

IMAGE ANALYSIS

AN OVERVIEW OF TOOLS
BY NOORSHER AHMED





The Evolution of Imaging

Light Microscopy

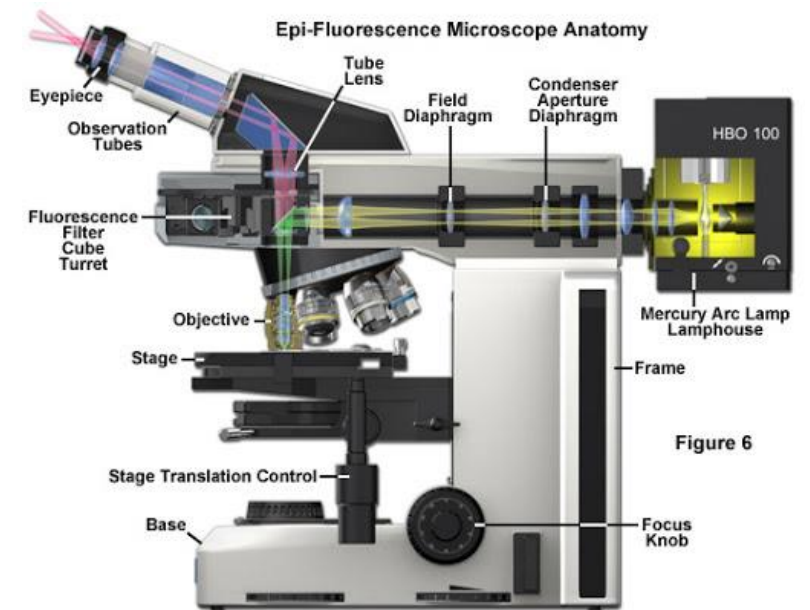
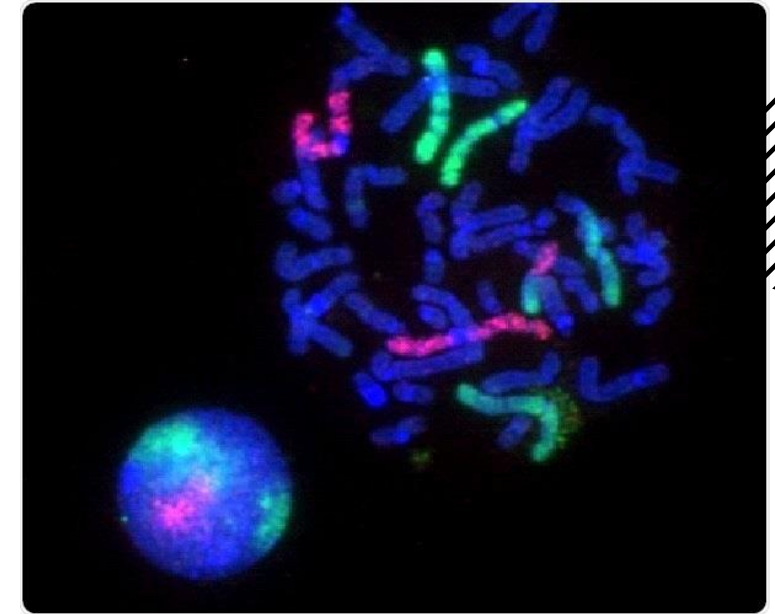
- Classic white light as source
- Low magnification
- Low resolution
- Large field of view



The Evolution of Imaging

Epi-fluorescent Imaging

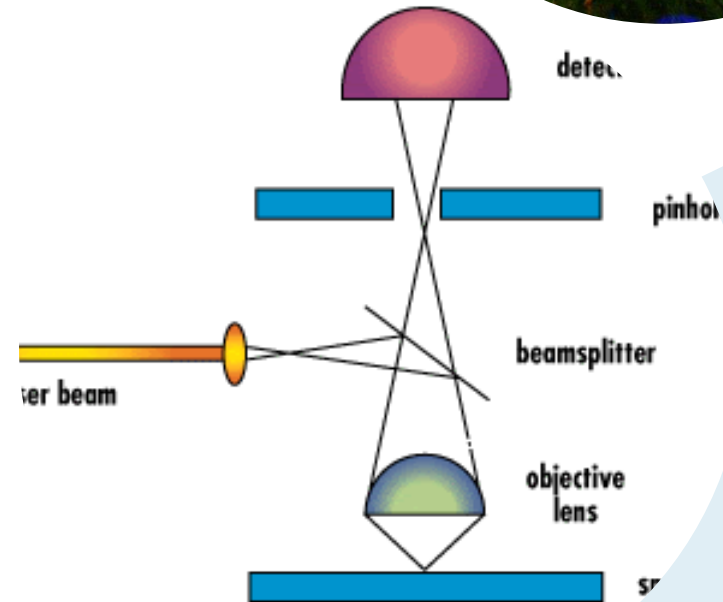
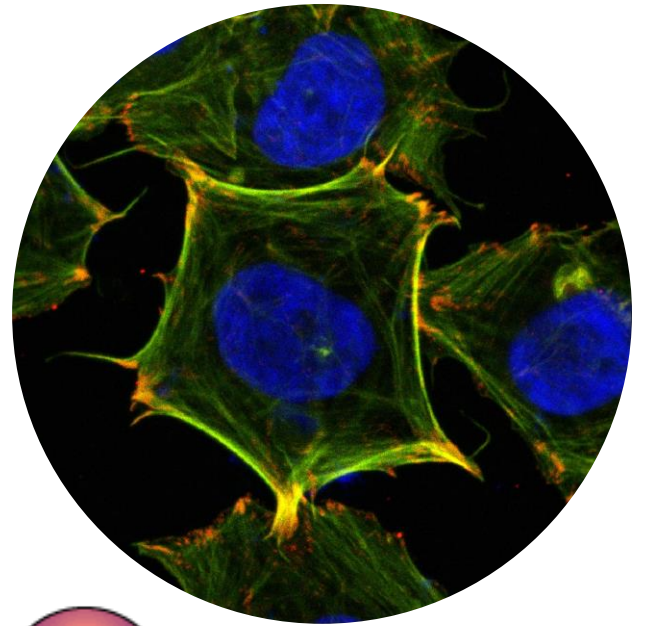
- Specified wavelength excitation
- Can use fluorescently tagged proteins
- Same mag/resolution as light microscopes



The Evolution of Imaging

Confocal Microscopy

- Laser light source of specific wavelength
- 100x magnification possible
- Higher resolution
- “3D” imaging (z-stacks)



Components Needed for HazeP

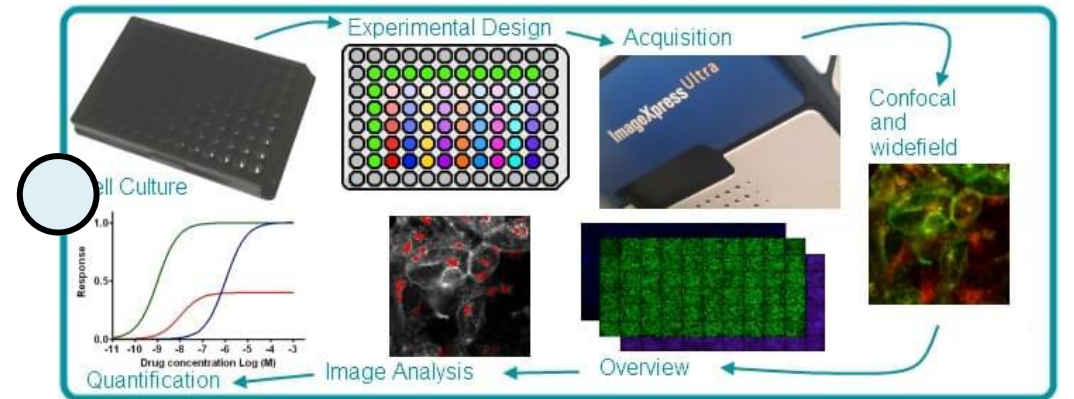
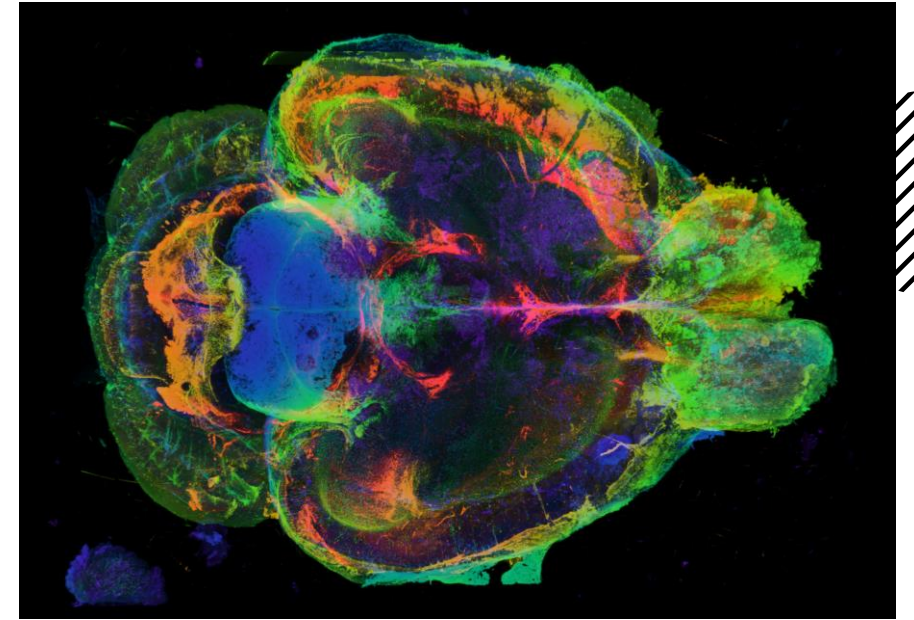


The Evolution of Imaging

High Content Imaging

- Combine Confocal Imaging with Robotics
- Thousands to millions of cells
- High mag/resolution

Big Data



The Evolution of Imaging

Super-resolution Microscopy

- Extremely high resolution (single molecule!)
- High magnification
- Large data formats
- Thousands of particles/features per cell

Big Data

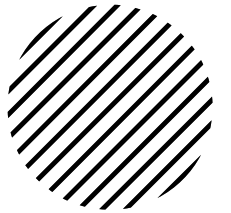
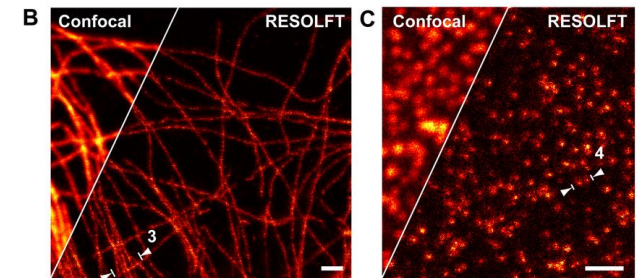
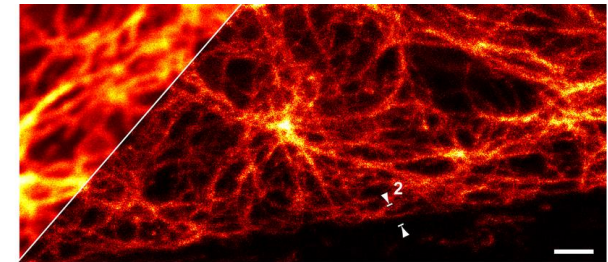
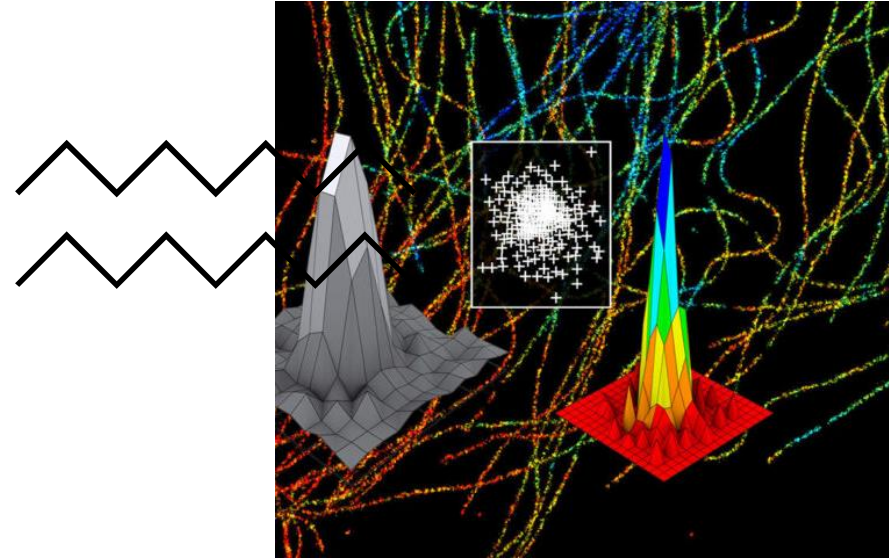


Image Analysis Tasks

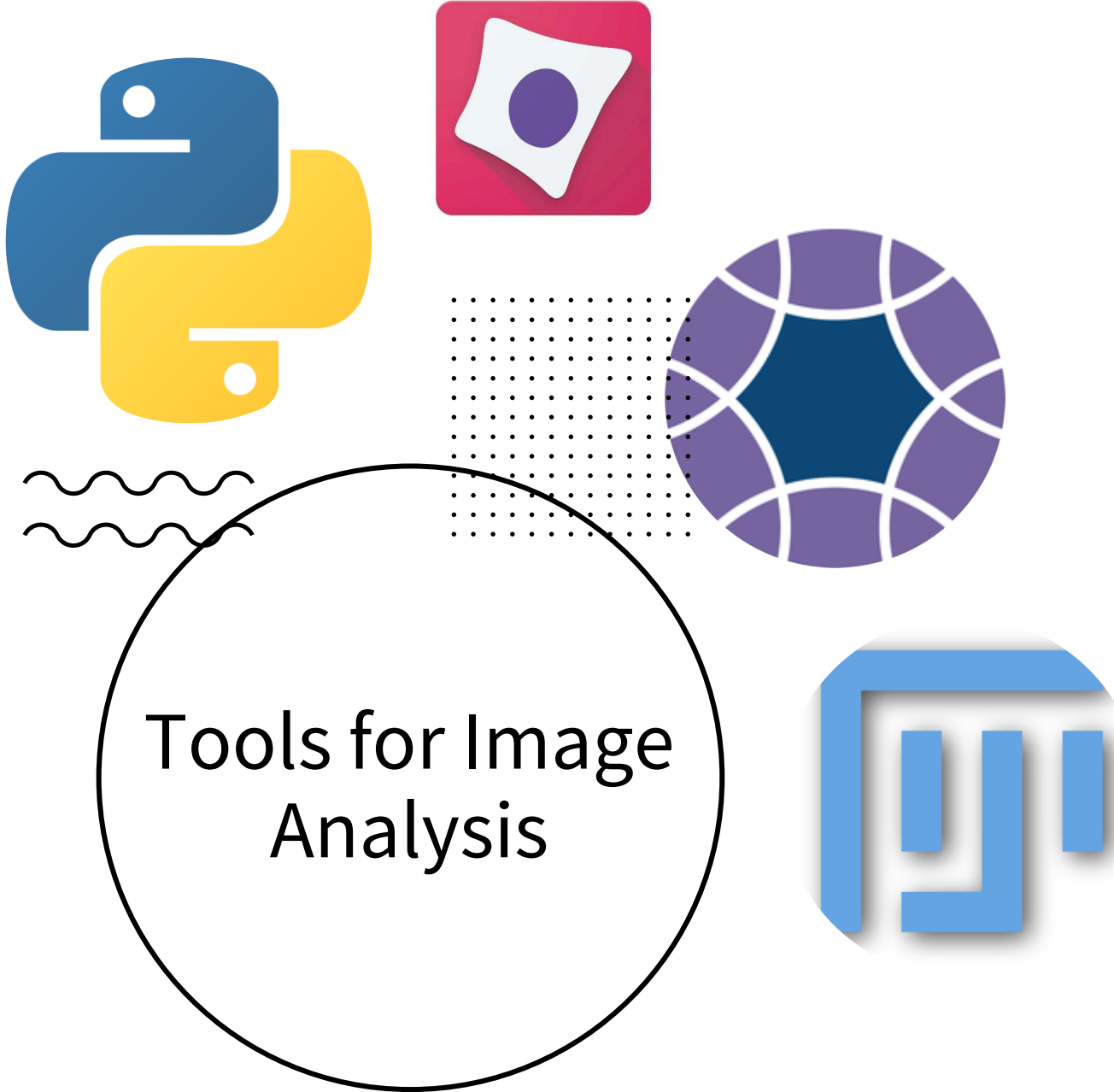
- You have your images, now what?
 - Count cells/particles
 - Segment cells, tissue, etc.
 - Fluorescent area / cell area ratio
 - Comparing fluorescent signal between samples/cells
 - Track cells/organism through time series
 - Changes in morphology

...Doing this by hand is a pain...



Download from [img](#)



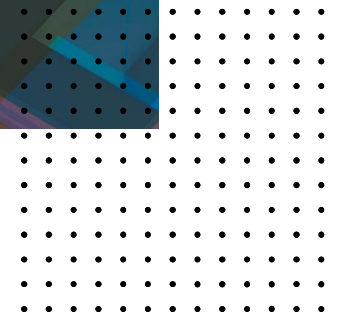
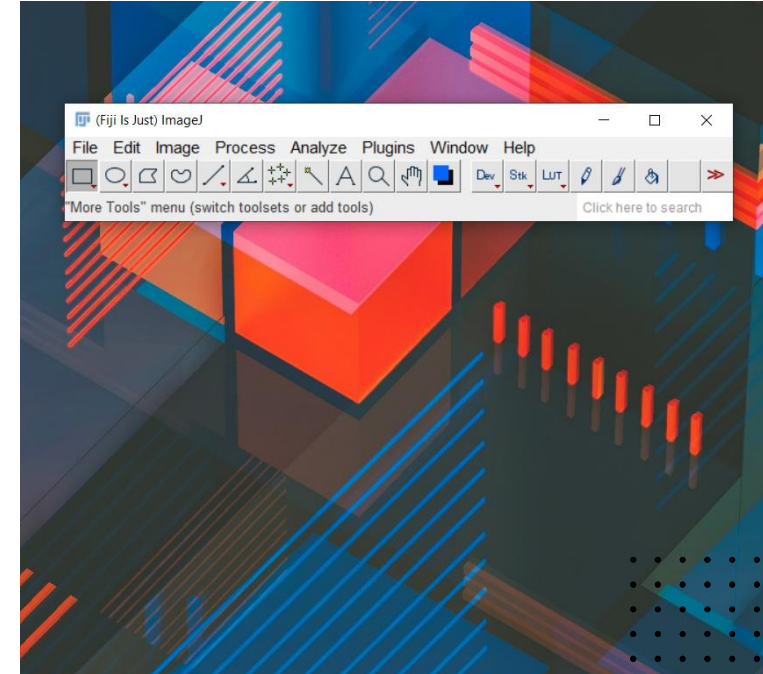
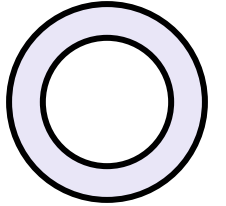
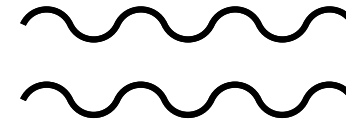


- FIJI
- CellProfiler
- AICS Segmenter
- Custom code...

FIJI (FIJI Is Just ImageJ)

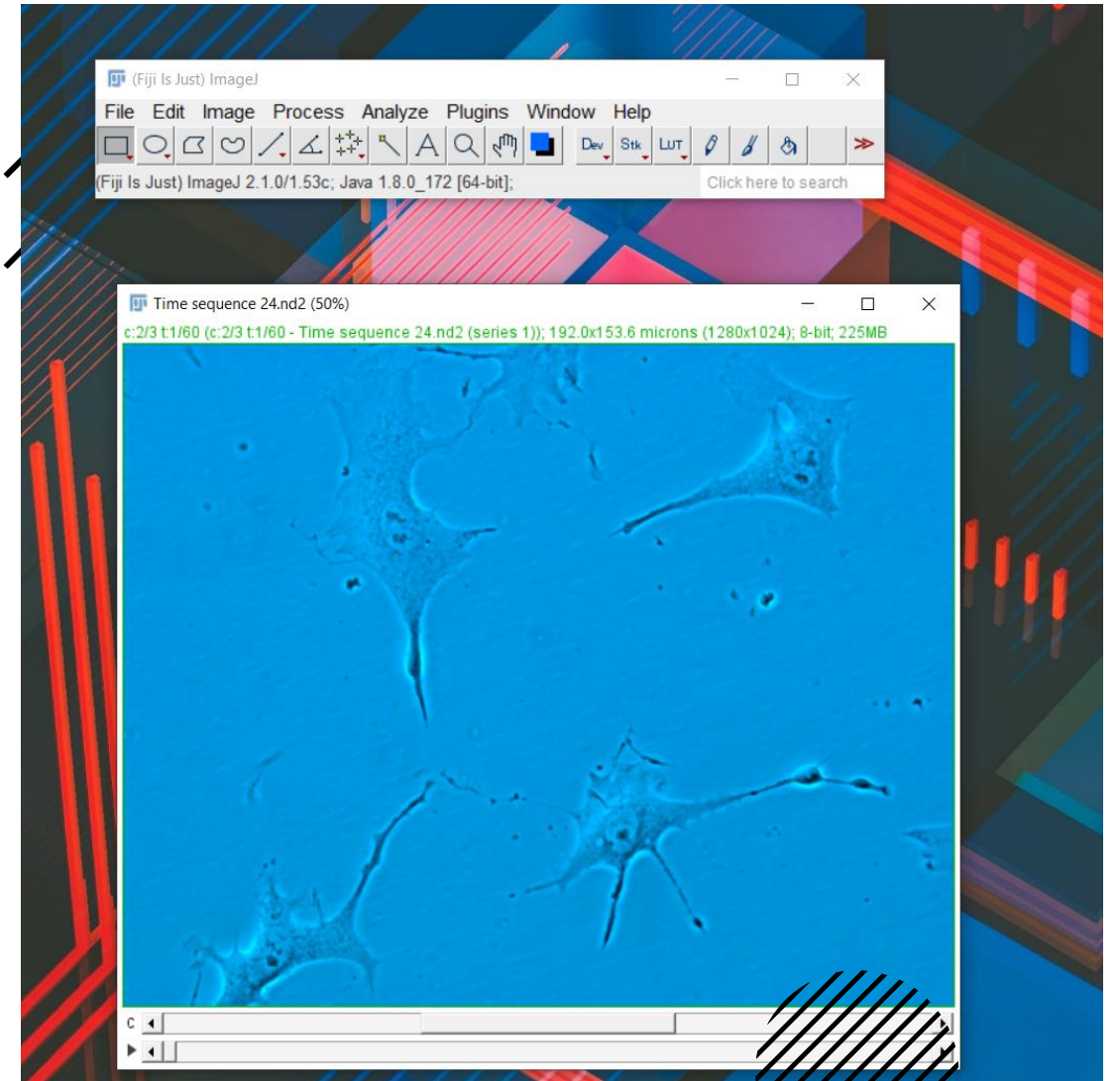
Starts with just a nifty toolbar

- Crop image
- Adjust brightness/contrast
- Annotate image
- The real power is in the menu items



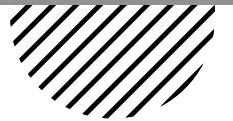
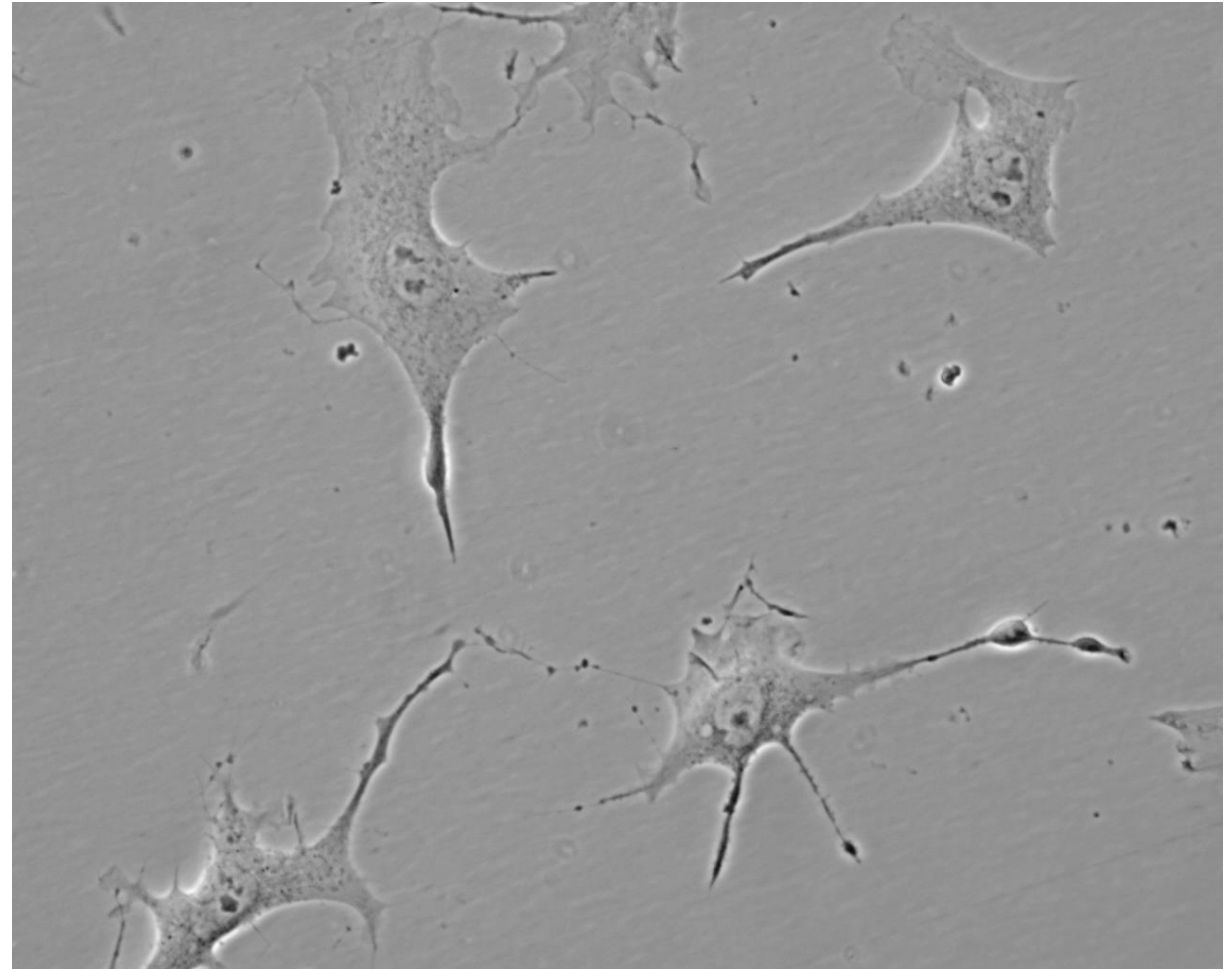
FIJI

- Open any type of image or microscopy file
- Creates “Hyperstacks” for images taken at multiple positions, z-slices, channels, and time series
- Export to make cool figures!



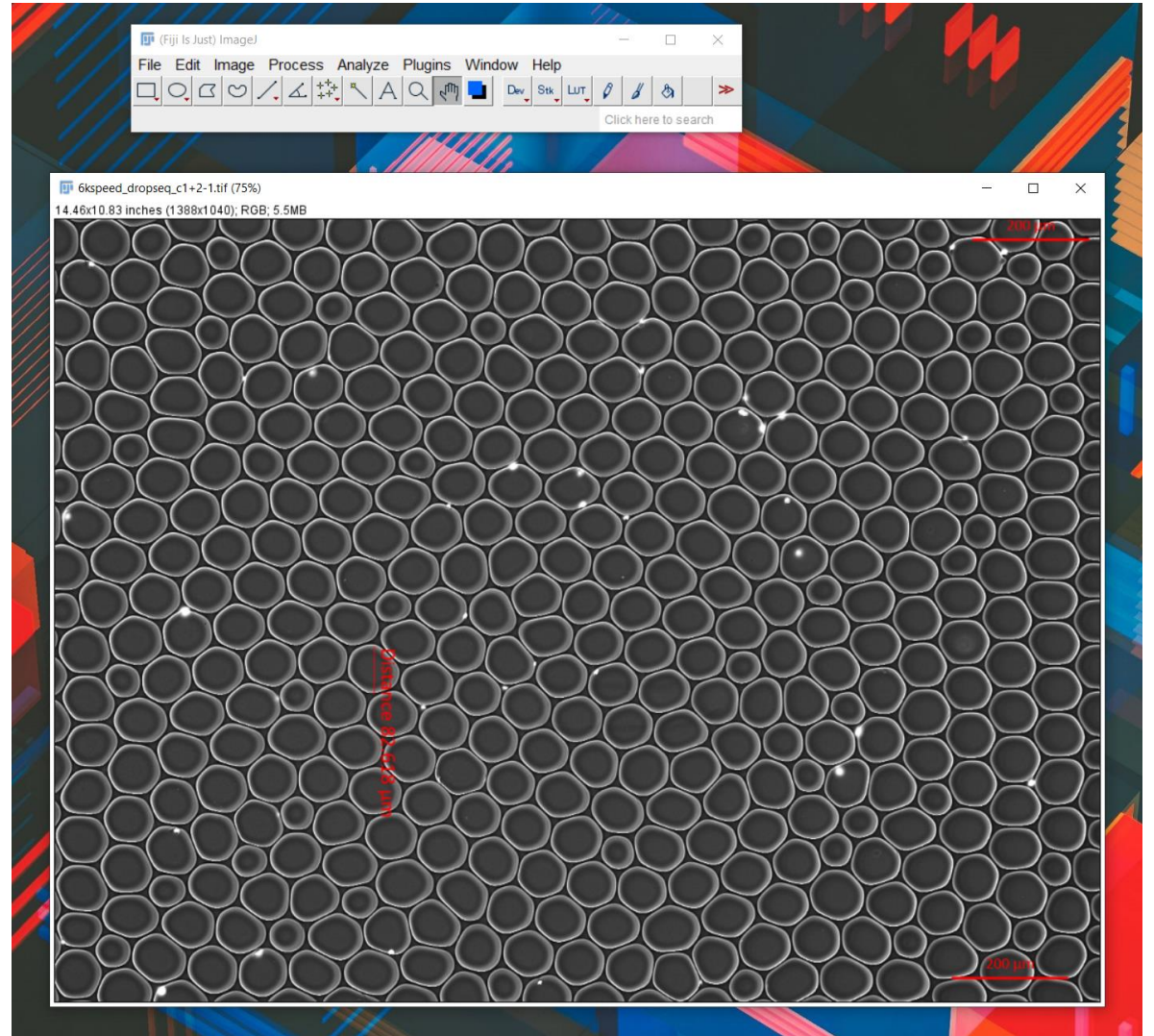
FIJI

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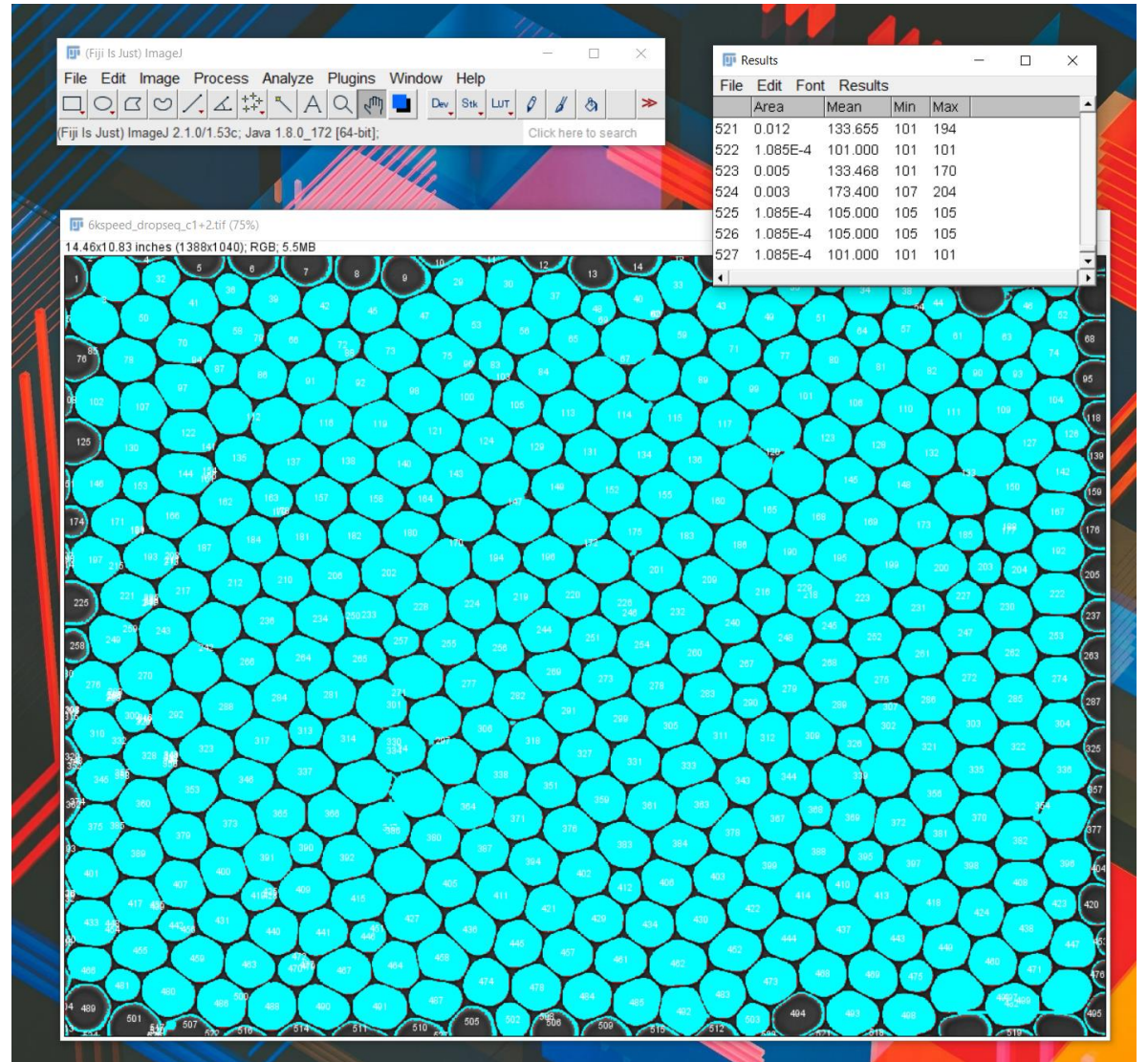
FIJI

- Automate counting features



FIJI

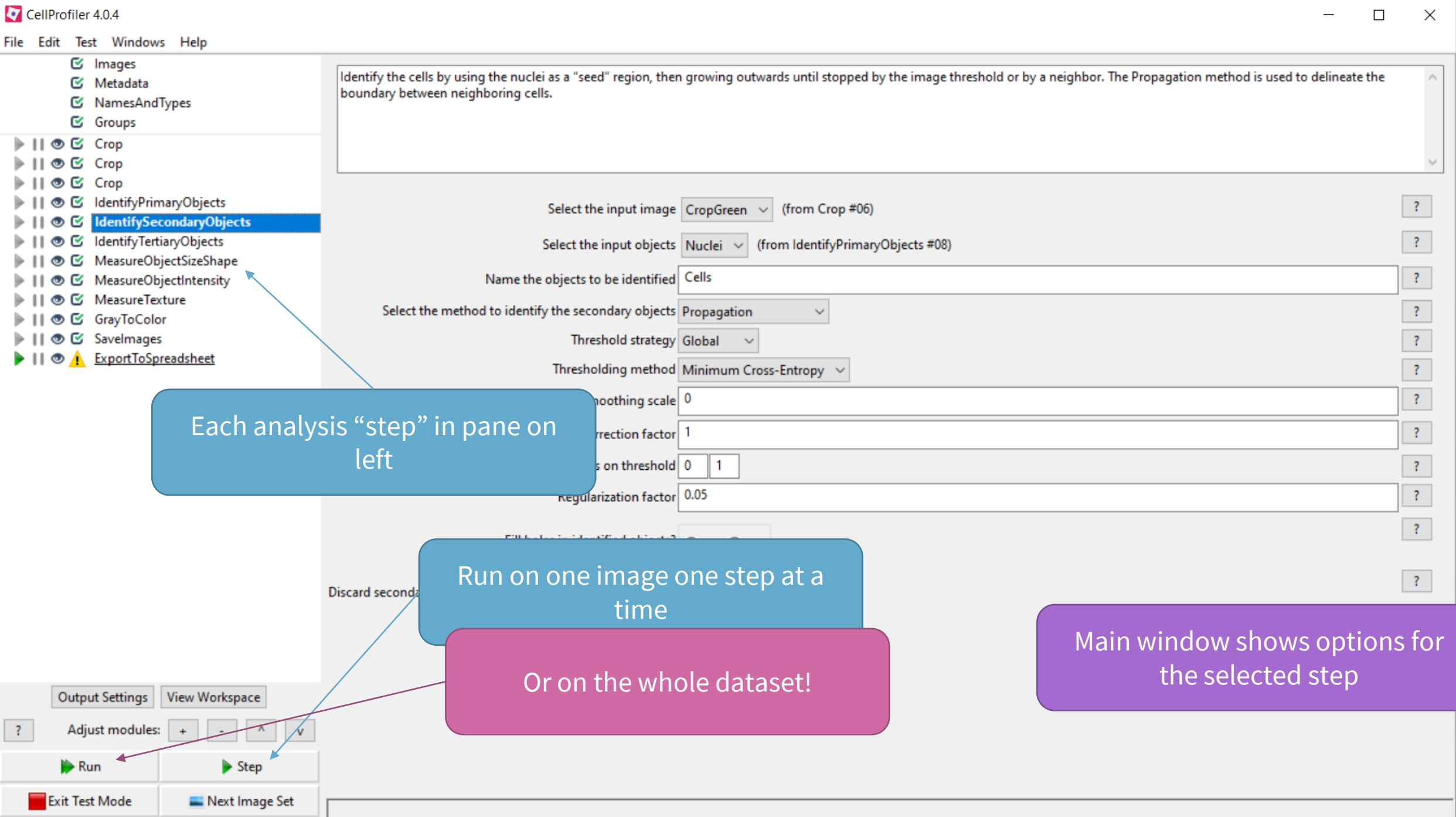
- Automate counting features
- You can also “record” yourself do an analysis and save it as a macro to apply to a whole folder of images!
- Export results into an excel file

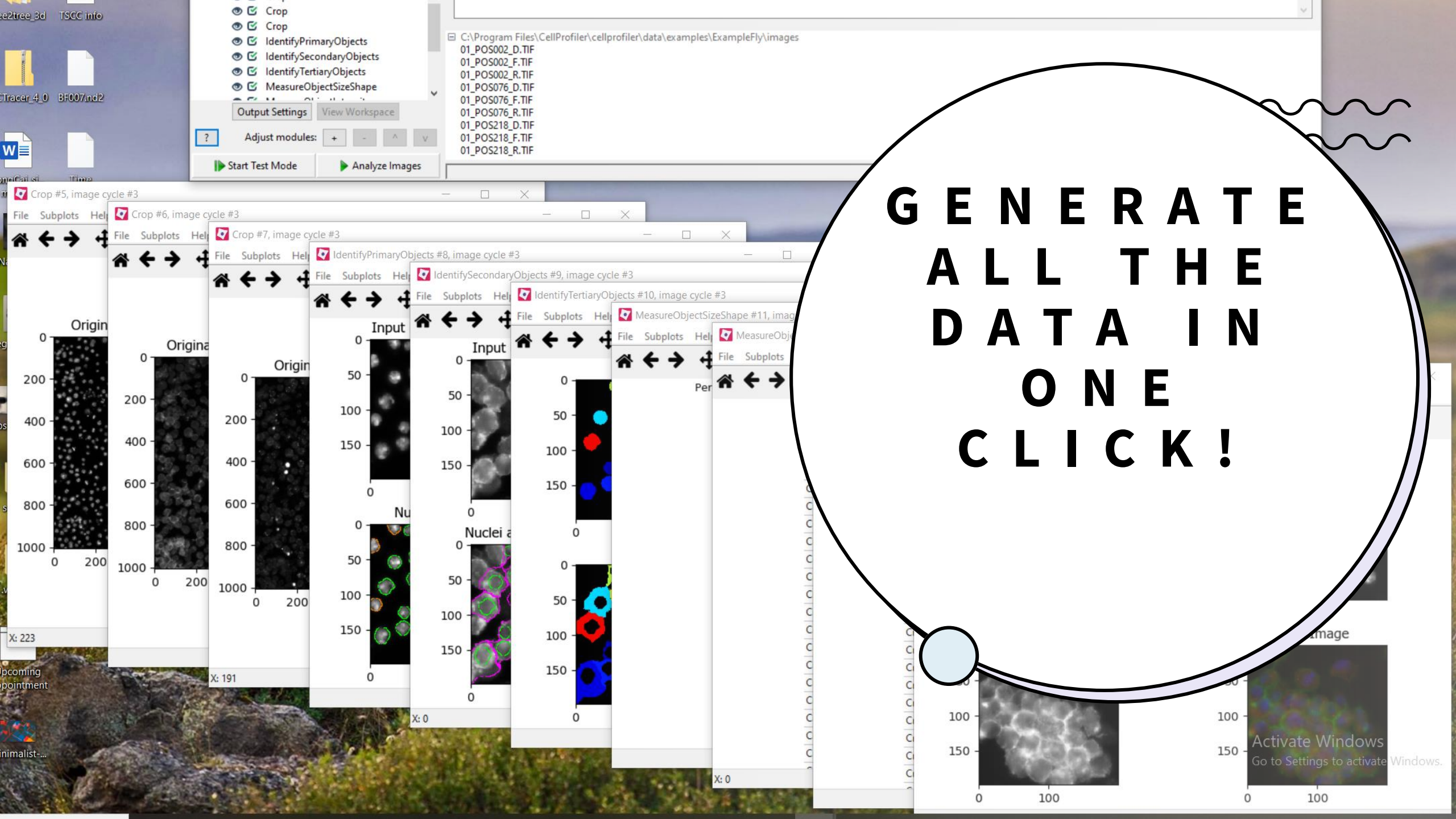


○ CellProfiler

- An easy to use free software tool to build an analysis pipeline
- Apply the pipeline to thousands of images and export data in any format you want
- Hundreds of different types of analyses available from simple (co-localization) to advanced (deep learning)
- About as easy to use as FIJI but much more powerful



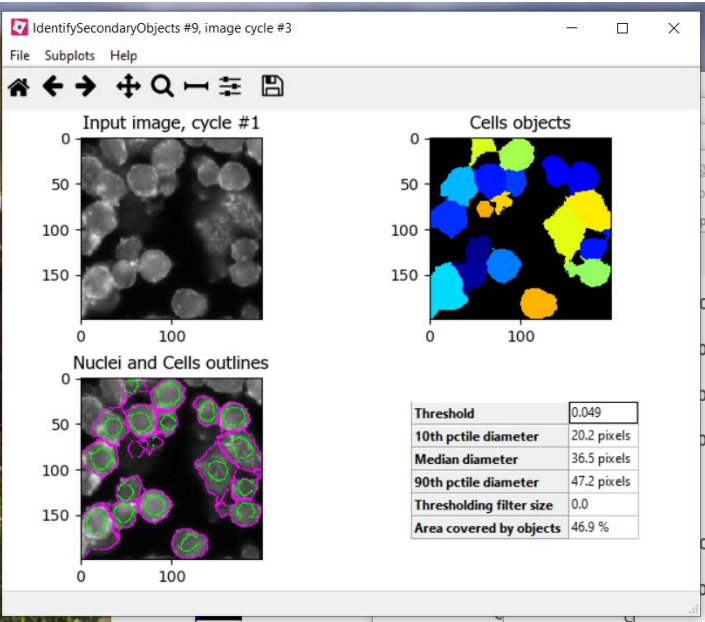
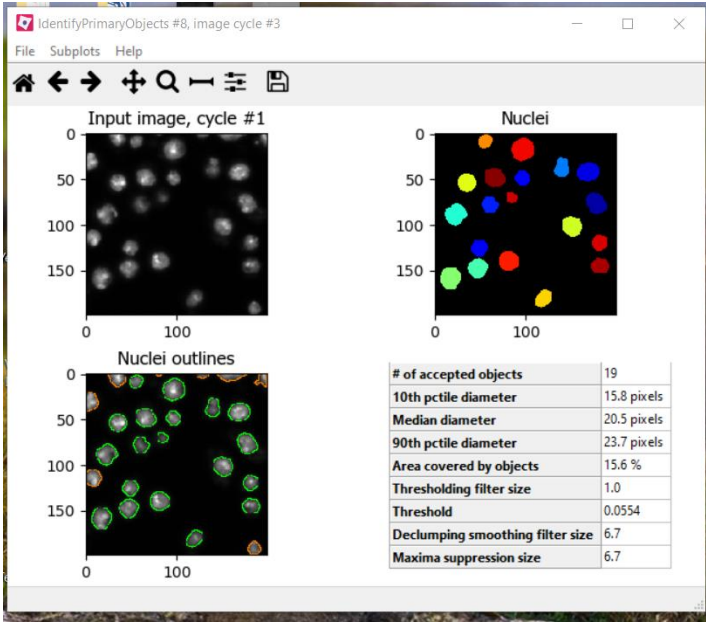
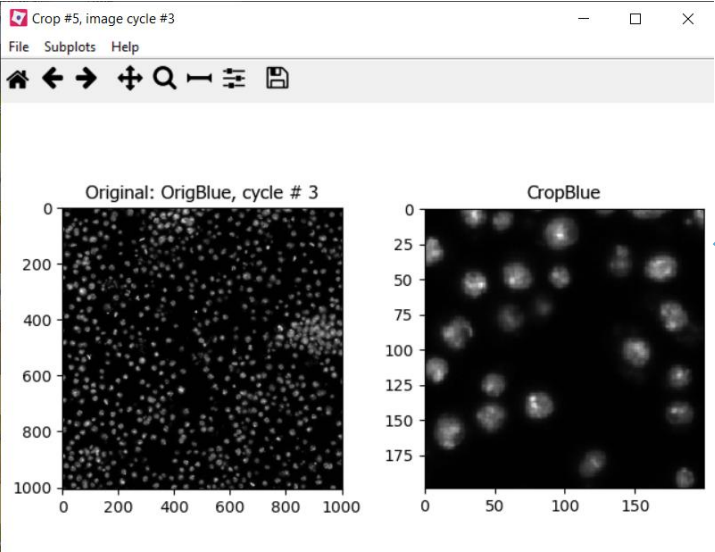




**GENERATE
ALL THE
DATA IN
ONE
CLICK!**

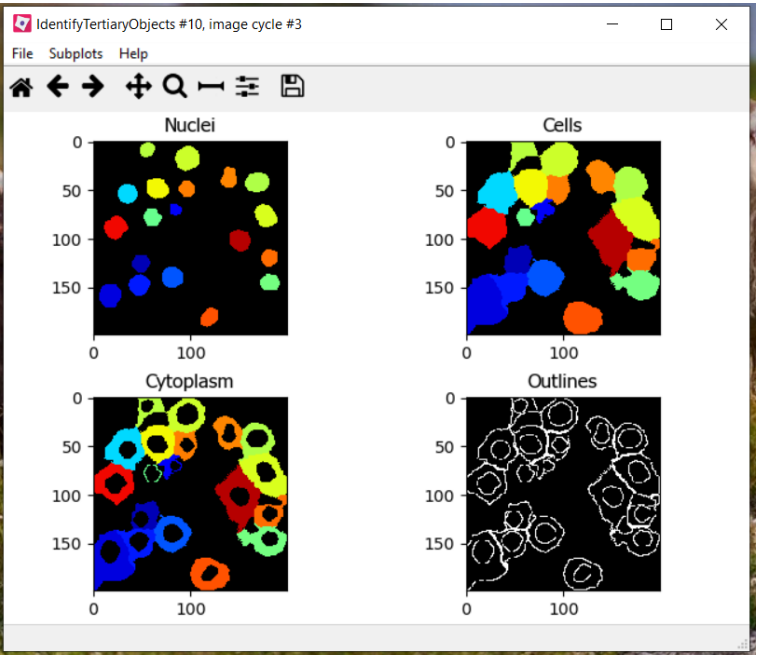


1. Original Green and Blue channel images



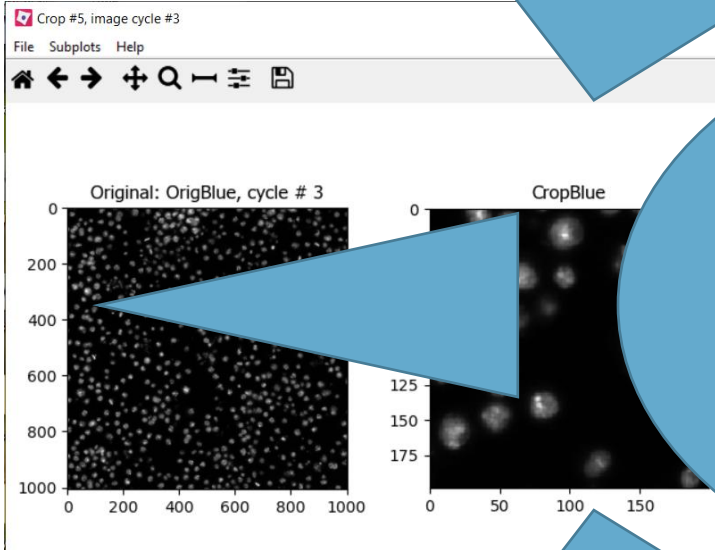
2. Segment nuclei and cells

3. Subtract and get Cytoplasm area and cell outlines!





1. Original Green and Blue channel images

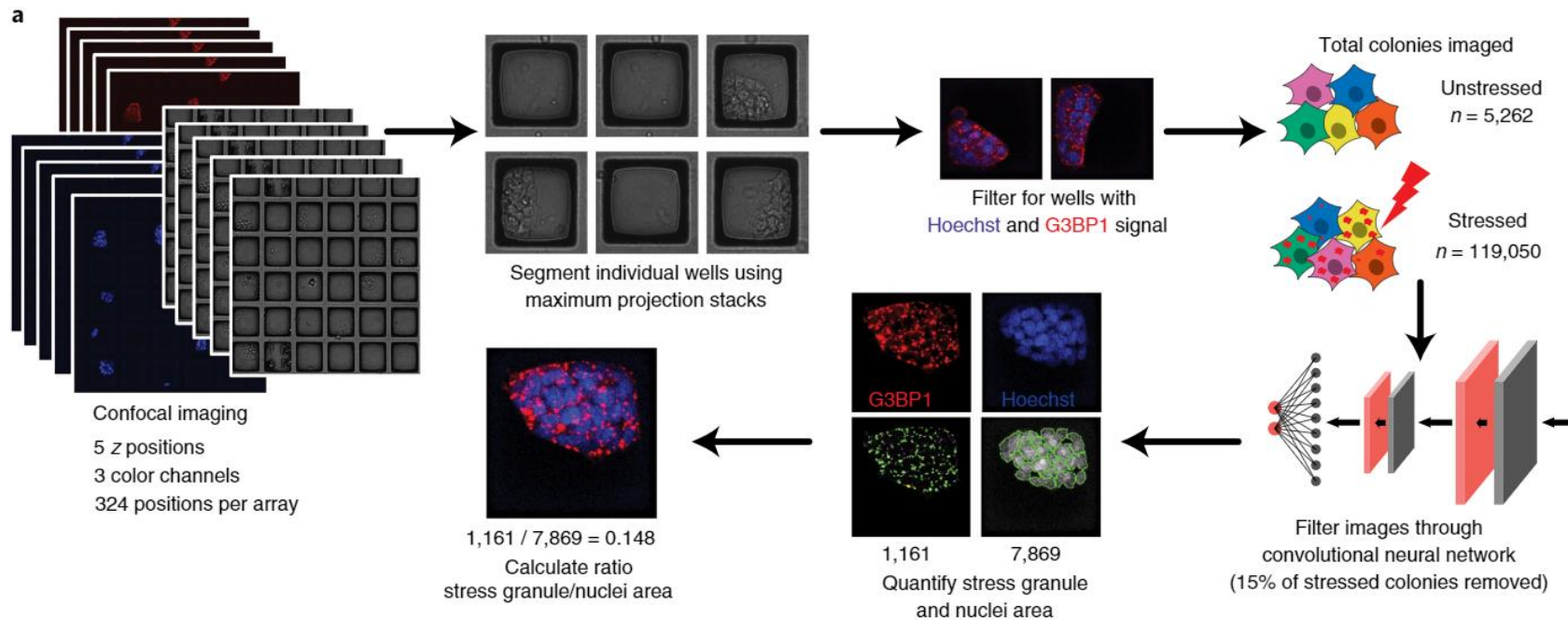


And not a line of code was needed!

3. Subtract and get Cytoplasm area and cell outlines!



CellProfiler – A case study

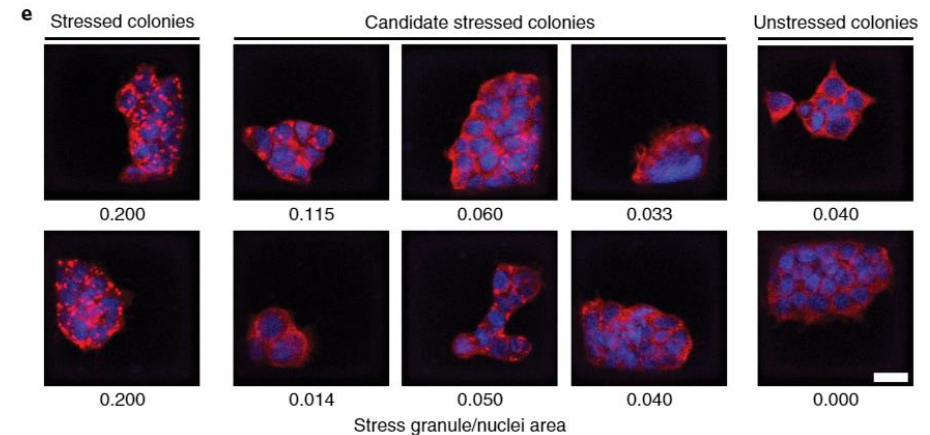
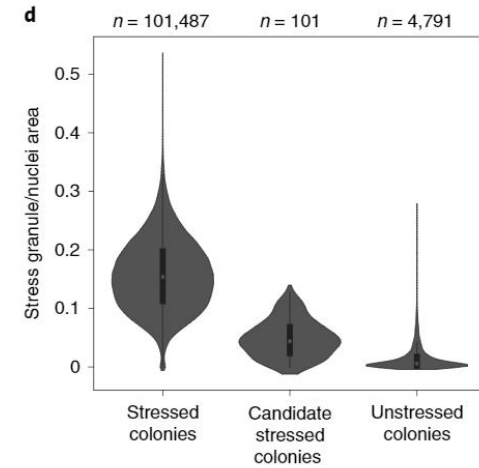
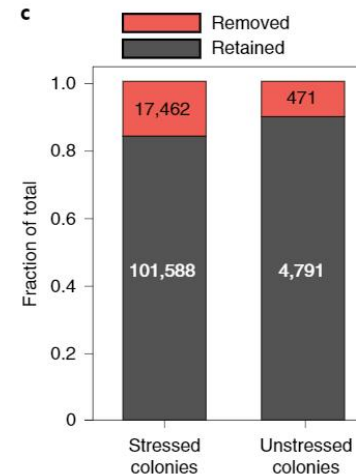
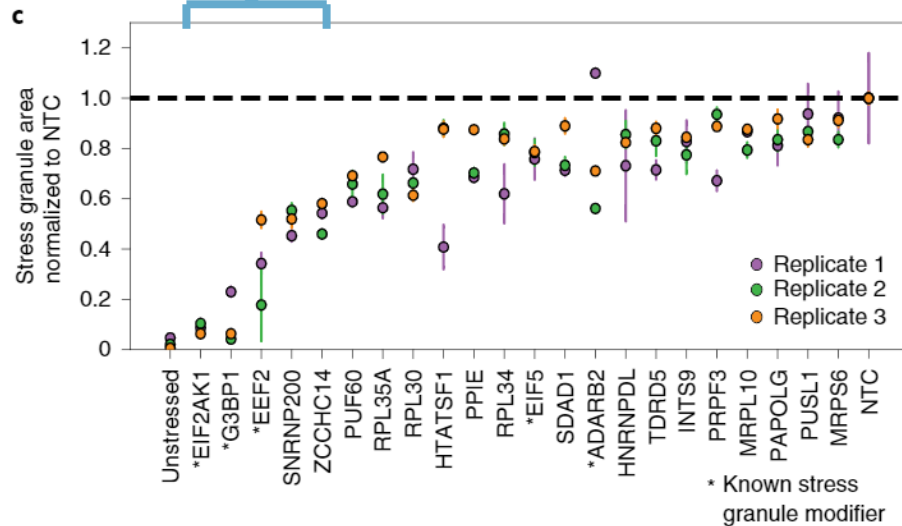


- 100k+ images
- Segment each well
- Quality control the image
- Stress granule area (G3BP1) / DAPI area ratio
- Look for wells with cells with very low ratio
- Sequence cells to find gene knockdown



CellProfiler – A case study

CellProfiler can help find the
needle in the haystack!

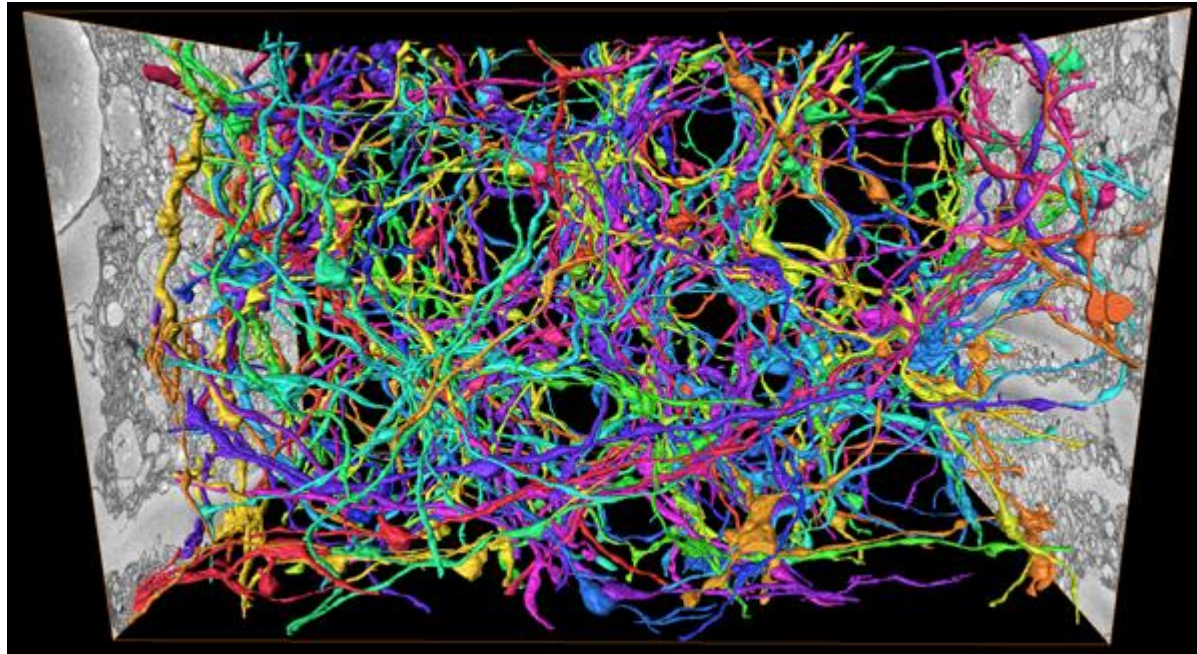


○ Image Analysis wizardry in Python

- Highly custom pipelines using libraries used across disciplines for image analysis
 - Scikit-image
 - OpenCV
 - Numpy (because images are just matrices after all...)
 - PyTorch/Tensorflow (for machine learning)
- Apply analysis on terabytes of data on supercomputing cluster (TSCC, AWS, etc.)



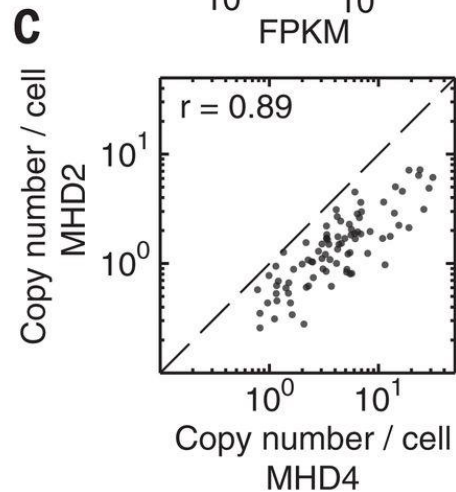
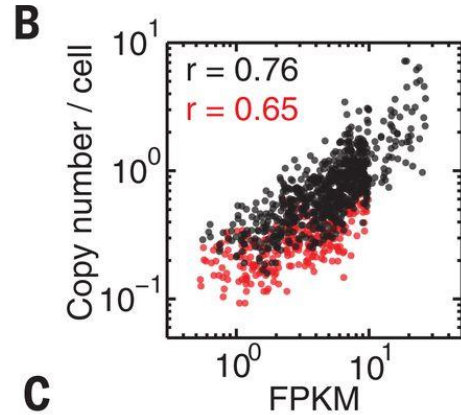
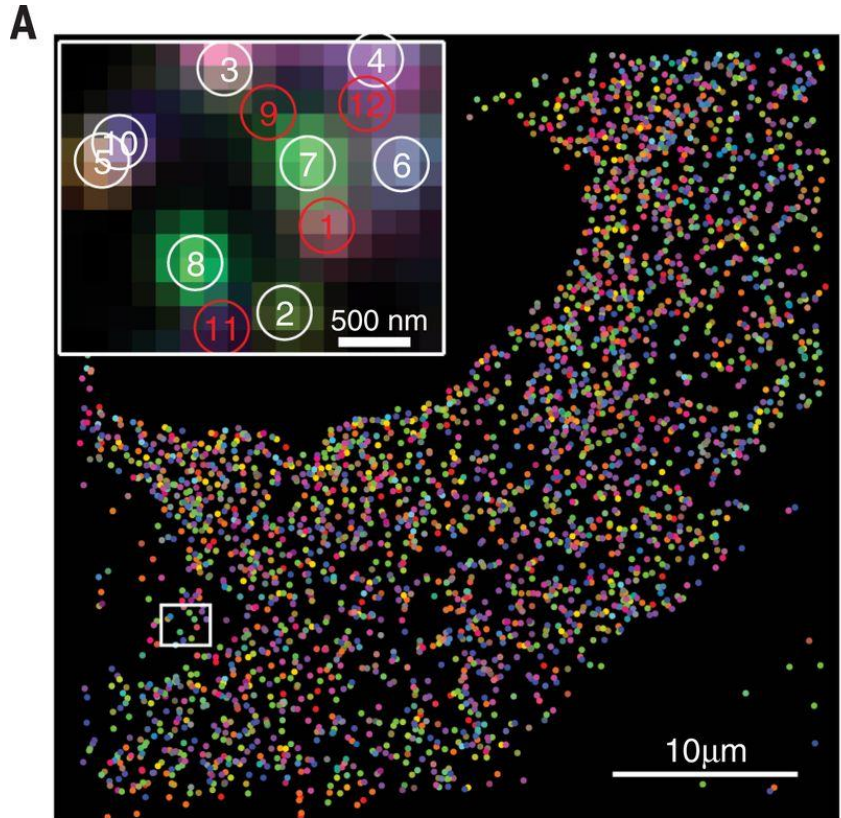
○ What is image analysis with code used for?



- Connectomics reconstruction (neurons)



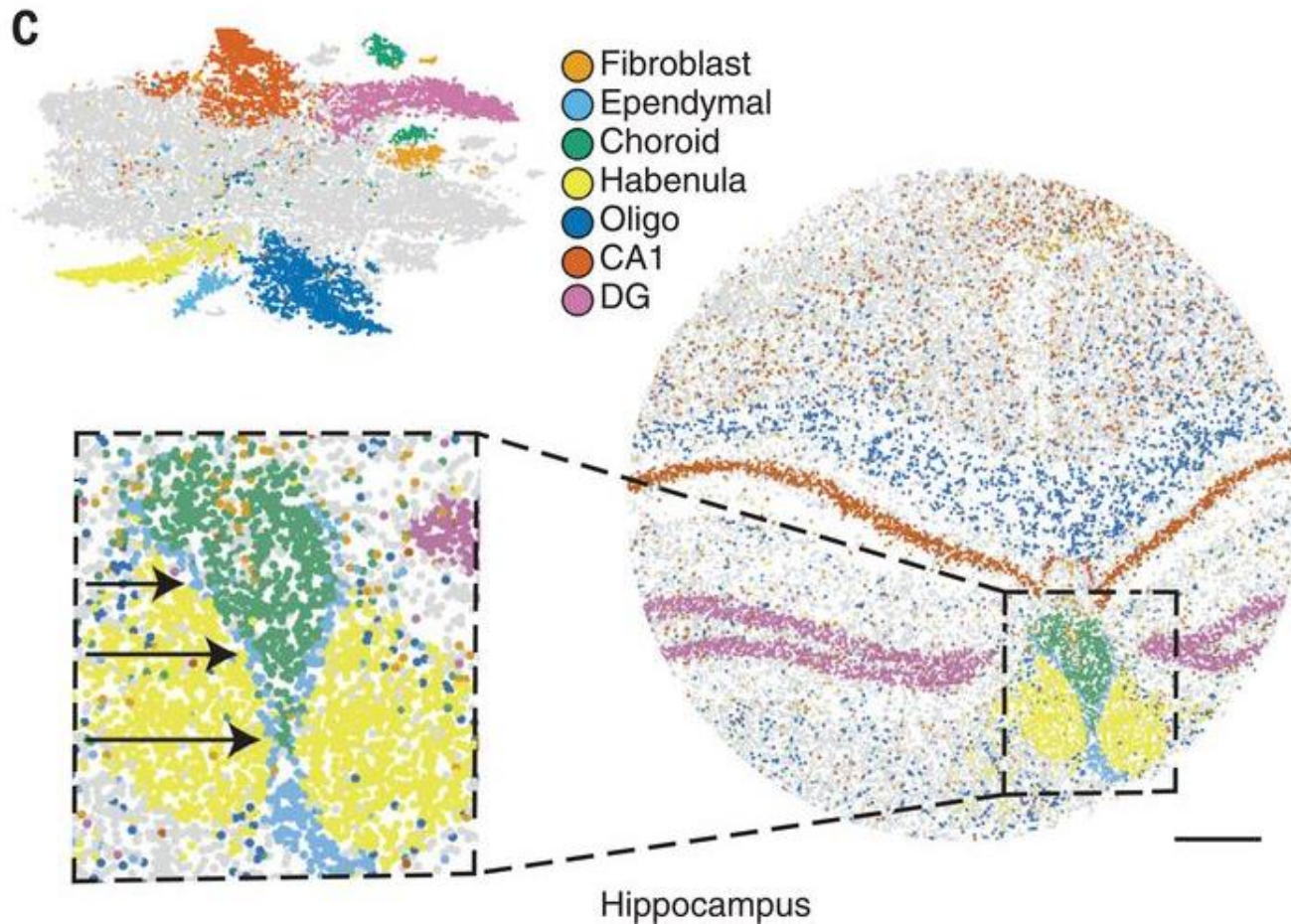
○ What is image analysis with code used for?



- Connectomics reconstruction (neurons)
- Single molecule detection



○ What is image analysis with code used for?



- Connectomics reconstruction (neurons)
- Single molecule detection
- Combine single-cell sequencing with imaging



AICS Segmenter

- Has very easy to use functions to segment features in confocal images
- Run inside of a Jupyter Notebook
- Nifty functions to visualize in 3D
- <https://www.allencell.org/3d-cell-viewer.html>

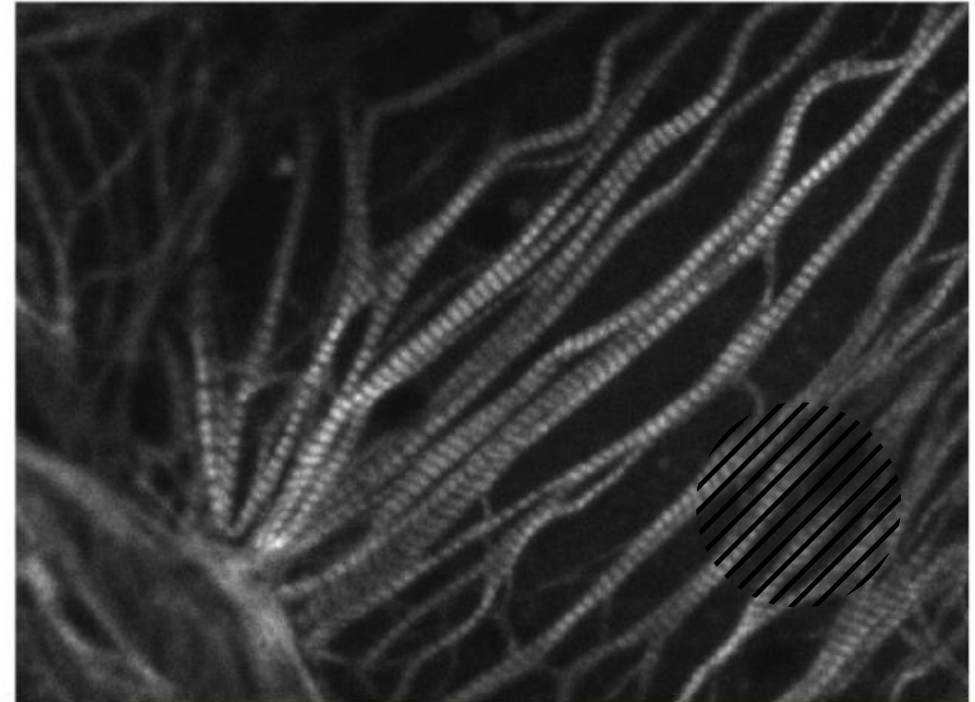
```
7 plt.rcParams["figure.figsize"] = [12, 8]  
  
ModuleNotFoundError: No module named 'aicssegmentation'
```

Loading the data

```
In [4]: FILE_NAME = '../demo_data/TNNI1_demo_data.tif'  
reader = AICSImage(FILE_NAME)  
IMG = reader.data  
  
print(IMG.shape)  
  
(1, 1, 60, 441, 555)
```

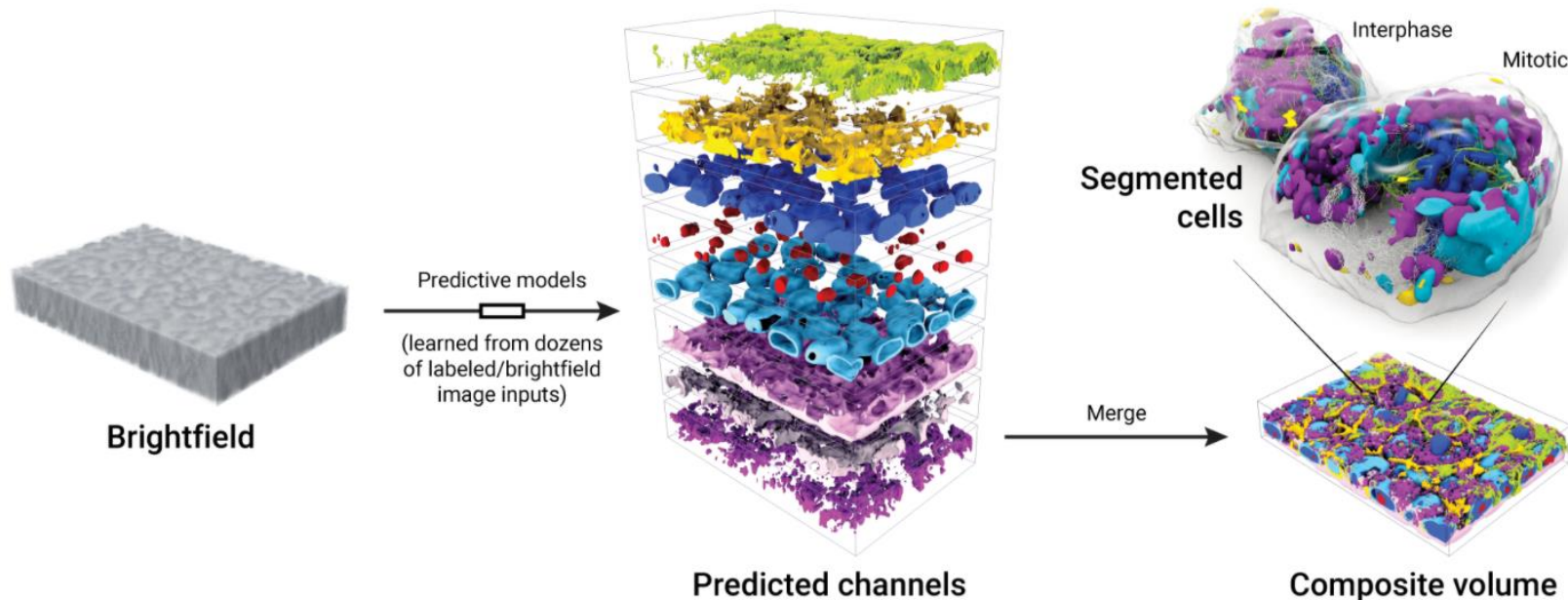
Preview of the image

```
In [3]: N_CHANNELS = IMG.shape[1]  
MID_SLICE = np.int(0.5*IMG.shape[2])  
  
fig, ax = plt.subplots(1, N_CHANNELS, figsize=(18,16), dpi=72, facecolor='w', edgecolor='k')  
if N_CHANNELS==1:  
    ax.axis('off')  
    ax.imshow(IMG[0,0,MID_SLICE,:], cmap=plt.cm.gray)  
else:  
    for channel in range(N_CHANNELS):  
        ax[channel].axis('off')  
        ax[channel].imshow(IMG[0,channel,MID_SLICE,:], cmap=plt.cm.gray)
```



Label-free “staining”

- Classically: limited in number of stains you can image
- Now: Image brightfield → predict all the other stains
- <https://www.allencell.org/label-free-determination.html>





Summary

- For your own sake, please don't do image analysis by hand
- You can do really simple analyses with almost no learning curve (FIJI)
- You can do really advanced high-throughput analysis with no coding! (CellProfiler)
- Using python for image analysis, you can defy the limitations imposed by the laws of physics!!

