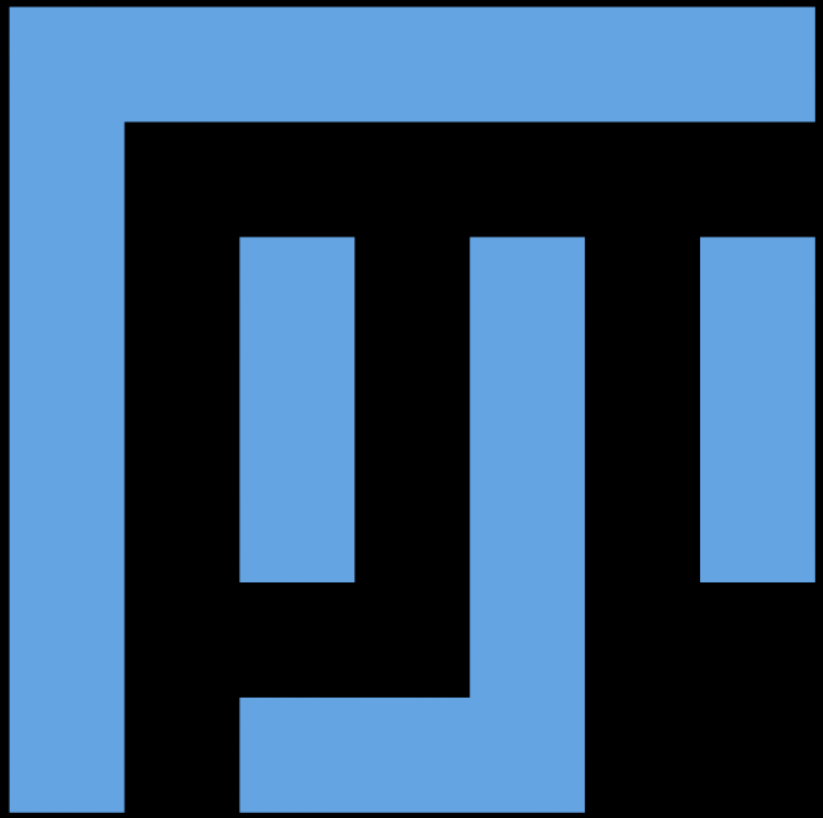
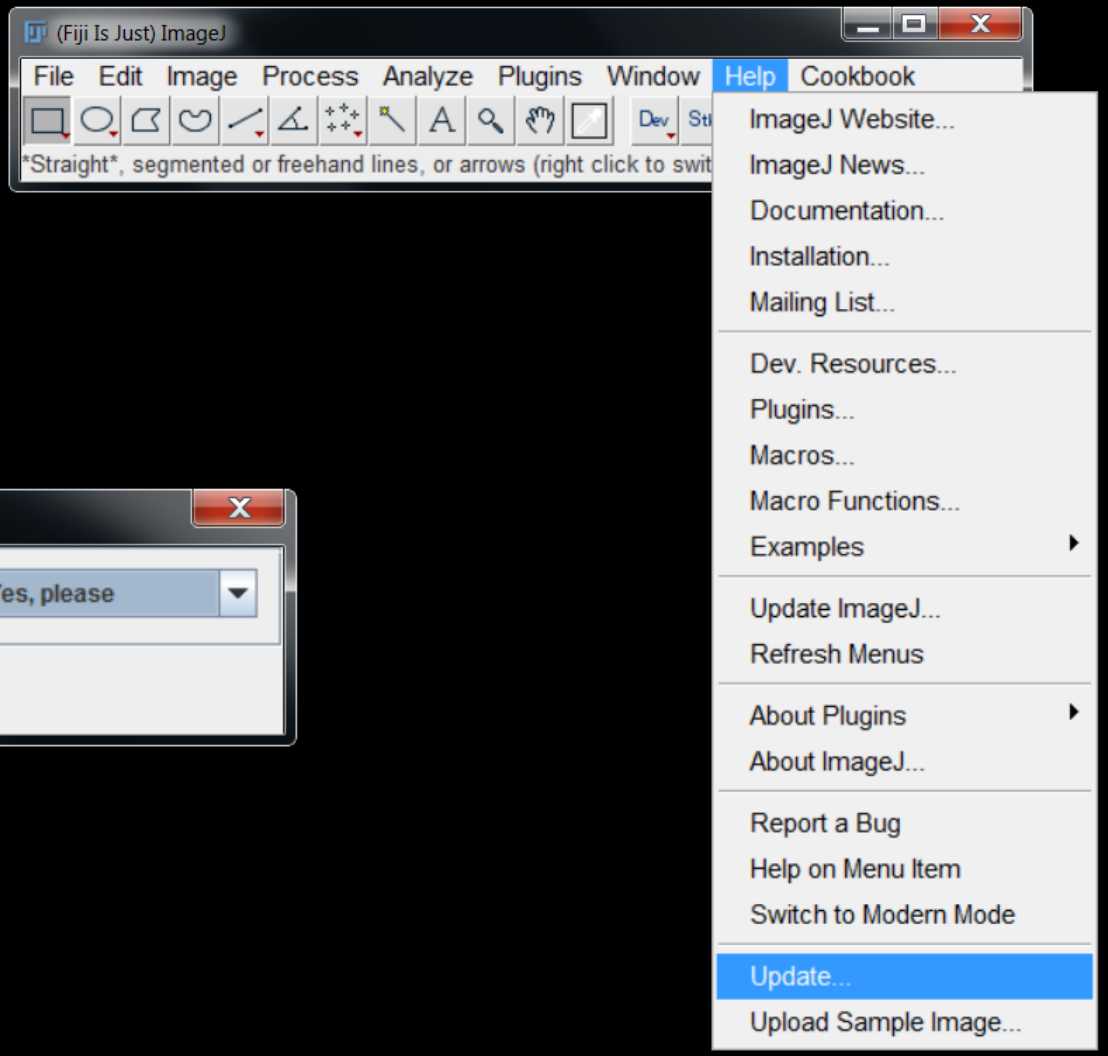
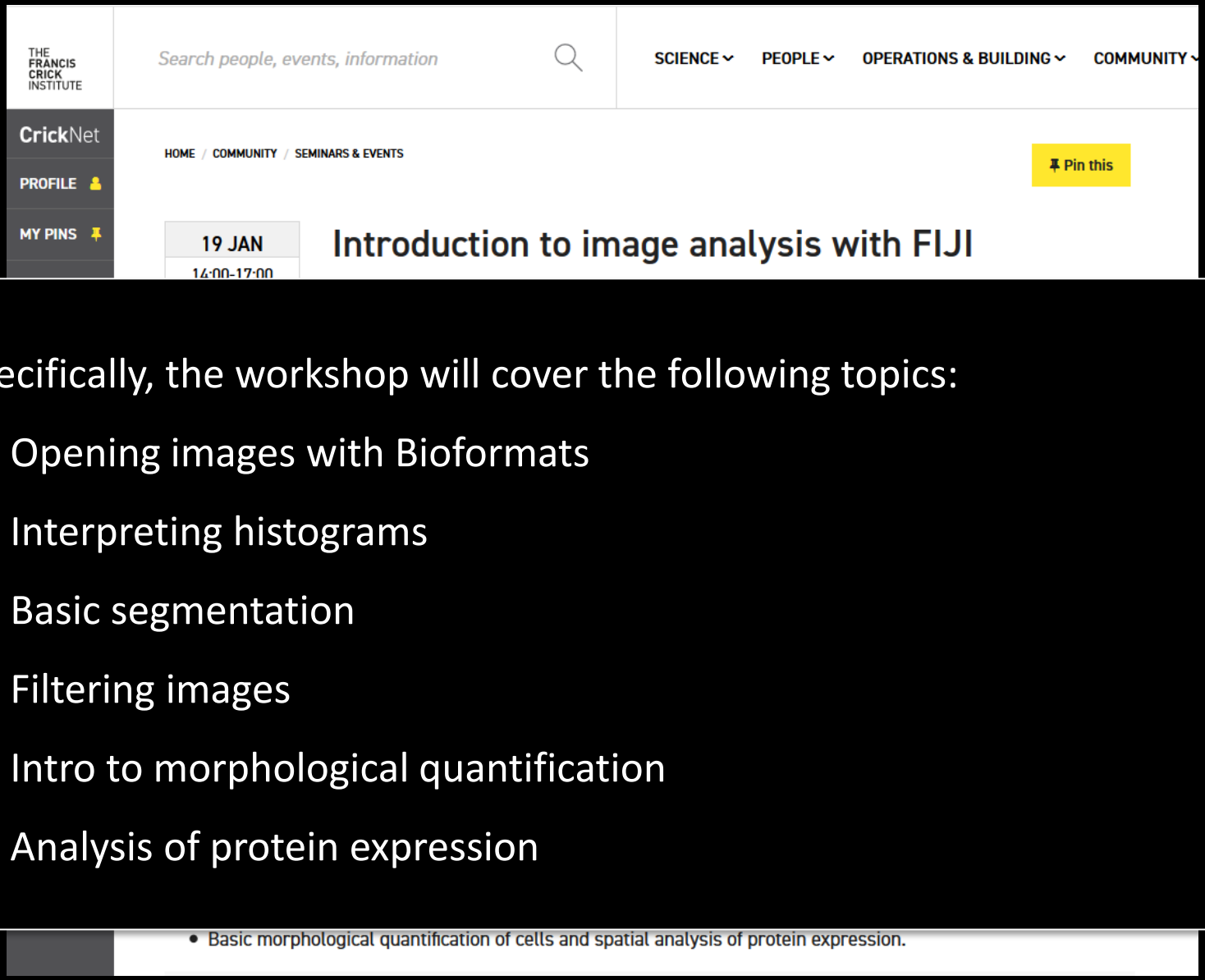
Introduction to Image Analysis with



PLEASE ENSURE FIJI IS INSTALLED CORRECTLY!



WHAT DO WE HOPE TO ACHIEVE?



Specifically, the workshop will cover the following topics:

1. Opening images with Bioformats
2. Interpreting histograms
3. Basic segmentation
4. Filtering images
5. Intro to morphological quantification
6. Analysis of protein expression

AIMS

- Introduction to image analysis concepts
- Gentle introduction to FIJI

FORMAT

- General overview
- Small chunks of theory/demonstration, each followed by a practical.
- Challenges
- Break for tea/coffee at 15:30
- Finish about 17:00

HOUSEKEEPING

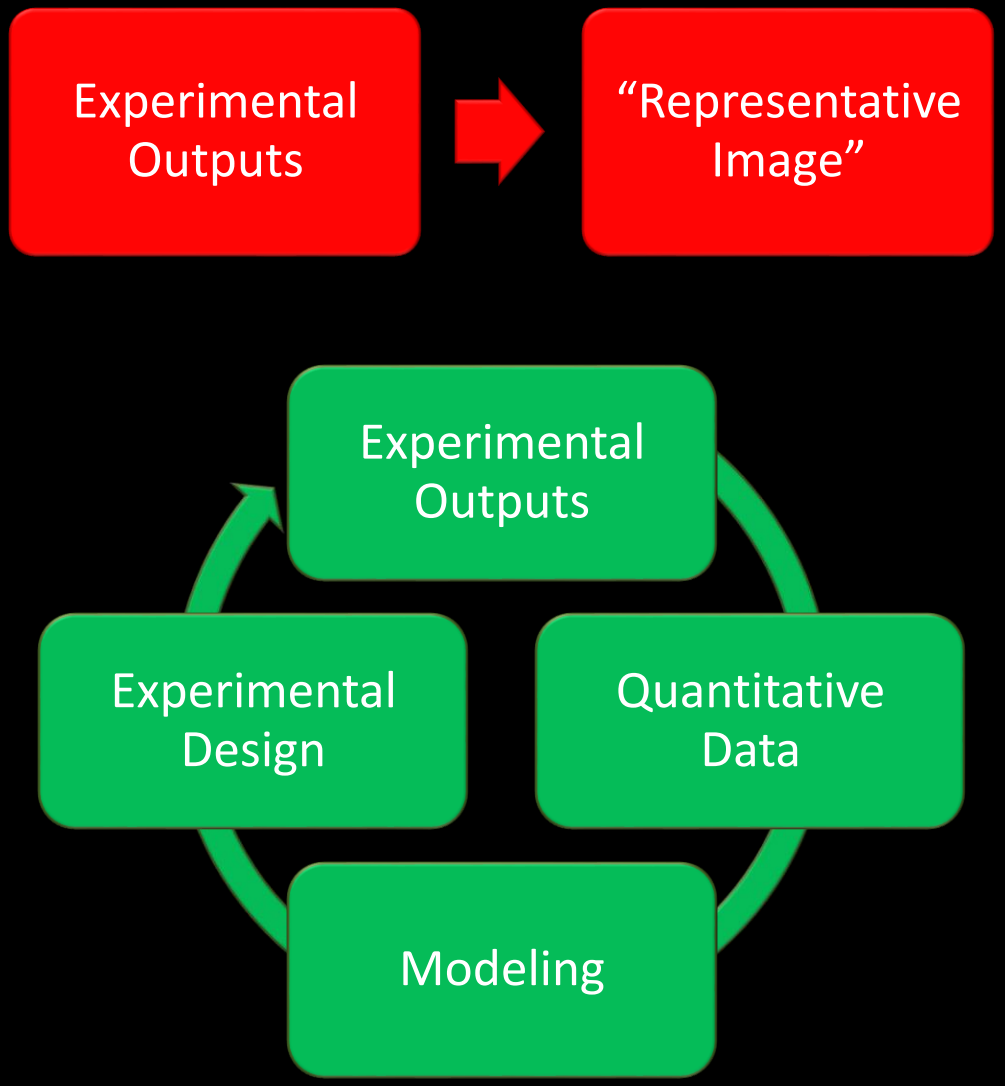
You don’t need to take notes – I will send you the slides after the workshop

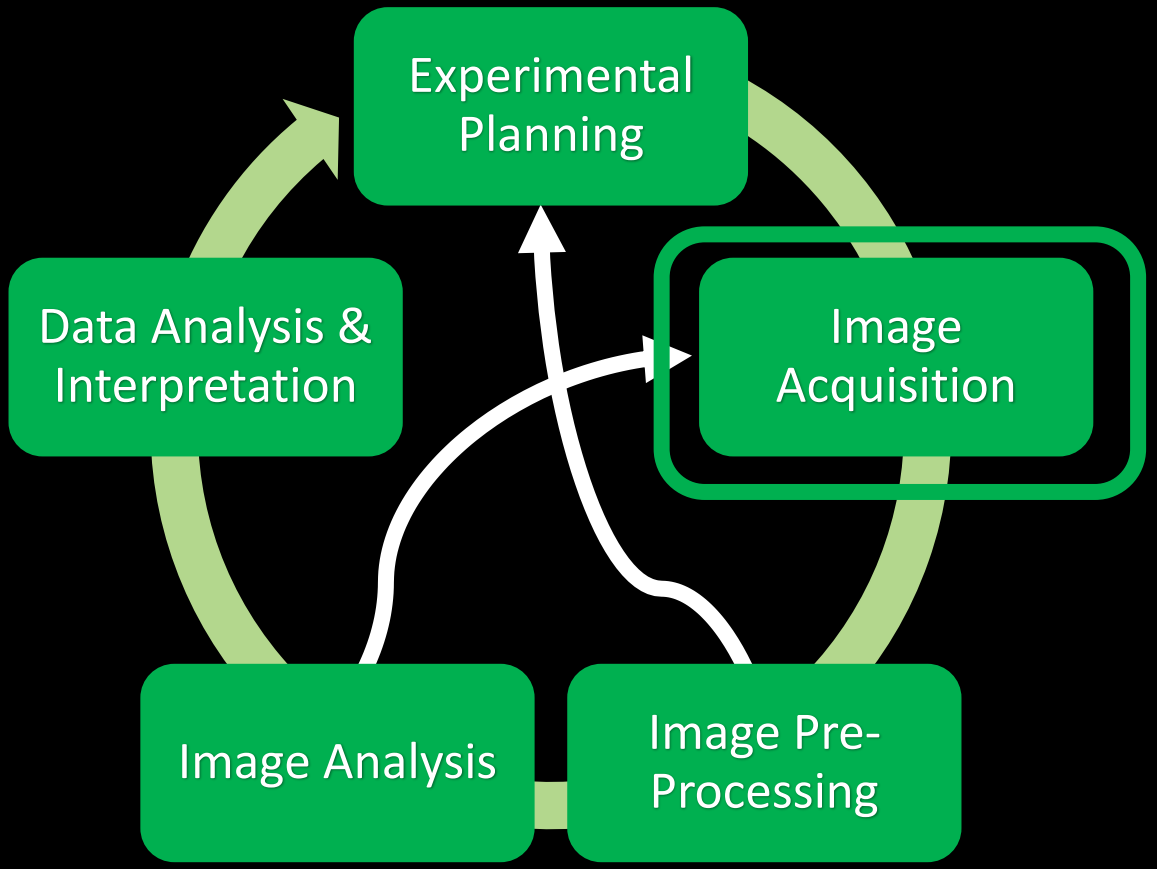
Please sign the sign-in sheet

Please feel free to ask questions

WHY USE QUANTITATIVE IMAGE ANALYSIS?

- Microscopy historically qualitative
- New technology facilitates quantification
- Limited uptake among biologists





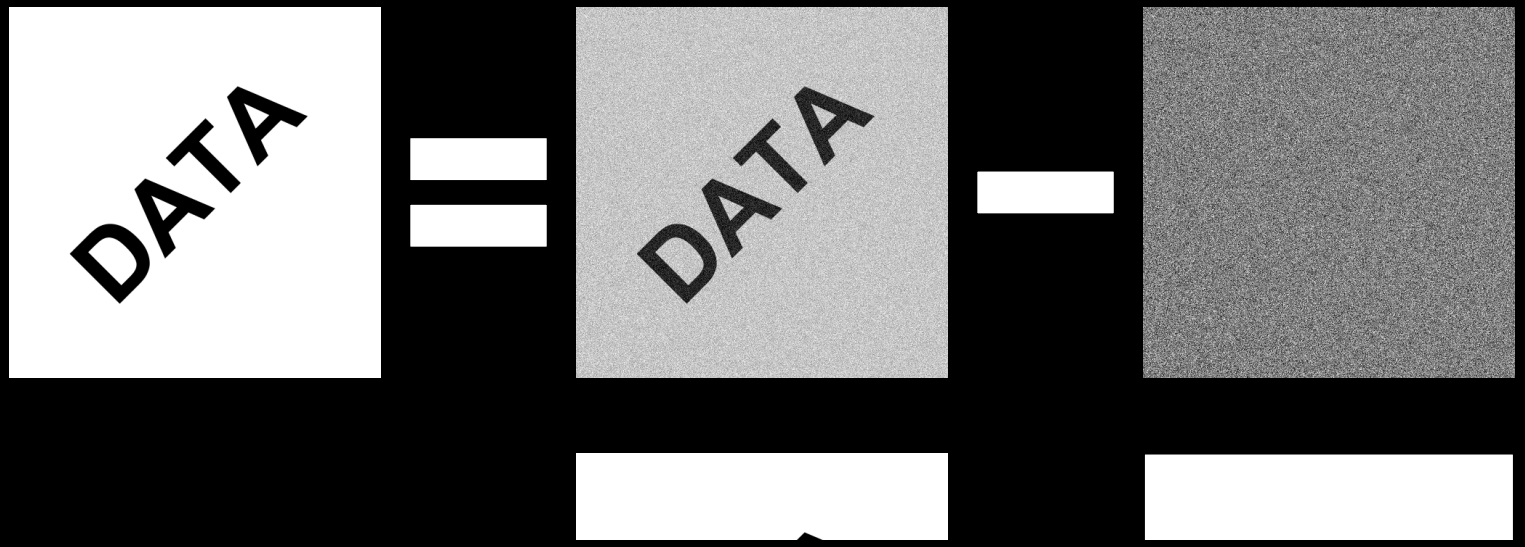
- Experimental design is an iterative process
- High quality images absolutely crucial
- Scale up gradually

Fixed coverslips → Live cell single well → Live cell multi-well

IMAGE ANALYSIS V IMAGE PROCESSING ?

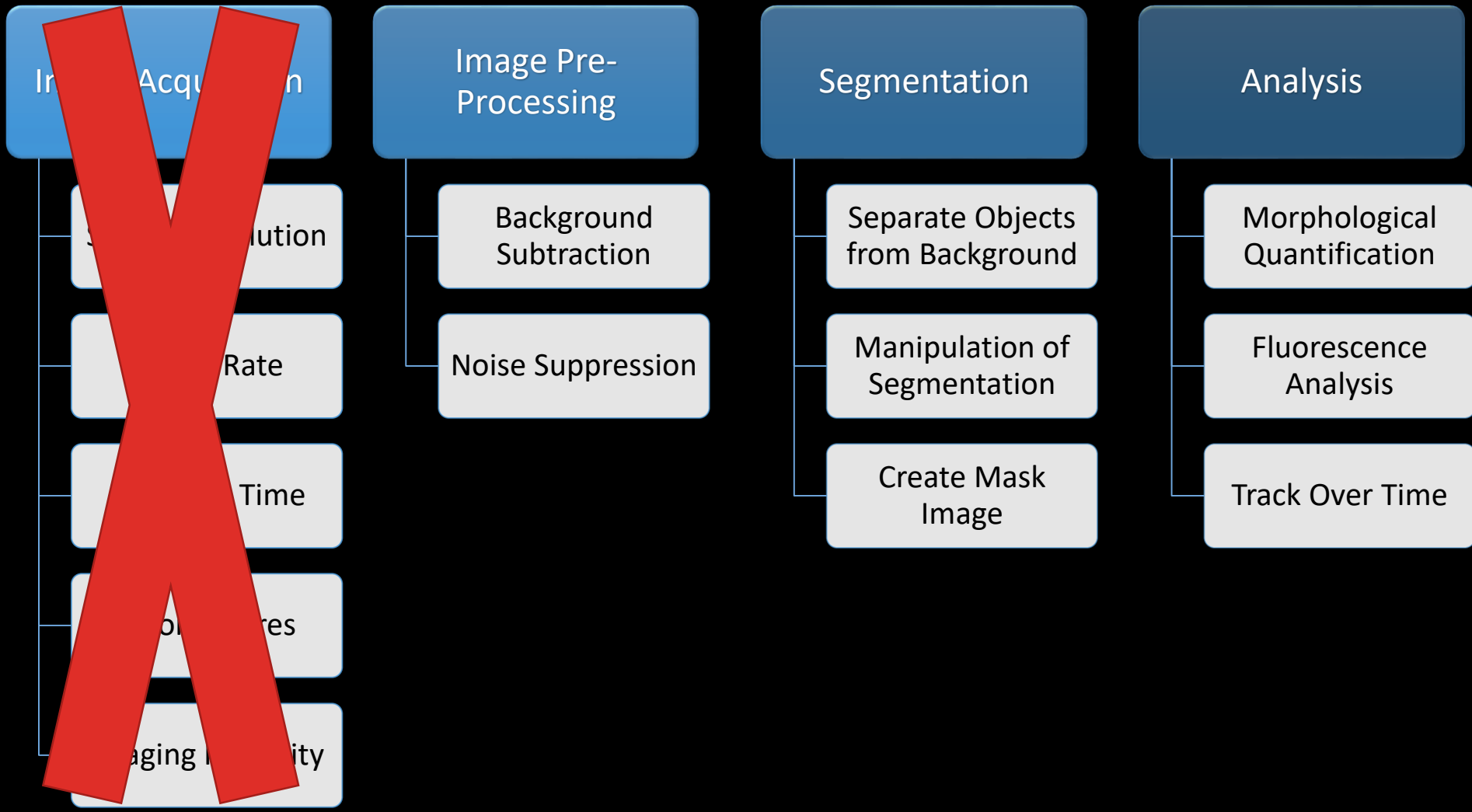
- Image Processing:
  - Enhancement, filtering for noise reduction, image registration, etc.
- Image Analysis:
  - Analysis of data contained within an image. For example, quantification of cell area.

Processing:

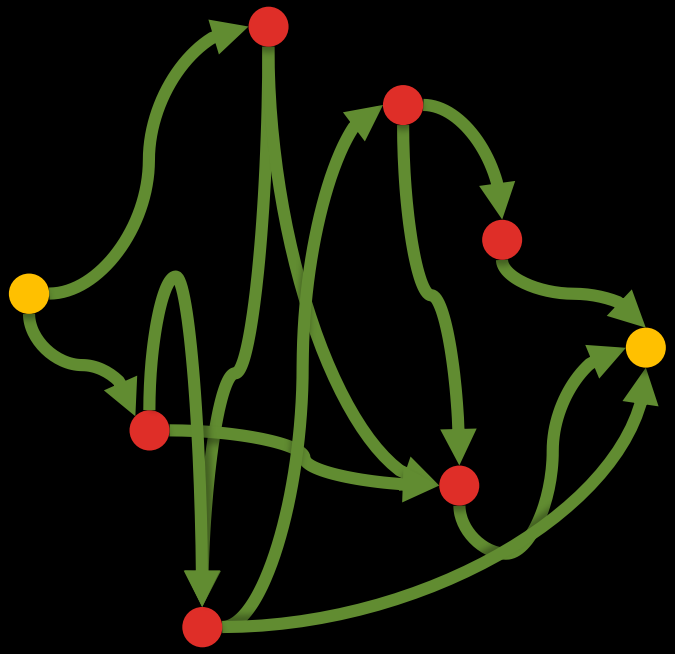


Processing should be kept to a minimum – reduces information content in image

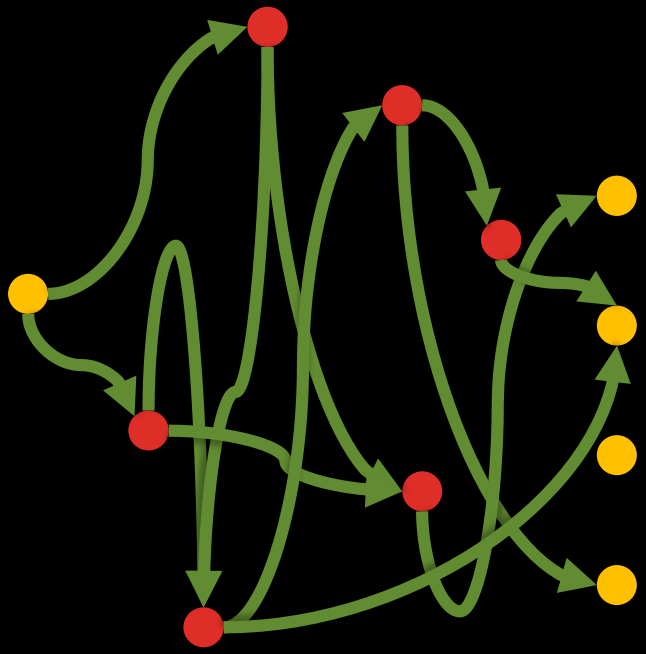
TYPICAL IMAGE ANALYSIS WORKFLOW

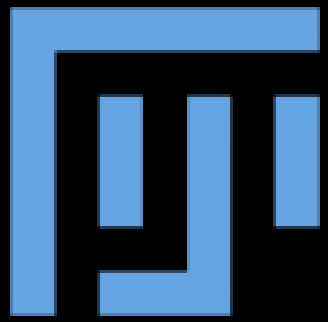


1. There are several different ways to arrive at a solution



2. There is rarely one single correct solution





- **FIJI:**
- Fiji Is Just ImageJ
- Actively maintained, with frequent updates.

ImageJ:

- Open source
- Public domain, cross-platform.
- Read most image formats (via bioformats).
- Same standard functions as proprietary packages.
- Open architecture.

CellProfiler

cell image analysis software

BROAD INSTITUTE

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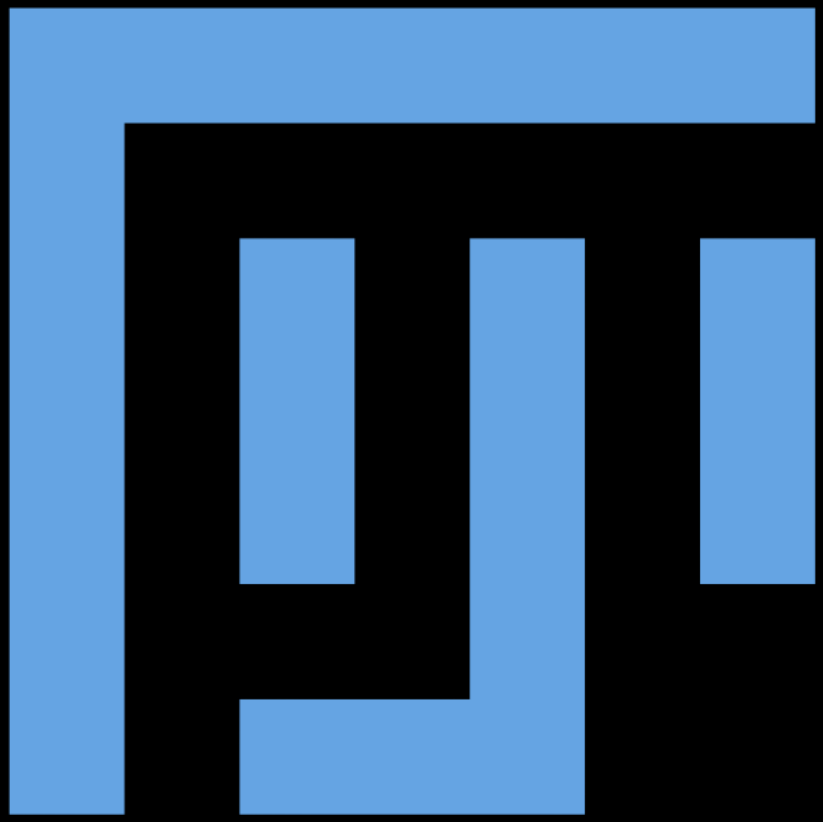
CellProfiler Download

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. See our papers on analyzing cell images and non-cell images.

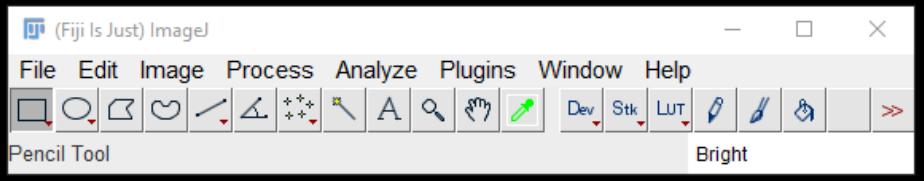
CellProfiler Analyst Download

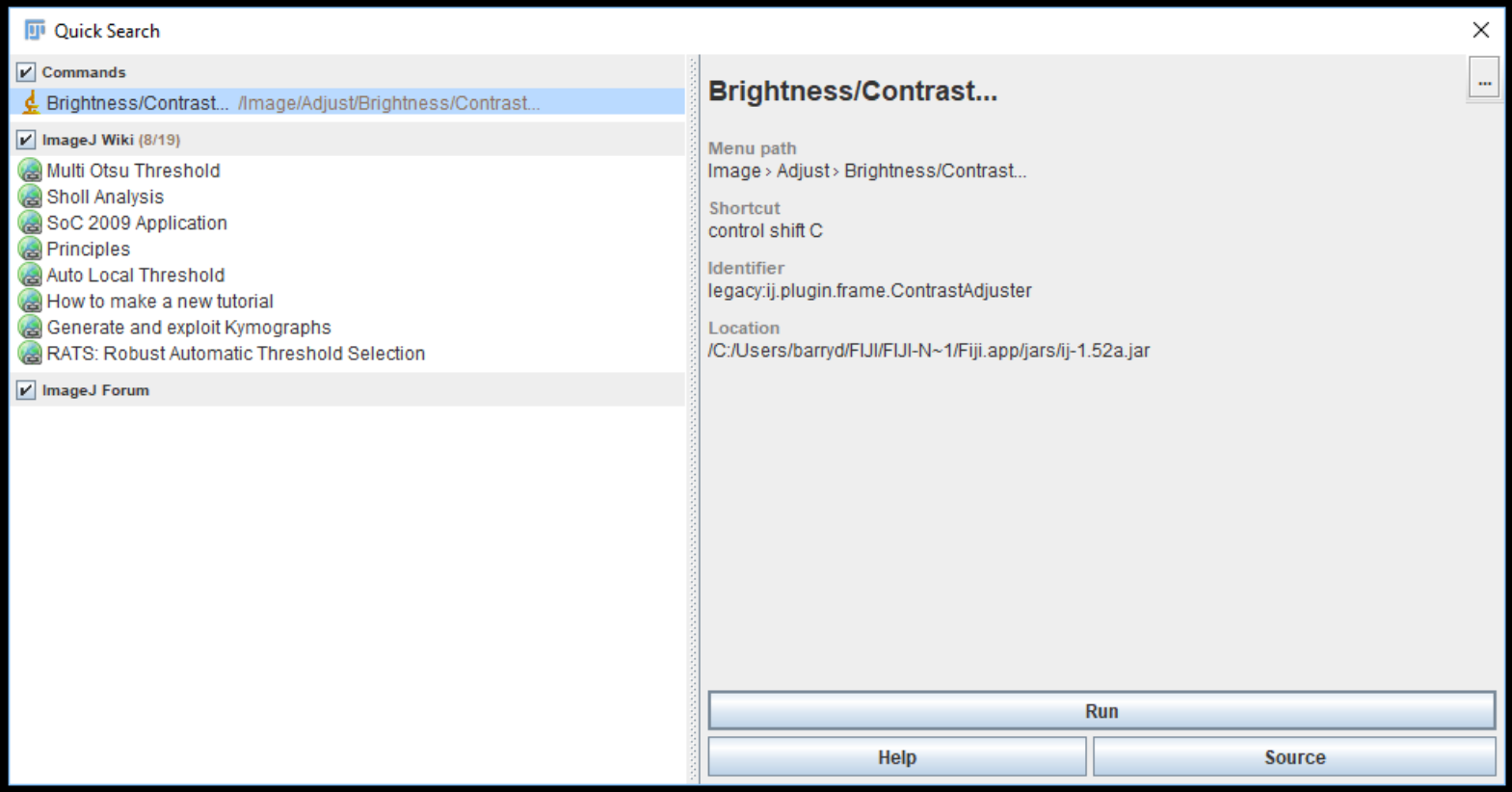
CellProfiler Analyst is free open-source software for exploring and analyzing large, high-dimensional image-derived data. It includes machine learning tools for identifying complex and subtle phenotypes. See our papers on data visualization and machine learning.



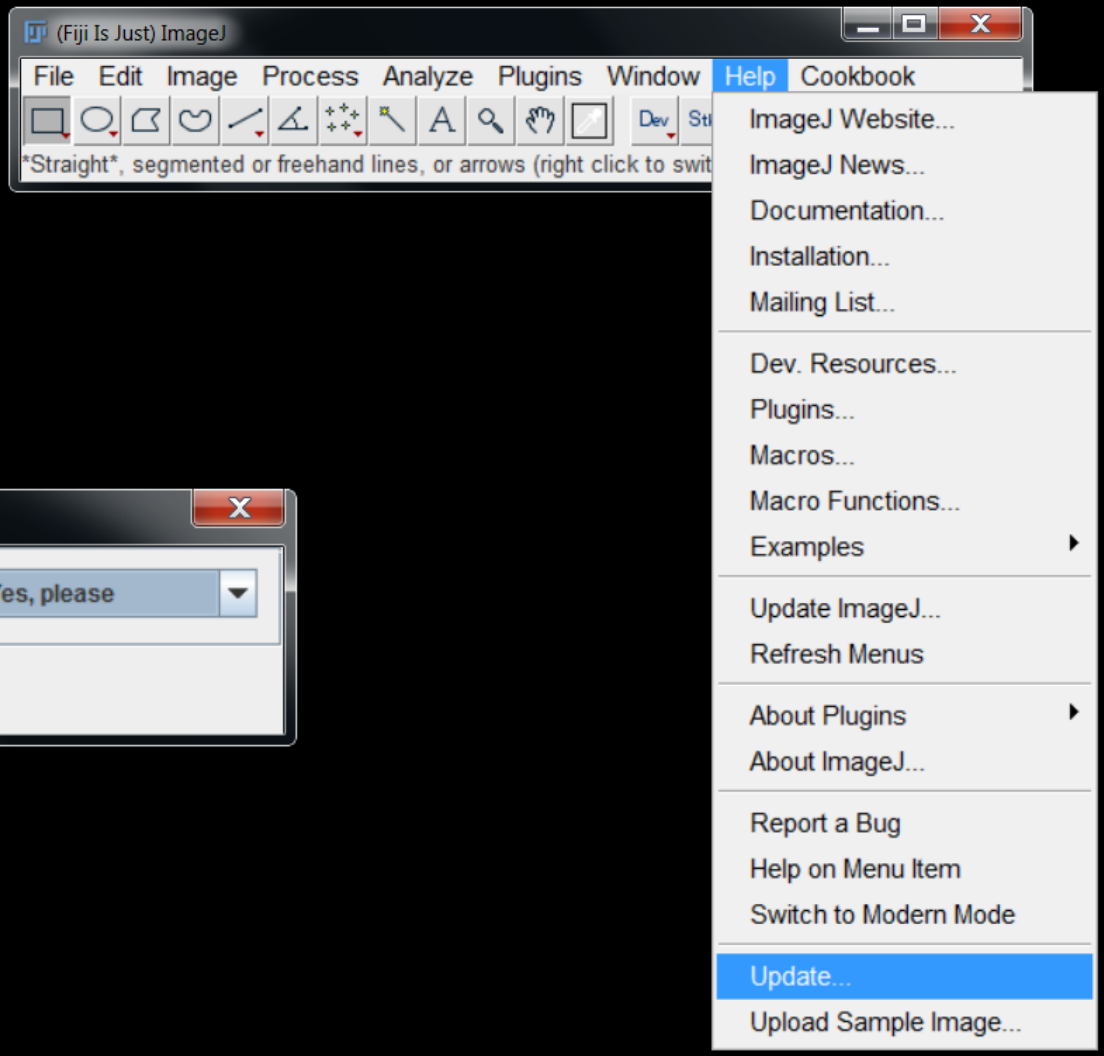
Let us begin…

IF YOU FORGET HOW TO ACCESS SOMETHING…



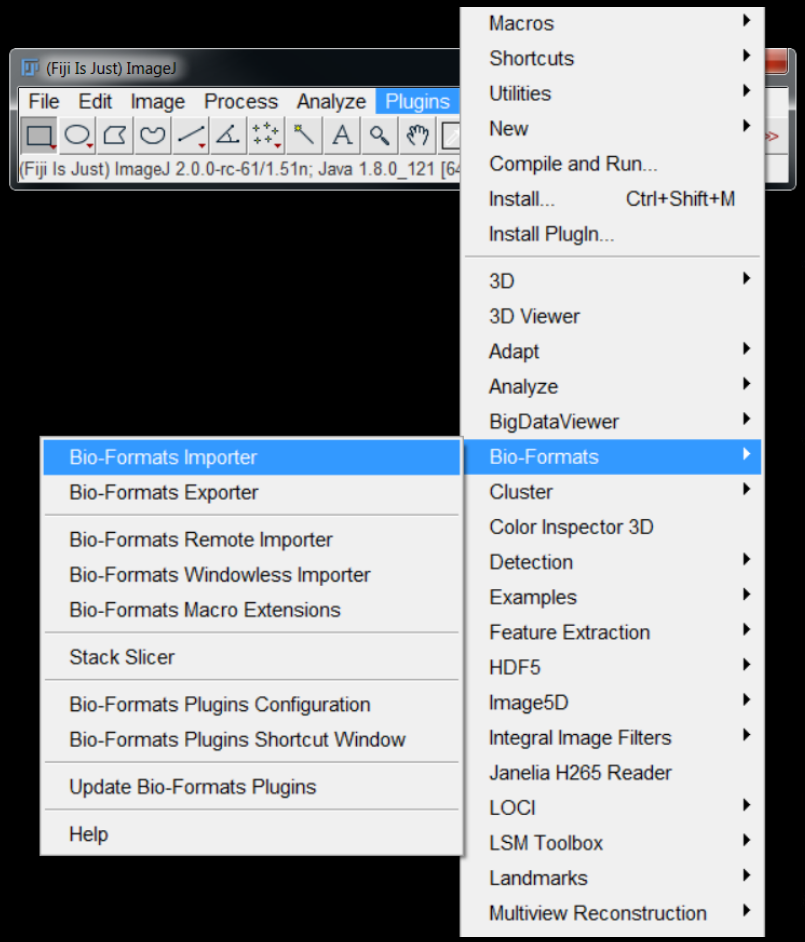


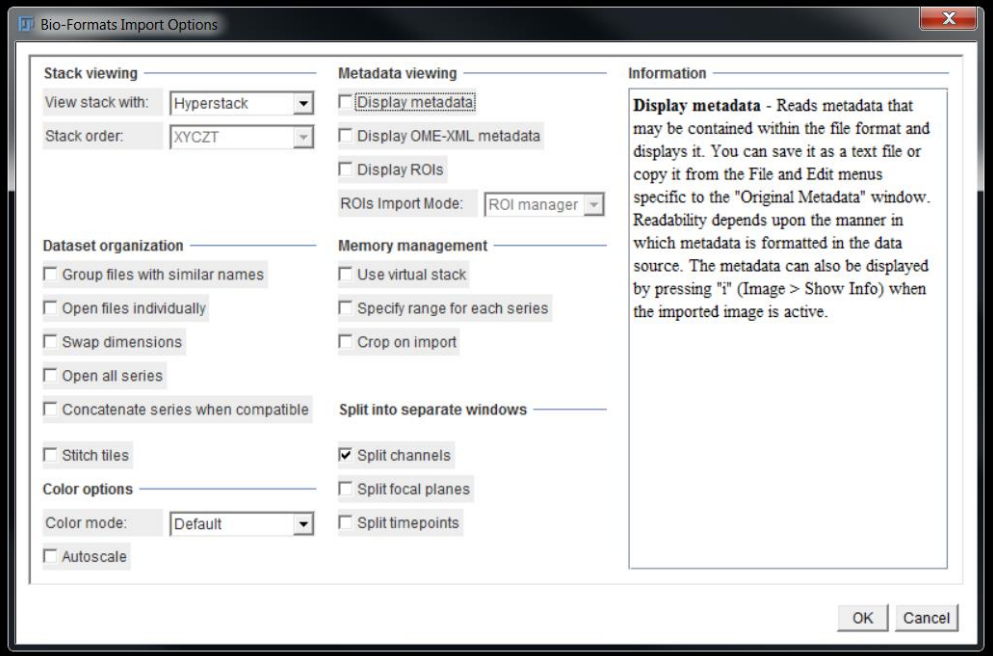
UPDATING FIJI



OPENING AN IMAGE

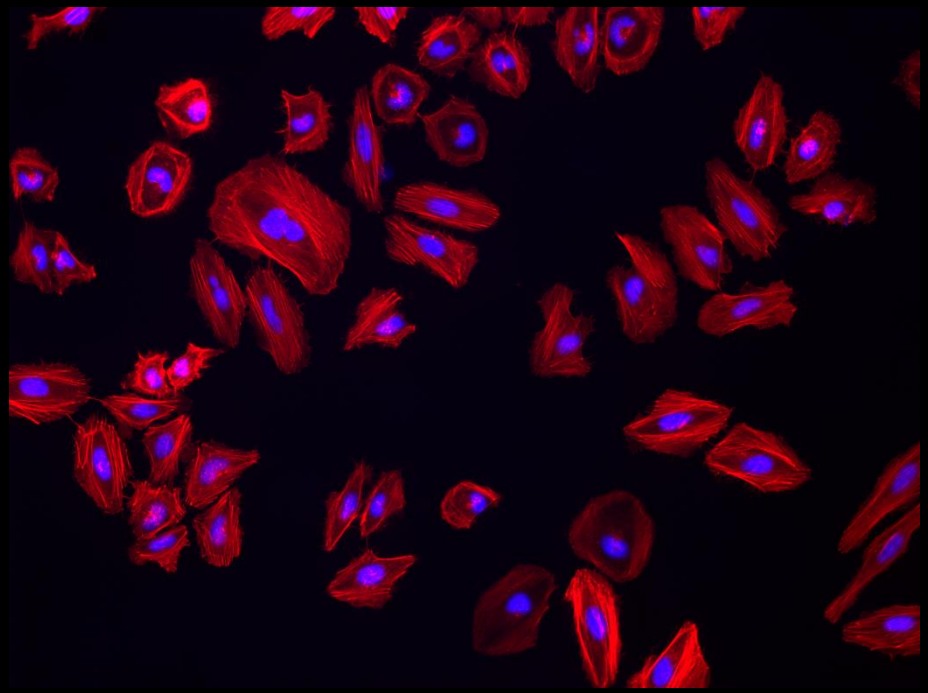
- Don’t Drag & Drop
- Bioformats ensures consistent reading of metadata
  - Independent project distributed with FIJI



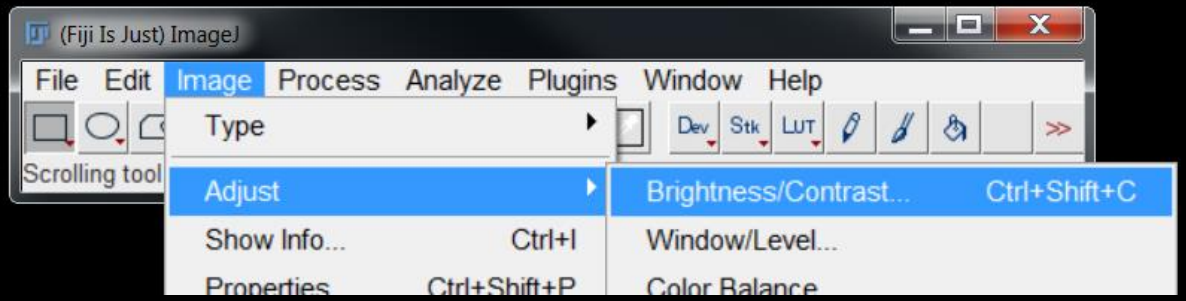


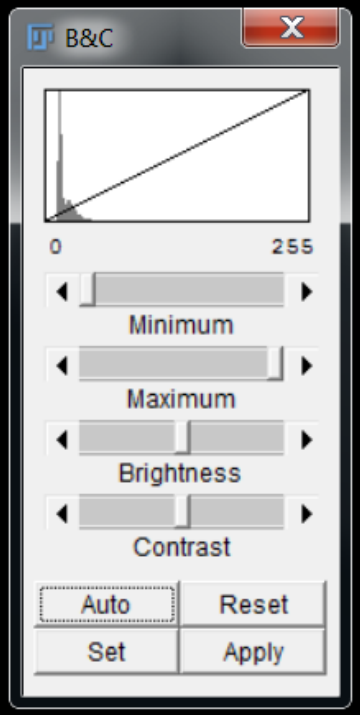
DEMO 1 – OPENING IMAGES WITH BIOFORMATS

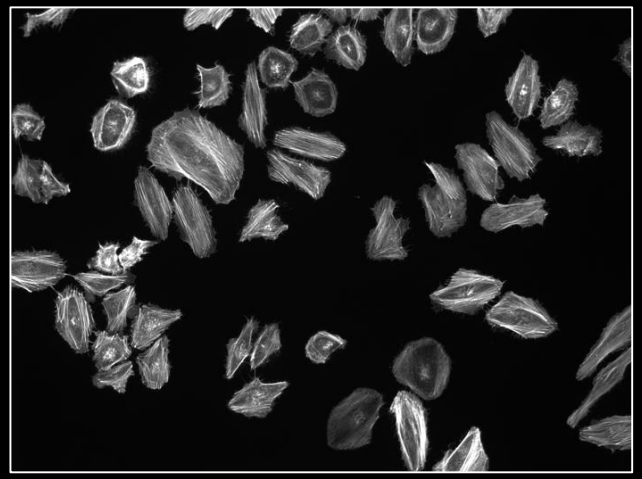
- Import Metamorph (TIFF) Dataset:
  - Overview of various options presented in Bioformats GUI
  - Illustration of reading of MetaData
  - Images can *appear* black, but pixels have values greater than zero



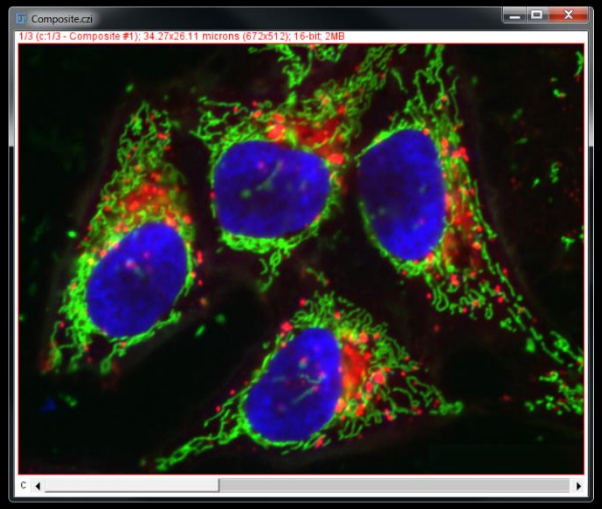
ADJUSTING CONTRAST

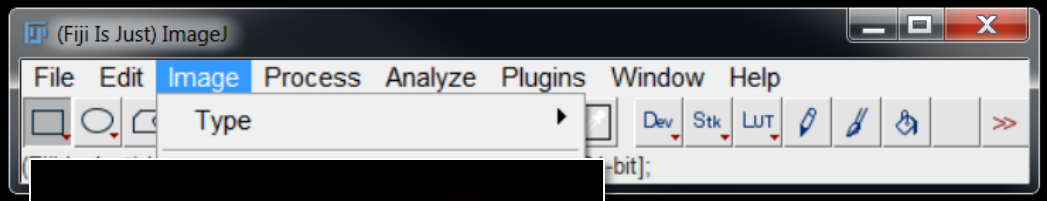


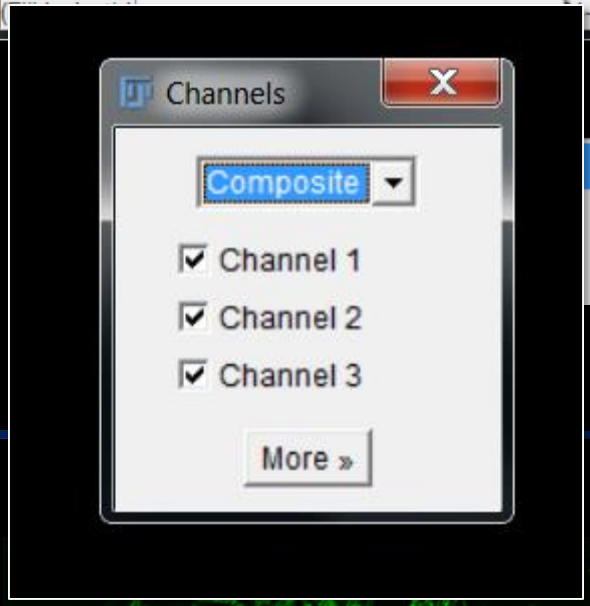


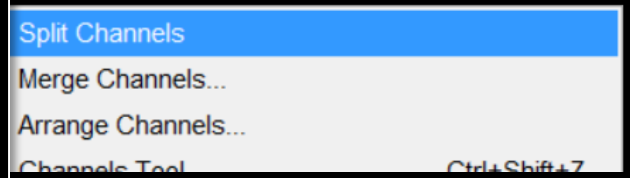


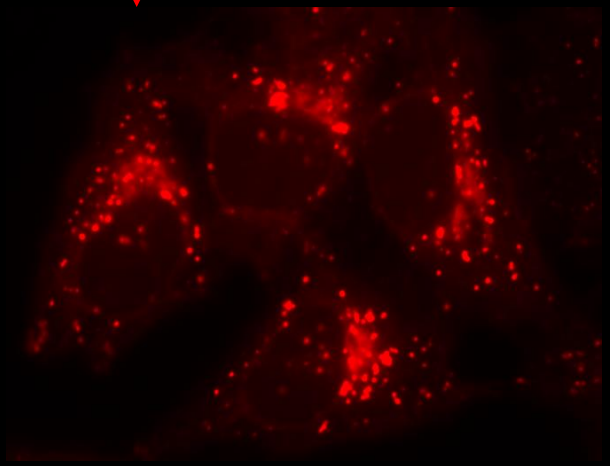
WORKING WITH CHANNELS

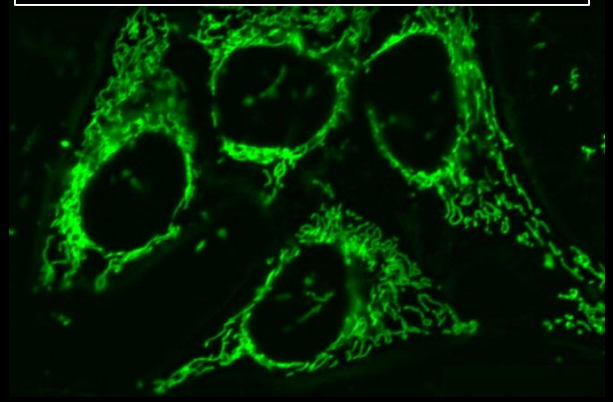


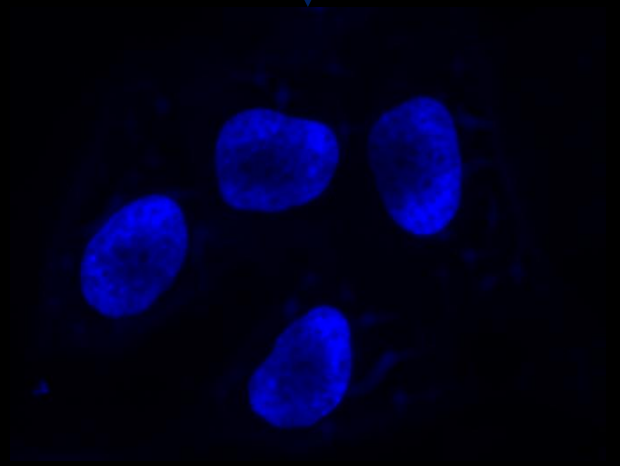






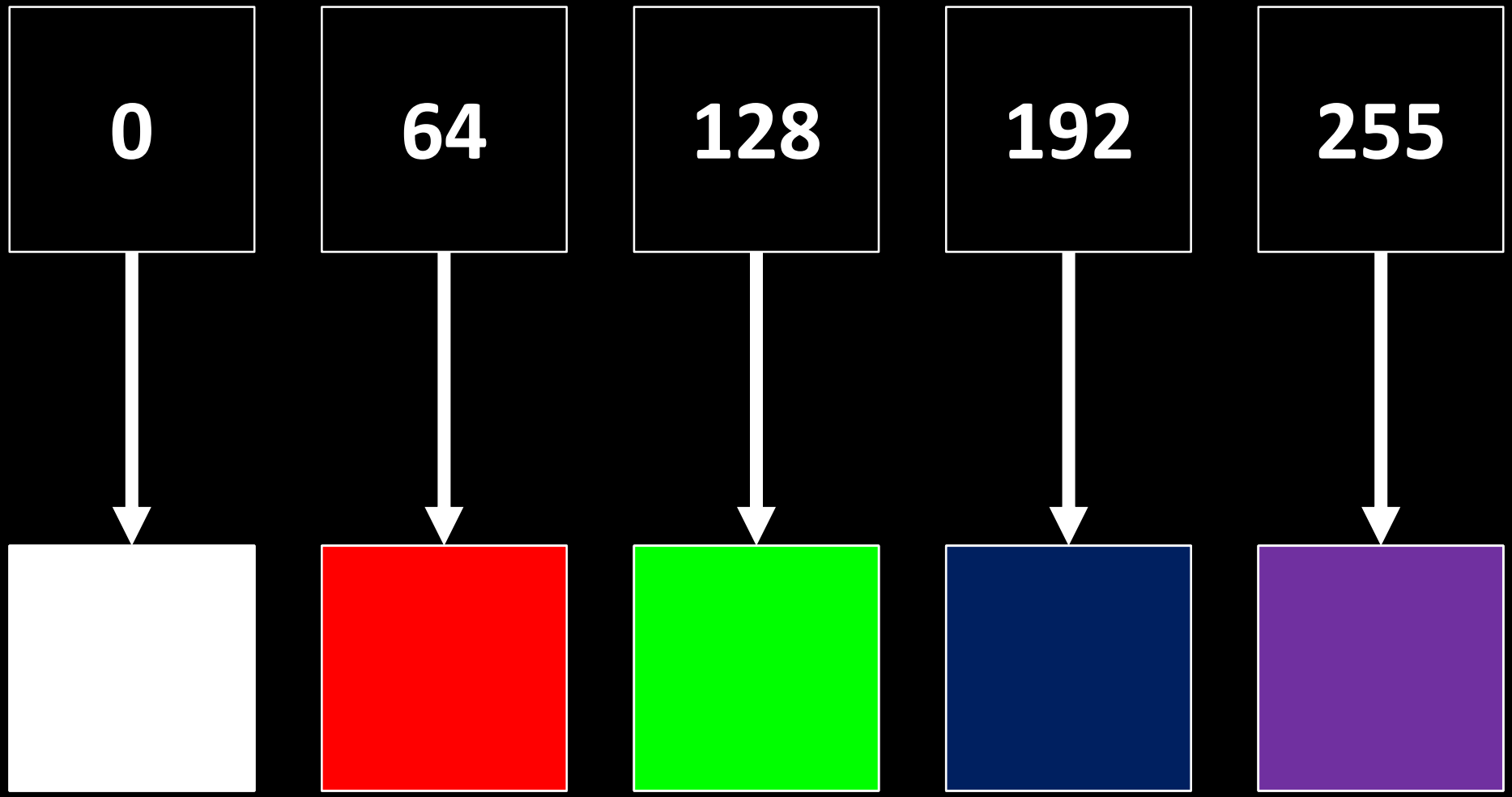






LOOK-UP TABLES (LUTS)

By default, pixel values are mapped to grey levels…



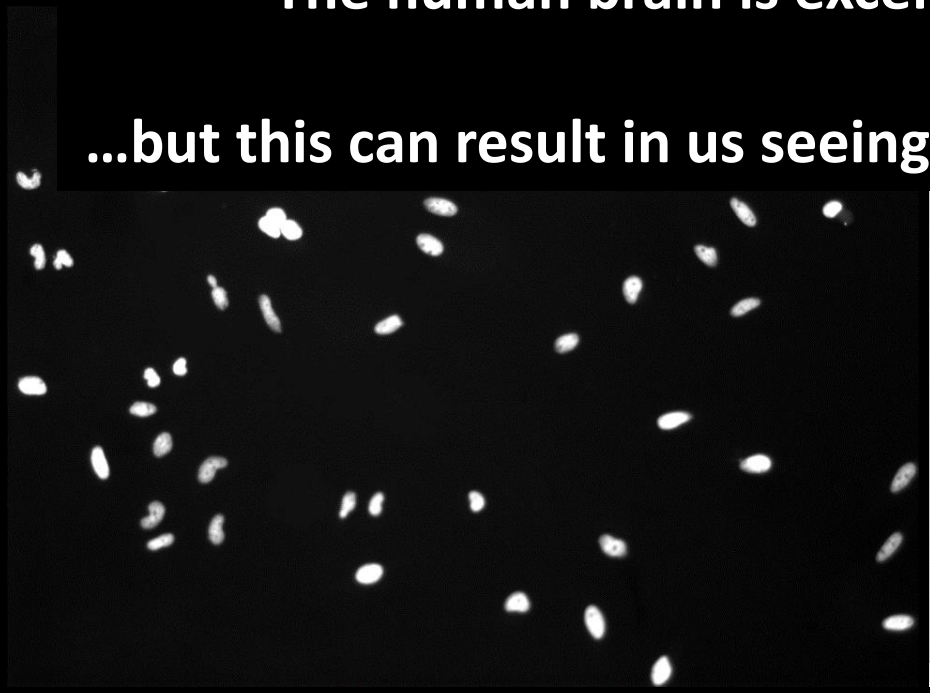
…but there is no reason why this has to be the case.

IMAGES ARE JUST NUMBERS

"Solutions to image analysis problems often appear simple, particularly when easily accomplished by the human visual system, which is complex and poorly understood."

The human brain is excellent at pattern matching…

…but this can result in us seeing "patterns" that don't really exist



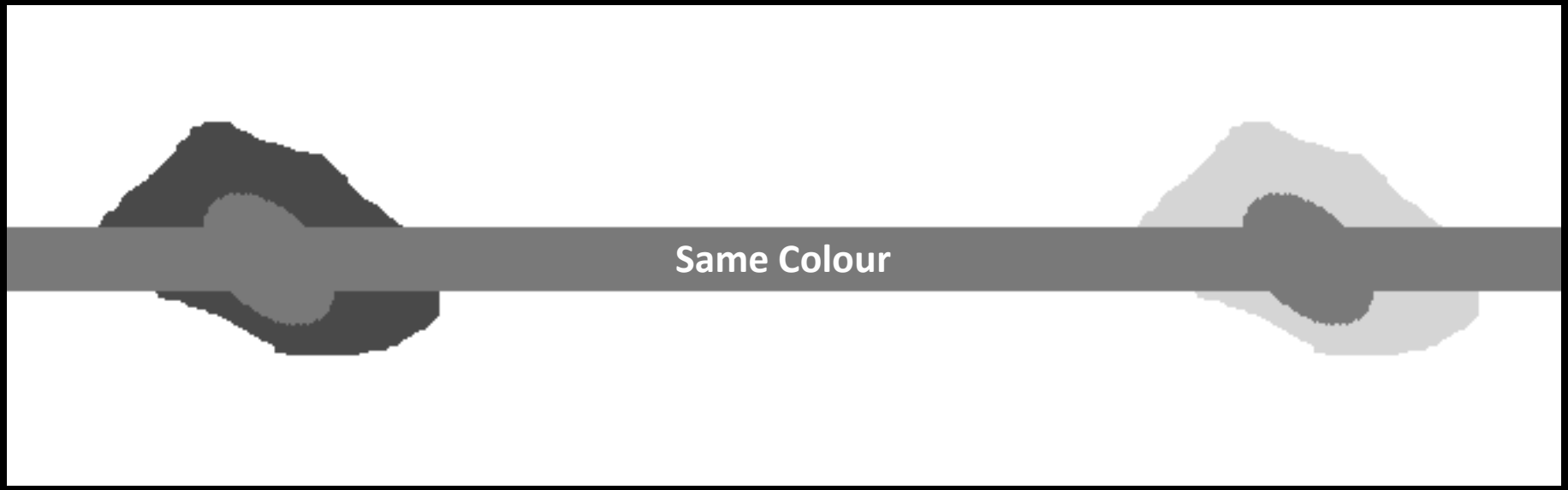
THIS CAN CAUSE PROBLEMS…

Pareidolia is a psychological phenomenon in which the mind responds to a stimulus by perceiving a familiar pattern where none exists (e.g., in random data).

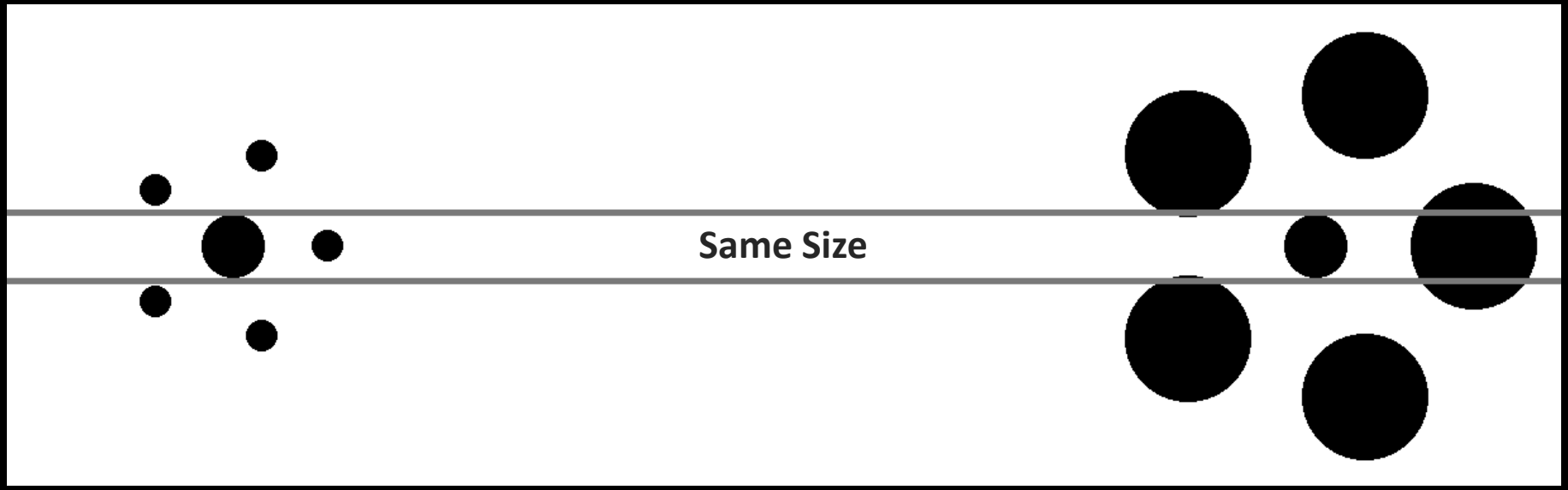
1976, Viking 1

2001, Mars Global Surveyor

Which nucleus is brighter?



Which centre circle is bigger?



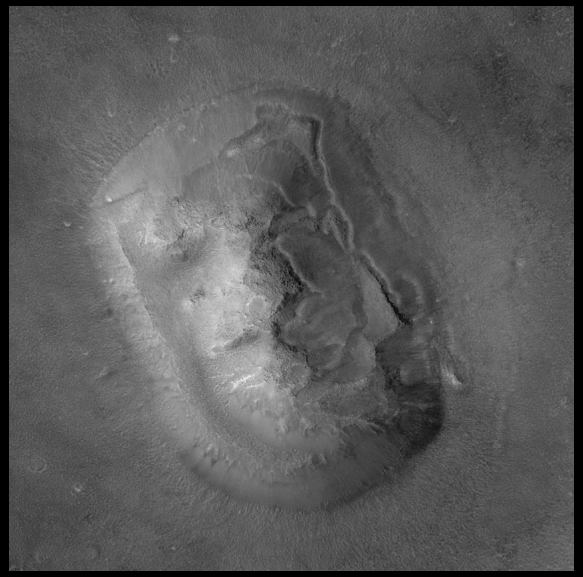
WHAT'S YOUR POINT DAVE?!?!?

We're here to learn image analysis – you're preaching to the choir!

People will very often design an analysis pipeline to confirm what **they think they see** visually….

…which often results in significant frustration.

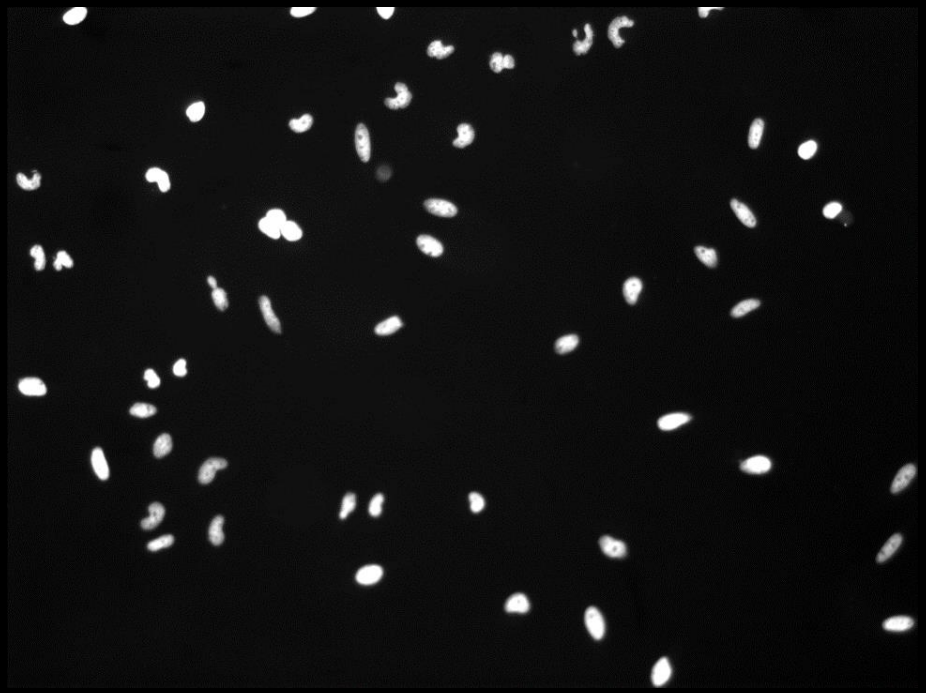
Expected Result: Humanoids on Mars

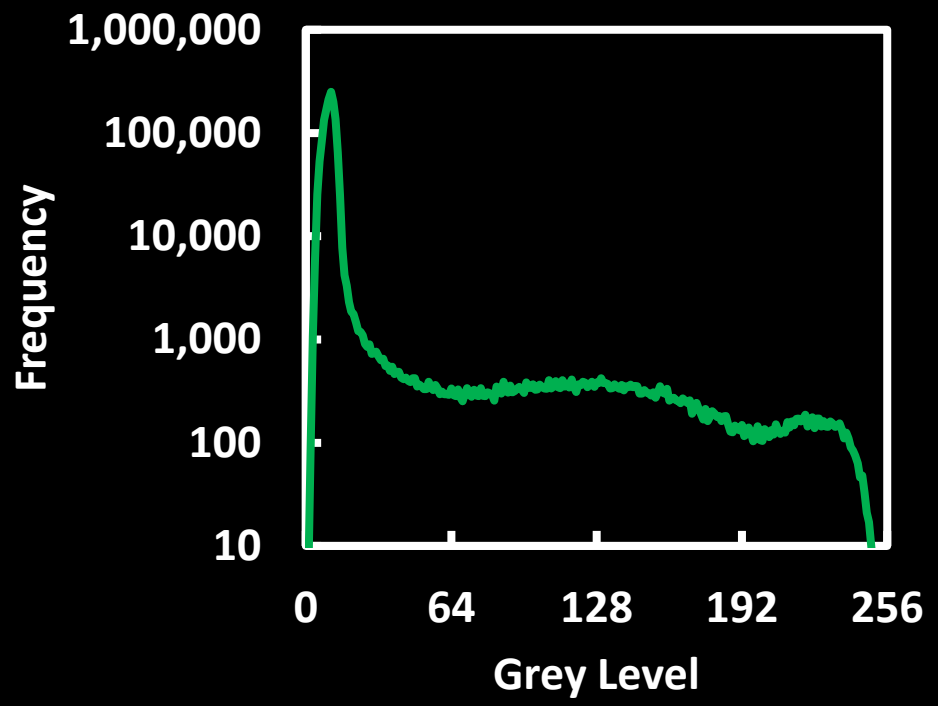


Actual Result: Big Rock

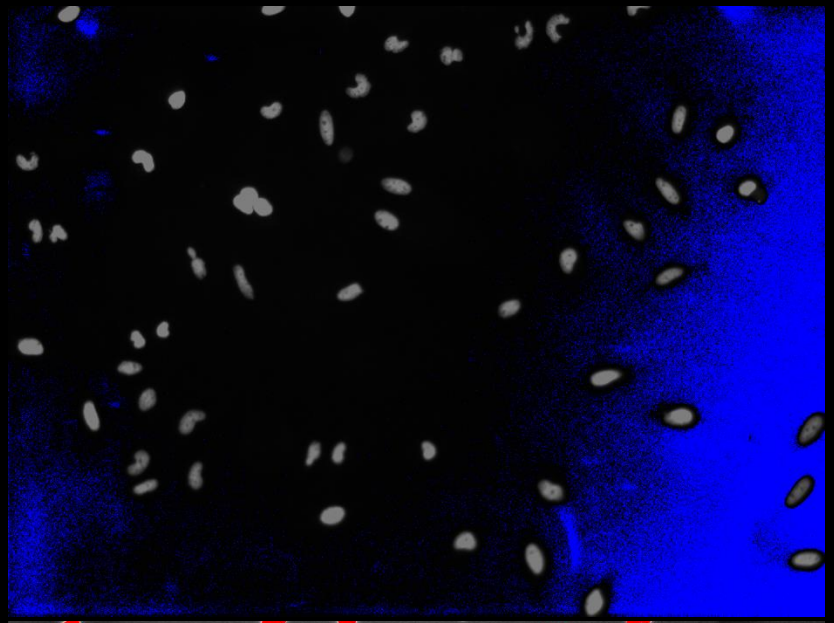
HISTOGRAMS

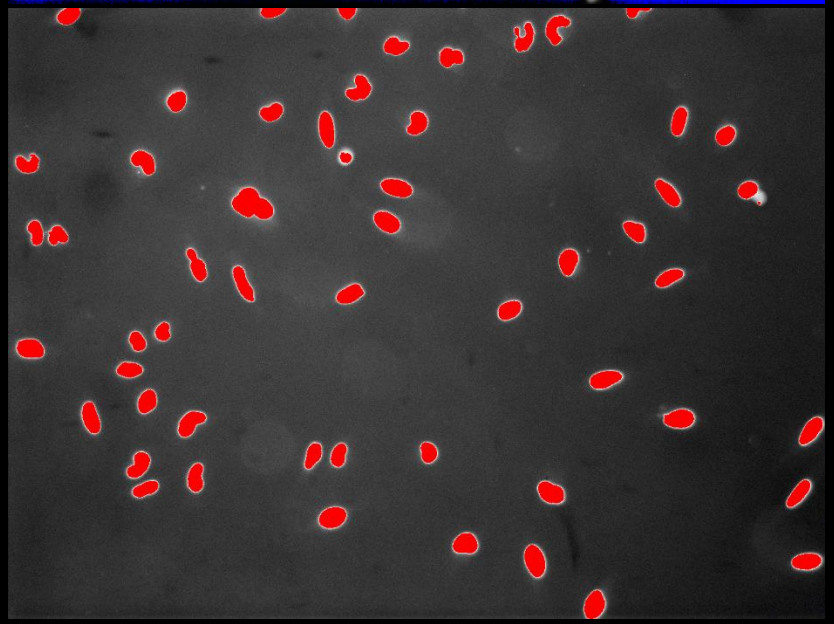
A graphical representation of the distribution of numerical data

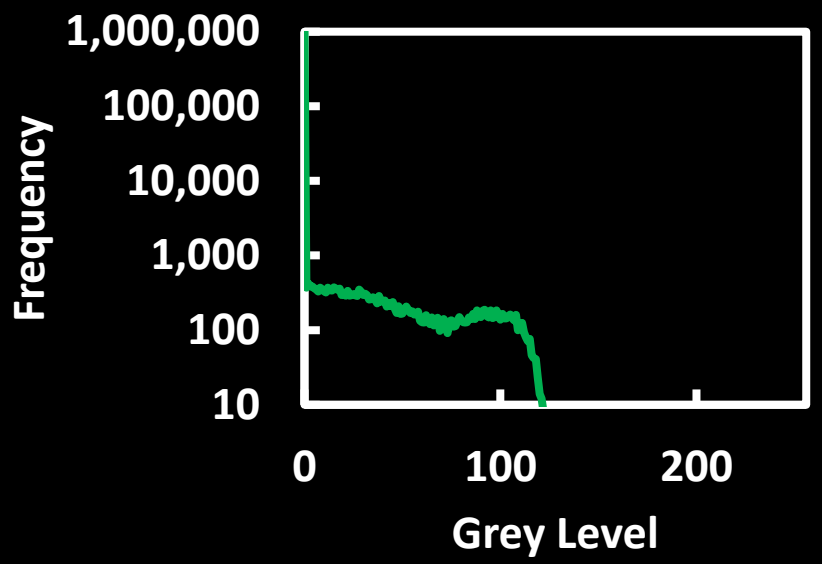


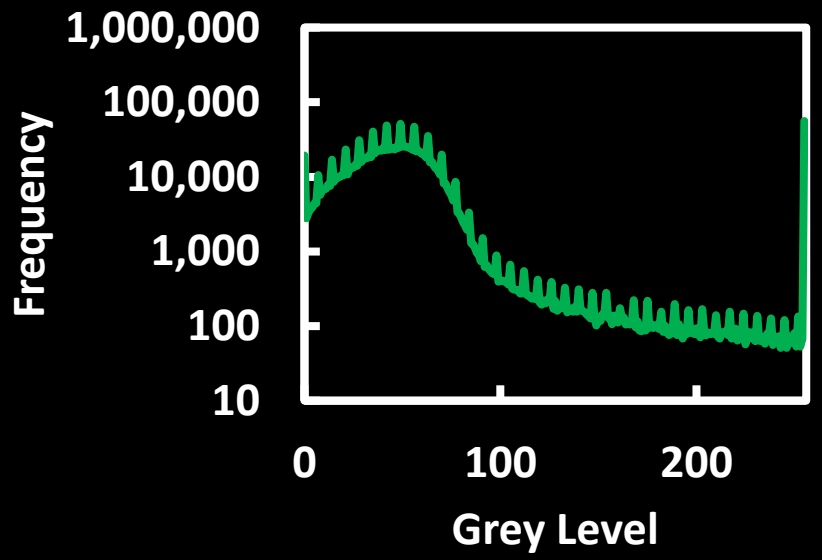


INTERPRETING HISTOGRAMS





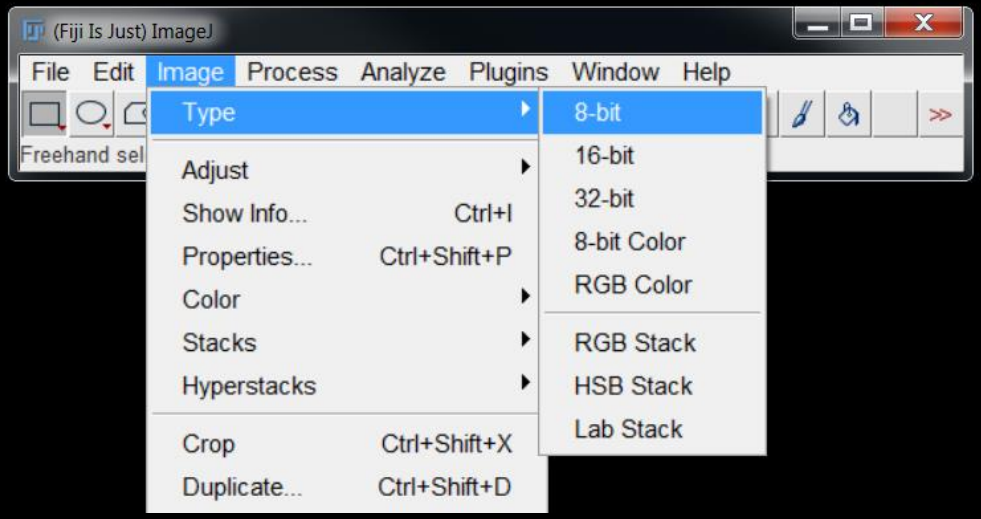




BIT DEPTH

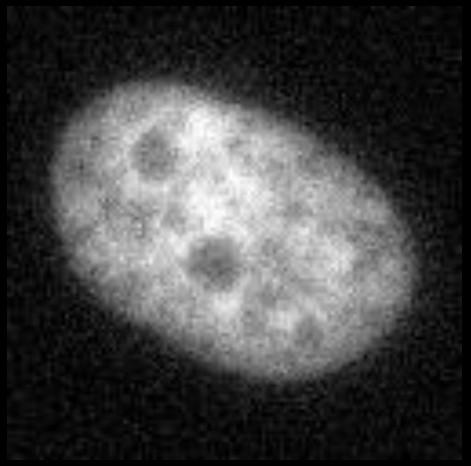
Range of values a pixel can represent

Bits per pixel	Number of values	Range of values
8	2^8	0 – 255
12	2^{12}	0 – 4,095
16	2^{16}	0 – 65,535
32	2^{32}	0 – 4,294,967,295

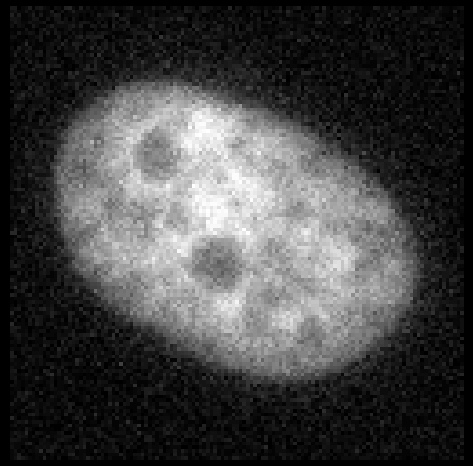


Greater bit depth means larger file sizes

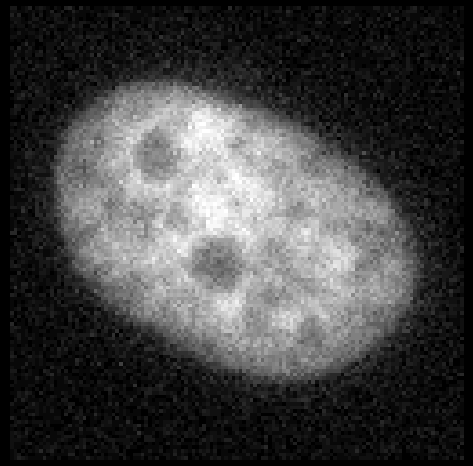
REDUCING BIT DEPTH LOSES INFORMATION



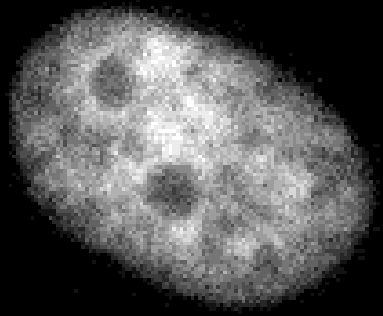
8-bit



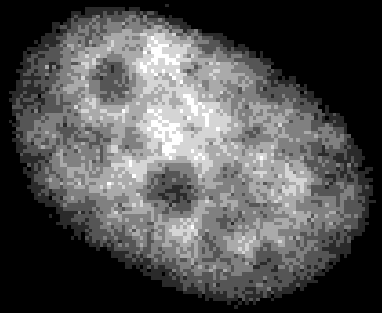
7-bit



6-bit

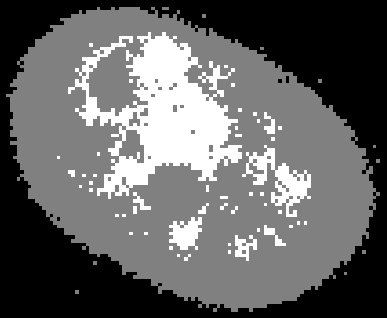


5-bit



4-bit

3-bit



2-bit

1-bit

DEMO 2 – MANIPULATING PIXEL VALUES

- Reducing bit depth incurs loss of data
- Best to deal with raw values
  - Operations performed more precise (e.g. lower rounding error)
- Compress for presentation

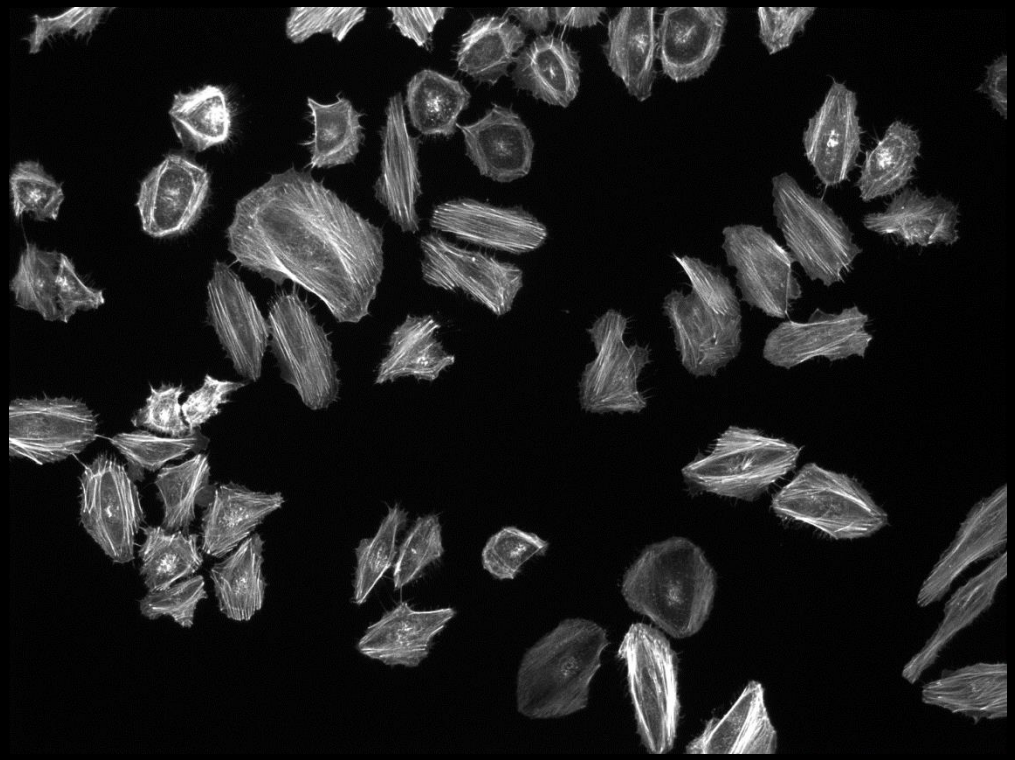


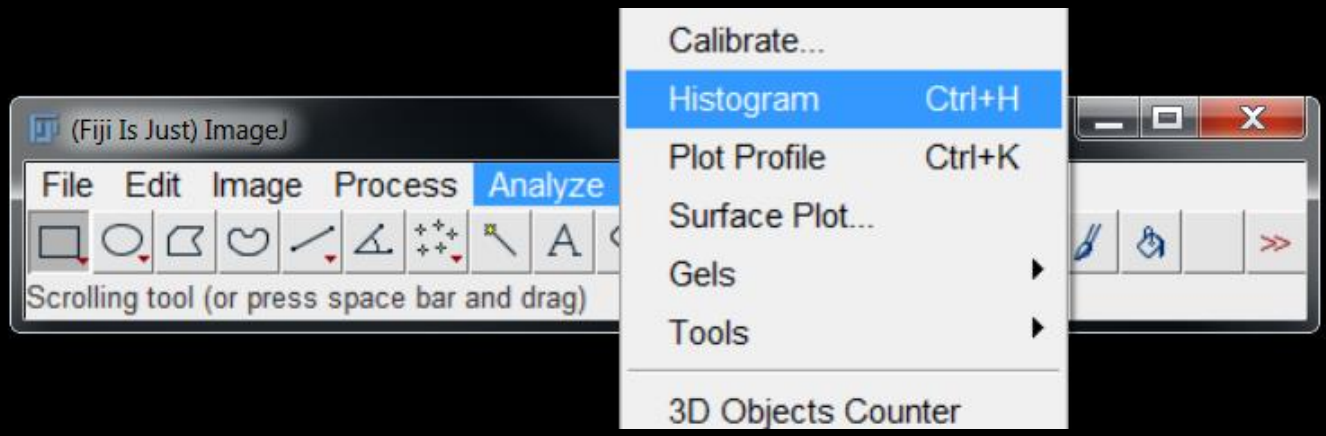
IMAGE COMPRESSION

- Lossless:
  - All image information is preserved when saved.

Lossy Compression: Anything that changes pixel values

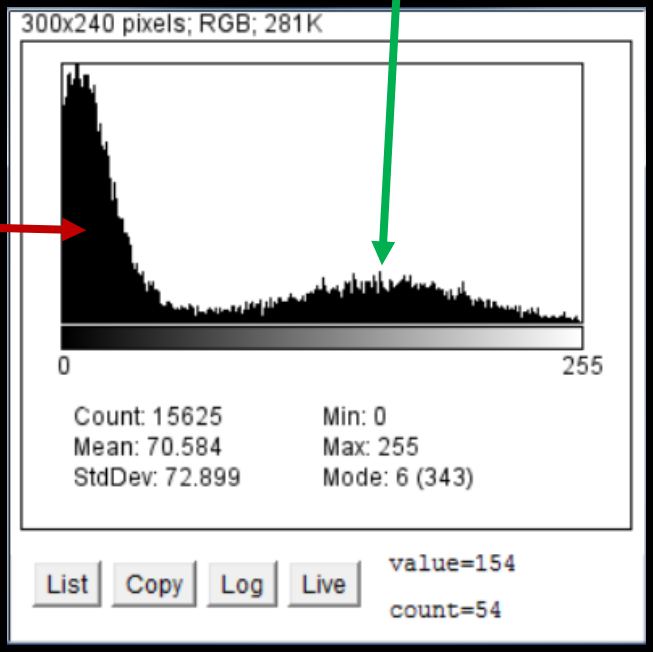
- Image information is irretrievably lost when saved.
- JPEG, GIF
- Typically results in small file sizes

INTERPRETING HISTOGRAMS FURTHER



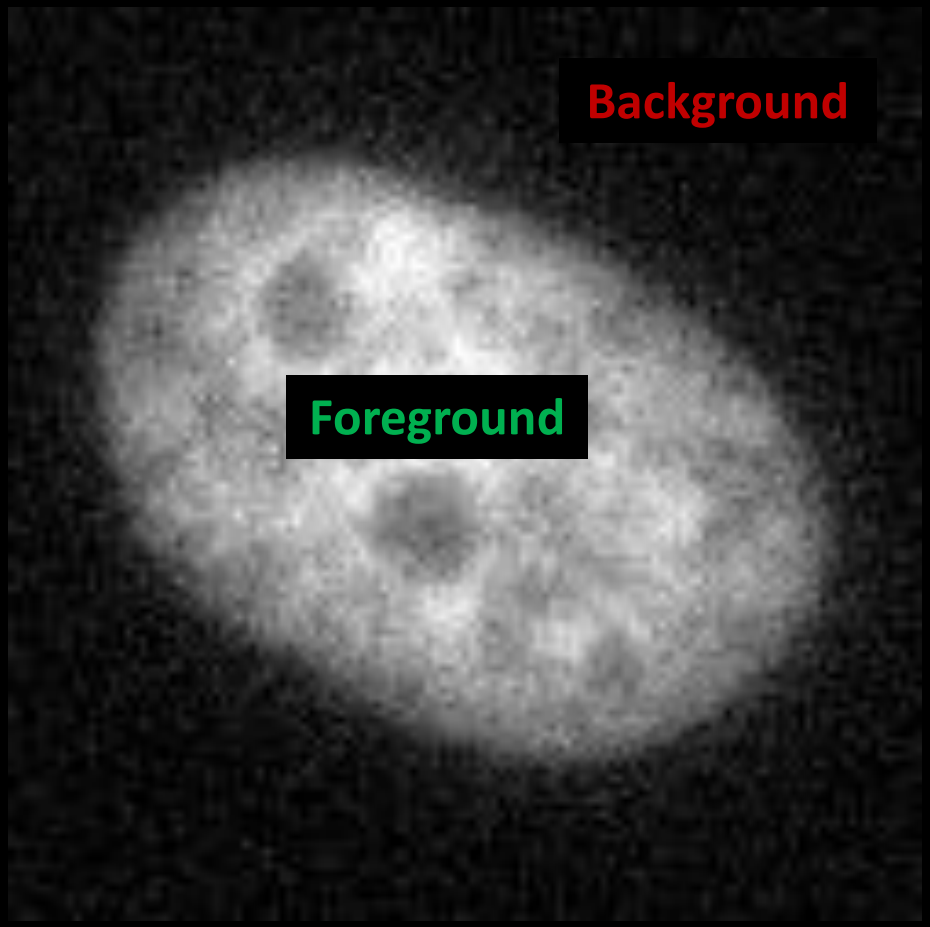
"Background"

"Foreground"

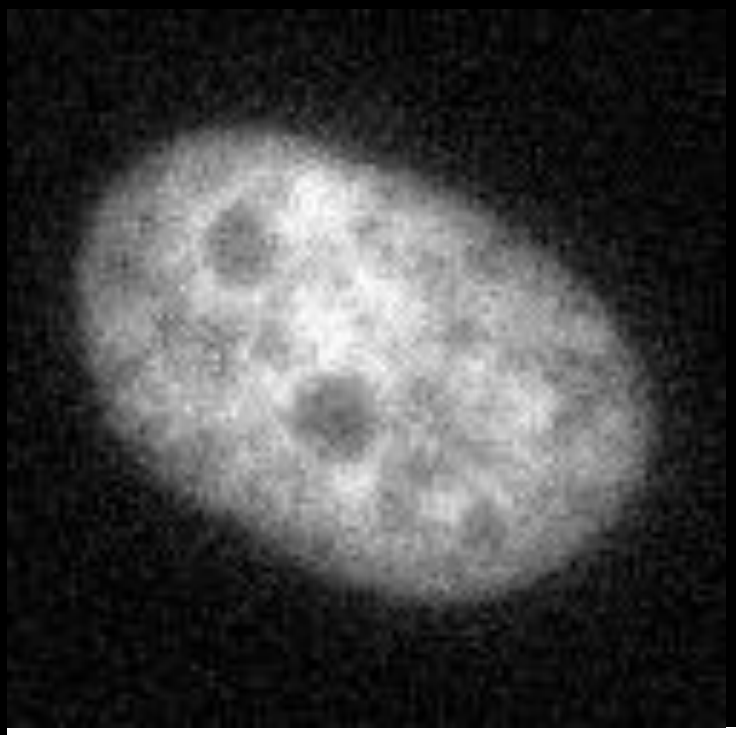


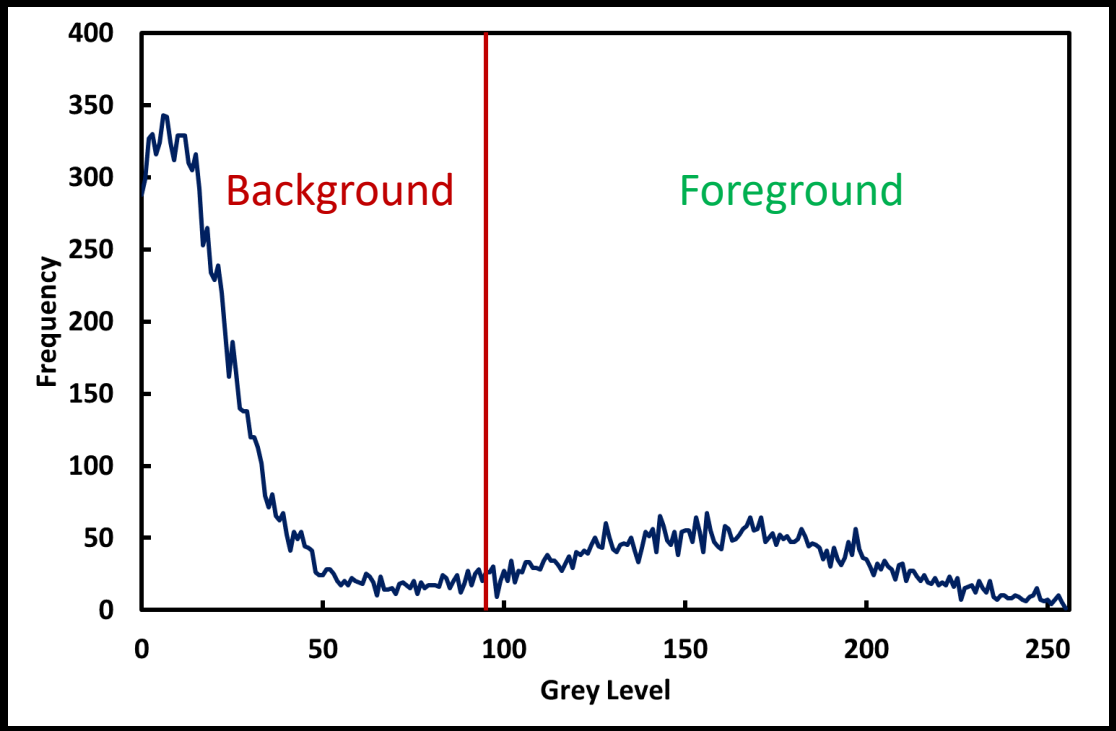
Can be exploited for segmentation

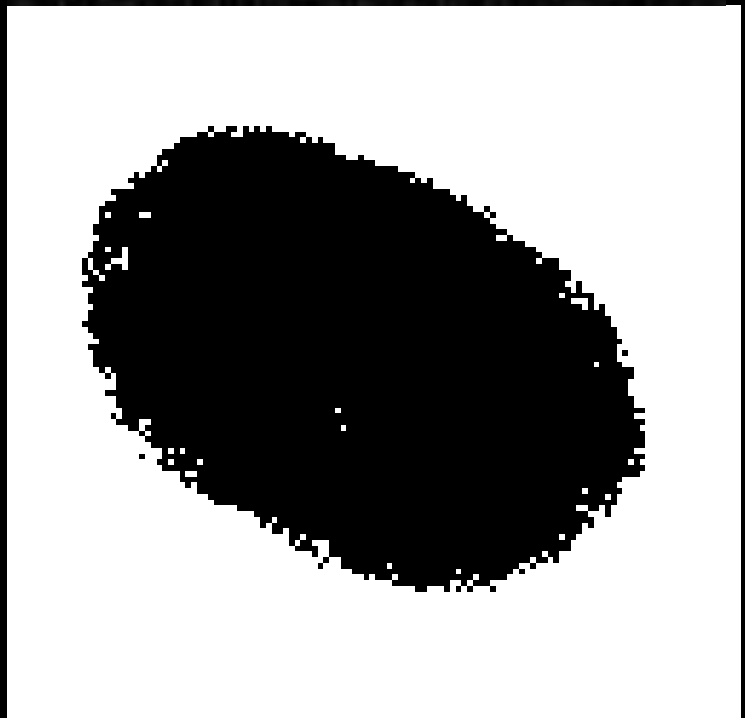
WHAT IS IMAGE SEGMENTATION?



- The process of dividing an image into different regions
- Assigning a label to each pixel within an image
- Pixels within a region should have similar properties

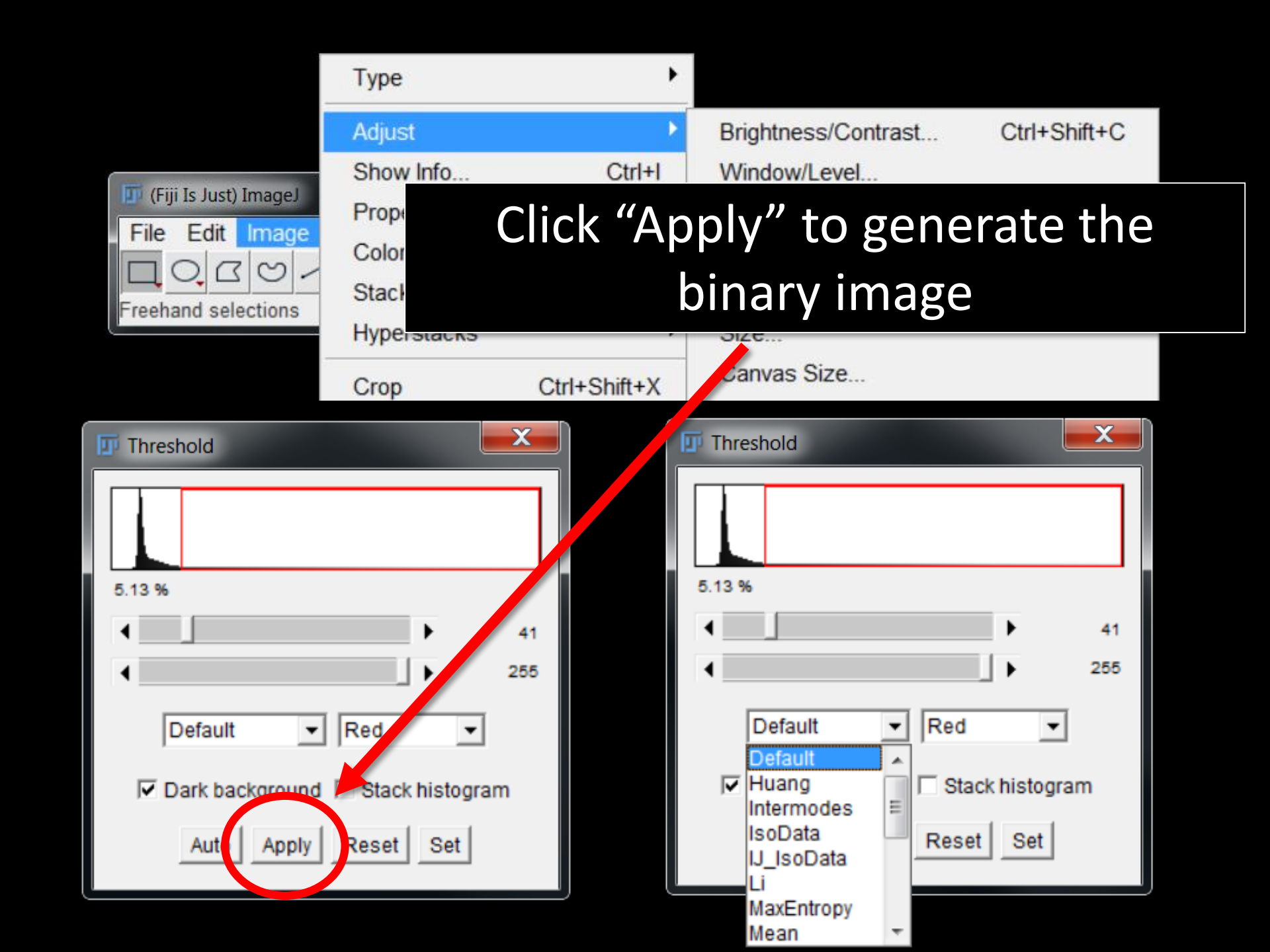




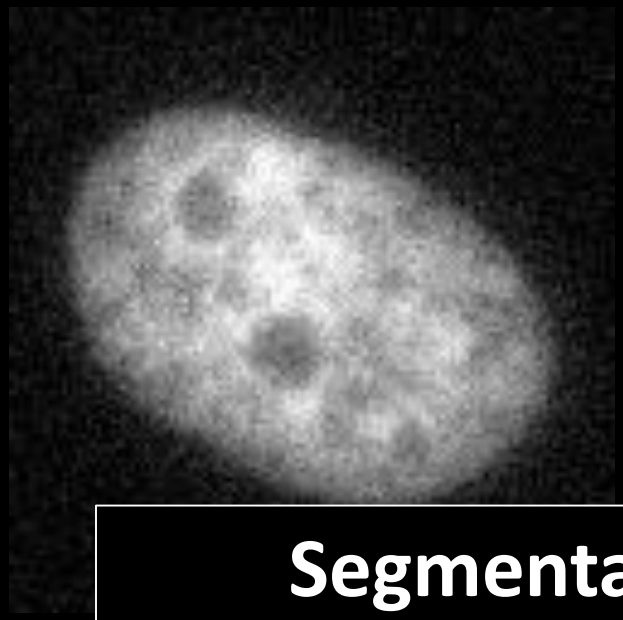


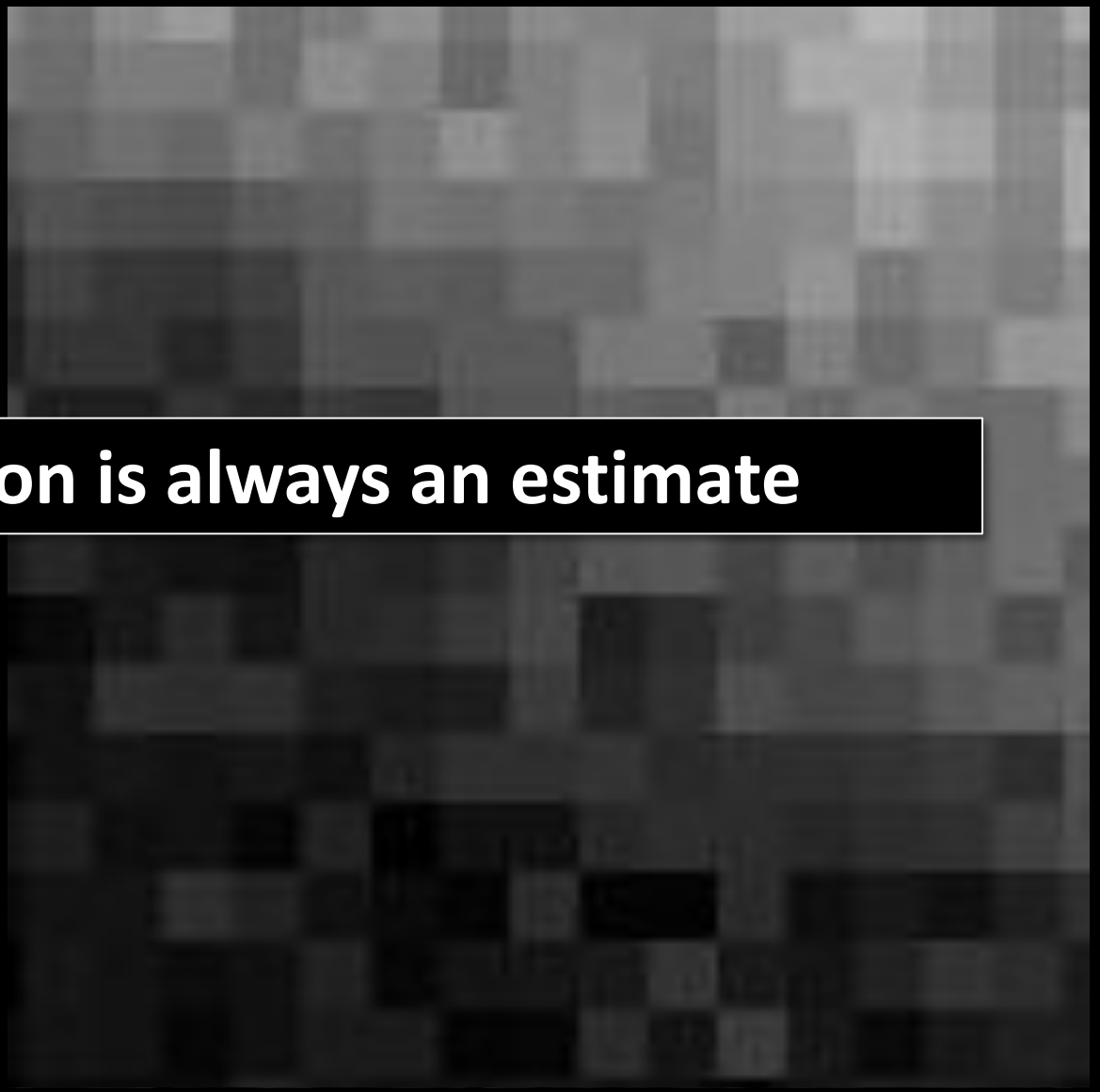
$$T > \frac{\text{Average of Foreground Pixels} + \text{Average of Background Pixels}}{2}$$

- FIJI has several variations on this algorithm
- Each produces different results
- **Result referred to as binary (or mask) image**

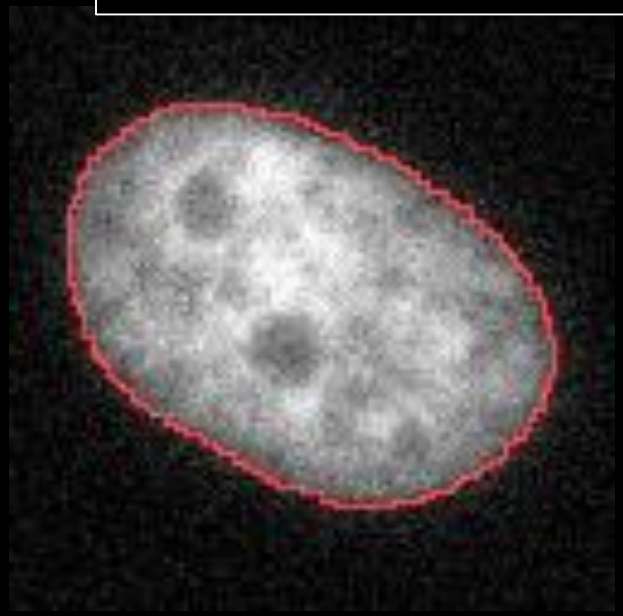

Type
Adjust
Show Info... Ctrl+I
Brightness/Contrast... Ctrl+Shift+C
Window/Level...
Crop Ctrl+Shift+X
Canvas Size...
(Fiji Is Just) ImageJ
File Edit Image
Freehand selections
Click “Apply” to generate the binary image
Threshold
5.13 %
41
255
Default
Red
Dark background
Stack histogram
Aut
Apply
Reset
Set
Threshold
5.13 %
41
255
Default
Red
Default
Huang
Intermodes
IsoData
IJ_IsoData
Li
MaxEntropy
Mean
Stack histogram
Reset
Set

BOUNDARY BETWEEN REGIONS IS AMBIGUOUS

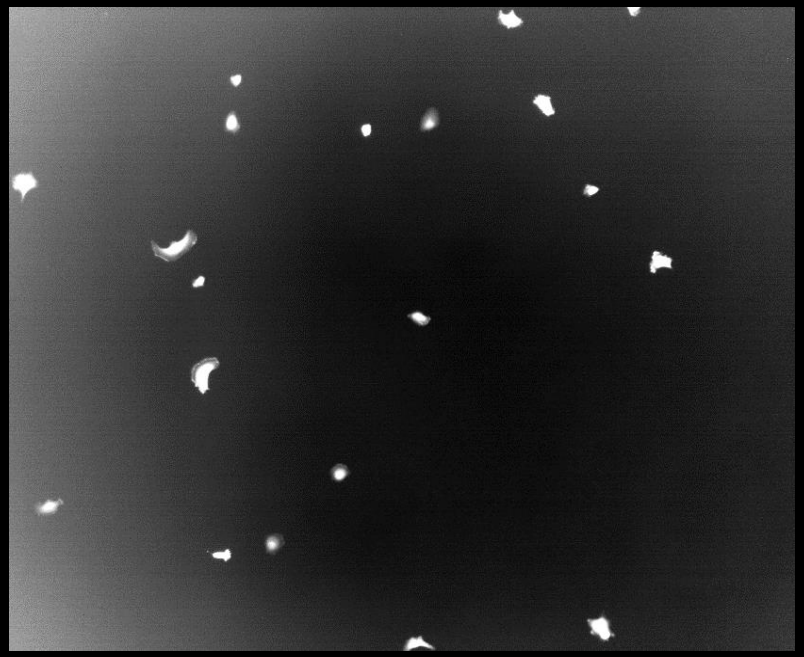


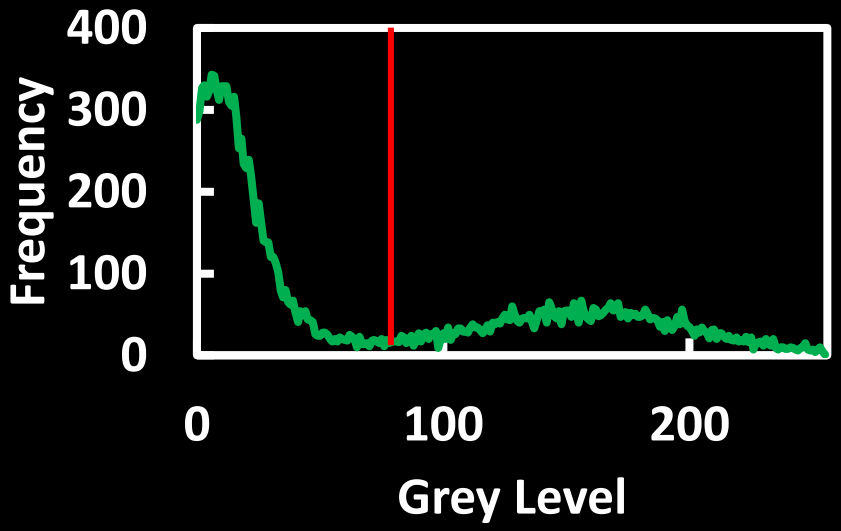


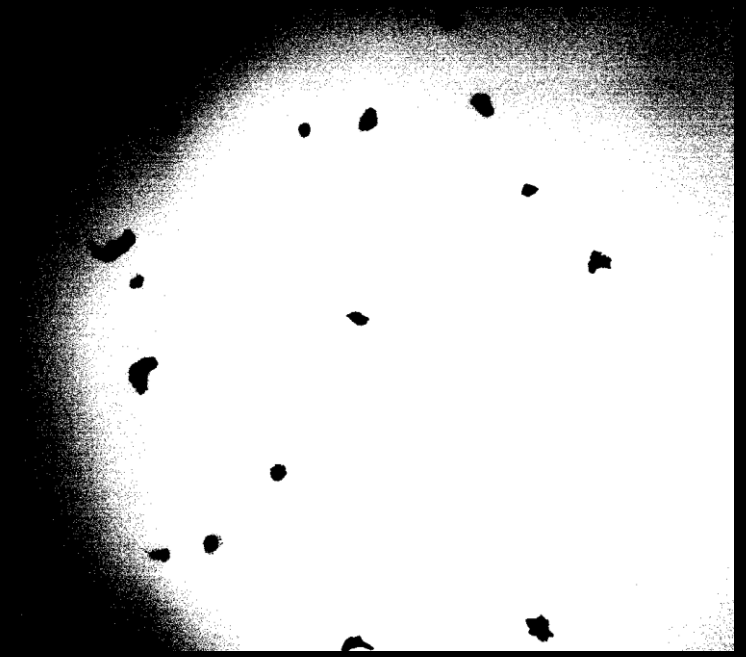
Segmentation is always an estimate

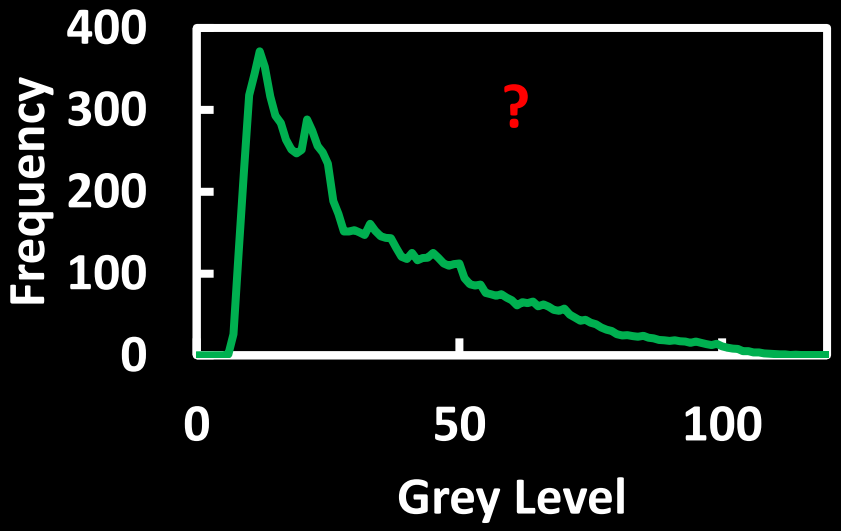


UNEVEN BACKGROUND POSES PROBLEMS

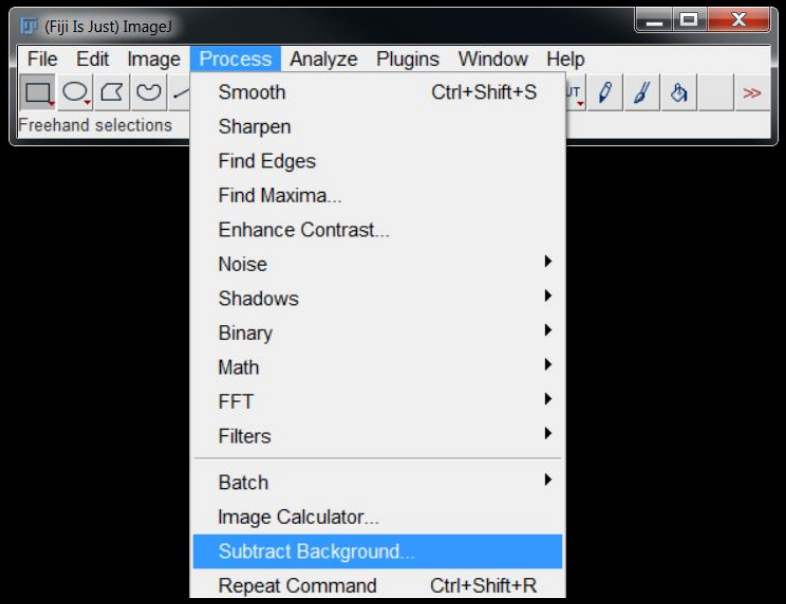


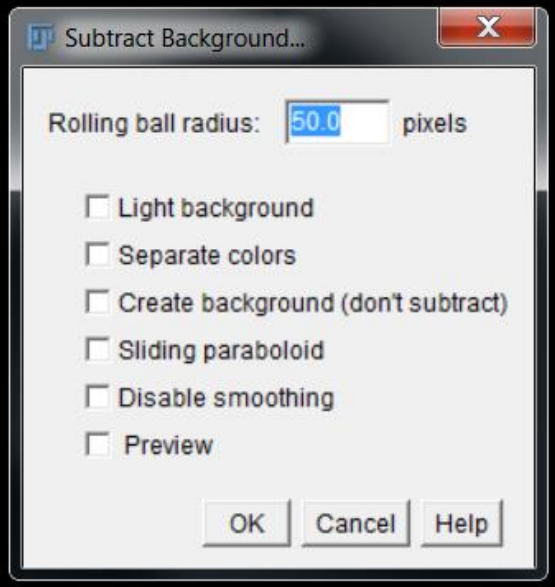






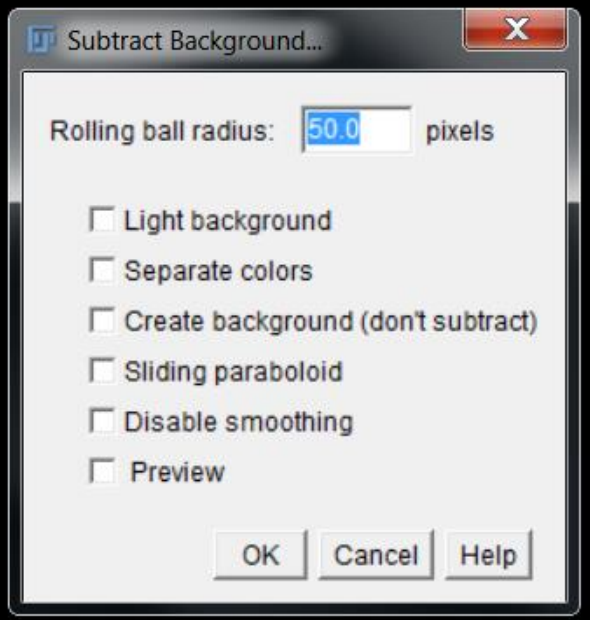
BACKGROUND SUBTRACTION



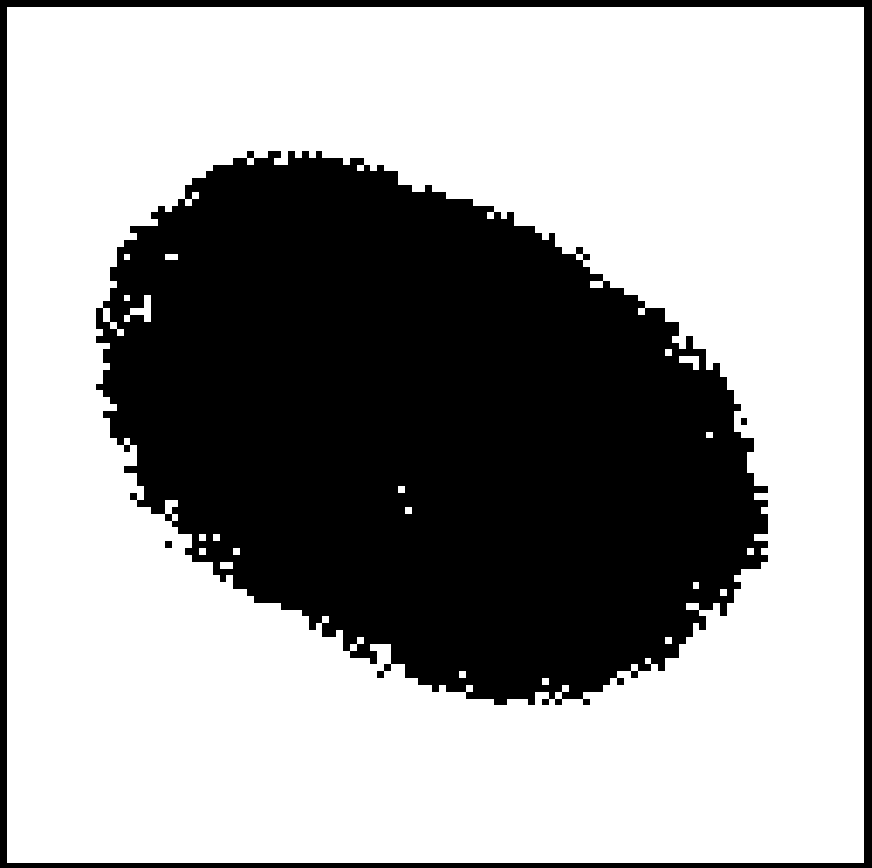


DEMO 4 – CORRECTING UNEVEN BACKGROUND

- Investigate influence of filter radius
- Background subtractor creates an estimate of background and removes from image

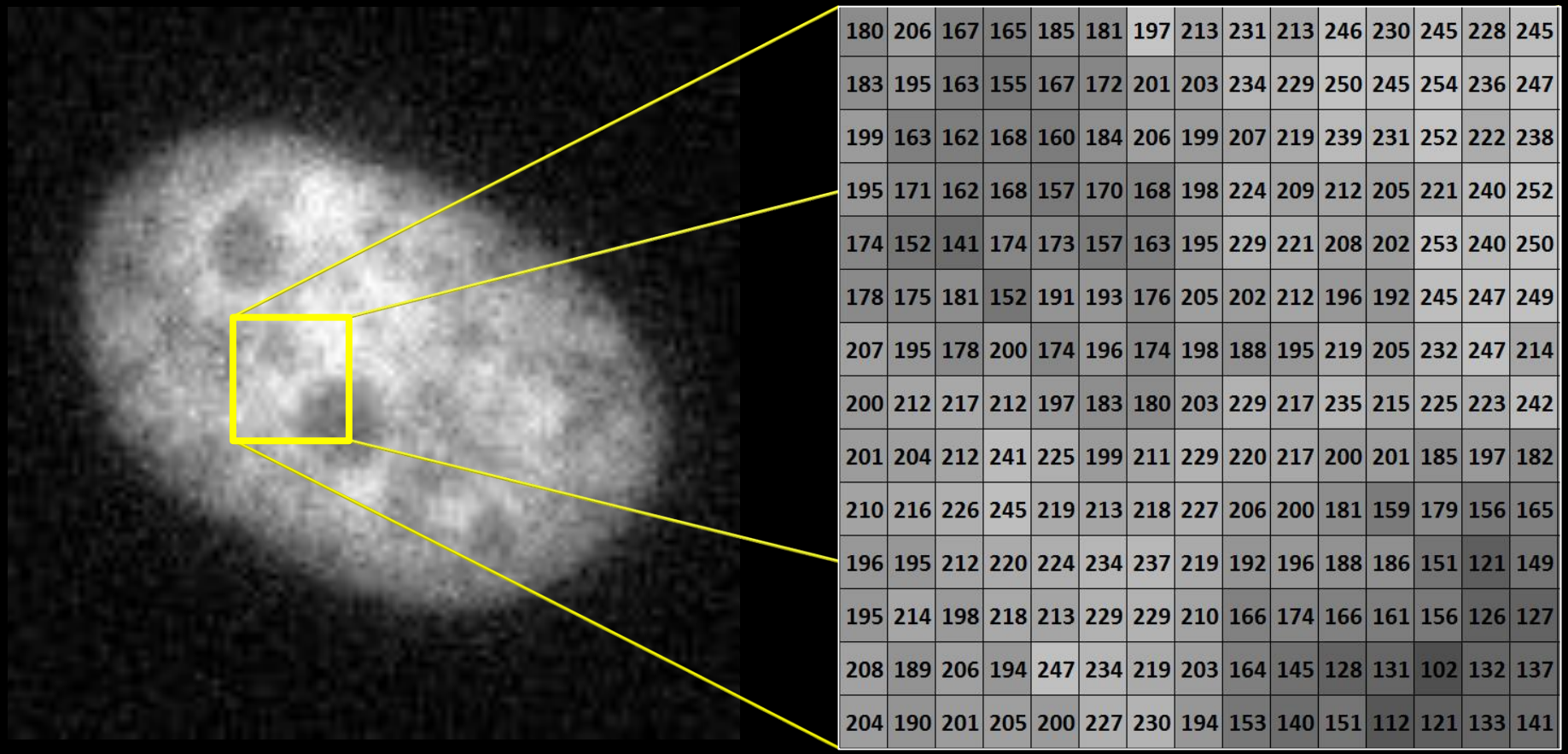


ANOTHER OBSTACLE TO “GOOD” SEGMENTATIONS IS SPECKLE NOISE…



Filtering can be employed to improve segmentation

WHAT IS FILTERING?



180	206	167	165	185	181	197	213	231	213	246	230	245	228	245
183	195	163	155	167	172	201	203	234	229	250	245	254	236	247
199	163	162	168	160	184	206	199	207	219	239	231	252	222	238
195	171	162	168	157	170	168	198	224	209	212	205	221	240	252
174	152	141	174	173	157	163	195	229	221	208	202	253	240	250
178	175	181	152	191	193	176	205	202	212	196	192	245	247	249
207	195	178	200	174	196	174	198	188	195	219	205	232	247	214
200	212	217	212	197	183	180	203	229	217	235	215	225	223	242
201	204	212	241	225	199	211	229	220	217	200	201	185	197	182
210	216	226	245	219	213	218	227	206	200	181	159	179	156	165
196	195	212	220	224	234	237	219	192	196	188	186	151	121	149
195	214	198	218	213	229	229	210	166	174	166	161	156	126	127
208	189	206	194	247	234	219	203	164	145	128	131	102	132	137
204	190	201	205	200	227	230	194	153	140	151	112	121	133	141

- Generally refers to simple arithmetic operations on small numbers of pixels

MEAN/AVERAGING FILTERING

243	185	185
19	246	105
225	221	119

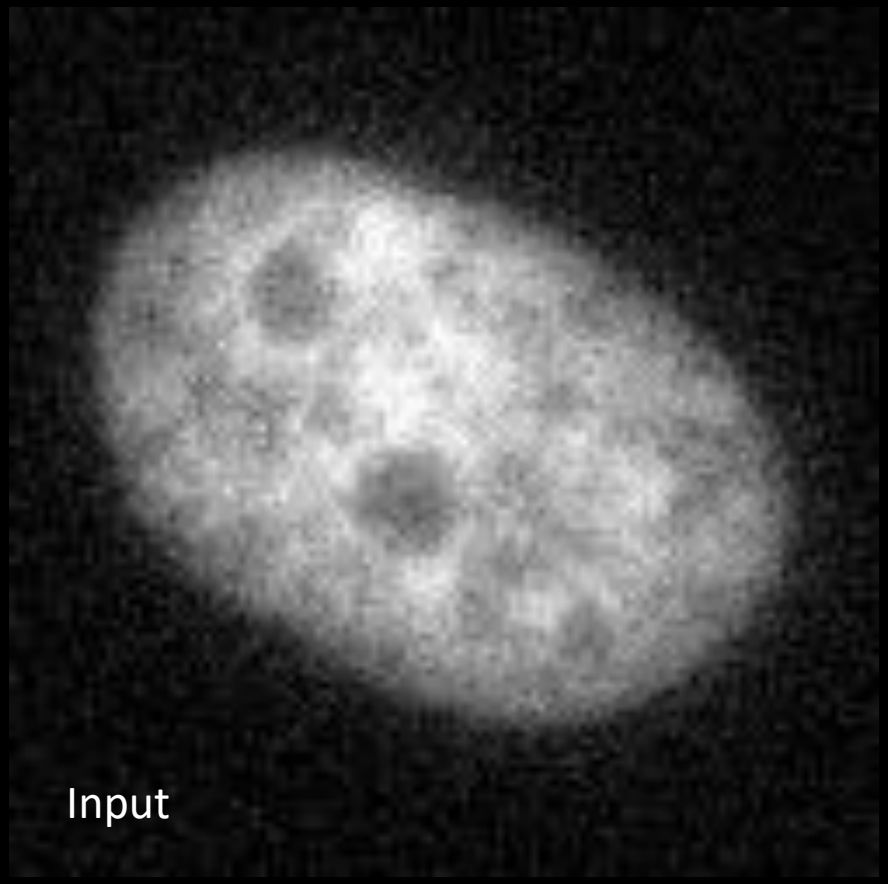
243	185	185
19	172	105
225	221	119

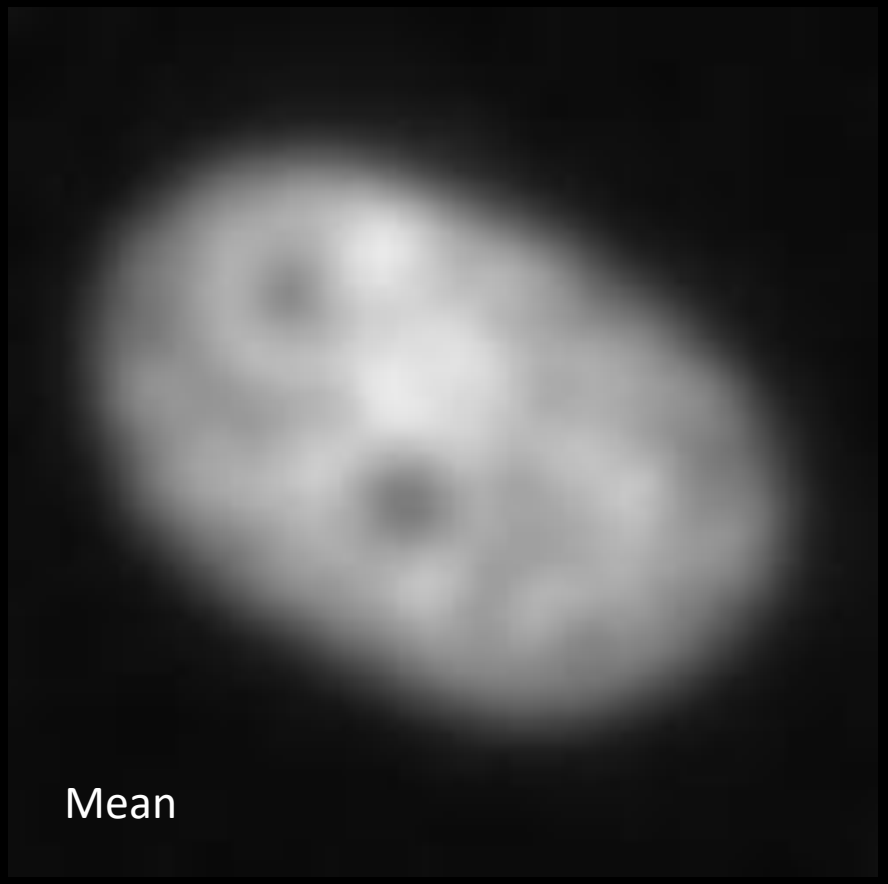
Replaces central value with average of all values

FILTERING IN ACTION

Input **Output**

MEAN FILTERING “BLURS” NOISE





But remember, information is also lost!

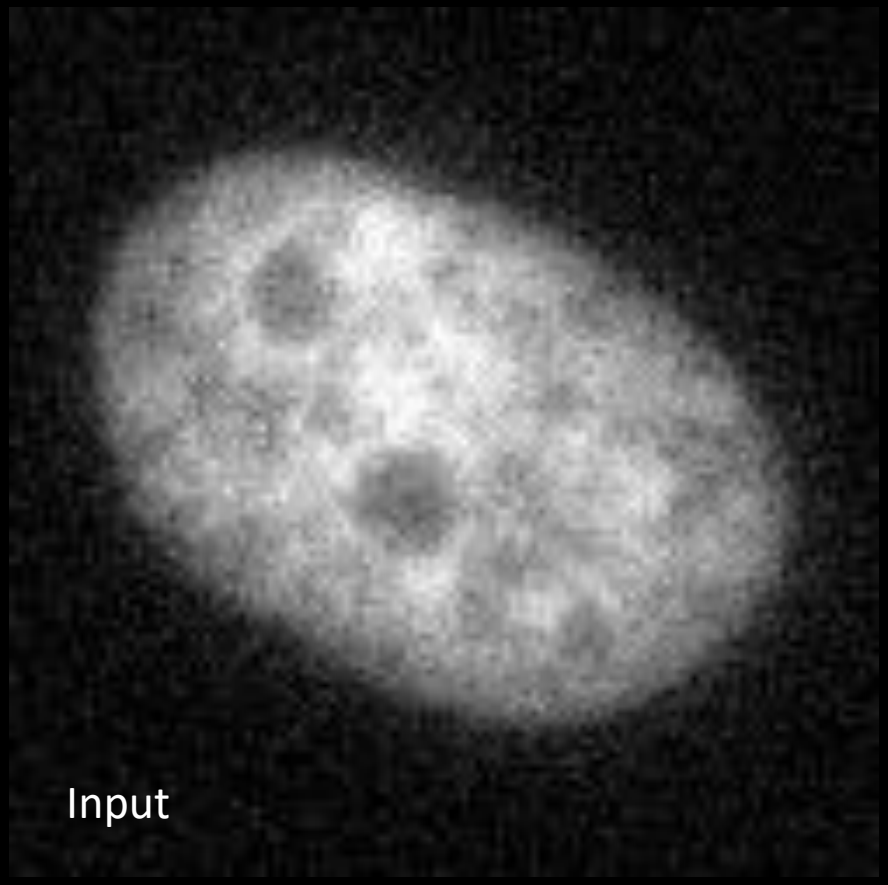
MEDIAN FILTERING

243	185	185
19	246	105
225	221	119

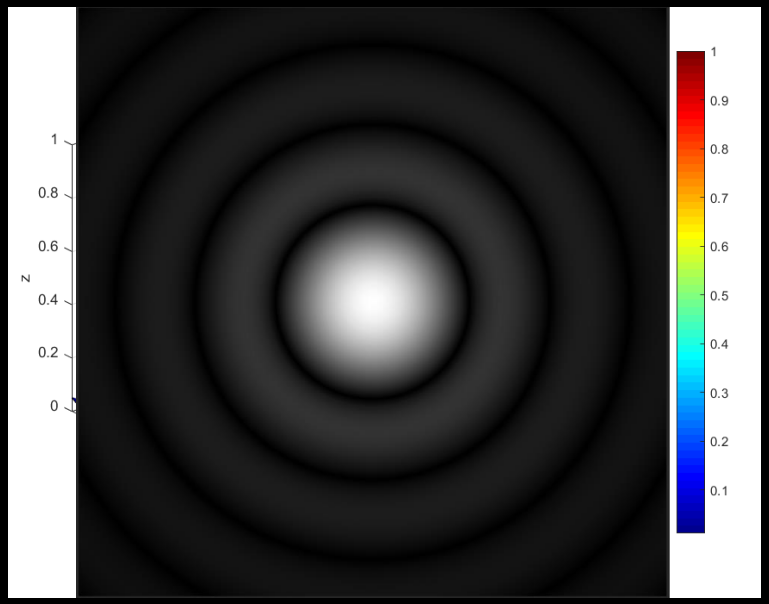
243	185	185
19	185	105
225	221	119

Replaces central value with median value

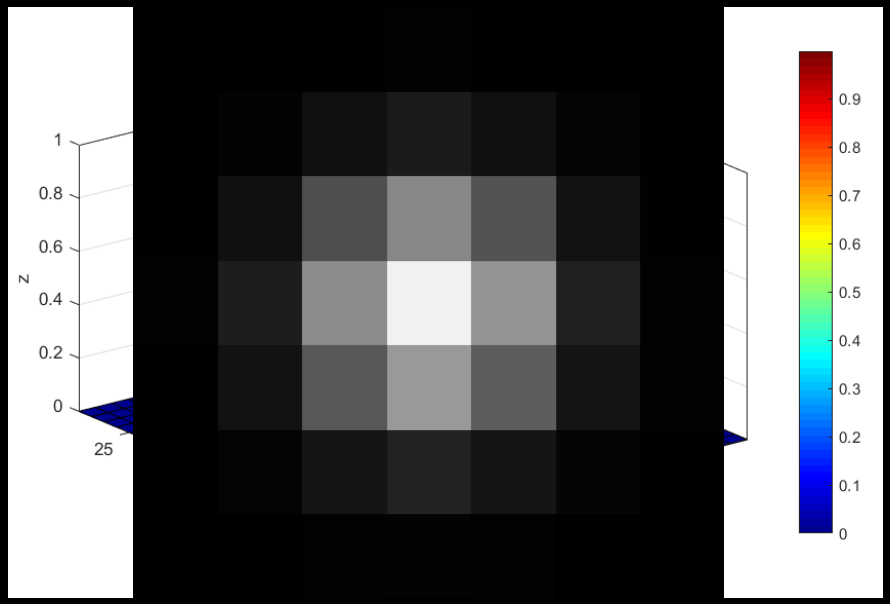
MEDIAN FILTERING PRESERVES EDGES



GAUSSIAN FILTERING



Airy Disk



2D Gaussian

- Approximation of Airy Disk
- Essentially a weighted mean filter

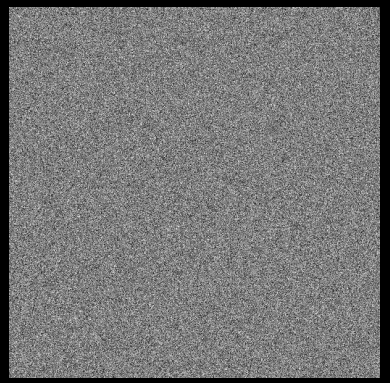
1.00	1.00	1.00
1.00	1.00	1.00
1.00	1.00	1.00

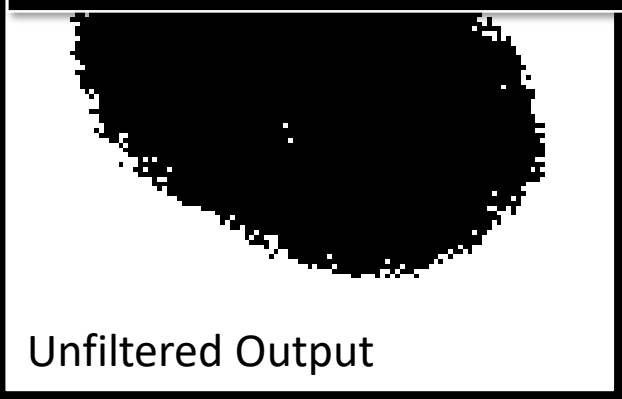
Gaussian Filter

Processing:

=

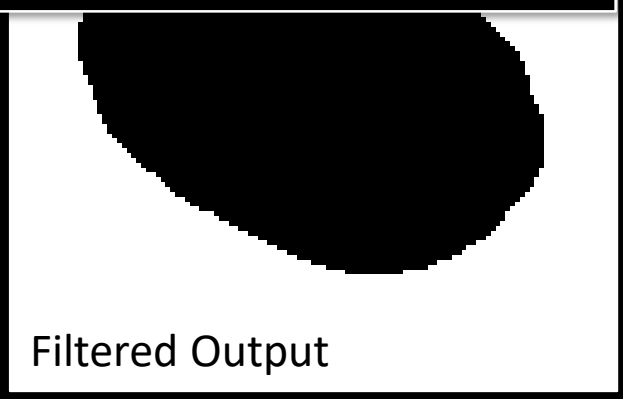
−





Unfiltered Output

Median

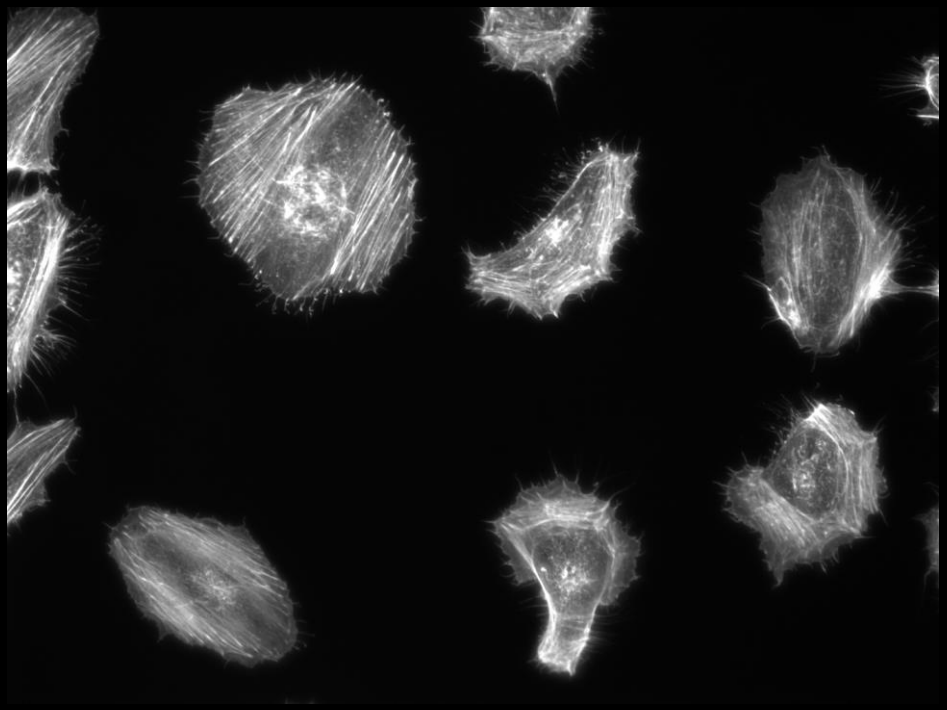


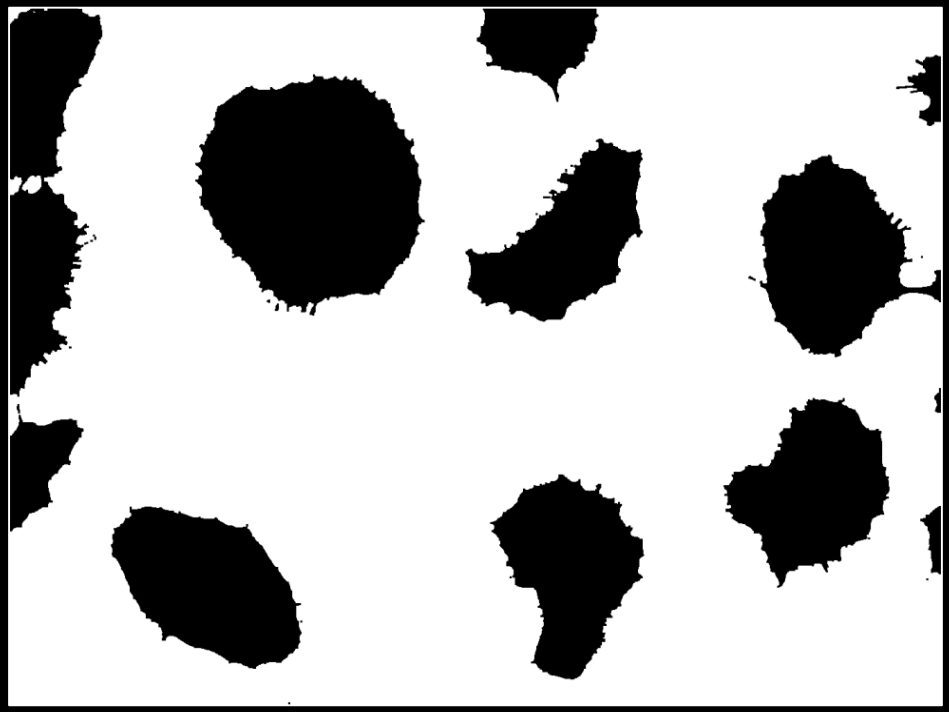
Filtered Output

DEMO 5 - FILTERS

- Notice the effect of varying filter radius
- Observe the difference in edge preservation between mean and median filters

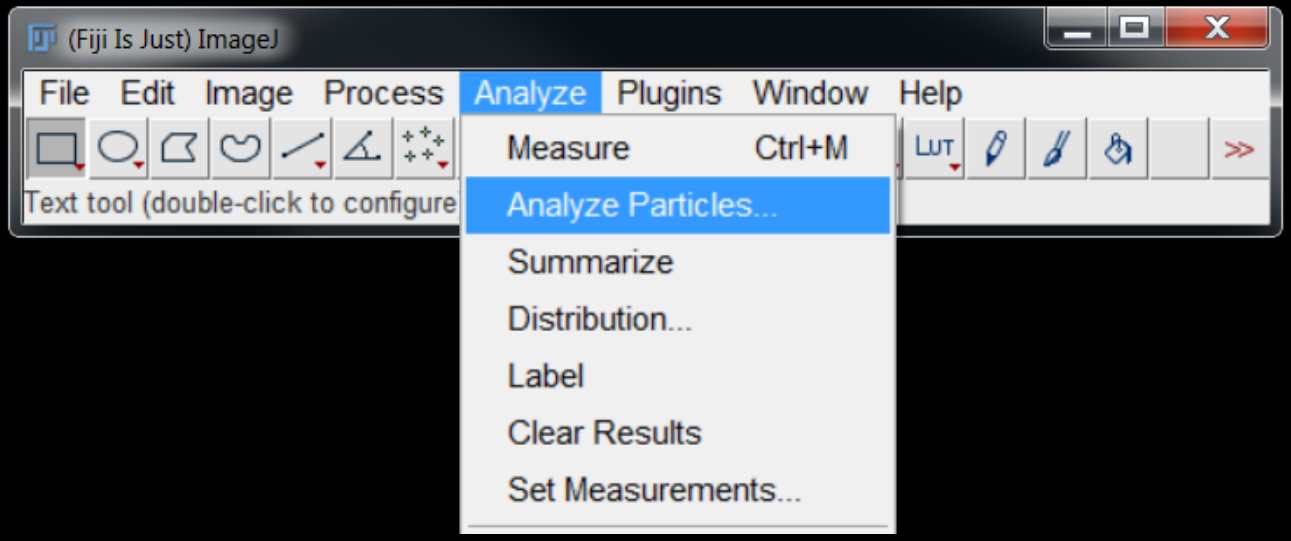
MORPHOLOGICAL ANALYSIS

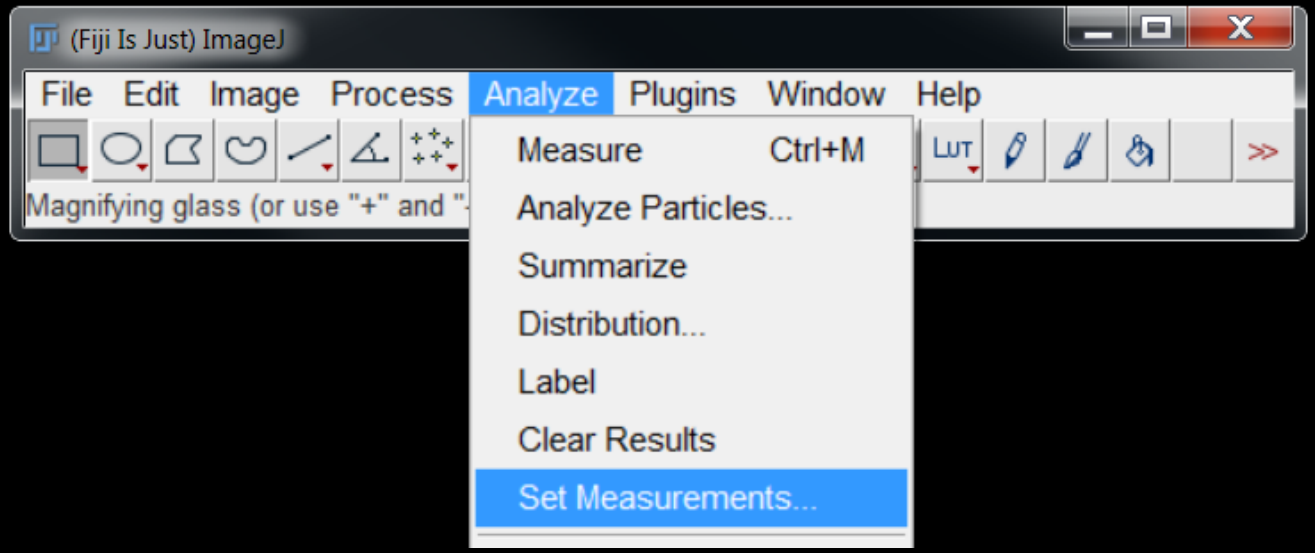


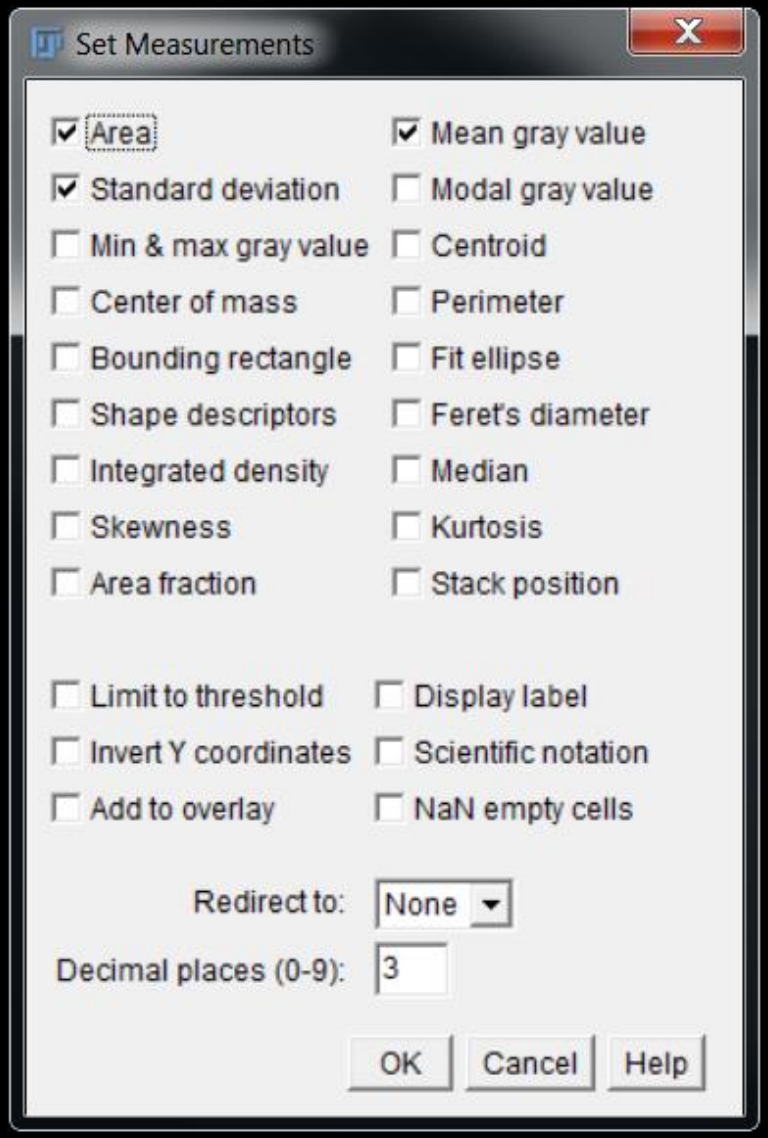


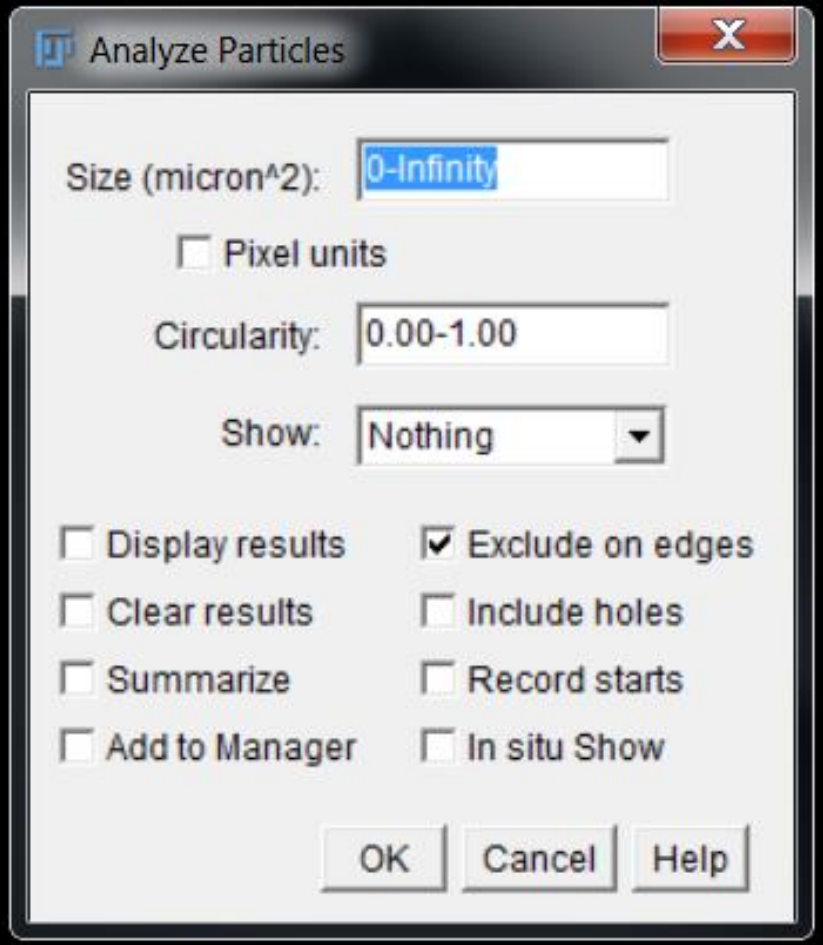
How do we extract numerical data from segmented images?

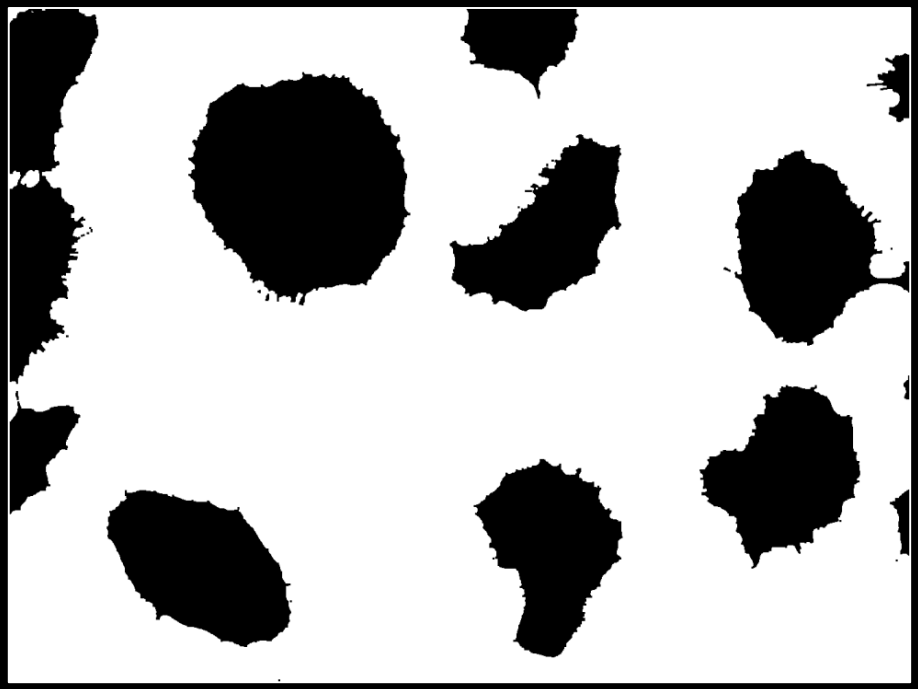
MORPHOLOGICAL ANALYSIS

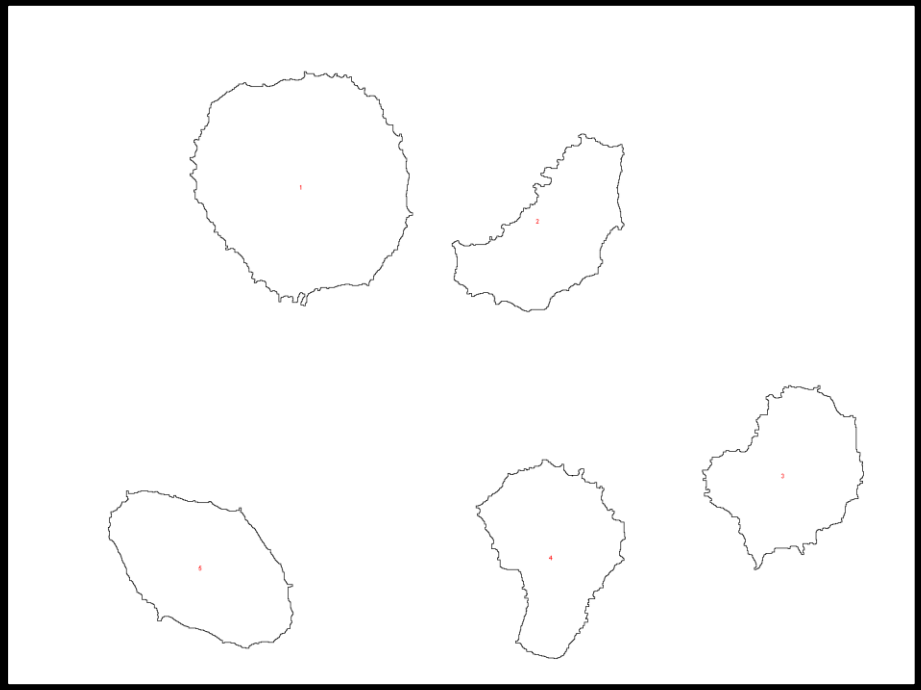





Set Measurements
Area
Mean gray value
Standard deviation
Modal gray value
Min & max gray value
Centroid
Center of mass
Perimeter
Bounding rectangle
Fit ellipse
Shape descriptors
Feret's diameter
Integrated density
Median
Skewness
Kurtosis
Area fraction
Stack position
Limit to threshold
Display label
Invert Y coordinates
Scientific notation
Add to overlay
NaN empty cells
Redirect to:
None
Decimal places (0-9):
3
OK
Cancel
Help


Analyze Particles
Size (micron^2):
0-Infinity
Pixel units
Circularity:
0.00-1.00
Show:
Nothing
Display results
Exclude on edges
Clear results
Include holes
Summarize
Record starts
Add to Manager
In situ Show
OK
Cancel
Help





Results

File Edit Font Results

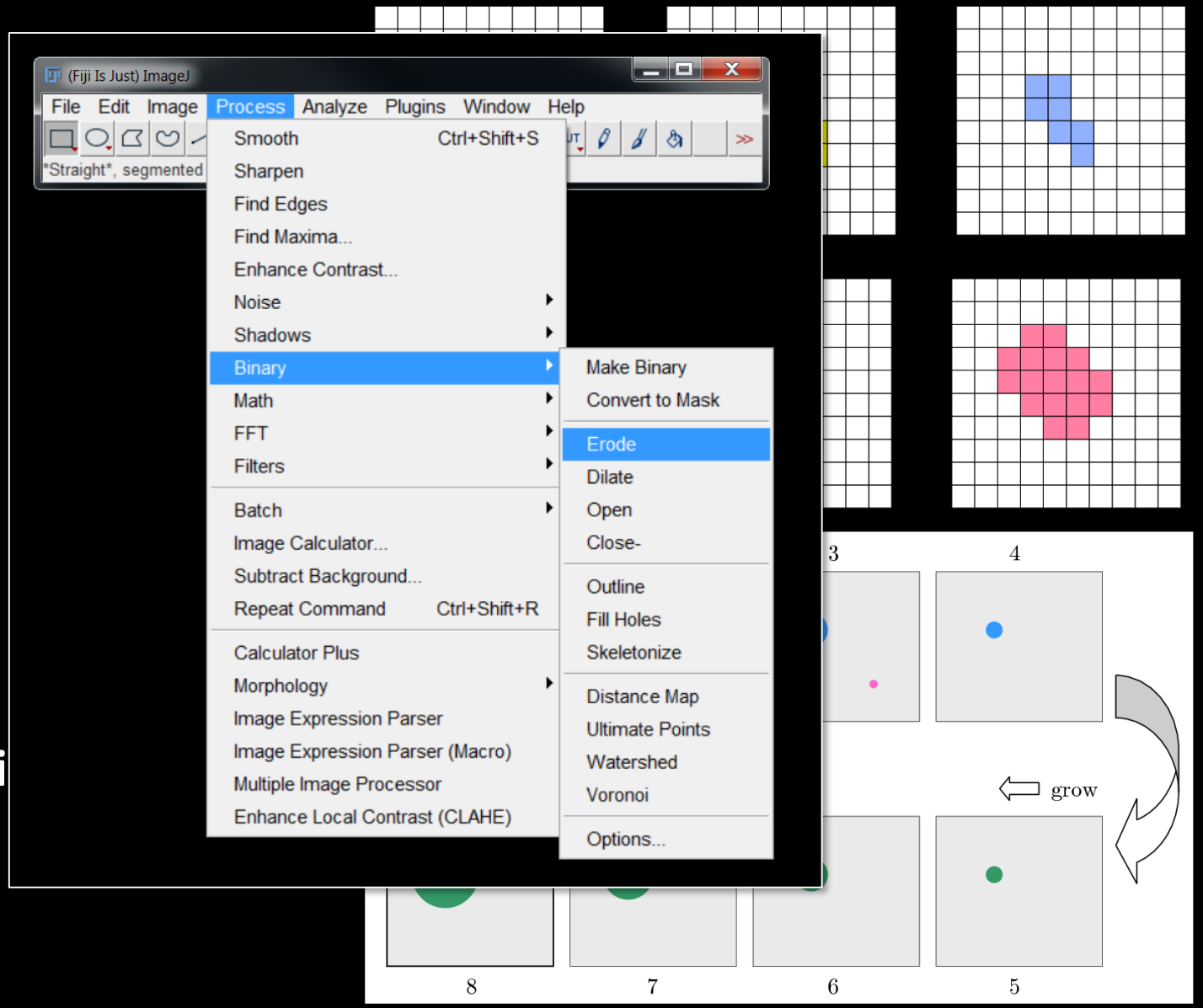
	Area	X	Y	XM	YM	Perim.	BX	BY	Width	Height	Major	Minor	Angle	Circ.	Feret	IntDen	RawIntDen	FeretX	FeretY	FeretAngle	MinFe
1	88461	452.335	269.404	452.335	269.404	1385.894	277	99	343	360	351.863	320.102	126.303	0.579	371.602	22557555	22557555	311	146	130.635	324.8
2	37578	833.182	346.780	833.182	346.780	1097.744	681	195	265	273	311.118	153.787	46.201	0.392	332.182	9582390	9582390	684	419	38.768	181.8
3	41450	1201.315	717.108	1201.315	717.108	1062.590	1067	582	248	283	260.470	202.617	55.433	0.461	300.483	10569750	10569750	1147	865	70.359	216.0
4	40950	837.361	834.134	837.361	834.134	1044.815	718	696	230	306	281.859	184.983	95.828	0.471	306.863	10442250	10442250	820	696	94.298	213.8
5	45631	296.057	861.770	296.057	861.770	949.034	151	744	285	242	316.443	183.601	145.191	0.637	329.509	11635905	11635905	155	776	146.889	206.4

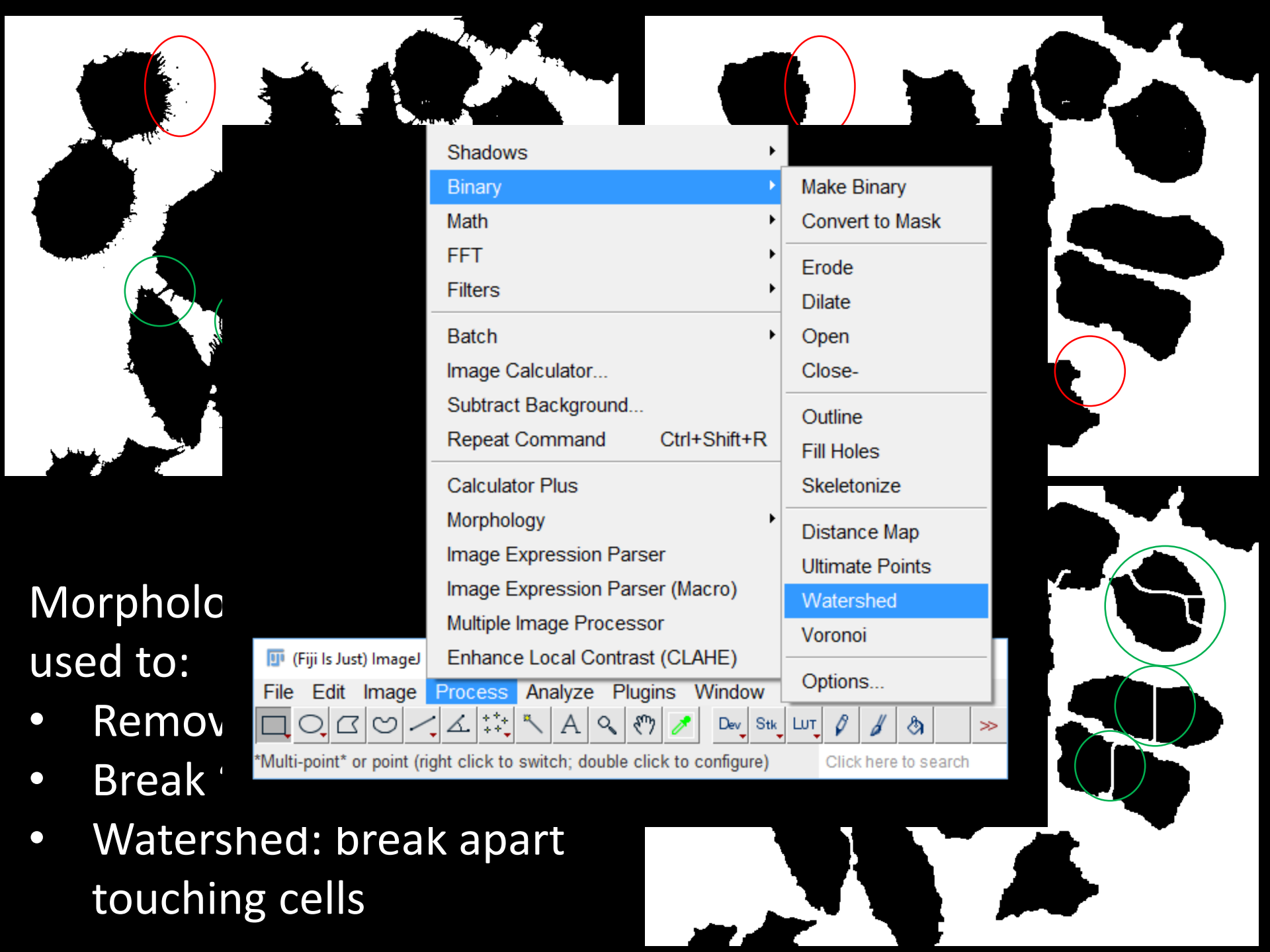
MORPHOLOGICAL FILTERING

Erosion

Dilation

Erosion + Dilati



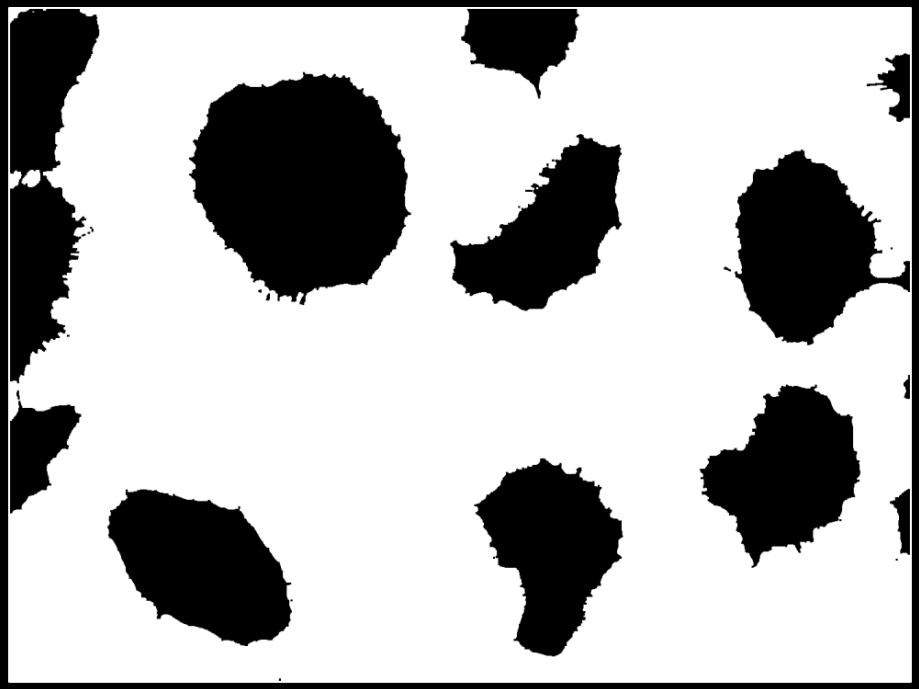


Morpholo
used to:

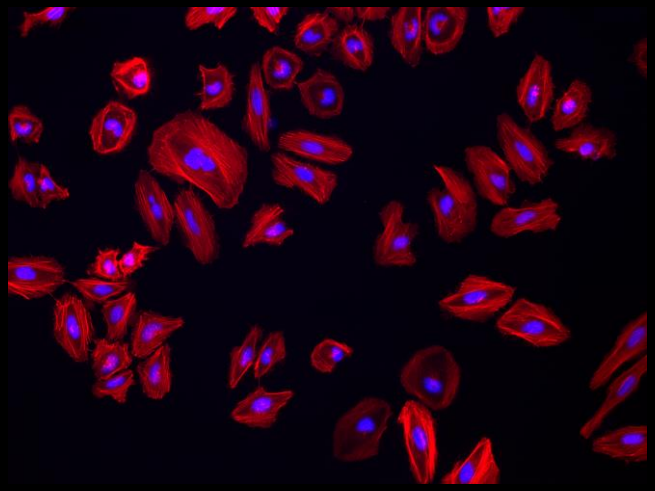
- Remov
- Break
- Watershed: break apart touching cells

DEMO 6 – WORKING WITH BINARY IMAGES

- Demo particle analyser and morphological filters
- Show how to specify background colour for analyser



CHALLENGE 1



1. Count the number of cells
2. Estimate the mean cell area

Note: You may find it helpful to duplicate and/or rename images as you work

Filter Noise	• Process > Filters
Segment Cells From Background	• Image > Adjust > Threshold
Manipulate Segmentation	• Process > Binary
Specify Morphological Measurements	• Analyze > Set Measurements
Quantify Morphology	• Analyze > Analyze Particles

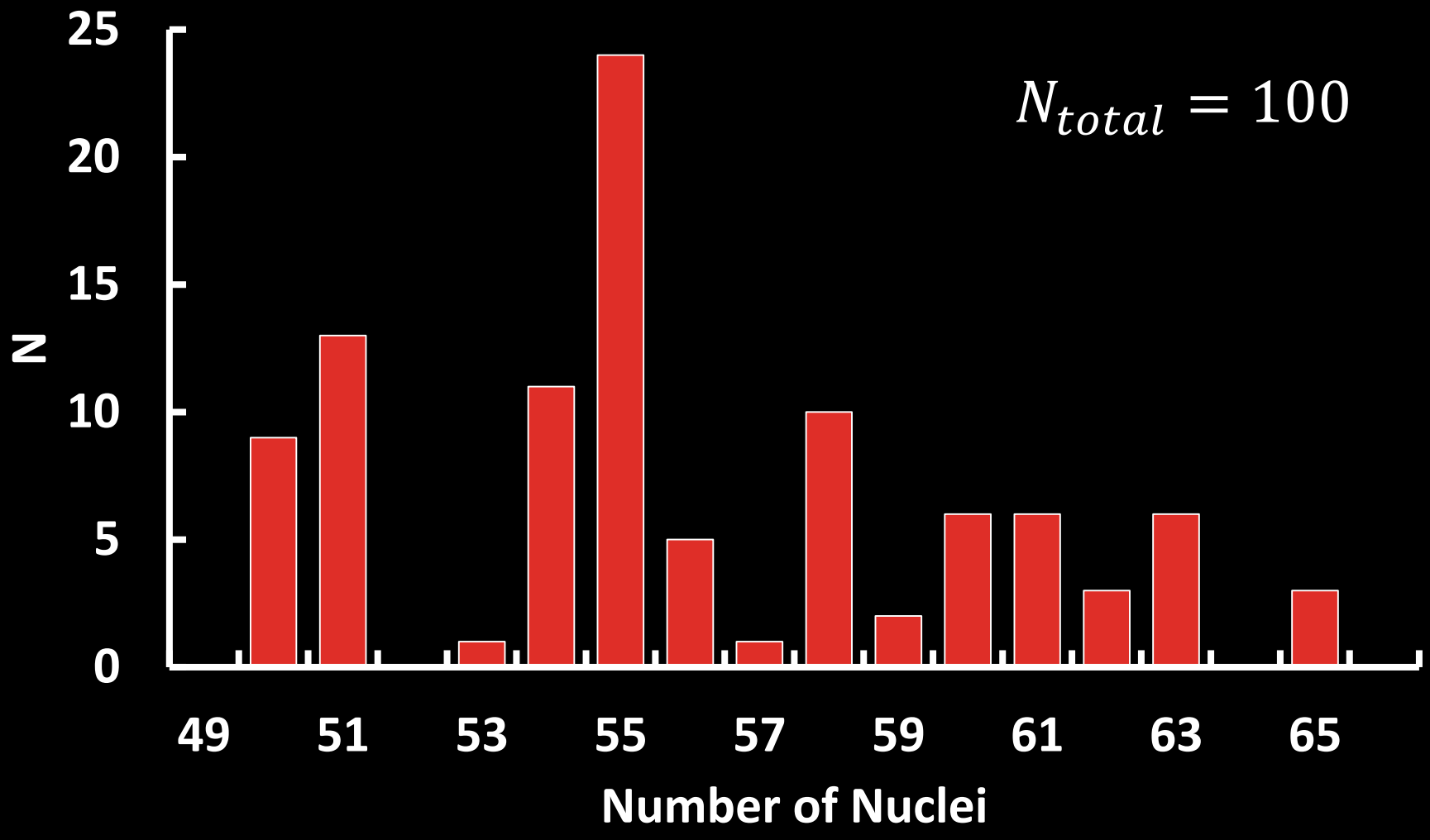
CHALLENGE 1

Filter Noise	• Process > Filters
Segment Cells From Background	• Image > Adjust > Threshold
Manipulate Segmentation	• Process > Binary
Specify Morphological Measurements	• Analyze > Set Measurements
Quantify Morphology	• Analyze > Analyze Particles

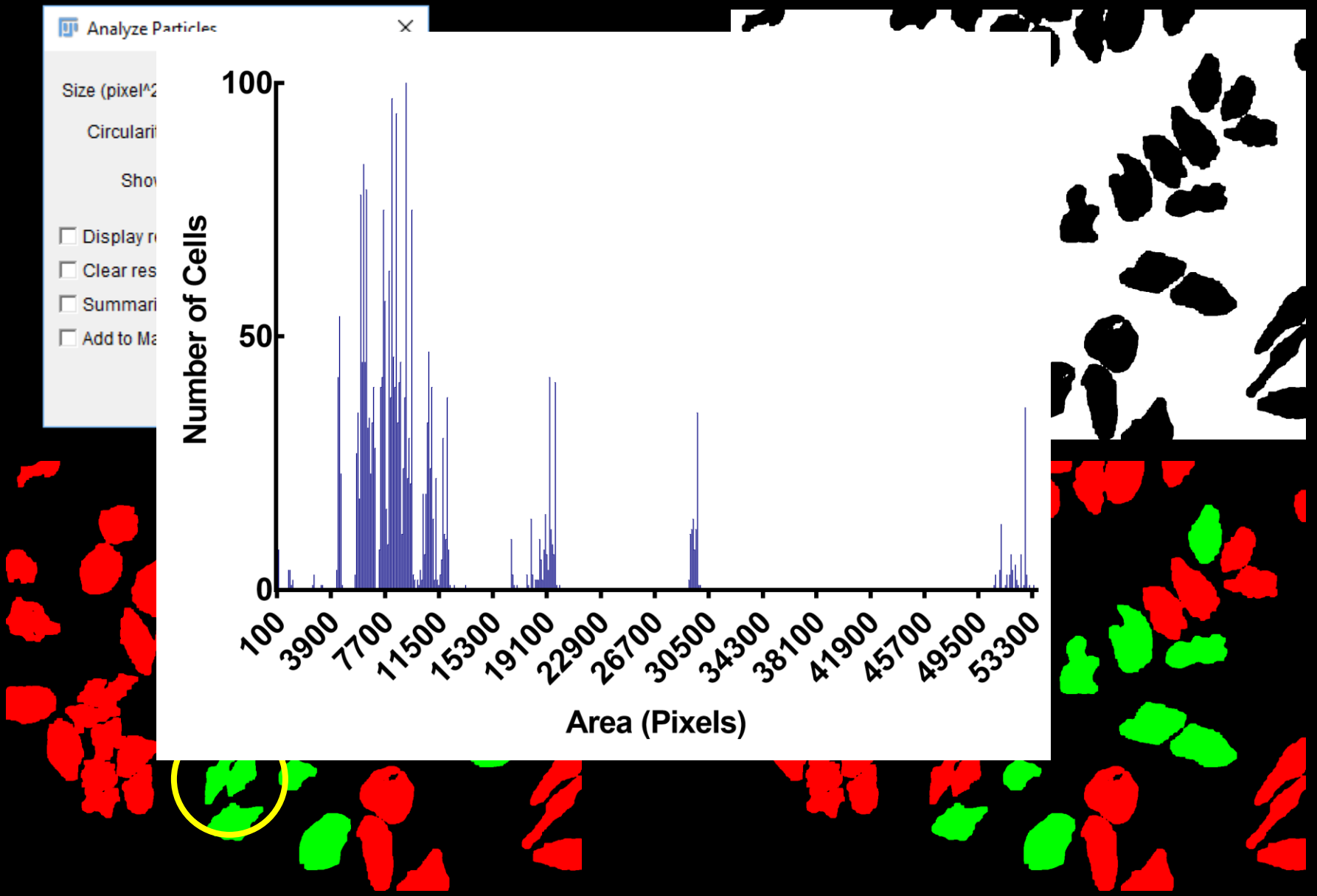
- Which variables in your analysis pipeline will have the greatest impact on your result?
- Could the images be improved in any way to facilitate easier analysis?
- Can you think of an alternative approach?

SOLUTION TO CHALLENGE 1

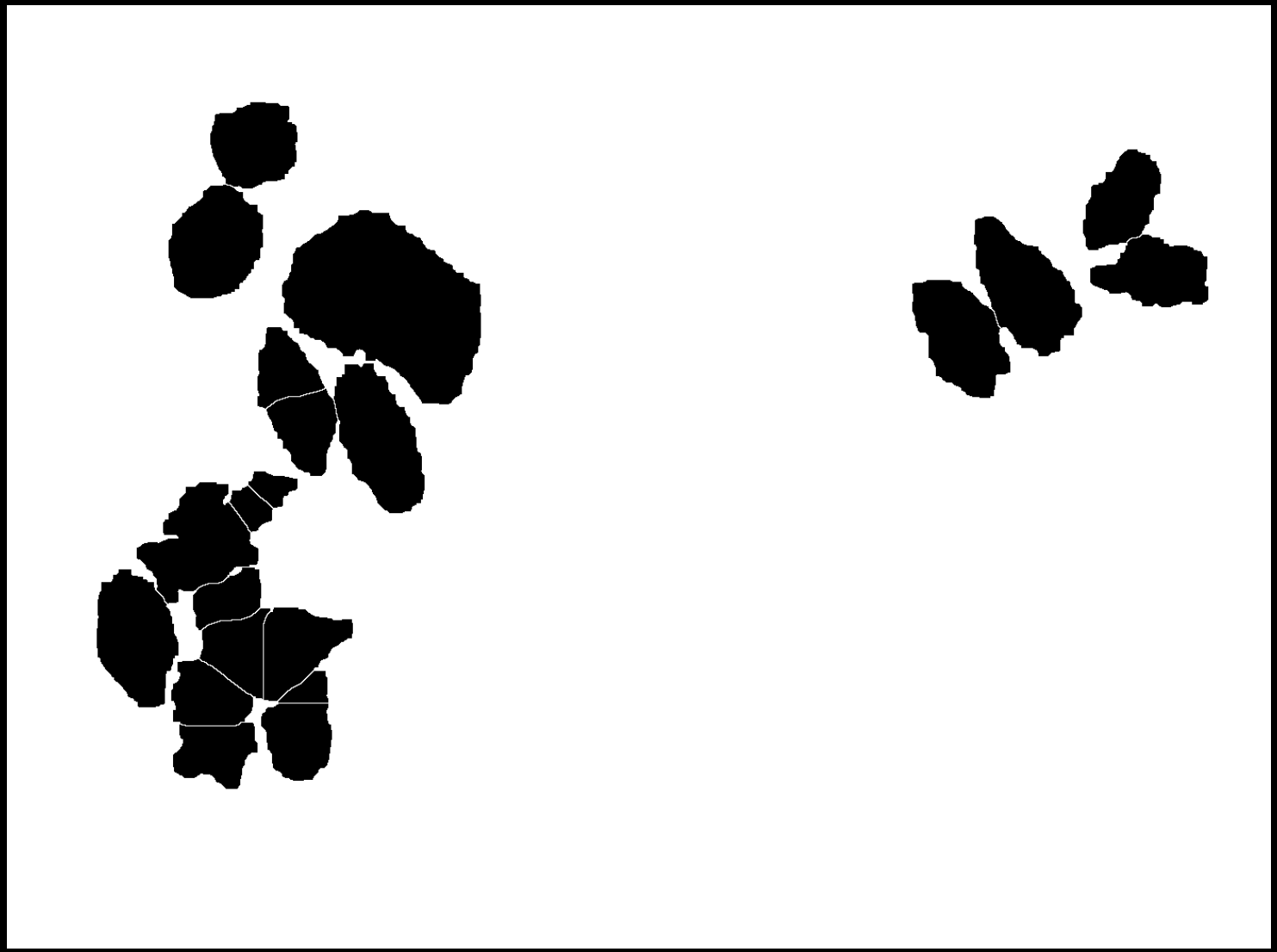
HOW DO PARAMETER VALUES AFFECT THE RESULT?



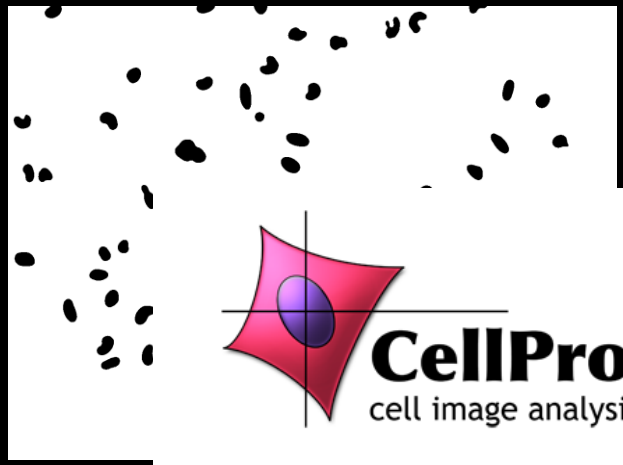
USING MORPHOLOGICAL CRITERIA

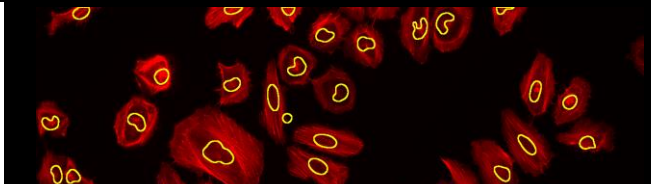


REPEAT ANALYSIS ON CLUMPED CELLS

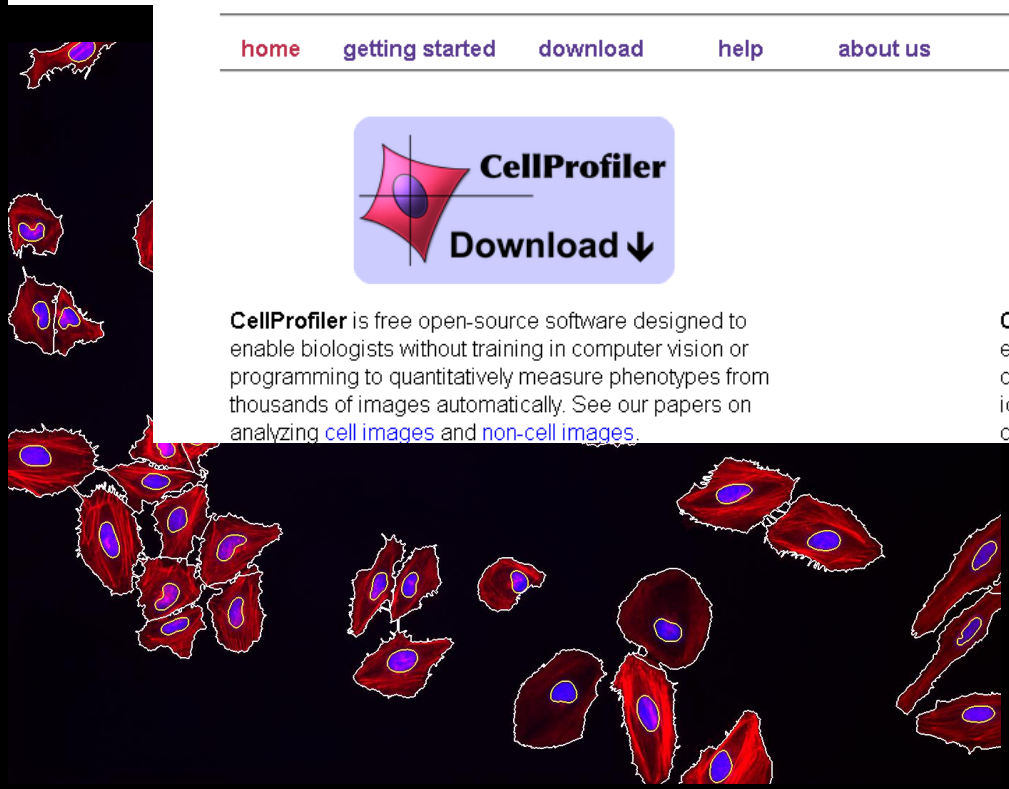


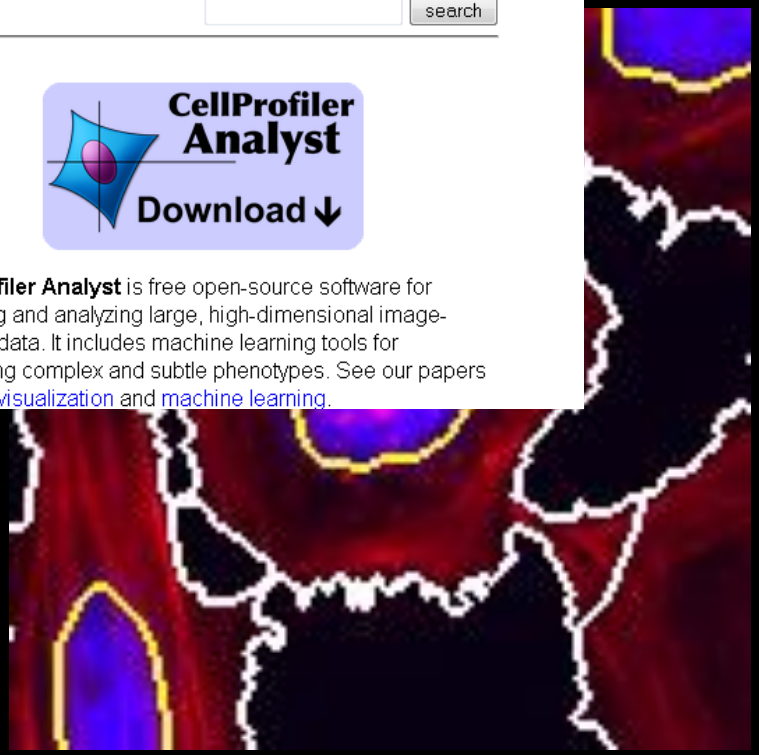
ALTERNATIVE APPROACH: REGION-GROWING





Use nuclei as seeds





CellProfiler
cell image analysis software

BROAD INSTITUTE

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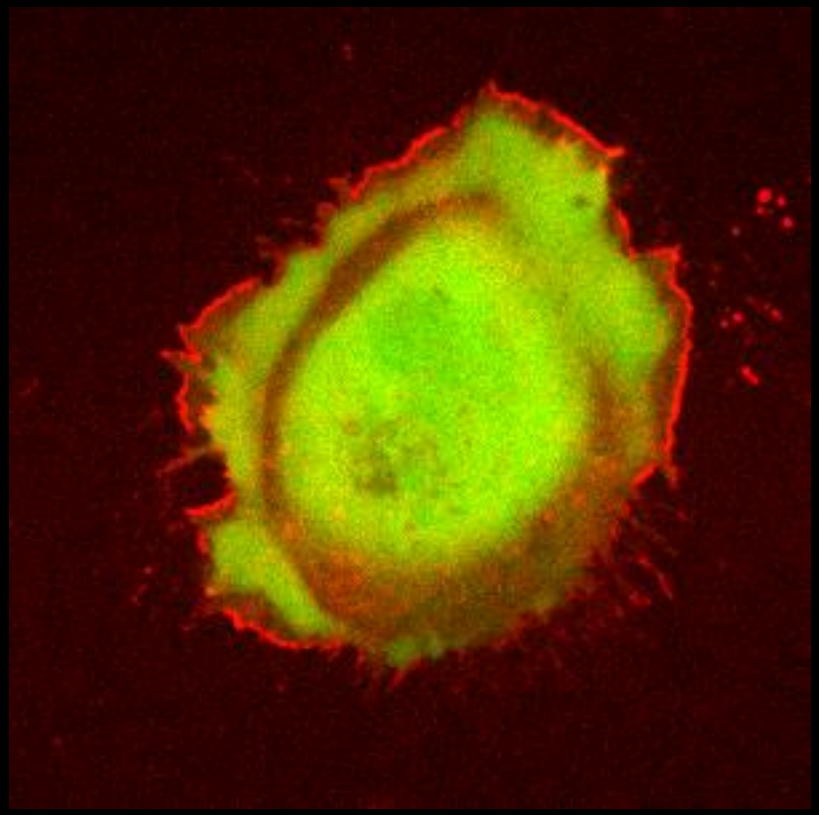
CellProfiler Download

CellProfiler Analyst Download

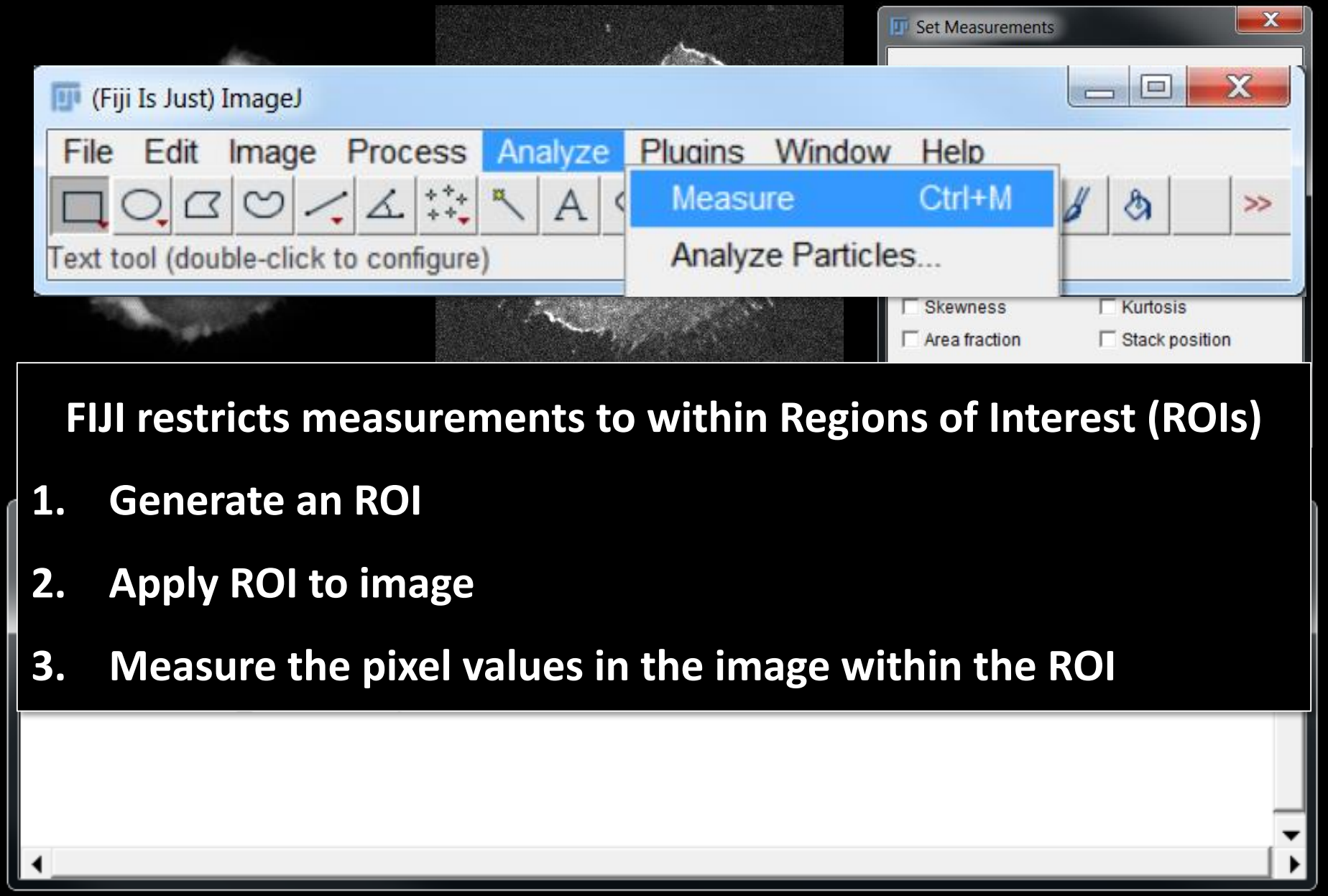
CellProfiler is free open-source software designed to enable biologists without training in computer vision or programming to quantitatively measure phenotypes from thousands of images automatically. See our papers on analyzing cell images and non-cell images.

CellProfiler Analyst is free open-source software for exploring and analyzing large, high-dimensional image-derived data. It includes machine learning tools for identifying complex and subtle phenotypes. See our papers on data visualization and machine learning.

ANALYSING MULTIPLE CHANNELS



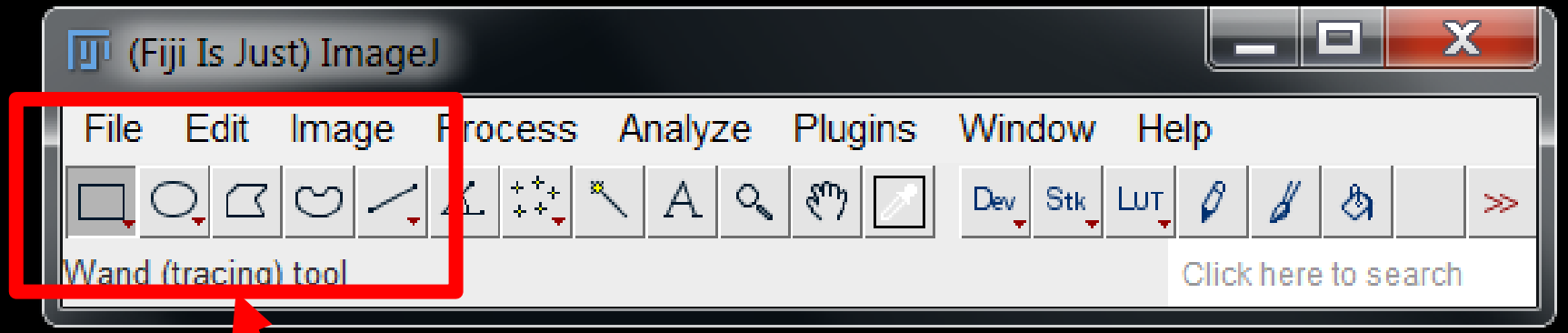
What if we want to analyse protein expression?



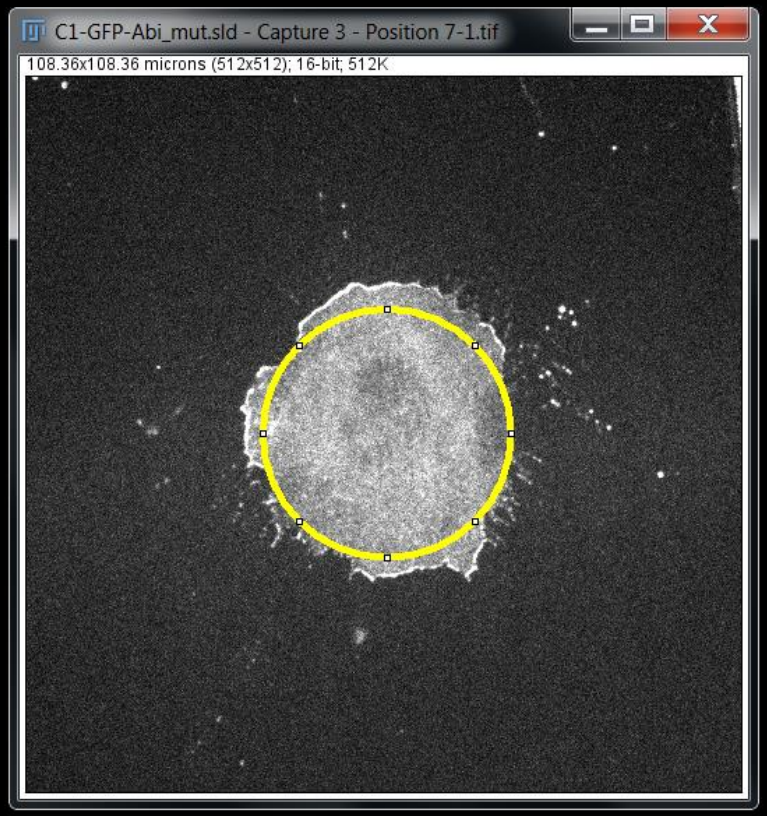
FIJI restricts measurements to within Regions of Interest (ROIs)

1. **Generate an ROI**
2. **Apply ROI to image**
3. **Measure the pixel values in the image within the ROI**

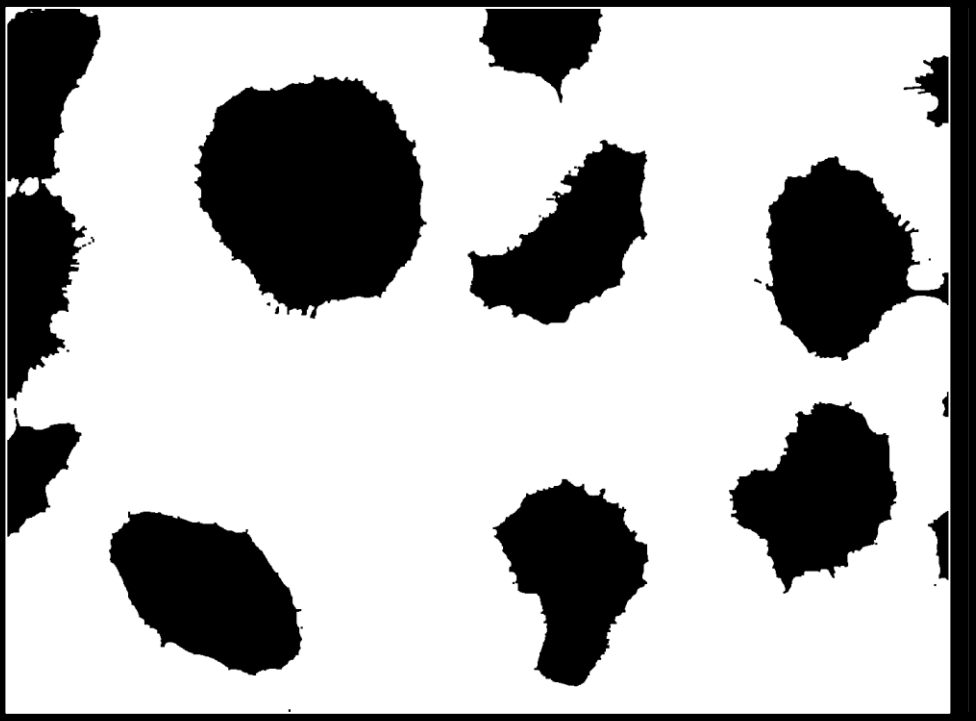
IT'S POSSIBLE TO SPECIFY ROIS MANUALLY



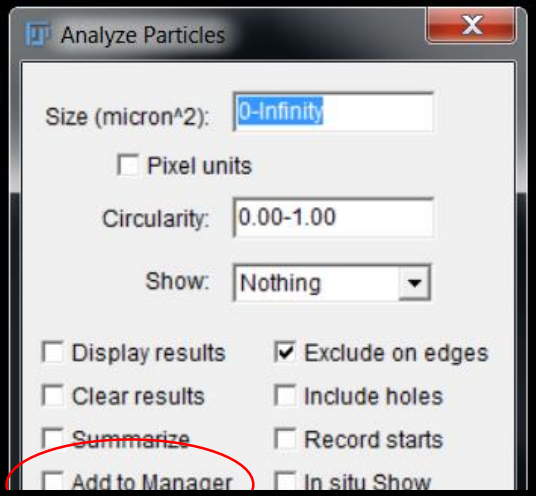
ROI Drawing Tools

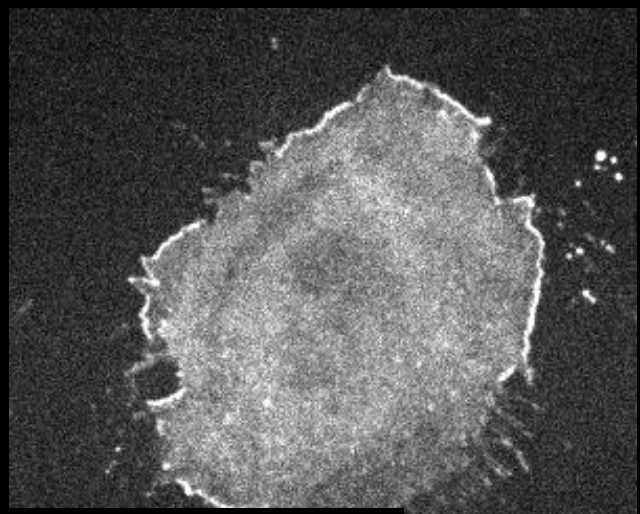


PARTICLE ANALYSER GENERATES ROIS “BEHIND THE SCENES”

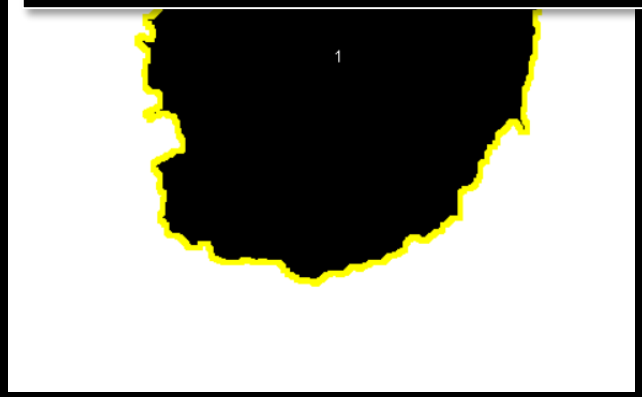


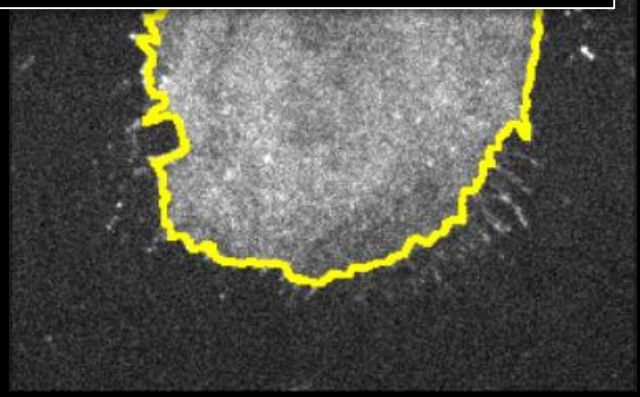
Masks and ROIS can be considered interchangeable



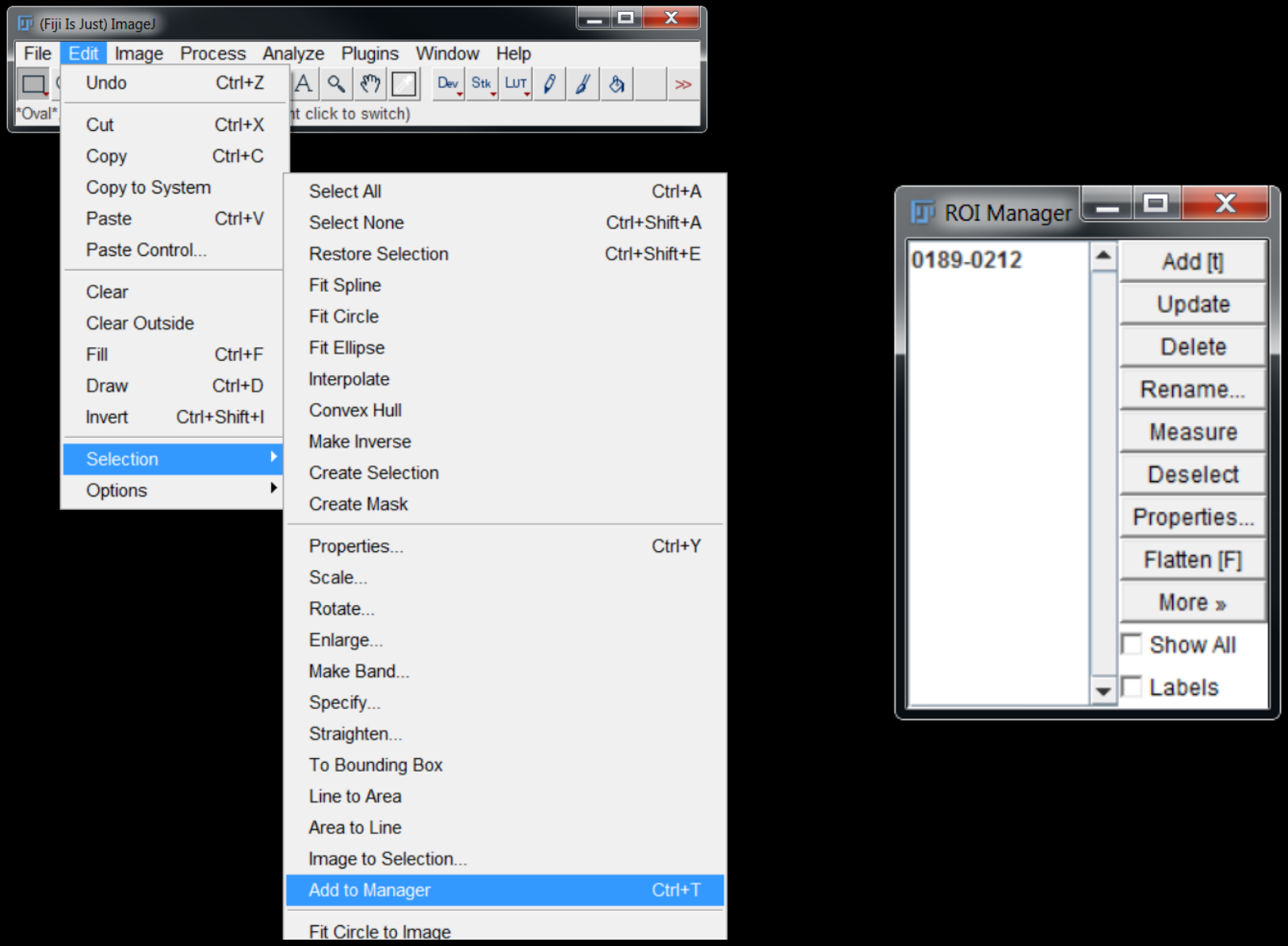


1. Using Particle Analyser to generate an ROI
2. Apply ROI to image
3. Measure the pixel values in the image within the ROI



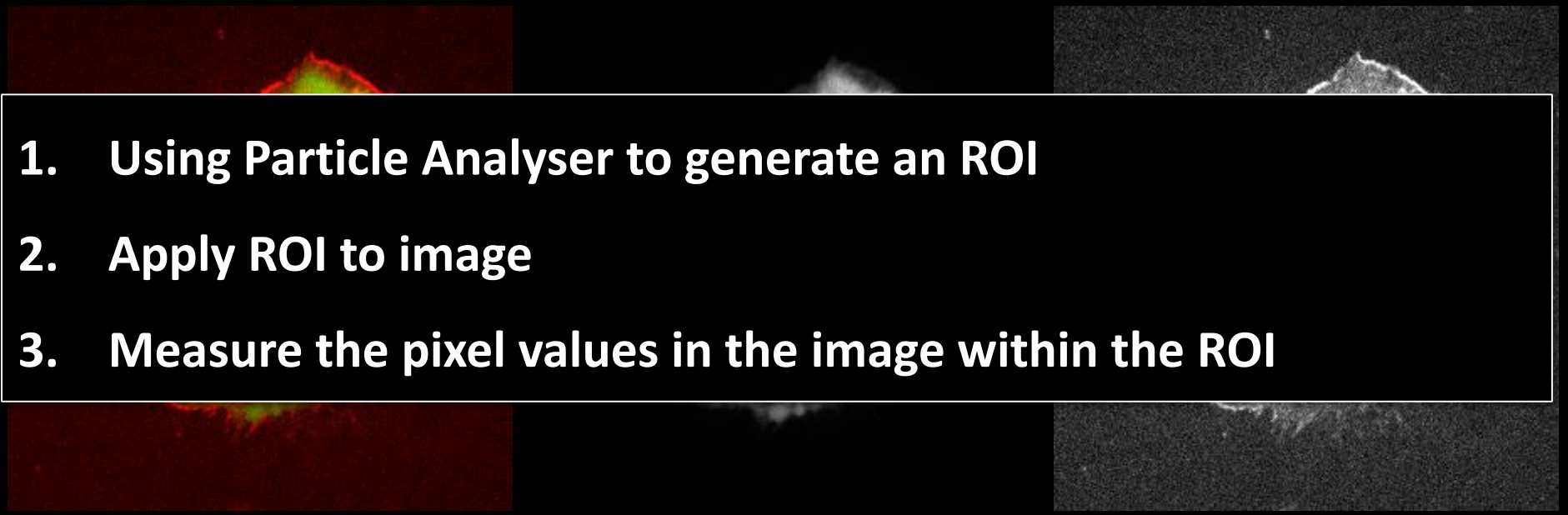


ROI MANAGER CAN ALSO BE ACCESSED MANUALLY…

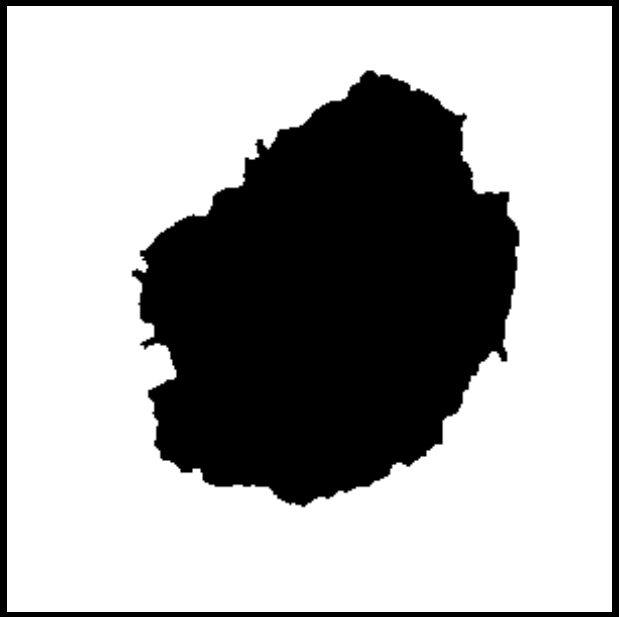


DEMO 7 – GENERATING ROIS AUTOMATICALLY

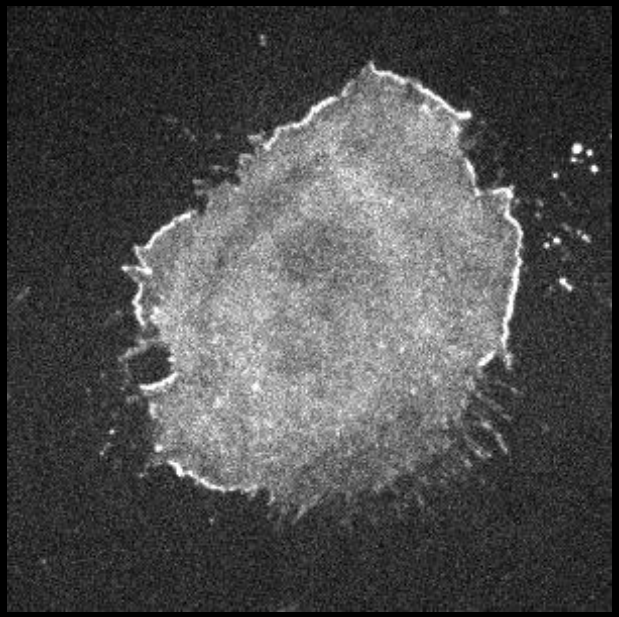
Demonstration of Particle Analyser's ability to generate regions of interest



1. **Using Particle Analyser to generate an ROI**
2. **Apply ROI to image**
3. **Measure the pixel values in the image within the ROI**



Binary Mask



Fluorescent Signal

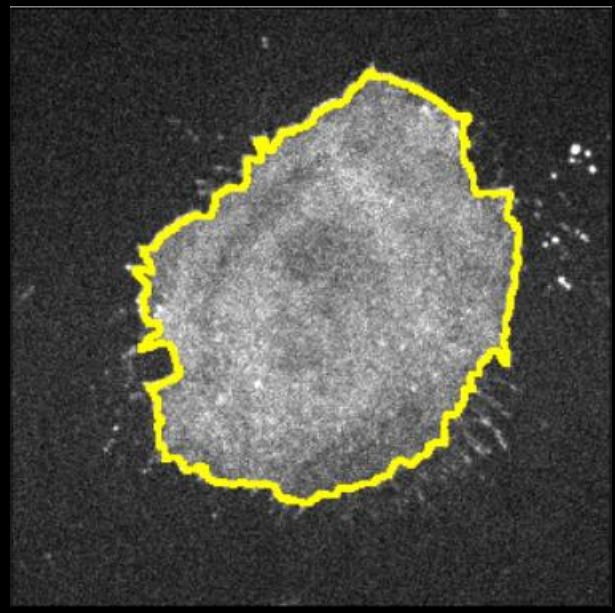
Set Measurements

☑ Area	☑ Mean gray value
☑ Standard deviation	☑ Modal gray value
☑ Min & max gray value	☐ Centroid
☐ Center of mass	☐ Perimeter
☐ Bounding rectangle	☐ Fit ellipse
☐ Shape descriptors	☐ Feret's diameter
☐ Integrated density	☐ Median
☐ Skewness	☐ Kurtosis
☐ Area fraction	☐ Stack position
☐ Limit to threshold	☐ Display label
☐ Invert Y coordinates	☐ Scientific notation
☐ Add to overlay	☐ NaN empty cells

Redirect to: Fluorescent Signal

Decimal places (0-9): 3

OK Cancel Help



FIJI will always apply measurements to whatever image is specified here

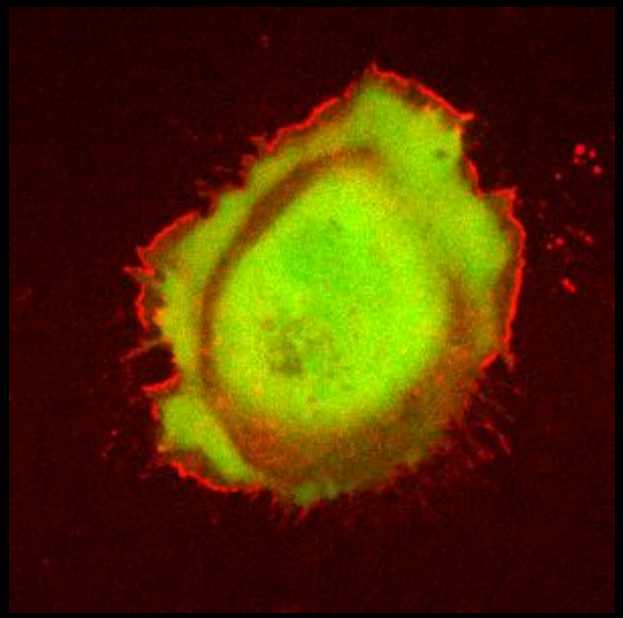
Results

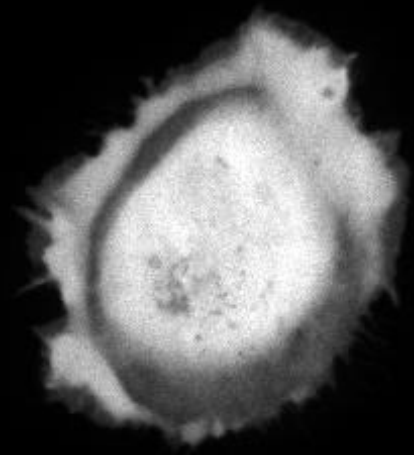
File Edit Font Results

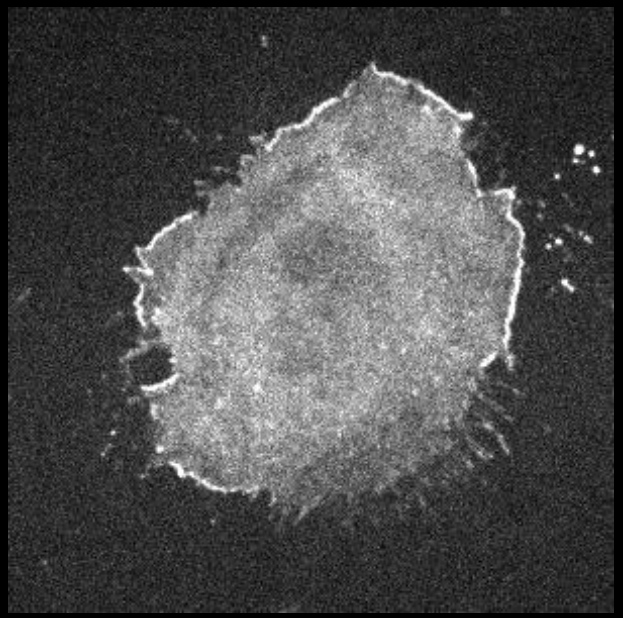
	Label	Area	Mean	StdDev	Mode	Min	Max	IntDen	Median	Skew	Kurt	RawIntDen
1	C1-GFP-Abi_mut.sld - Capture 3 - Position 7-1.tif	655.794	1745.410	213.500	1816	979	2718	1144628.426	1740	0.196	0.075	25554545

DEMO 8 – QUANTIFYING FLUORESCENCE

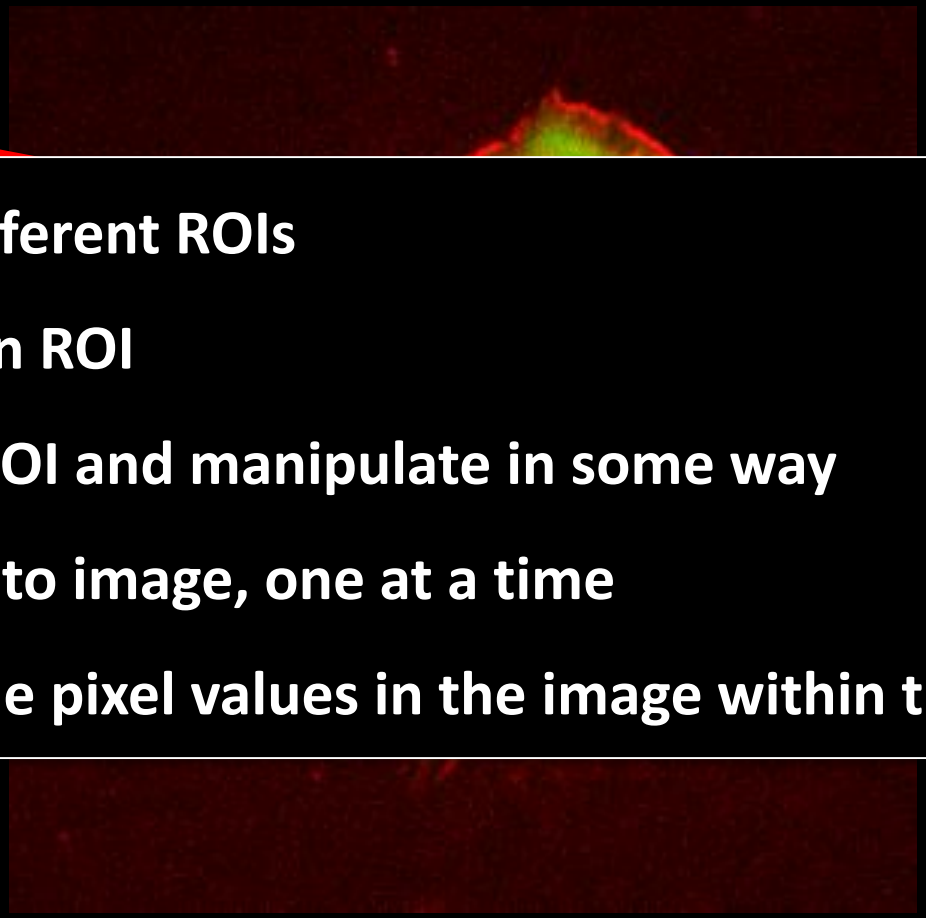
Demonstration of Particle Analyser's ability to apply ROIs to measure grey levels







WHAT IF WE WANT TO EXAMINE DIFFERENCES IN PROTEIN EXPRESSION…



…between here

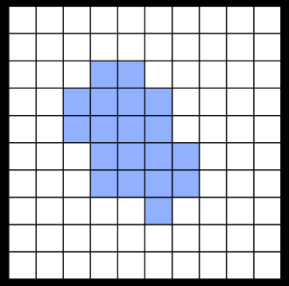
…and here

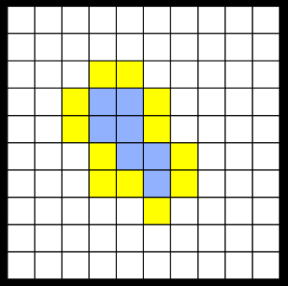
Require two different ROIs

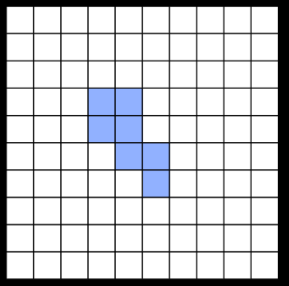
1. **Generate an ROI**
2. **Duplicate ROI and manipulate in some way**
3. **Apply ROIs to image, one at a time**
4. **Measure the pixel values in the image within the ROIs**

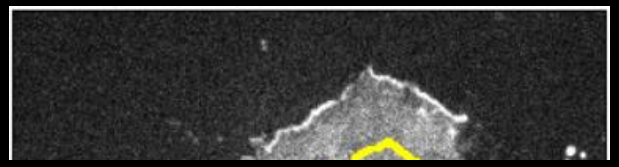
POSSIBLE TO MANIPULATE MASK PRIOR TO ROI GENERATION

Erosion

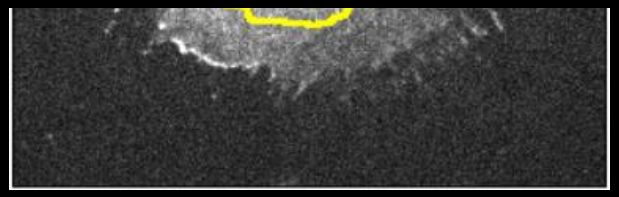


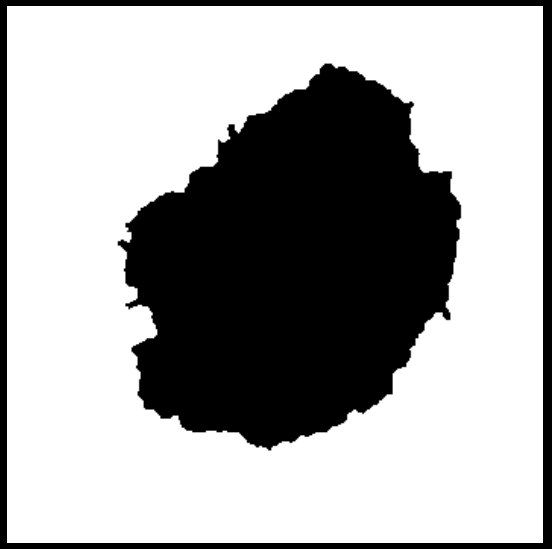


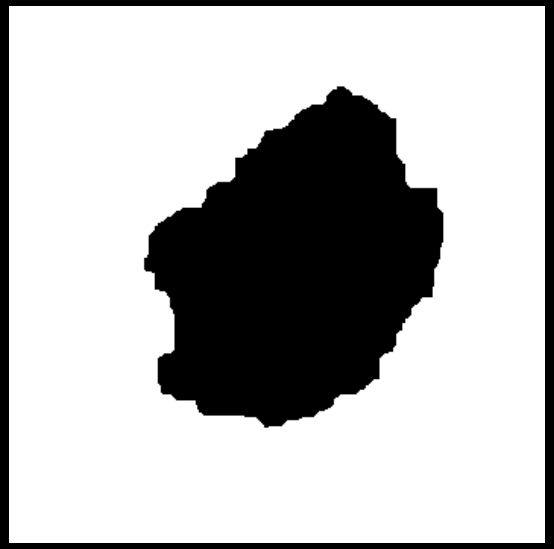


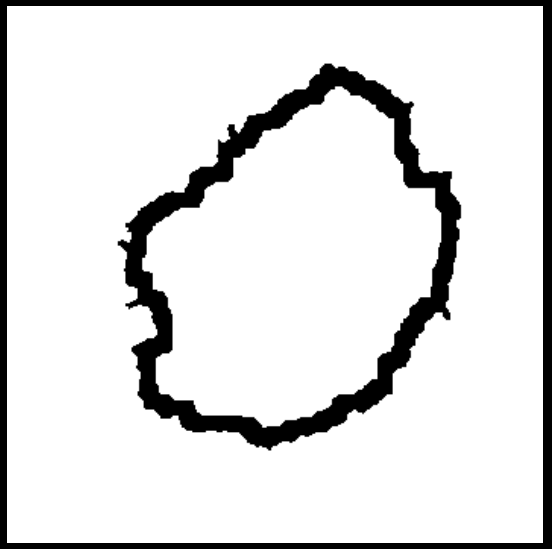


How do we generate a mask to represent the cell boundary?



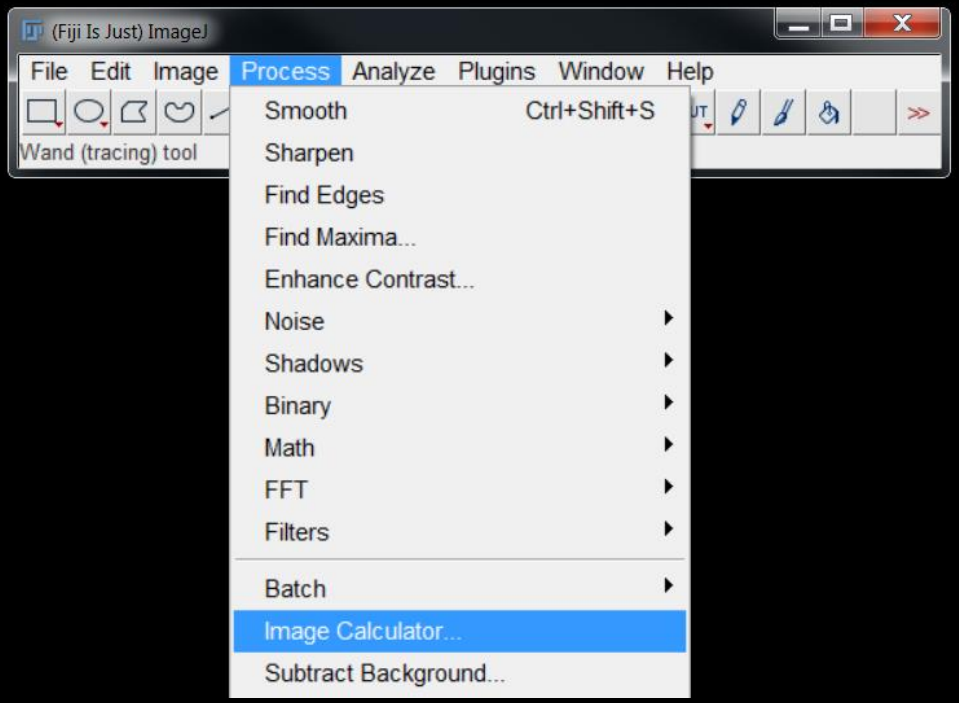


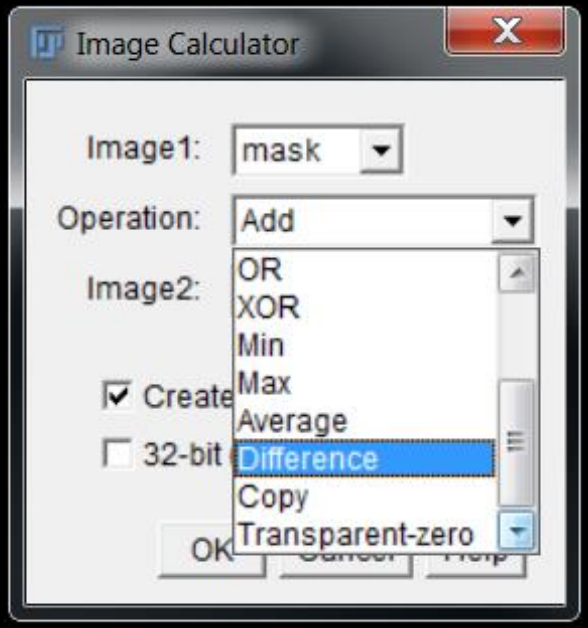




Calculate difference between these…

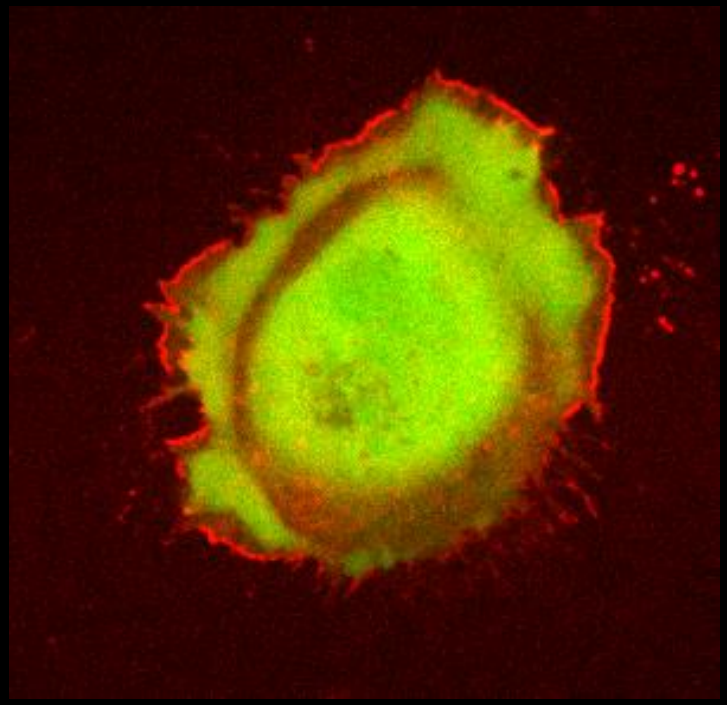
…to produce this.





CHALLENGE 2

Estimate the difference in mCherry expression between the cell edge and the cell centre



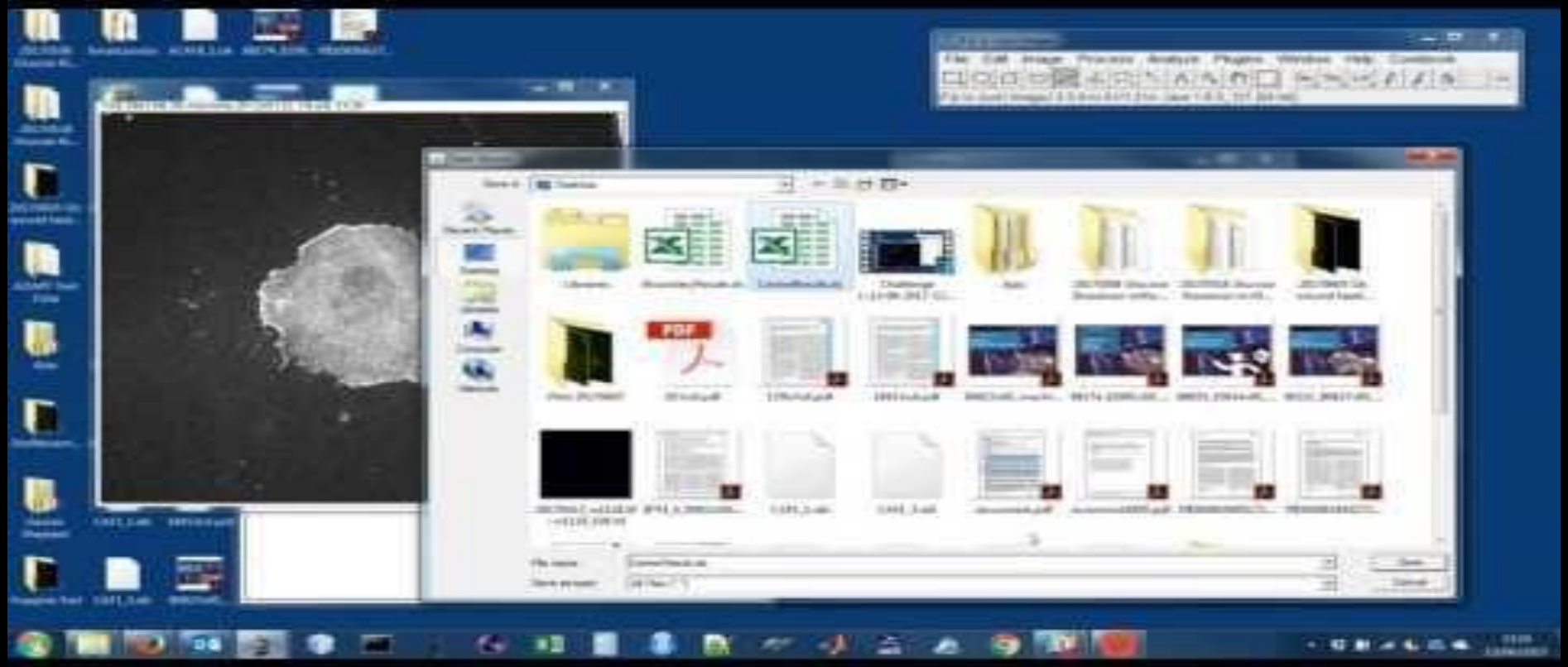
Filter Noise	• Process > Filters
Segment cells from background	• Image > Adjust > Threshold
Manipulate Segmentation	• Process > Binary
Create New Mask Image	• Process > Image Calculator
Specify Morphological Measurements	• Analyze > Set Measurements
Quantify Morphology & Fluorescence	• Analyze > Analyze Particles

CHALLENGE 2

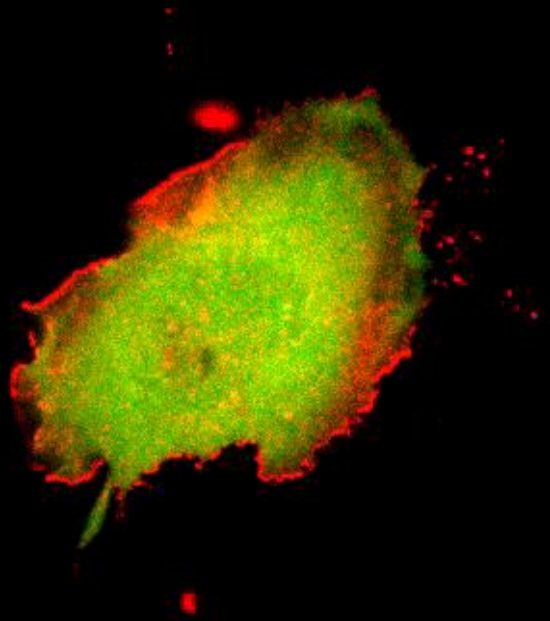
Filter Noise	• Process > Filters
Segment cells from background	• Image > Adjust > Threshold
Manipulate Segmentation	• Process > Binary
Create New Mask Image	• Process > Image Calculator
Specify Morphological Measurements	• Analyze > Set Measurements
Quantify Morphology & Fluorescence	• Analyze > Analyze Particles

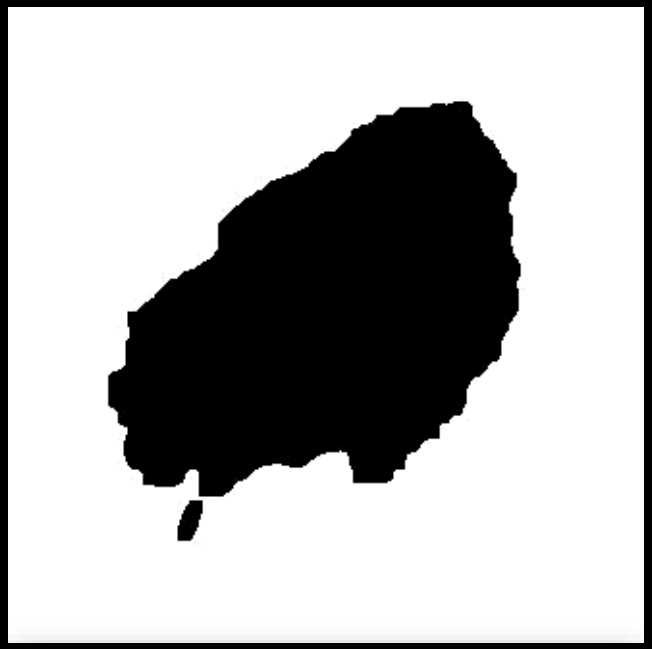
- Which variables in your analysis pipeline will have the greatest impact on your result?
- Is the result what you expected?
  - Why?
  - What could explain any discrepancy between what you see “visually” and what you obtain quantitatively.

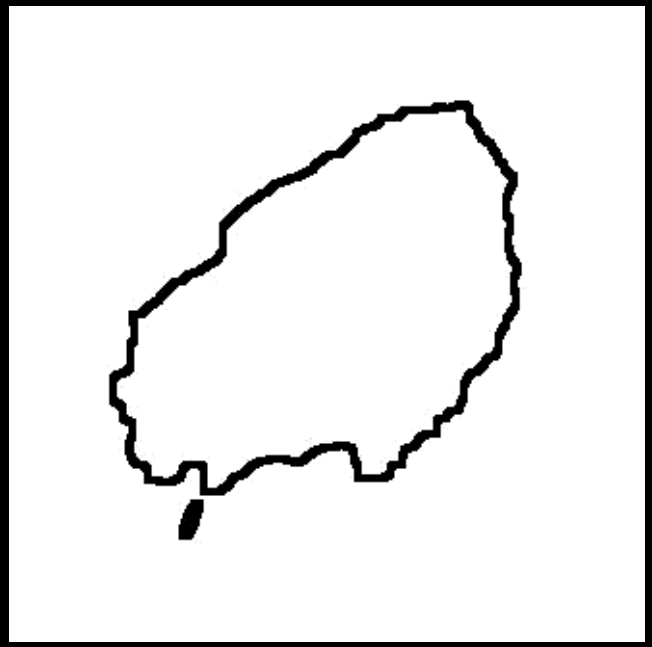
SOLUTION TO CHALLENGE 2

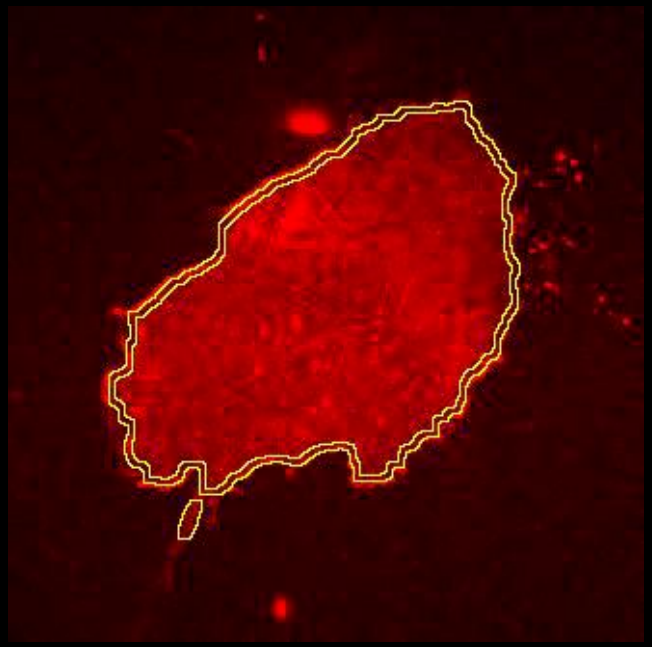


Everything we have done can also be applied to 3- & 4-D datasets



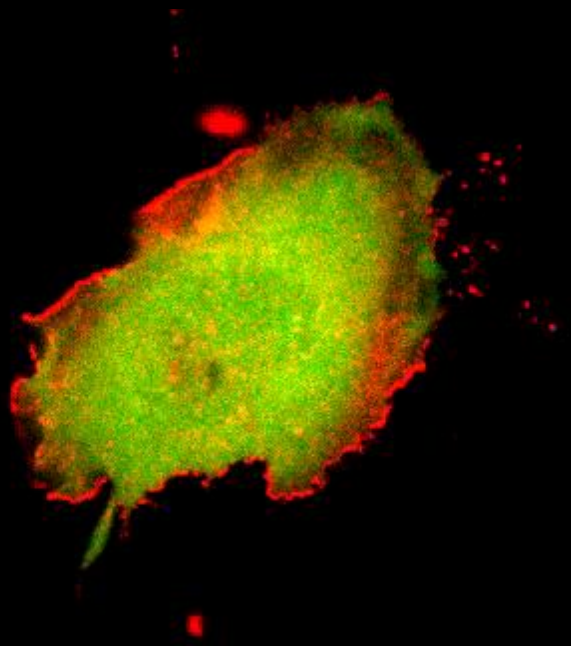




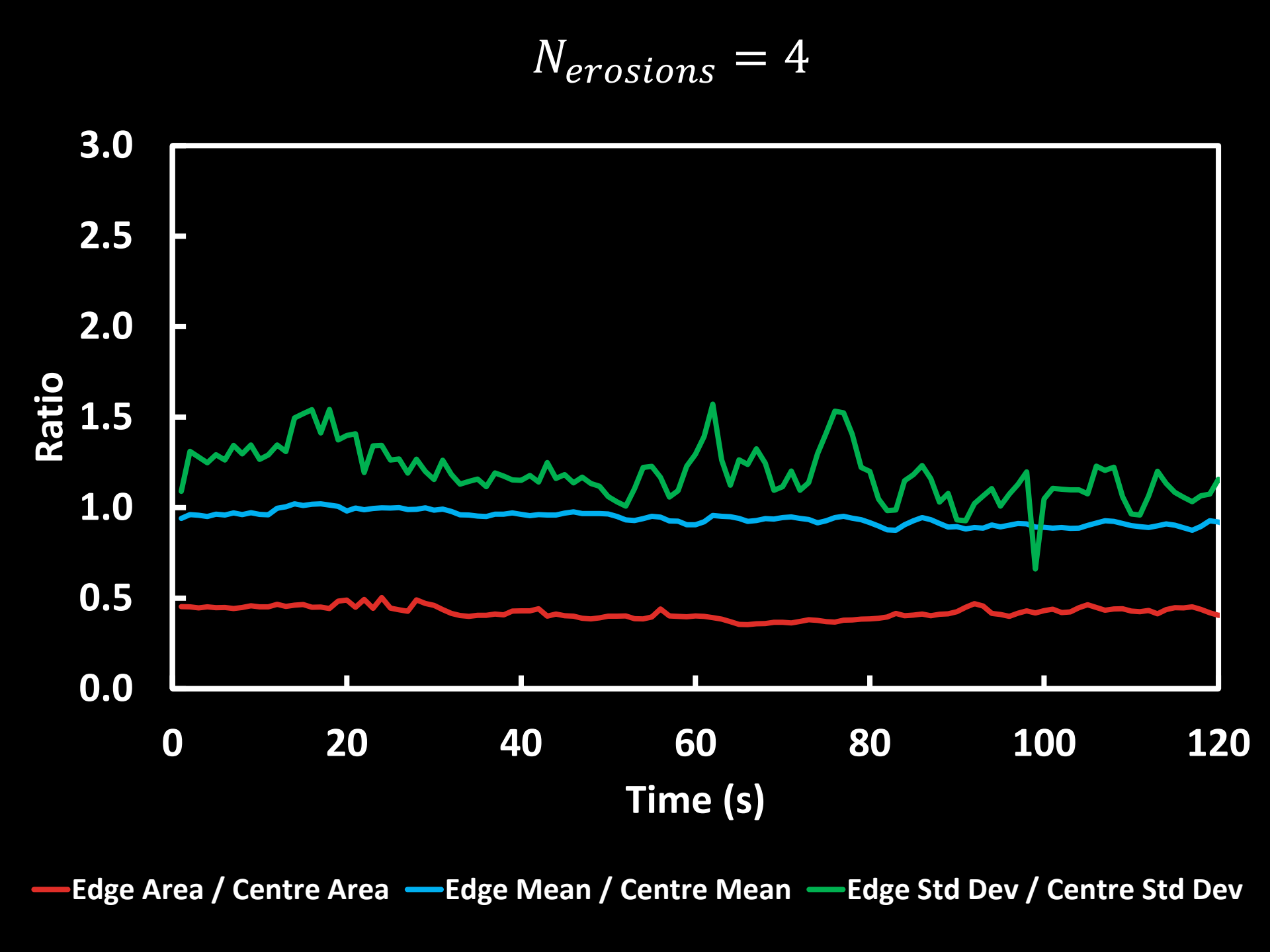


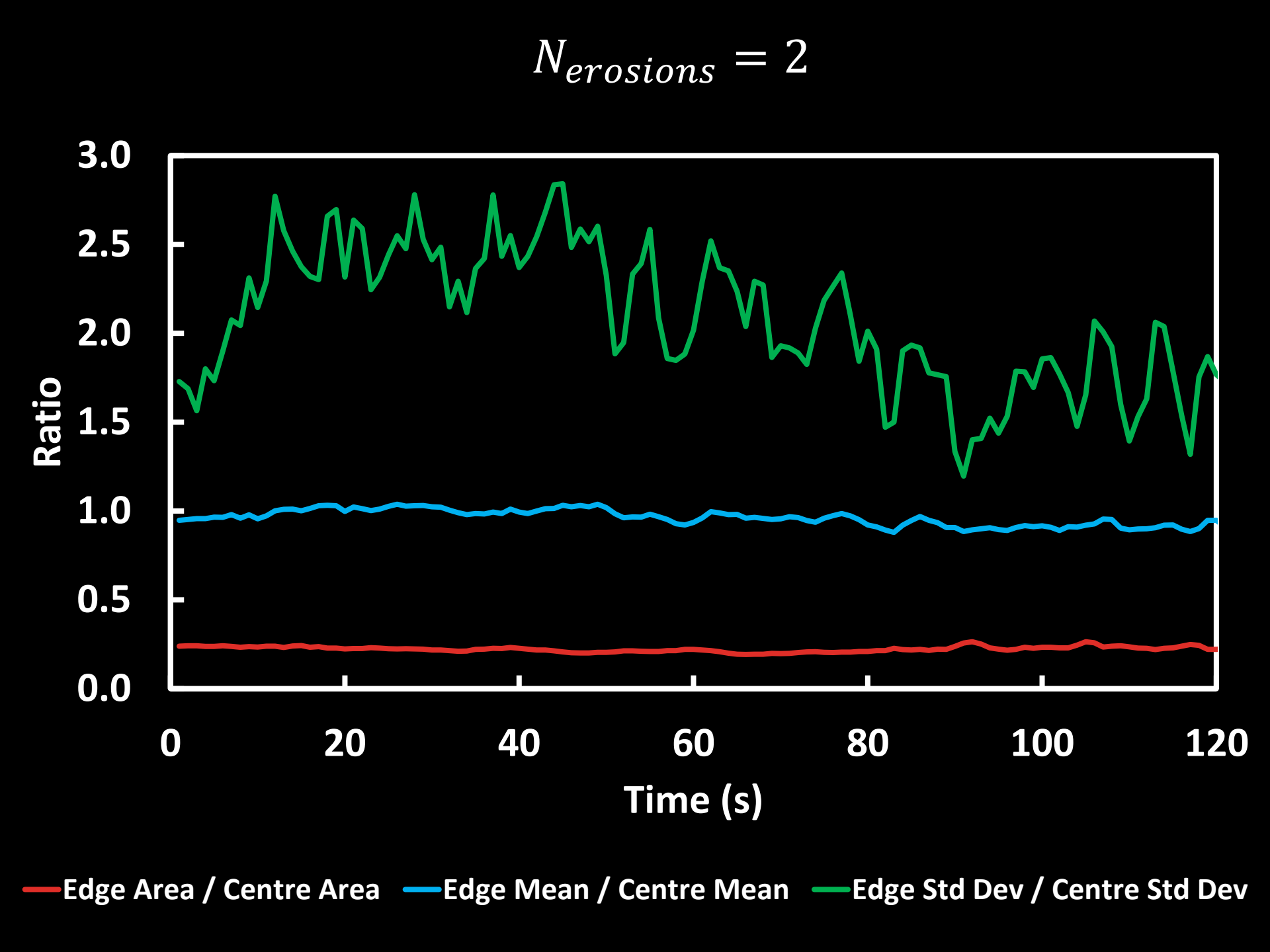
CHALLENGE 3

Determine whether mCherry localisation varies over time



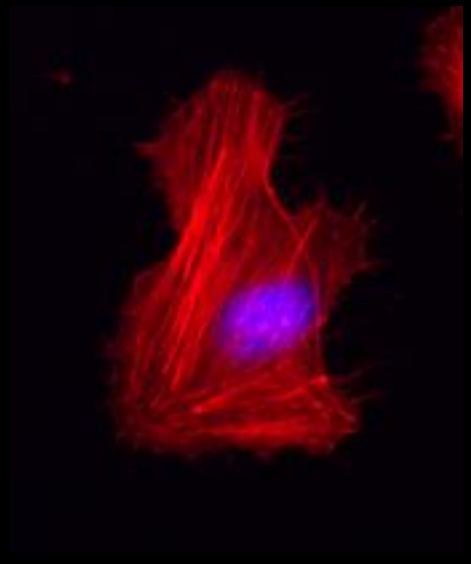
Filter Noise	• Process > Filters
Segment cells from background	• Image > Adjust > Threshold
Manipulate Segmentation	• Process > Binary
Create New Mask Image	• Process > Image Calculator
Specify Morphological Measurements	• Analyze > Set Measurements
Quantify Morphology & Fluorescence	• Analyze > Analyze Particles

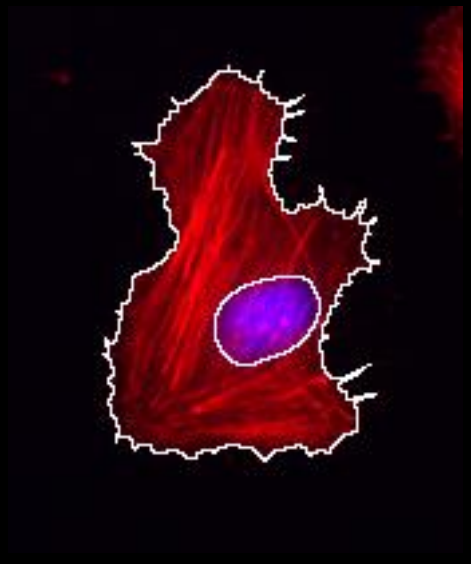

$N_{erosions} = 4$
3.0
2.5
2.0
1.5
1.0
0.5
0.0
Ratio
0
20
40
60
80
100
120
Time (s)
Edge Area / Centre Area
Edge Mean / Centre Mean
Edge Std Dev / Centre Std Dev

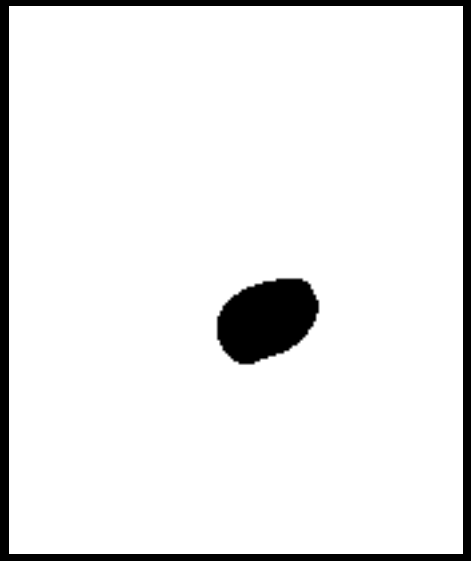

$N_{erosions} = 2$
3.0
2.5
2.0
1.5
1.0
0.5
0.0
Ratio
0
20
40
60
80
100
120
Time (s)
Edge Area / Centre Area
Edge Mean / Centre Mean
Edge Std Dev / Centre Std Dev

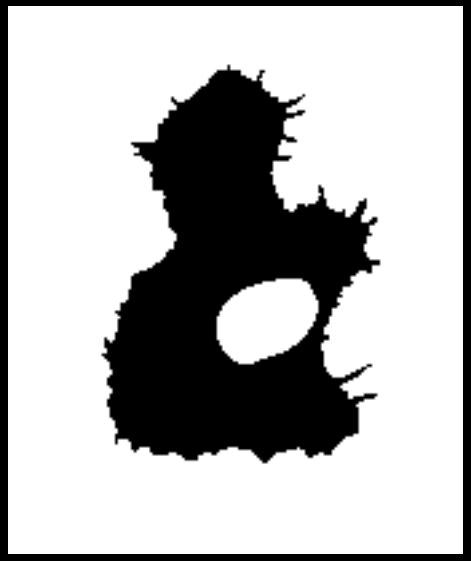
EASY TO EXTEND THIS APPROACH…

For example, to compare nuclear & non-nuclear expression



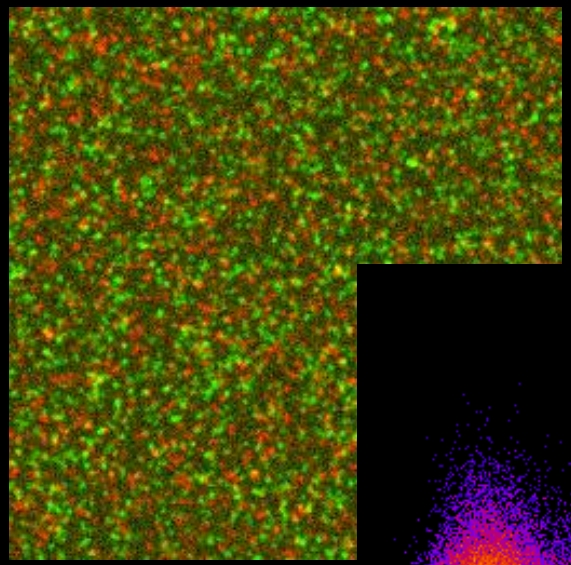


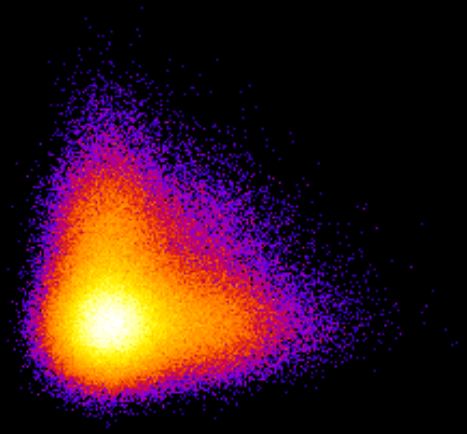


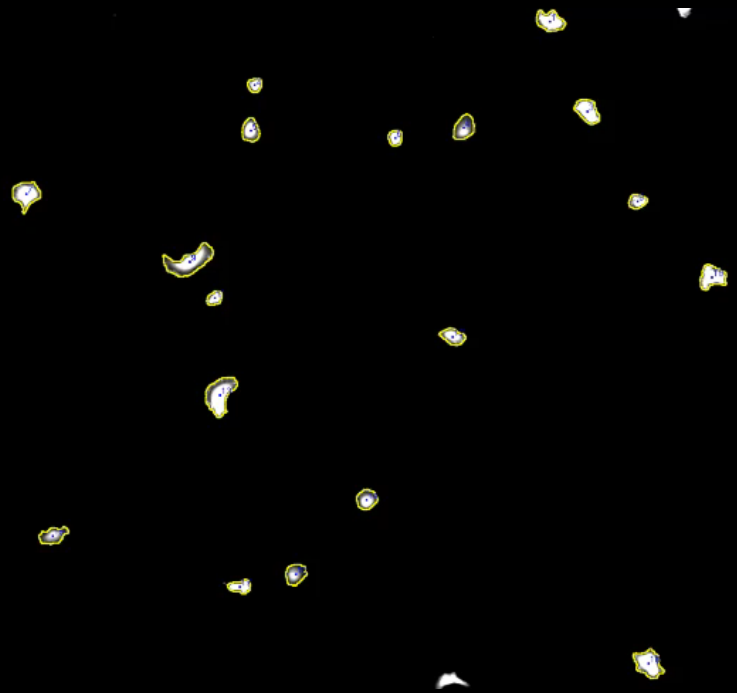


ADVANCED TOPICS

- Object Tracking
- Colocalisation analysis
- Writing macros & plugins







```
import ij.plugin.frame.RoiManager as RM
import fiji.plugin.kymographbuilder.KymographFactory as KFactory


def validDataset(dataset):
    """Assess if dataset has suitable dimensions"""
    from net.imagej.axis import Axes
    z = dataset.dimension(dataset.dimensionIndex(Axes.Z))
    t = dataset.dimension(dataset.dimensionIndex(Axes.TIME))
    return z * t > 1


rm = RM.getInstance()
counter = 0
if validDataset(dataset) and rm and rm.getCount():
    for roi in rm.getRoisAsArray():
        if roi.isLine():
            kfactory = KFactory(context, dataset, roi)
            kfactory.build()
            counter += 1
            title = "Kymograph" + str(counter).zfill(3) + "_" + roi.getName()
            ij.ui().show(title, kfactory.getKymograph())
    log.info("MultiKymographBuilder Finished. " + str(counter) + " ROIs processed")
else:
    log.error("Either the ROI Manager is empty or " + dataset.getName() +" has invalid dimensions")

```

Mon 26 Jun - Wed 28 Jun 2017
09:30, ...

Venue: Bioinformatics Training Room, Craik-Marshall Building, Downing Site

Provided by: Bioinformatics

Booking

Bookings cannot be made on this event (Event is completed).

Other dates:

No more events

[Show past events]

Register interest

Register your interest - if you would be interested in additional dates being scheduled.

Map

Image Analysis for Biologists

Prerequisites Updated

Description

This course will focus on **computational methods for analysing cellular images** and **extracting quantitative data from them**. The aim of this course is to familiarise the participants with computational image analysis methodologies, and to provide hands-on training in running quantitative analysis pipelines.

On day 1 we will introduce **principles of image processing and analysis**, giving an **overview of commonly used algorithms** through a series of talks and practicals based on **Fiji**, an extensible open source software package.

On day 2, we will describe the open **Icy platform** developed at the Institut Pasteur. Icy is a next-generation, user-friendly software offering powerful **acquisition, visualisation, annotation and analysis algorithms for 5D bioimaging data**, together with unique automation/scripting capabilities (notably via its graphical programming interface) and tight integration with existing software (e.g. ImageJ, Matlab, Micro-Manager).

On day 3, we will cover time series processing and cell tracking using **TrackMate**. In the afternoon, we will present the **Image Data Resource**, an added-value platform that combines data from multiple independent imaging experiments and imaging modalities and integrates them into a single resource for reanalysis in a convenient, scalable form.

Please note that if you are not eligible for a University of Cambridge Raven account you will need to book or register your interest by linking here.

Target audience

- Researchers who are applying or planning to apply image analysis in their research
- **Graduate** students, **Postdocs** and **Staff members** from the **University of Cambridge**, **Affiliated Institutions** and other external Institutions or individuals
- Please be aware that these courses are **only free for University of Cambridge students**. All other participants will be charged a registration fee in some form. Registration fees and further details regarding the charging policy are available here
- Further details regarding eligibility criteria are available here

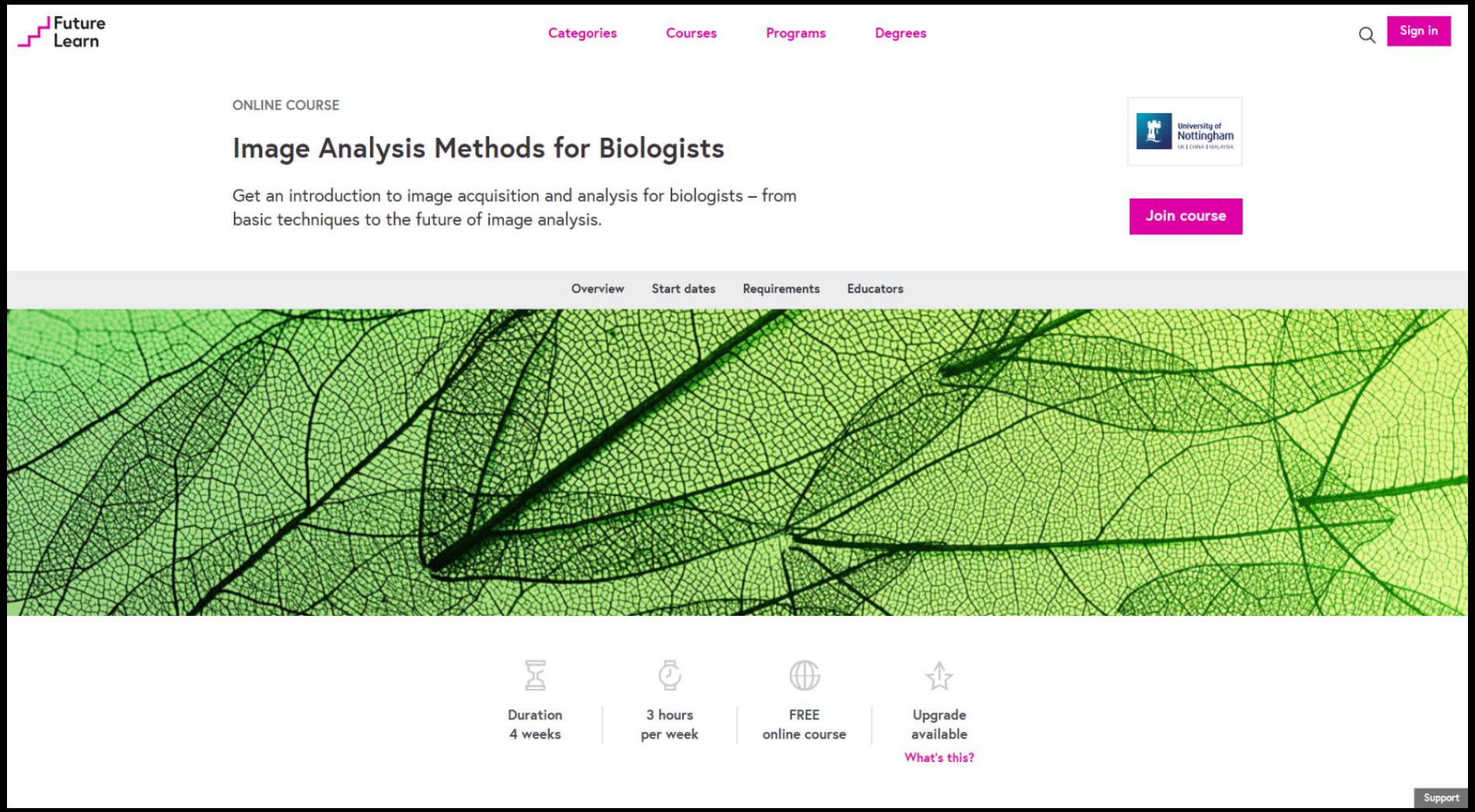
Prerequisites

Basic skills in mathematics and programming are an advantage, but not a requirement.

Sessions

Number of sessions: 3

#	Date	Time	Venue		Trainers
1	*Mon 26 Jun 2017*	*09:30 - 17:30*	*Bioinformatics Training Room, Craik-Marshall Building, Downing Site*	map	*Richard Butler, Jeremy Pike*



https://www.futurelearn.com/courses/image-analysis

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Image analysis help desk

Email alerts Contribute

Sharing knowledge and expertise to help research analyse image datasets.

Meets 2nd and 4th Wednesday of the month at 16:00 in the Crick bar.

Many of you are involved in acquiring microscopy image datasets and one of the aims of the Light Microscopy STP is to equip you with the necessary knowledge and expertise to analyse such datasets effectively.

However, we are aware that this may seem daunting to the uninitiated.

With this in mind, we have created an informal **Image Analysis "Hacking Club"**.

This will involve us situating ourselves in the coffee bar area from 16:00 (we will attempt to make ourselves easily identifiable) and anyone can drop by to ask us any kind of image-analysis related questions you can think of. This may be, for example, some pointers on analysing some images you have already acquired, or advice on designing future

IMAGEJ

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FIJI

Fiji is an image processing package—a "batteries-included" distribution of ImageJ, bundling a lot of plugins which facilitate scientific image analysis.

- **For users** - Fiji is easy to install and has an automatic update function, bundles a lot of plugins and offers comprehensive documentation.
- **For developers** - Fiji is an open source project hosted in a Git version control repository, with access to the source code of all internals, libraries and plugins, and eases the development and scripting of plugins.

Contents [hide]

1 Downloads
2 License
3 Contributing
4 Publication

Fiji Is Just ImageJ

Overview
Using Fiji
Featured Fiji Projects
Fiji Publications
Links

Developing Fiji [-]
Building Fiji from source
Developing Fiji

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FIJI Workshop 18.07.2017 Survey

* 1. On a scale of 1 to 10, where 10 represents the highest level, what was your overall level of satisfaction with the workshop?

1 10

* 2. The workshop ran for approximately three hours - what do you think the ideal length would be?

1 hour 5 hours

3. How did you find the balance between lecturing and practical demonstrations?

- Too much time was spent explaining theory and providing background information.
- The balance was about right
- Not enough time was spent explaining theory and providing background information.

* 4. On a scale of 1 to 10, where 10 represents the highest level, how difficult did you find the challenges?

1 10

Have a Nice Weekend