

# Using ImageJ and FIJI

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# Learning outcomes of the course

- What is ImageJ and Fiji
- Basic features of image analysis using this software
  - Add annotations
  - Intensity measurements
  - Drift corrections
  - Measure distances
  - Co-localization analyses
  - Basic features of analyzing time-lapse images

# What is ImageJ and FIJI?

- ImageJ and FIJI are freeware used for image analysis in life sciences
- Freeware: nobody will ask you money for its use.

## Collaboration

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The Fiji project is driven by a strong desire to improve the tools available for life sciences to process and analyze data. To this end, Fiji collaborates closely with the following projects:



ImageJ2



Bio-Formats



OME



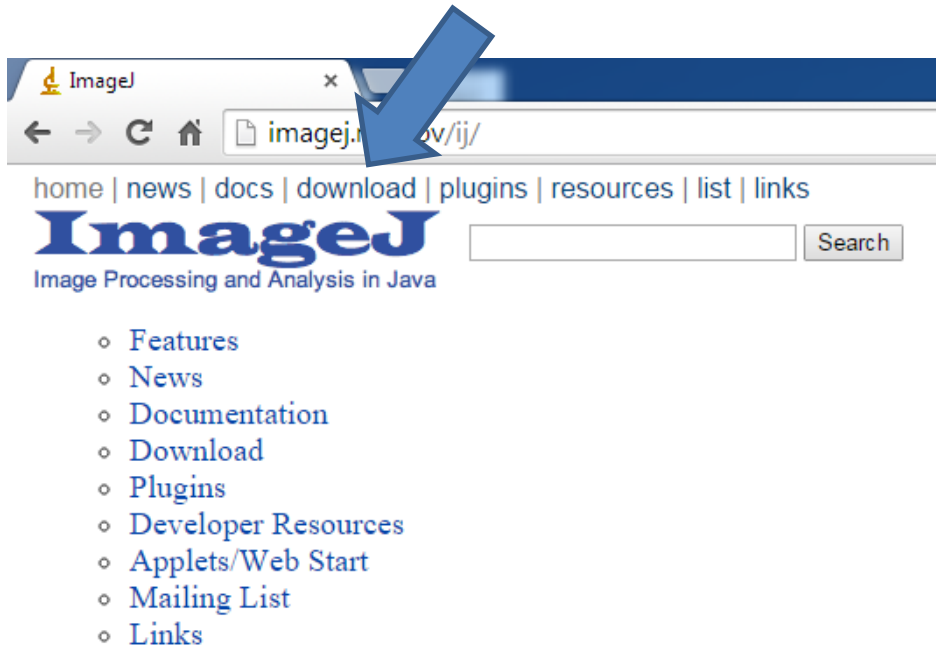
µManager



KNIME

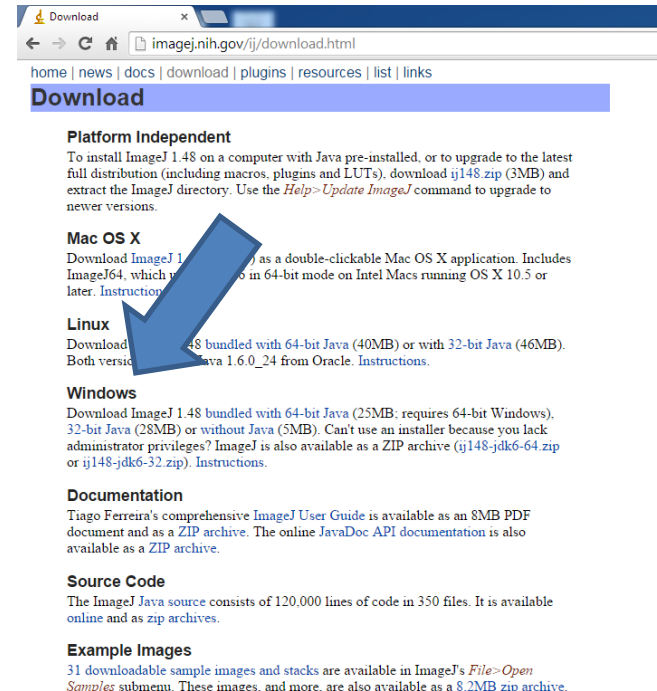
# How to get started?

## Step 1



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## Step 2

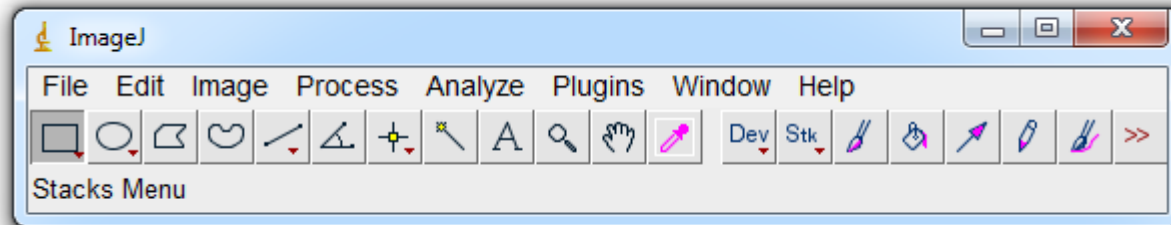


You can also browse the ImageJ download directory at [imagej.nih.gov/ij/download/](http://imagej.nih.gov/ij/download/). Refer to the [release notes](#) for a list of new features and bug fixes.

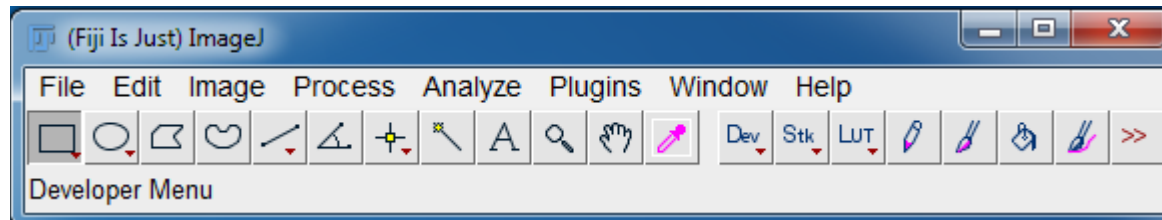
[top](#) | [home](#) | [news](#) | [docs](#) | [download](#) | [plugins](#) | [resources](#) | [list](#) | [links](#)



# Interface of the software



OR?



# Assume that you have a time-lapse image. So what is next?

- Check the size of the image (dimensions should be at least 512x512 dpi during image acquisition; French et al., 2008-course literature)
- Do you need to analyze it?

# How do I know which is the size of my image

The image shows the ZEN 2012 software interface. The main window displays the 'Info' tab for a file named 'TSN2 TIP8 30 min 5.avi'. The 'Dimensions' section is highlighted with a red box, showing 'x: 463, y: 512, time: 18, channels: 2, 8-bit'. A blue arrow points to the 'Info' tab in the left sidebar. A calculator window is open, showing the calculation  $0.227 \times 463 = 105.101$ . The status bar at the bottom indicates CPU usage at 0% and Free RAM at 2.4 GB.

**Method**

- Maximum intensity projection
- Color-coded projection
- Image calculator
- Average
- Filter
- Linear unmixing
- Ion Concentration
- Correlation
- Modify Series
- HDR- imaging
- Channel Alignment
- Copy

**Method Parameters**

Input image:  Select

**Info**

Name: TSN2 TIP8 30 min 5

Description:

Notes:

User: eogu0001

Scaling X: 0.227  $\mu$ m

Scaling Y: 0.227  $\mu$ m

Scaling Z:

Dimensions: x: 463, y: 512, time: 18, channels: 2, 8-bit

Image size: x: 104.99  $\mu$ m, y: 116.12  $\mu$ m

Scan Mode: plane, time series

Zoom: 3.7

Objective: Plan-Apochromat 20x/0.8 M27

Pixel dwell: 1.75  $\mu$ s

Average: line 4

Master gain: Ch1: 928, Ch2: 535

Digital gain: 1.00

Digital offset: 0.00

Pinhole: 250  $\mu$ m

Filters: Ch1: 431 - 504, Ch2: 529 - 595

Beam splitters: MBS: MBS 458/514, MBS\_InVis: MBS -405

Lasers: 458 nm: 5.0 %, 514 nm: 0.3000 %

**Calculator**

View Edit Help

0.227 \*  
463

MC MR MS M+ M-  
← CE C ± √  
7 8 9 / %  
4 5 6 \* 1/x  
1 2 3 - =  
0 . +

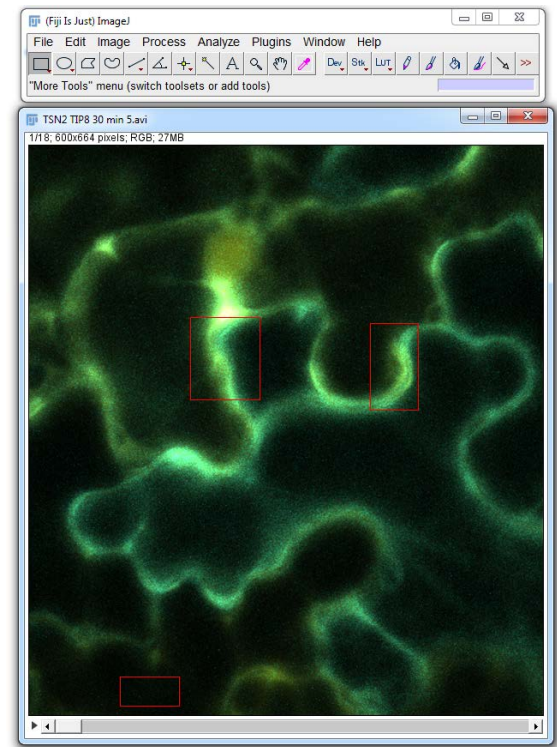
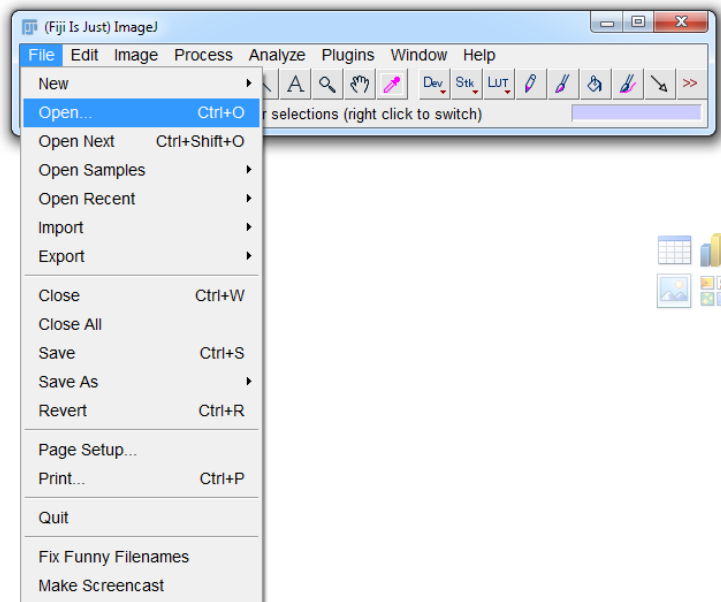
**Images and Documents**

- 3 b.lsm 0.25 MB
- 3 b.lsm 0.25 MB
- TSN2 ...n 5.avi 8.1 MB

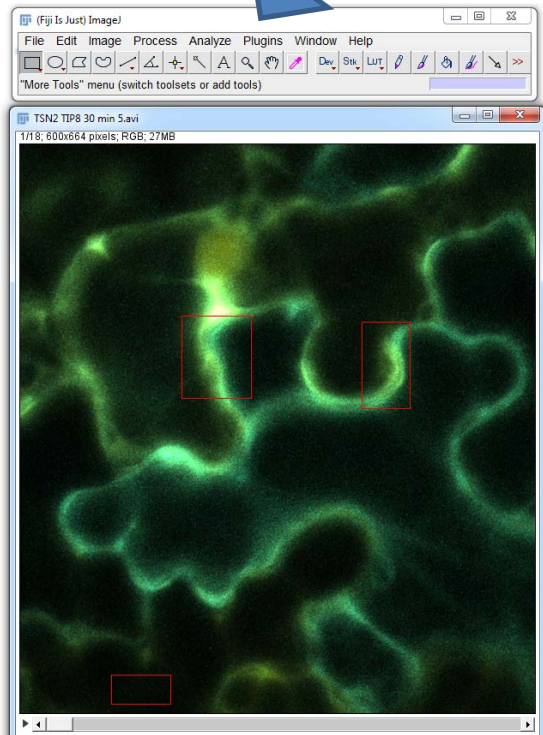
CPU: 0% Free HD: 0.33 TB  
Free Ram: 2.4 GB

# Open your file with FIJI

- FIJI is compatible with 'czi'!!!!

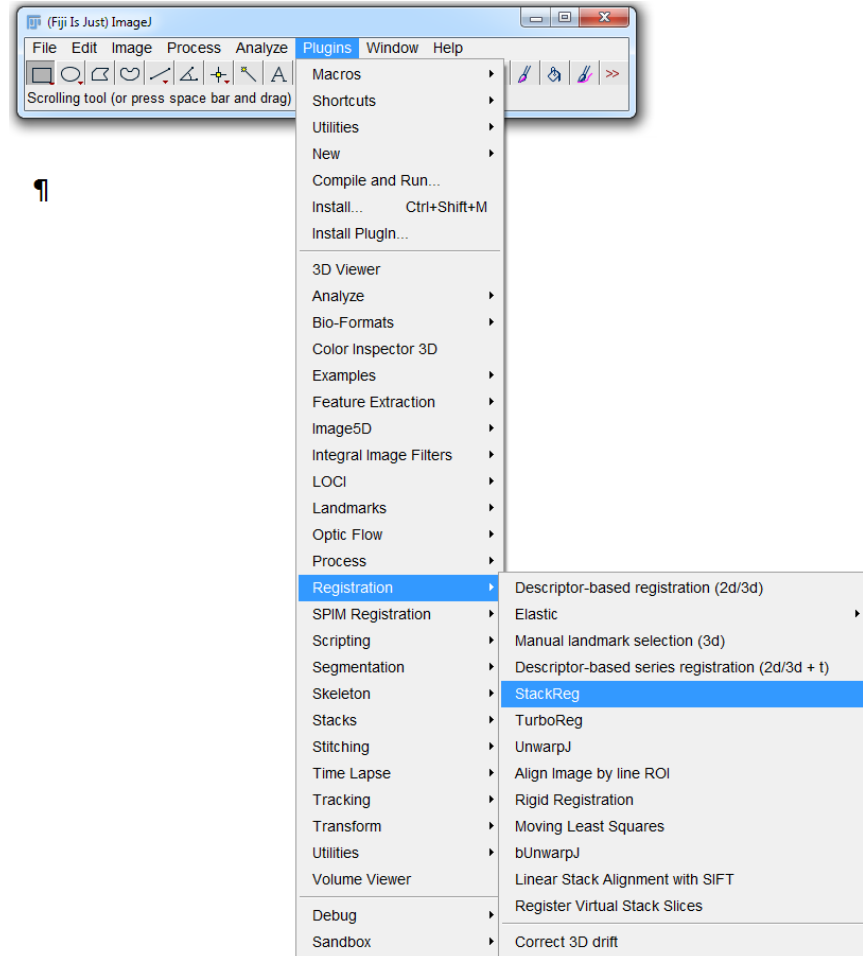


# My image is 'drifting'. What shall I do?

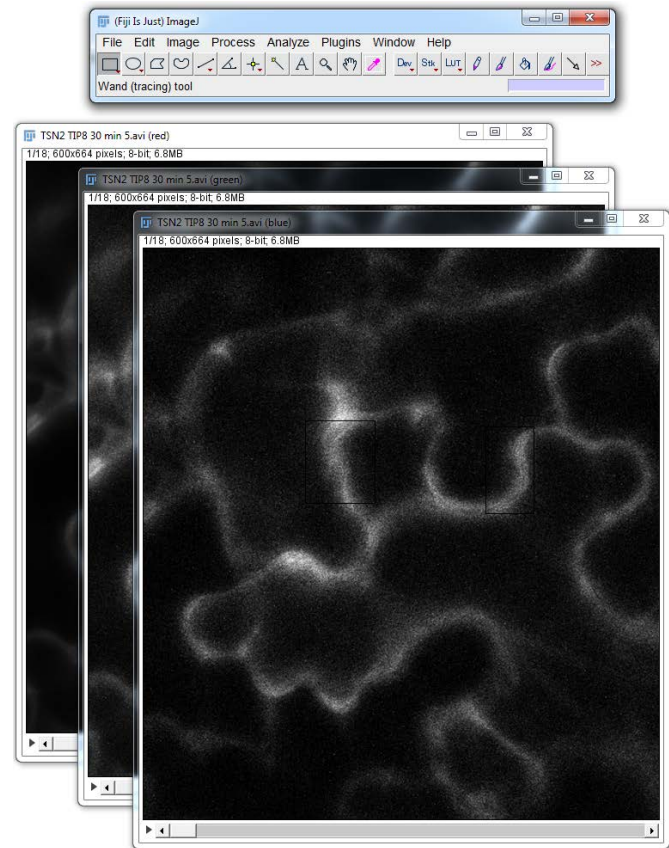
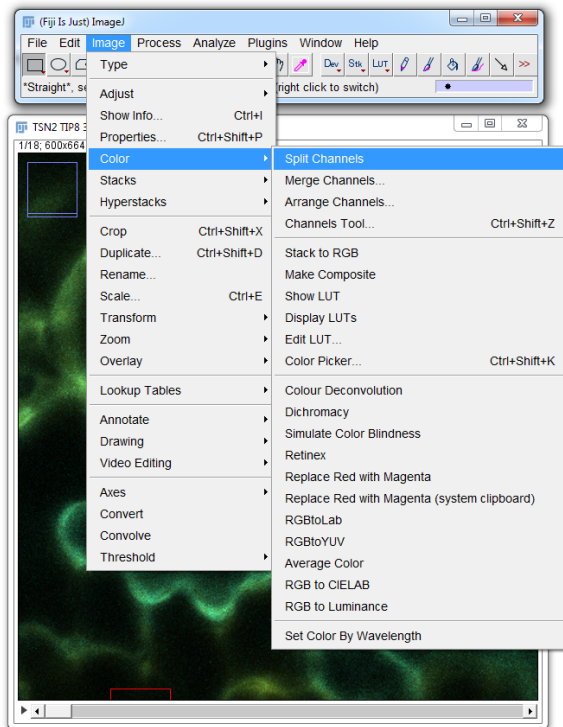


How does it work?

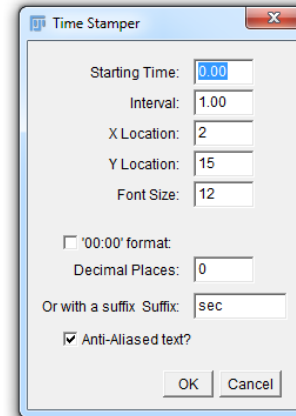
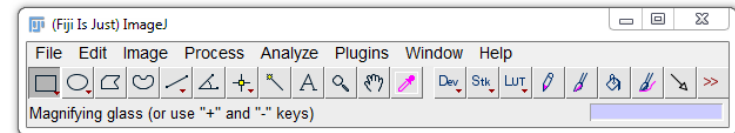
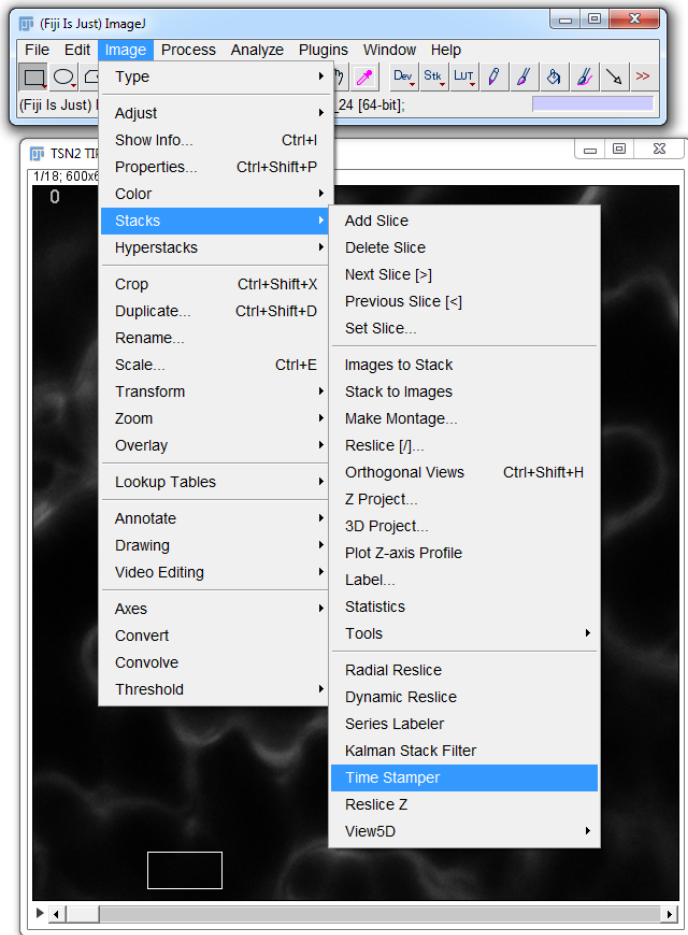
- [We are using Rigid body transformations](#)
- <http://bigwww.epfl.ch/thevenaz/stackreg/>



# If you have channels you can split them

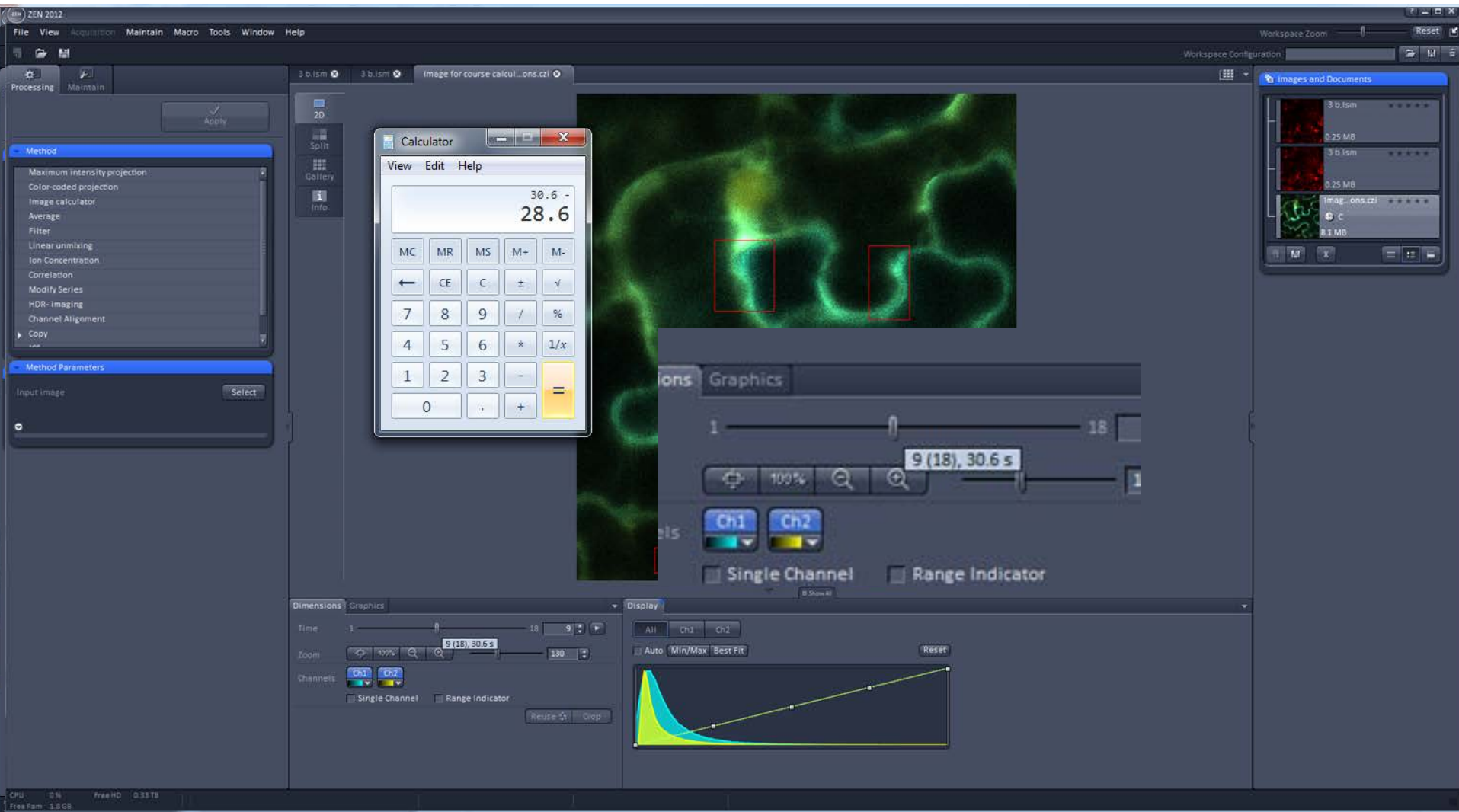


# Lets add time stamps

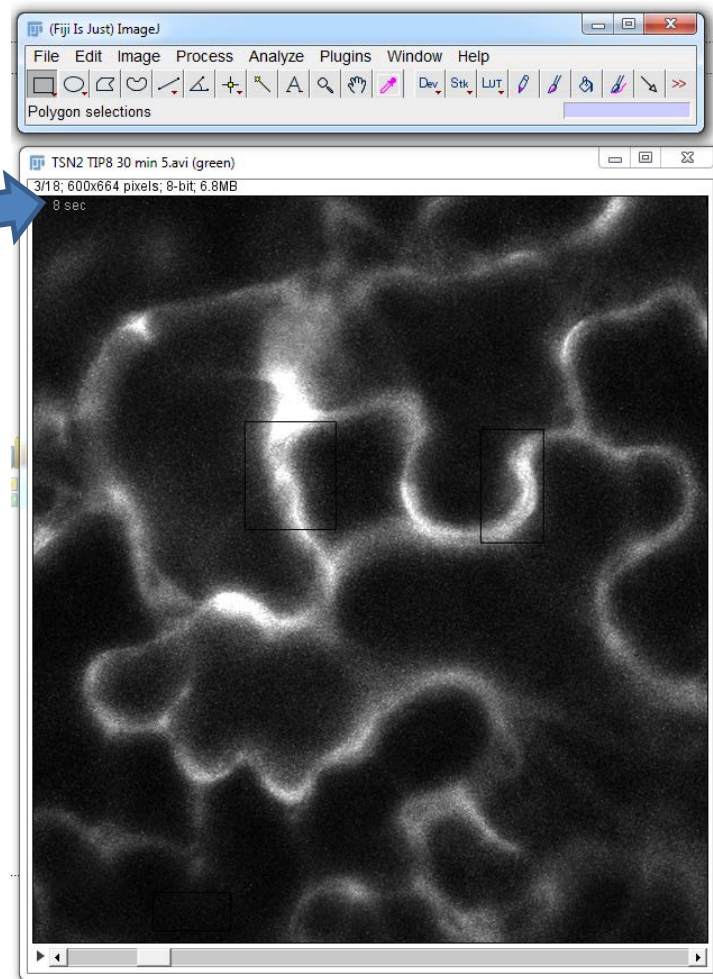
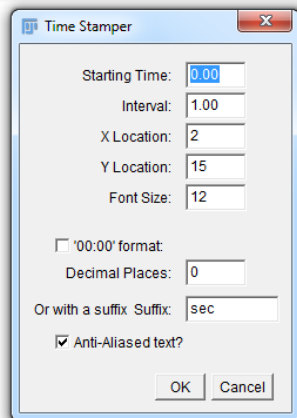
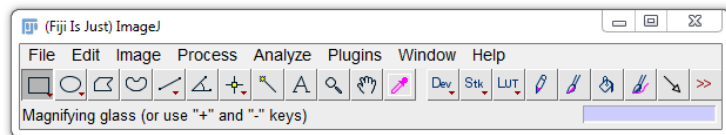




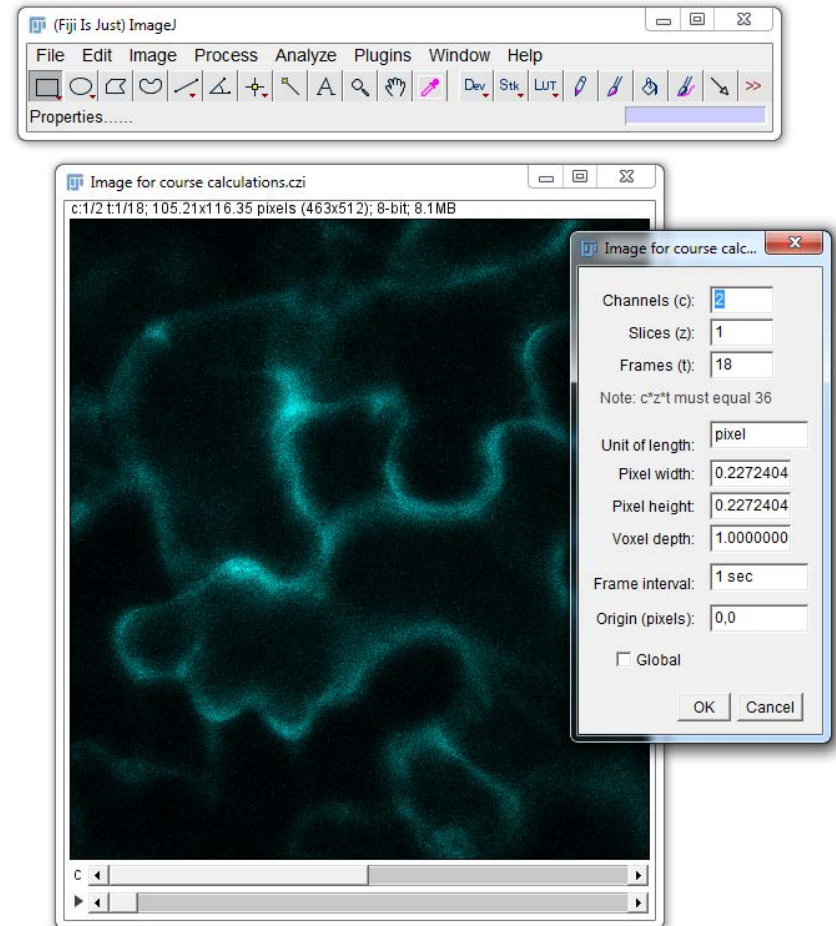
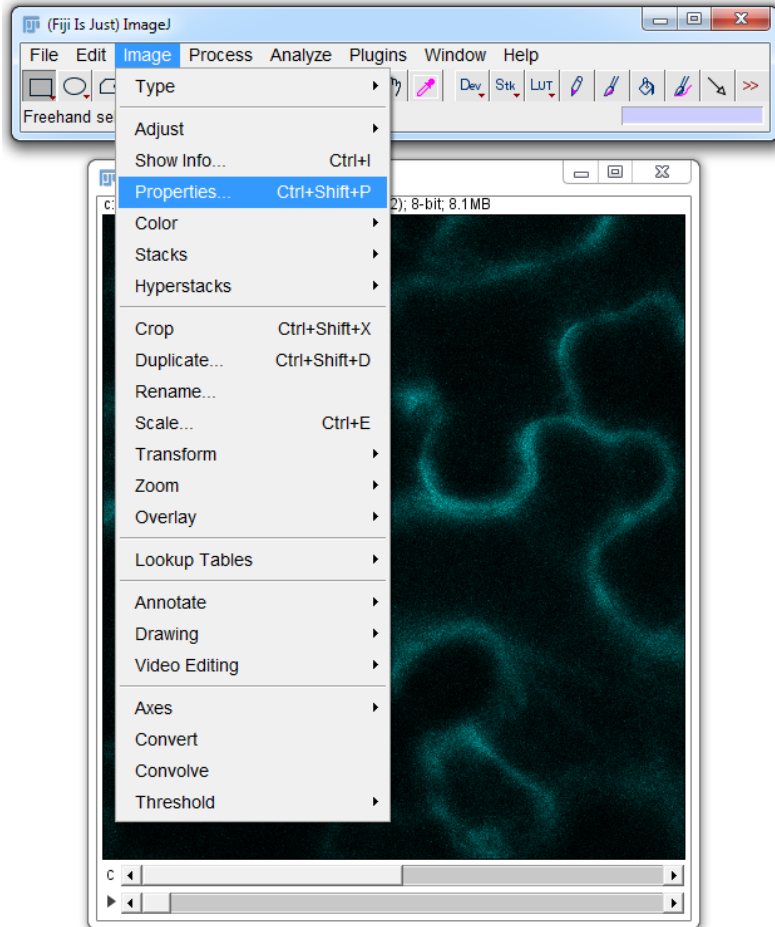
# Calculation of interval time

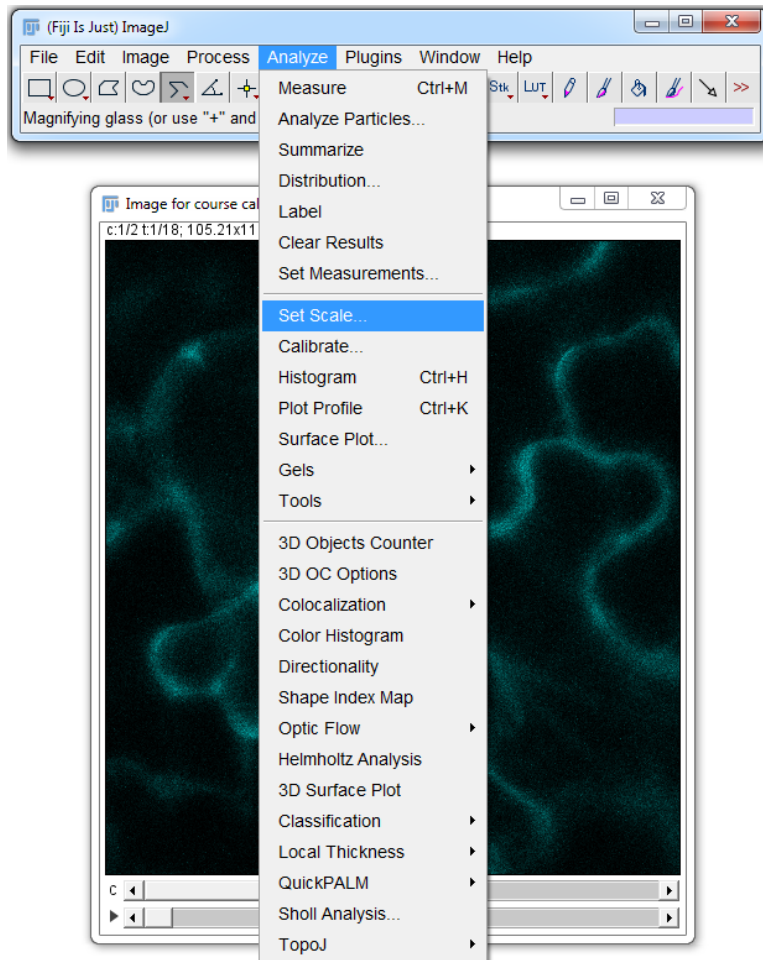




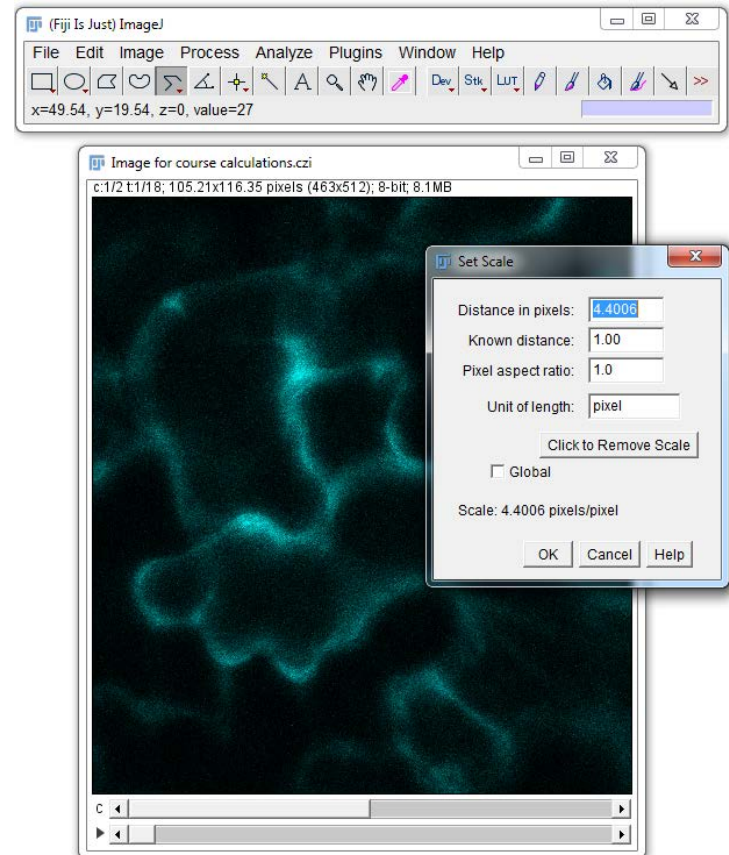


# Set up scale bars

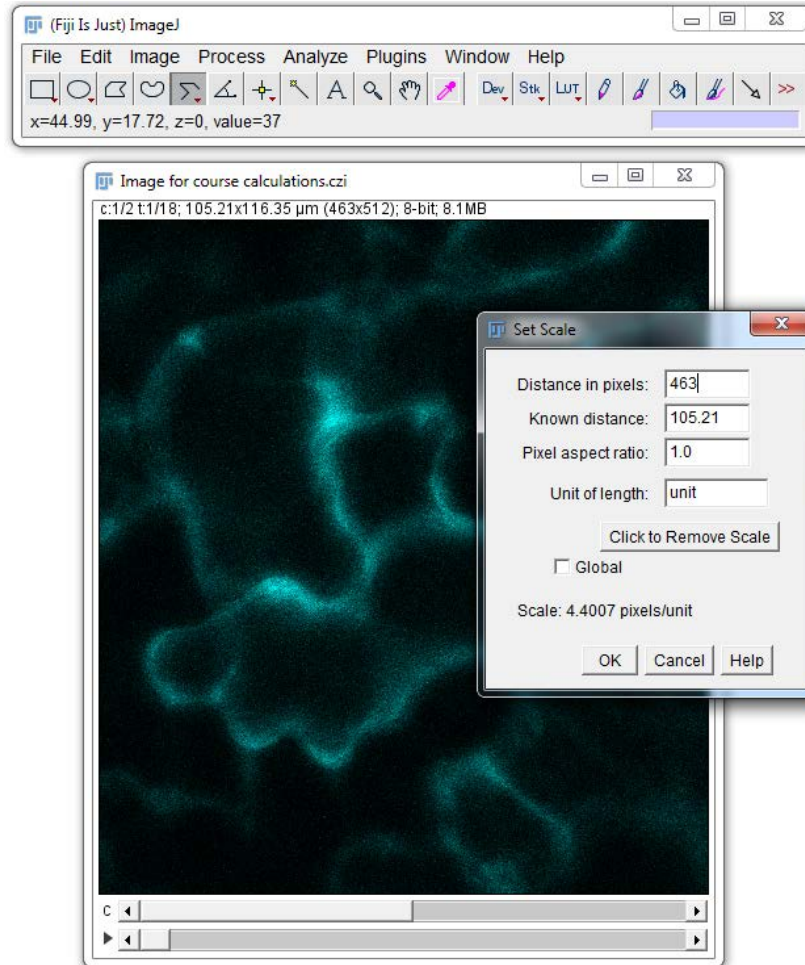




## 1. If you have 'CZI' files



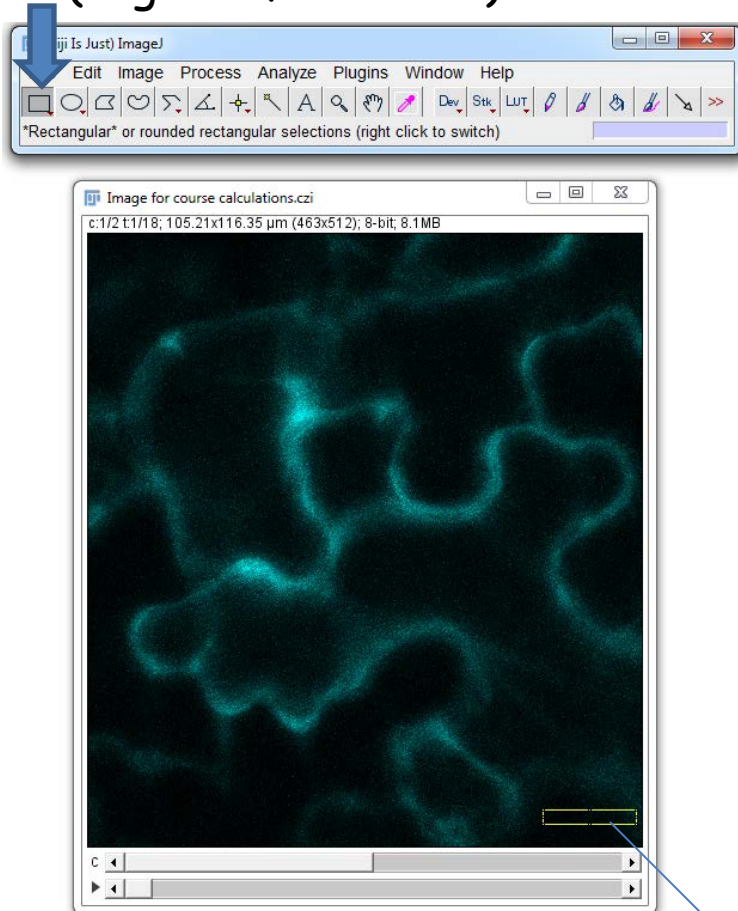
## 2. If you do not have 'CZI' files (e.g. 'avi' files etc.)



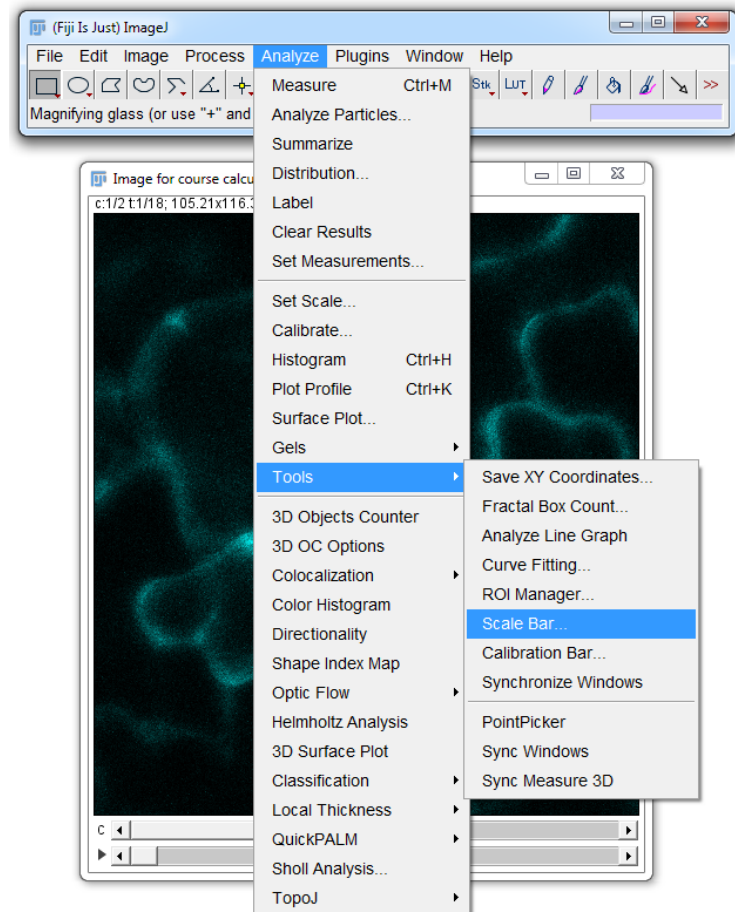


# Adding the scale bar on the image

Step 1: select where you want the scale bar  
ROI (region of interest)

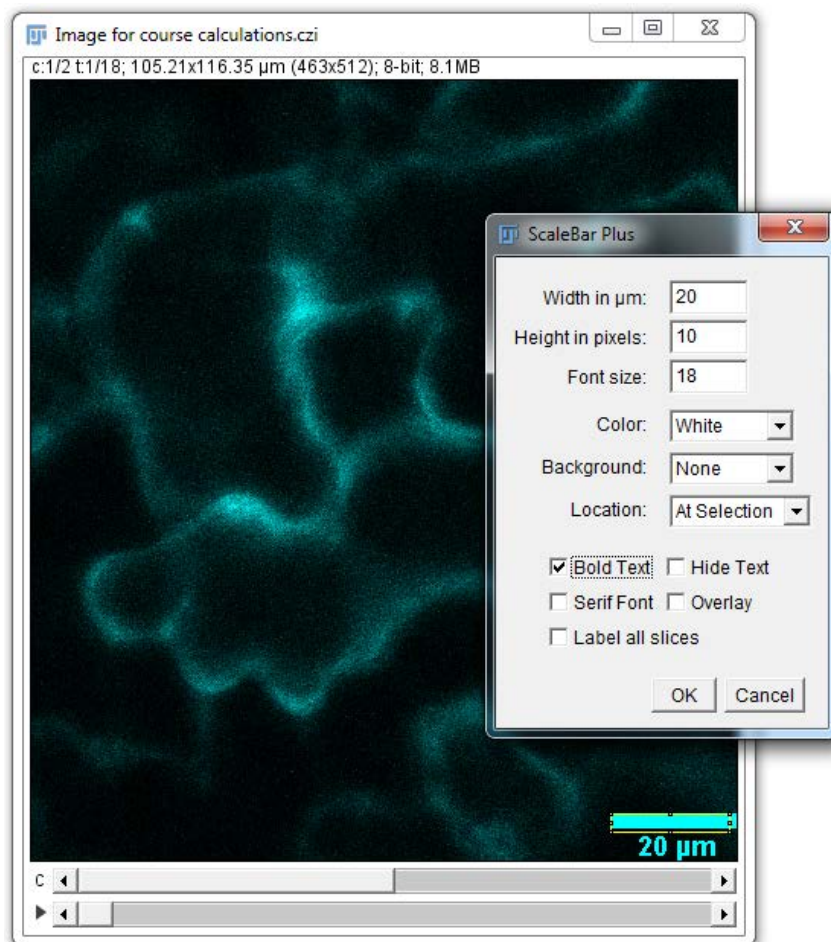


Step 2: do the following

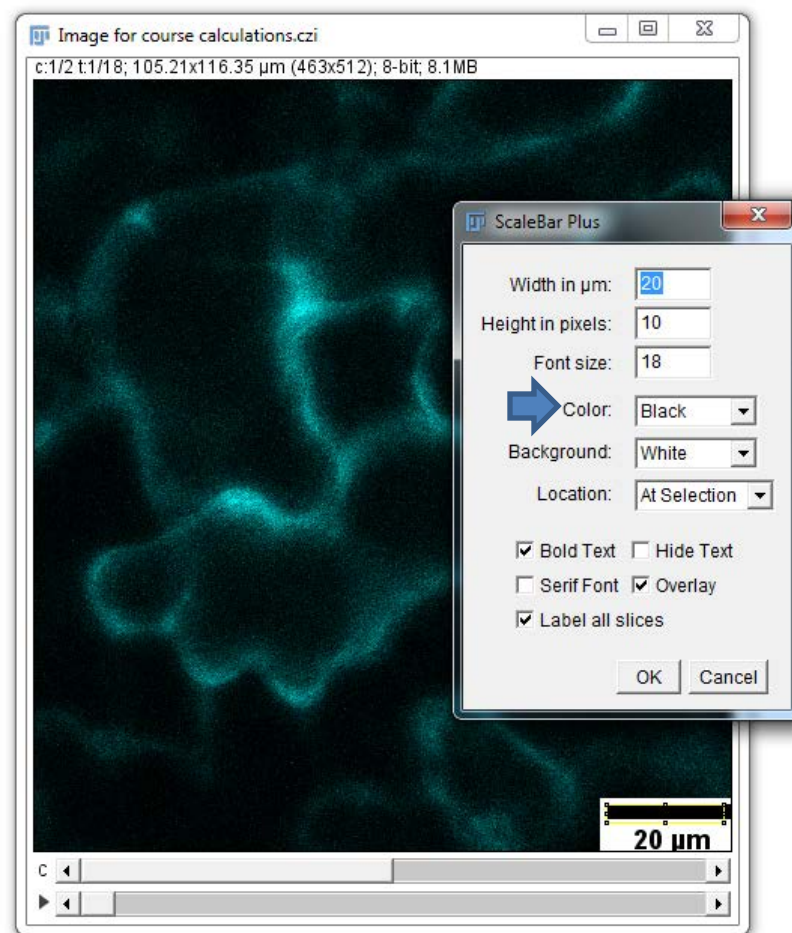


I want my scale bar here

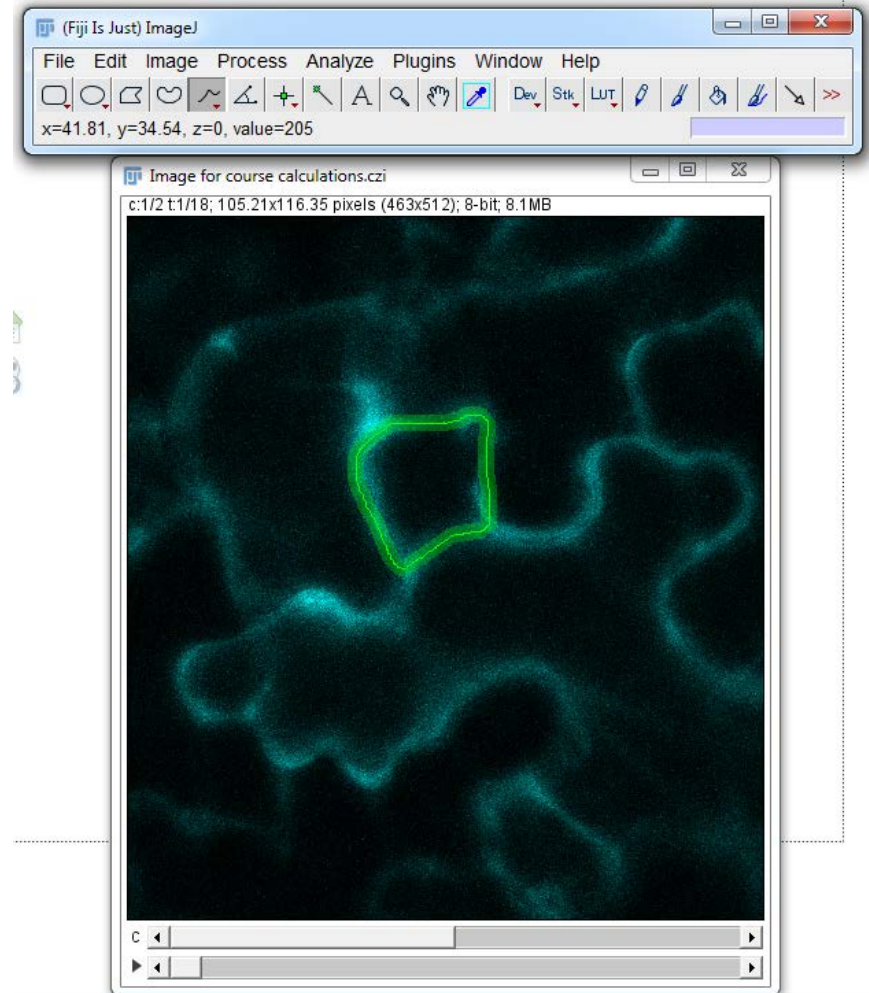
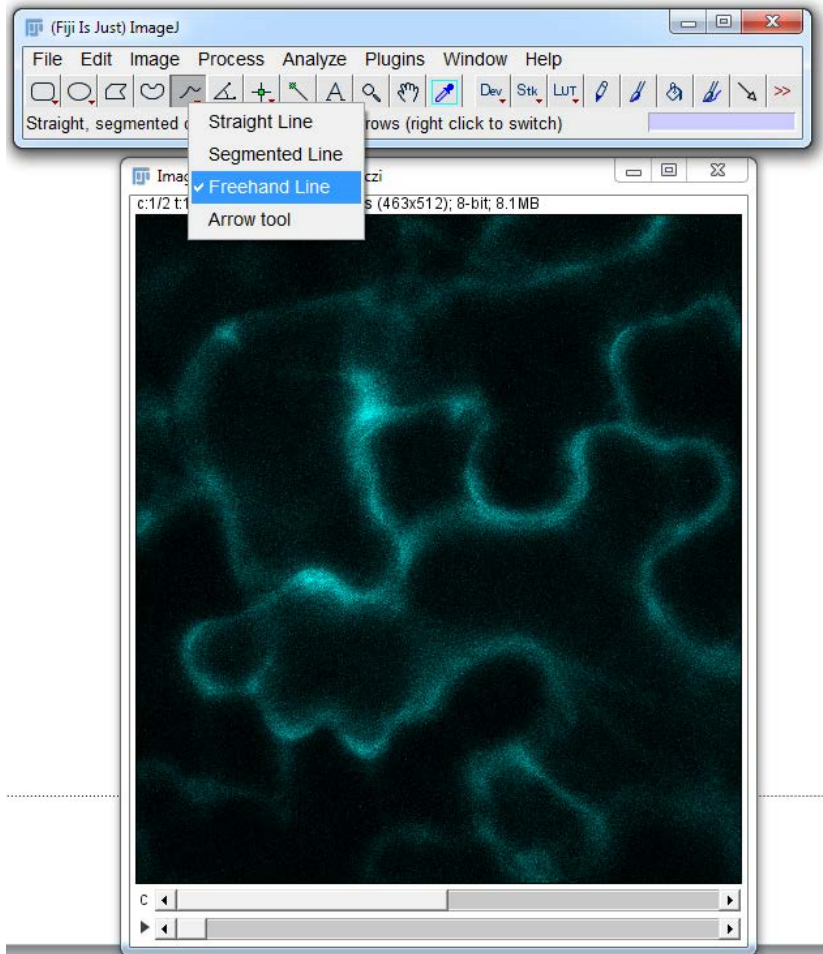
Step 3: this box appears.



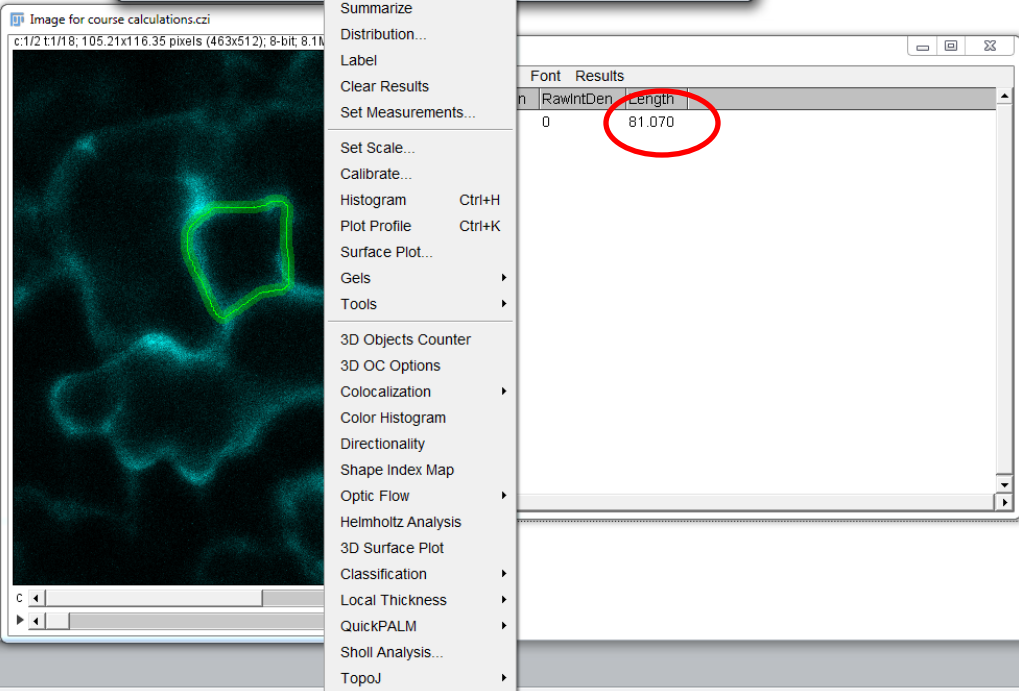
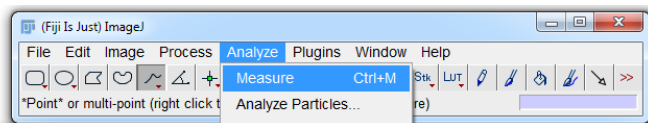
Step 4: adjust 'color' and...done.



# Now I can make dimension measurements

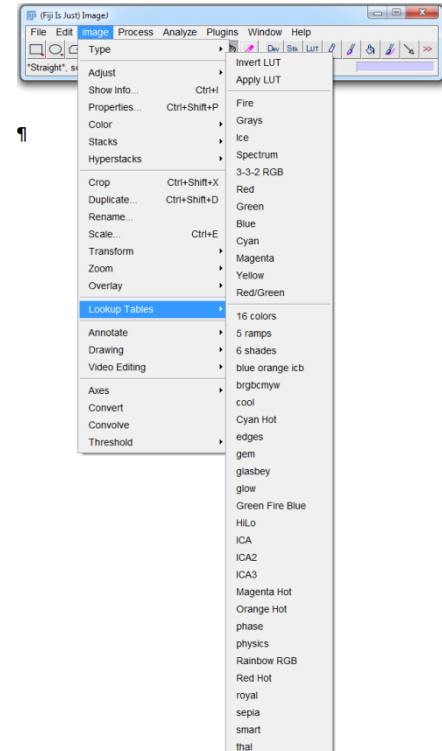
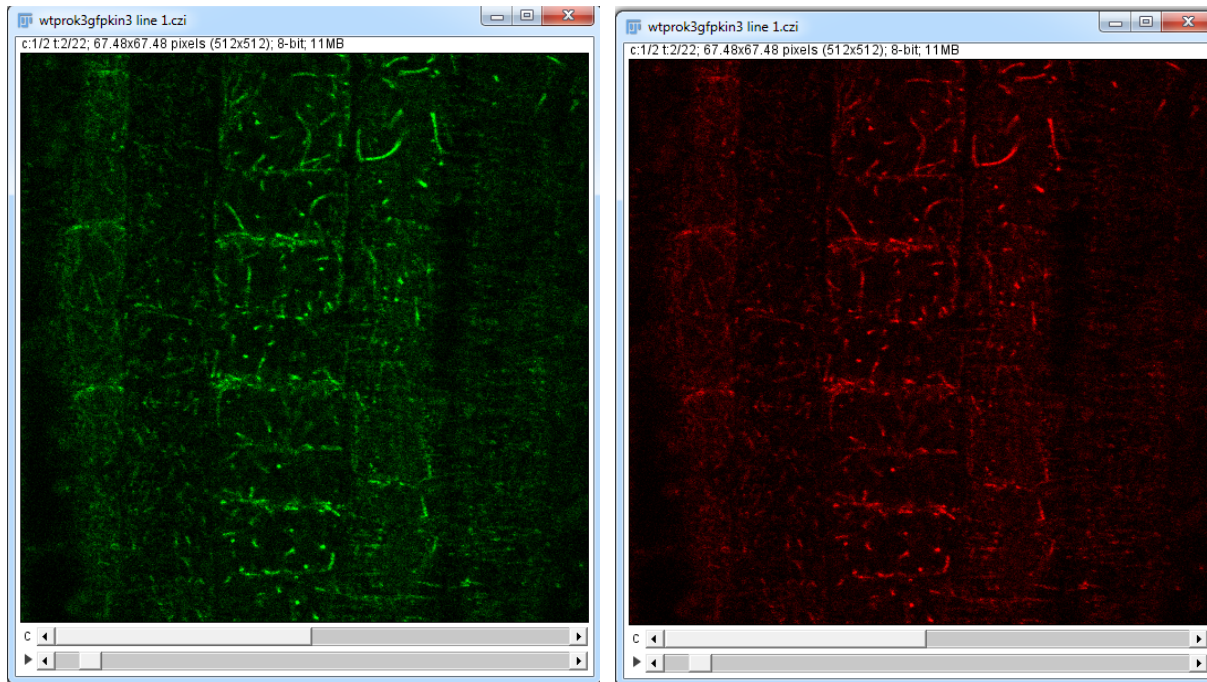




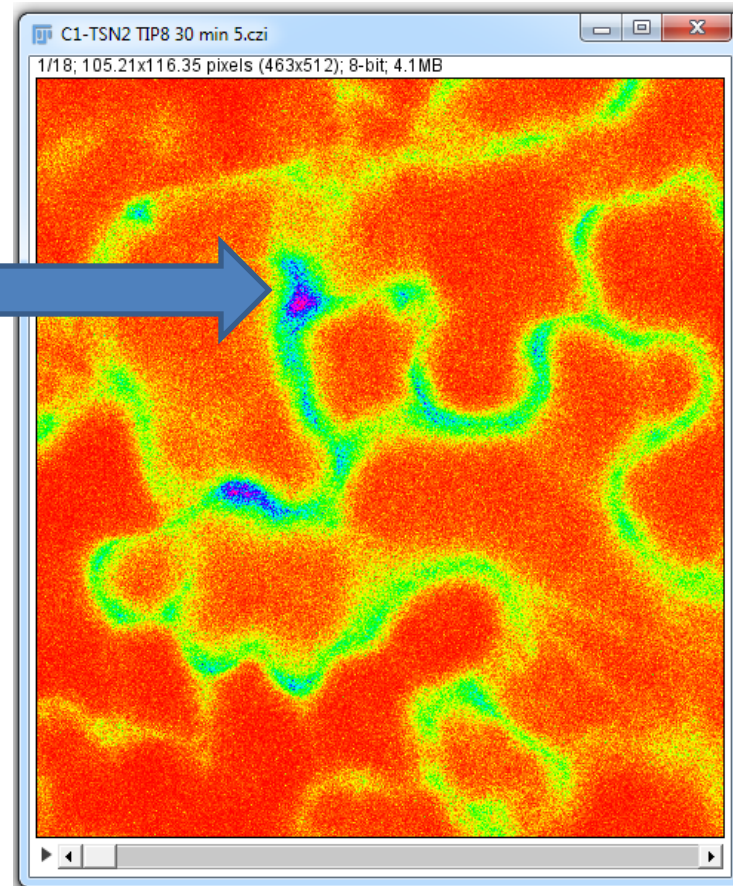
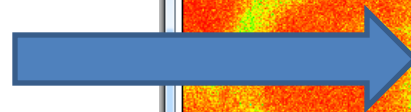
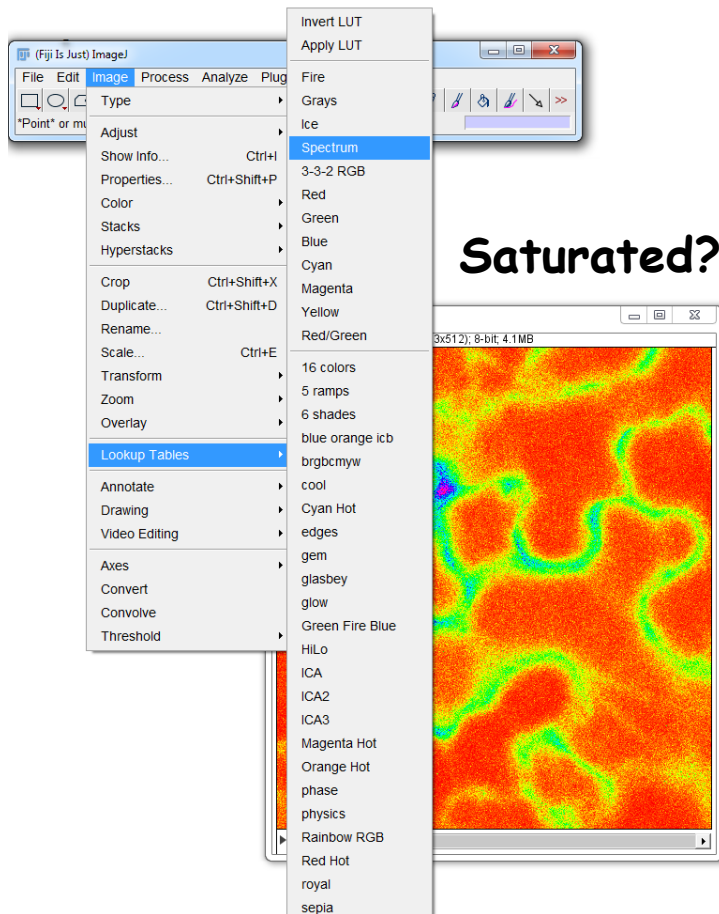




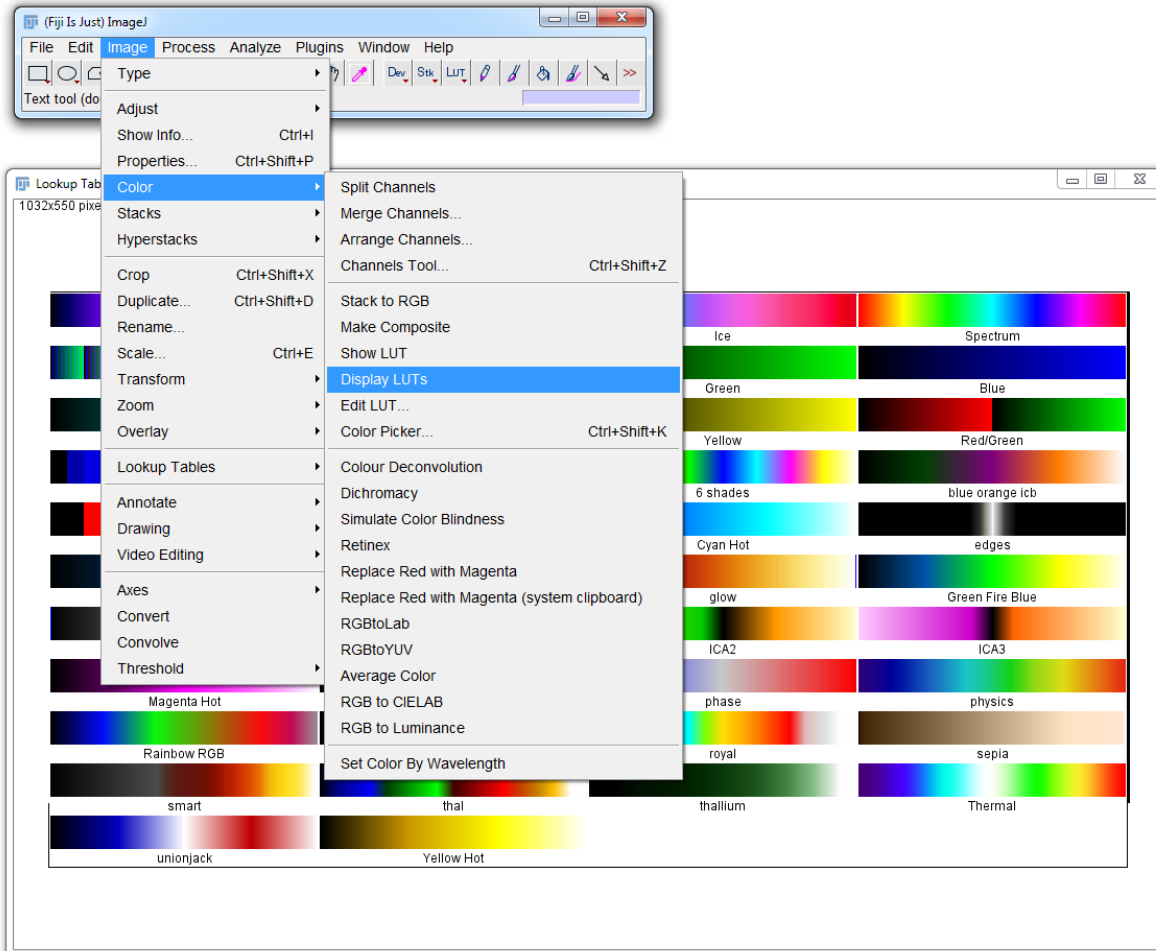
# Adjusting colors



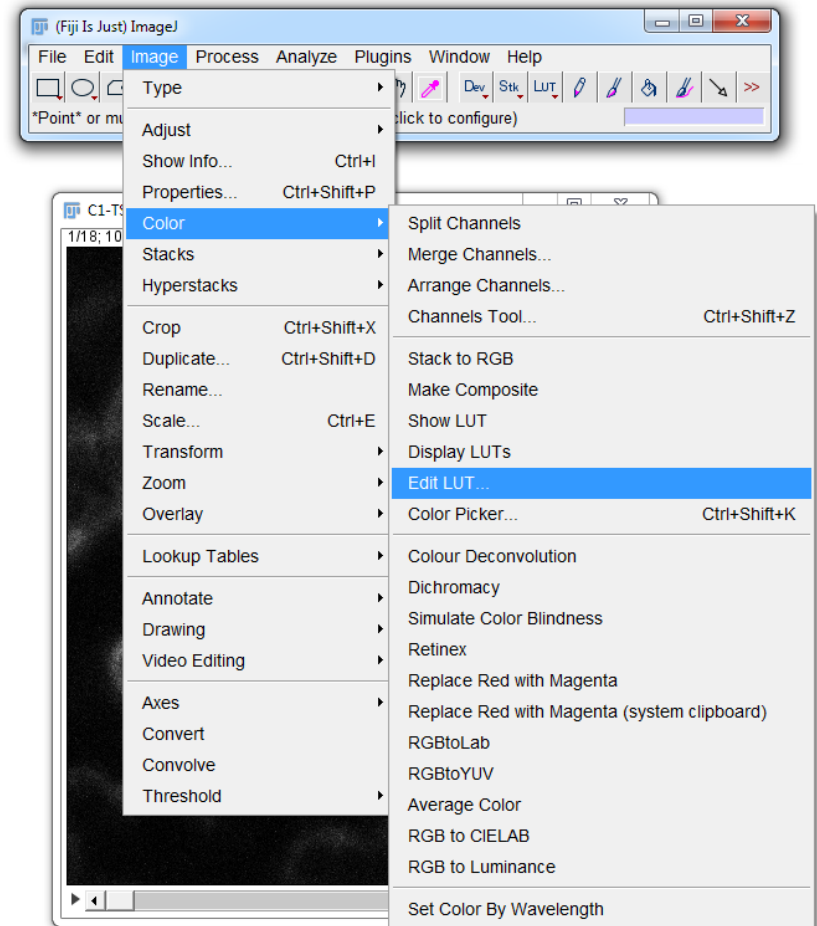
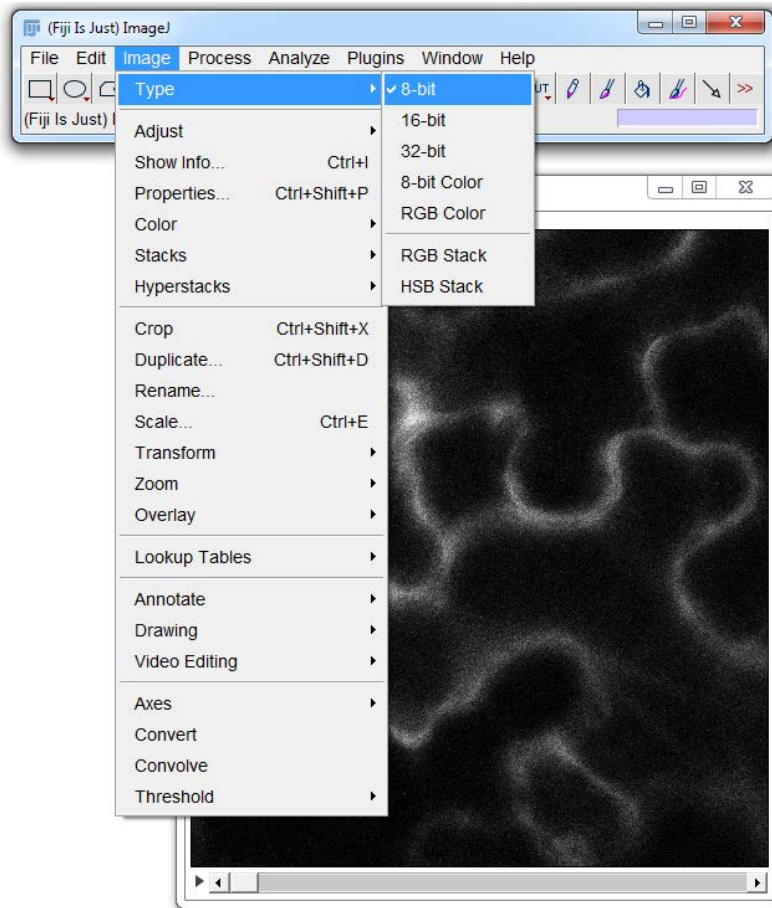
Solution: Use grey scale images



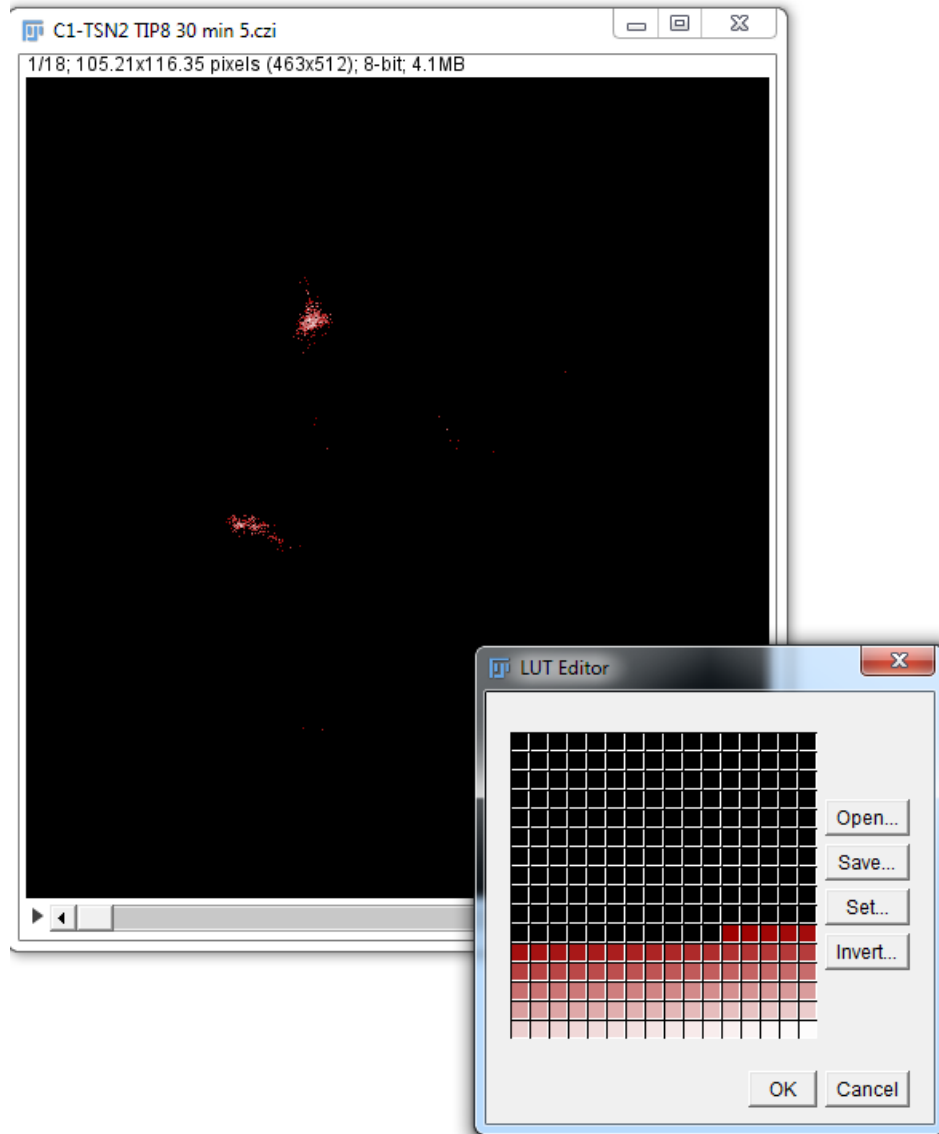
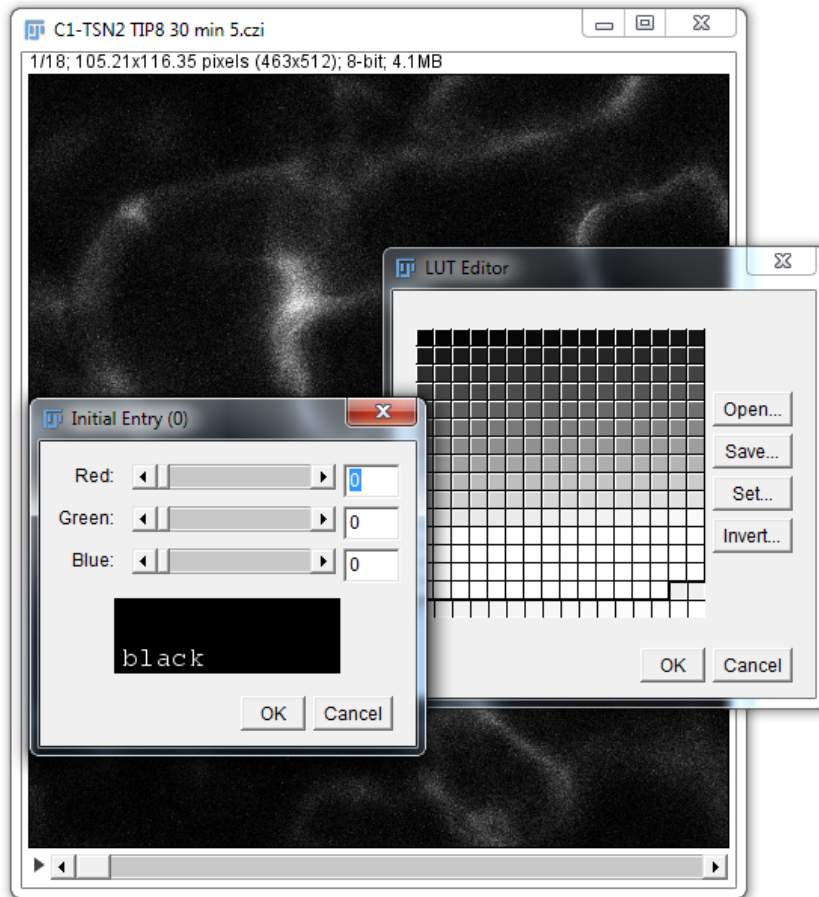
# What is a Look Up Table (LUT)?



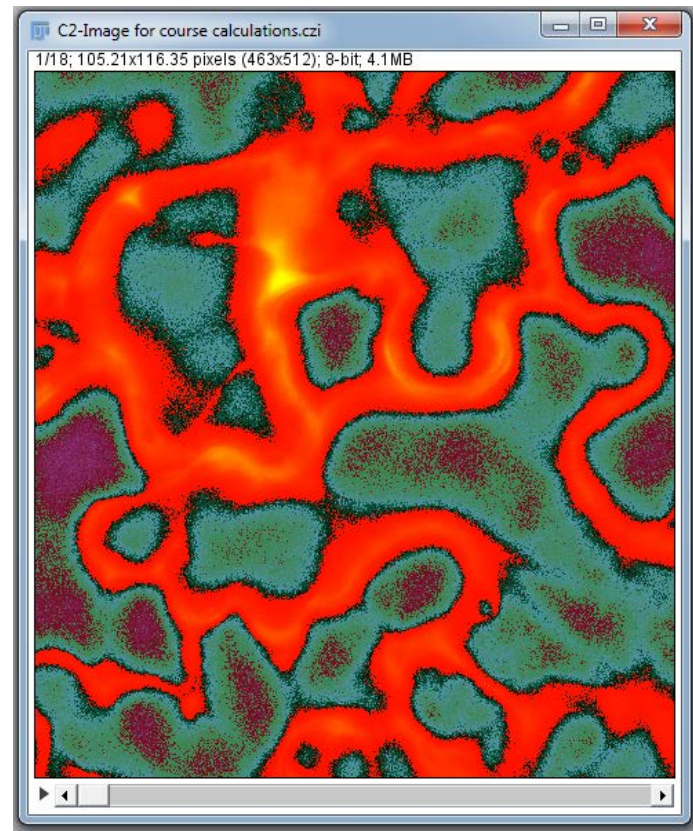
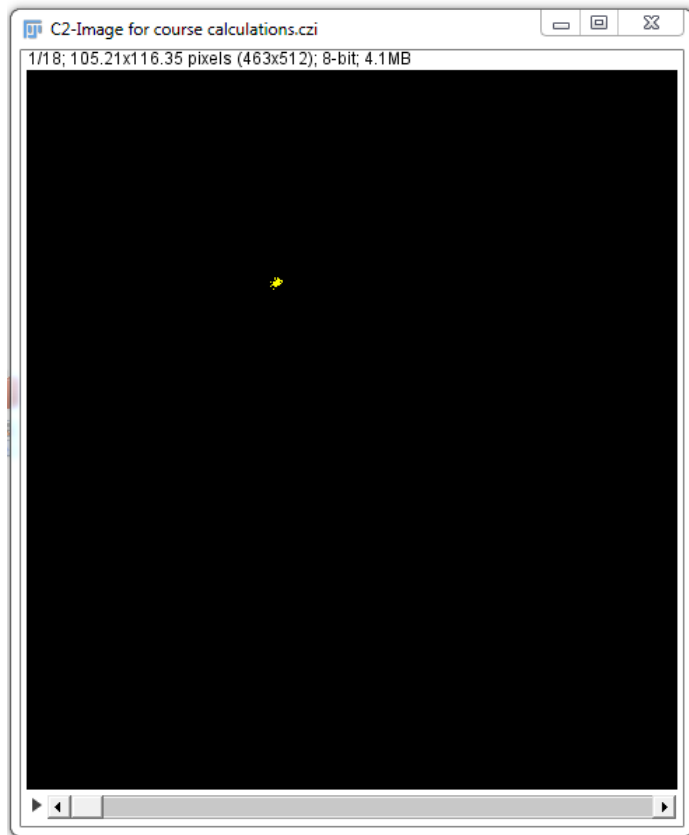
# Highlighting certain signal intensities



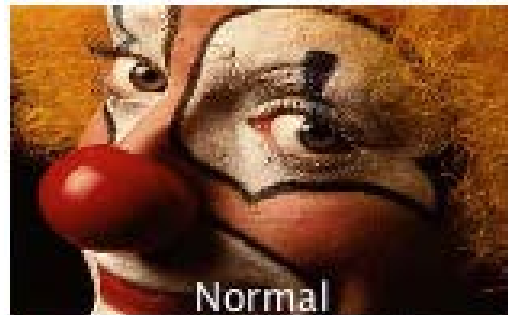
# Are my colors in linear range?







# Types of color blindness



Normal



Protanopia (no red)



Deutanopia (no green)



Tritanopia (no blue)



Protanomaly (low red)



Deuteranomaly (low green)



Tritanomaly (low blue)

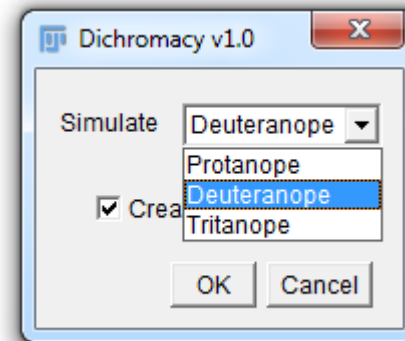
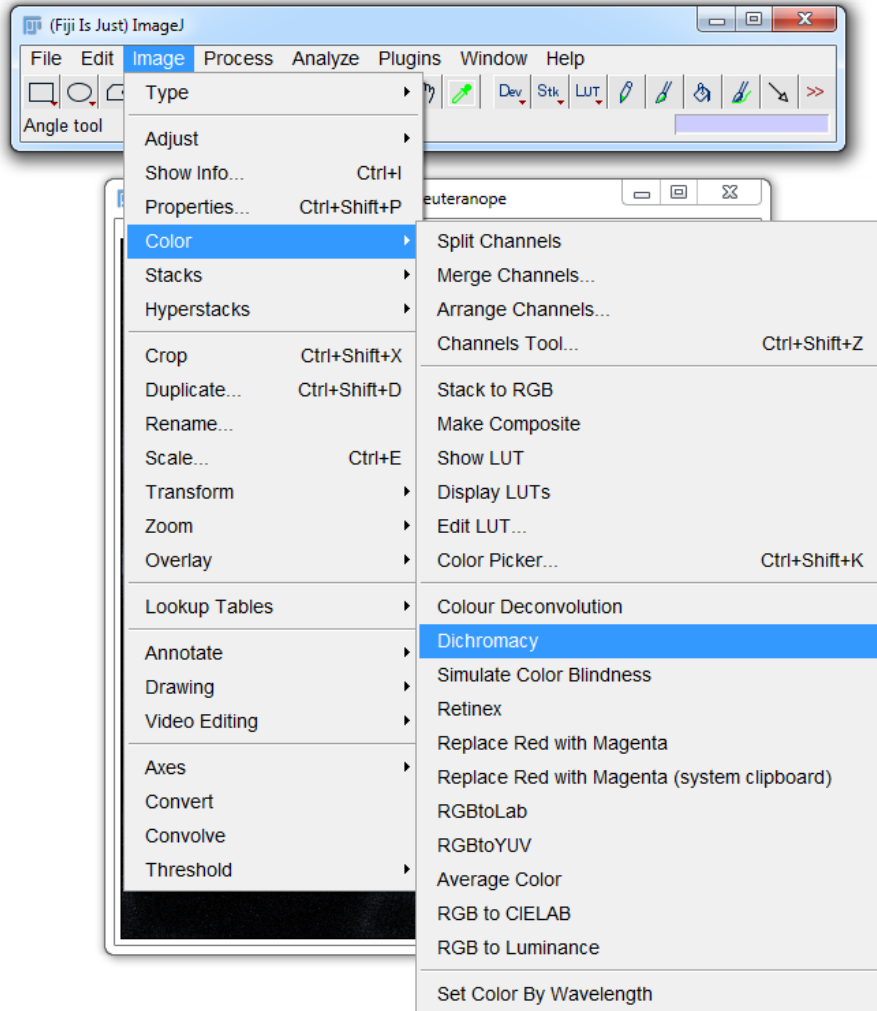


Typical Monochromacy

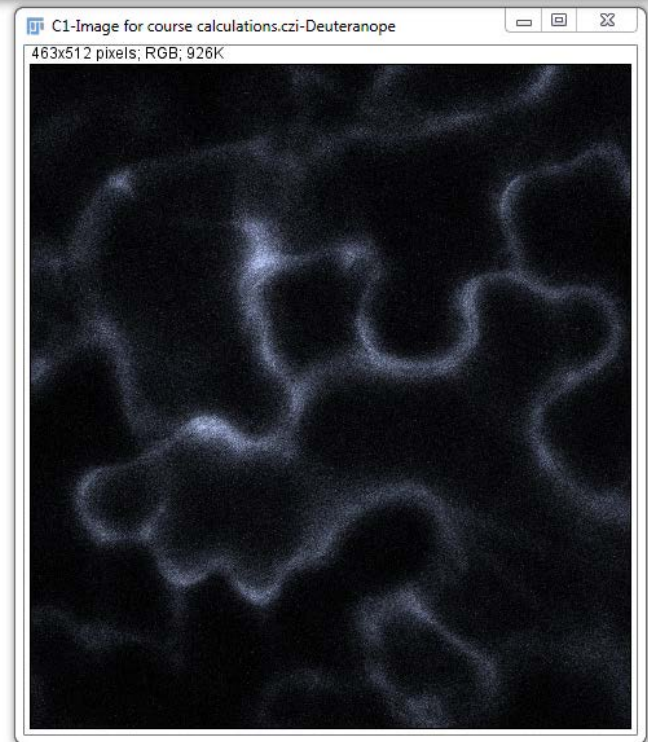
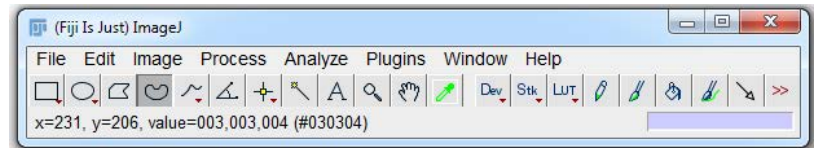
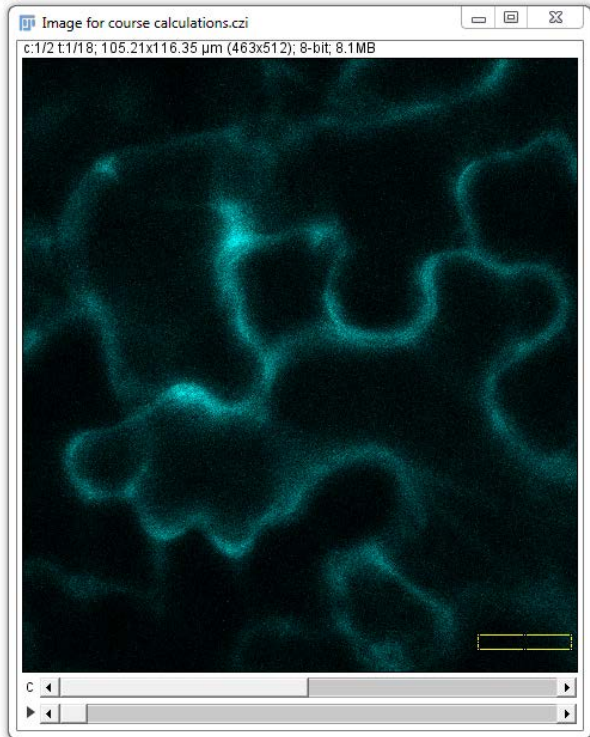
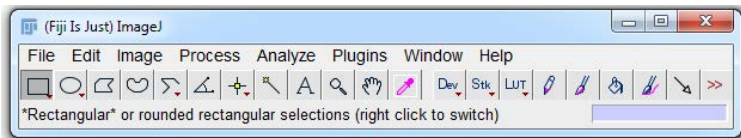


Atypical Monochromacy

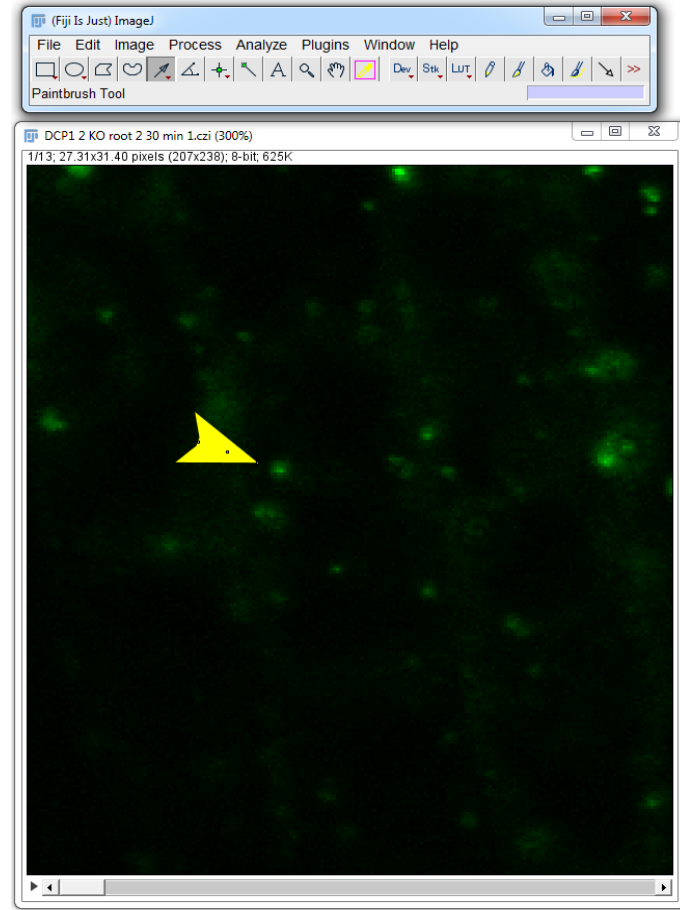
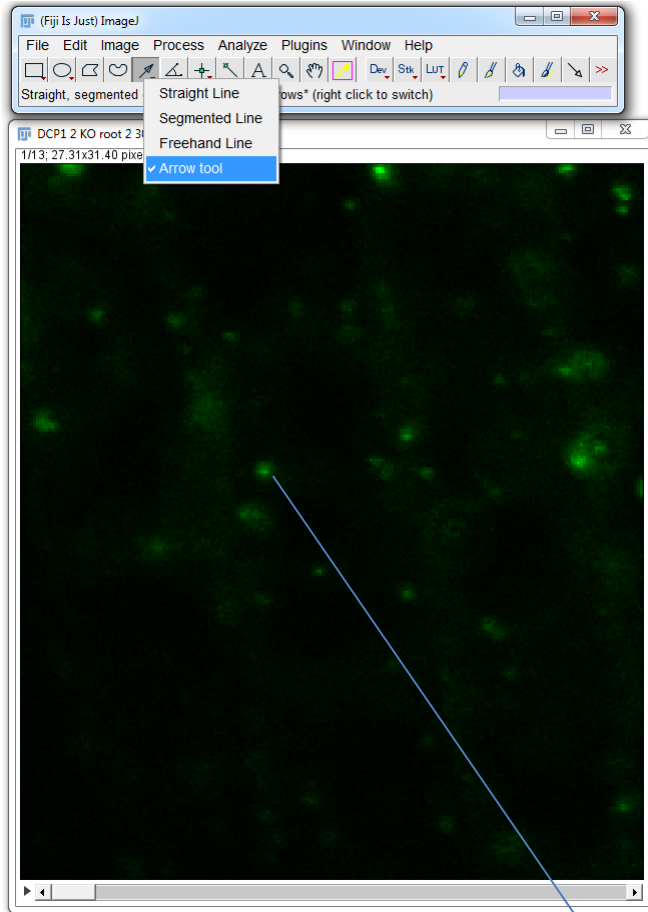
# Simulate color blightness





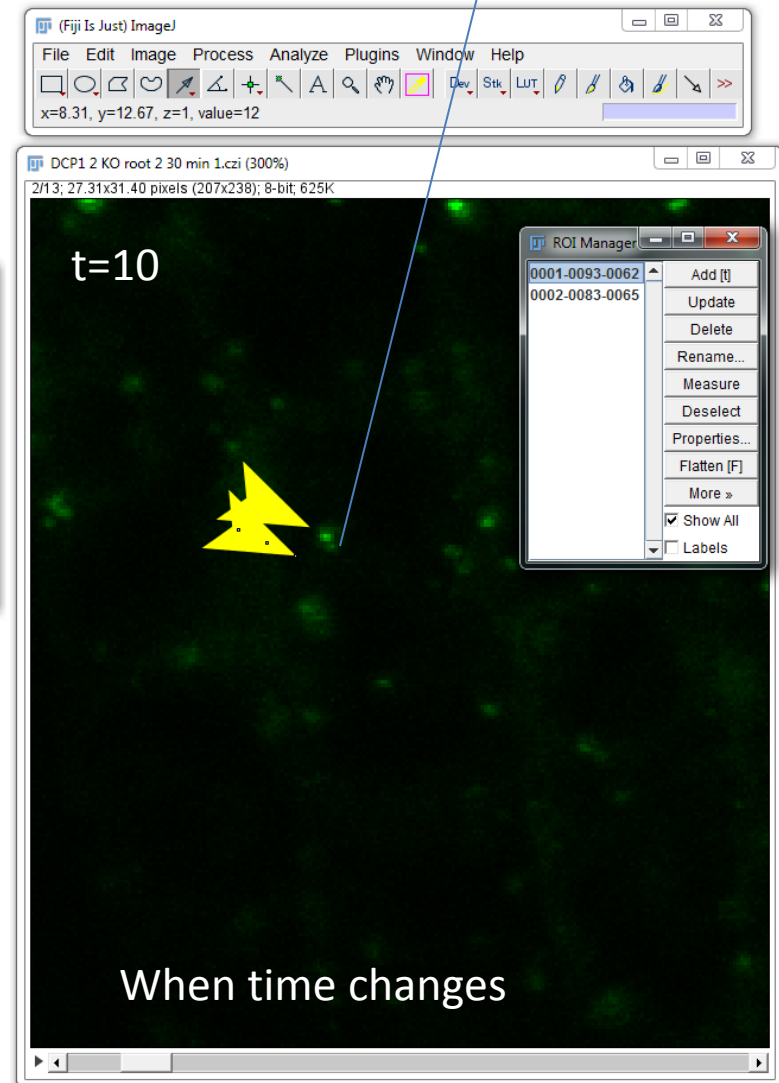
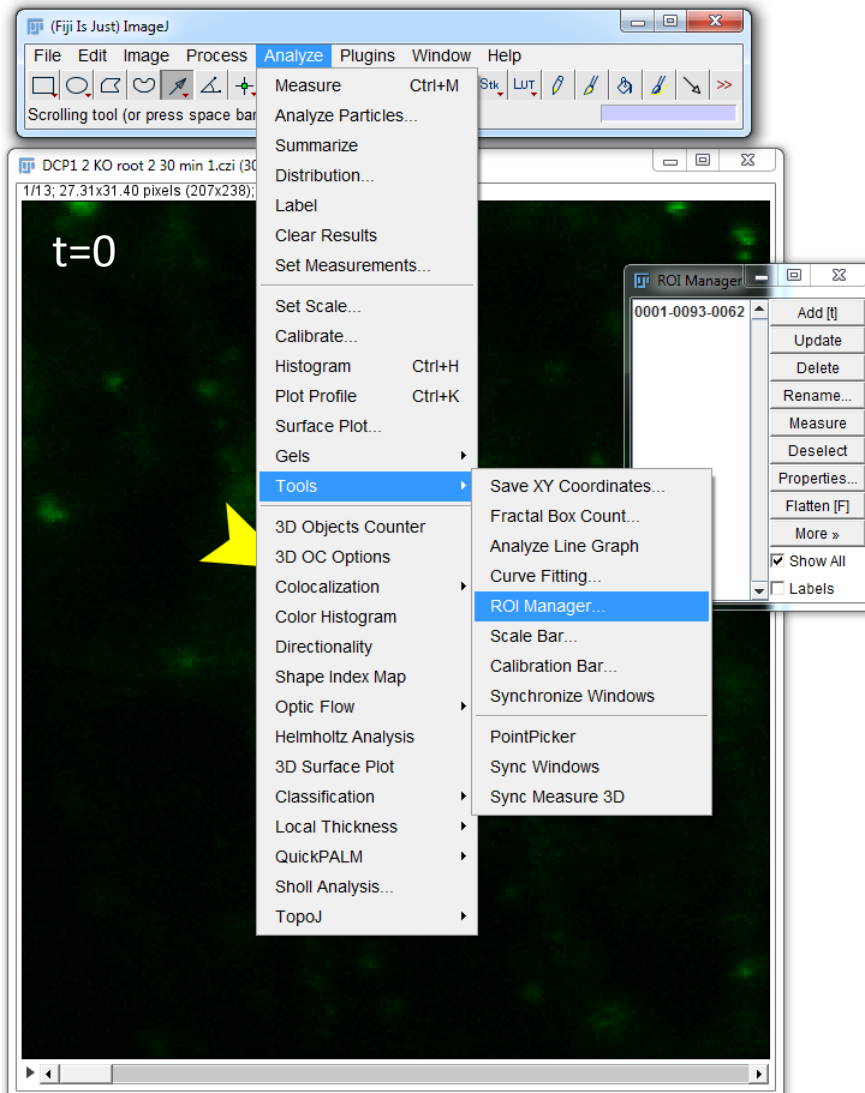


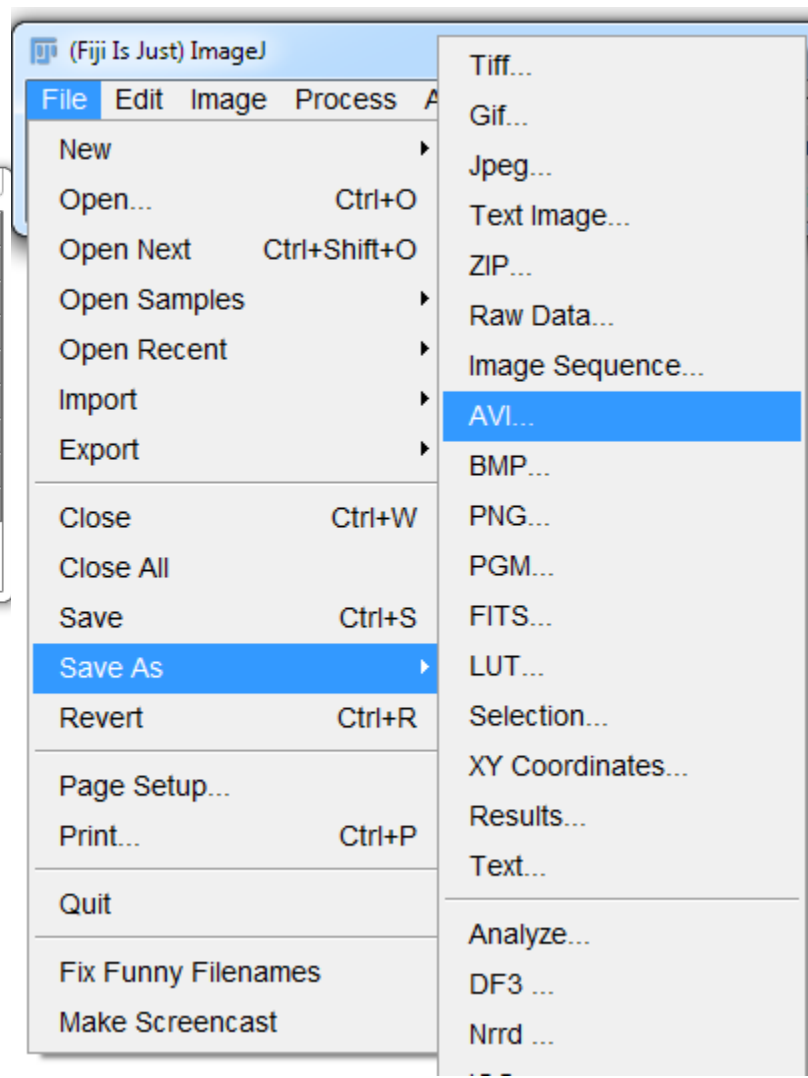
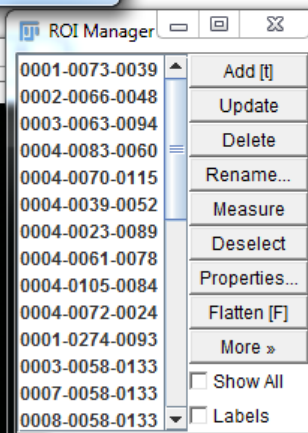
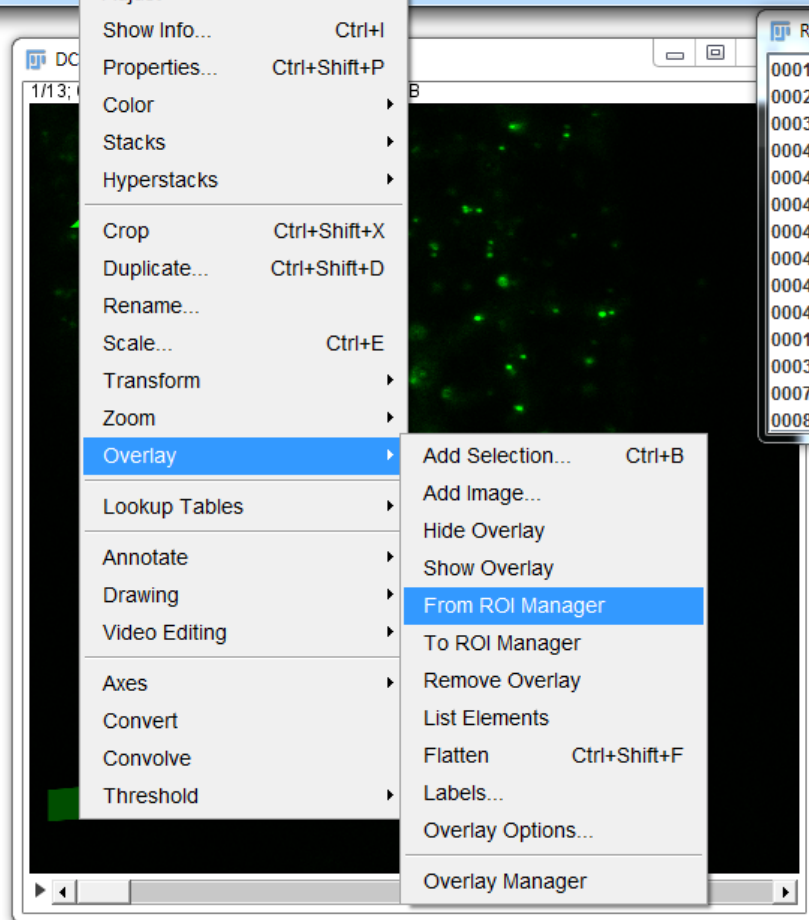
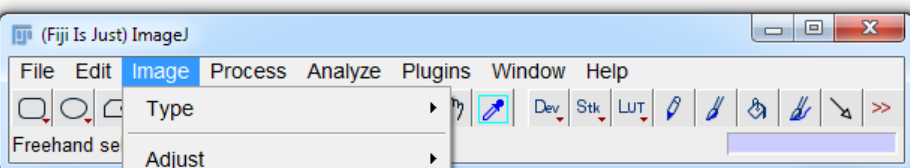
# Designate structures on your images

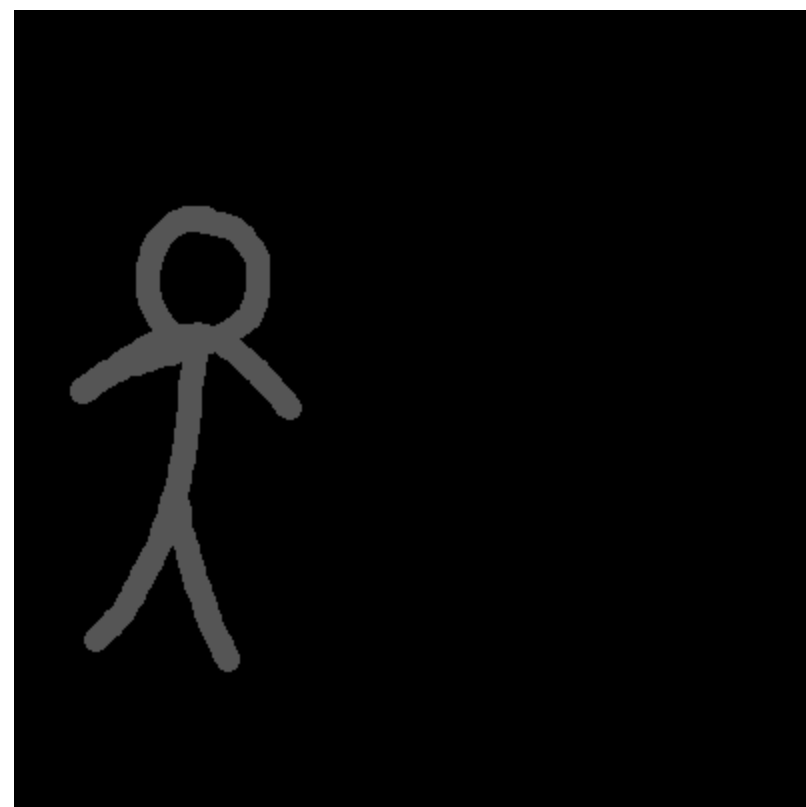
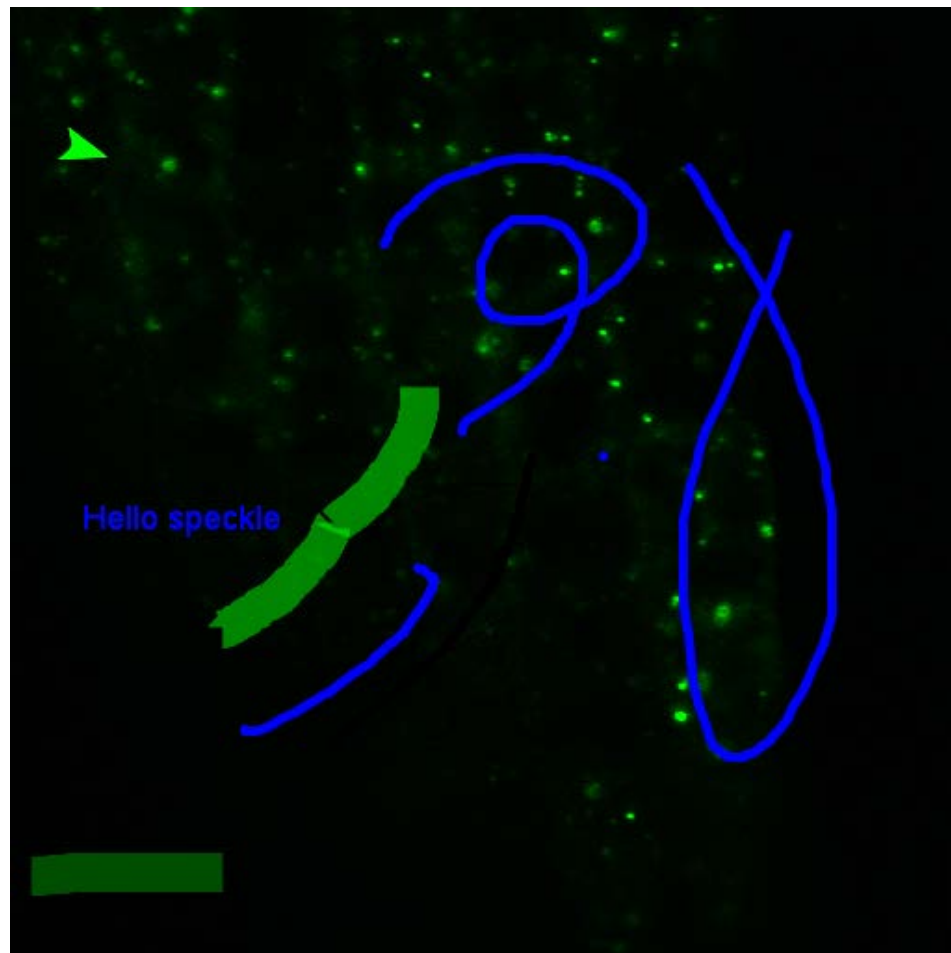


I am interested on this spot

My spot is  
moving...







# Do my structures co-localize?

Are the intensities of green and red correlating:

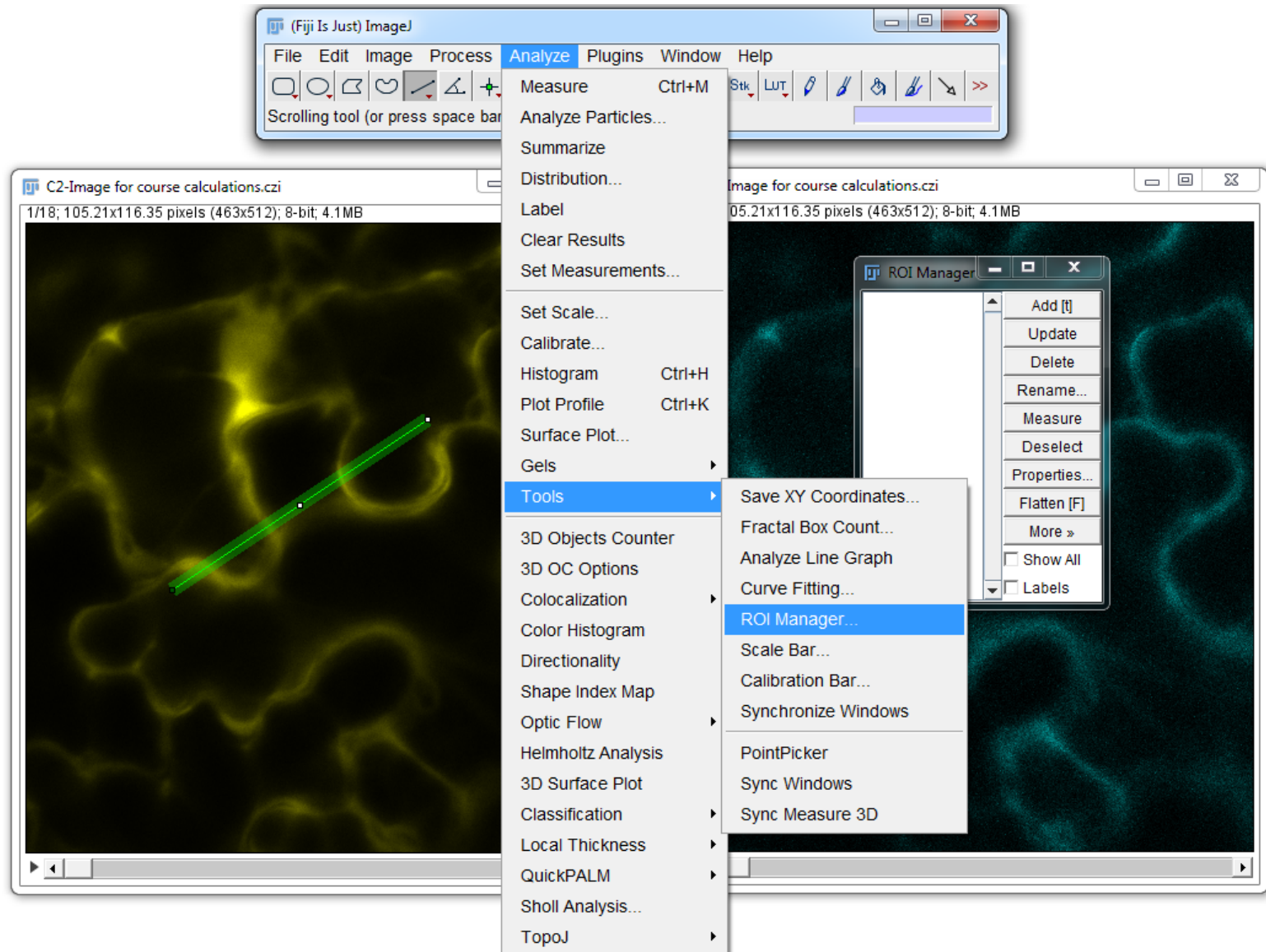
**Pearson's correlation coefficient.** Requires linear relationship between the two channel intensities.

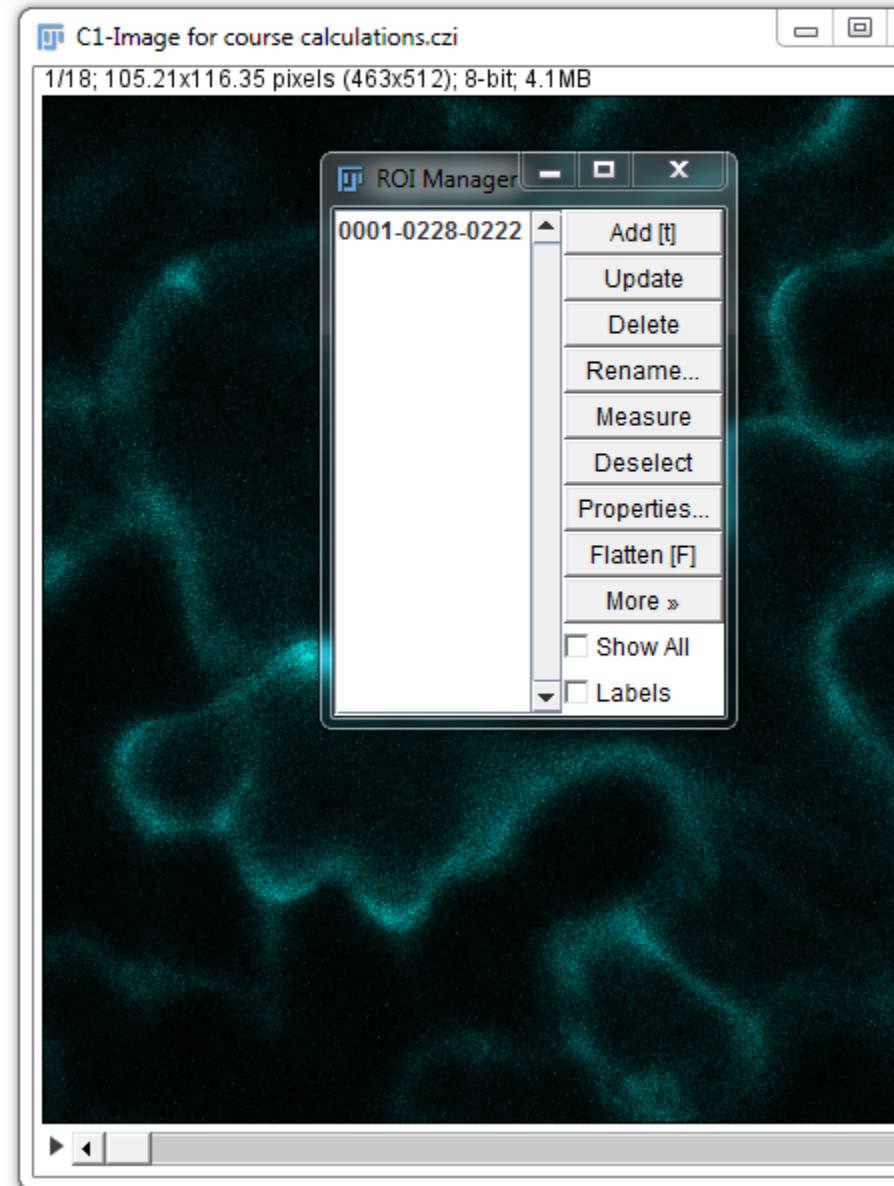
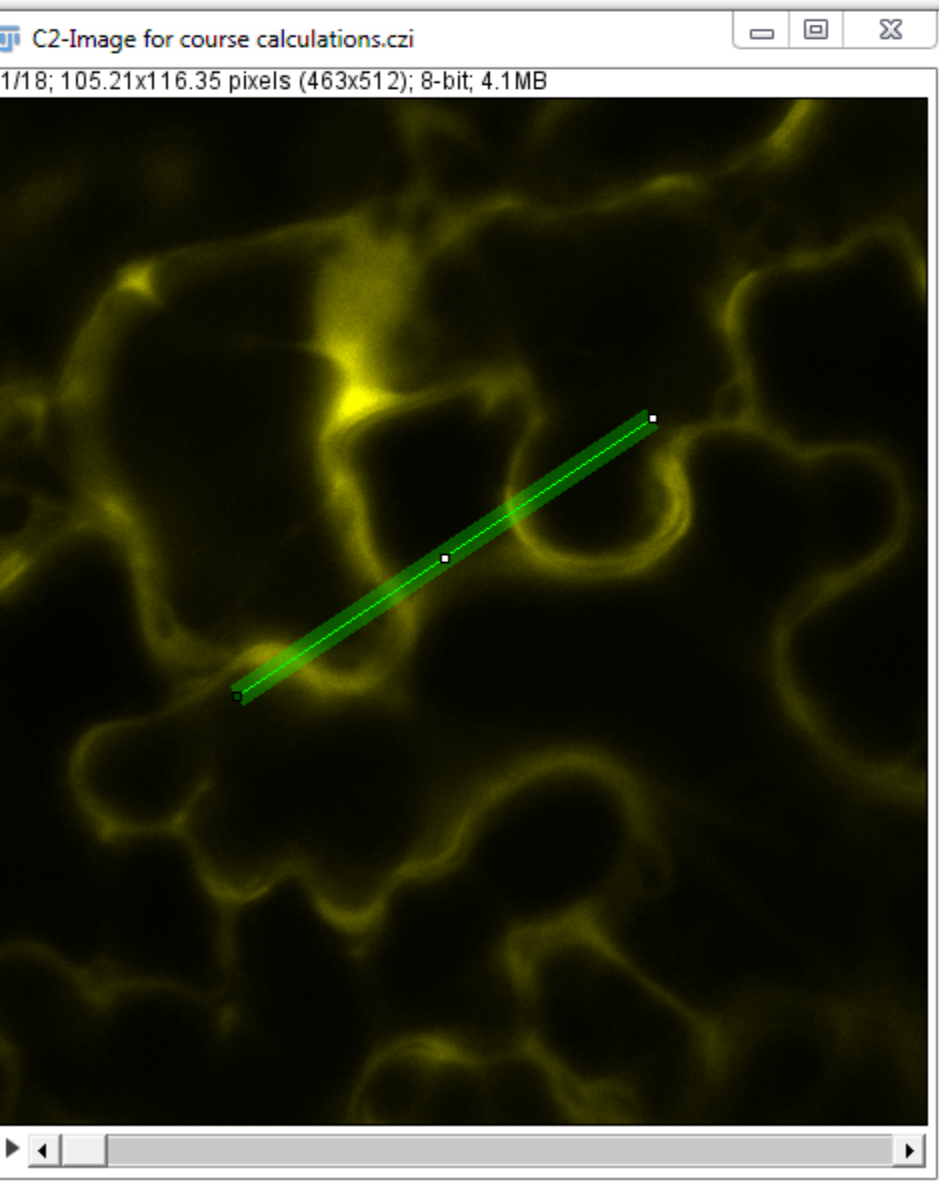
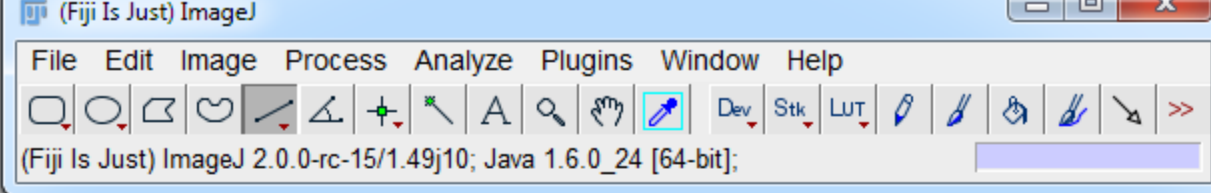
**Mander's coefficient.** Proportional to the amount of fluorescence of the co-localizing objects in each component, which is dependent on the intensities of the signals.

**Spearman's rank coefficient.** Pearson correlation coefficient between ranked variables



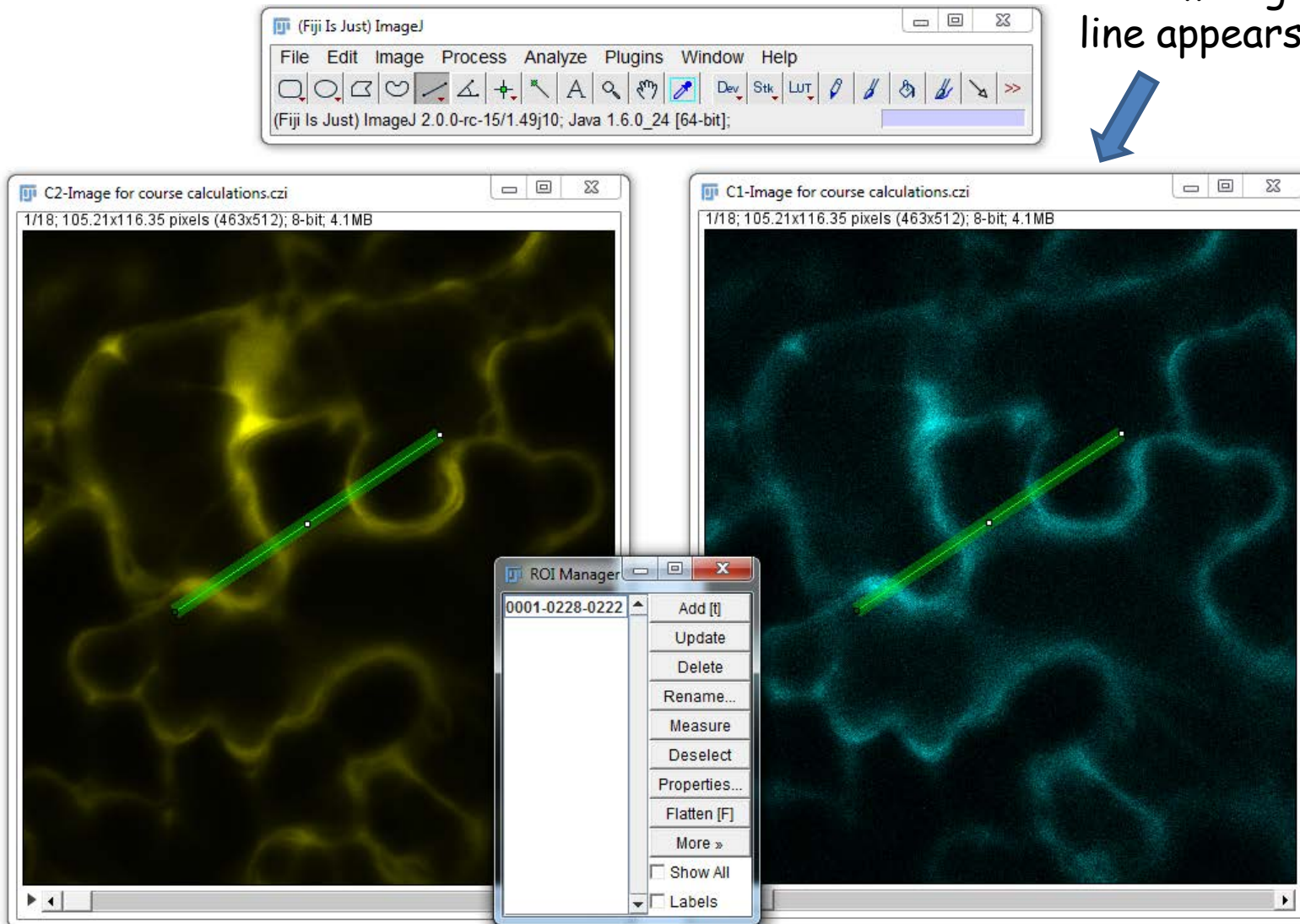
# Plot profiles of the intensities



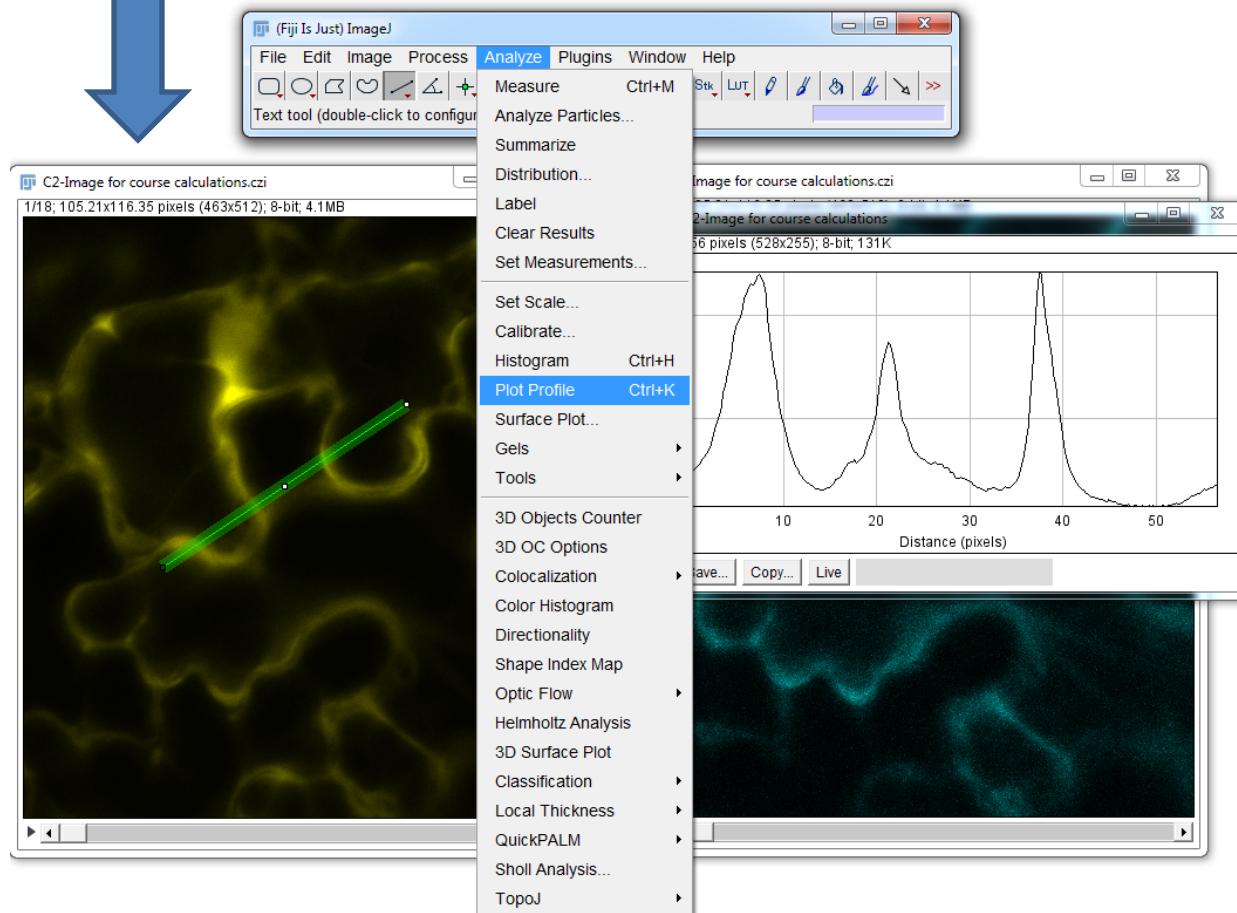


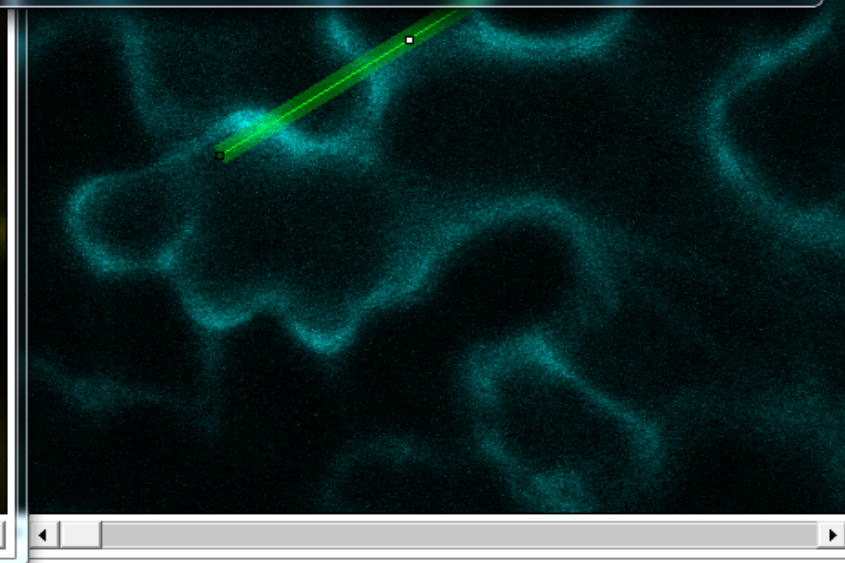
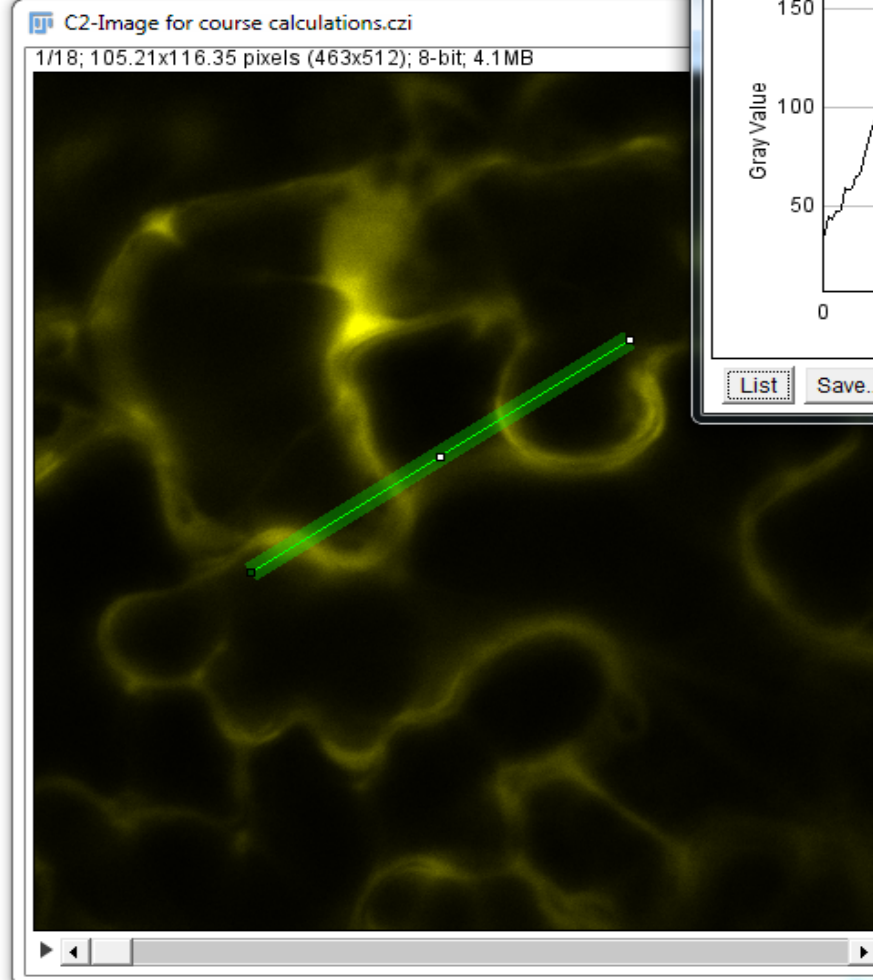
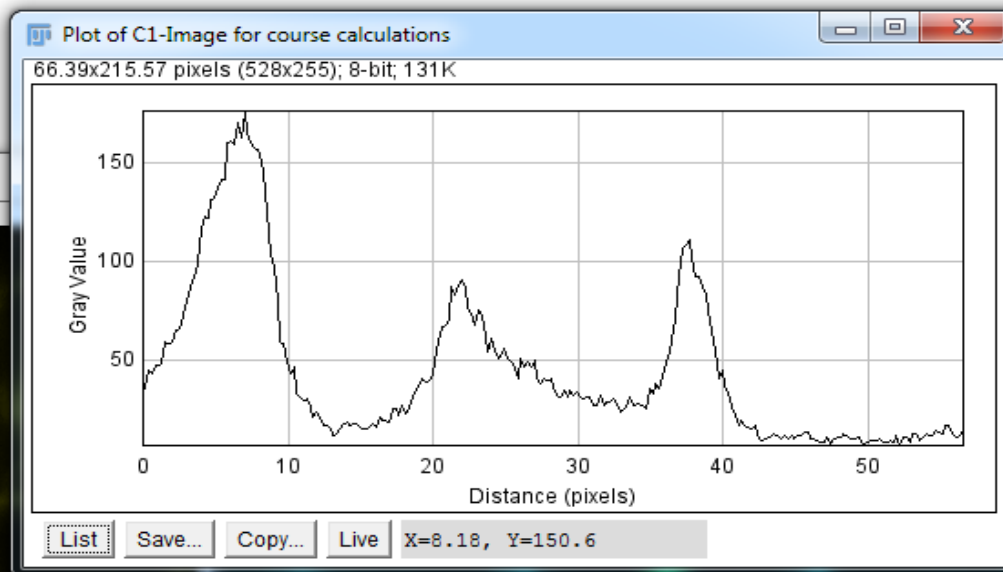
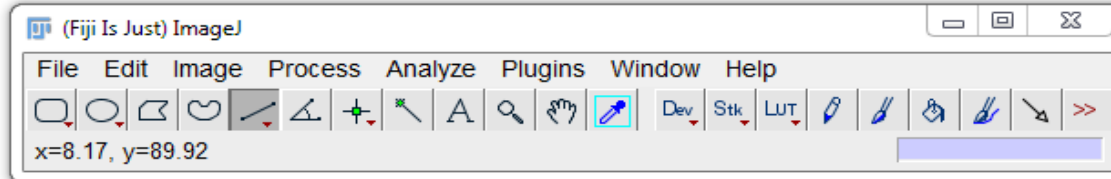


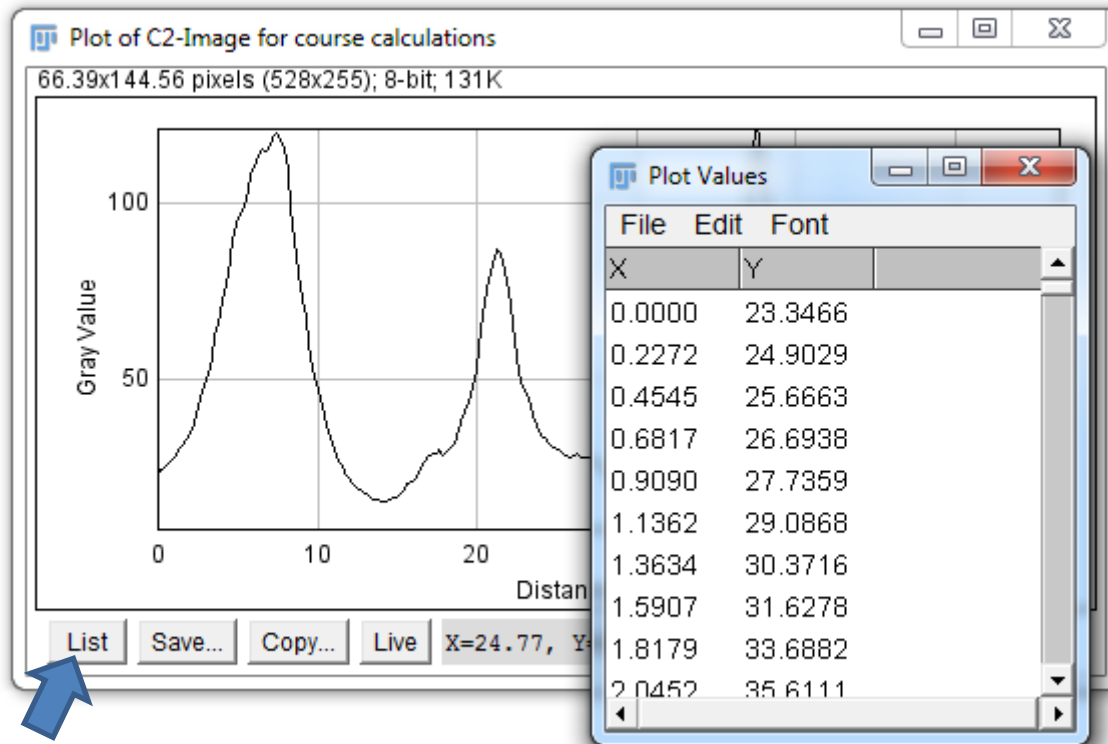
I select this window  
and the ROI from the  
ROI manager and the  
line appears here



Select each window and then  
'analyze'-'>'plot profile'

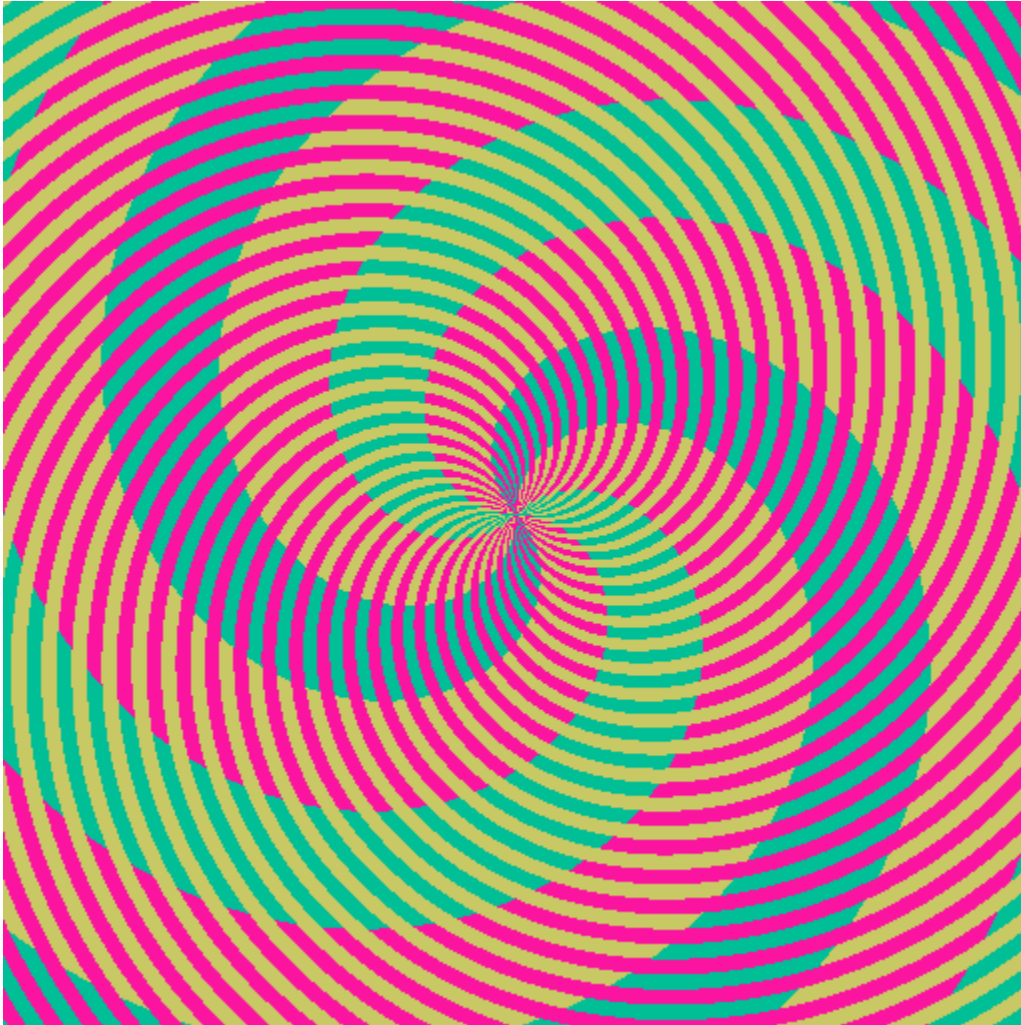


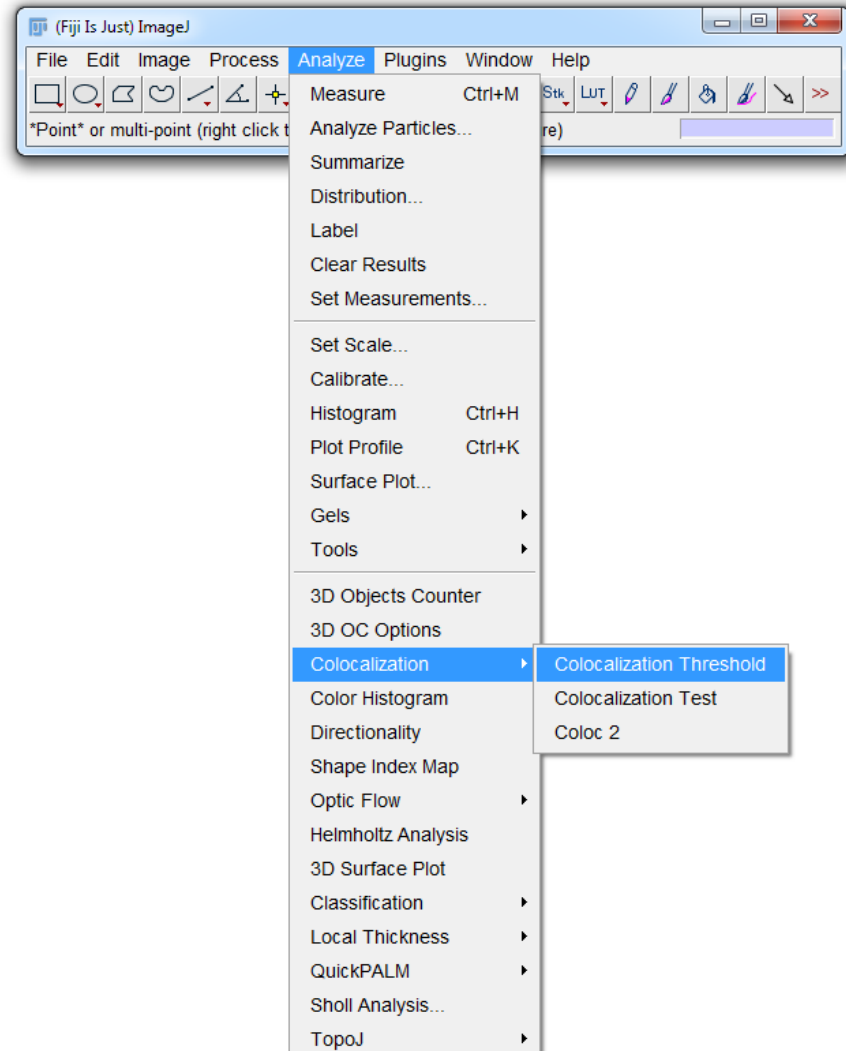
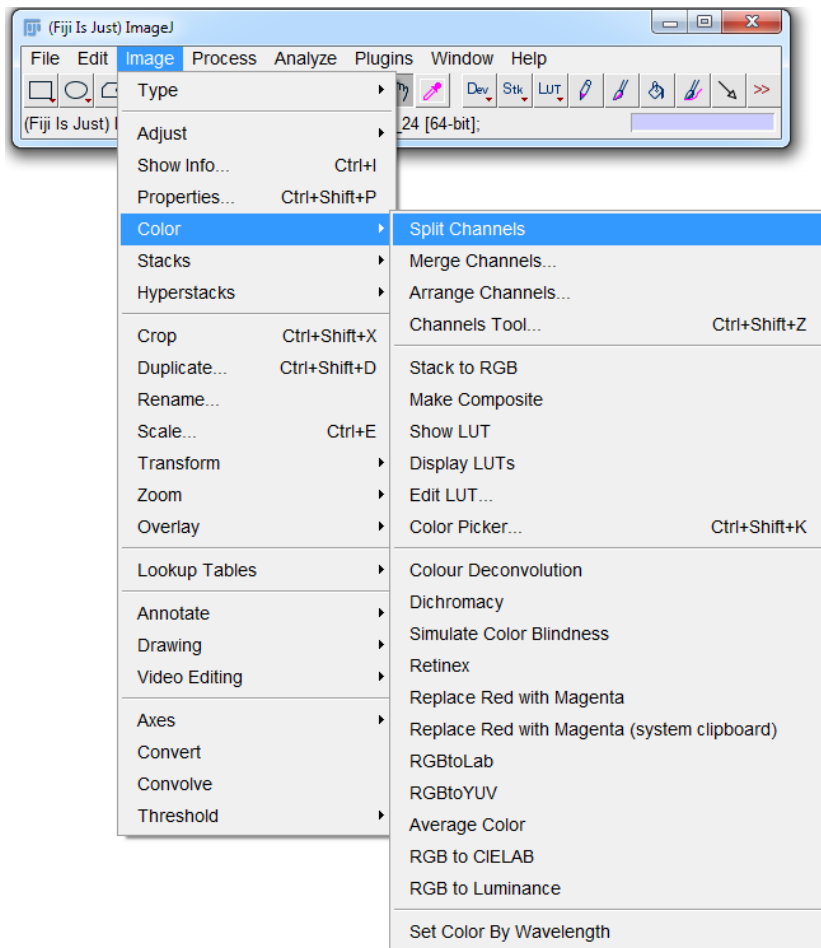




Click on the 'list' button and take the values that appear in the 'plot value' box to Excel sheet and plot them

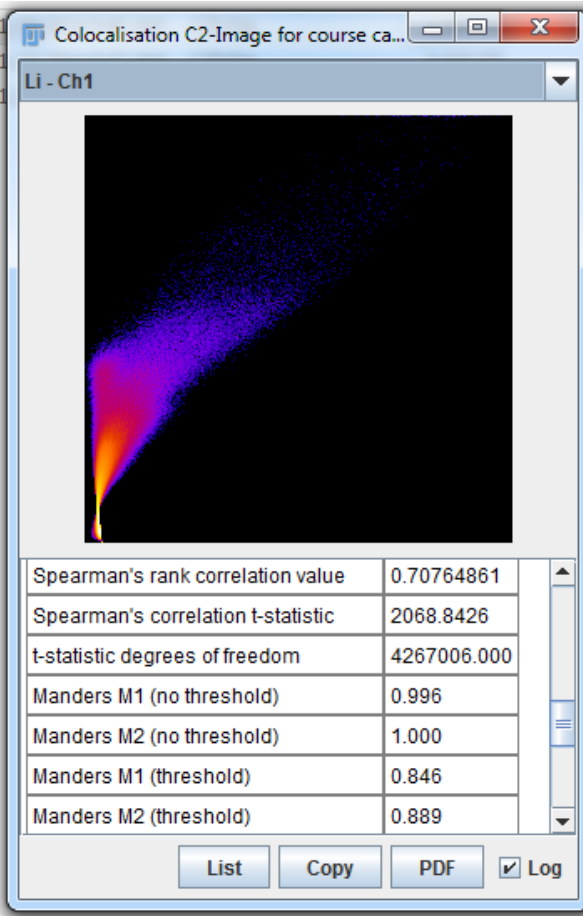
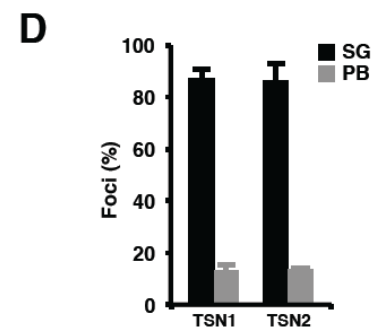
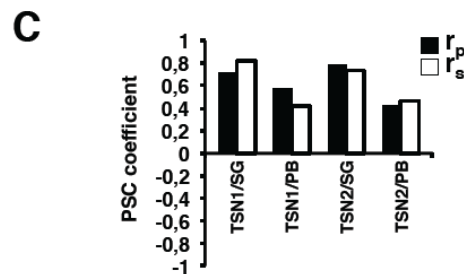
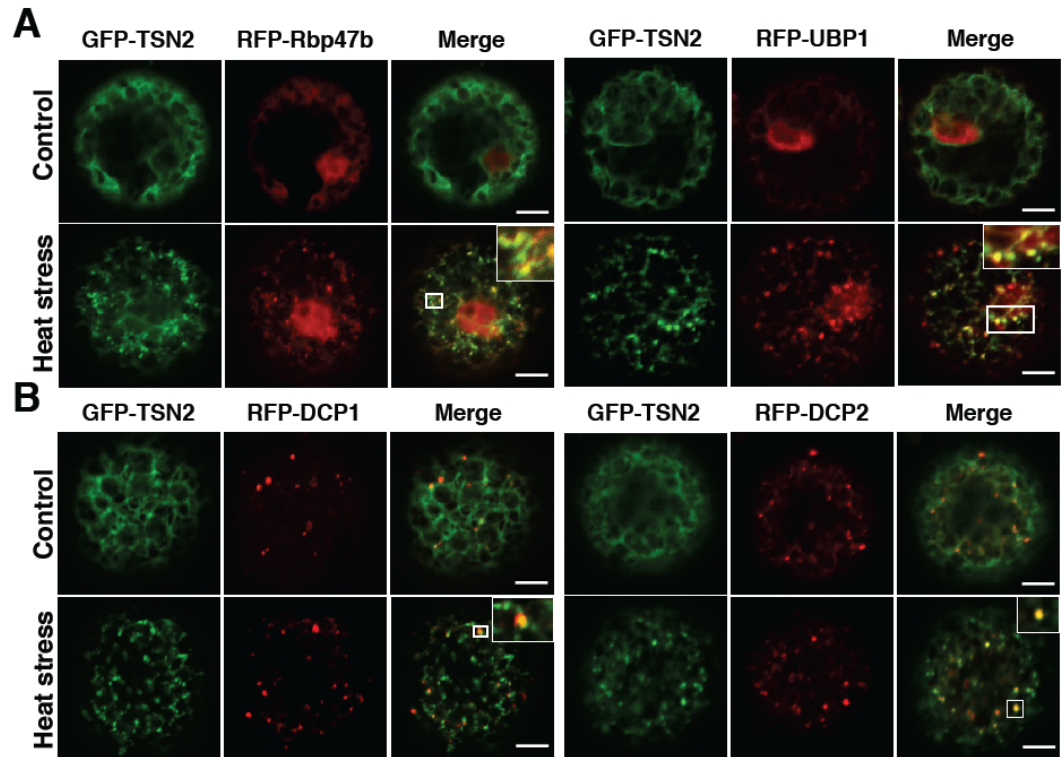
# Ok! I need some math now!



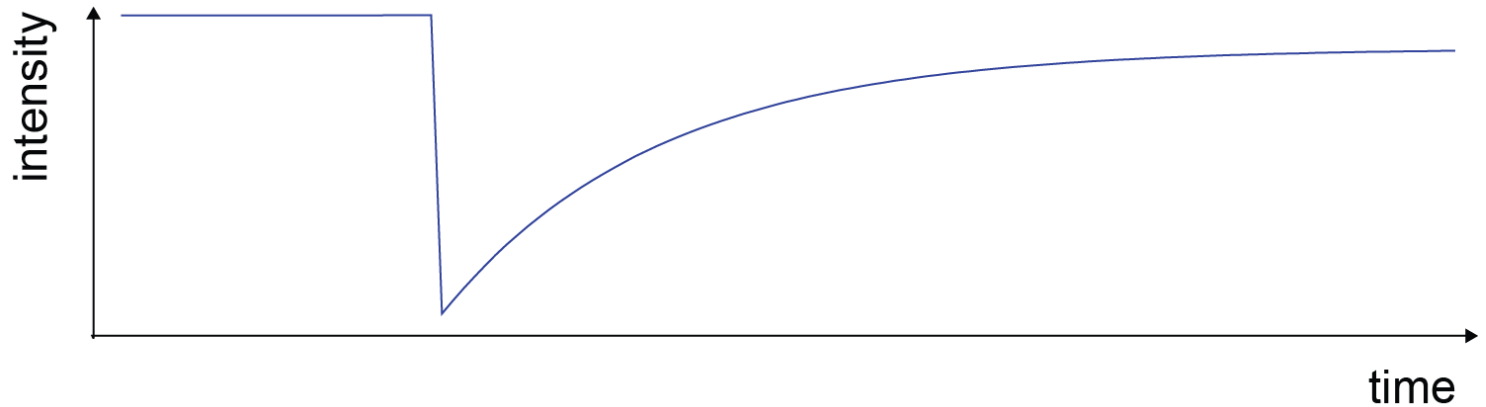
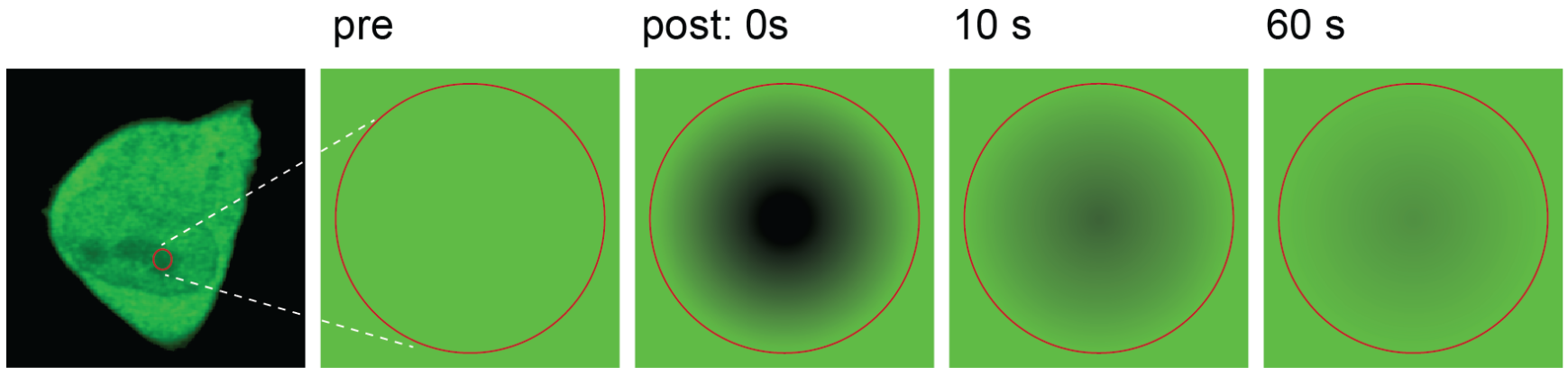


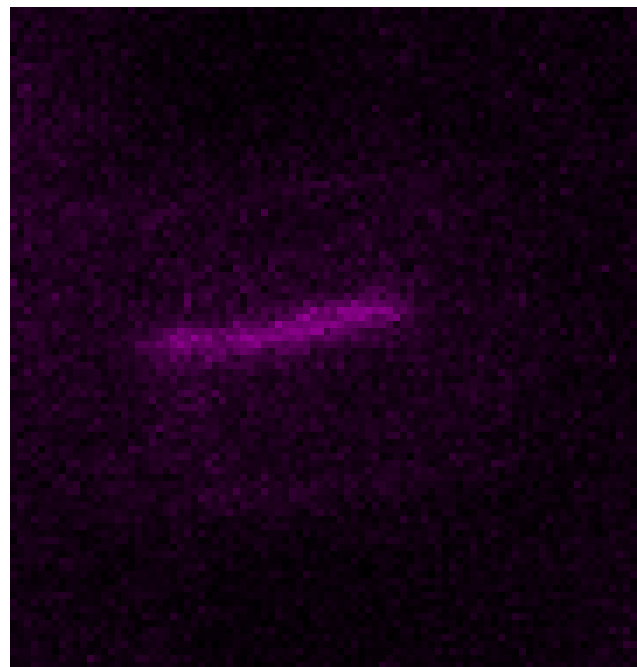
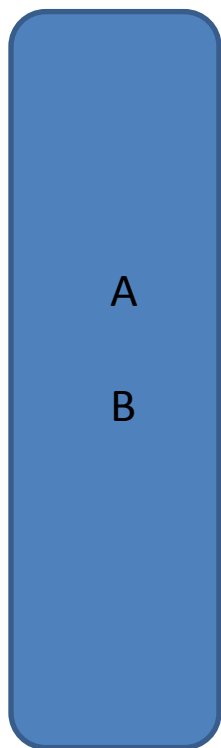
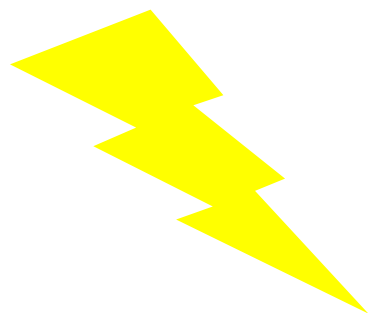


# Data presentation of colocalization and some regular



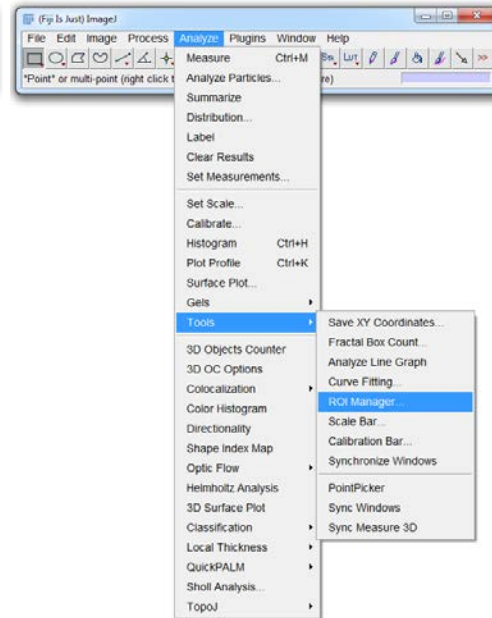
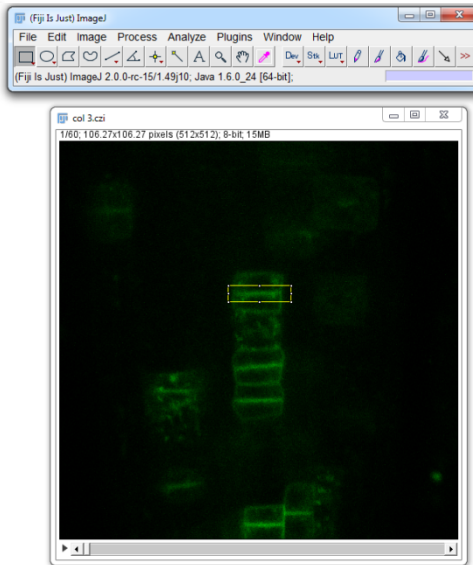
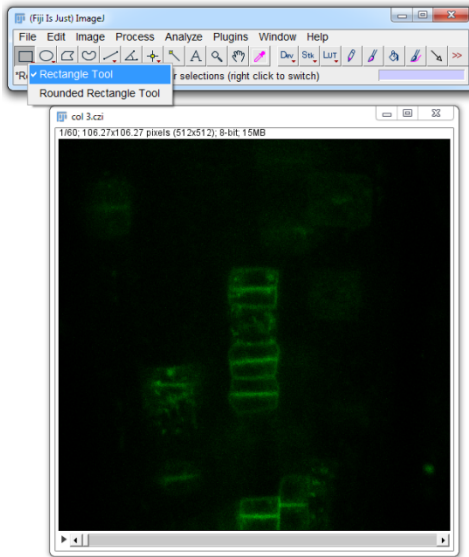
# Fluorescence recovery after photo-bleaching



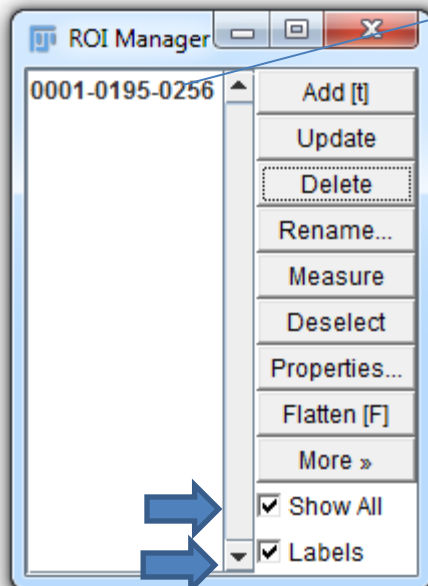


# Analyzing FRAP data

Select the ROI → Use the rectangle tool to select the ROI → Select the ROI manager

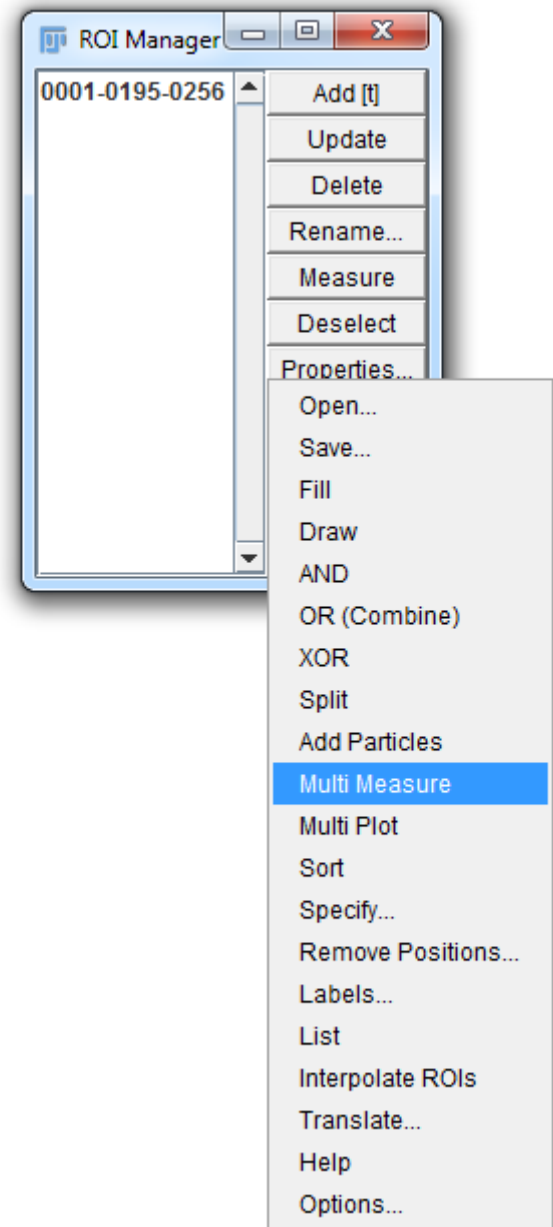


2. Click on 'show all' and 'labels'



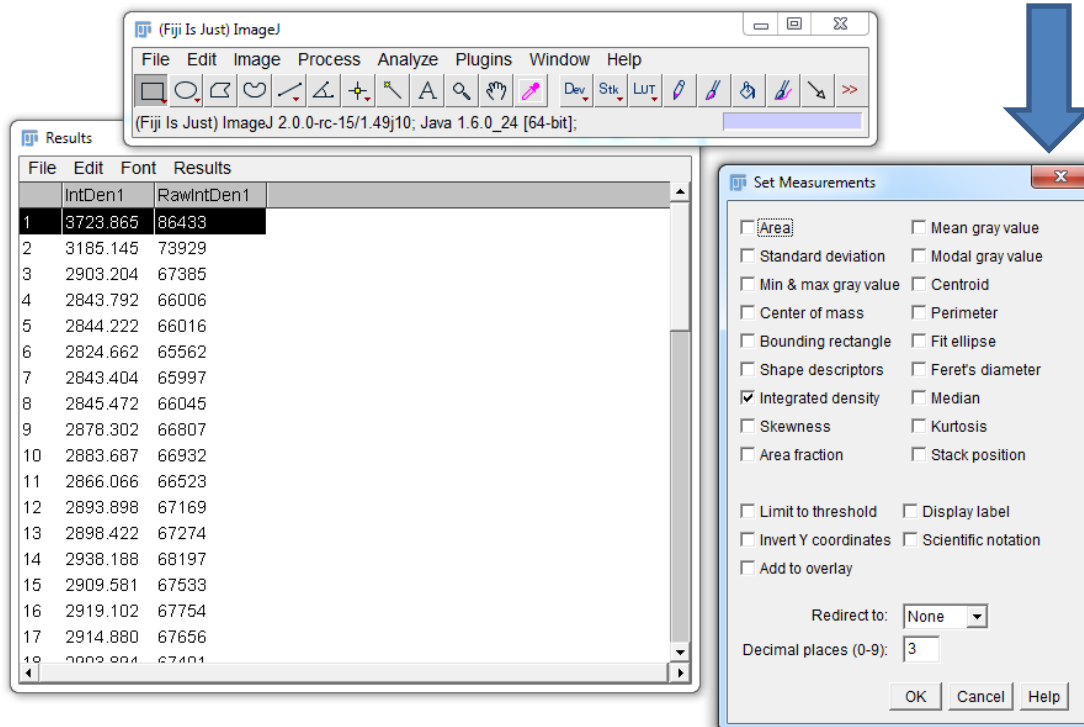
This is my ROI

3. Select 'more' and on drop-down menu select 'Multi measure'



- 4. You end up with an intensity measurement table


*Make sure that 'integrated density' is selected (Results-> Set measurements...)*






- 5. Copy and paste the data from the table to an Excel file

Time in sec (or min)

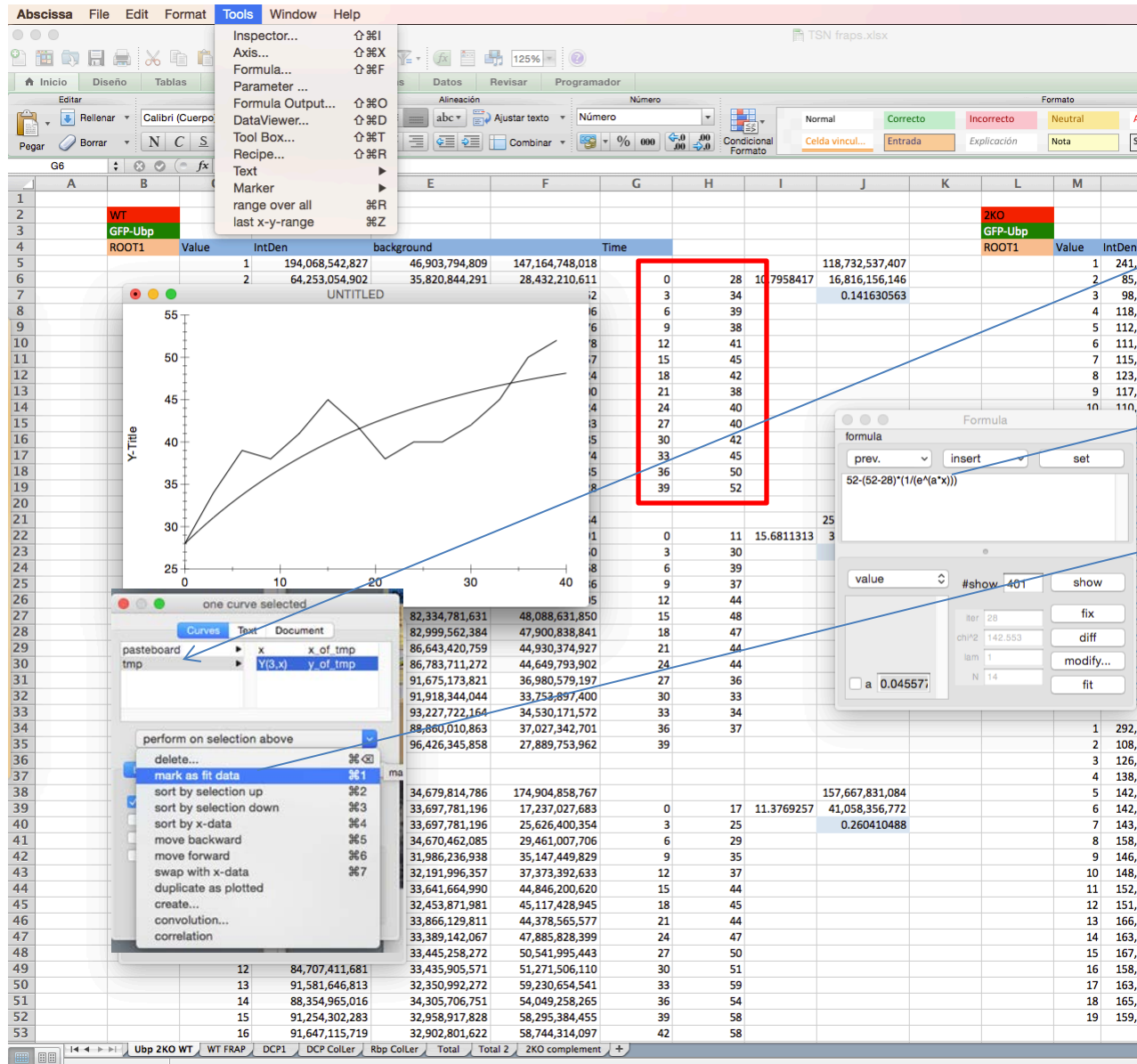


	B	C	D	E	F	G	H
WT							
GFP-Ubp							
ROOT1	Value	IntDen	background		Time		
	1	194,068,542,827	46,903,794,809	147,164,748,018			
	2	64,253,054,902	35,820,844,291	28,432,210,611	0	28	
	3	75,289,241,916	40,871,302,754	34,417,939,162	3	34	
	4	81,892,248,723	42,638,963,217	39,253,285,506	6	39	
	5	82,836,871,509	43,901,577,833	38,935,293,676	9	38	
	6	85,820,383,084	44,696,557,406	41,123,825,678	12	41	
	7	93,050,020,848	47,801,654,091	45,248,366,757	15	45	
	8	91,413,298,197	48,690,160,673	42,723,137,524	18	42	
	9	88,990,948,675	50,888,045,375	38,102,903,300	21	38	
	10	91,114,011,770	50,579,406,246	40,534,605,524	24	40	
	11	91,937,049,445	49,662,841,562	42,274,207,883	27	40	
	12	89,813,986,350	50,785,165,665	39,028,820,685	30	42	
	13	85,988,731,699	53,609,681,325	32,379,050,374	33	45	
	14	85,876,499,289	54,470,129,804	31,406,369,485	36	50	
	15	87,662,865,153	52,524,768,025	35,138,097,128	39	52	



Normalized  
intensity (my  
intensity-  
background)

# Use curve fitting



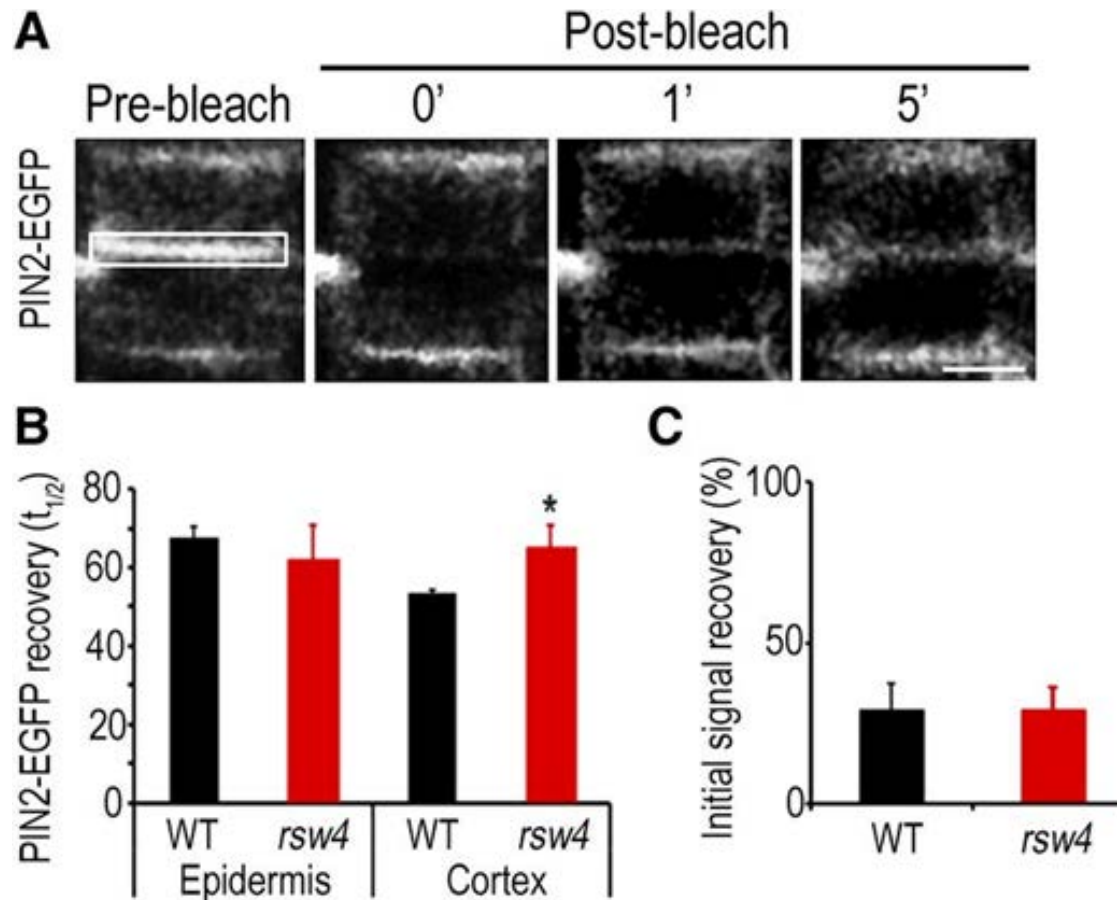
7. Paste your data here

8. Set up your equation  

$$F(t) = F_{inf} - (F_{inf} - F_0) * \exp(-t * a)$$

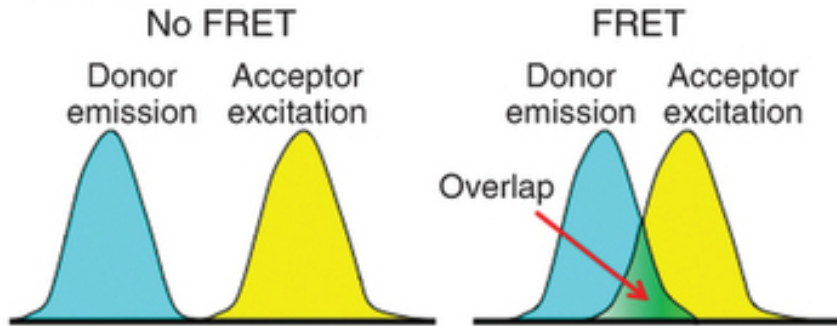
8. Select 'mark as fit data'

# Presentation of FRAP data and control experiments required

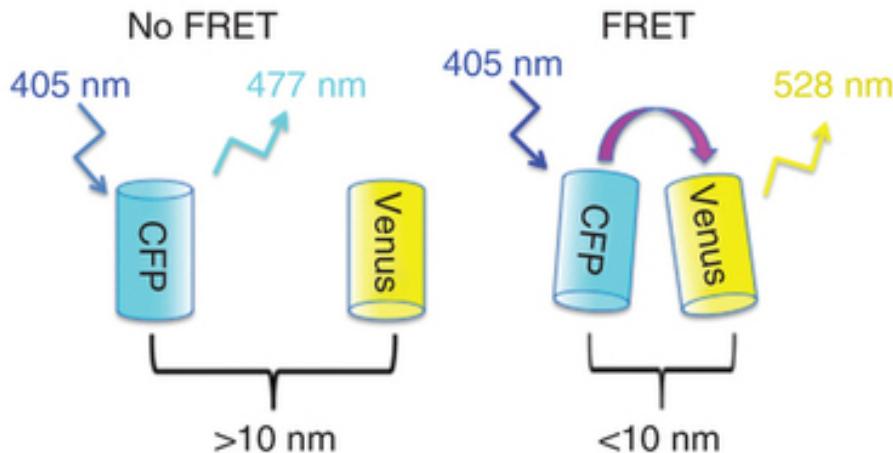


# Försters resonance energy transfer (FRET)

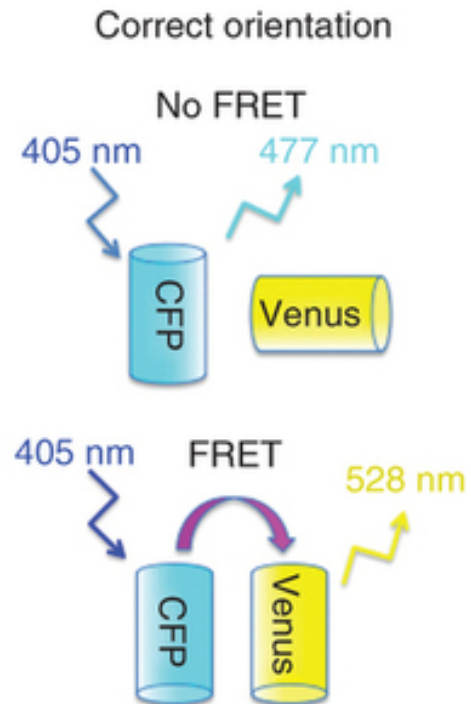
**a** Spectral overlap



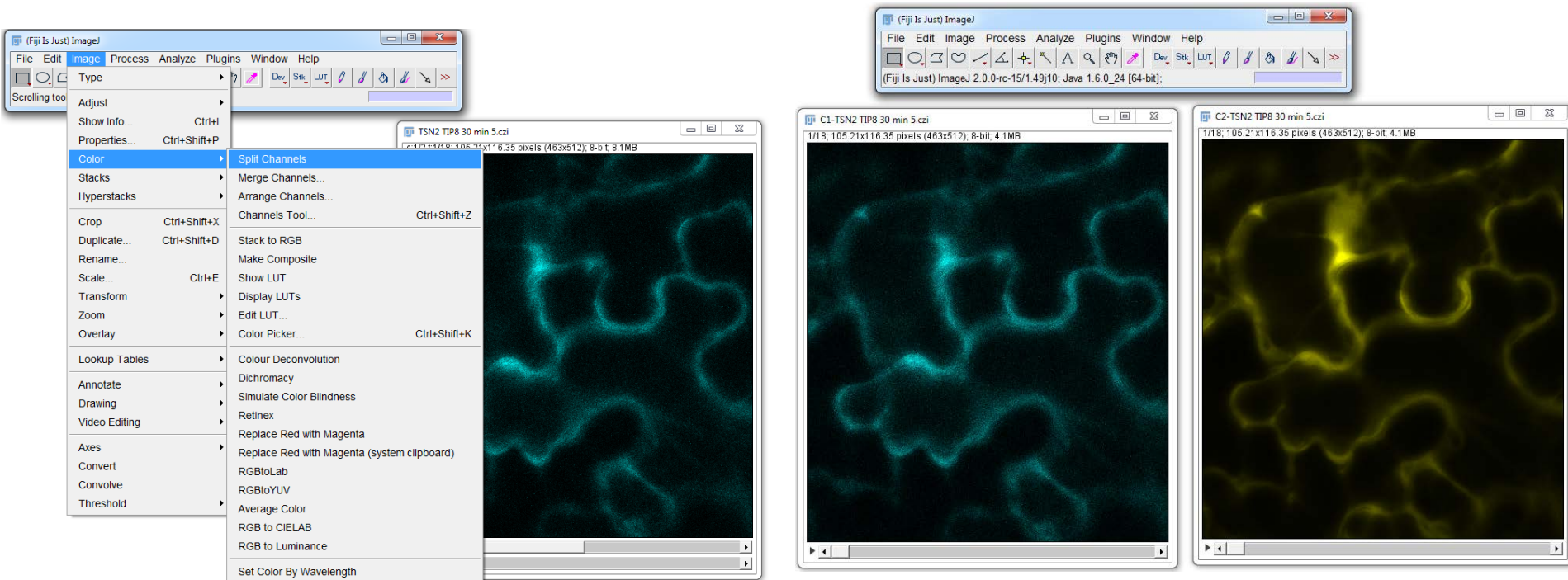
**b** Distance <10 nm



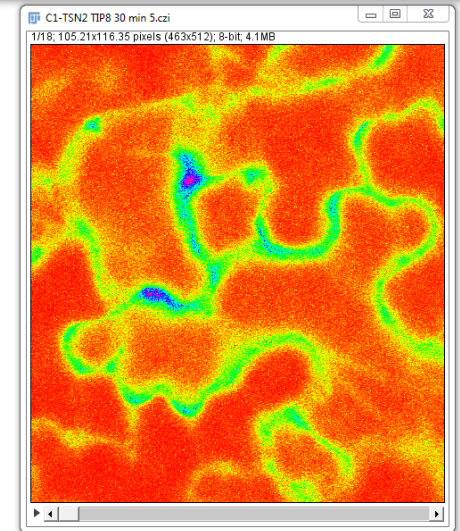
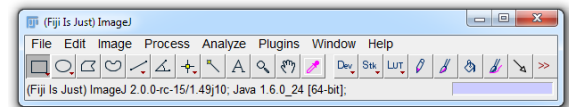
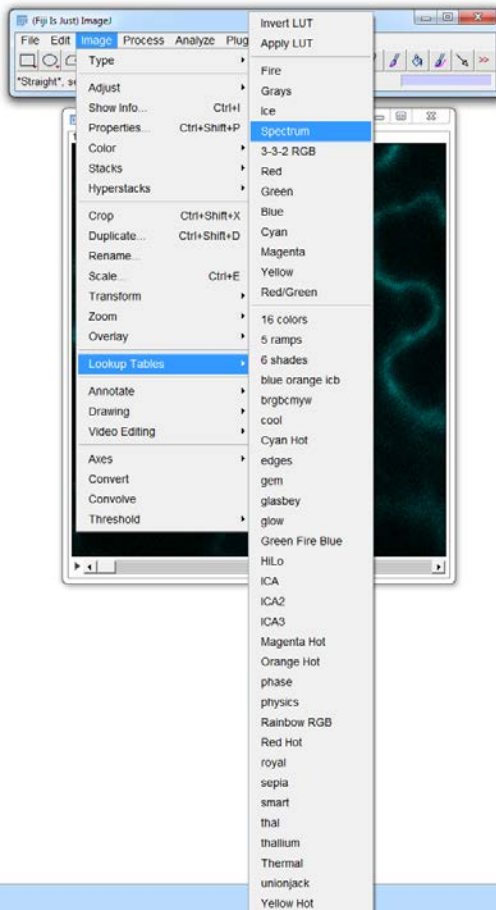
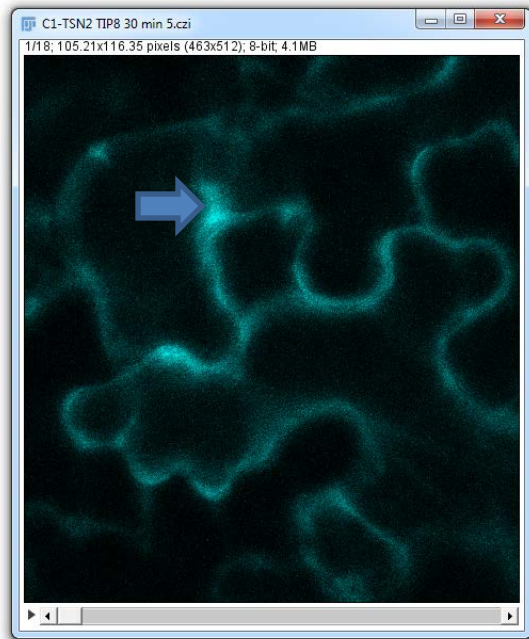
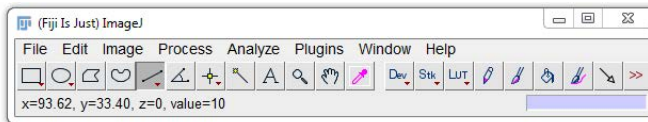
**c**



# Acceptor photo-bleaching

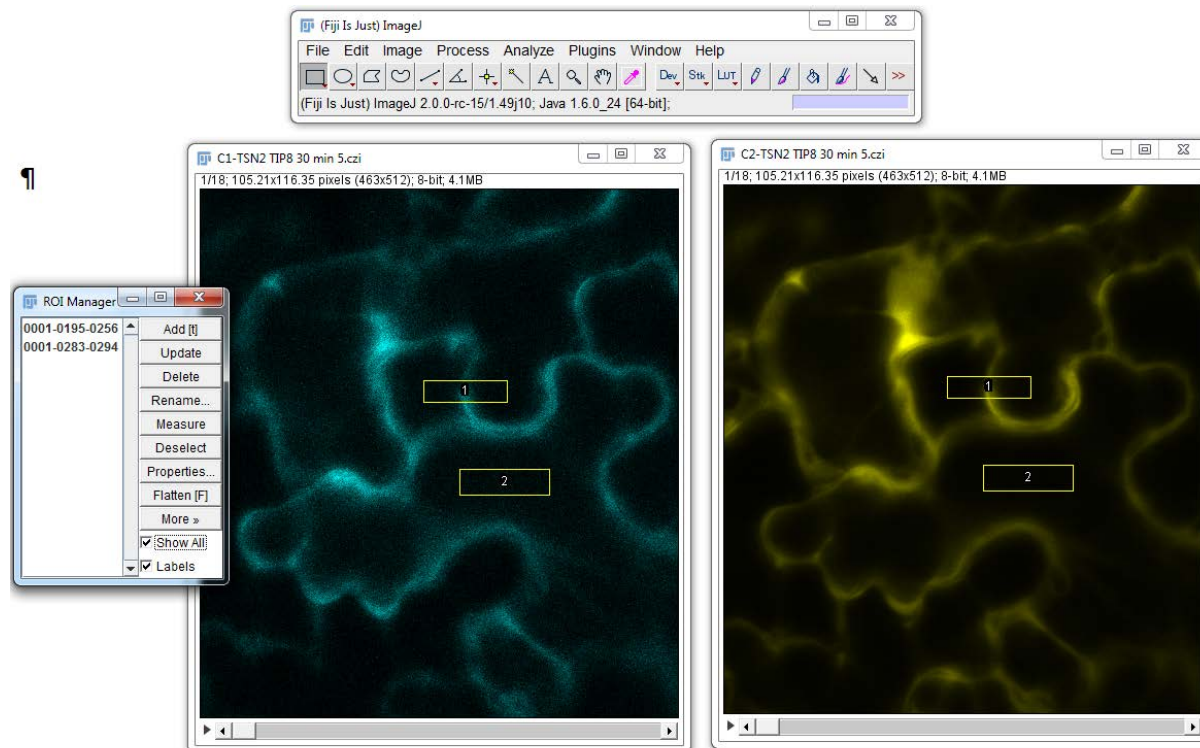




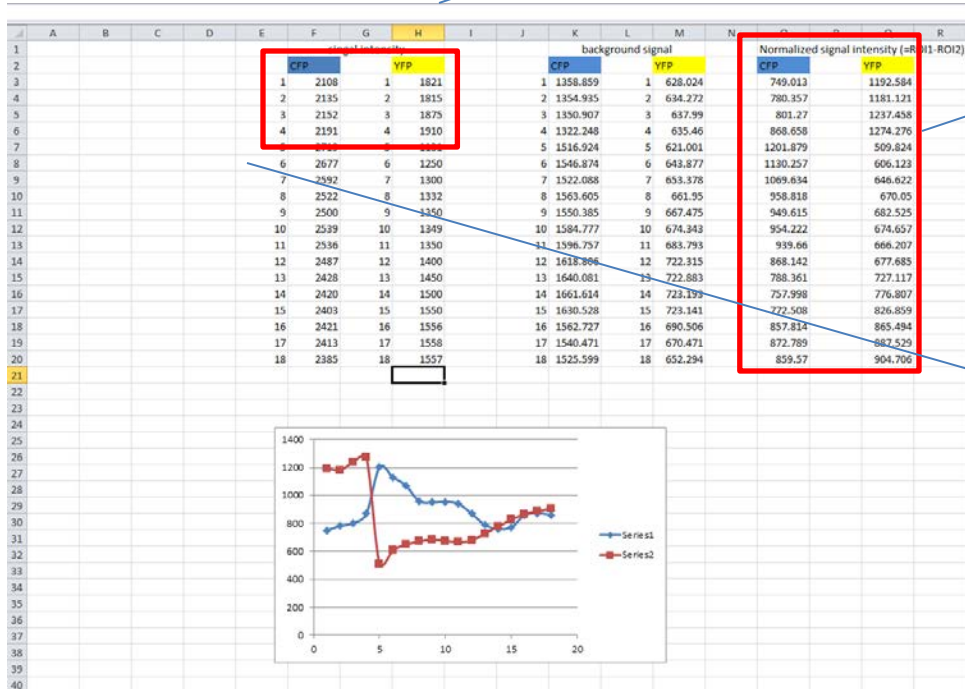




¶



No significant changes in intensity



I plot these data

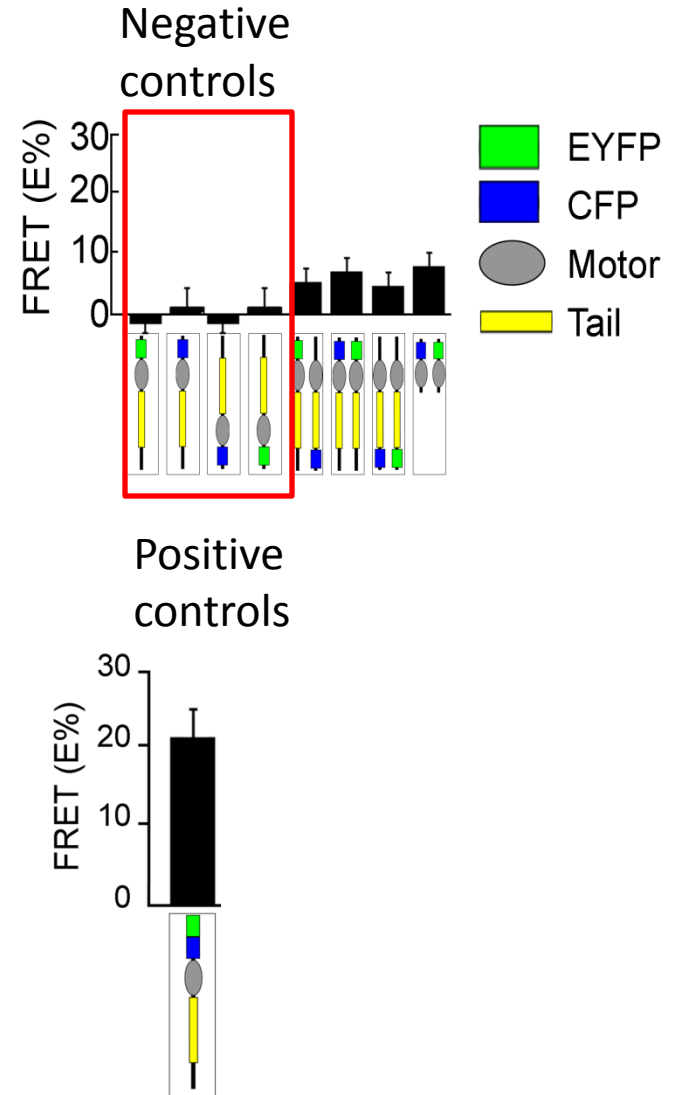
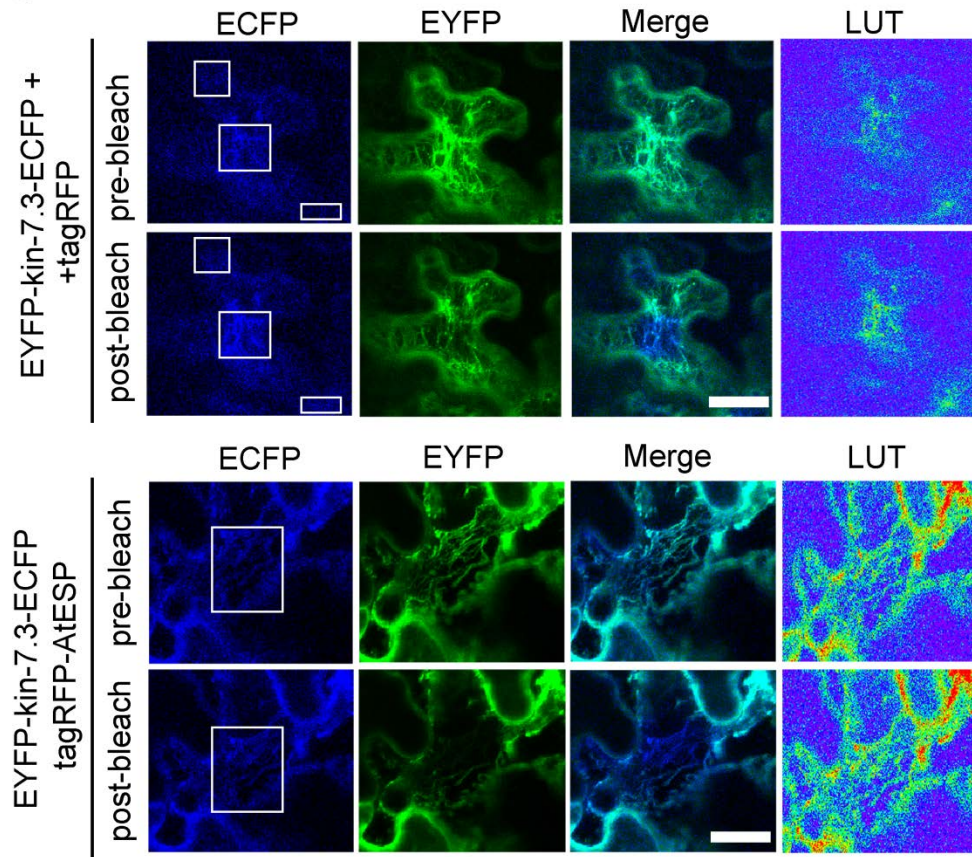
Keep in mind that FRAP takes some time (depending on the iterations). Therefore, I should always check that the increased intensity is not due to 'relaxation' of the CFP

# Calculate FRET efficiency

$$\text{Efret}(\%) = (\text{Int. final} - \text{Int. initial}) / (\text{Int. final})$$

[illegible]

# Data presentation for FRET



# Further reading

- <http://fiji.sc/Cookbook>
- [http://fiji.sc/Time Stamper](http://fiji.sc/Time%20Stamper)
- [http://fiji.sc/Annotating Images](http://fiji.sc/Annotating%20Images)
- <http://occm.otago.ac.nz/resources/Making-a-Look-Up-Table---LUT.pdf>
- [http://fiji.sc/Image Intensity Processing](http://fiji.sc/Image%20Intensity%20Processing)
- Abcissa software <http://rbruehl.macbay.de/>
- FRAP theory (Balinski paper in the course literature)  
<http://jcs.biologists.org/content/114/21/3885.full.pdf+html>

# Where does 'F(t) = F<sub>inf</sub> – (F<sub>inf</sub> – F<sub>0</sub>)\*exp(–t\*a)' comes?

Assuming that molecule *A* can bind reversibly to a spatially-fixed site *B* to form a complex *AB*, then the reaction equilibrium is given by



The forward reaction rate (units: M s<sup>-1</sup>) is

$$r_{\text{on}} = k_{\text{on}}[A][B] \quad (\text{A2})$$

where *k<sub>on</sub>* is the bimolecular association rate constant (units: M<sup>-1</sup> s<sup>-1</sup>) and the reverse reaction rate (units: M s<sup>-1</sup>) is

$$r_{\text{off}} = k_{\text{off}}[AB] \quad (\text{A3})$$

where *k<sub>off</sub>* is the unimolecular dissociation rate constant (units: s<sup>-1</sup>) and all the bracketed quantities are the molar concentrations of the indicated species. At equilibrium these two rates are equal (*r<sub>on</sub>*=*r<sub>off</sub>*) and the corresponding association equilibrium constant, *K*, is defined by

$$K = \frac{k_{\text{on}}}{k_{\text{off}}} = \frac{[AB]_e}{[A]_e[B]_e} = \frac{1}{K_D} \quad (\text{A4})$$

where the subscript 'e' indicates the concentration at equilibrium. Given the reaction in Eqn A1, the rate of formation of *AB* at any arbitrary time is given by

$$\frac{d[AB]}{dt} = k_{\text{on}}[A][B] - k_{\text{off}}[AB] . \quad (\text{A5})$$

In the FRAP experiments, we use a brief laser pulse to photobleach the fluorescent species *A* when it is bound to *B*,

so that at time t=0, [AB] will be 0. We assume that the photobleaching has little effect on the fluorescence of [A] because the bleached *A* subunits readily leave the bleached region by diffusion and are replaced by unbleached subunits at an equivalent concentration. Also, it is assumed that the amount of *A* that is bleached is small compared with the total amount in the cell. Assuming that Eqn A1 has reached equilibrium prior to the bleaching event at t=0, and that [A] and [B] are unaffected by the bleaching process, then

$$[A] = [A]_e \text{ and } [B] = [B]_e \quad (\text{A6})$$

so that by combining Eqns A4 and A6

$$K_{\text{on}} = \frac{k_{\text{off}}[AB]_e}{[A]_e[B]_e} . \quad (\text{A7})$$

Substituting Eqn A7 into Eqn A5,

$$\frac{d[AB]}{dt} = k_{\text{off}}[A][B]_e - k_{\text{off}}[AB] . \quad (\text{A8})$$

Assuming that [AB]=0 at t=0, then the solution to equation A8 is given by

$$\frac{[AB]}{[AB]_e} = 1 - e^{-k_{\text{off}}t} \quad (\text{A9})$$

which applies regardless of the degree of binding site saturation at equilibrium. Therefore, given the stated assumptions, the rate constant for FRAP recovery is identical to the dissociation rate constant, *k<sub>off</sub>*.