



Getting started with image analysis in Fiji

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BIO-204

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Determine Transfection Efficiency with Fiji

- 24h after transfection (lab 8) cells were fixed and stained with DAPI
- file names
 - transfection = Amy2-CDS-His + GFP
 - mock = no DNA
- identical imaging conditions for transfection and mock
- representative fluorescence images were acquired in two channels
 - GFP: excitation 488 nm
 - DAPI: excitation 405 nm
- download images (Moodle)
- follow step-by-step guidelines



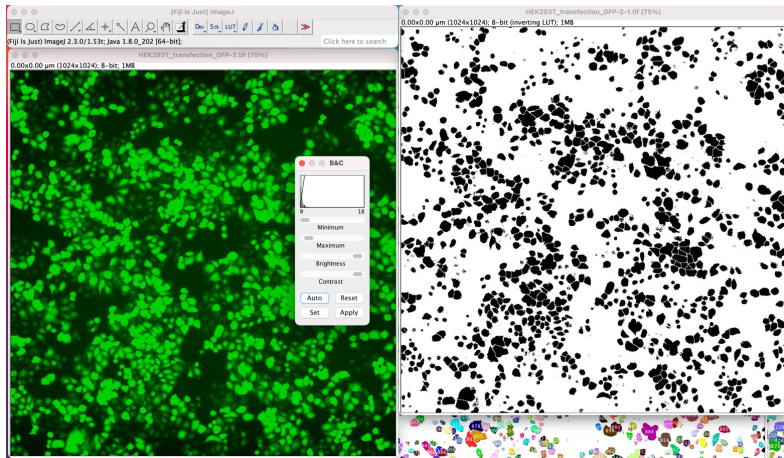
Download image processing software Fiji

open source

Fiji=Fiji is just ImageJ (with plugins)

professional software with many functions

<https://imagej.net/software/fiji/downloads>



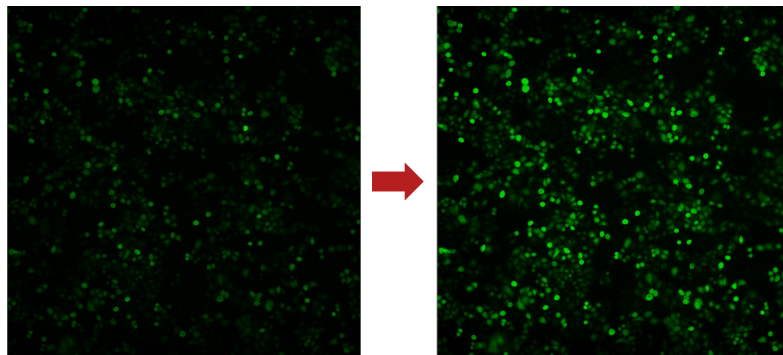
Tasks

- A) Merge DAPI + GFP images
- B) Determine Transfection efficiency

A)

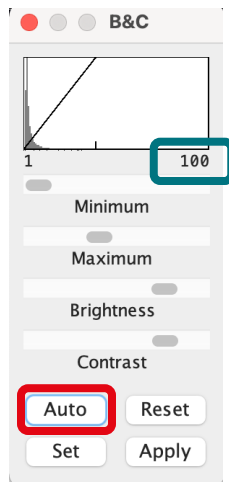
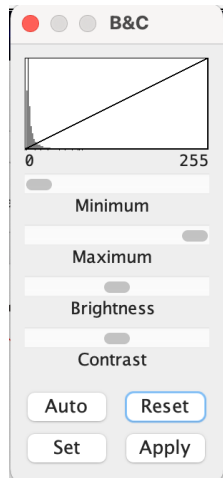
How to merge (overlay) DAPI + GFP images

- adjust contrast of individual images
- merge images



For Good Visibility by Eye: Adjust Contrast

- open image(s)
- image > adjust > brightness/ contrast / auto
 - value can be different for each image
- alternative: move the min/ max for manual adjustment

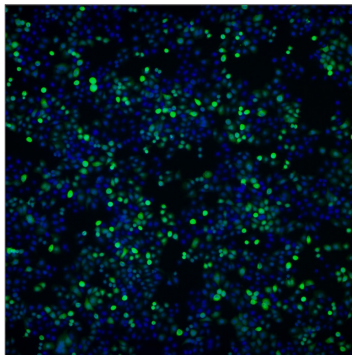
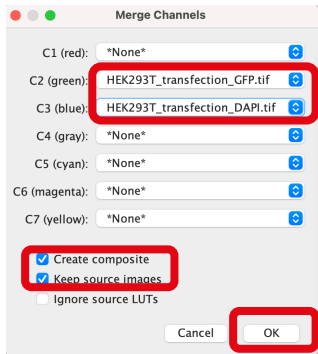
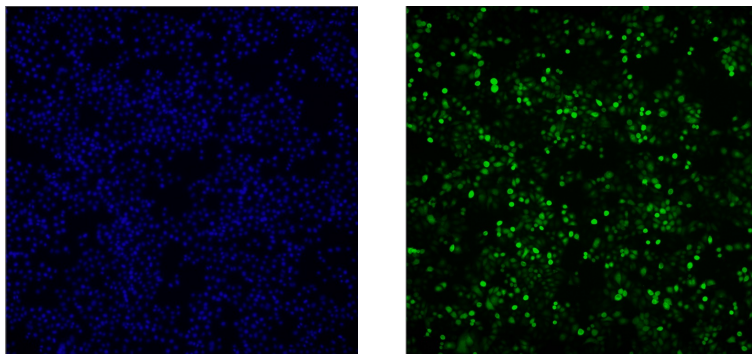


for comparison between different conditions
use **same value**

- first set GFP contrast (transfection image)
- then use the **same value** to display the mock image

To Overlay Individual Images: Merge Channels

- open images (GFP and DAPI)
- image> color> merge channels
- select files for green and blue channel
- save as> tiff (for scientific processing)
- save as> jpg (compressed format, use for illustration purpose only, ELN OK)
- name: *original filename_merge*
- now you have 3 image files (DAPI; GFP, merge)



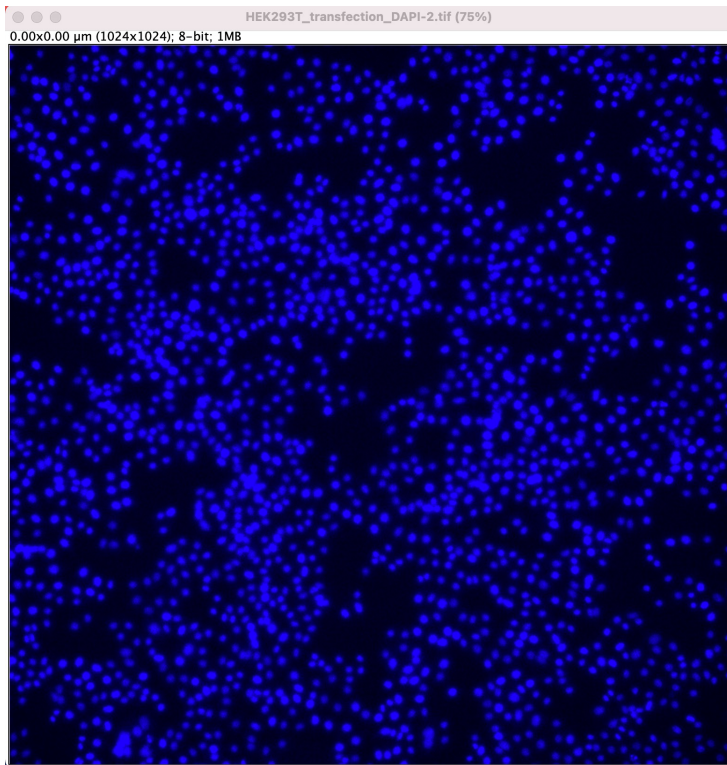
Create a Figure

- see figure guidelines BIO-203
 - panels A, B, C
 - label images (GFP transfected cells, nuclei, merge)
 - write figure legend

B)

How to count objects (pixels, nuclei, cells, ...)

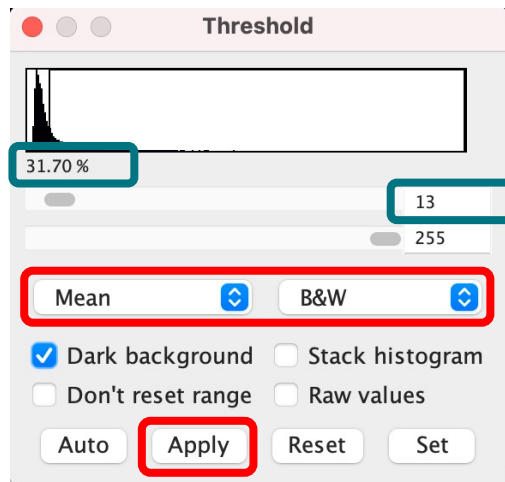
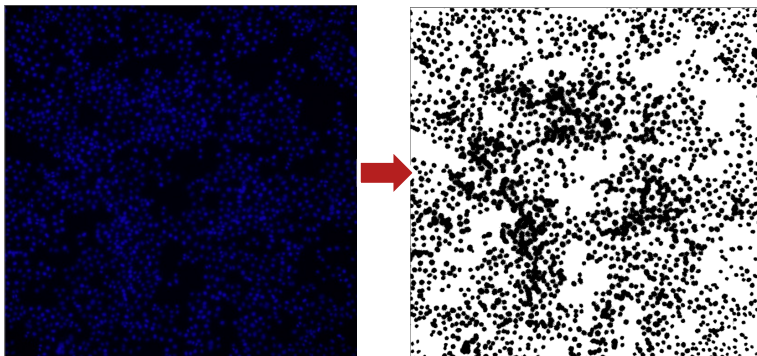
- process image
- analyse



Process DAPI image

- nuclear fluorescence uniform (signal intensity, size, shape...)
- most nuclei are well separated

1) Adjust Treshold



- open image (single channel: DAPI)
- convert to grayscale with 254 gray levels
 - image> type> 8-bit
- adjust treshold
 - set to black and white = binary image
 - image> adjust> threshold>mean
 - value can be different for each image

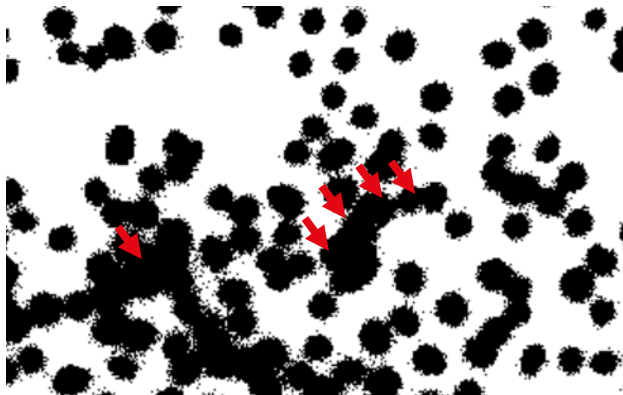
- (possible error message, continue):



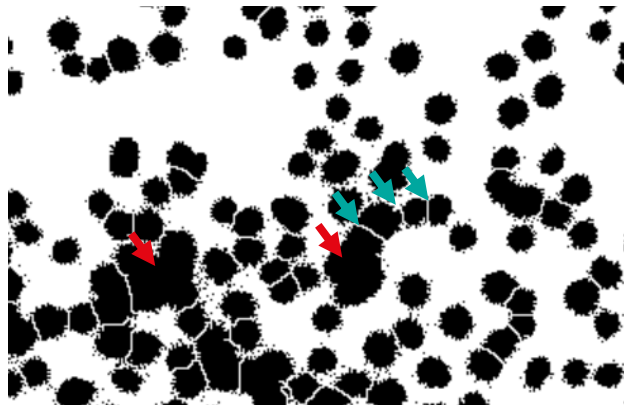
2) Separate Overlapping Objects (nuclei)

- process> binary> watershed
- separation **successful** or **failed**
- (can be further optimized if needed, here ok)

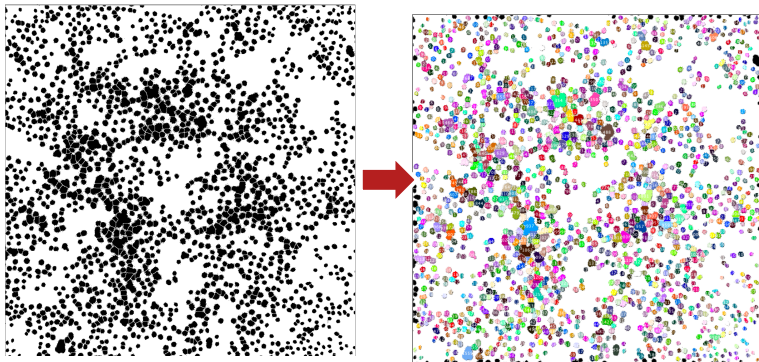
some nuclei are in proximity and difficult to distinguish



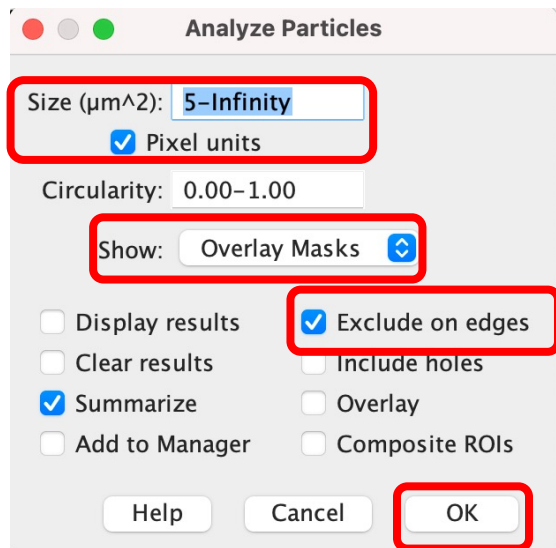
most nuclei separated
(see white lines)



3) Count Objects (Nuclei)



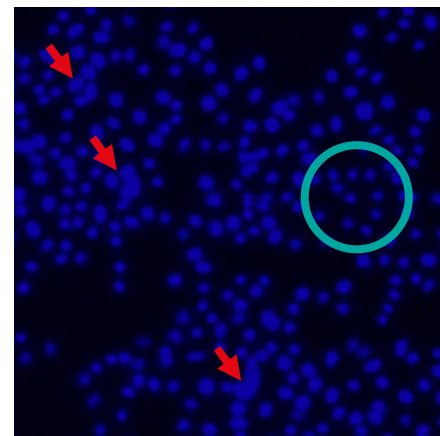
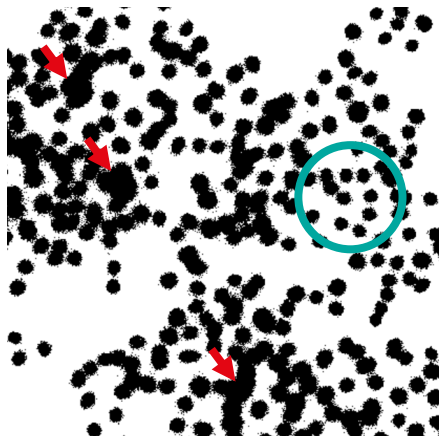
- example: count all black objects with minimum size 5x5 pixels (if only 1-2 pixels are black it is probably not a nucleus)



- `analyze> analyze particles`
 - set size: 5-Infinity
 - exclude on edges (since we lack information for cells that are not entirely inside the image we exclude them from the analysis)

Does the automatic nuclei detection work?

- in the output image each object is shown with a color (count number in white can be ignored here)
 - Compare by eye if the color mask corresponds to what you see in raw image
- **successful** counting in areas with low nuclei density (majority of nuclei)
- ↘ **less accurate** when nuclei are close (signal not separated)



Results are in Table

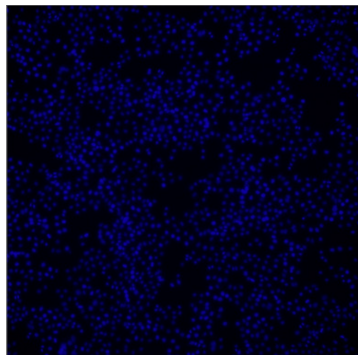
Summary						
Slice	Count	Total Area	Average Size	%Area	Mean	IntDen
HEK293T_transfection_DAPI-5.tif	1624	1.680E-6	1.034E-9	29.547	255	2.637E-7

- Count: 1624 objects (here: nuclei)

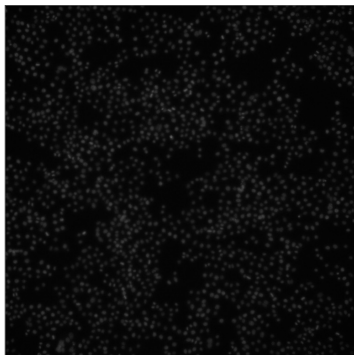
Summary:

Image Processing for Nuclei Count (DAPI)

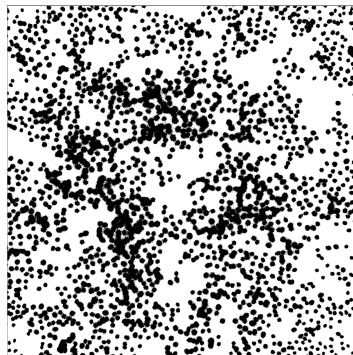
raw image



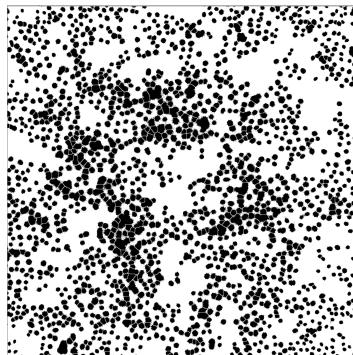
greyscale
(8-bit)



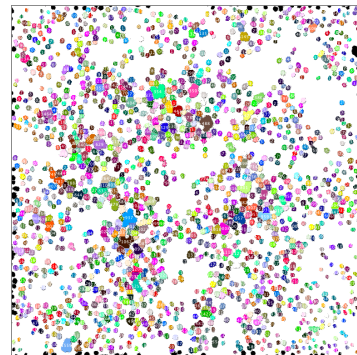
threshold
(black + white)



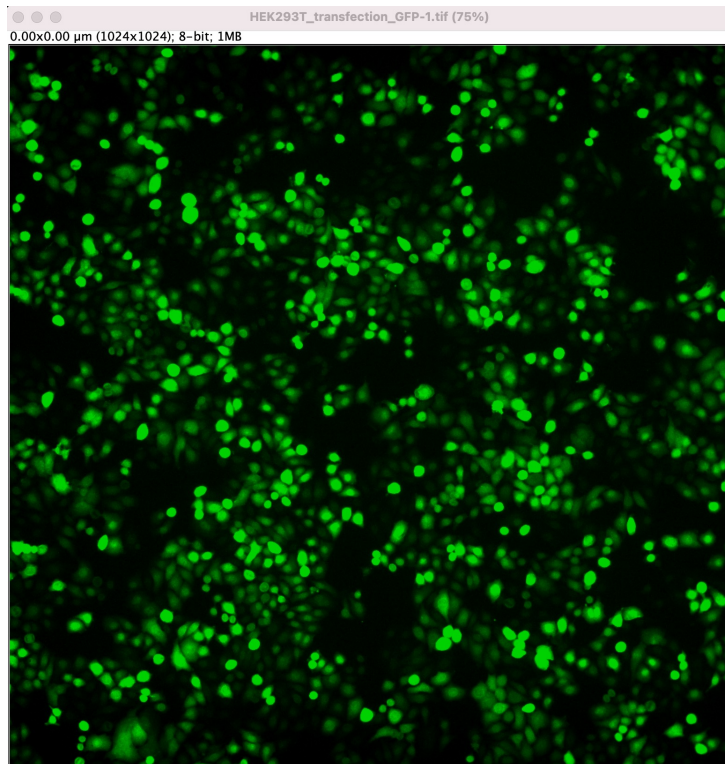
separate
(watershed)



count objects



Slice		Count
HEK293T_transfection_DAPI-5.tif		1624



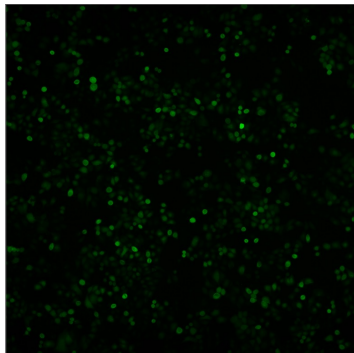
Process GFP image (same steps as with DAPI image)

- intensity of GFP fluorescence is variable: strong vs weak expression
- difficult to count
 - cells in close contact
 - weak expressing cells
 - strong expressing cells

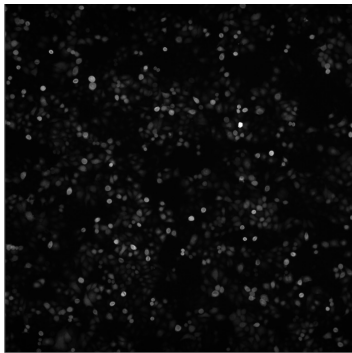
Summary:

Image Processing for GFP Expressing Cells

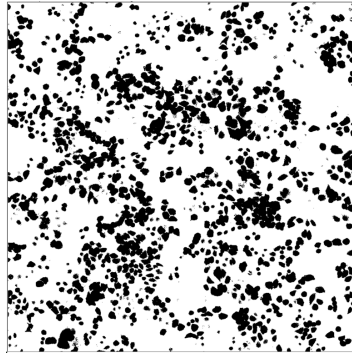
raw image



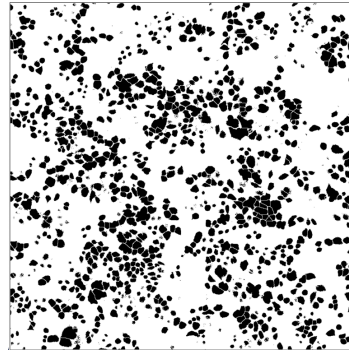
greyscale
(8-bit)



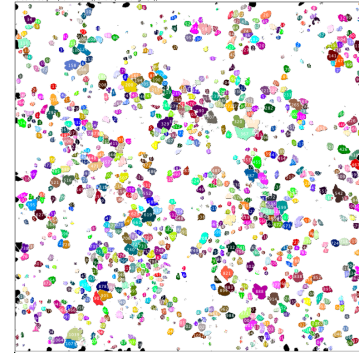
threshold
(black + white)



separate
(watershed)



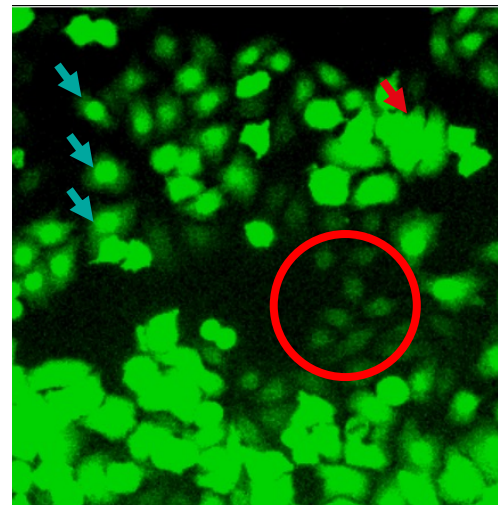
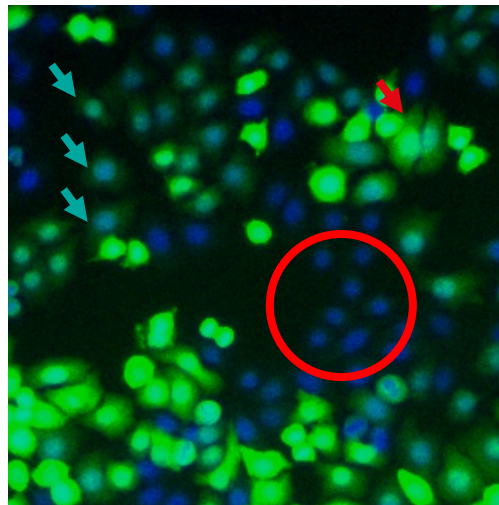
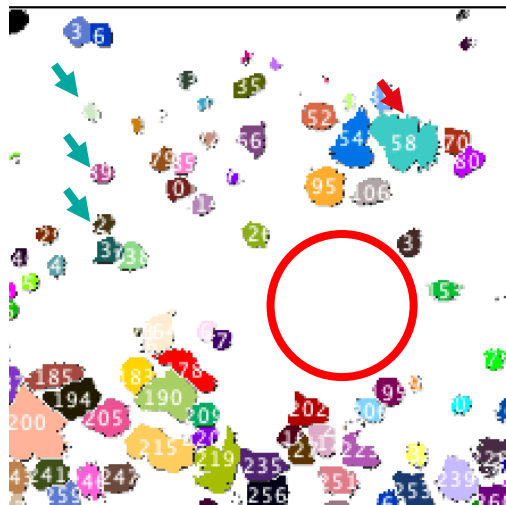
count objects

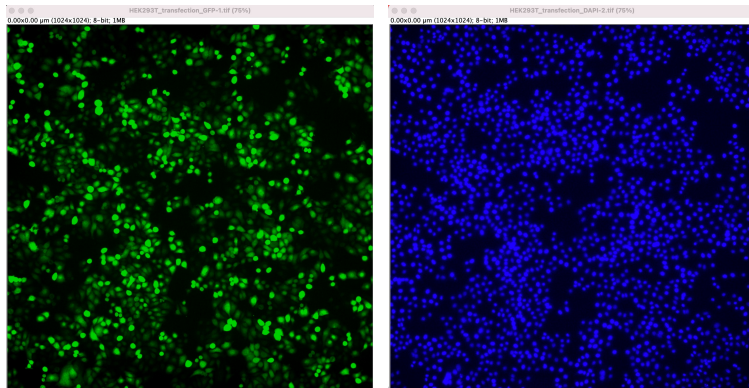


Summary	
Slice	Count
HEK293T_transfection_DAPI-5.tif	1624
HEK293T_transfection_GFP.tif	1100

Note Some GFP Detection Issues

- Compare by eye color mask and raw data
 - **successful** counting for cells with 'mean' expression level
 - **underestimation** of cell counts due to:
 - very weak expression - below threshold- not counted
 - ↘ very strong expression, high cell density: cells not well separated
- count merge GFP + DAPI GFP enhanced contrast





Calculate % Transfection Efficiency

Transfected Cells (GFP): 1100

All cells (DAPI nuclei): 1624

Transfection efficiency

$$1100/1624 = 68\%$$

Every image is different

- optimize !
 - experimental setup (cell density, expression duration...)
 - image acquisition
 - processing
- if you have acquired many images use batch processing

