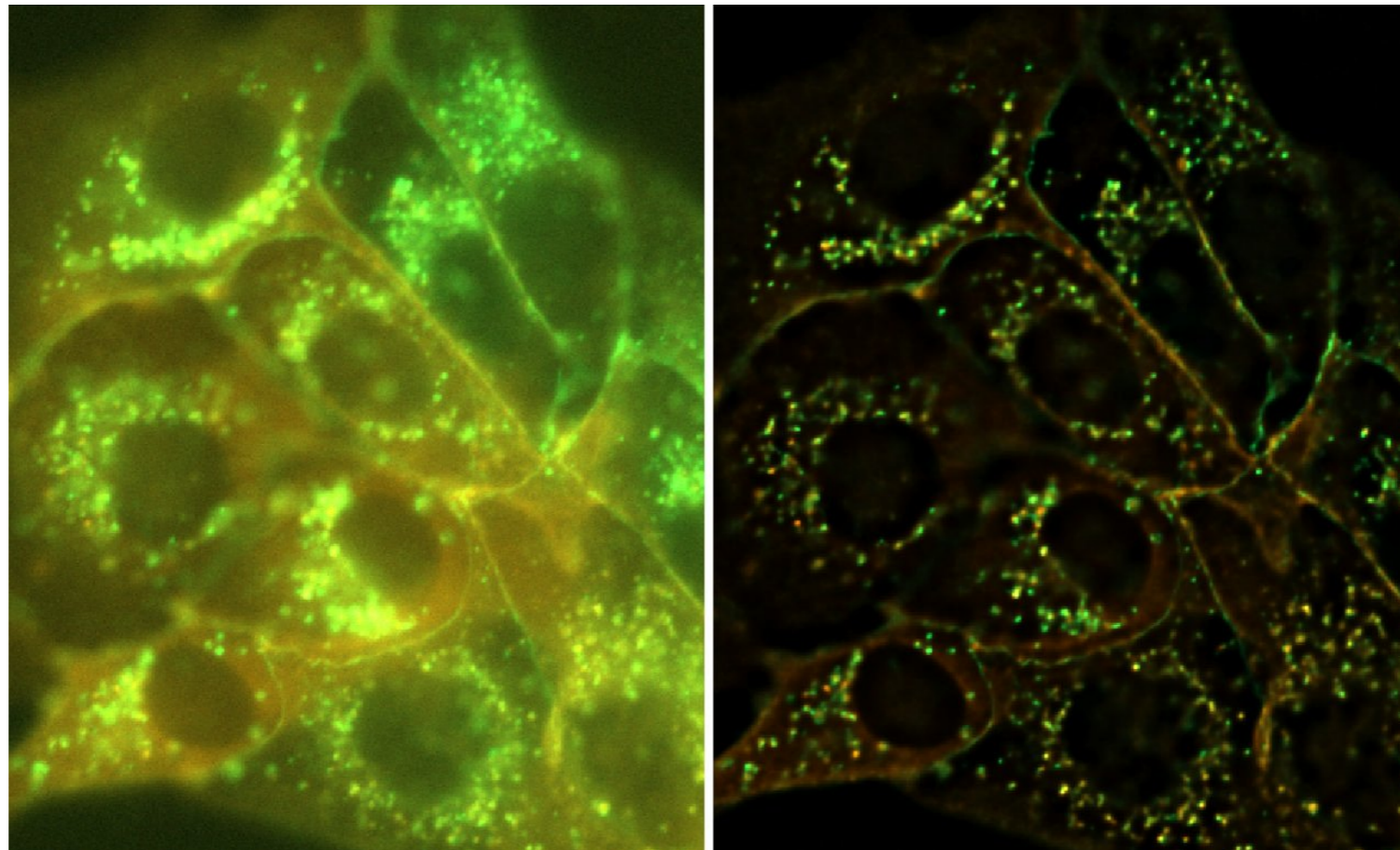
peak 1: 100

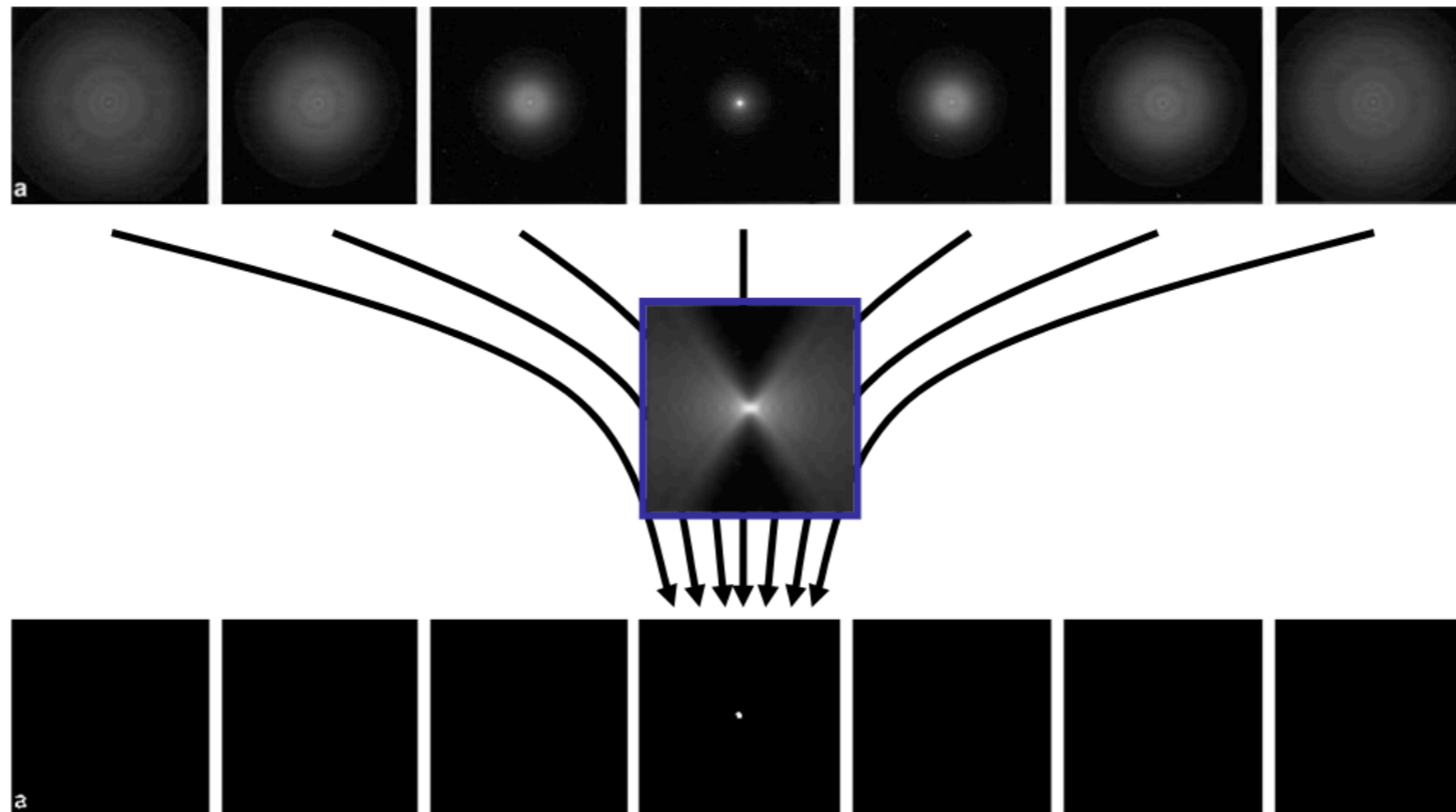


peak 1: 100



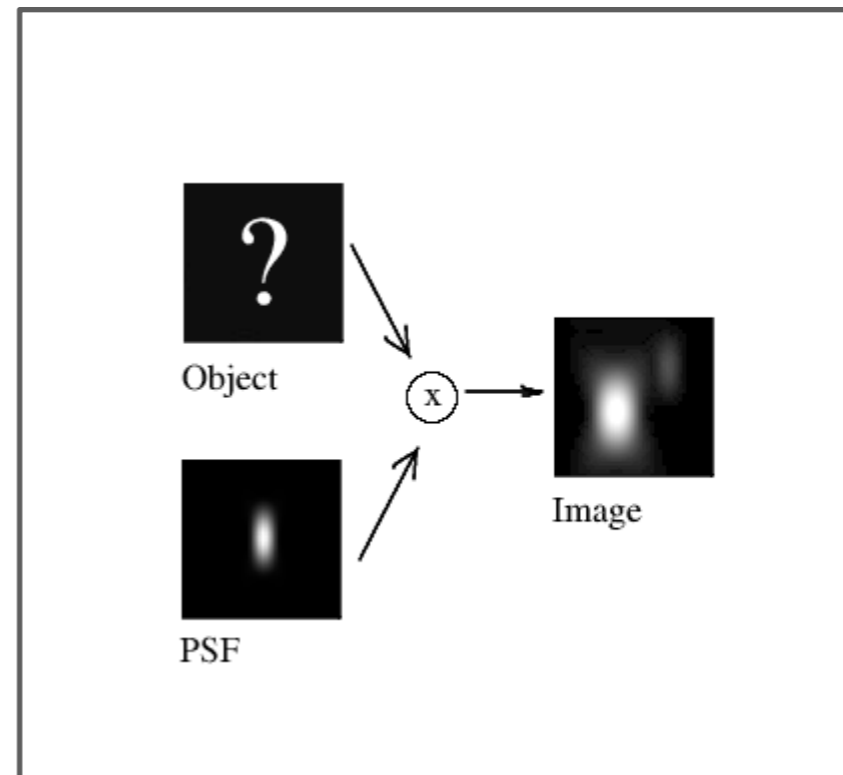
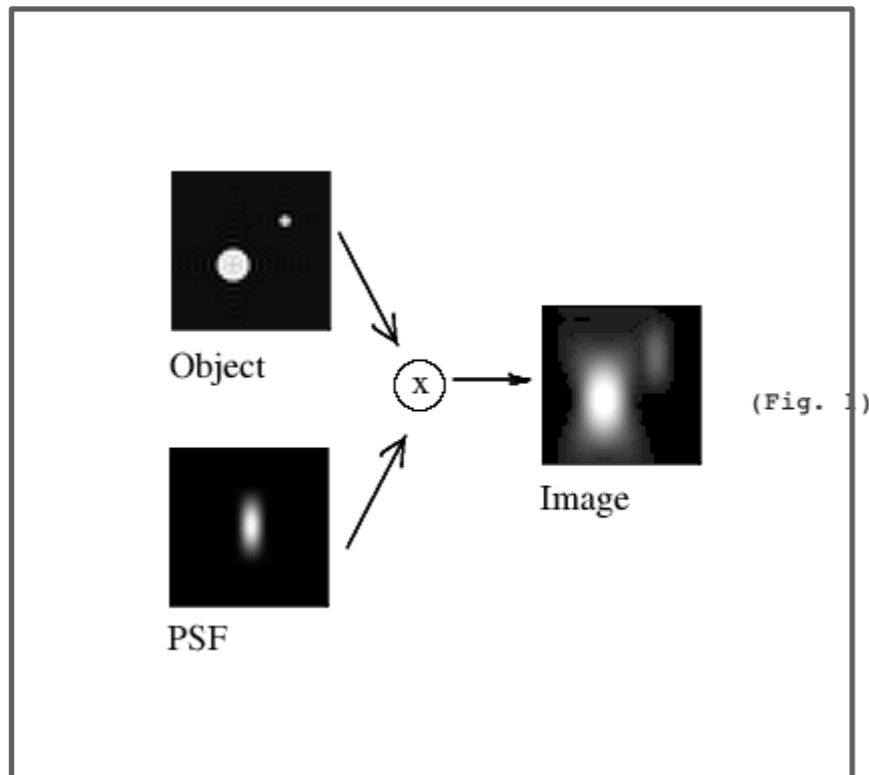
Deconvolution





Out-of-focus information is moved back to its estimated origin

Deconvolution



Deconvolution software

Deconvolution

- Image restoration
- Volume Visualisation
- Some analysis

Software is Expensive.

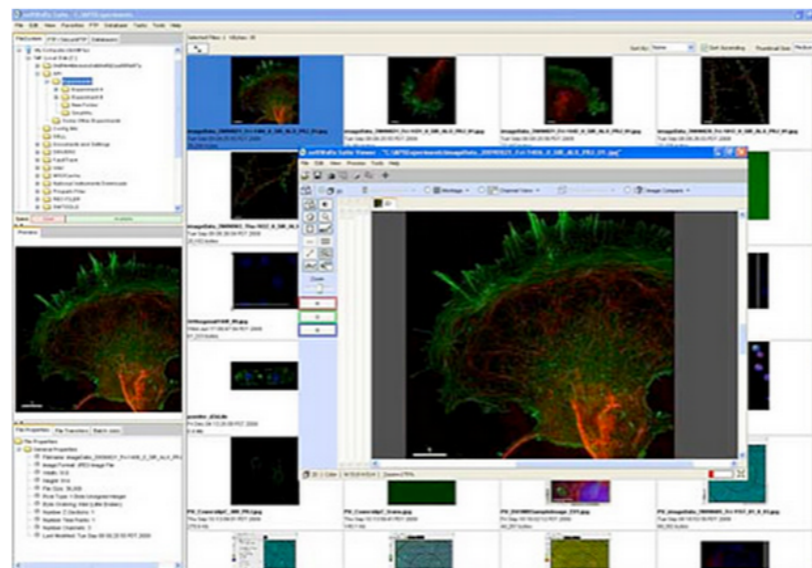
Some new deep learning solutions are becoming available.

e.g. CARE

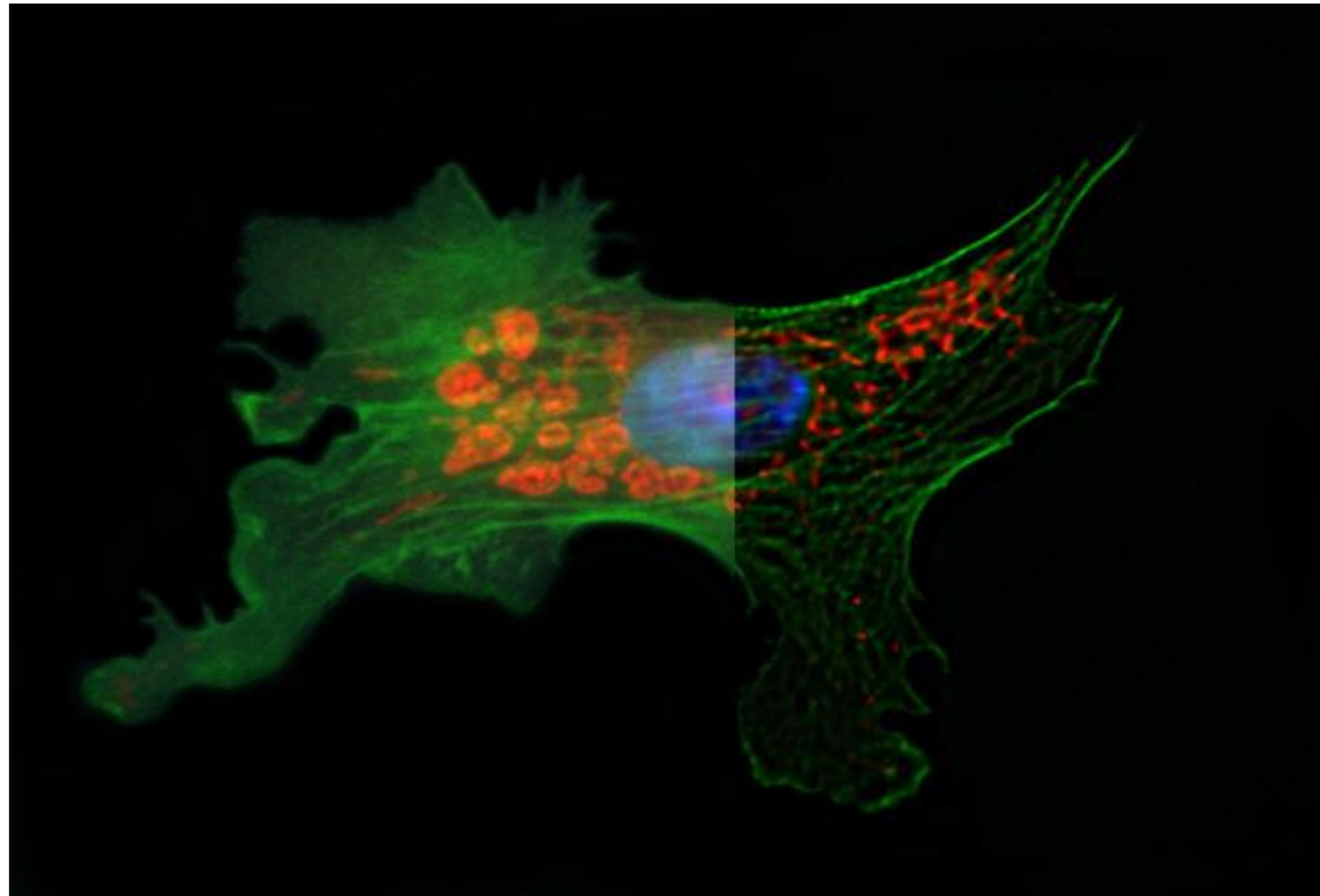
<http://csbdeep.bioimagecomputing.com/>



SoftWoRx



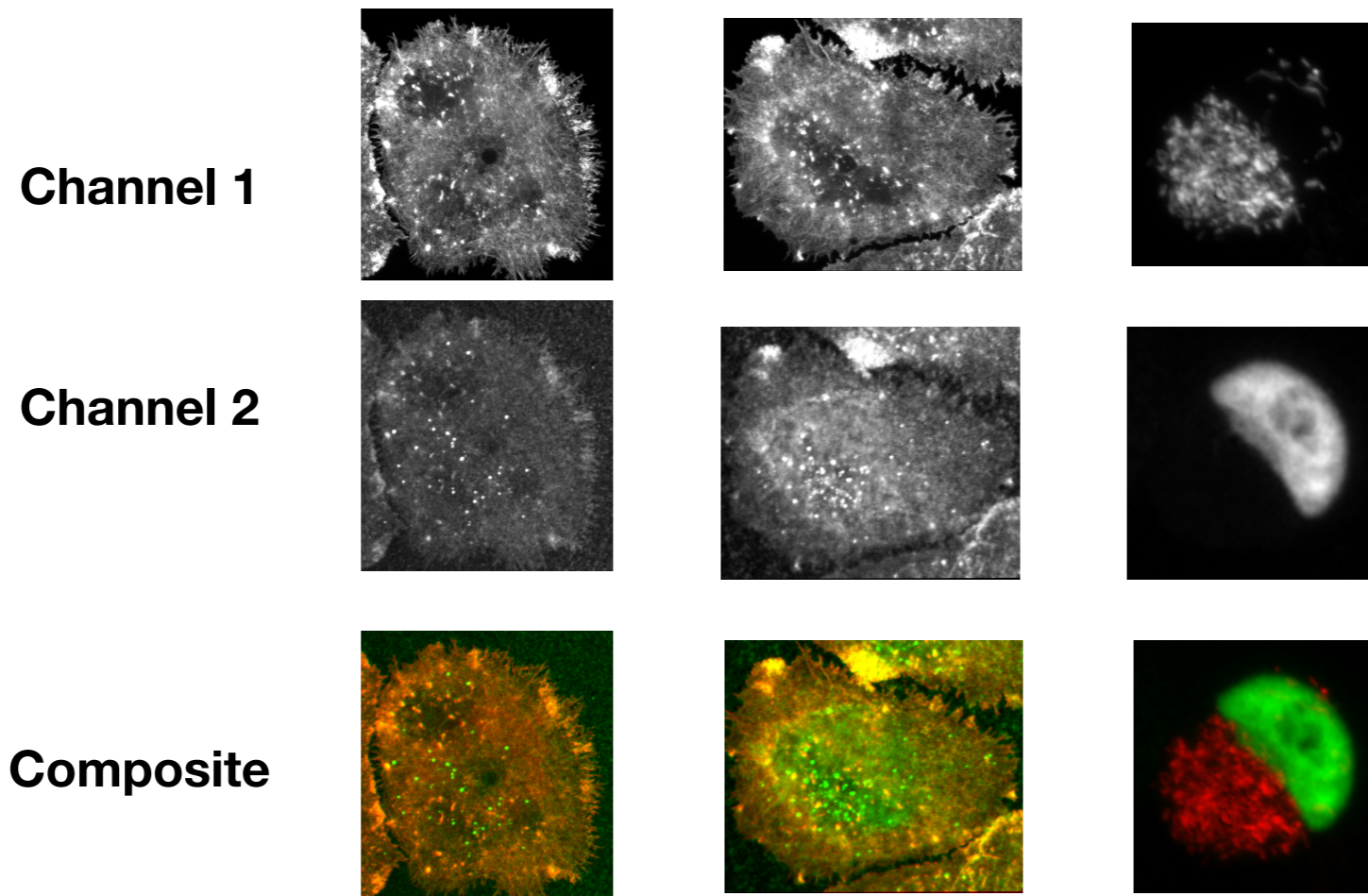
Deconvolution



Be aware of artefacts!

Colocalisation statistics

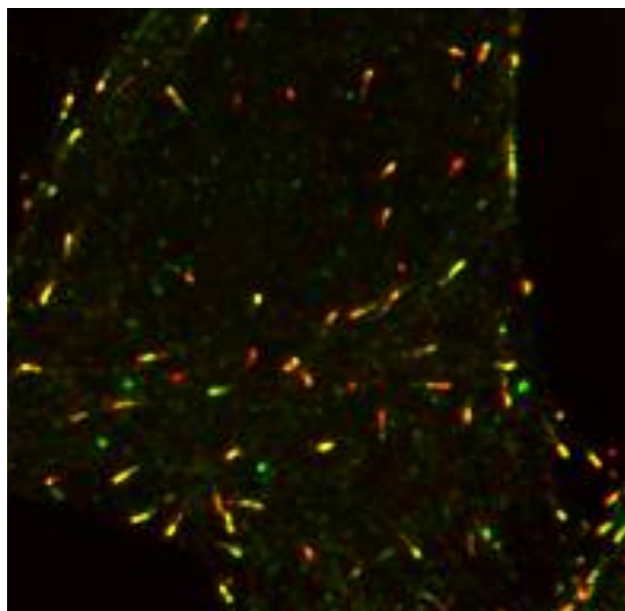
How similar are these images?



Three ways to evaluate colocalisation

Visualisation

First, apply a LUT to each channel, then overlay them



Quantification

Image considered as a **collection of pixels**

Look for a link between intensities from both channels

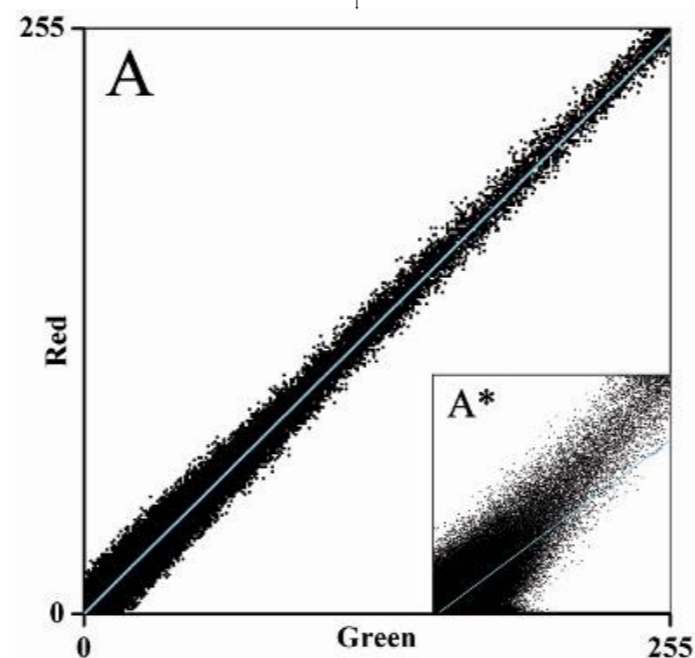
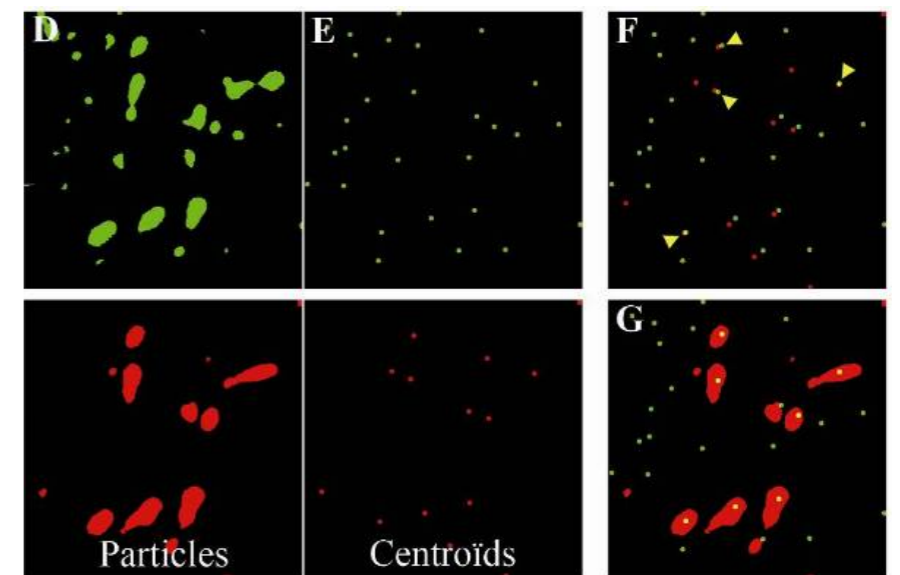
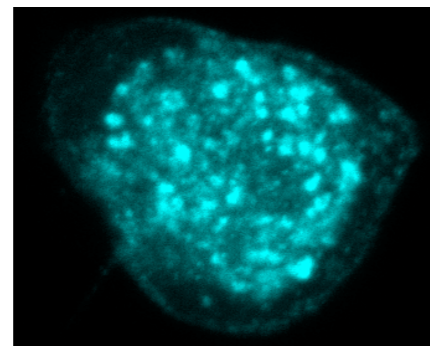


Image considered as a **collection of objects**

First, identify the structures, then look for an overlap, either partial or total between objects



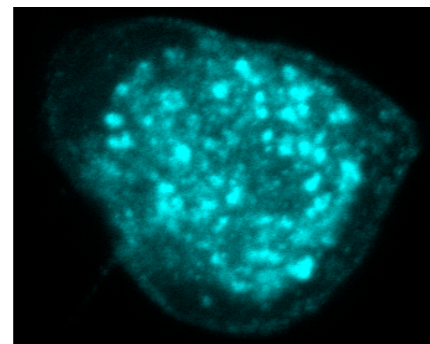
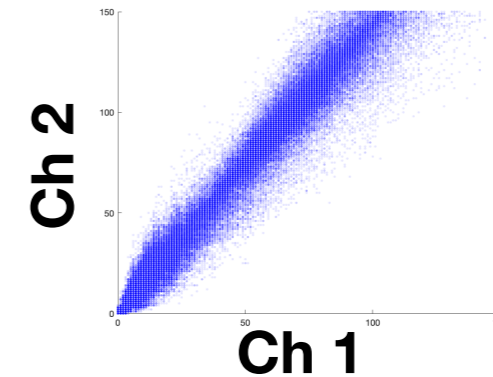
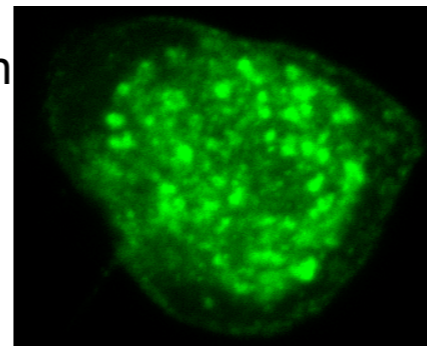
Pearson's Correlation Coefficient



correlation

0.8

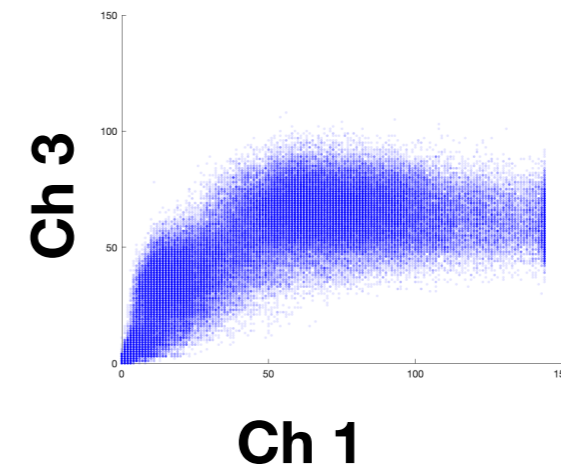
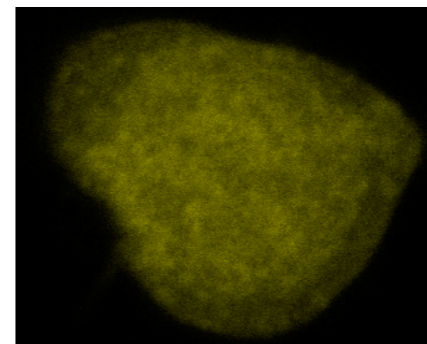
VS



correlation

0.2

VS



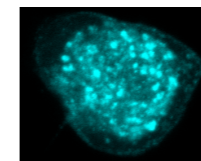
Images which have similar 'spatial' distribution of pixel values will be highly-correlated. We can use this to establish colocalisation.

Pearson's product-moment correlation test

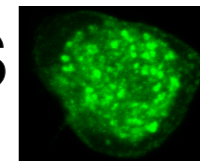
Pearson's equation:

$$r = \frac{\sum (R_i - \bar{R}) \times (G_i - \bar{G})}{\sqrt{\sum (R_i - \bar{R})^2 \times \sum (G_i - \bar{G})^2}}$$

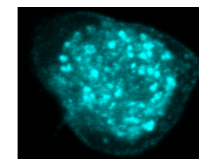
if r is 1.0 means correlation
if r is close to '0.0' no correlation.
if r is -1.0 it means anti-correlation.
R refers to one channel, G refers to Green channel. G or R with a bar refers to mean intensity in that channel. 'i' refers to each pixel in image. Sigma (big E) refers to sum. So sum of all pixels minus their mean.



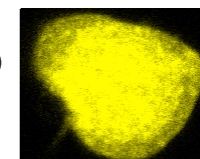
VS
high



r = 0.85



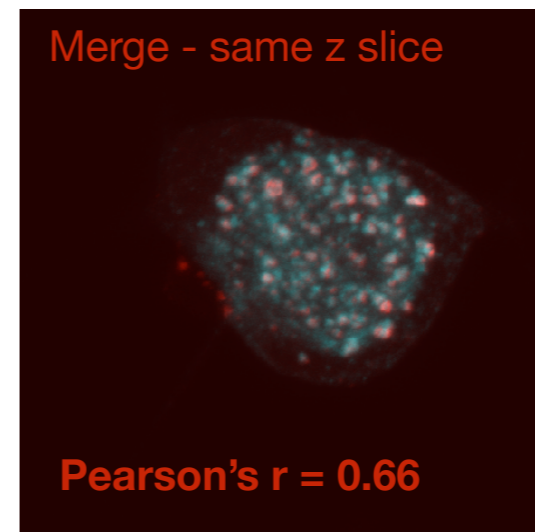
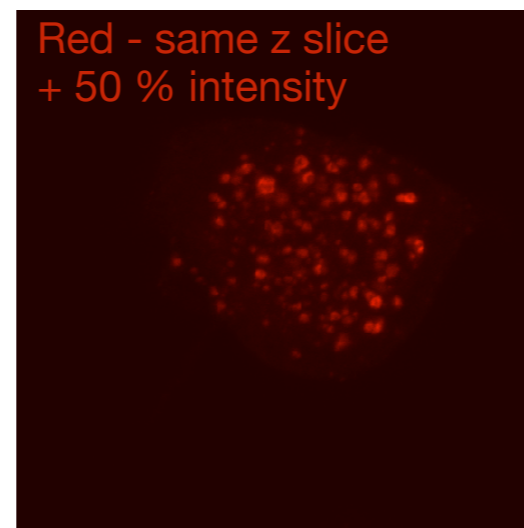
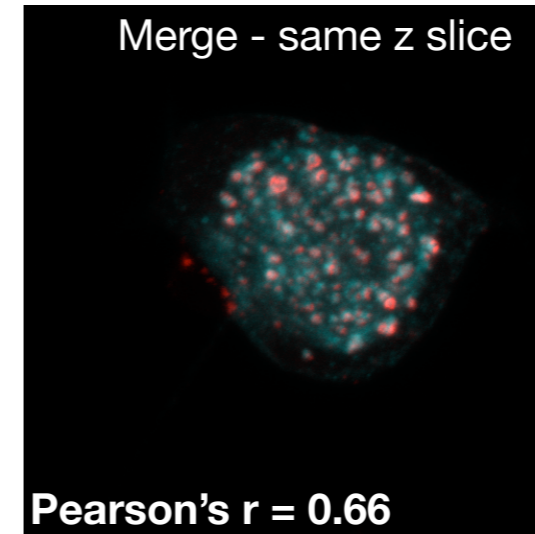
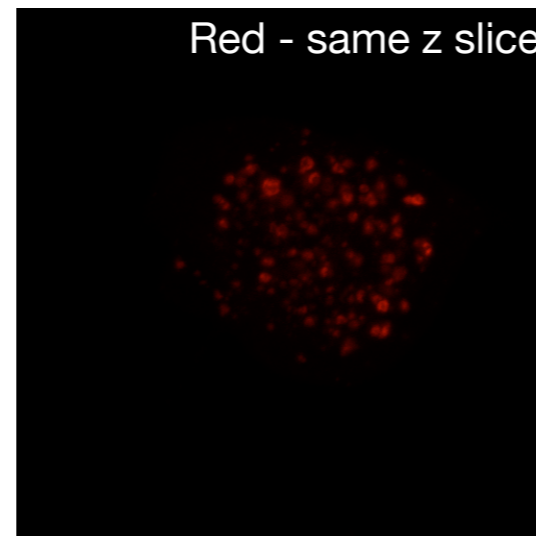
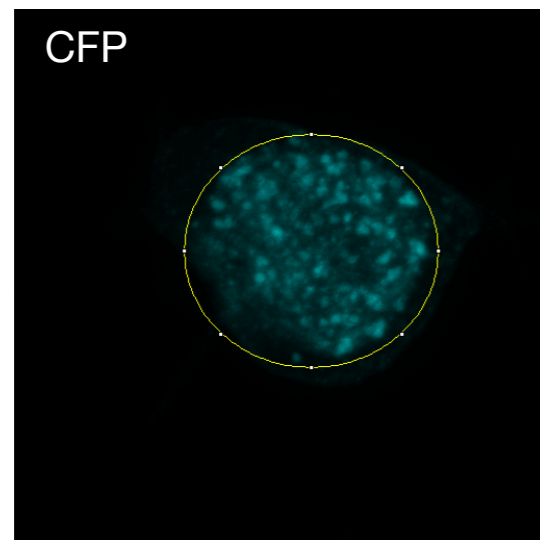
VS
low



r = 0.25

- Dimensionless and normalised comparison. Can be used on any two images as long as they are the same spatial size and don't have too many black pixels

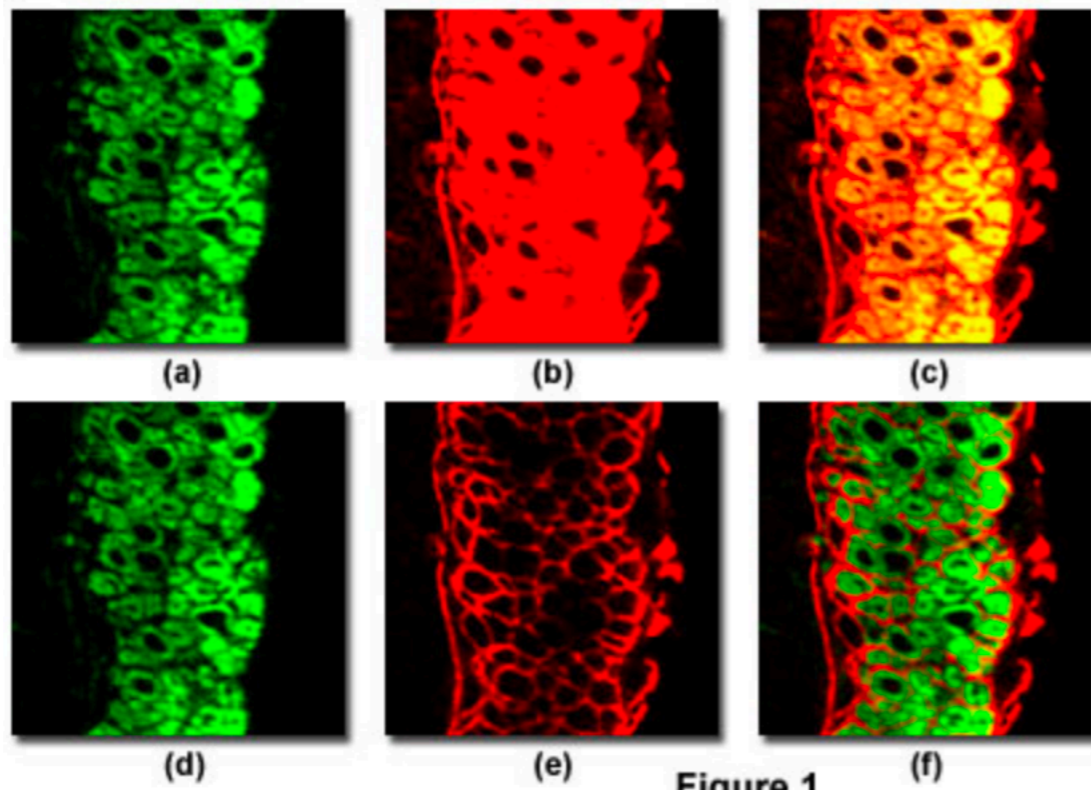
Pearson's test is insensitive to global intensity



- Pearson's test is (within reason) insensitive to linear changes in intensity.
- This is good, it looks at trends rather than absolute values.
- This means expression variation between cells does not ruin experiment

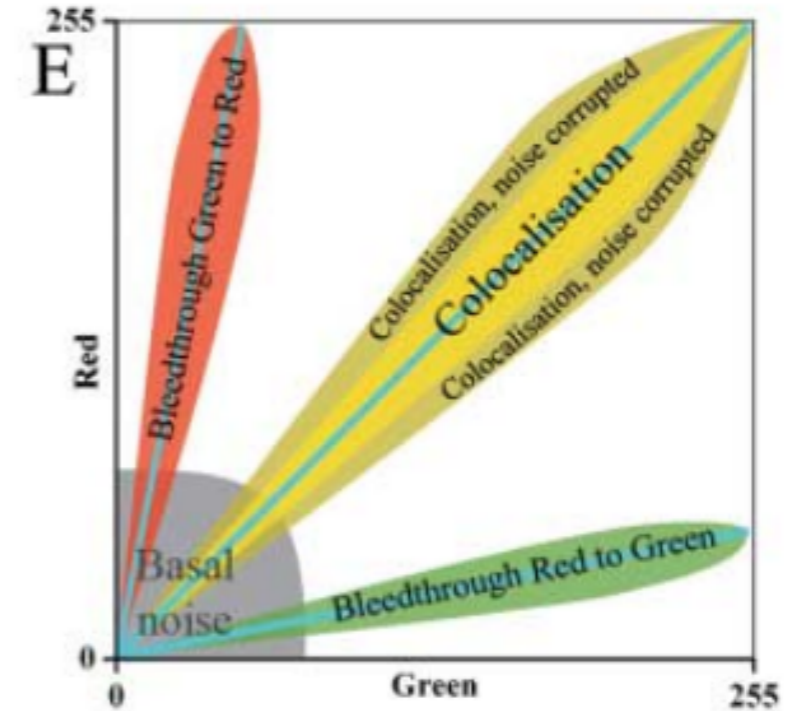
Pearson's test is sensitive to bleed-through and noise

Fluorophore Emission Bleed-Through in Confocal Microscopy



source: Olympus

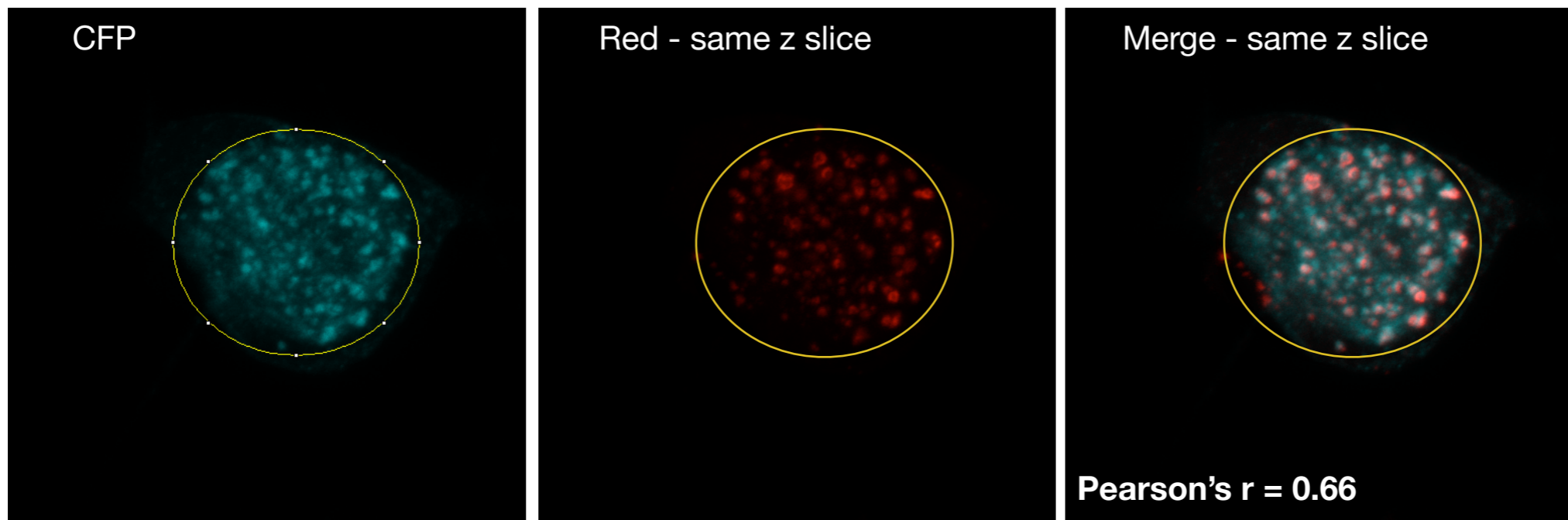
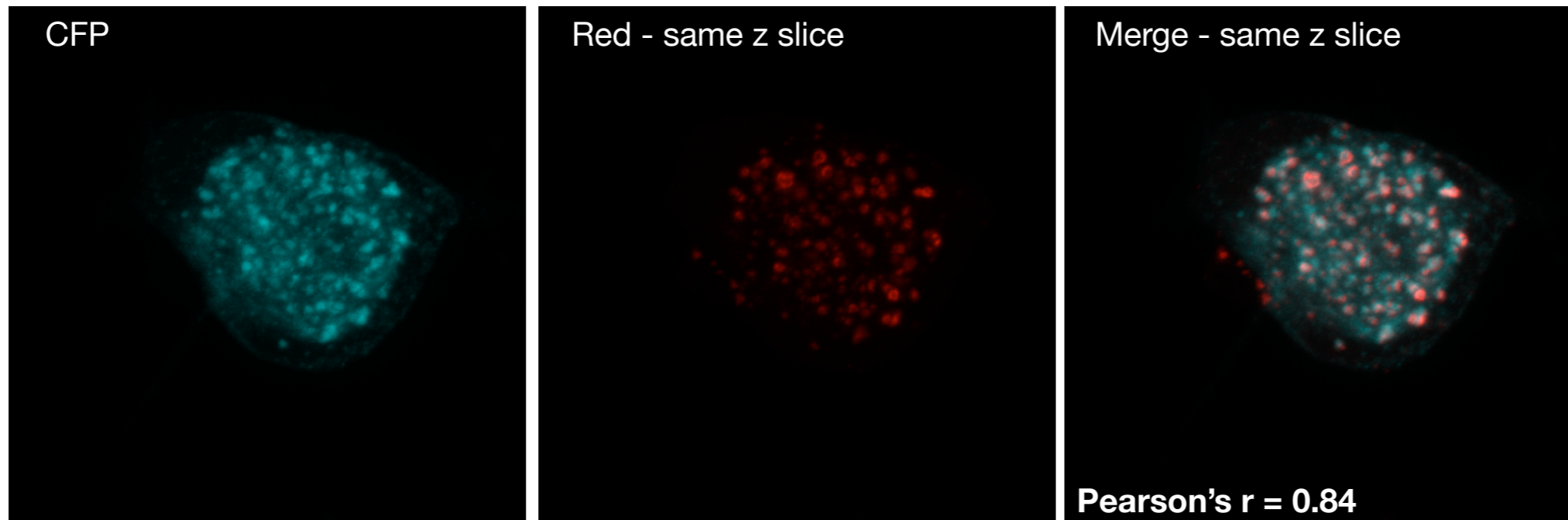
Figure 1



222 S. BOLTE AND F. P. CORDELIÈRES

- Spectral bleed through will artificially increase the correlation coefficient.
- Noise will artificially decrease the correlation coefficient.

P's test is sensitive zero pixels and saturation



- Pearson's test doesn't ignore '0' pixels and noise within calculation.
- Coloc 2 plugin does warn you however: The ratio between zero-zero pixels and other pixels is larger 0.37. Maybe you should use a ROI.

Sensitivity to resolution

The « diagnostic » placed for co-localisation should always be stated relative to a particular resolution and sampling rate.



- In cell biology:
the two proteins are at the same location
- The statistical point-of-view:
Considering the current resolution, it might not be excluded that the two proteins are indeed at the same location

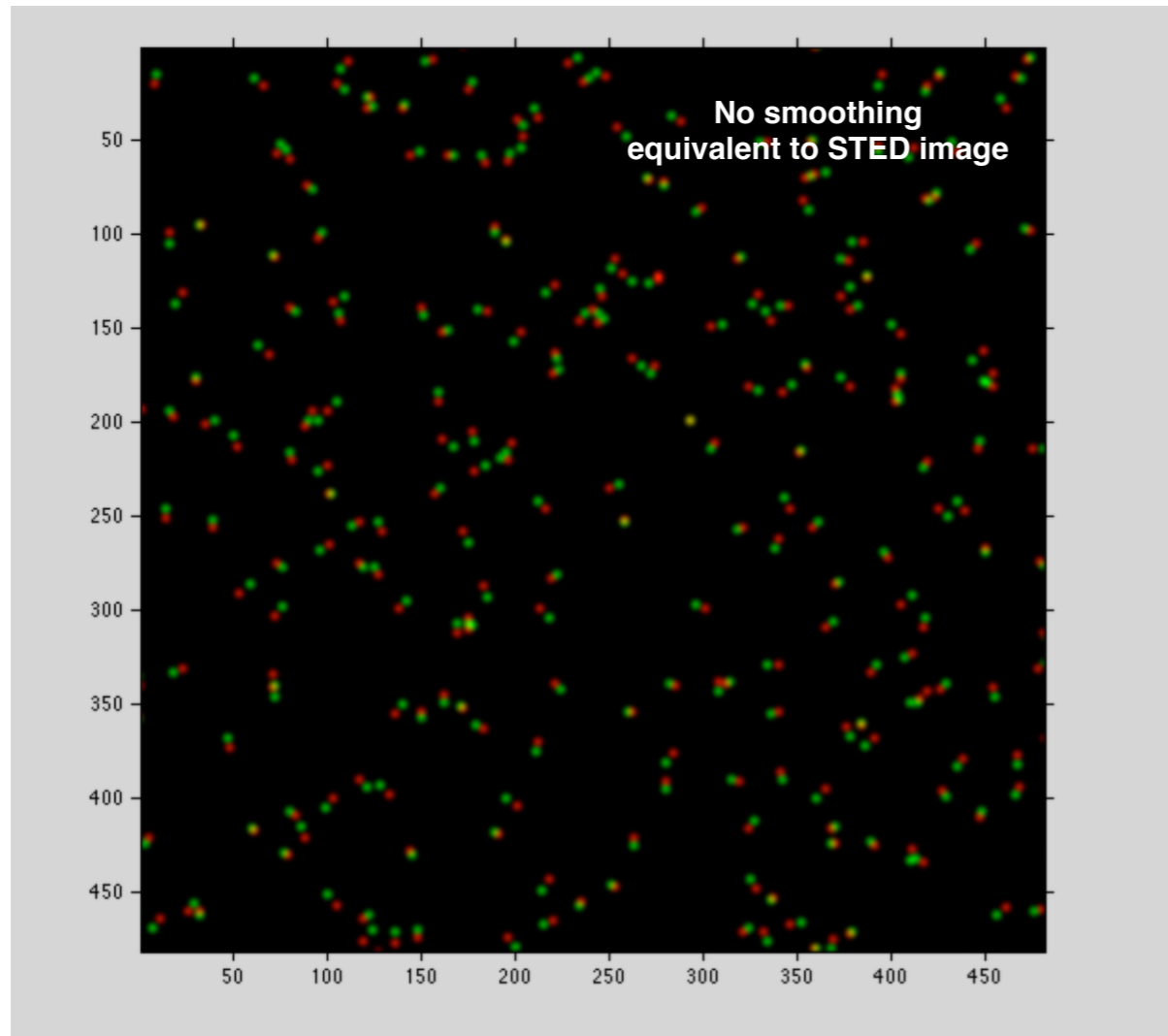
Sensitivity to resolution

The « diagnostic » placed for co-localisation should always be stated relative to a particular resolution and sampling rate.

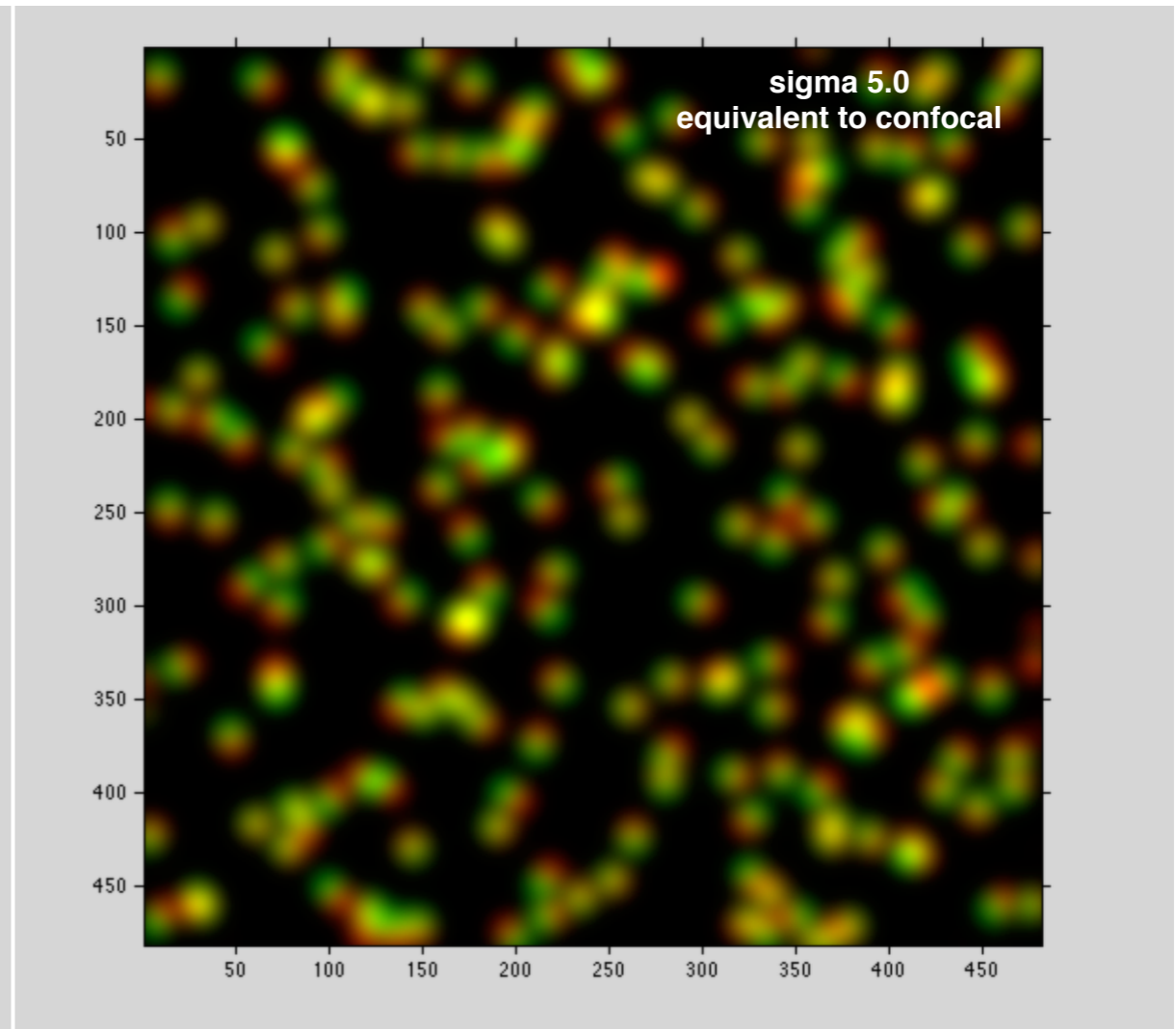


- In cell biology:
the two proteins are at the same location
- The statistical point-of-view:
Considering the current resolution, it might not be excluded that the two proteins are indeed at the same location

Sensitivity to resolution



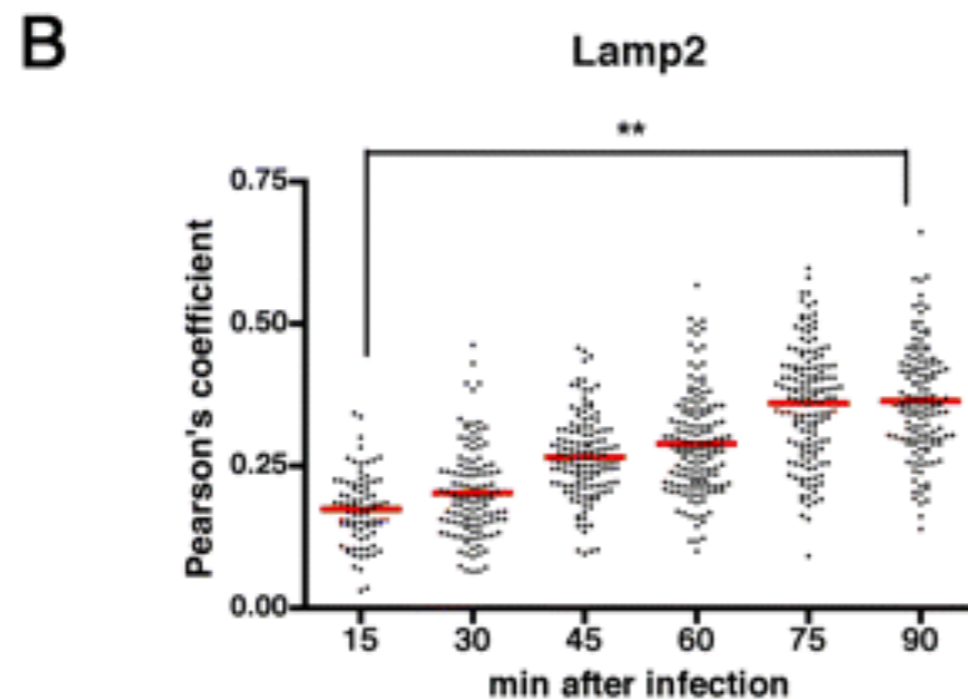
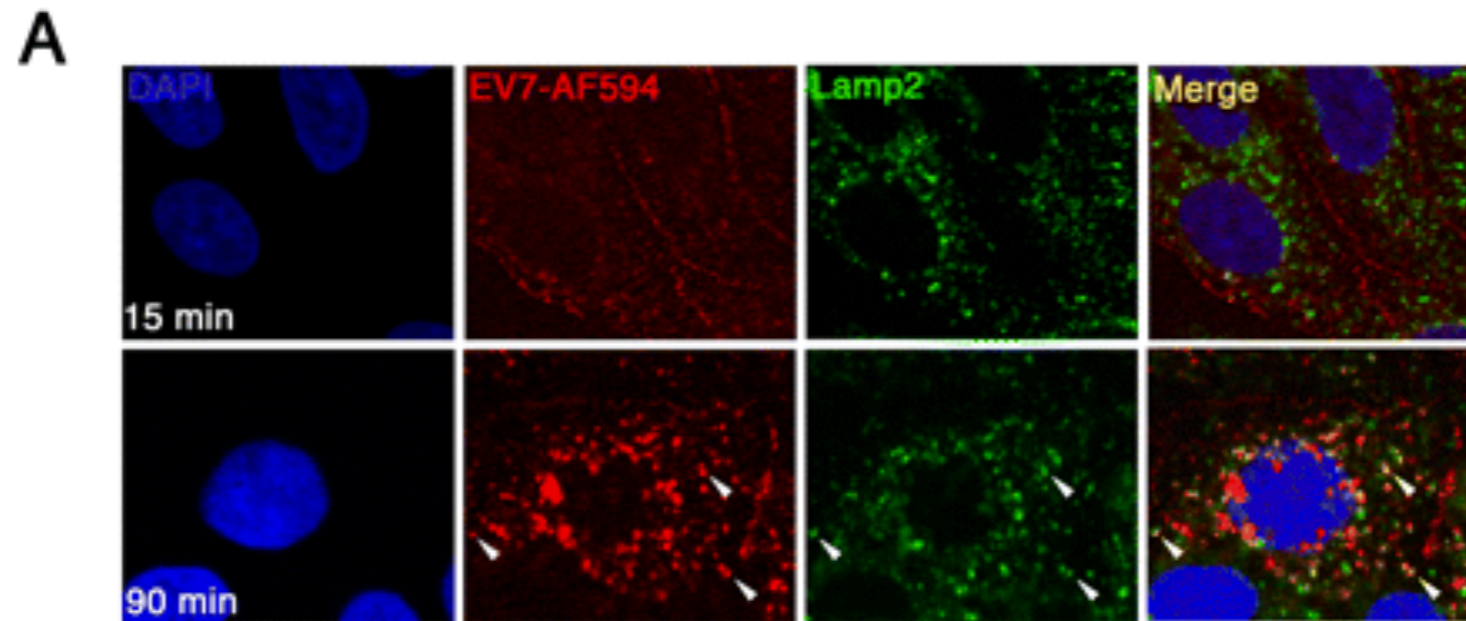
$$r = 0.23$$



$$r = 0.84$$

A good example of pearson's test for colocalisation

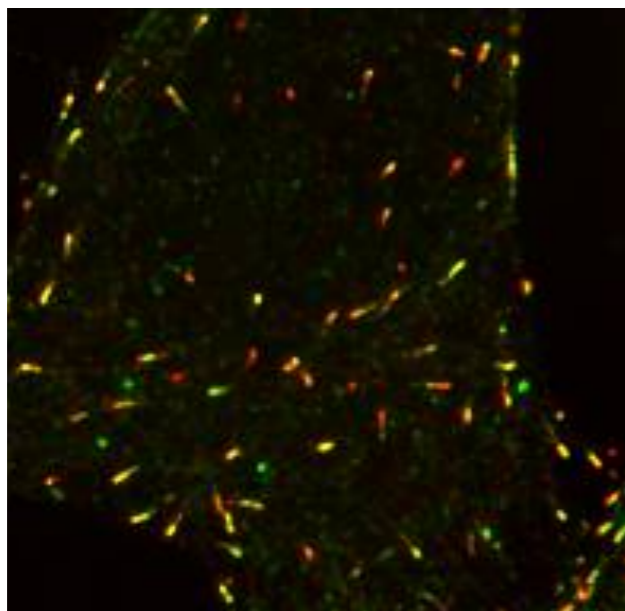
Comparing EV7 staining with Lamp2 over time.



Always consider the limitations of the method and chose your Experimental settings and controls carefully.

Visualisation

First, apply a LUT to each channel, then overlay them



Quantification

Image considered as a **collection of pixels**

Look for a link between intensities from both channels

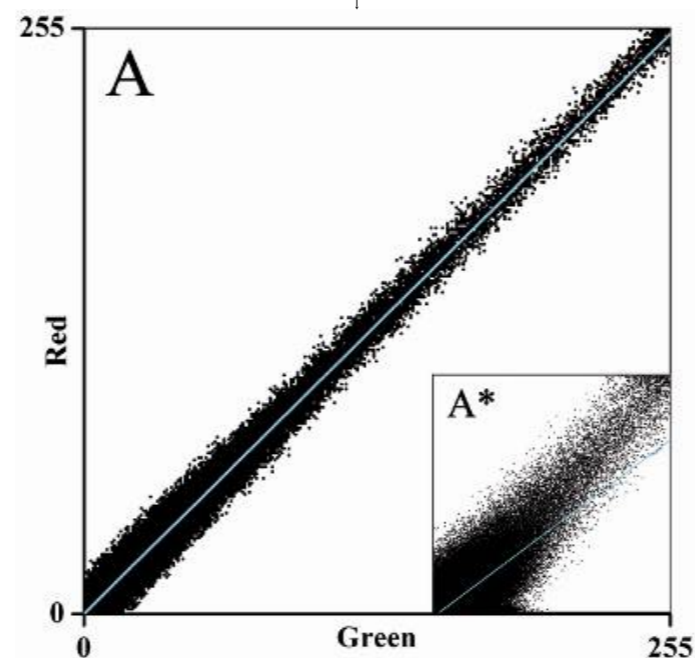
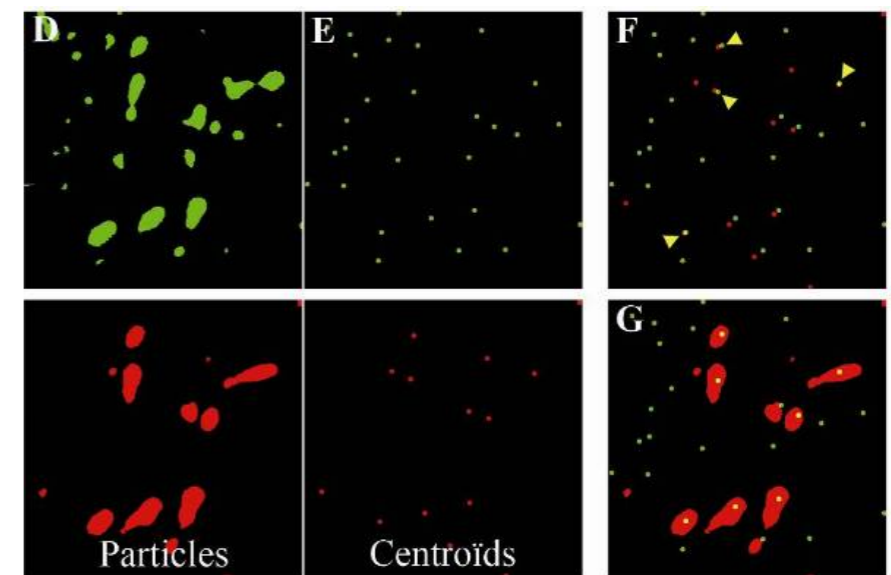
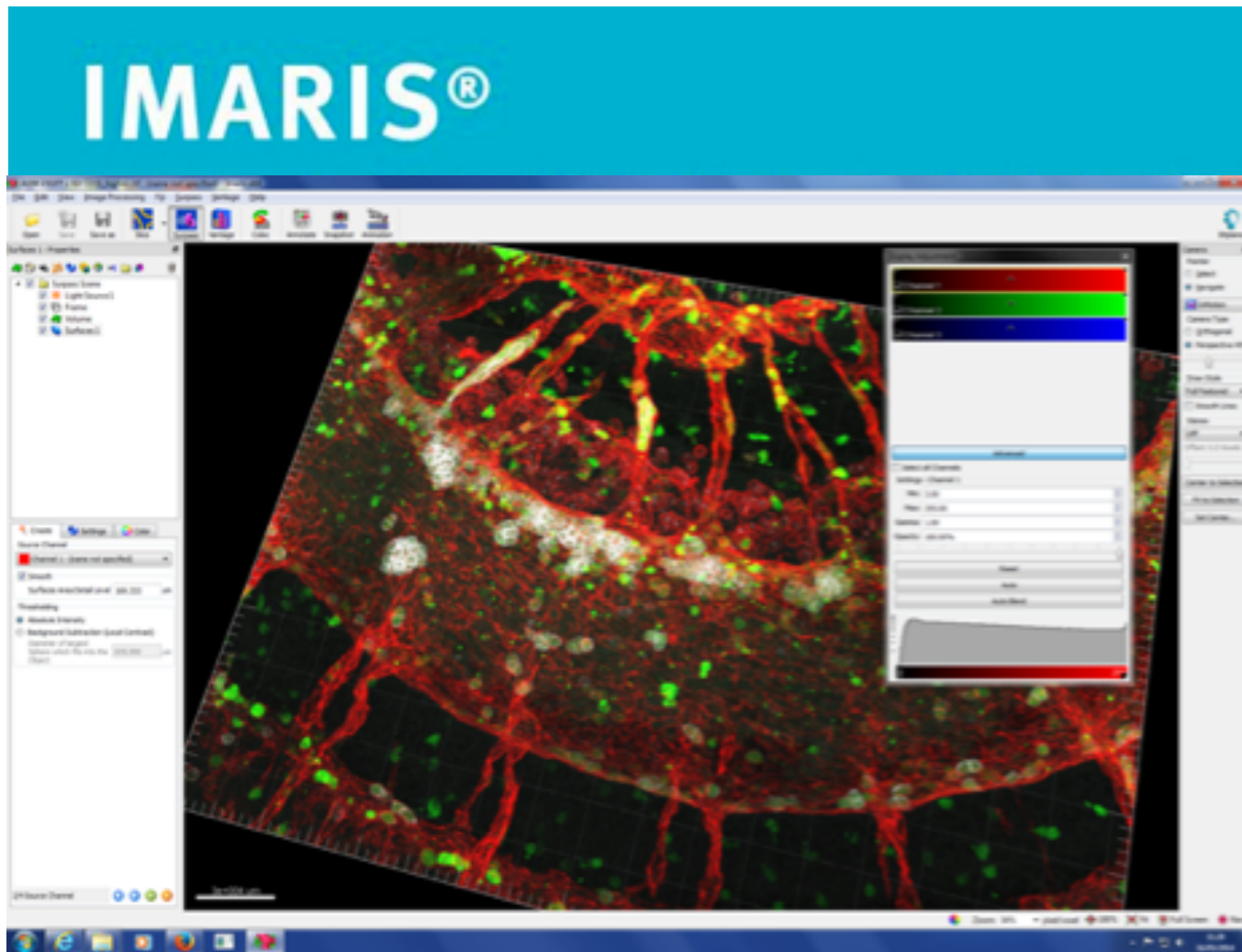


Image considered as a **collection of objects**

First, identify the structures, then look for an overlap, either partial or total between objects

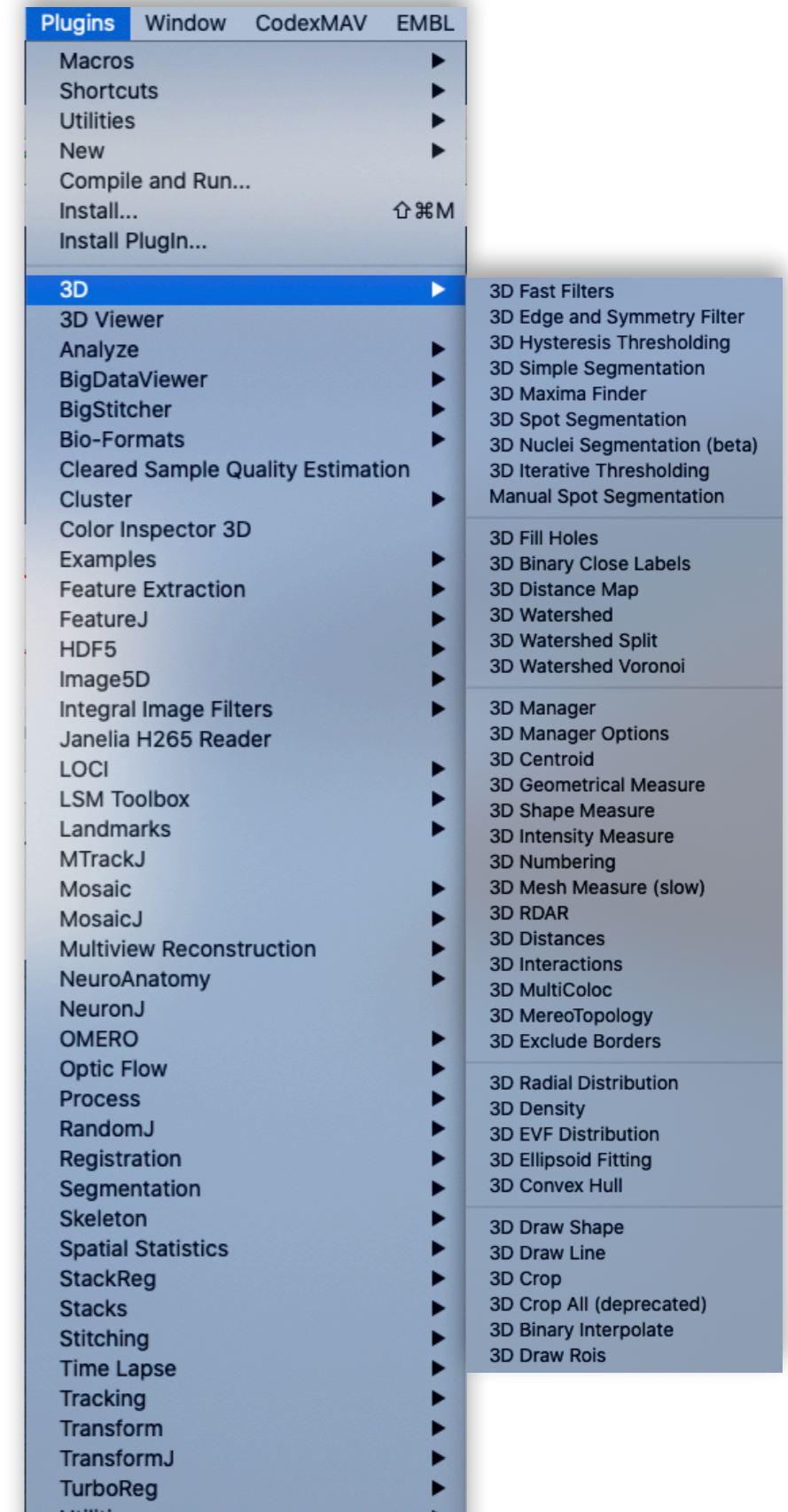
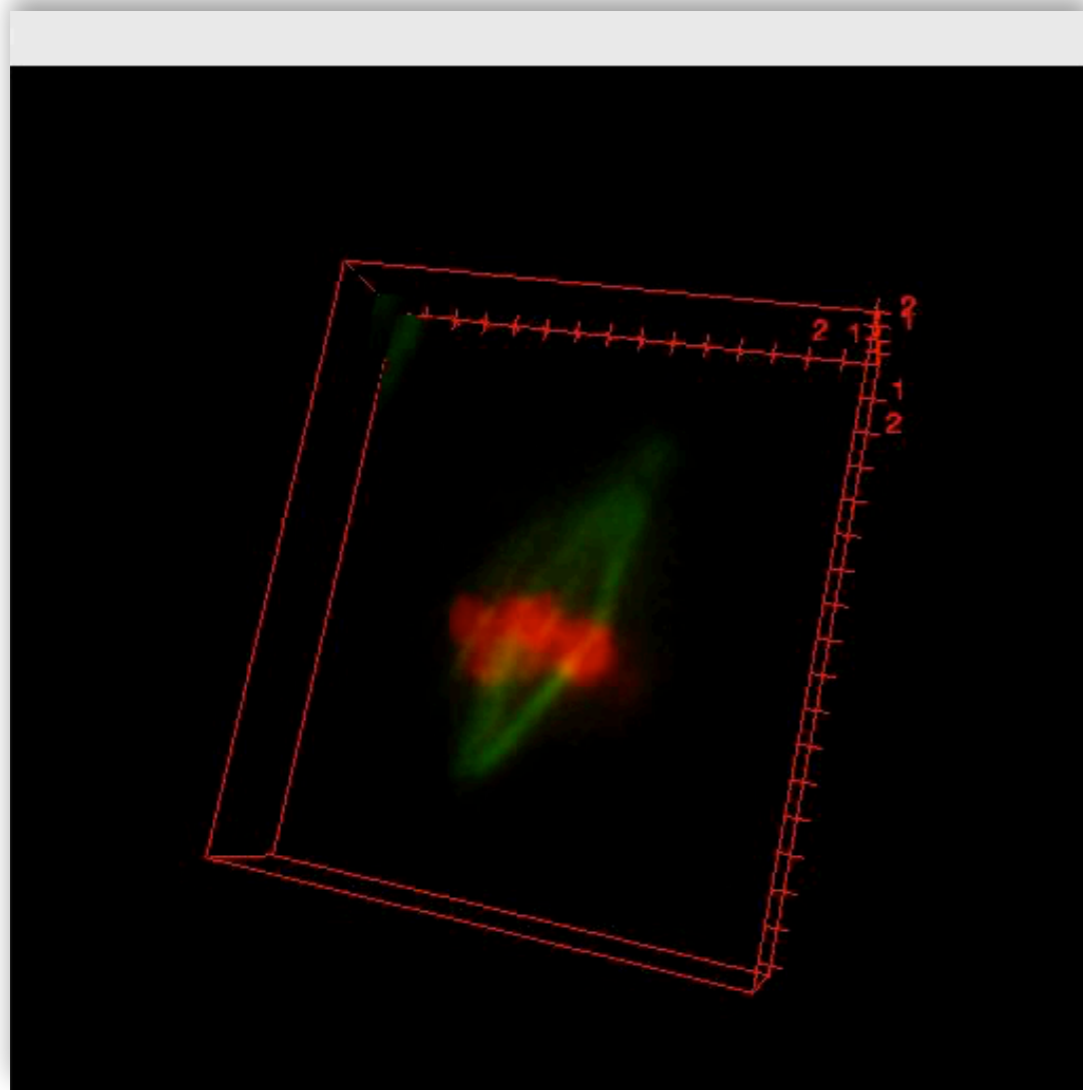


3D visualisation & Analysis

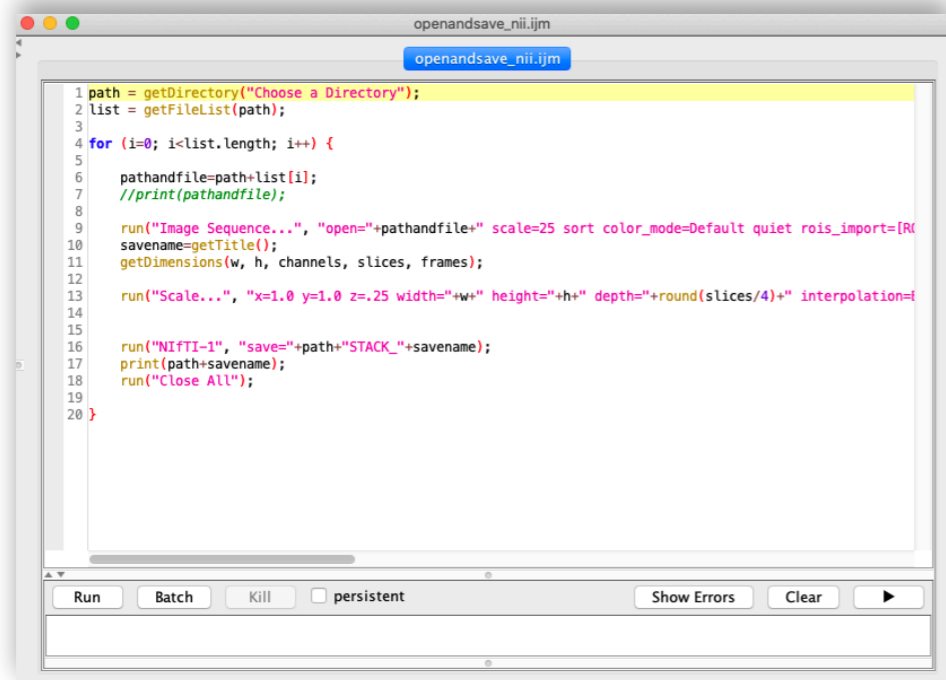


- Volume Visualisation
- Automatic and manual identification of objects in 3D
- Tracking and Colocalisation in 3D

3D visualisation & Analysis

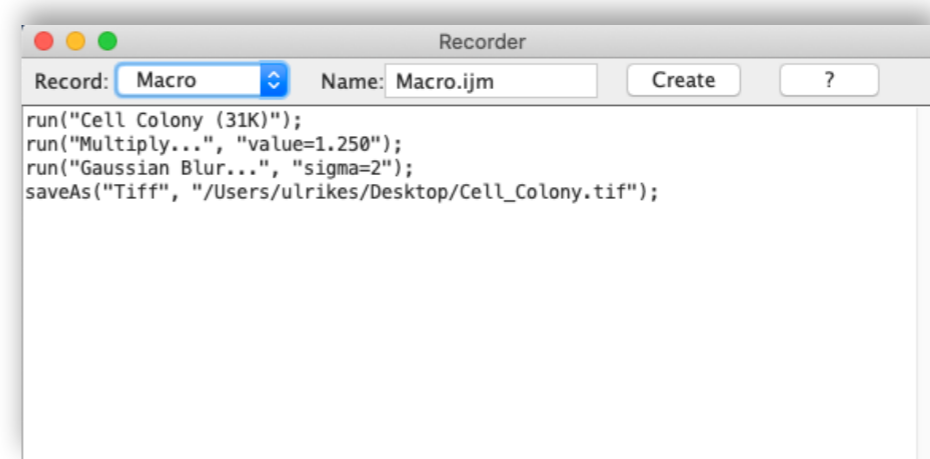


Macro Programming



```
1 path = getDirectory("Choose a Directory");
2 list = getFileList(path);
3
4 for (i=0; i<list.length; i++) {
5
6     pathandfile=path+list[i];
7     //print(pathandfile);
8
9     run("Image Sequence...", "open="+pathandfile+" scale=25 sort color_mode=Default quiet rois_import=[R
10     savename=getTitle();
11     getDimensions(w, h, channels, slices, frames);
12
13     run("Scale...", "x=1.0 y=1.0 z=.25 width="+w+" height="+h+" depth="+round(slices/4)+" interpolation=f
14
15
16     run("NIfTI-1", "save="+path+"STACK_"+savename);
17     print(path+savename);
18     run("Close ALL");
19 }
20 }
```

Run Batch Kill persistent Show Errors Clear ▶



Record: Macro Name: Macro.ijm Create ?

```
run("Cell Colony (31K)");
run("Multiply...", "value=1.250");
run("Gaussian Blur...", "sigma=2");
saveAs("Tiff", "/Users/ulrikes/Desktop/Cell_Colony.tif");
```

Take nice images!

- **No saturated pixels**
- **Good signal to noise**
- **Low background**

- **Keep imaging conditions the same: laser power, gain, resolution, etc.**

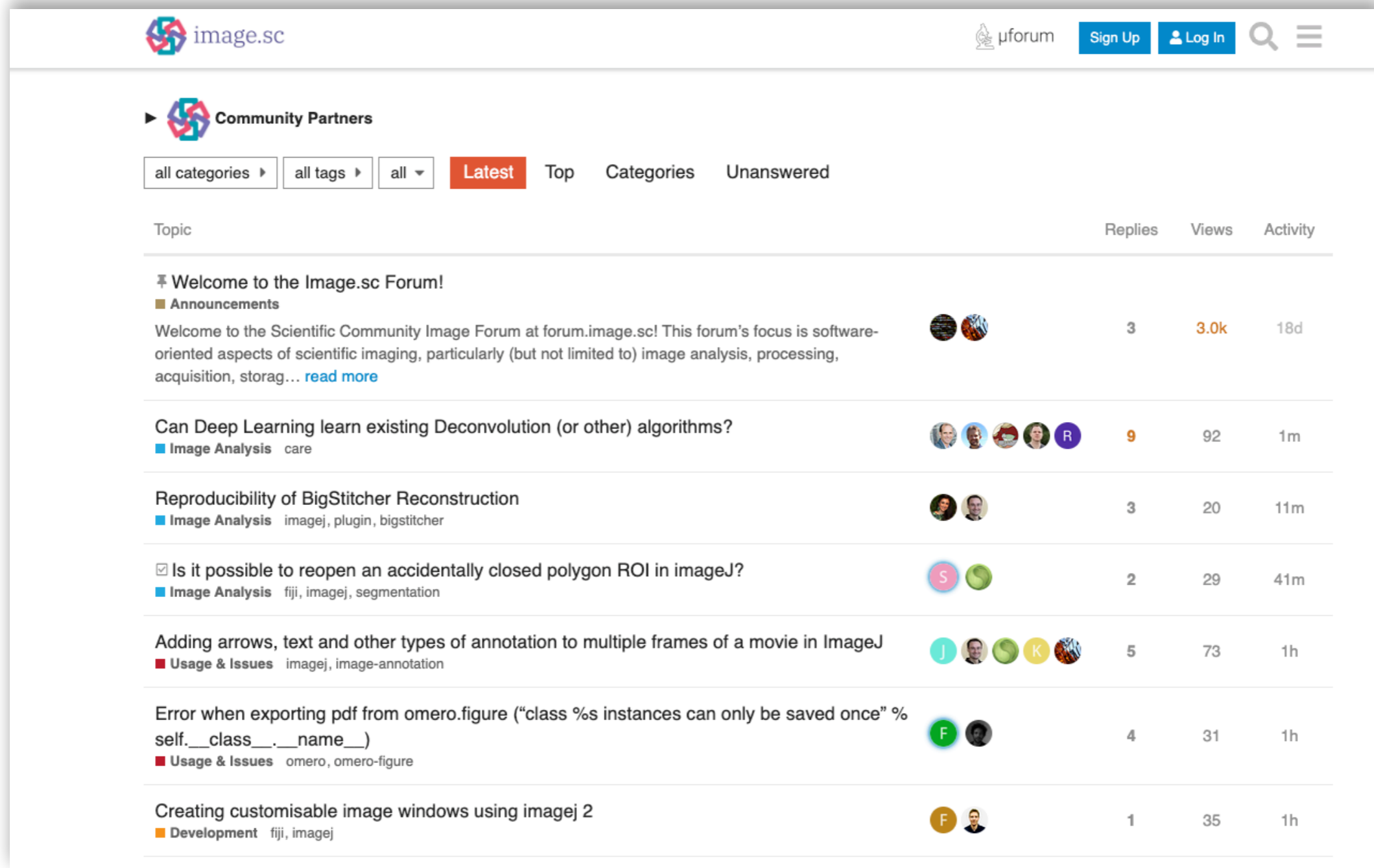
- **Microscopes have to be aligned**
- **Be mindful of chromatic aberrations**

- **Think about image Analysis before acquiring hundreds of images!**

Don't!

- **Adjust the brightness and contrast equally in each image or else include colour scale.**
- **Do not disguise faint structures in your image by adjusting brightness to hide it.**
- **Do not remove or change pixels in background.**
- **Don't apply non-linear transforms to image (e.g. change gamma).**
- **Don't do anything you cannot justify in your methods.**

Image Analysis questions for later



The screenshot shows the image.sc forum interface. At the top left is the image.sc logo. At the top right are links for 'forum', 'Sign Up', and 'Log In', along with search and menu icons. Below the header is a 'Community Partners' section. A navigation bar includes filters for 'all categories', 'all tags', and 'all', with 'Latest' selected. The main content is a table of forum topics with columns for Topic, Replies, Views, and Activity.

Topic	Replies	Views	Activity
Welcome to the Image.sc Forum! Announcements Welcome to the Scientific Community Image Forum at forum.image.sc! This forum's focus is software-oriented aspects of scientific imaging, particularly (but not limited to) image analysis, processing, acquisition, storag... read more	3	3.0k	18d
Can Deep Learning learn existing Deconvolution (or other) algorithms? Image Analysis care	9	92	1m
Reproducibility of BigStitcher Reconstruction Image Analysis imagej, plugin, bigstitcher	3	20	11m
<input checked="" type="checkbox"/> Is it possible to reopen an accidentally closed polygon ROI in imageJ? Image Analysis fiji, imagej, segmentation	2	29	41m
Adding arrows, text and other types of annotation to multiple frames of a movie in ImageJ Usage & Issues imagej, image-annotation	5	73	1h
Error when exporting pdf from omero.figure ("class %s instances can only be saved once" % self.__class__.__name__) Usage & Issues omero, omero-figure	4	31	1h
Creating customisable image windows using imagej 2 Development fiji, imagej	1	35	1h

Thank you!

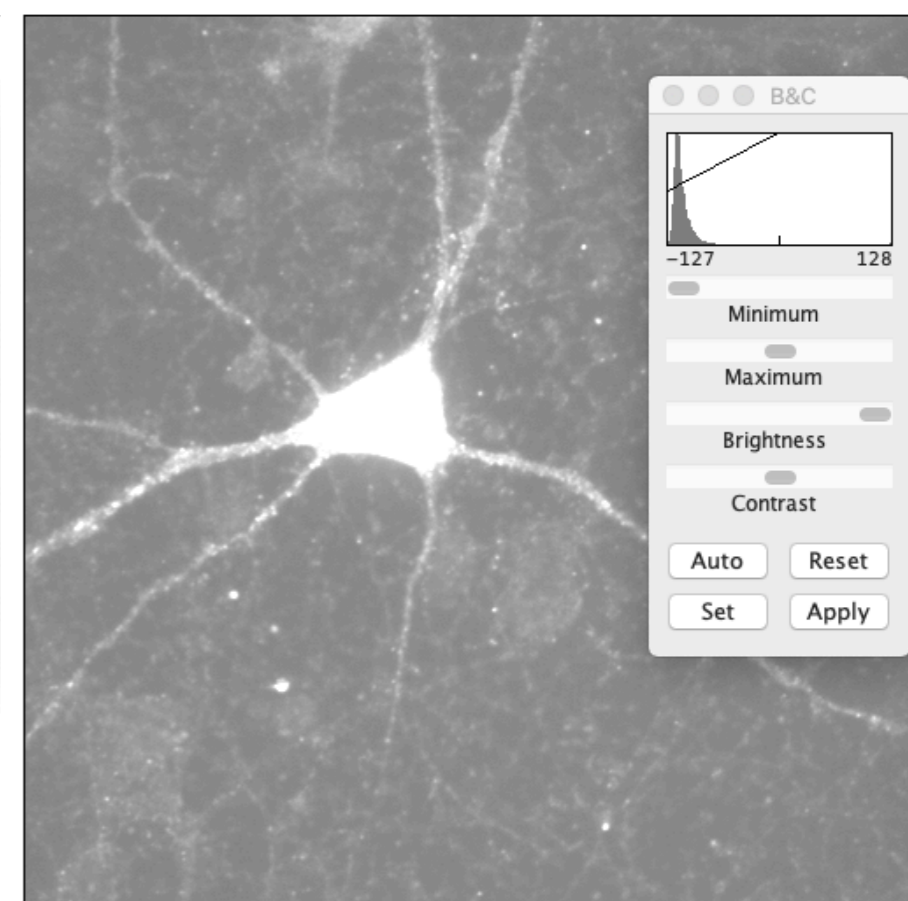
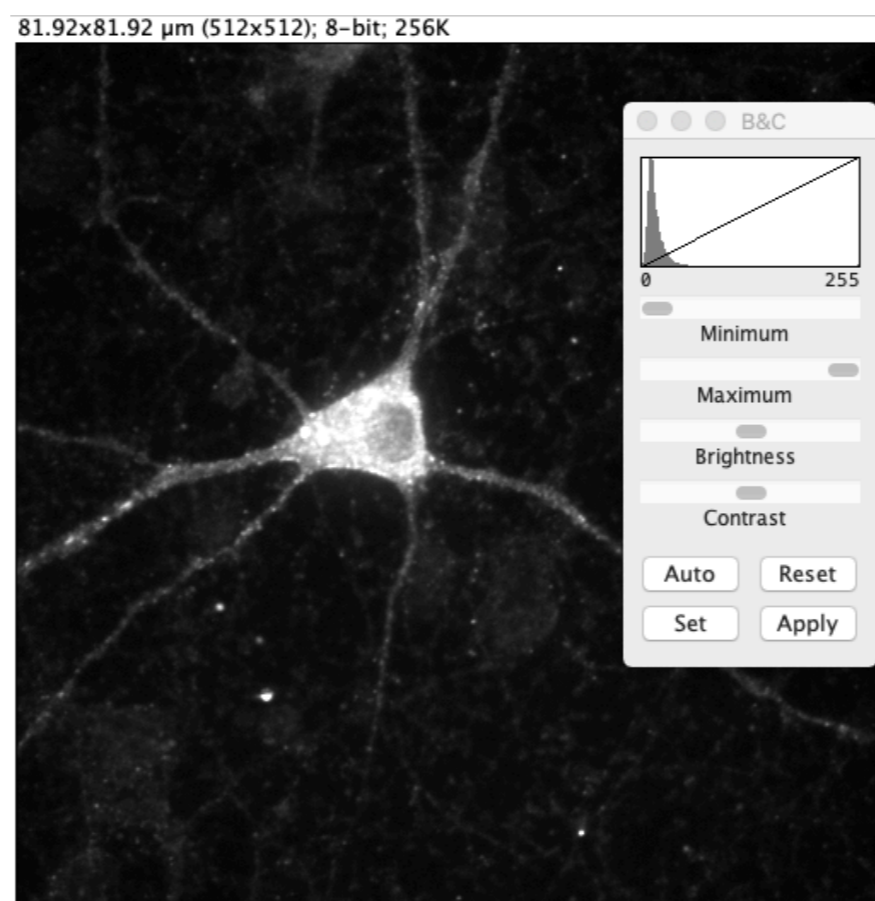
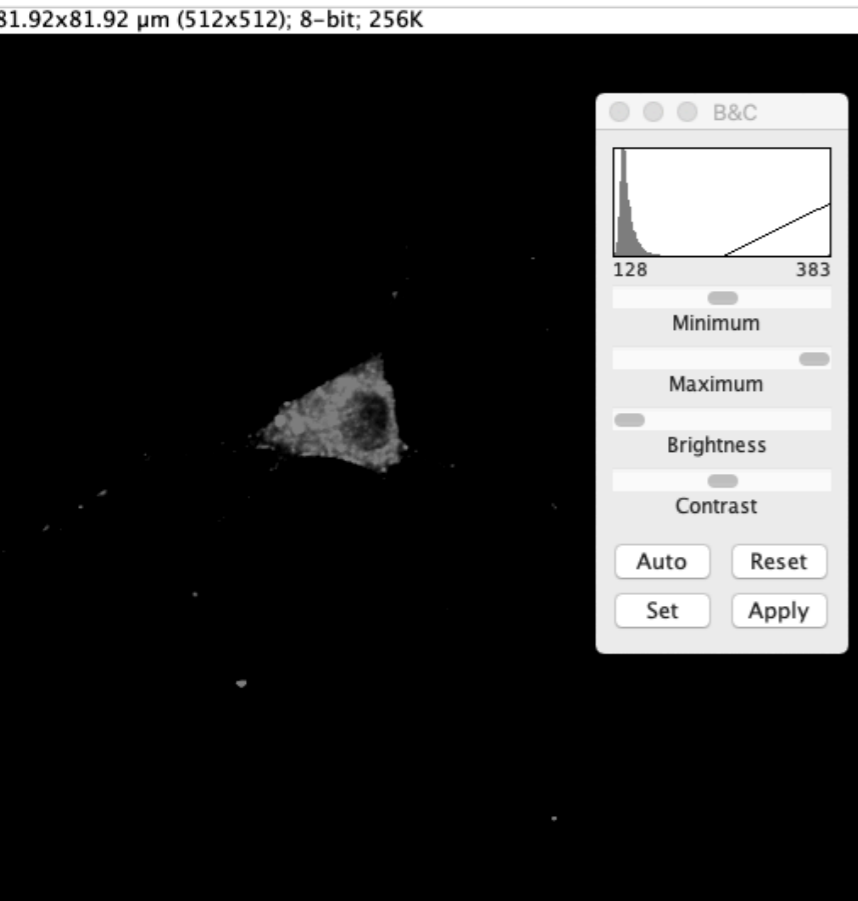
Ulrike.Schulze@rdm.ox.ac.uk

Thank you!

Ulrike.Schulze@rdm.ox.ac.uk

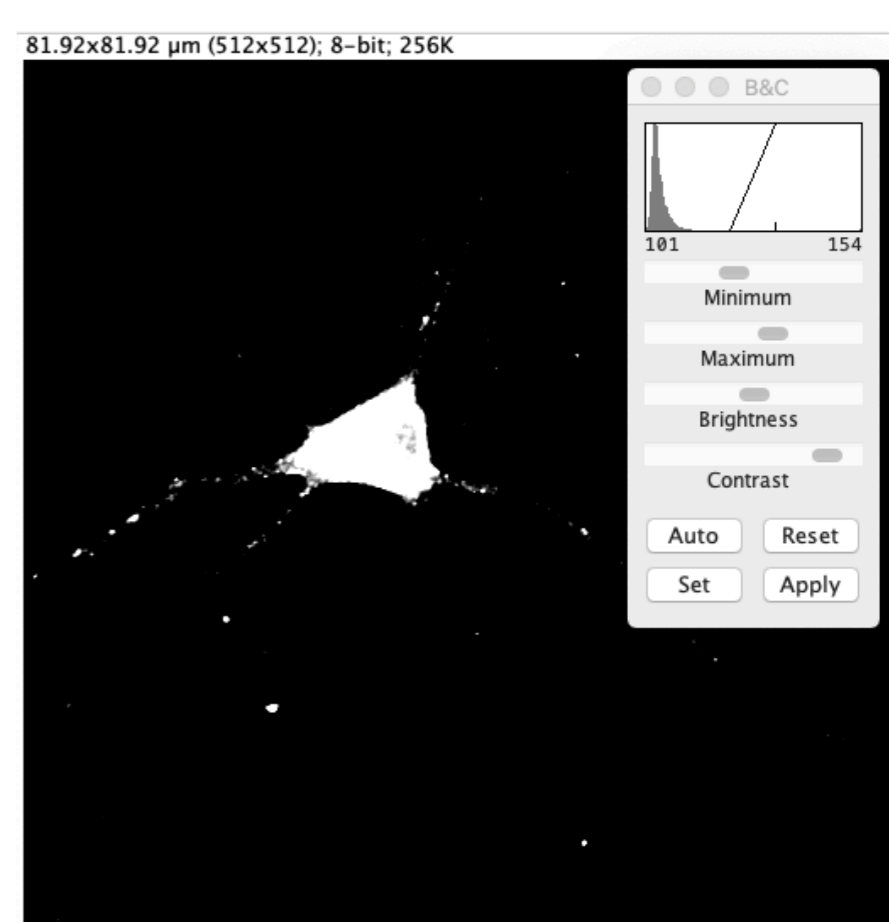
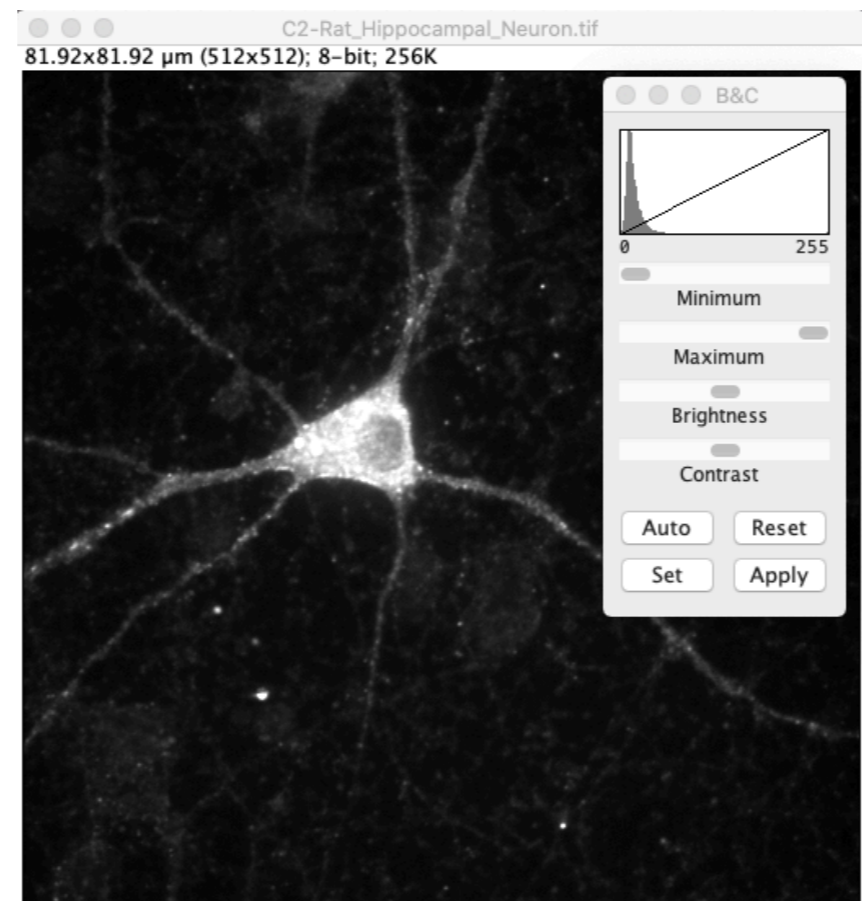
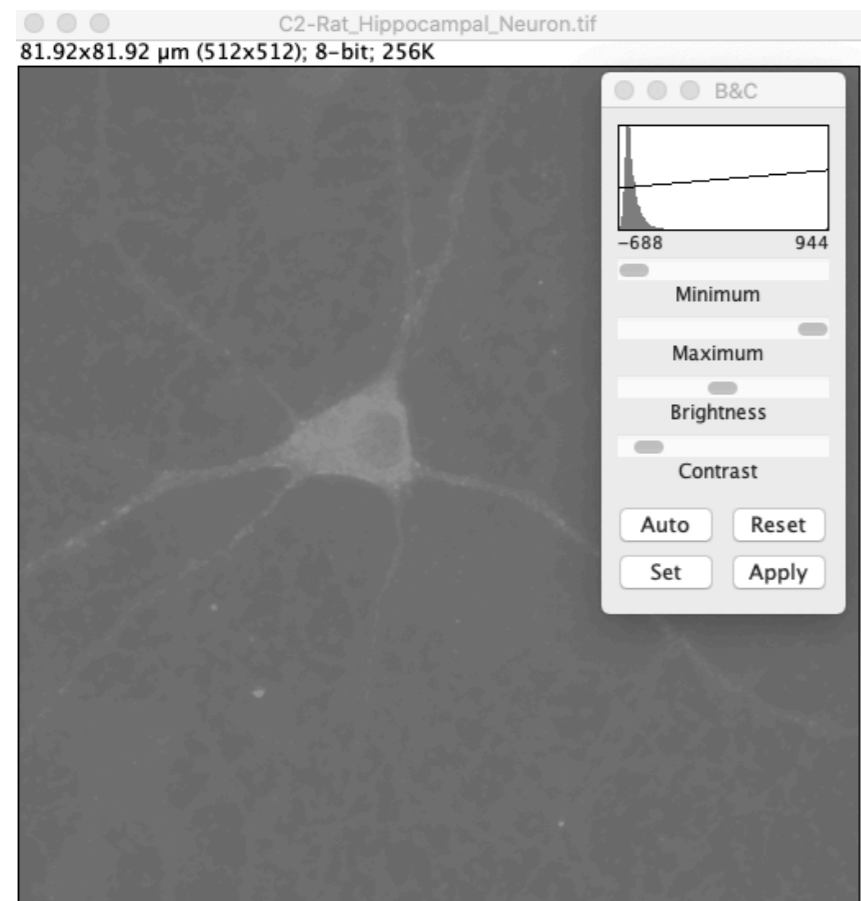
Brightness

Conversion of image intensity to display intensity



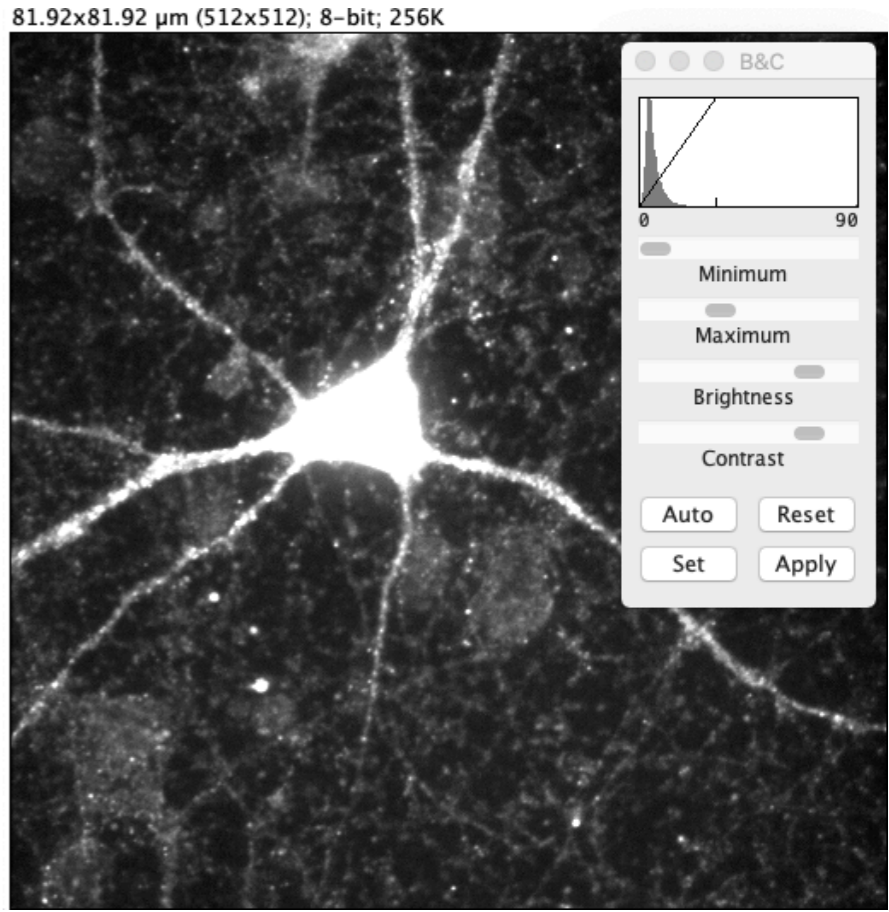
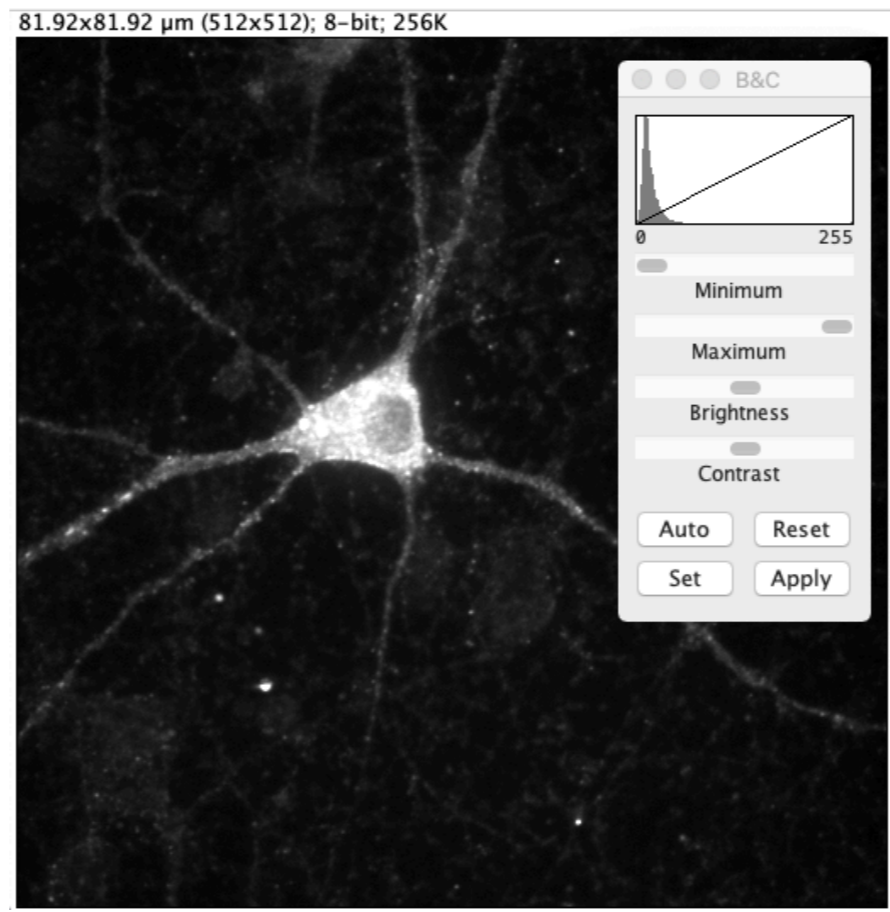
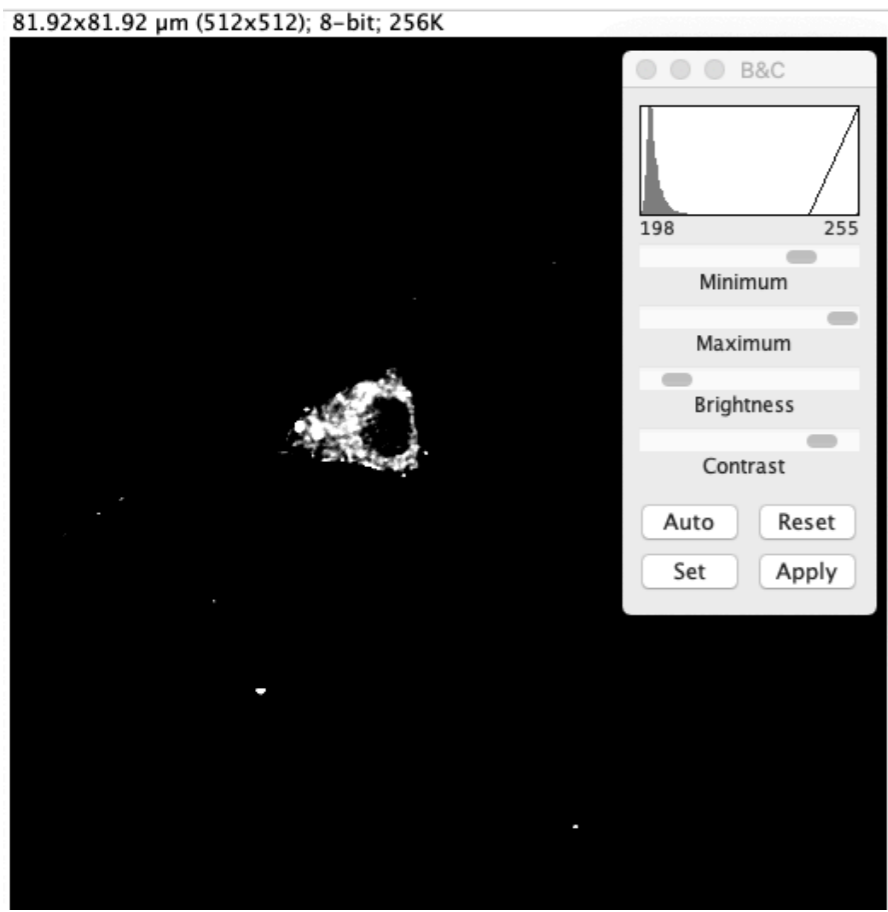
Contrast

ratio of the brightest spot to the darkest spot in the image.
It affects the range of the displayed image

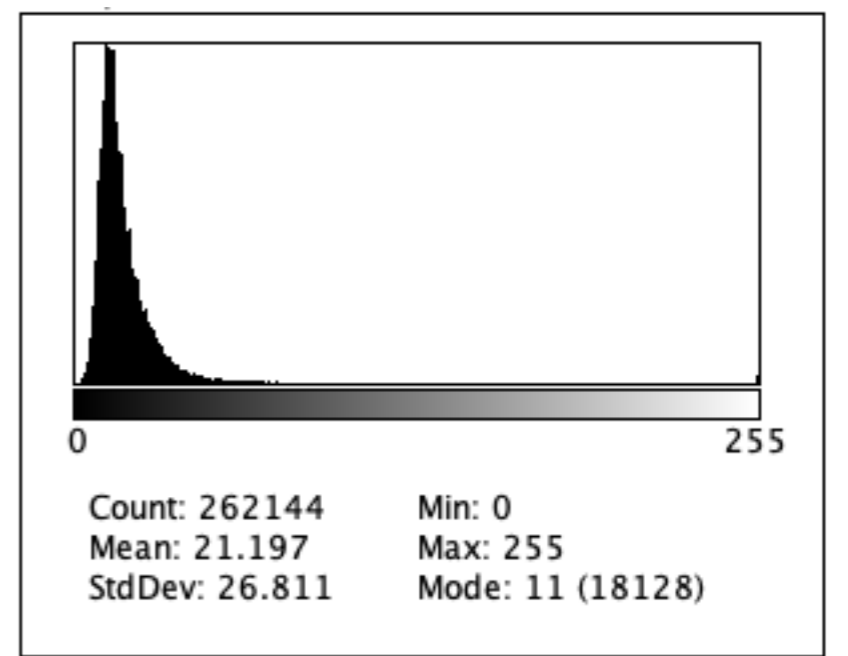
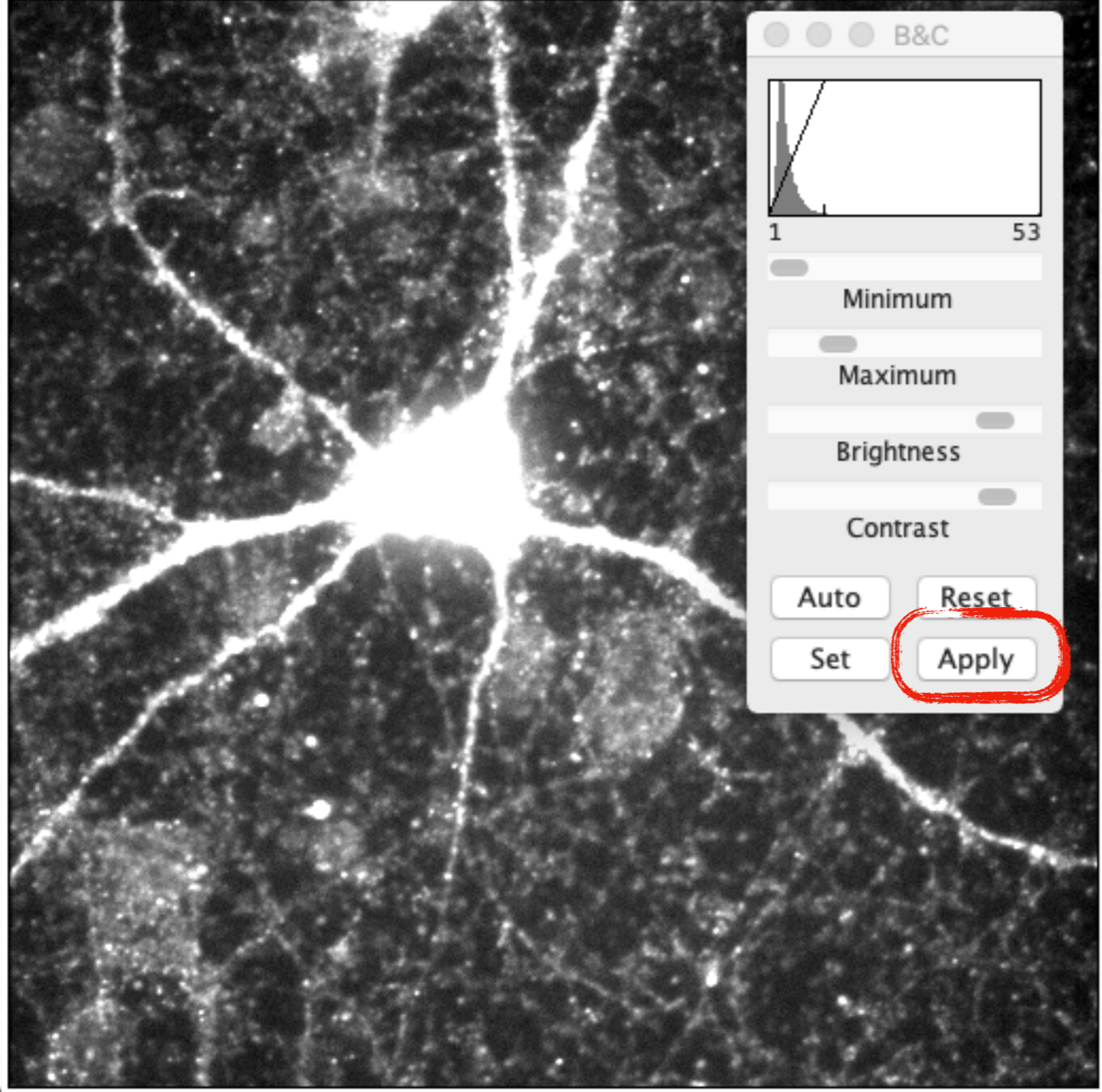


MinMax Slider

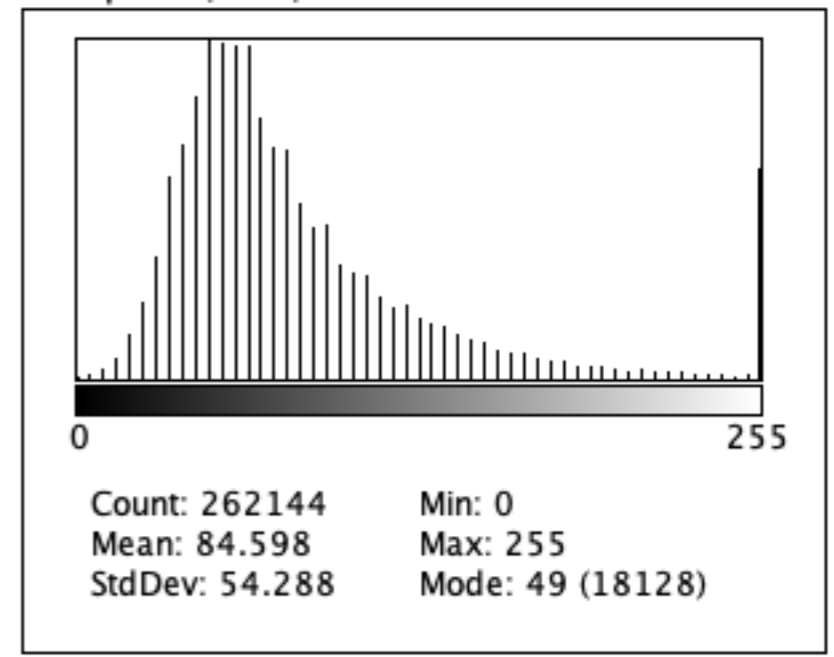
Change Brightness and Contrast simultaneously



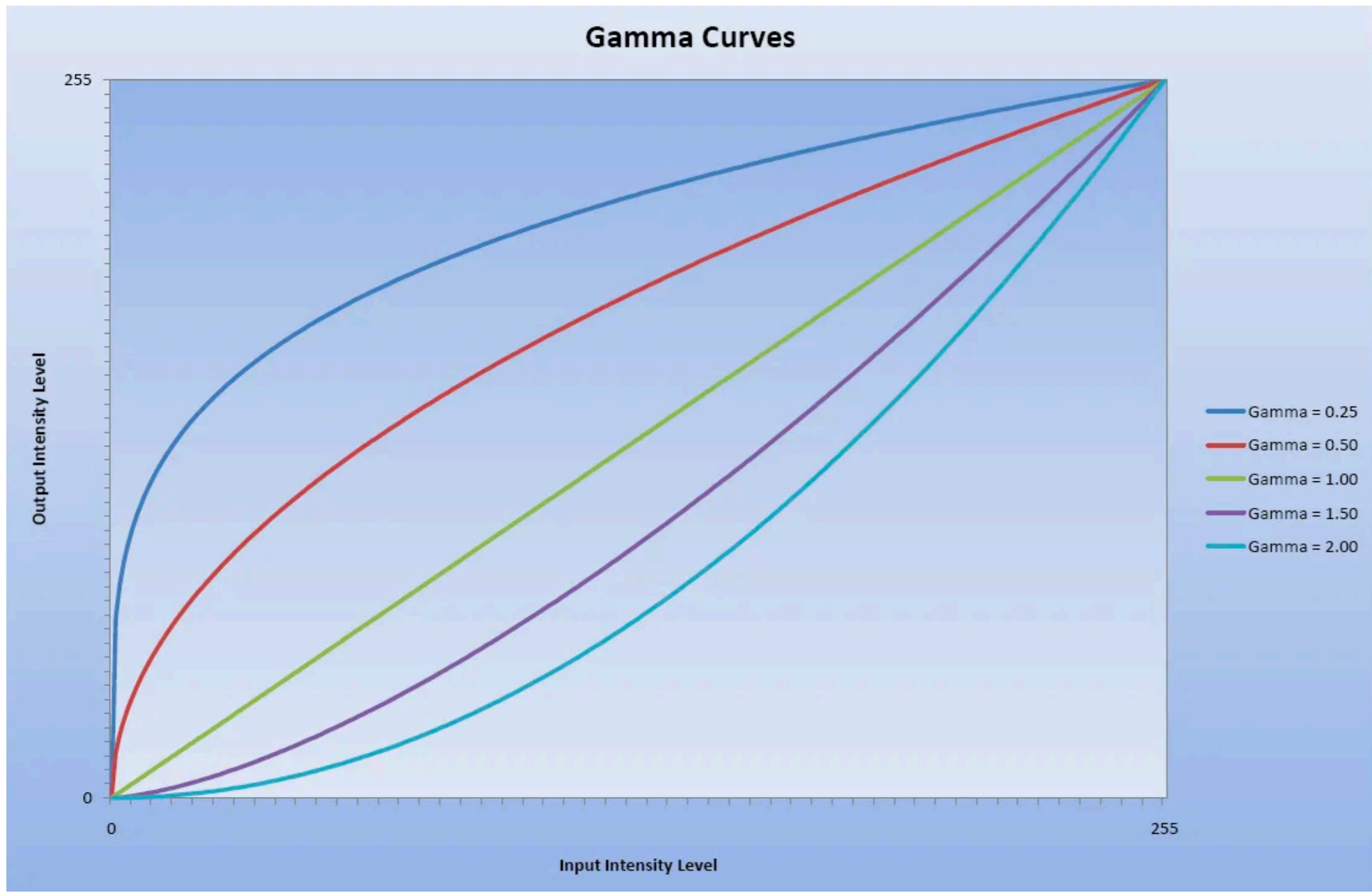
81.92x81.92 μm (512x512); 8-bit; 256K



List Copy Log Live 224 52

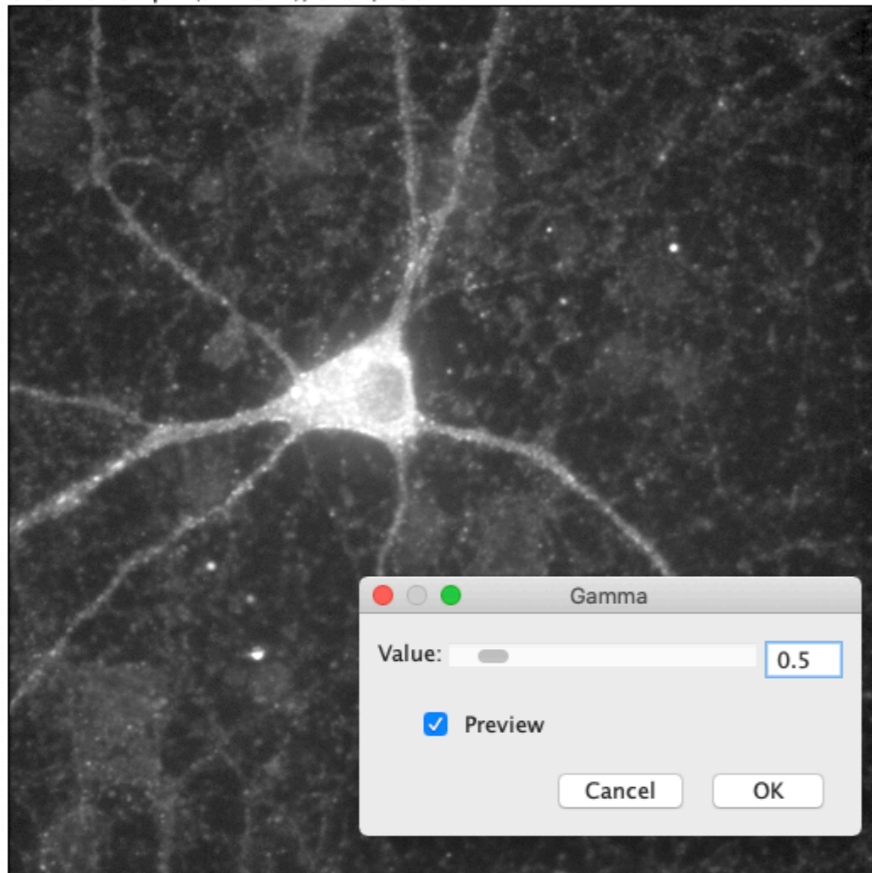


Gamma correction



<https://www.dfstudios.co.uk/articles/programming/image-programming-algorithms/image-processing-algorithms-part-6-gamma-correction/>

Gamma correction

81.92x81.92 μm (512x512); 8-bit; 256Kx81.92 μm (512x512); 8-bit; 256K