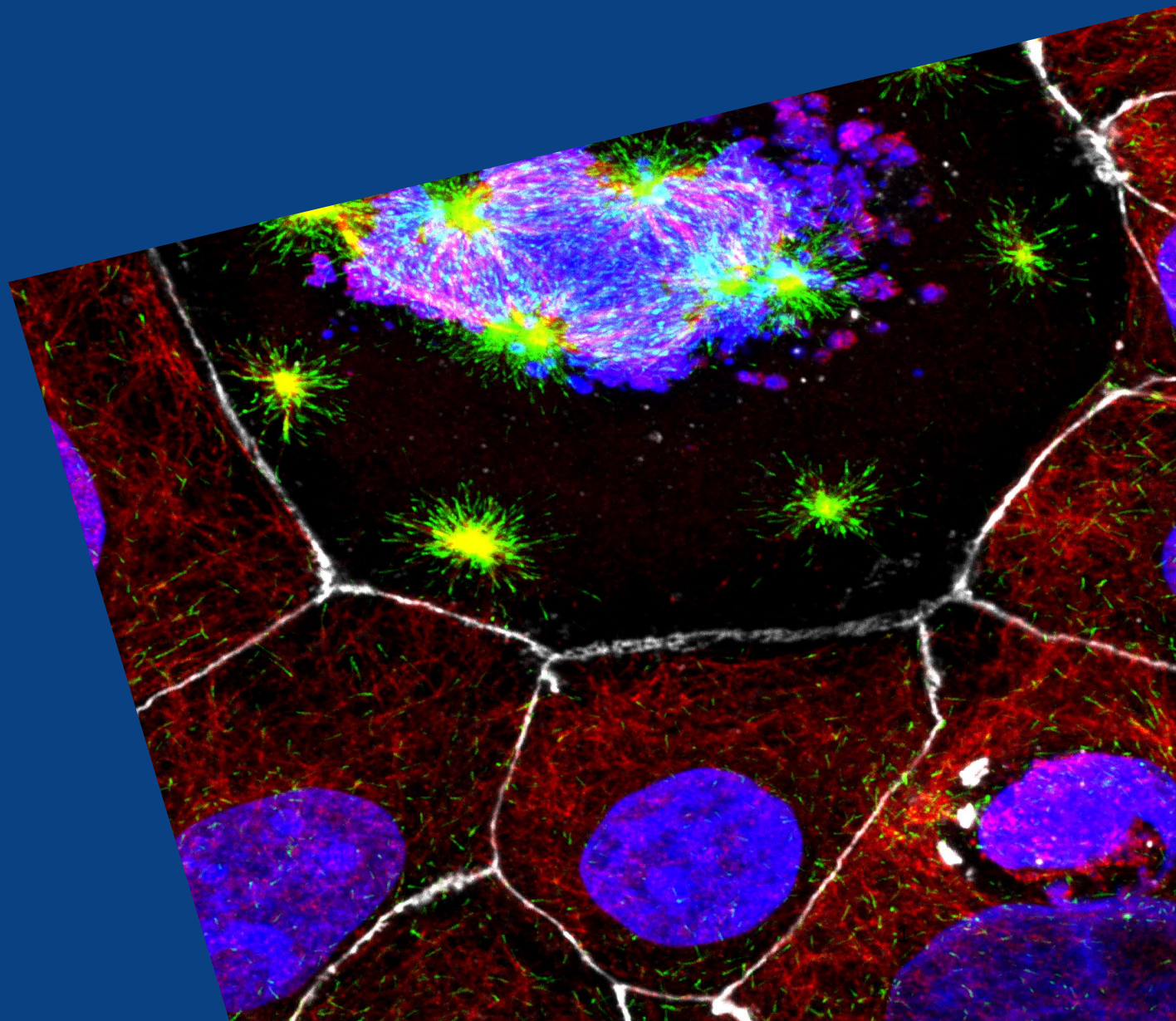
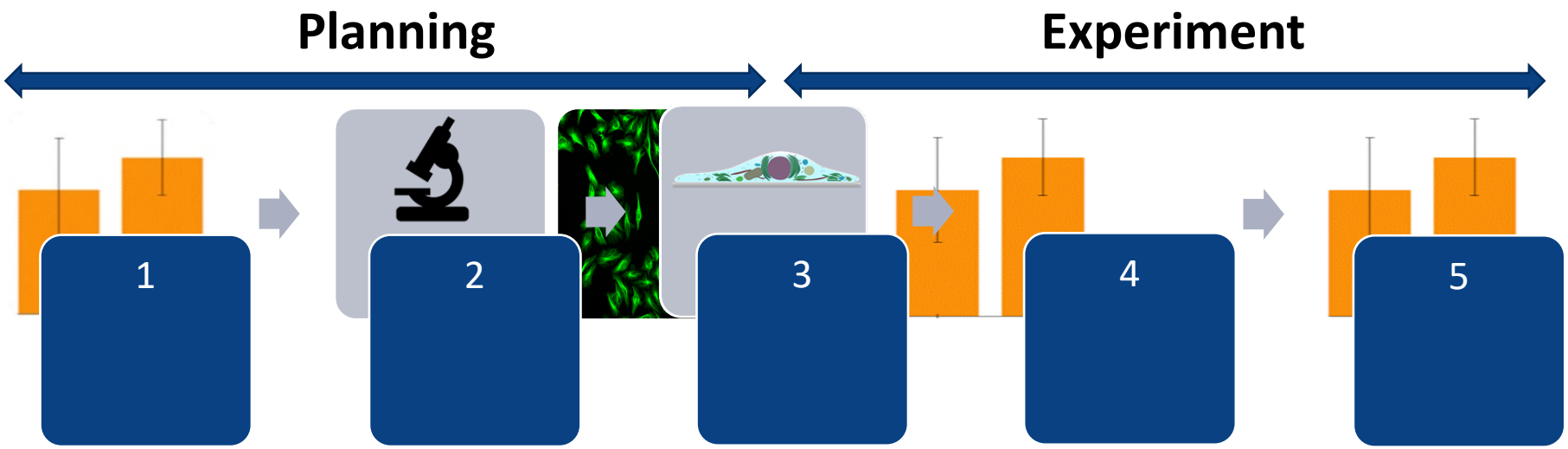
THE UNIVERSITY OF MELBOURNE

Introduction to Bioimage Analysis



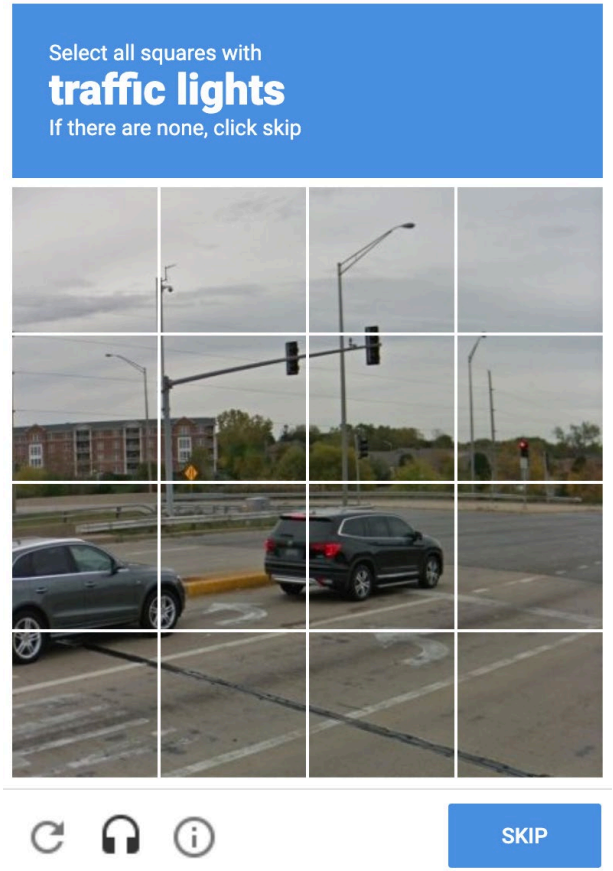
Dr Ellie Cho & Dr Shane Doris Cheung
Application Specialists
Biological Optical Microscopy Platform

Part 1. An Overview of BioImage Analysis



What is an object?

What is trivial for a human can be very difficult for a computer:

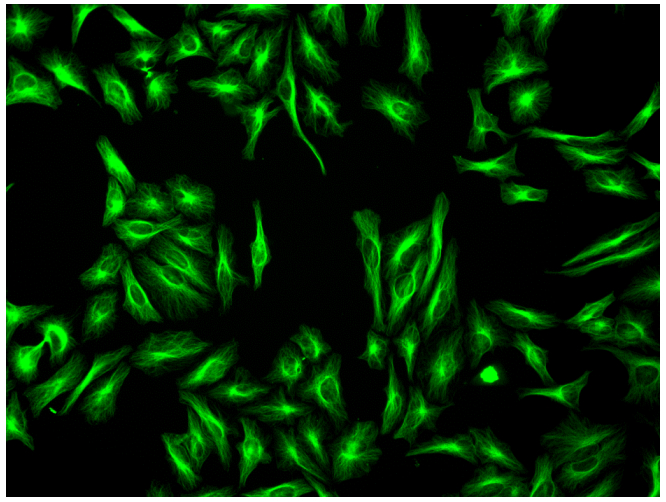


Bioimage Analysis

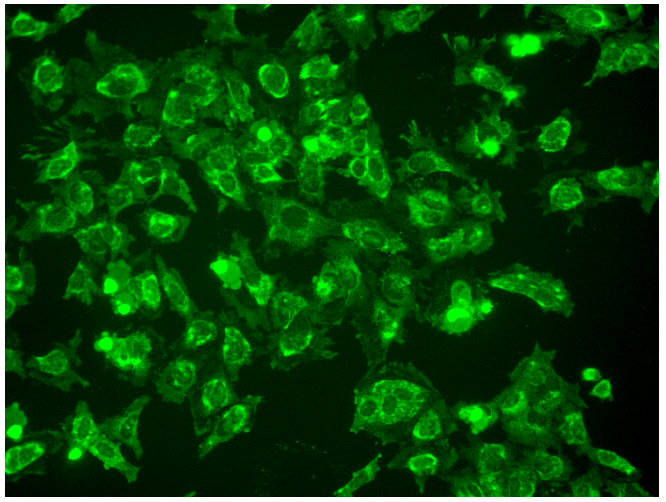
Goal:

Obtaining quantifiable information from microscopy images of biological sample

Control



Treated



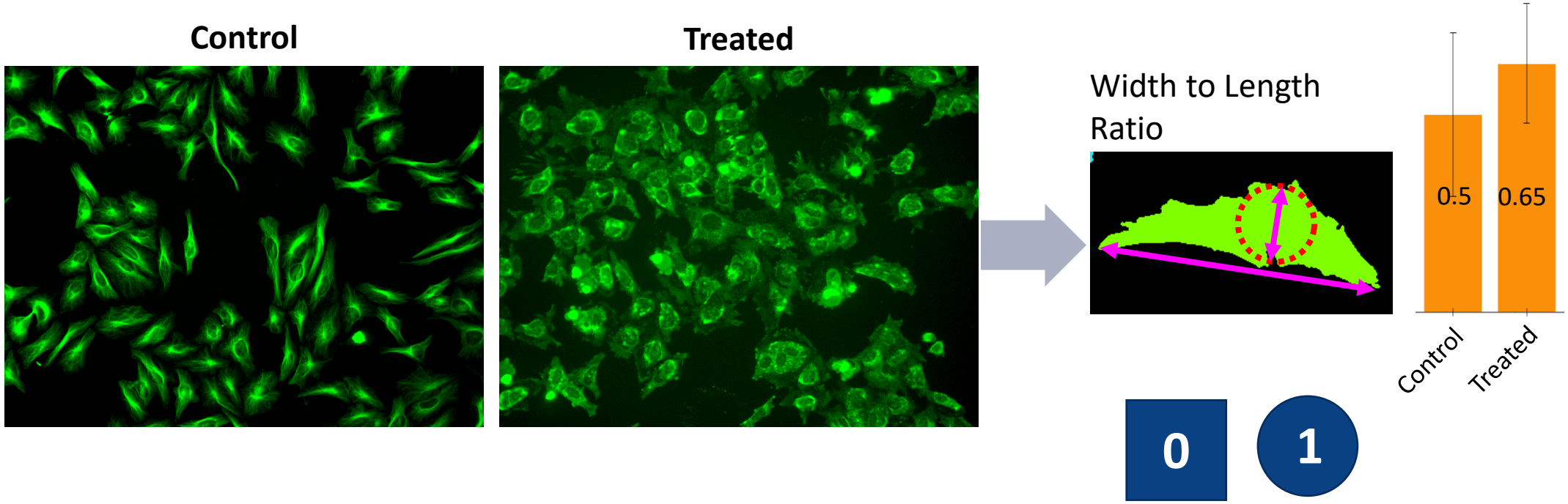
In the treated group, cell looks ‘rounder“…

But how much?

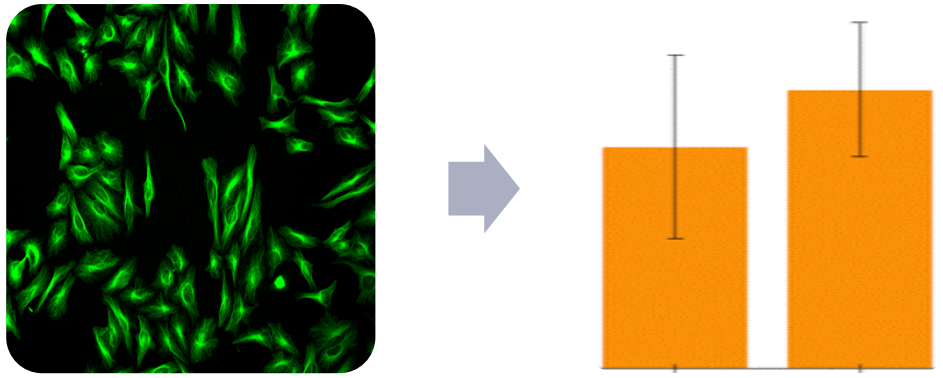
Bioimage Analysis

Goal:

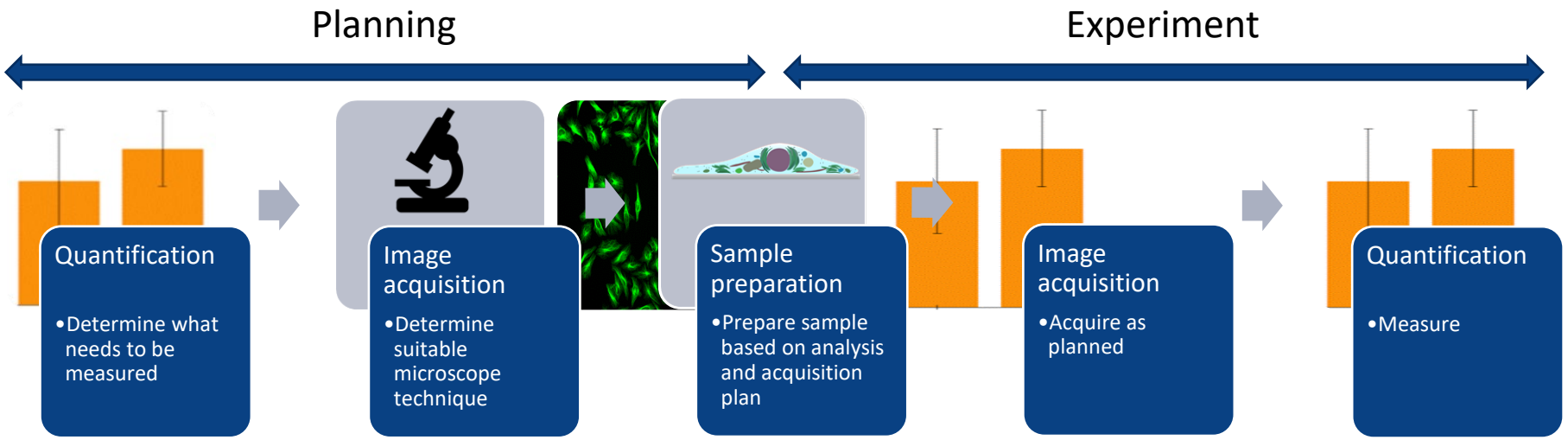
Obtaining quantifiable information from microscopy image of biological sample



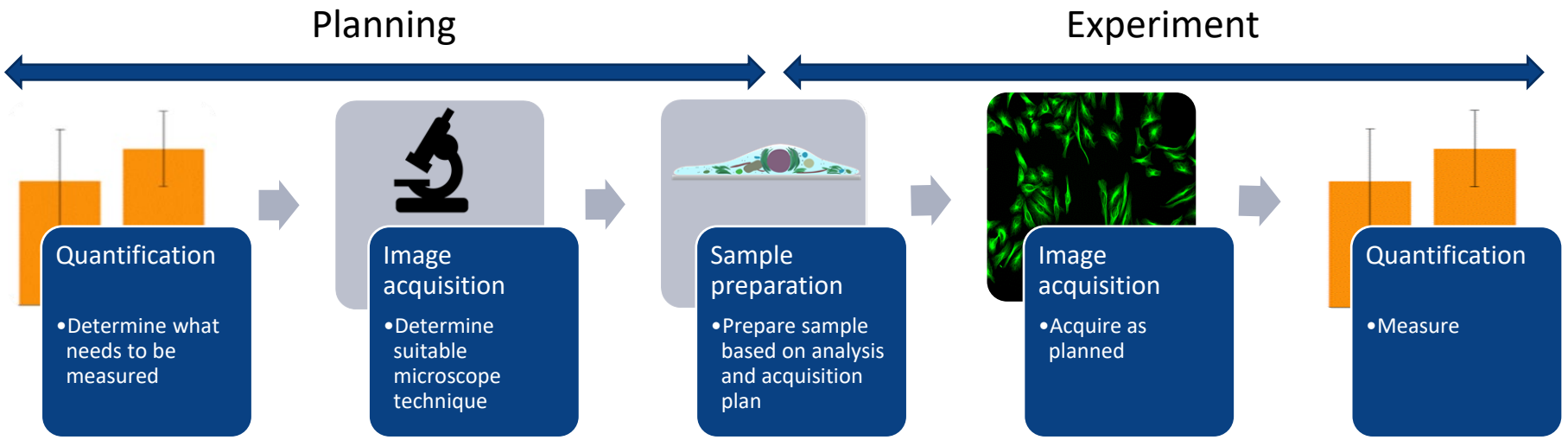
Planning for Bioimage Analysis



Planning for Bioimage Analysis



Planning for Bioimage Analysis

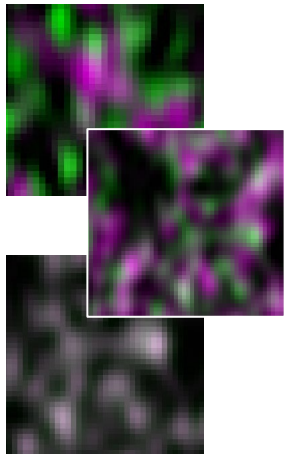


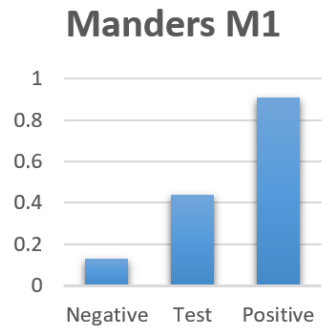
Colocalisation of 2 proteins in mitochondria

Super-resolution to resolve inner & outer membrane of mitochondria

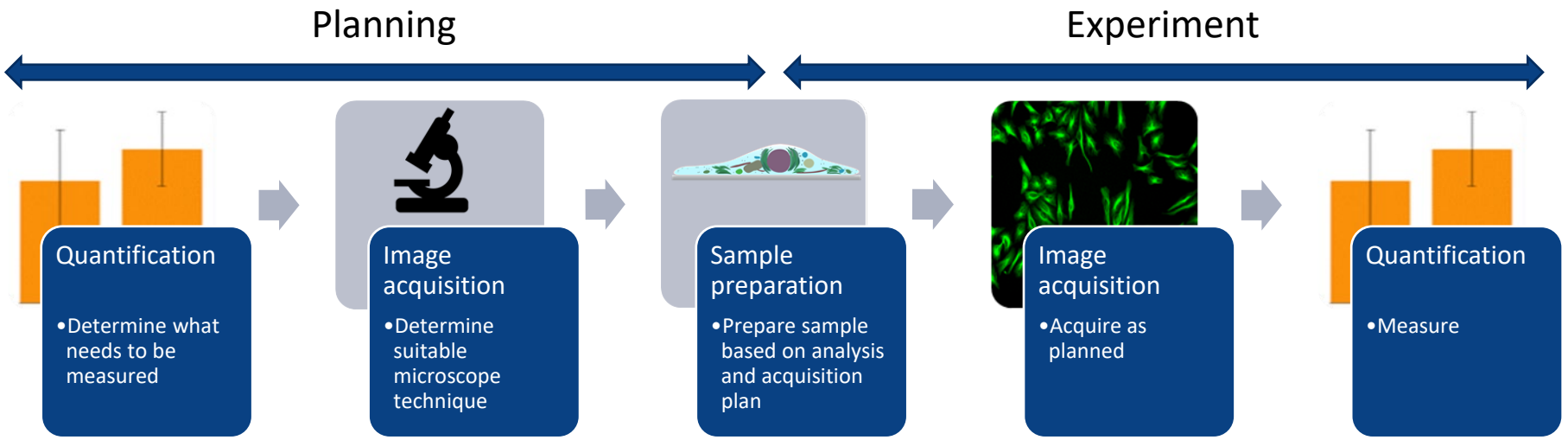
Monolayer cell culture on coverslip

- Negative control
- Positive control
- Test sample





Planning for Bioimage Analysis



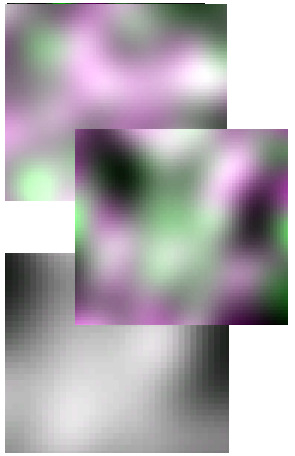
Colocalisation of 2 proteins in mitochondria

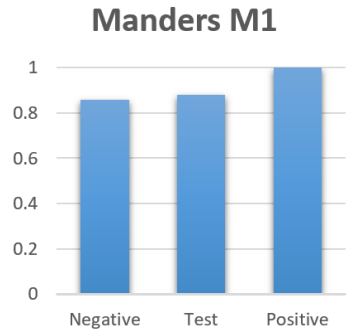
Super-resolu… to resolve in… outer …brane of mit… ndria

Low-resolution?

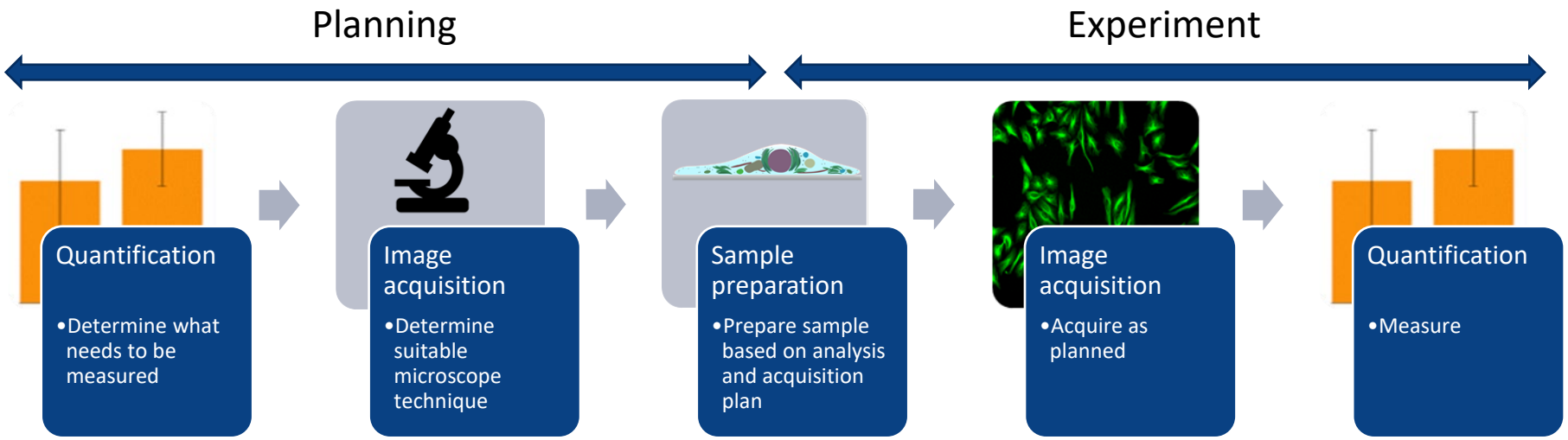
Monolayer cell culture on coverslip

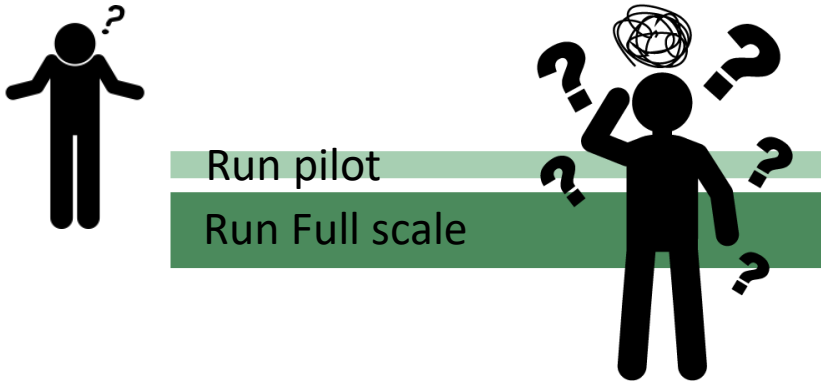
- Negative control
- Positive control
- Test sample





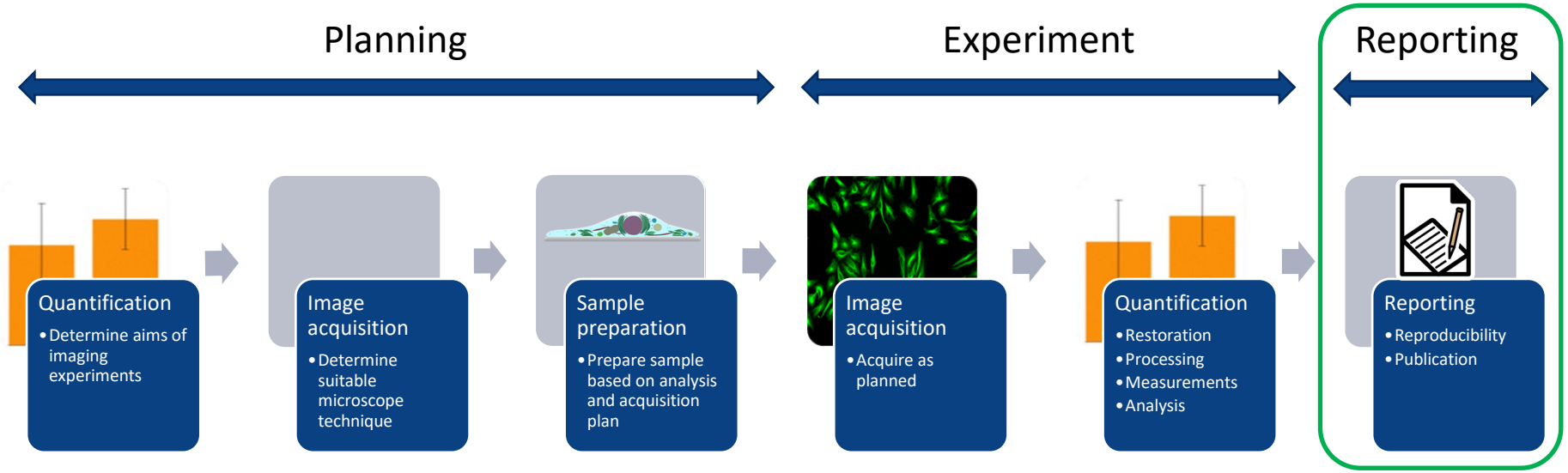
Planning for Bioimage Analysis



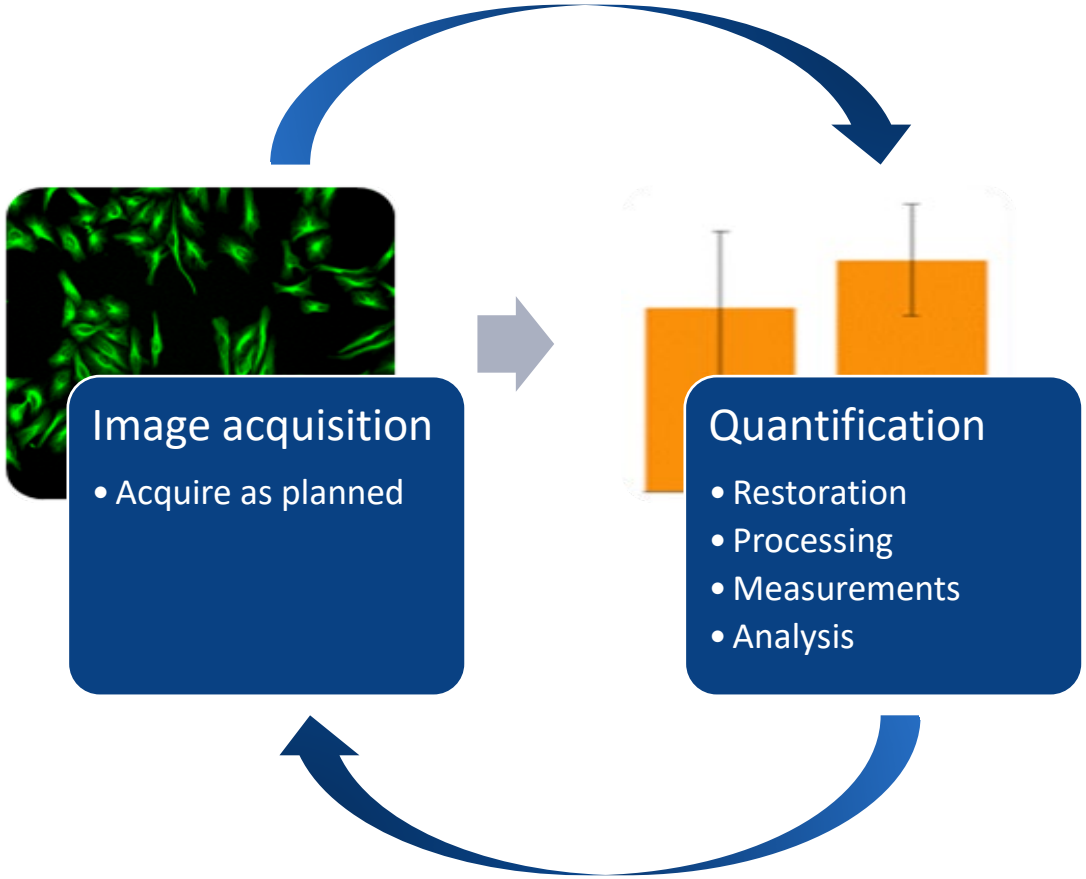


Consult with us
Biological Optical Microscopy Platform
bomp-enquiries@unimelb.edu.au

Planning for Bioimage Analysis



Planning for Bioimage Analysis



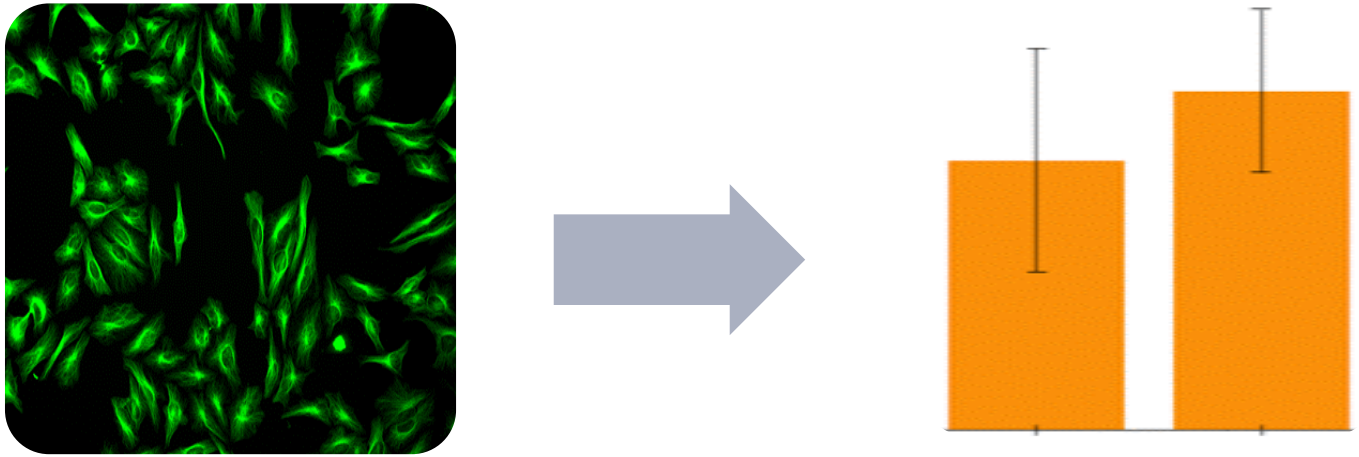
Do not image all of your samples and THEN
Try to do all of the analysis!

The quality images maybe not be sufficient!

Bin or reimage!

Image Analysis Workflow

How do we get from images to graphs…?



General Bioimage Analysis Workflows

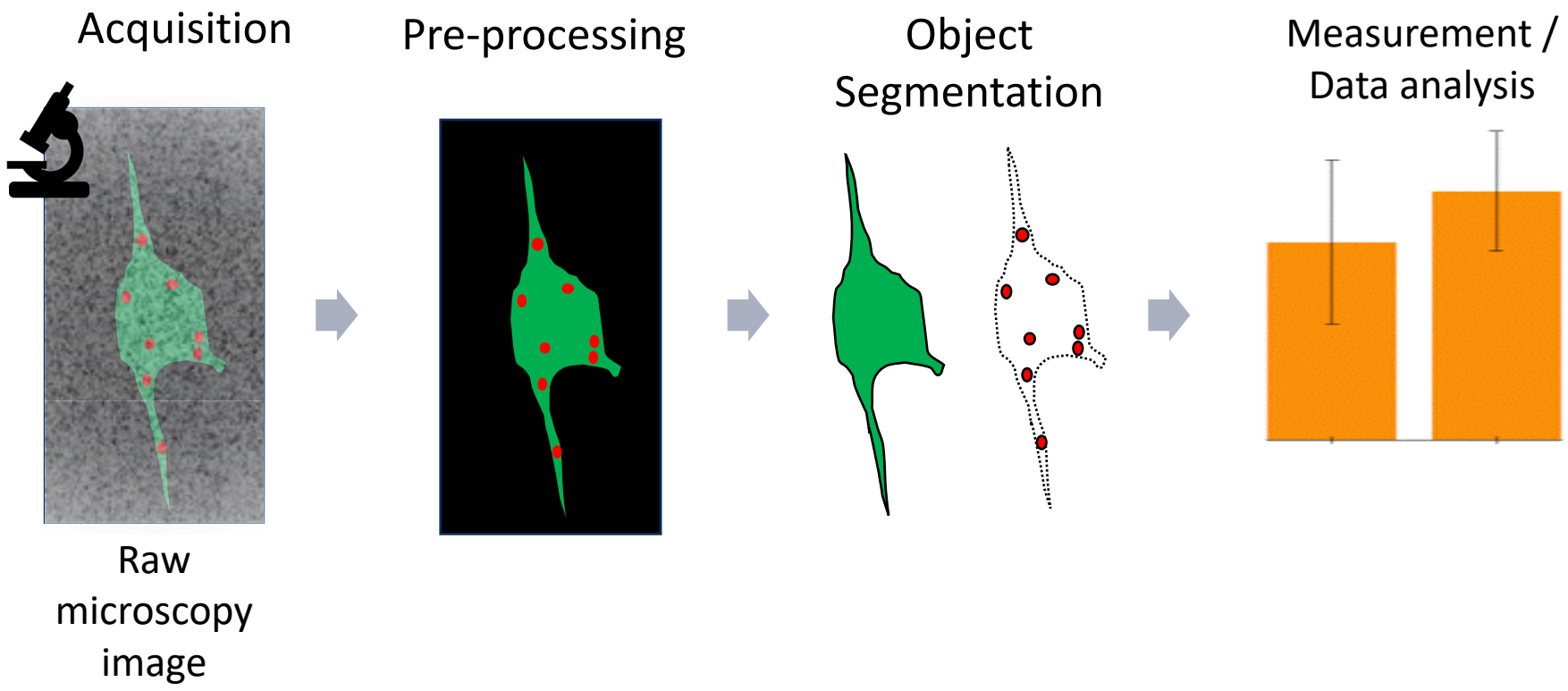
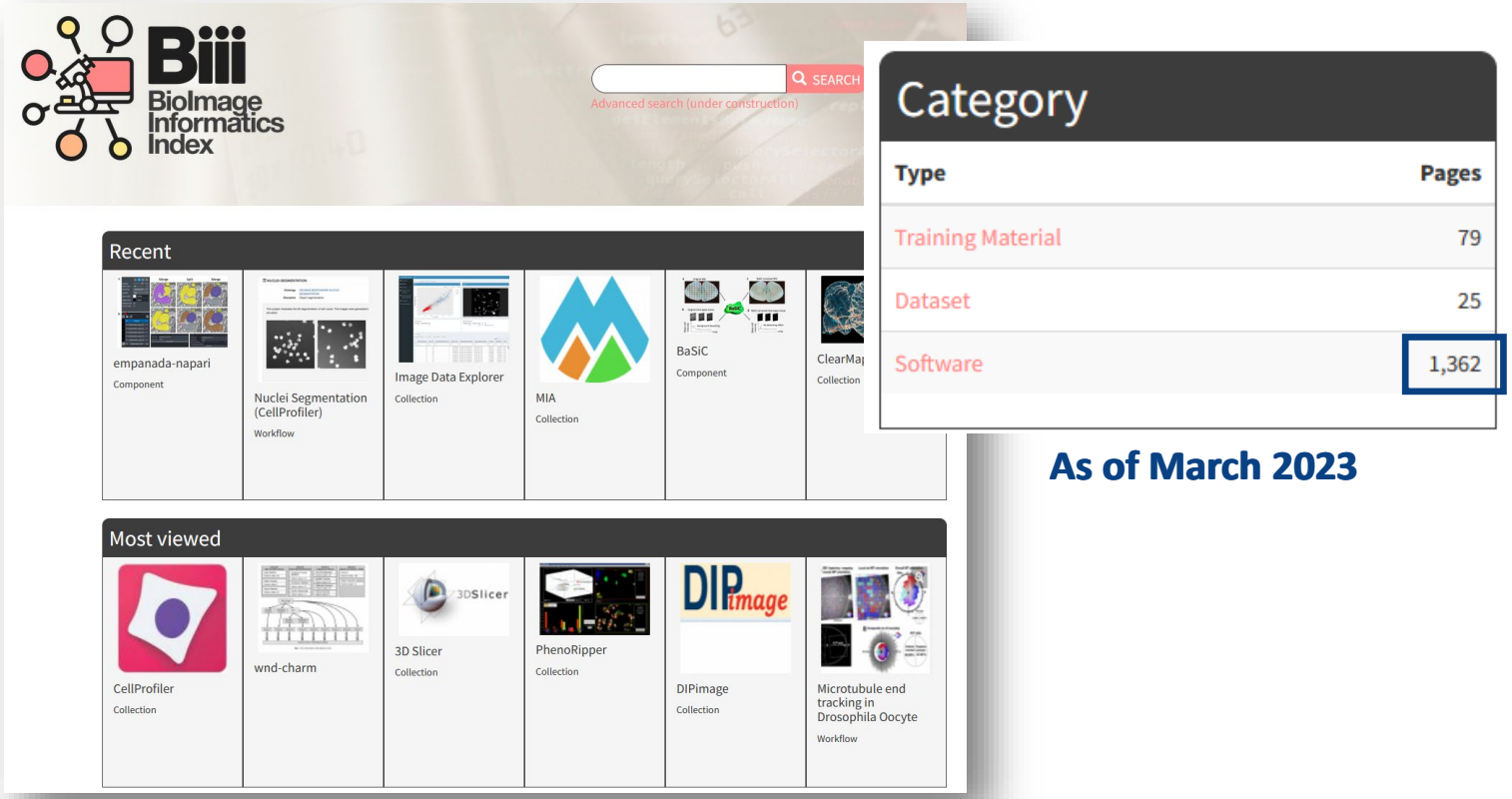


Image Processing Software

BioImage Informatics Index by Networks of European Bio-image Analysts (NEUBIAS): https://biii.eu/



Category	
Type	**Pages**
Training Material	79
Dataset	25
Software	1,362

As of March 2023

Reviews

Eliceiri et al., Nat Methods, 2012

Wiesmann et al., J Microsc, 2015

Baroux et al., Methods Mol Biol, 2018

Software name	Primary function
ImageJ	Image analysis
Fiji	Image analysis
BioImageXD	Image analysis
Icy	Image analysis
CellProfiler	Image analysis
Vaa3D	Visualization and image analysis
FarSight	Visualization
VTK	Bioimaging library
ITK	Bioimaging library
OpenCV	Bioimaging library
WND-CHARM	Machine learning
PSLID	Machine learning
Ilastik	Machine learning
CellProfiler Analyst	Machine learning and data analysis
PatternUnmixer	Machine learning
CellOrganizer	Machine learning, modeling and visualization
KNIME	Workflow system

Source: Eliceiri 2012

Image Processing Software @ BOMP

Freeware

ImageJ/Fiji

CellProfiler™
cell image analysis software

ilastik

Commercial

ZEN ZEISS

LEICA

NIS Elements
NIKON

FV Olympus

Harmony®
Perkin Elmer

SVI

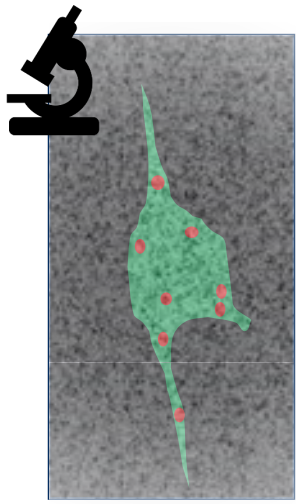
Volocity

MetaMorph®

Amira®

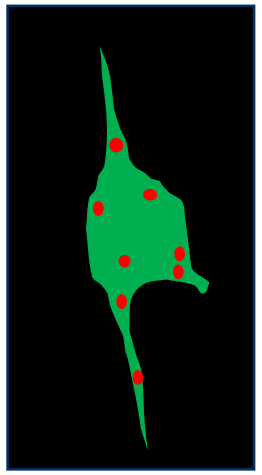
Part 2.
The Bioimage Analysis Workflow

Acquisition

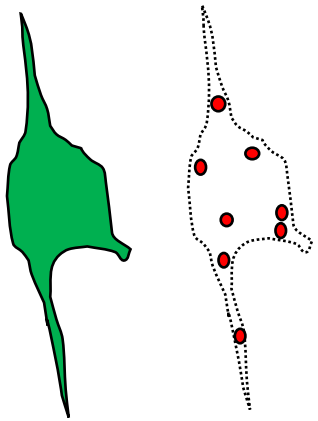


RAW Image

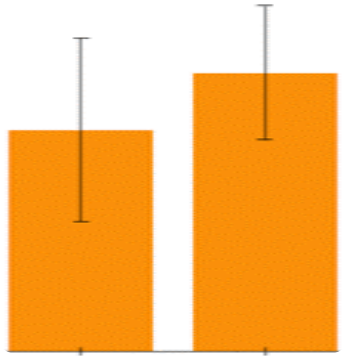
Pre-processing



Object Segmentation



Measurement / Data analysis



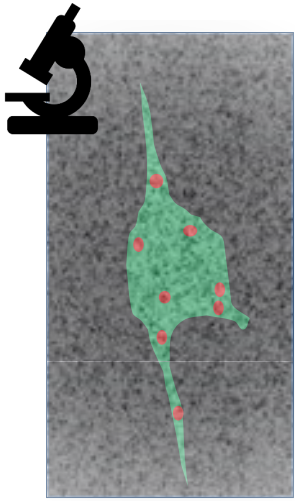
Reporting

Acquisition

Pre-processing

Object detection

Measurement / Data analysis

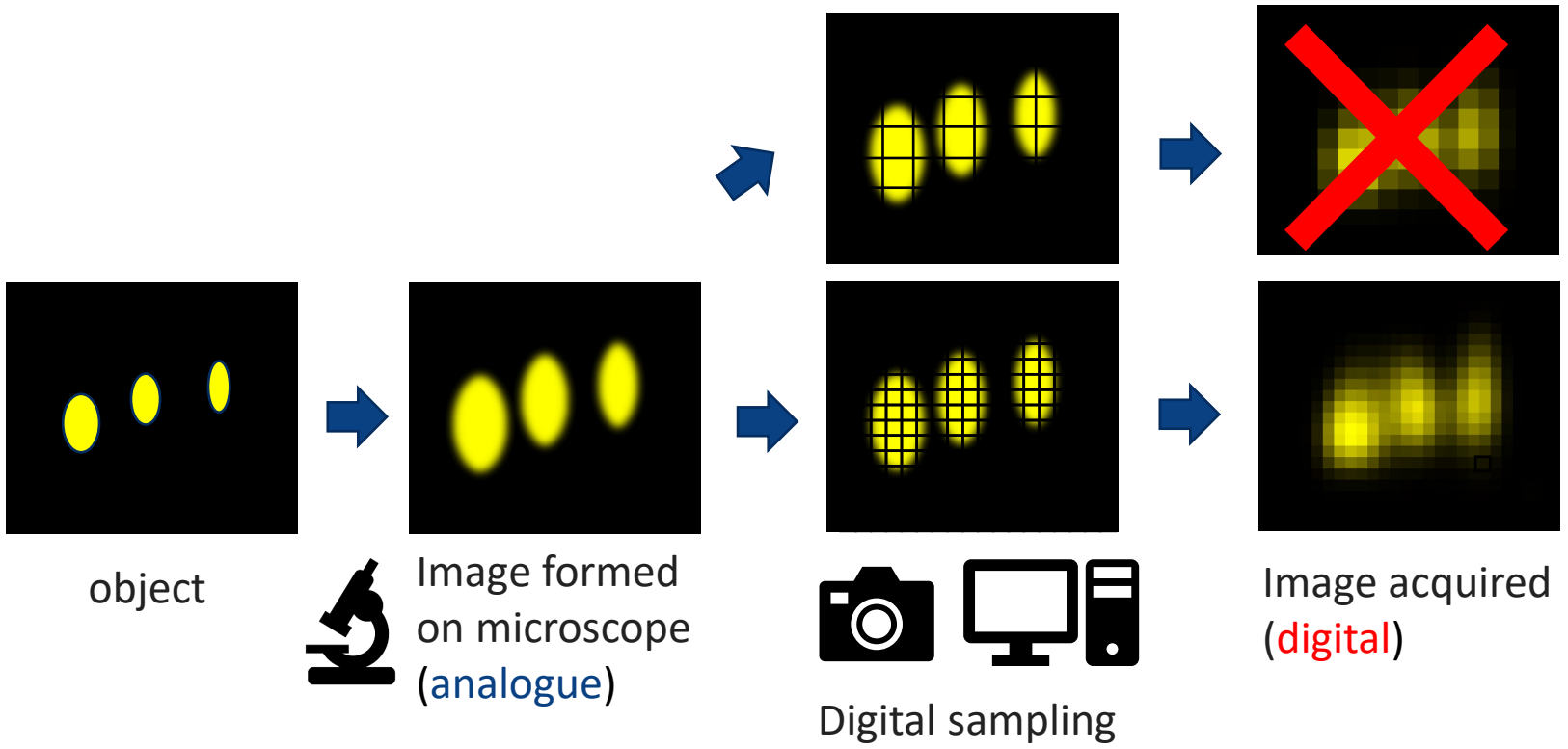


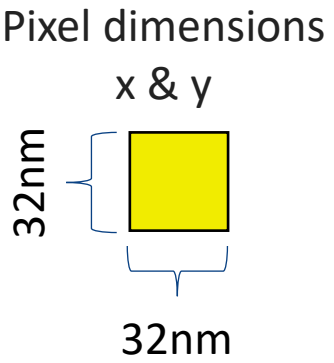
Raw microscopy image

During Acquisition

- Acquire with sufficient **sampling rate**
- Use **appropriate resolution**
- Decide on a **quantitative** or **qualitative** approach
- Use proper **bit depth**
- Avoid **saturation**
- Use whole **dynamic range**

Sampling Rate



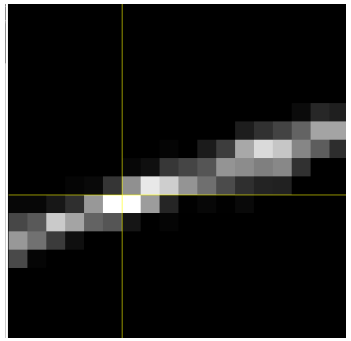


Acquire images with a sufficient **sampling rate**

Undersampling

- When the sampling rate is too low this is called undersampling and results in a pixelated image
- Particularly important depending on you desired quantificaiton
- Things to consider to avoid undersampling:
  - **Object size.** Determine expected size of the object from literature or experimentally
    - For example: if you wish to image lysosomes 300nm in diameter a pixel size 500 nm would lead to undersampling
  - Increasing the sampling rate allows use to image the shape

XY undersampling



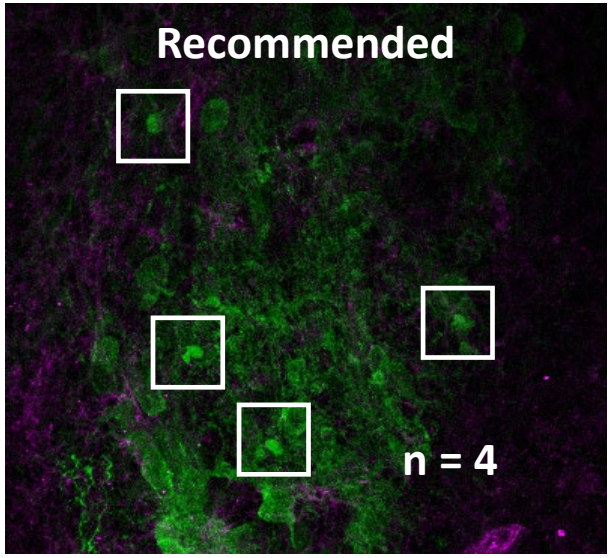
Oversampling

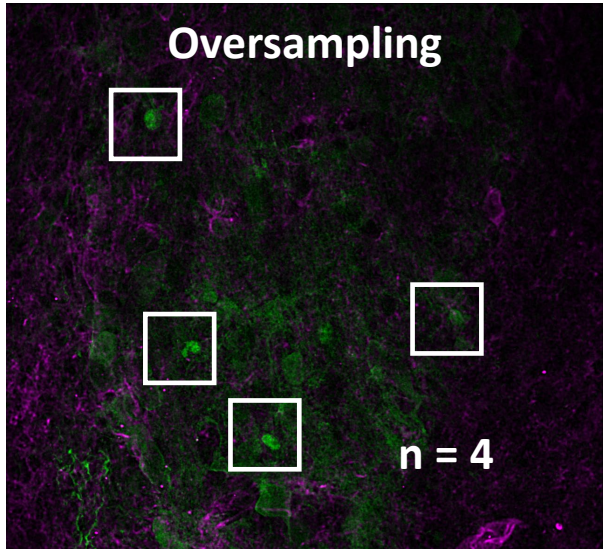
While we want sufficient resolution we need to avoid oversampling

- **Time**. Oversampling takes longer to acquire (and costs more!)
- **File size**. Larger file size means more storage required, slower data handling, longer processing time
- **Object size.** Use a sampling rate appropriate for your sample / quantification

➢ Example of Oversampling:
- Aim of imaging was to count neurons
- Acquisition settings used:

	Oversampling	Recommended
Pixel Size	40 nm	200 nm
Frame Size	1651 x 1651	512 x 512
Time	9 min	2 min
File Size	487 MB	25 MB
No. neurons	**4**	**4**





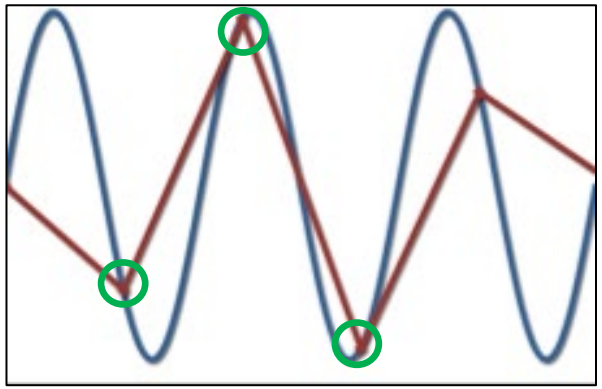
Nyquist-Shannon sampling theorem

- A microscope image results from the digital conversion of an analogue signal.
- Fundamental rule in analogue to digital conversion is the Nyquist-Shannon sampling theorem:
  - Sampling frequency must be **greater than 2.3 times the bandwidth** of the input signal for optimal reconstruction (or use pixels 1/3 the size of the smallest object)

Analogue signal

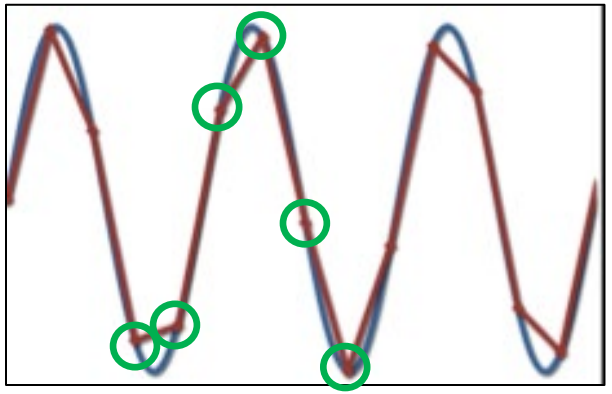
Digital sampling

Under-sampled



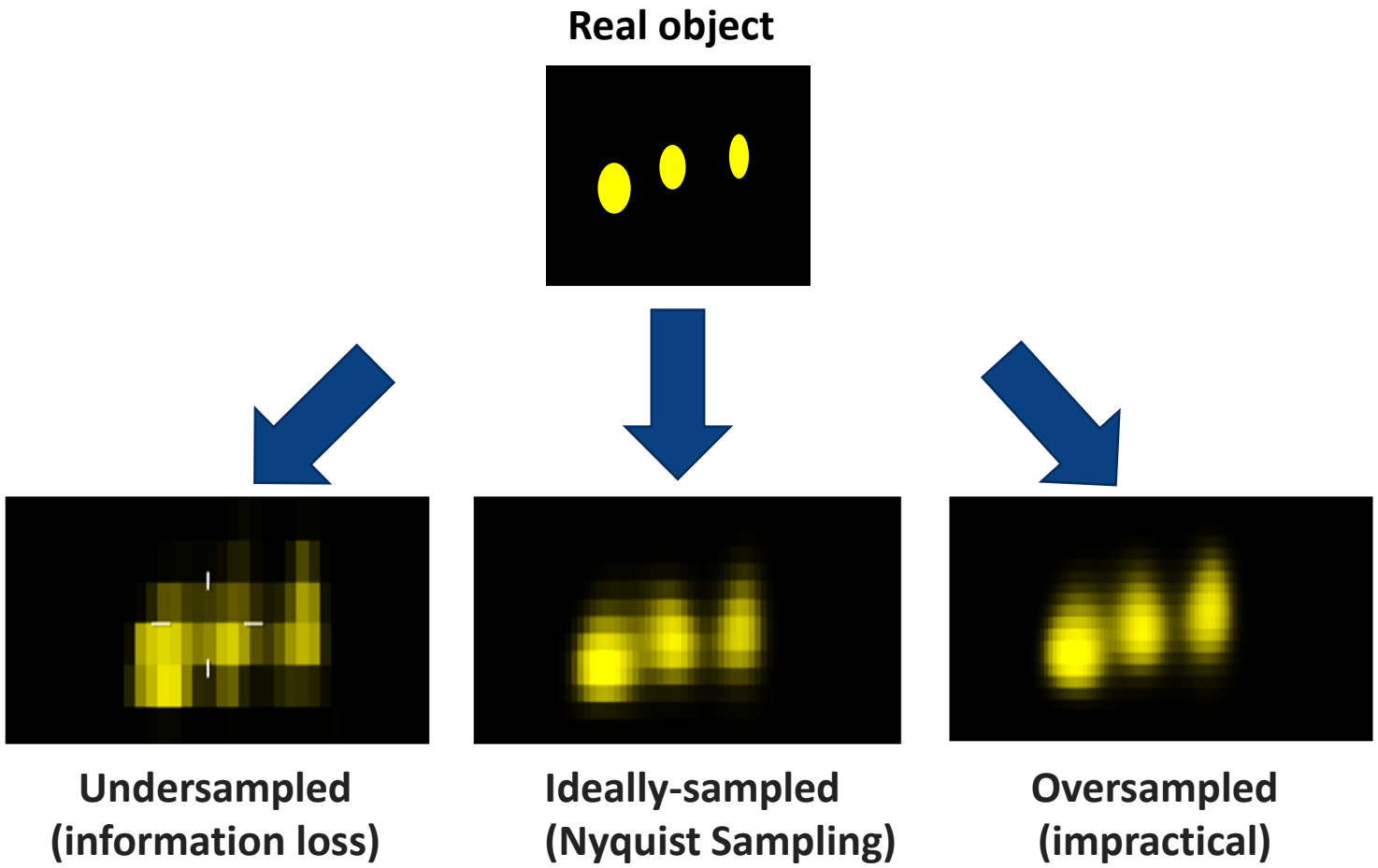
Sampling Frequency < 1

Ideally-sampled

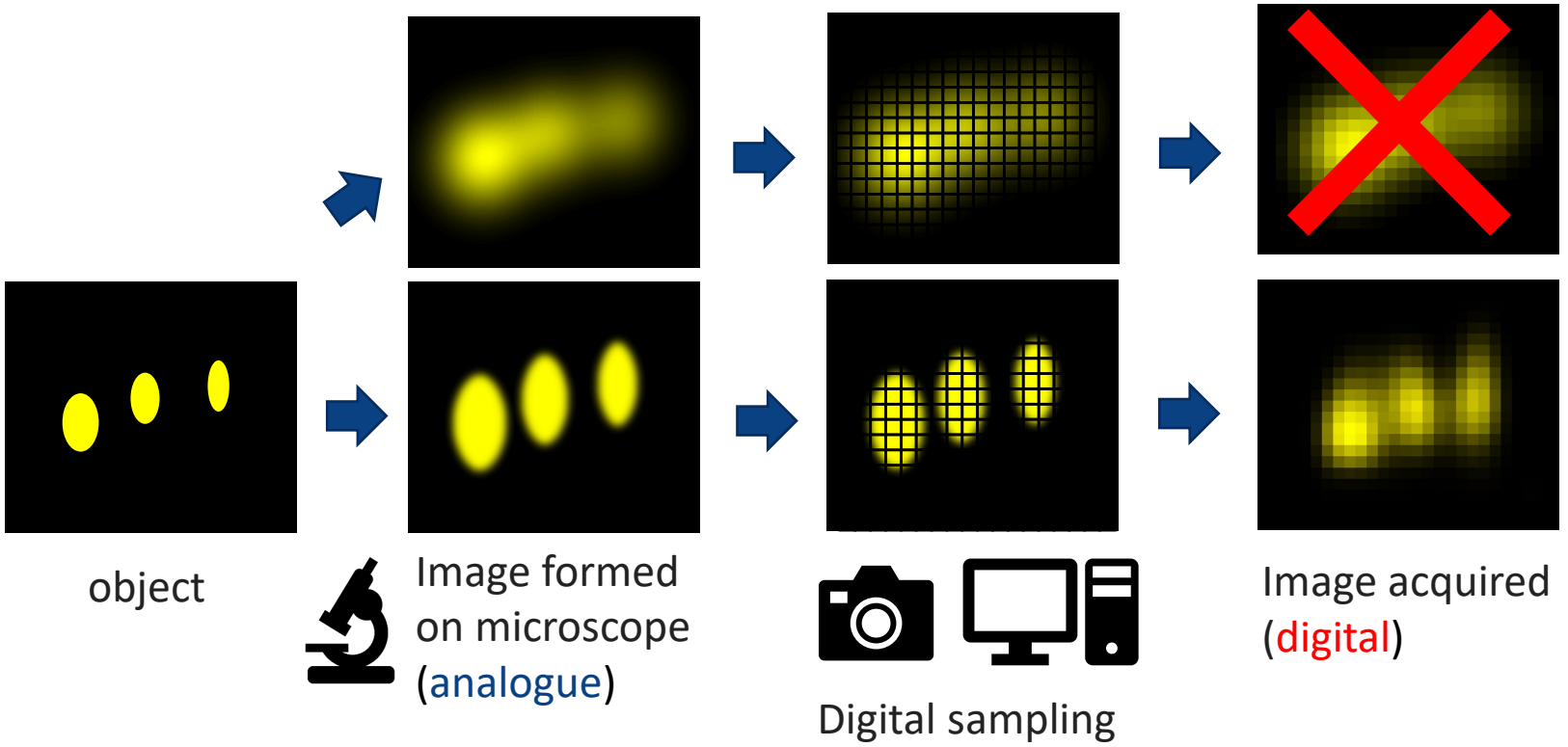


Sampling Frequency > 1

Sampling Summary



Optical Resolution



Appropriate an **resolution** for our object of interest

Quantity or Quality?

Is the aim of your imaging project is more about quantity or quality of images?

	Quantitative	Qualitative
No. images	A lot	Selected samples
Image quality / resolution	Sufficient quality	Best possible (oversampling)
Applications	• Large number of samples • Statistical demands	• Proof of concept • Complex structures • Visualisation
Notes	• Test settings (& processing) • Data management	• Is it scalable?

You can combine a quantitative and qualitative approach!

Qualitative AND Quantitative

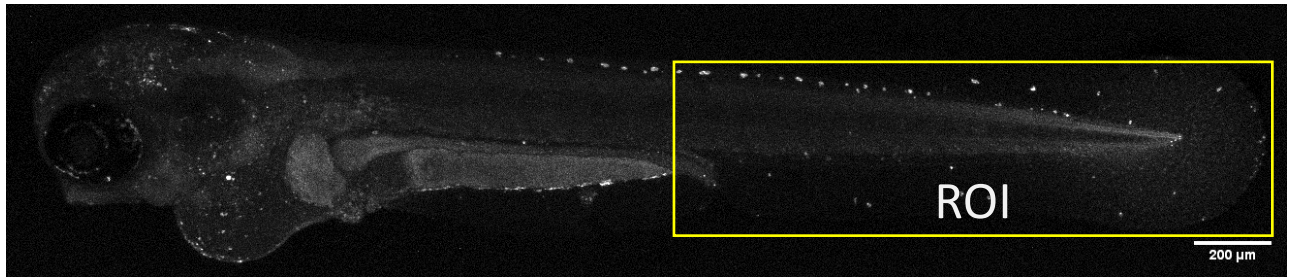
Qualitative (Confocal laser-scanning microscope)

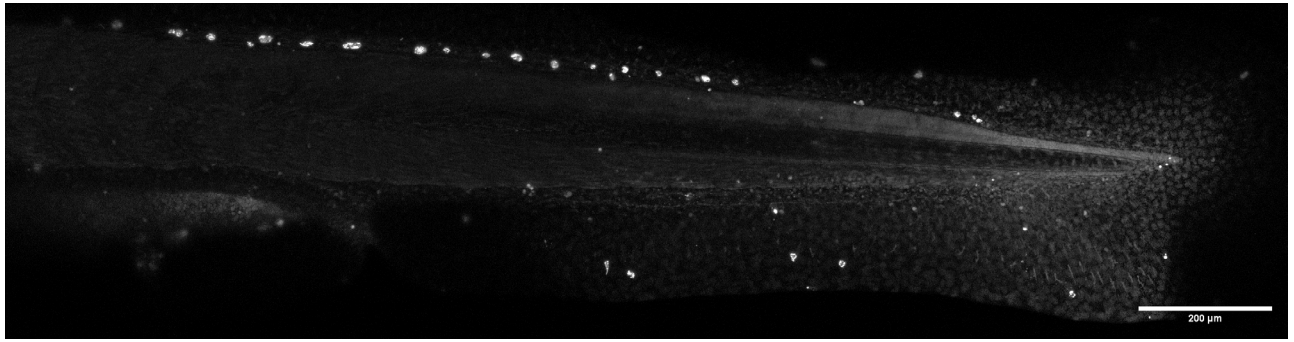
- Multiple z-stack images acquired at 20x, stitched together and used to create a maximum intensity projection.
- Time per image = 5 min. File size = 74 MB
- A ROI was cropped for analysis.

Quantitative (Benchtop widefield microscope)

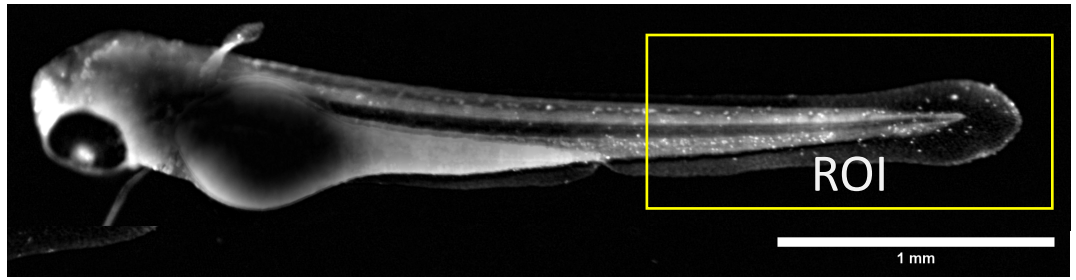
- Whole fish was imaged with single image at 2X.
- Time per image = 200ms. File size = 4 MB
- A ROI was cropped for analysis.

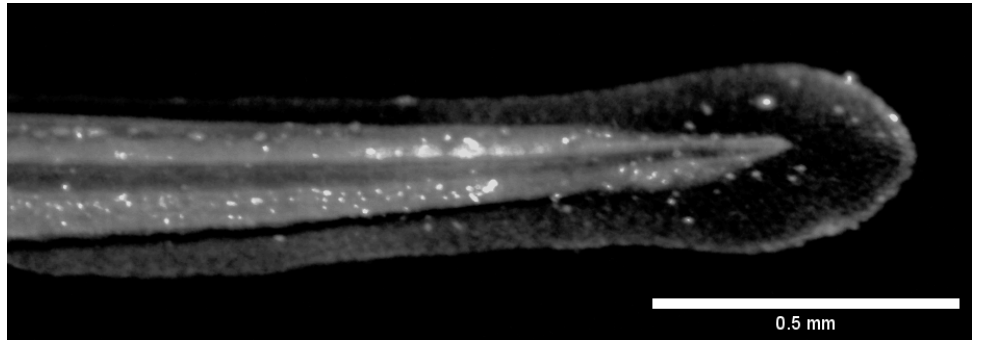
Confocal Imaging (Qualitative)



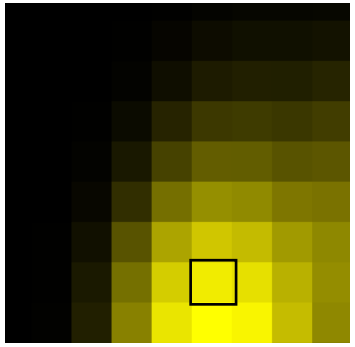


Widefield Imaging (Quantitative)

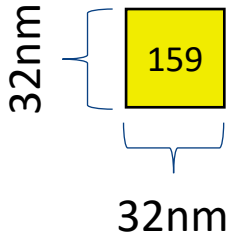




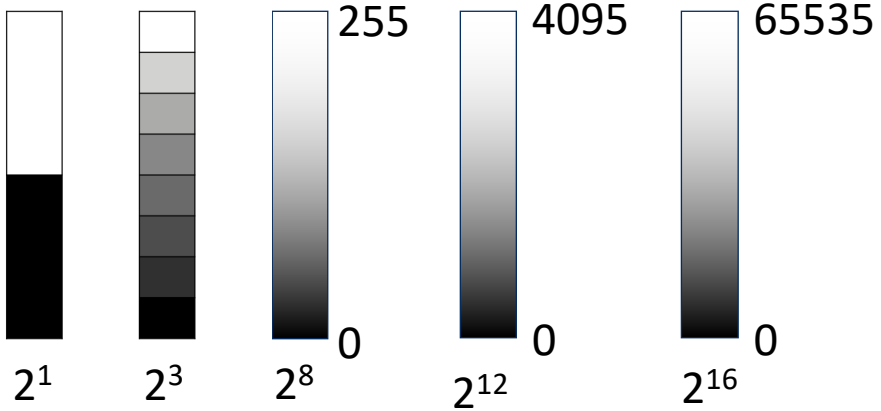
Bit-Depth

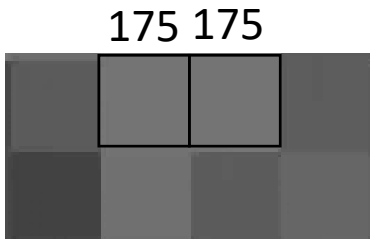


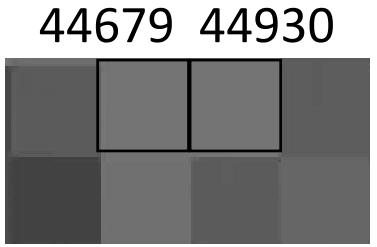
0	0	0	1	4	8	11	11	12
0	0	0	2	10	19	21	21	25
0	0	1	7	24	39	40	38	42
0	0	2	16	45	64	64	57	59
0	0	5	32	76	97	94	81	79
0	1	11	57	112	135	128	105	93
0	1	17	76	139	159	151	121	96
0	1	21	88	154	170	165	128	93



Binary + Dig**it** = **Bit**
1 bit = 0 or 1

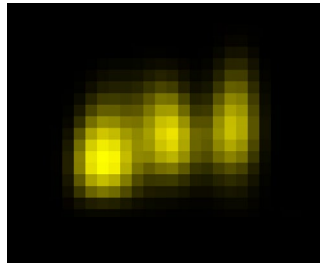


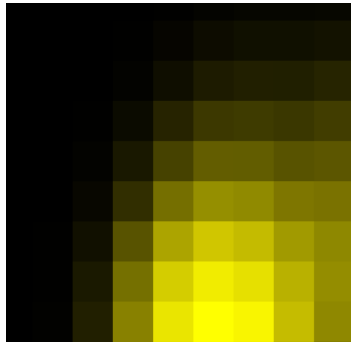




Use higher **bit depth** for intensity measurements

Dynamic Range & Saturation





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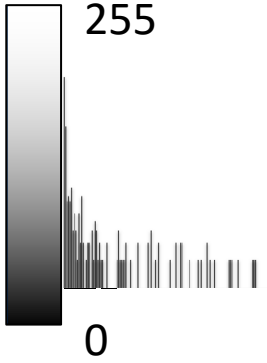
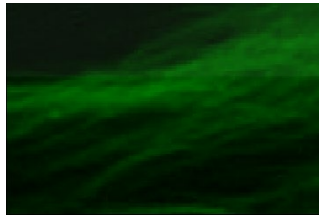
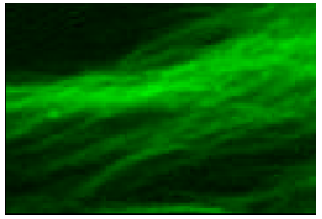
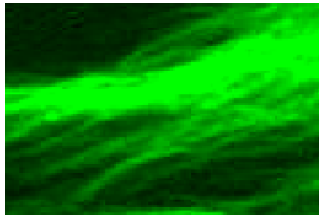
0	0	0	2	10	19	21	21	25
0	0	1	7	24	39	40	38	42
0	0	2	16	45	64	64	57	59
0	0	5	32	76	97	94	81	79
0	1	11	57	112	135	128	105	93
0	1	17	76	139	159	151	121	96
0	1	21	88	154	170	165	128	93

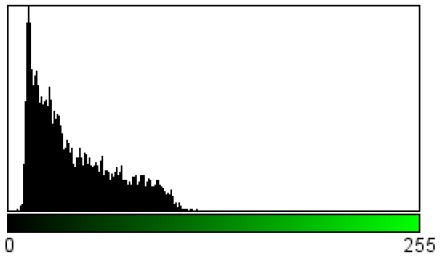


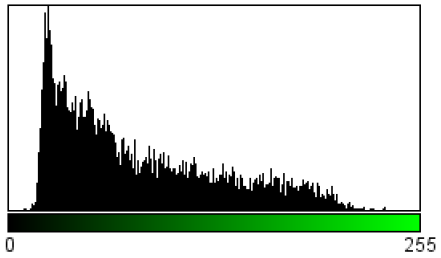
Frequency Histogram

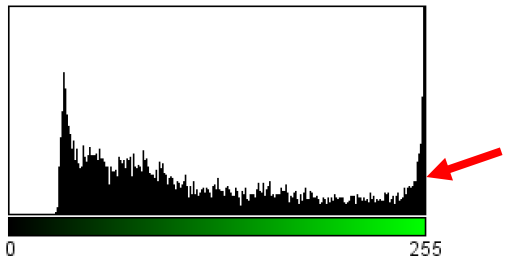












Use whole **dynamic range**

Avoid **saturation**

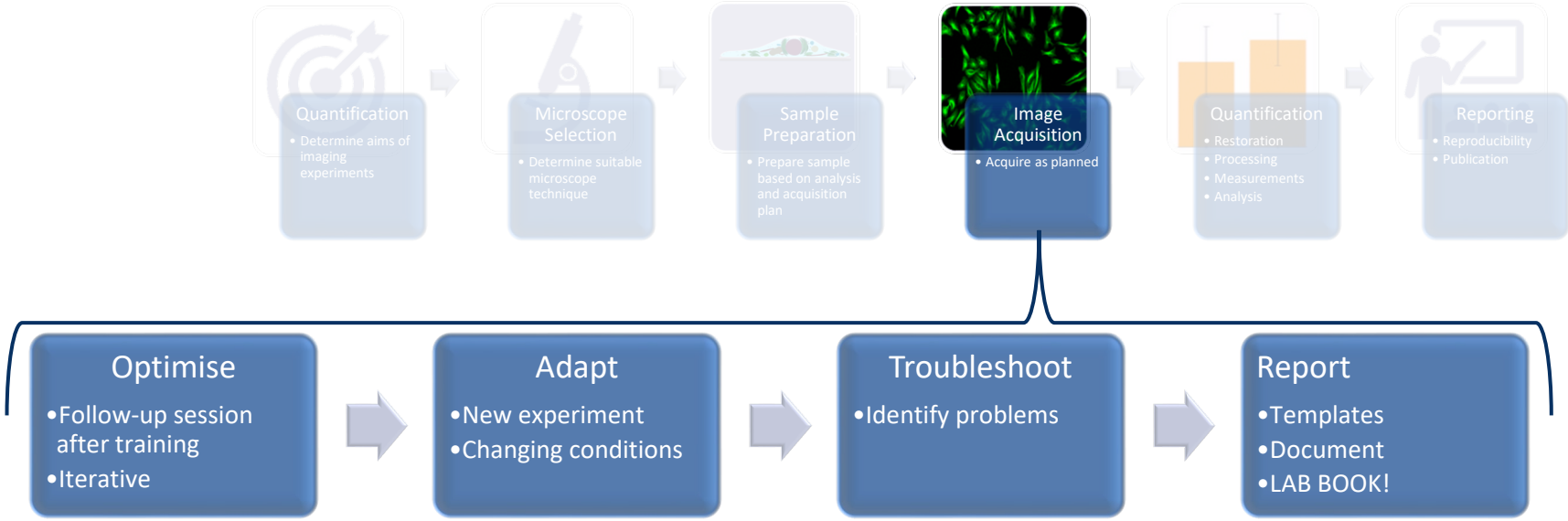
During Acquisition

- Images to be compared **MUST** be acquired (and processed) using the same settings
- Save the image using the microscopy raw format (CZI, LIF, OIB, ND2… OME-TIFF) to preserve metadata.
- Avoid saving as standard TIFF, JPG, PNG…

More detail on our other microscopy seminar series

https://microscopy.unimelb.edu.au/optical-microscopy/workshops-resources

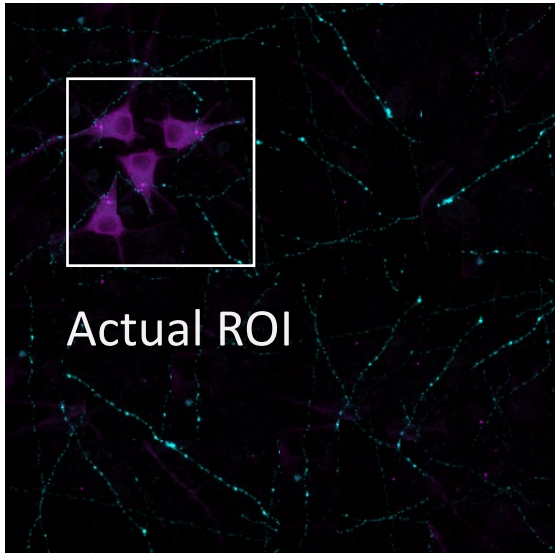
Optimising Acquisition After Training



- **Optimisation:** Fine tuning your settings is critical for the best results and efficiency
- **Adaptation:** Adjusting your setting for new samples (avoid copying settings)
- **Troubleshooting:** Identify problems…lookout for large files, slow imaging, difficult data management
- **Reporting:** Always document the acquisition tools used and save templates where possible

If in doubt reach out to BOMP for advice and guidance!

Case Study in Sub-optimal Setup

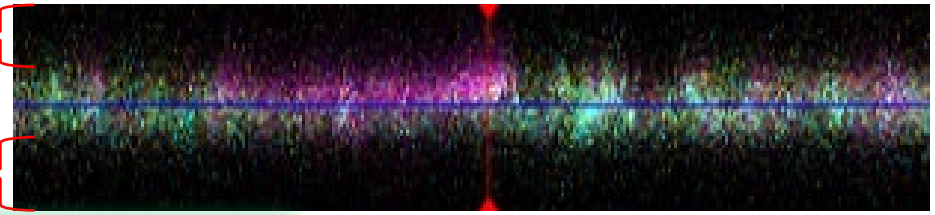


Question. Simple Yes/No question - is marker (blue) in cells (purple)?

Warnings!

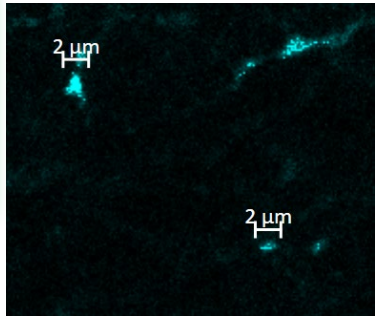
- Raw data size is **61.5 GB**
- File opening in Zen took **45 min**
- 12 tiles x 45 slices x 5.32 s per frame = **48 min**

Suggestions for improvement:



- **Tiling,** 12 tiles used but only half of 25 % image contains ROI
  - ✓ Take low resolution overview instead
- **Z-stack,** 60 % of slices are empty ~40 GB
  - ✓ Check first and last slice before starting
  - ✓ Crop after acquiring

With correct settings:
File = approx 1.6 GB
Acquisition = approx. 1.5 min

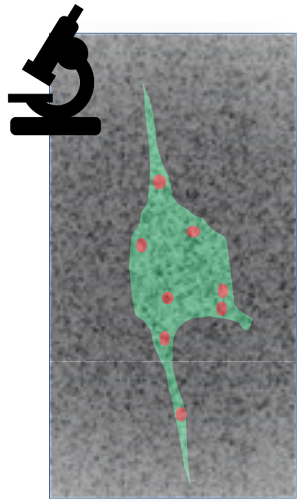


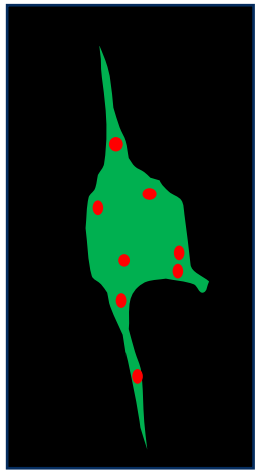
- **Sampling,** objects are ~2 µm in size but pixels are 0.15 µm
  - ✓ Minimum requirement is 0.86 µm (6x smaller)
- **Scanning mode** was set to unidirectional and doubled acquisition time
  - ✓ Use bidirectional scanning

Pre-processing

Object detection

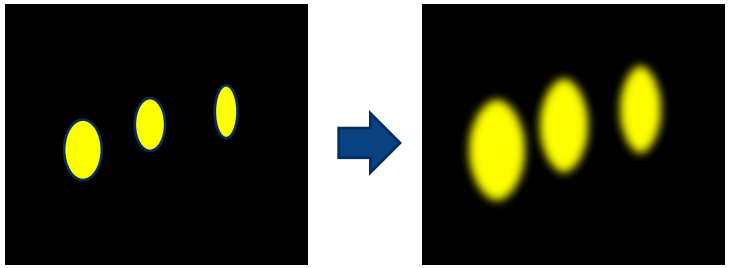
Measurement / Data analysis





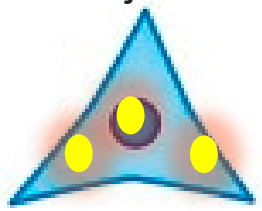
Raw microscopy image

Pre-processing



Fluorescent signal from object

Image formed on microscope



Think of all the lenses, filters and mirrors fluorescent light has to pass through to get to the detector!

- De-noising
- Background correction
- Bleaching correction (in time, in Z)
- Alignment
- Deconvolution

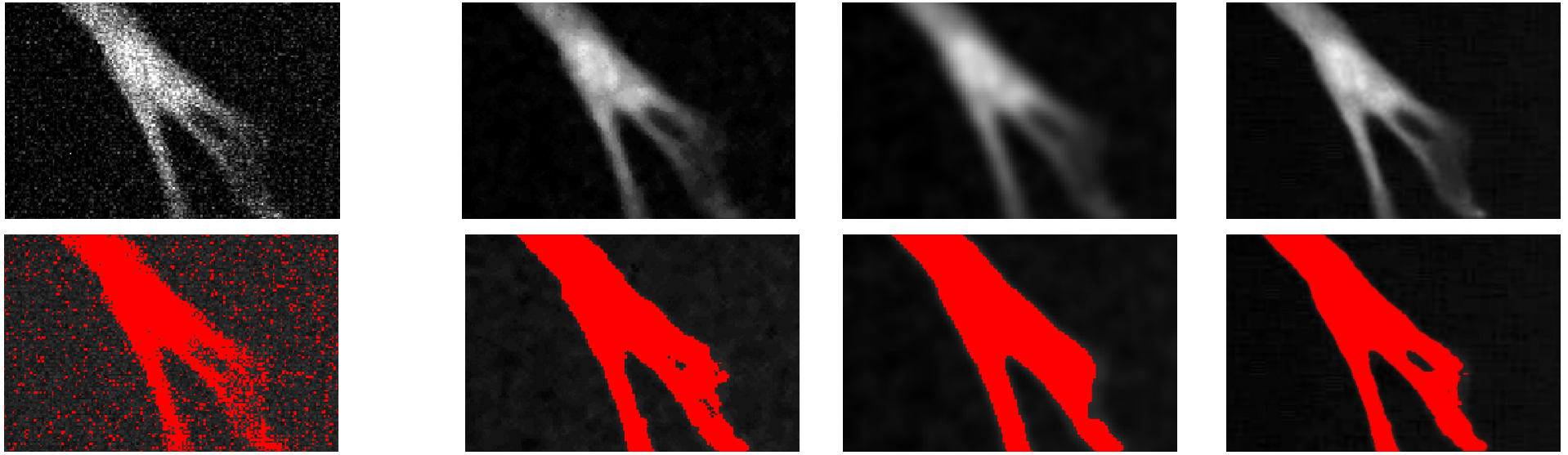
De-noising

Raw data

Median Filter (preserves edge)

Gaussian Filter (smoothing,blurring)

Deep learning

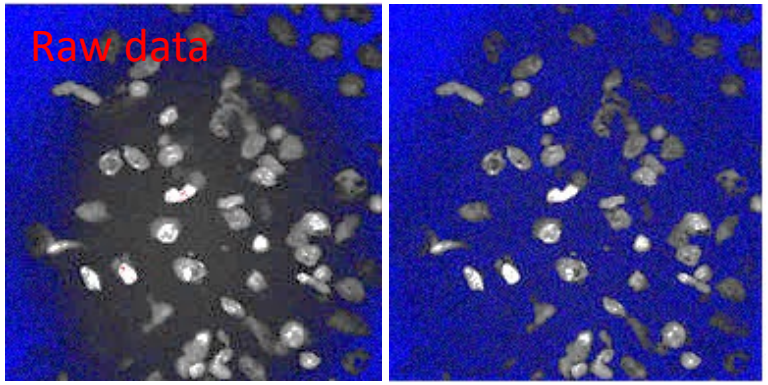


Noise2Void (Krull 2019)
https://github.com/juglab/n2v

Image : Celltrackingchallenge dataset Fluo-C2DL-MSC

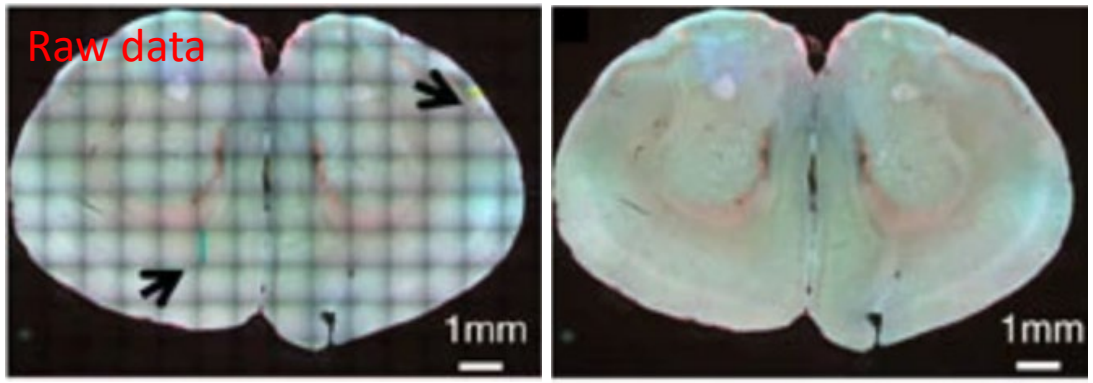
Background Correction

Background Subtraction



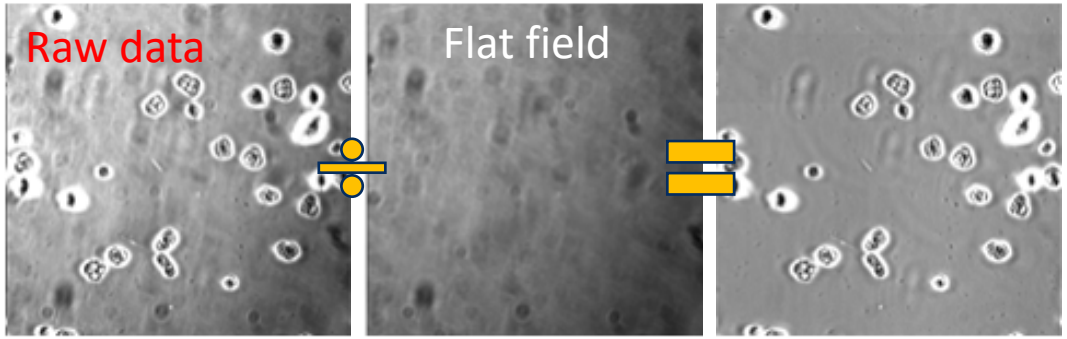
'Rolling Ball' (Castle and Keller 2007)

Shading Correction

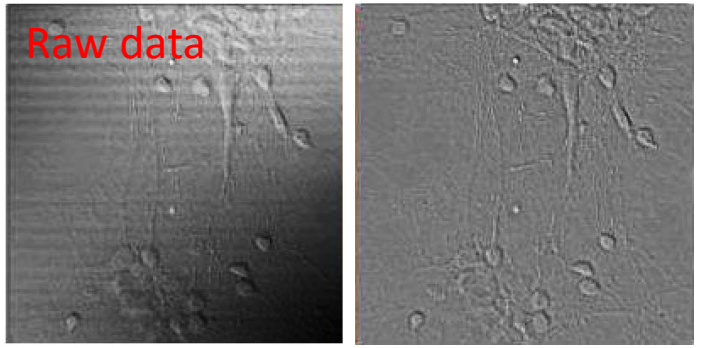


BaSiC (Peng 2017)

Flat Field Correction



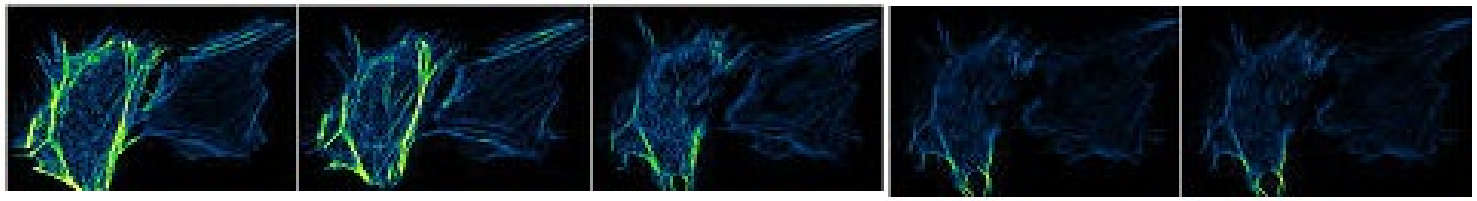
Suppress stripes (Bandpass Filter)



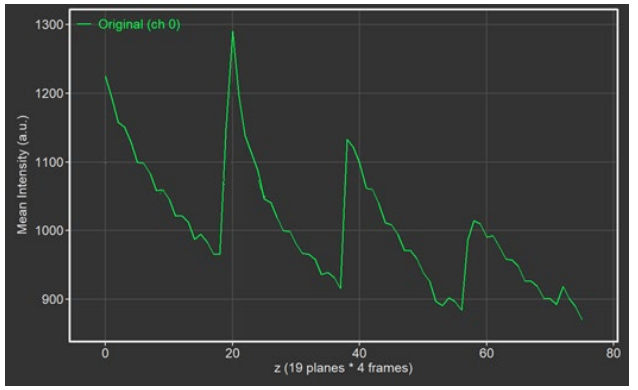
https://imagej.net/Image_Intensity_Processing#Background_correction

Bleaching correction

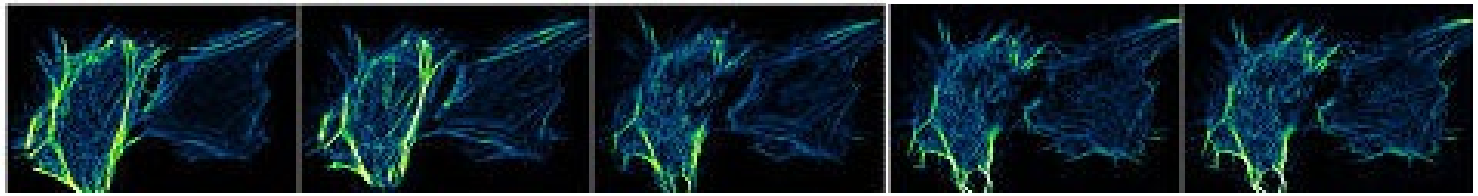
Stack intensity decreasing



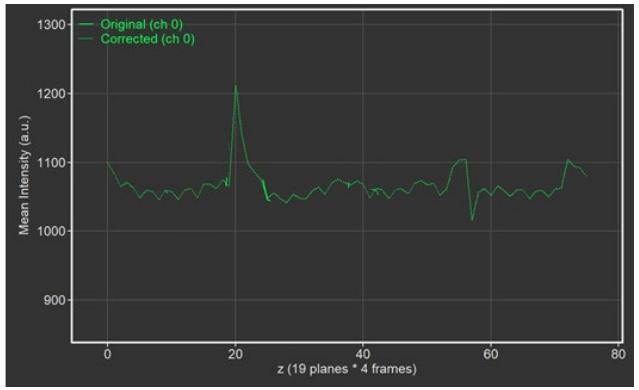
Intensity profile



Stack intensity corrected



Intensity profile

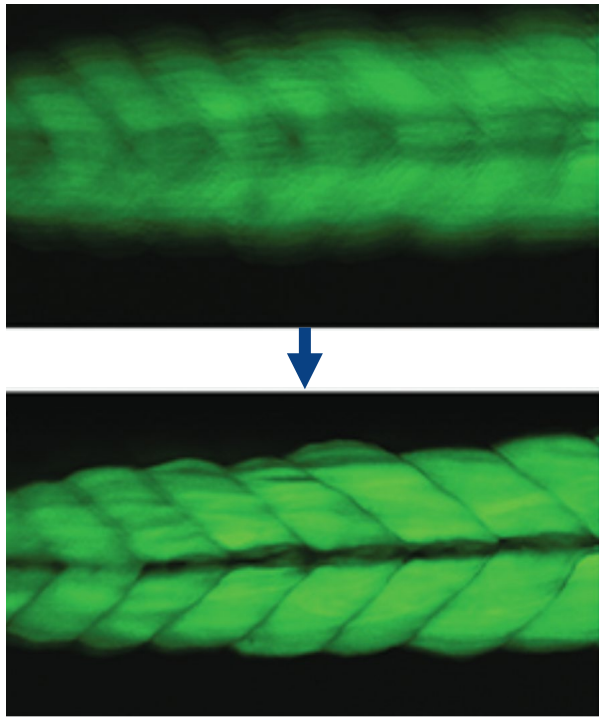


‘Bleach Correction’

‘Bleaching Corrector’

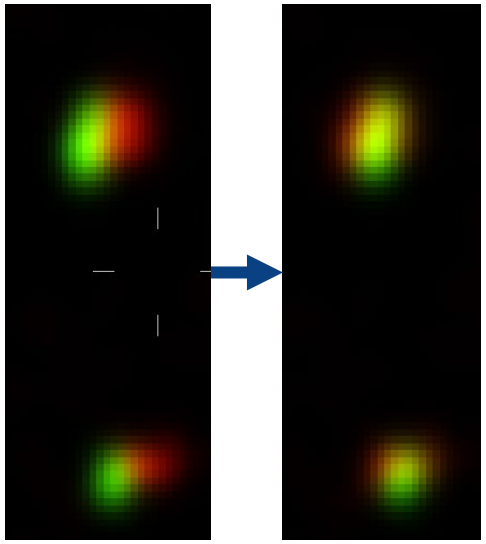
Alignment

Drift correction in x, y, z, t



'Correct 3D Drift' (Parslow 2014)

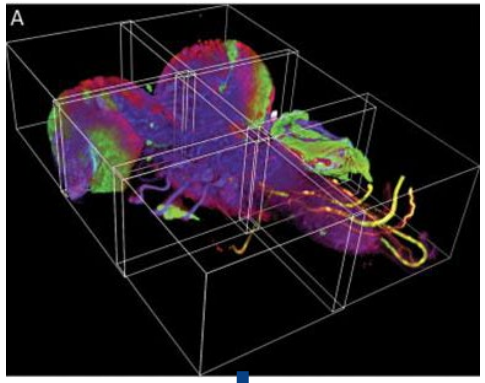
Chromatic shift correction

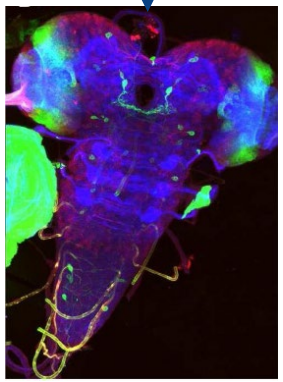


'TransformJ' (Meijering 2001)

'Chromatic Aberration corrector'

Stitching



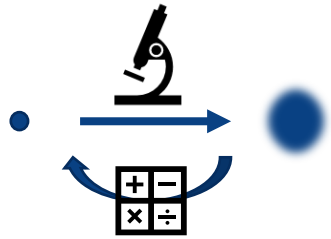


'BigStitcher' (Preibisch 2009)

More details: https://imagej.net/Category:Registration

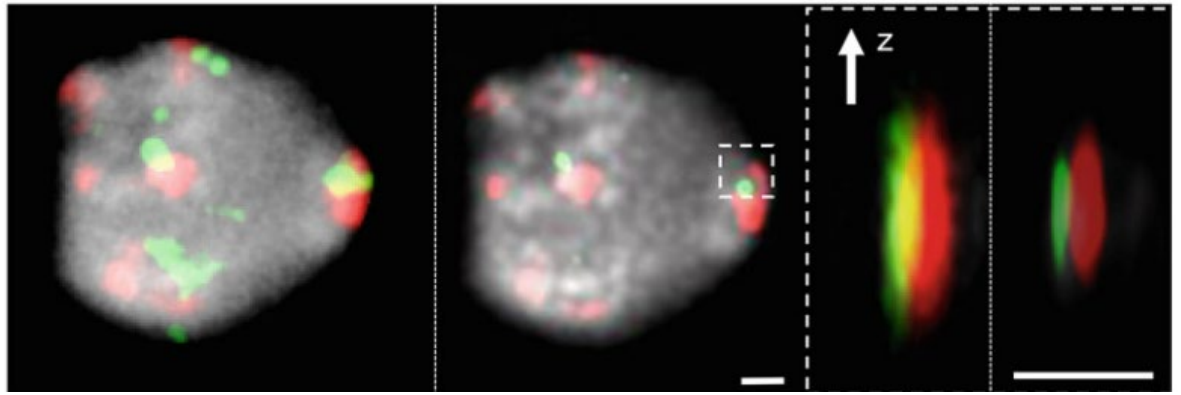
Deconvolution

Mathematical image restoration method

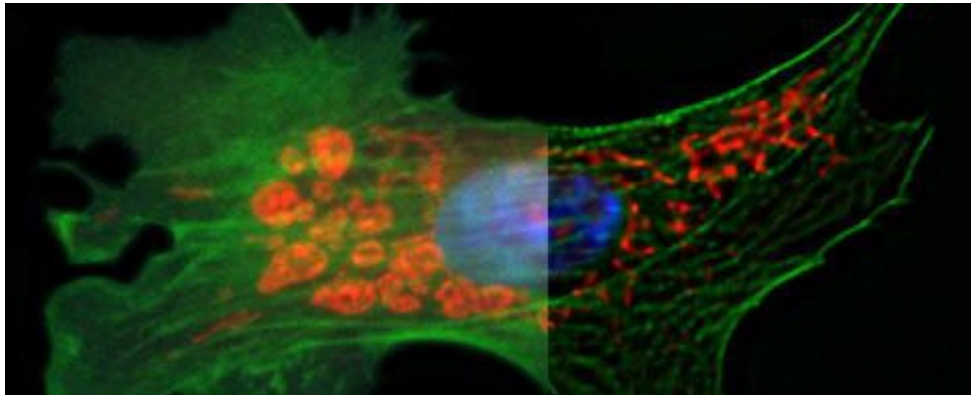


- Increase resolution in x,y,z
- Increase contrast
- Remove noise

Thereby improves the quality of data visualisation and analysis



Baroux 2018



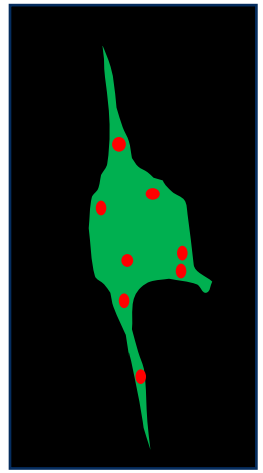
www.svi.nl

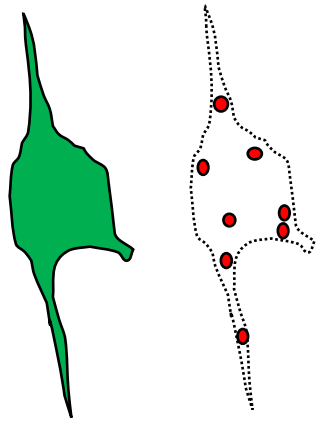
Image created by Dr. Jeff Tucker and Dr. Holly Rutledge from NIEHS, NIH, USA

Huygens Image Deconvolution Workshop (https://microscopy.unimelb.edu.au/)

Object Detection

Raw microscopy image

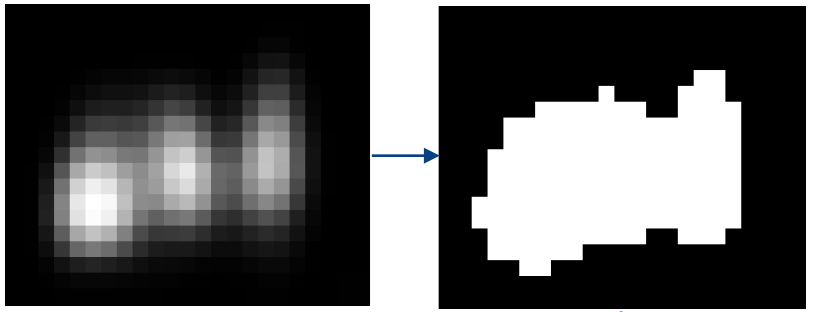




Measurement / Data analysis

Object Detection

- 1) Pixel segmentation



- Conventional
- Machine learning
- Deep learning
- Template matching

- 2) Binary processing

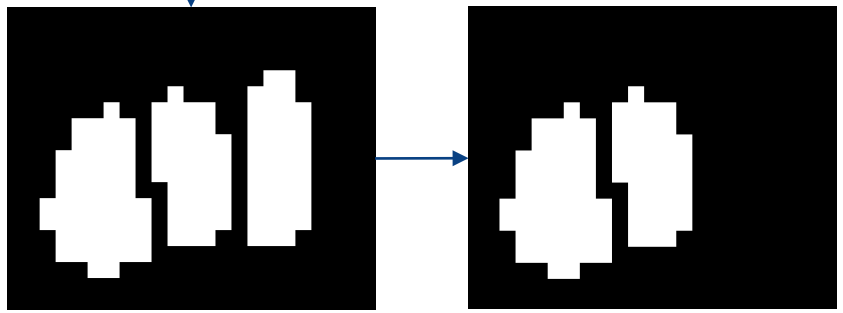
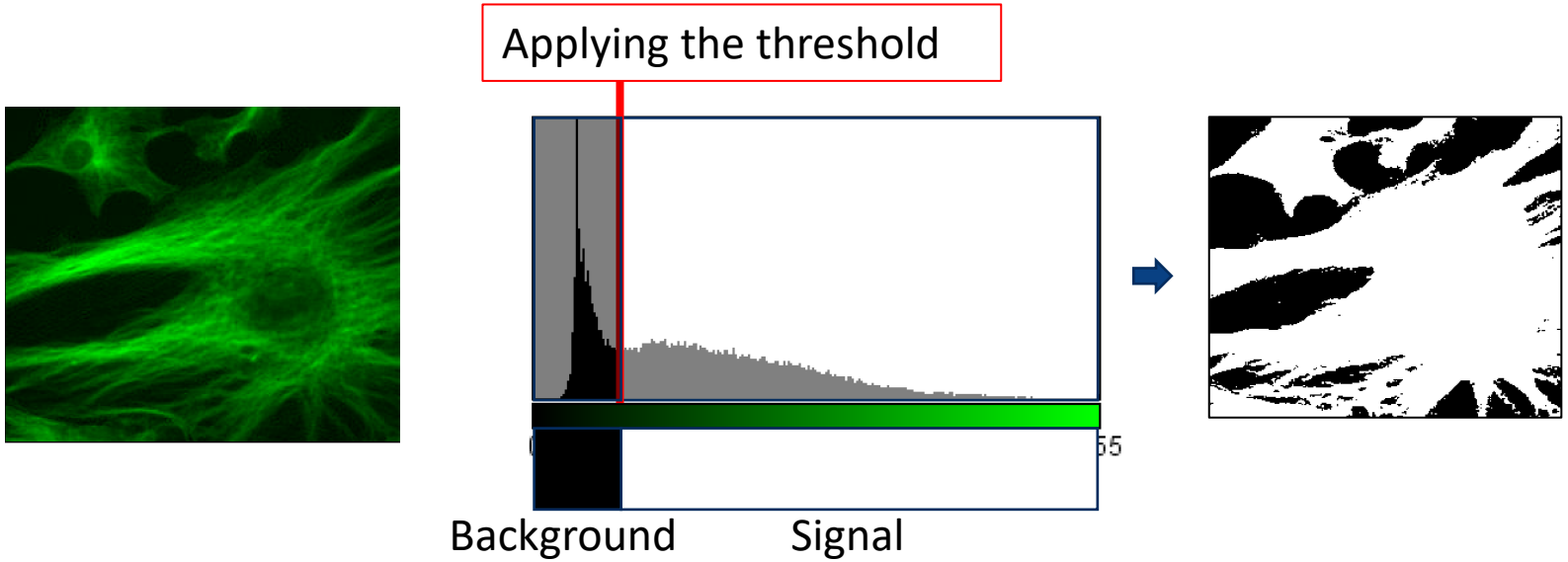


Image Segmentation Workshop (https://microscopy.unimelb.edu.au/)

Conventional Segmentation



- Find threshold using ‘negative control’ image or from the ‘background’ area
- To be ‘objective’, apply same threshold to all images

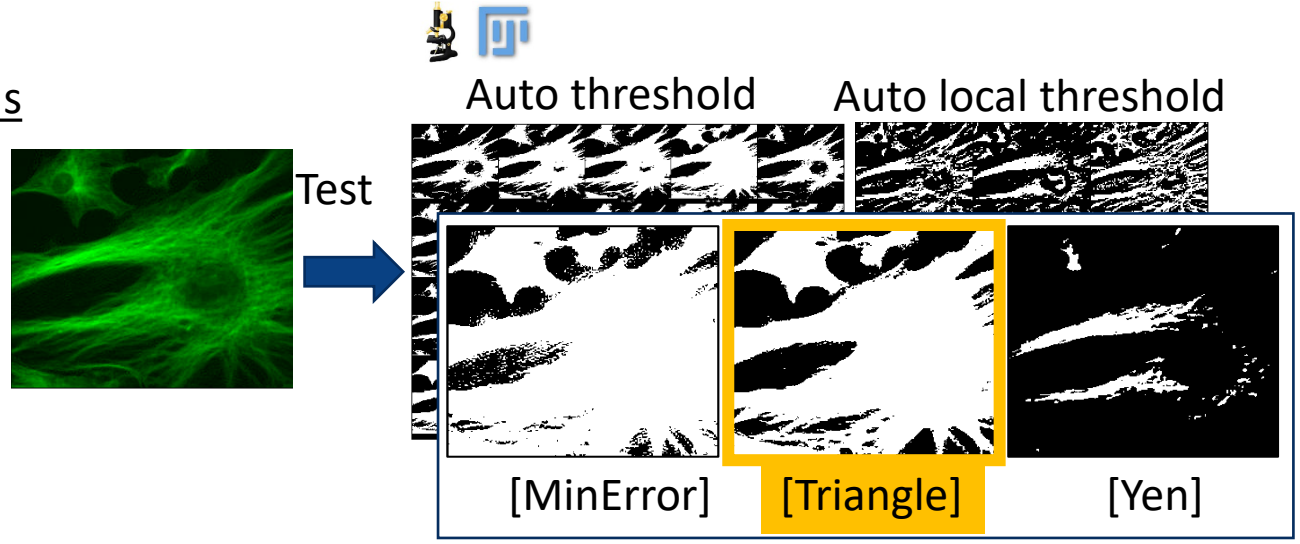
Conventional Segmentation

But

- Many ‘real’ images have different background levels
- Background level may change over time in the same sample in live cell imaging

Auto-threshold algorithms

Huang (1995)	Doyle(1962)
Prewitt (1966)	Shanbhag(1994)
Ridler(1978)	Zack (1977)
Li (1993)	Yen (1995)
Kapur(1985)	Bernsen(1986)
Glasbey(1993)	Soille(2004)
Kittler(1986)	Niblack(1986)
Tsai(1985)	Phansalskar(2011)
Otsu(1979)	Sauvola(2000)
	…any many more

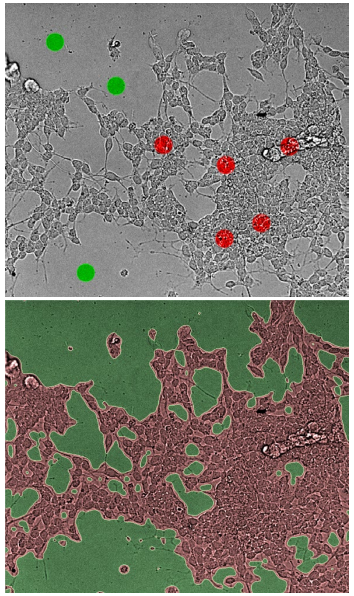


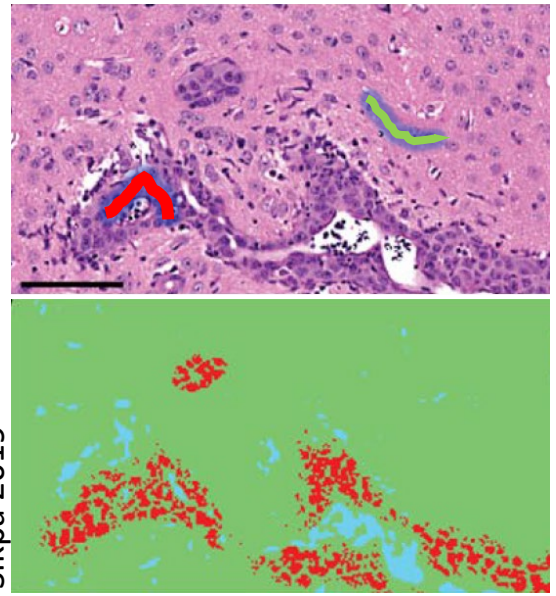
To compensate different background issue,

- Test different Auto-threshold methods
- Apply same auto-threshold algorithm for each image

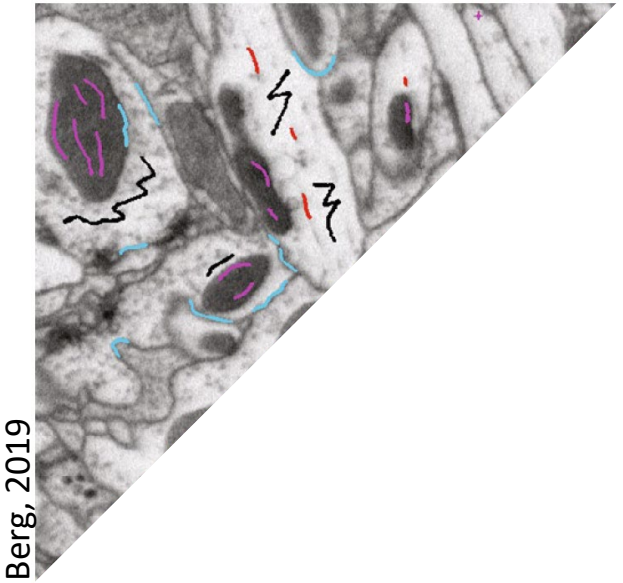
Machine Learning

- Thresholding doesn't work well with non-fluorescence images
  e.g. brightfield, phase contrast, colour, or EM images
- Segmentation using few manual annotations
- Interactive, user-friendly
- No machine learning expertise required





Sikpa 2019



Berg, 2019

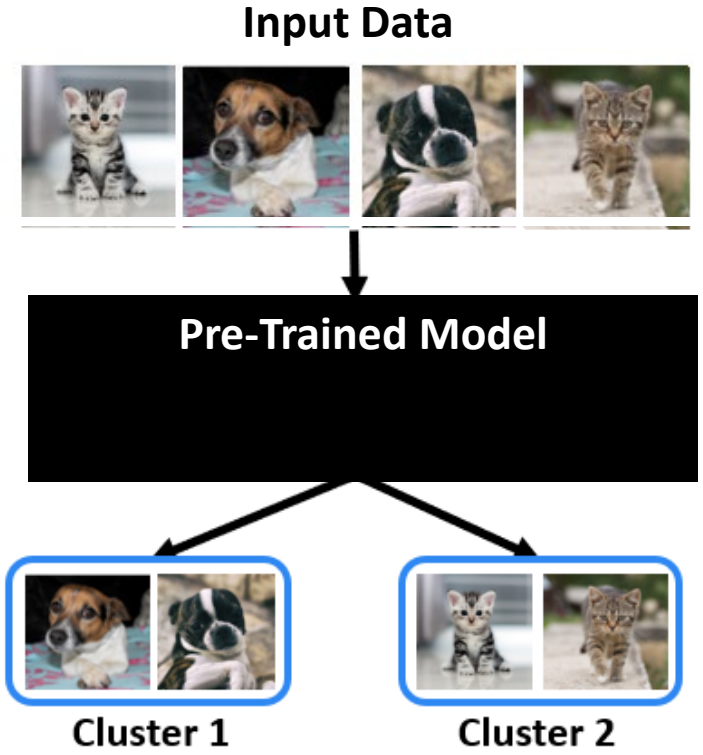
Harmony®

trainable WEKA

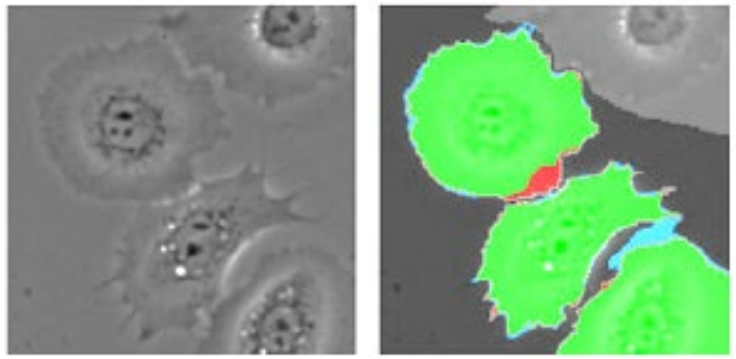
Ilastik

Deep Learning

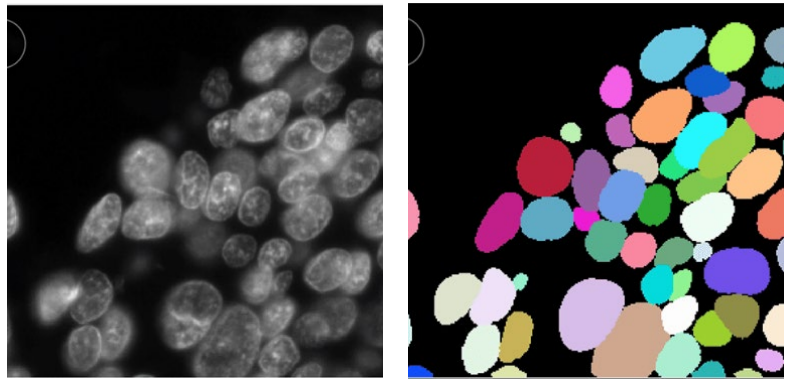
- Automatically extracts inherent image features or structures
- Models can be trained with ground truth annotations
- Pre-trained models compare input data to a known target
- Some ‘pre-trained’ models for bioimage analysis are accessible via user friendly software



U-net (Falk 2019)(via DeepImageJ)



StarDist (Schmidt 2018)

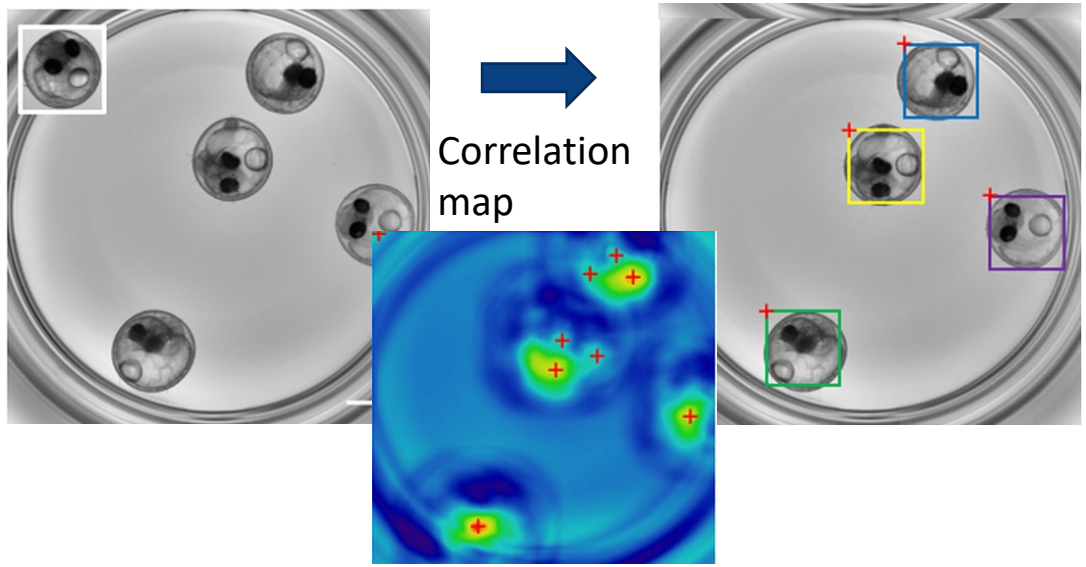


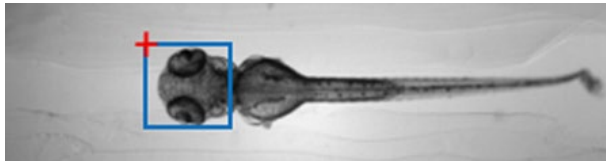
Template Matching

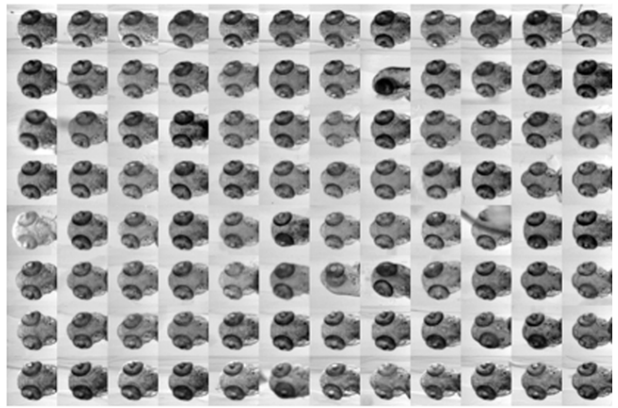
- No manual annotation
- Minimal computation – computes the probability to find one (or several) template images provided by user into a large image
- Good for finding similar structure in time-lapse or tissue micro-array
- No programming skill required

Template & Target

Matched image



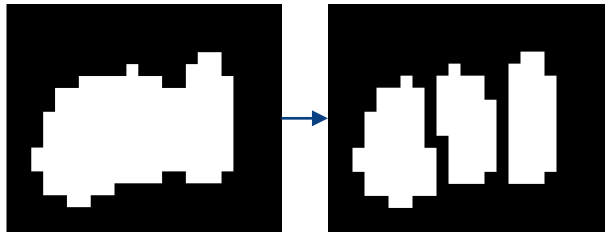




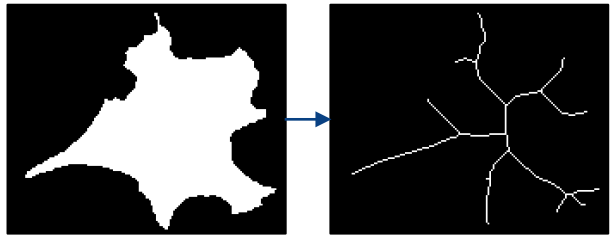
‘MultiTemplateMatching’ (Thomas & Gehrig 2019)

Binary Processing

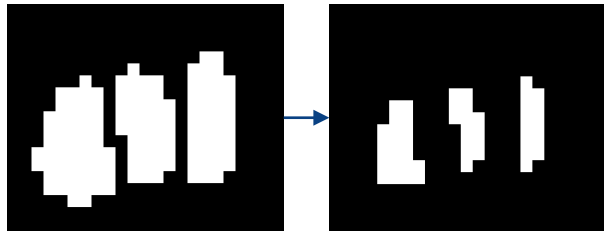
Watershed



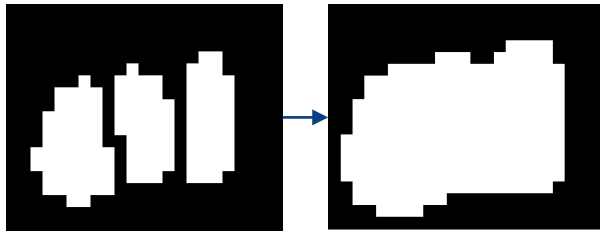
Skeletons



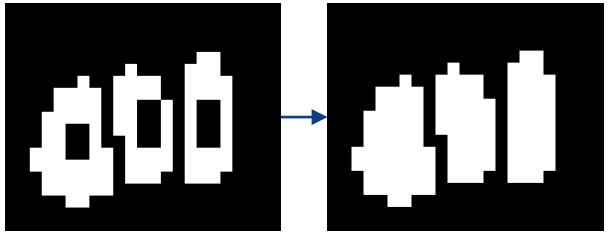
Erode



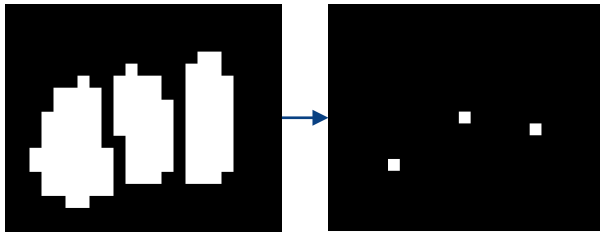
Dilate



Fill Holes

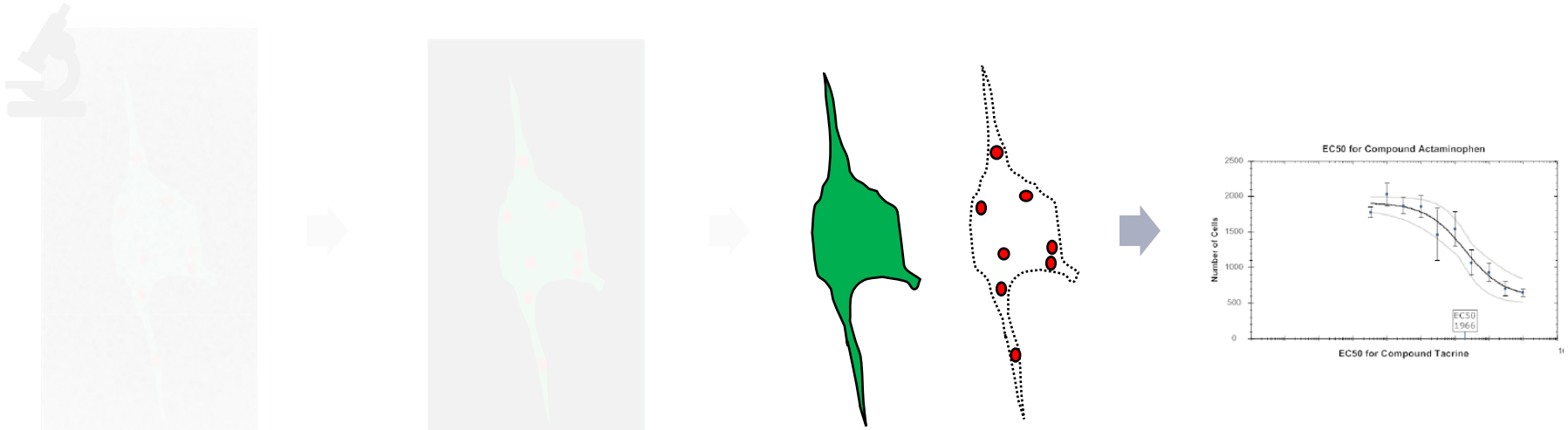


Ultimate eroded points



… many more

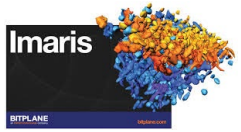
Measurement / Data Analysis

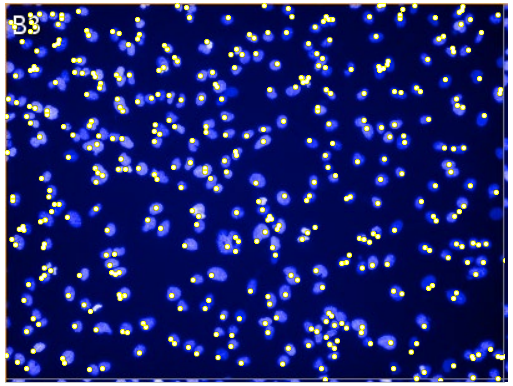


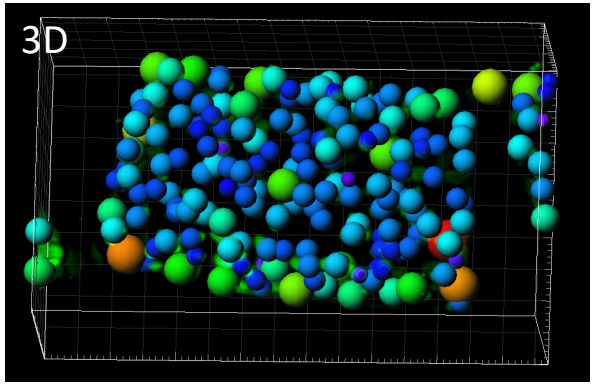
Measurement

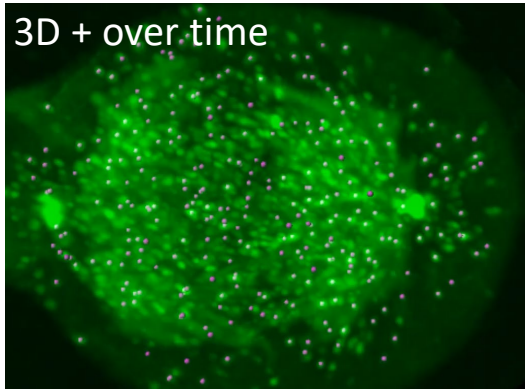
- Number
- Intensity
- Shape
- Distance (spatial analysis)
- Colocalisation / Co-occurrence
- Tracking

Number



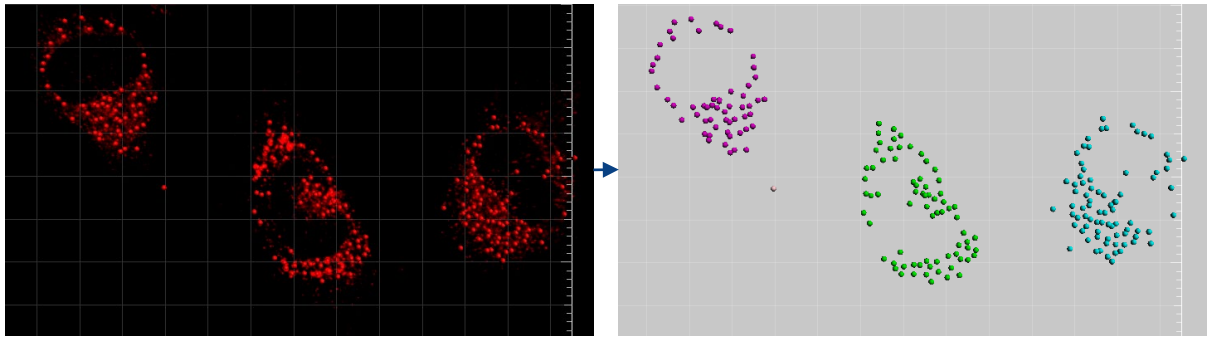






(Yamashita 2015)

Count per region of interest (ROI)

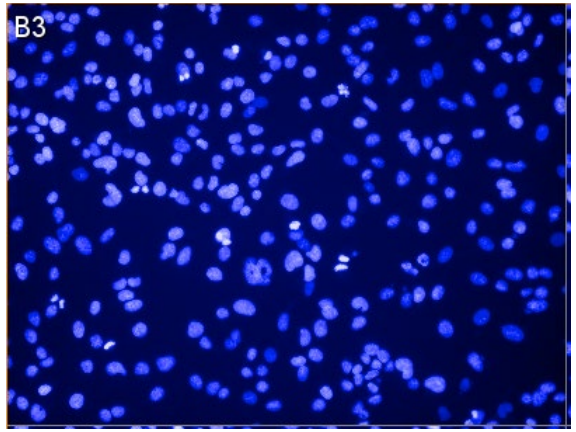


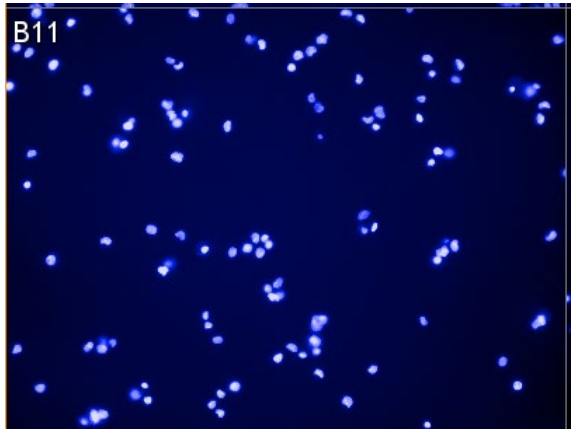
Number of Cell / Measured Area (volume)
Number of Cell / container (ROI)

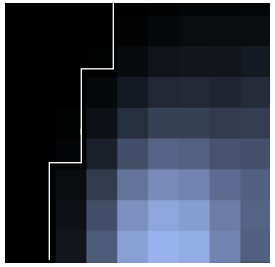
Avoid manual counting!
- Time consuming/ Impossible
- Biased

Intensity

Control **Treatment**

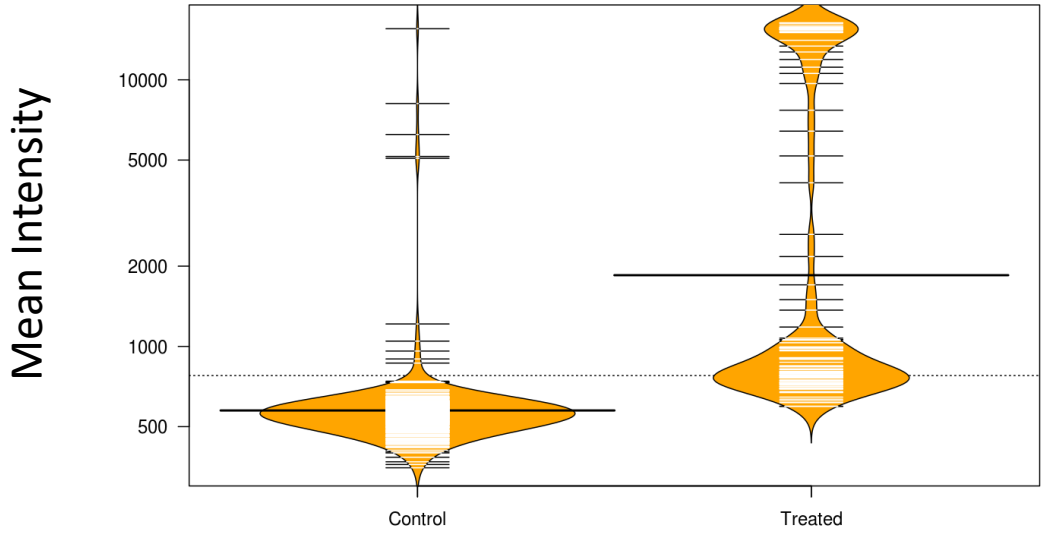






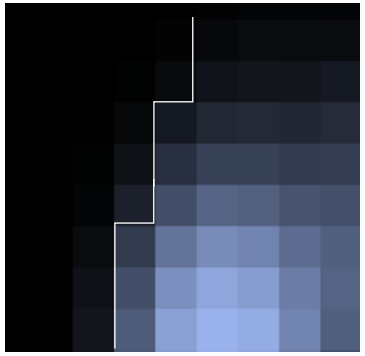
0	0	0	1	4	8	11	11	12
0	0	0	2	10	19	21	21	25
0	0	1	7	24	39	40	38	42
0	0	2	16	45	64	64	57	59
0	0	5	32	76	97	94	81	79
0	1	11	57	112	135	128	105	93
0	1	17	76	139	159	151	121	96
0	1	21	88	154	170	165	128	93

Mean Intensity
= sum intensity / area



- Treated cells are brighter
- Treated cells shows 2 distinctive populations

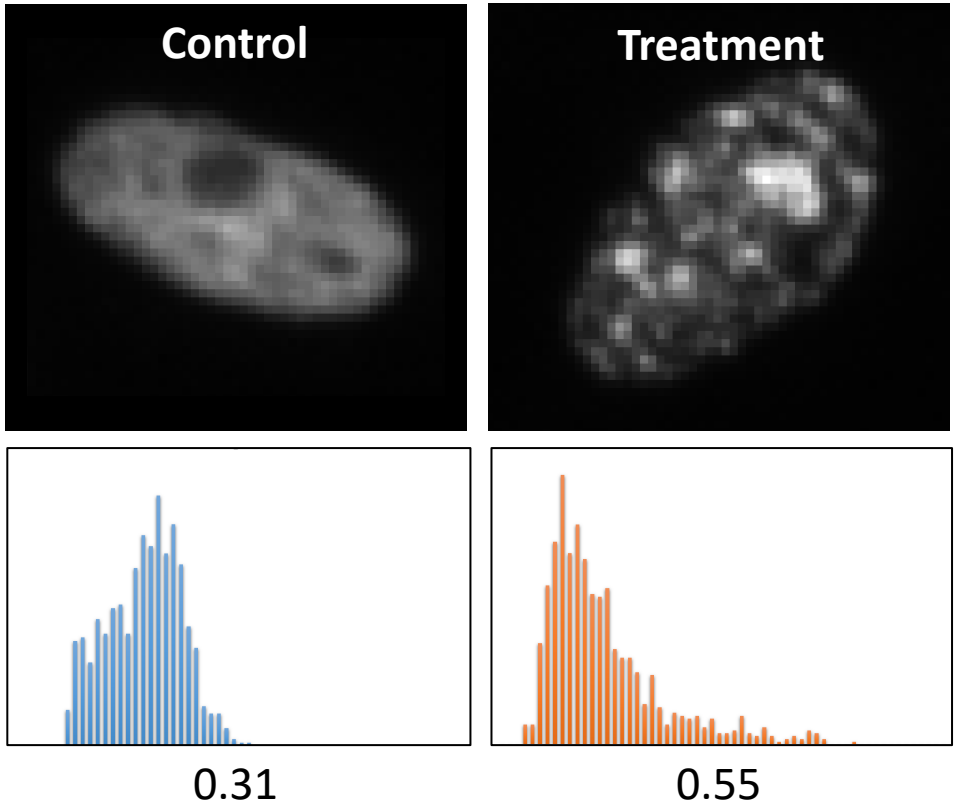
Intensity



0	0	0	1	4	8	11	11	12
0	0	0	2	10	19	21	21	25
0	0	1	7	24	39	40	38	42
0	0	2	16	45	64	64	57	59
0	0	5	32	76	97	94	81	79
0	1	11	57	112	135	128	105	93
0	1	17	76	139	159	151	121	96
0	1	21	88	154	170	165	128	93

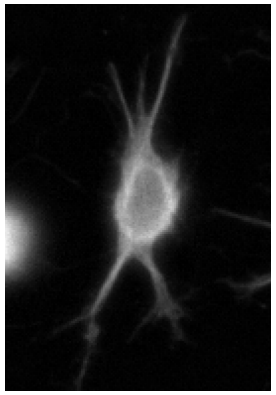
- Mean
- Minimum
- Maximum
- Median
- Sum
- StdDev

Measuring Fragmentation



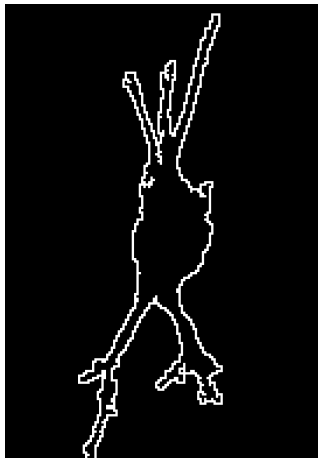
Coefficient of Variation
(StdDev/Mean)

Shape/ Morphology

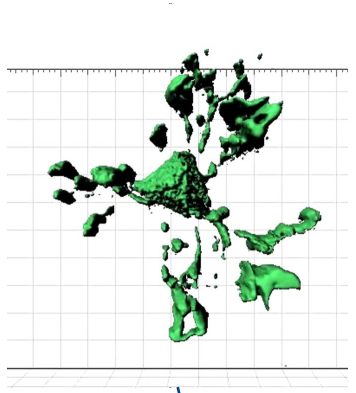


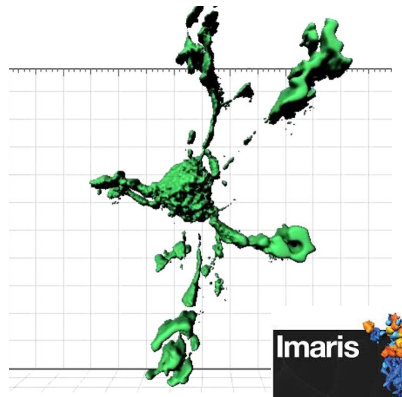
2D: Area
3D: Volume

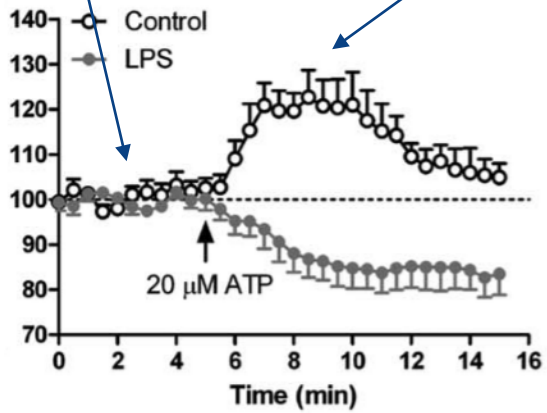
2D: Perimeter
3D: Surface Area



Ramification
(% Surface Area:Volume Ratio)

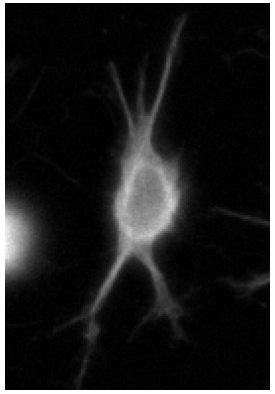




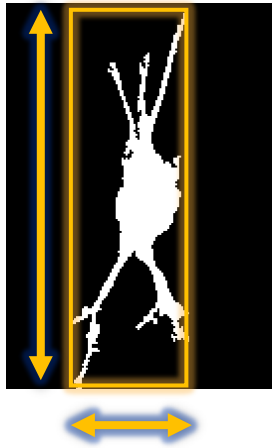


(Gyoneva 2014)

Shape/ Morphology

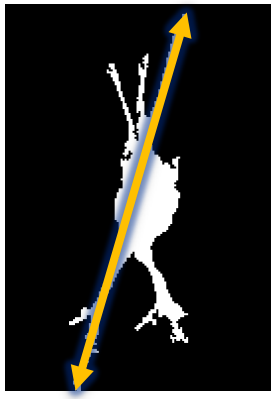


Min. bound rectangle



Aspect Ratio = :

Max Feret Diameter

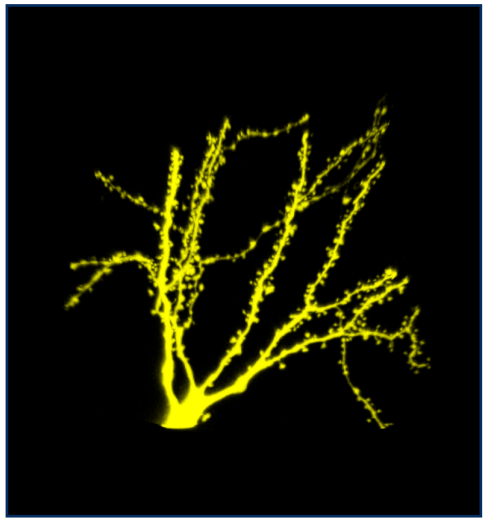


Orientation (Angle) =

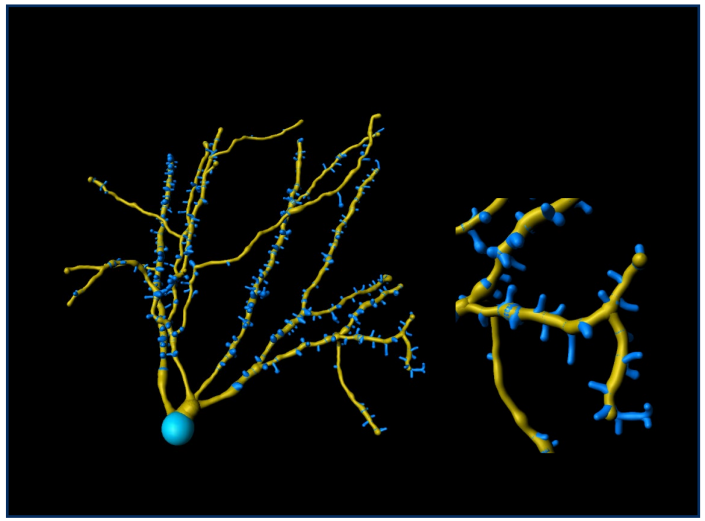
Convex Hull

Neuronal Morphology

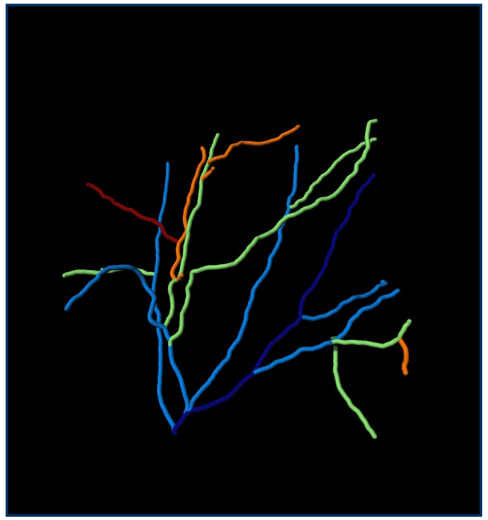
3D Volume



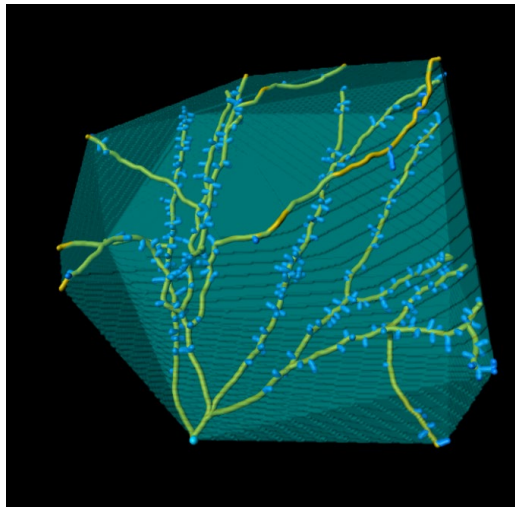
Branch & Spine

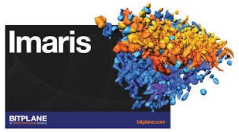


Branch level, length, angle..

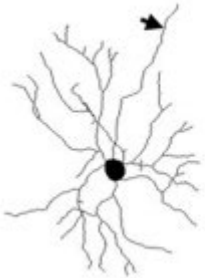


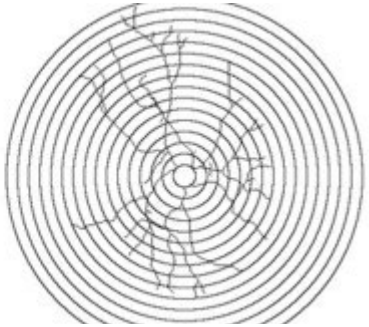
Convex Hull 3D



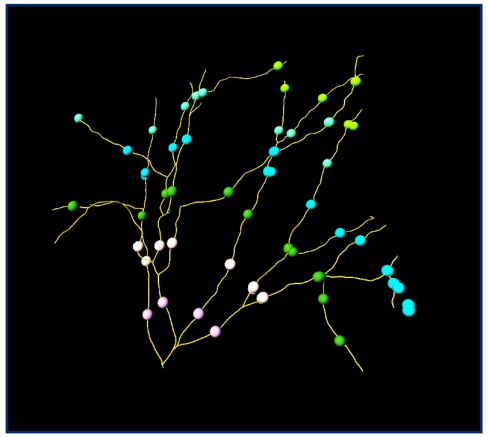


Sholl analysis:
Branch number per concentric shell



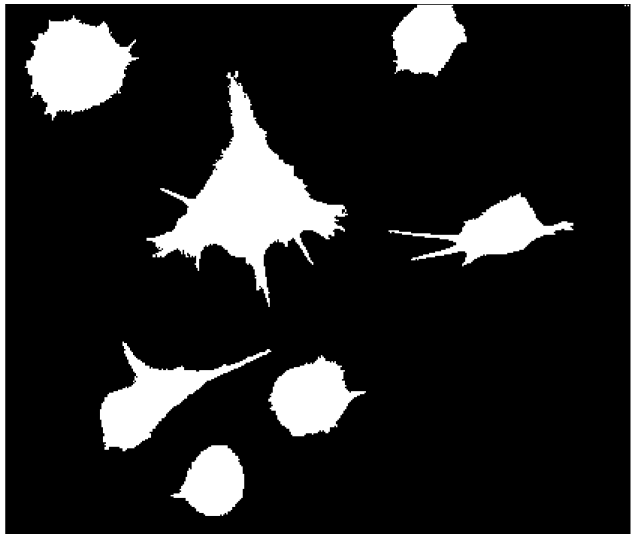


(Binley2014)

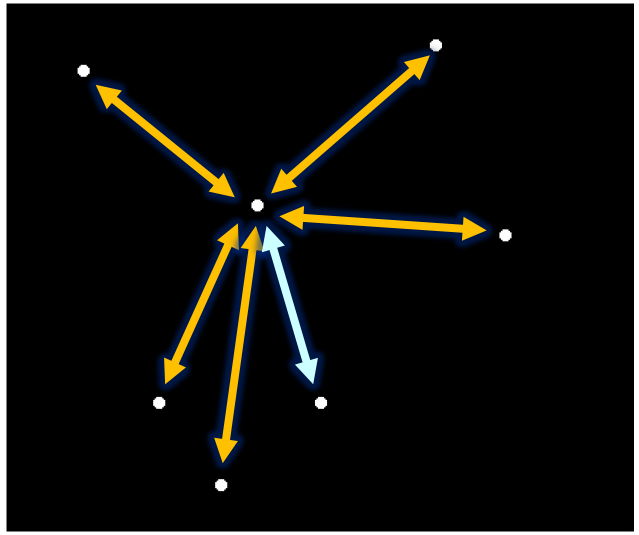


Distance

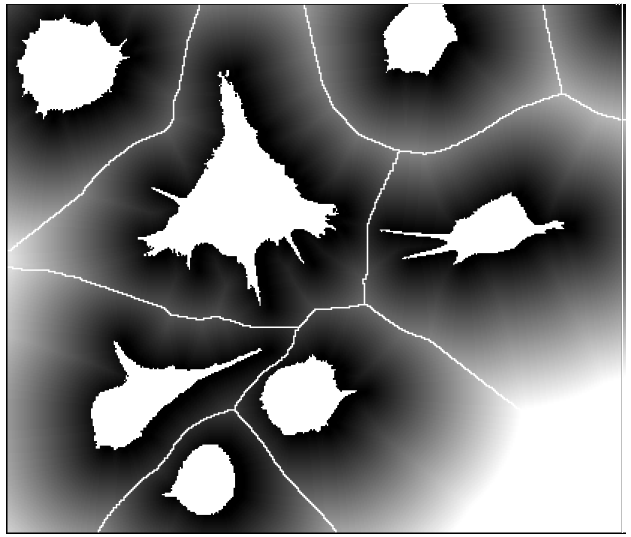
Neighbour relationships ?



Nearest Neighbour Distance
(centroid-centroid)

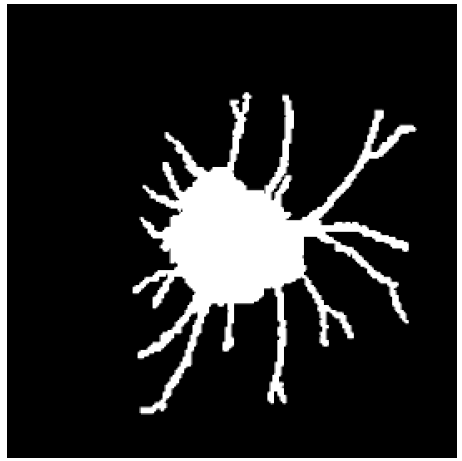


Minimum Separation Distance
(edge to edge)

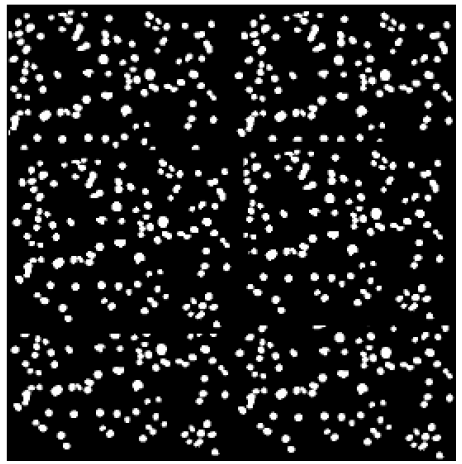


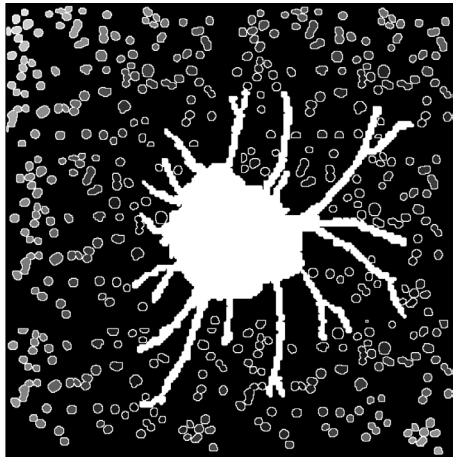
Distance

Finding touching objects

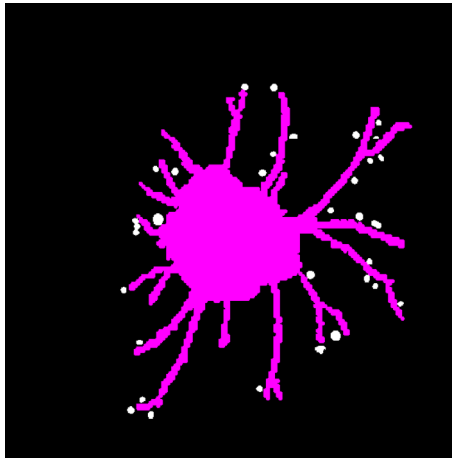


Euclidean distance map

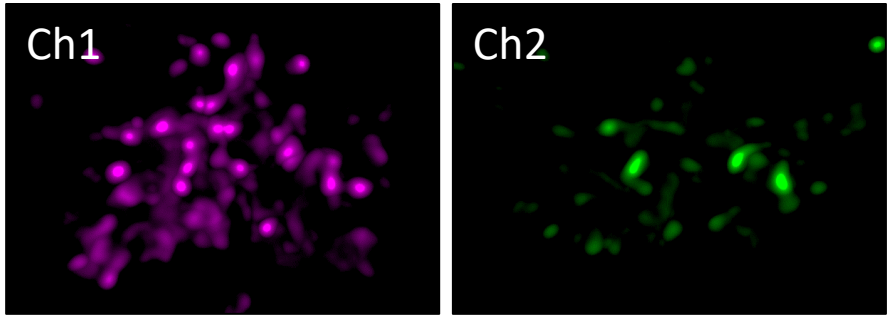




Result
(spots touching cell)

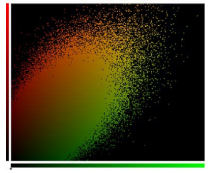


Colocalisation



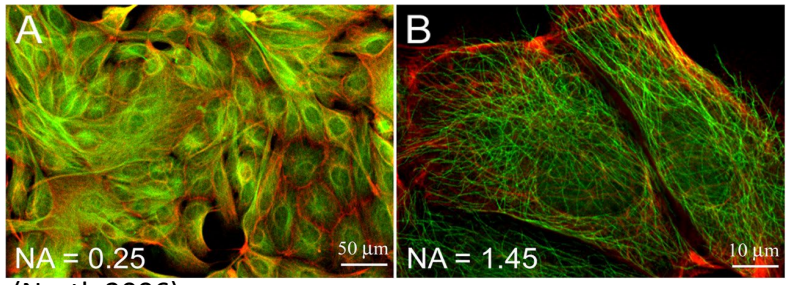
Indication of that two fluorophores are **generally near** each other

molecules are on the *same location*
molecules are *interacting*



- Correlation - Is there a relationship between intensities? (Pearson's)
- Co-occurrence - Are the fluorophores are generally near each other ?
  - Intensity based : Mander's Coefficient
  - Object based : overlapping area or volume

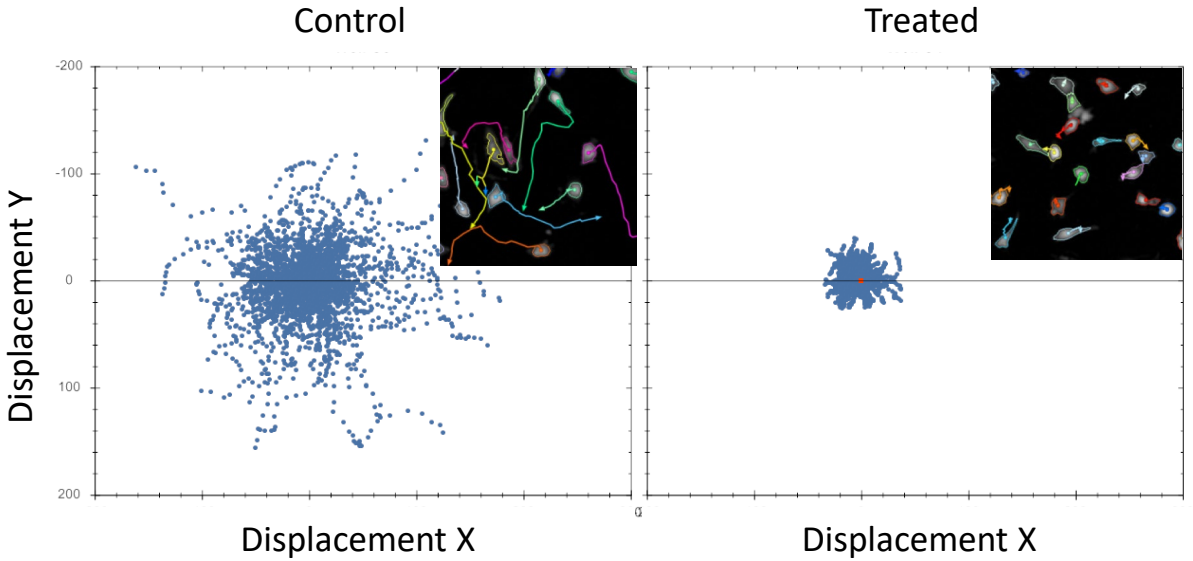
Quantification is heavily dependent on the resolution of acquisition system so careful planning is required

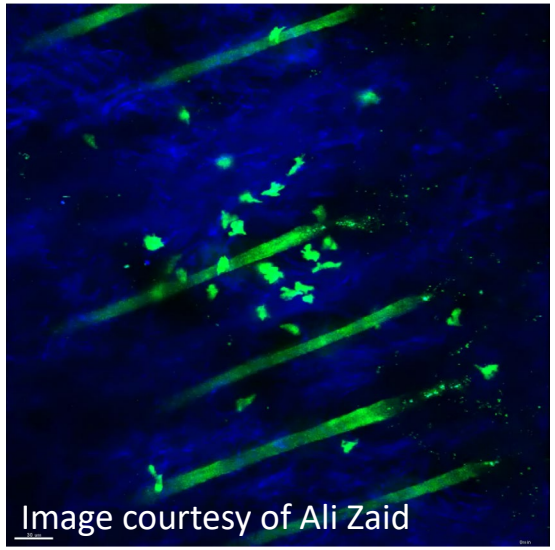


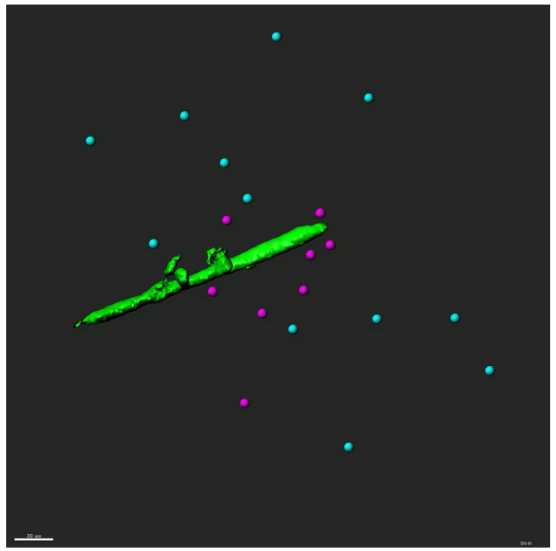
(North 2006)

Colocalisation Workshop (https://microscopy.unimelb.edu.au/)

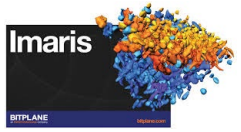
Tracking





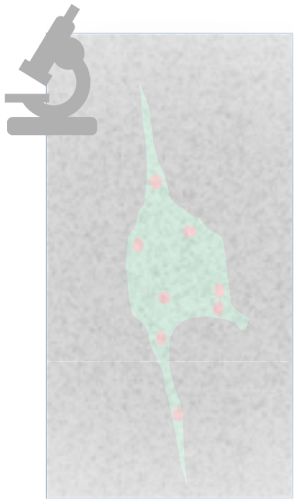


- Speed (µm/s)
- Displacement (µm)
- Accumulated distance (µm)
- Straightness
- Duration (s)



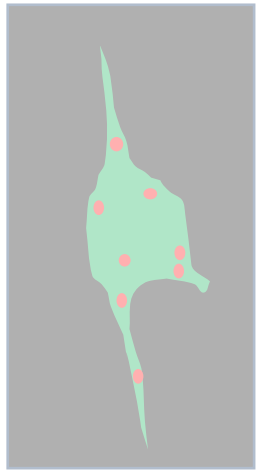
Reporting

Acquisition

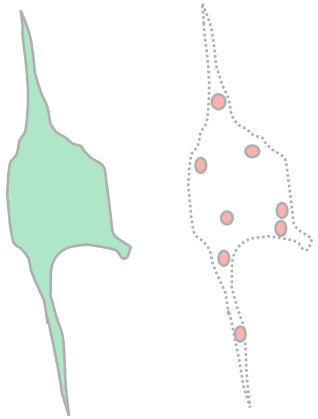


Raw microscopy image

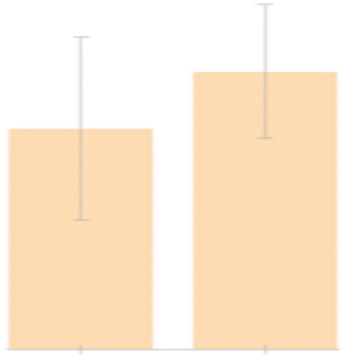
Pre-processing



Object Segmentation

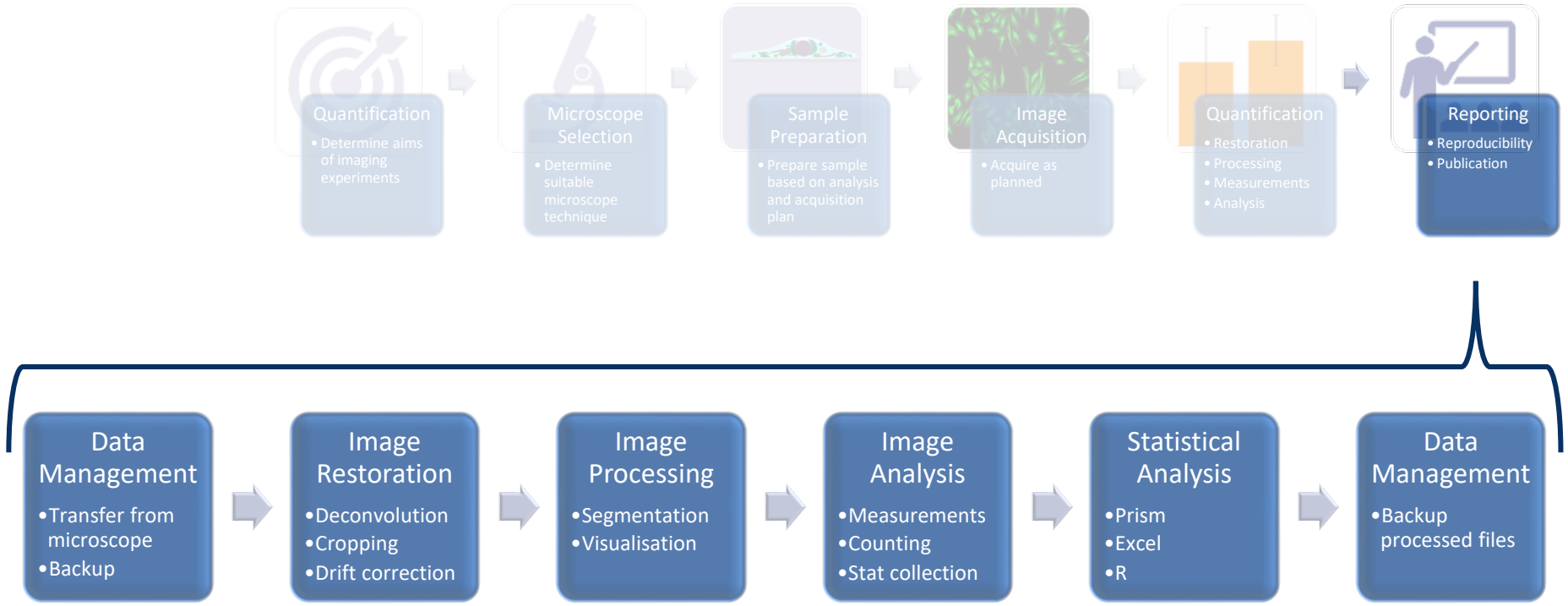


Measurement / Data analysis



Reporting

Performing Bio-image Analysis



- Complex workflows require a detailed reporting
- Reporting also includes being able to track down your data

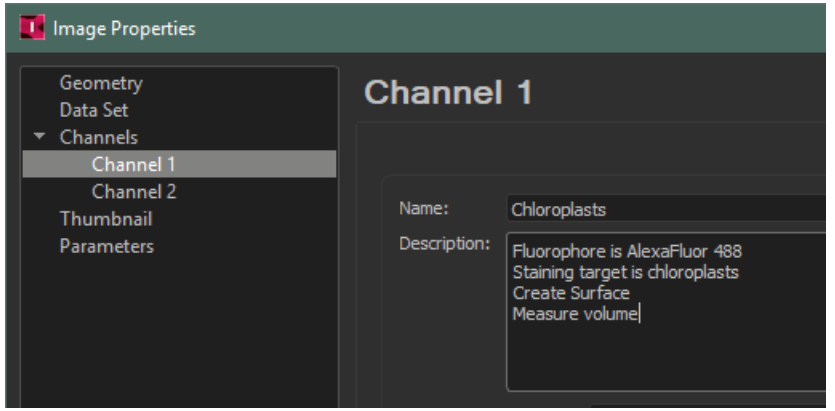
Reporting Analysis (or Acquisition)

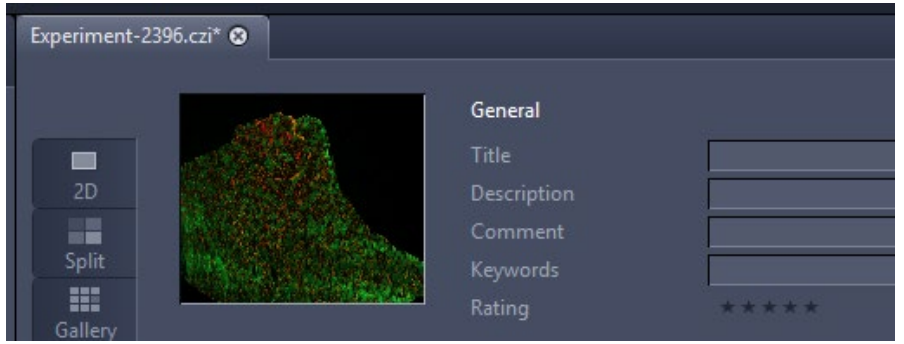
Aim:

1. Reproducibility (individually or within a group)
2. Knowledge retention
3. Materials and Methods

Reporting / recording:

- Take note of main steps and parameters in your analysis workflow (acquisition)
- Add experimental information in files e.g:
  - channel descriptions in Imaris
  - editing Track names in Zen
  - Adding comments in any program if possible



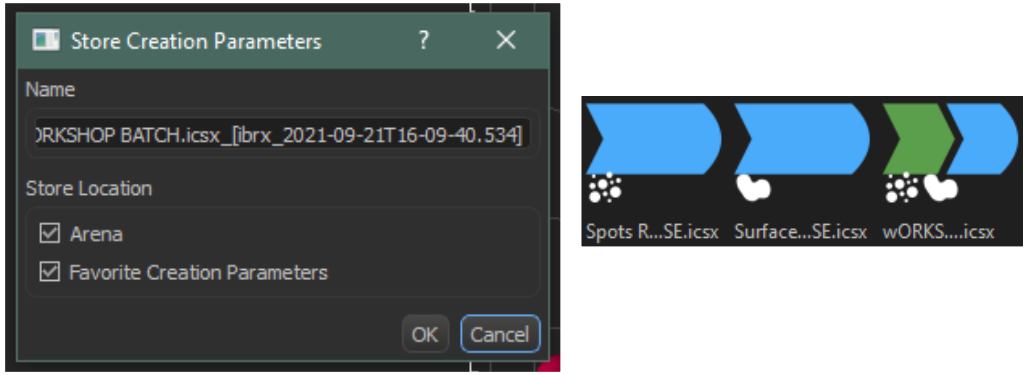


Keeping a Digital Record

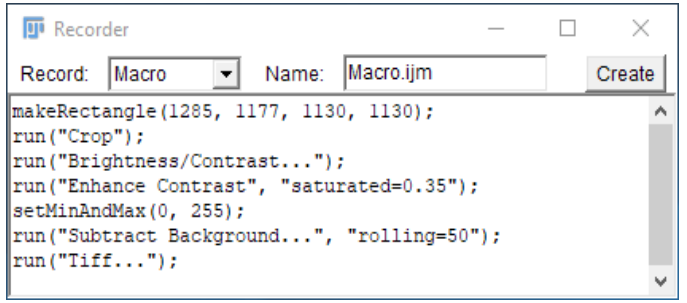
Save templates / settings files

- Programs with exportable settings files are Imaris, Huygens, CellProfiler, Harmony

Imaris templates



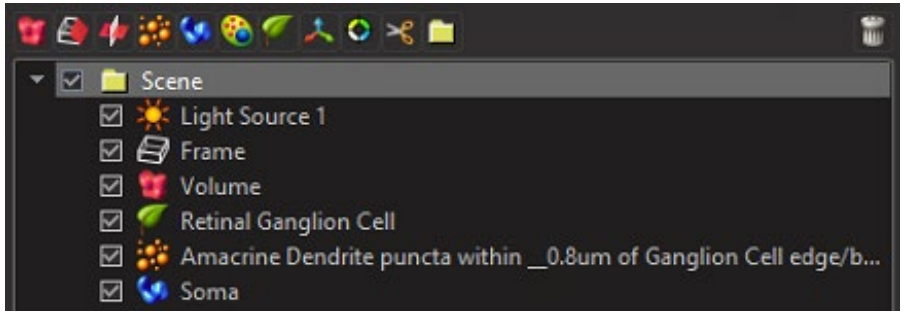
- FIJI recorder can record all processing steps and save as a text file



Representative example

- Pros: reproducibility, contains more information than you can write down
- Easier troubleshooting

Imaris Example



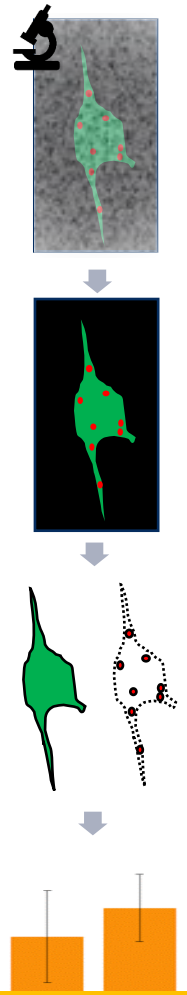
Bioimage Analysis Workflow

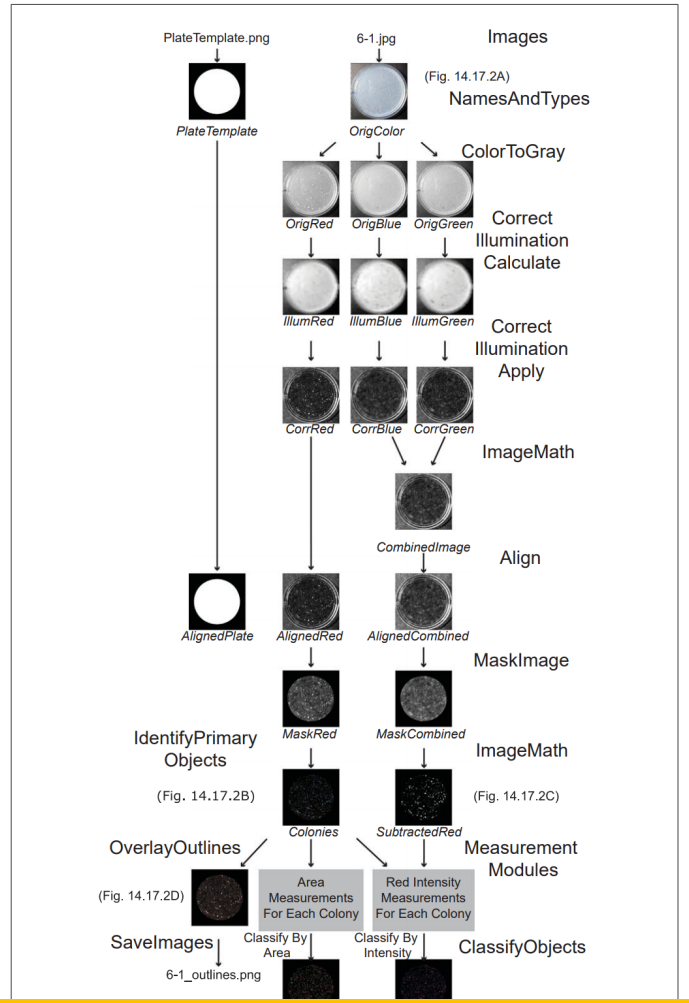
Acquisition

Pre-processing

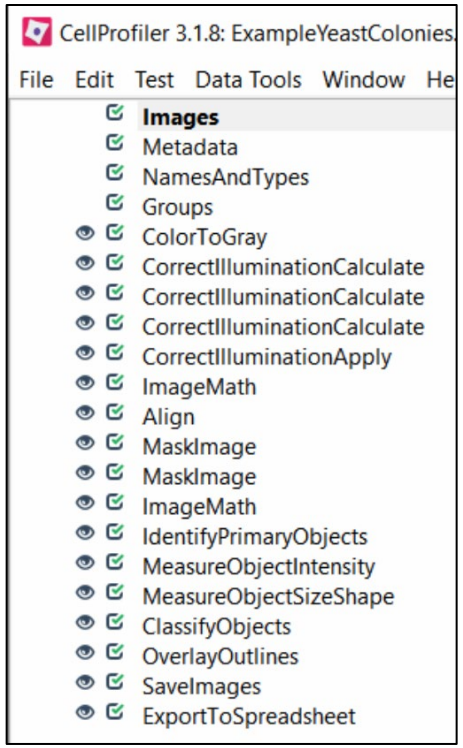
Object Segmentation

Measurement / Data analysis





Cell Profiler



CellProfiler Workshop (https://microscopy.unimelb.edu.au/)

(Bray 2015)

Automate Analysis


ImageJ macro
(save as .ijm)

*Process_Folder.ijm

```
#@ File (label = "Input directory", style = "directory") input
#@ File (label = "Output directory", style = "directory") output
#@ String (label = "File suffix", value = ".tif") suffix

// See also Process_Folder.py for a version of this code
// in the Python scripting language.

processFolder(input);

// function to scan folders/subfolders/files to find files with correct suffix
function processFolder(input) {
    list = getFileList(input);
    list = Array.sort(list);
    for (i = 0; i < list.length; i++) {
        if(File.isDirectory(input + File.separator + list[i]))
            processFolder(input + File.separator + list[i]);
        if(endsWith(list[i], suffix))
            processFile(input, output, list[i]);
    }
```

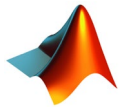
ImageJ Macro writing workshop (https://microscopy.unimelb.edu.au/)

Icy


Python w Scikit-Image

apeer

QuPath



Matlab

Knime

...more

Collaborate with us (bomp-enquiries@unimelb.edu.au)

BOMP Workshop Resources

- Workshops run once a year, but workshop resources available online all-year round!
  - https://microscopy.unimelb.edu.au/bomp/capabilities/workshops-resources
- Good source for getting knowledge
- Other good resources:

Forum on Bioimage analysis https://forum.image.sc/

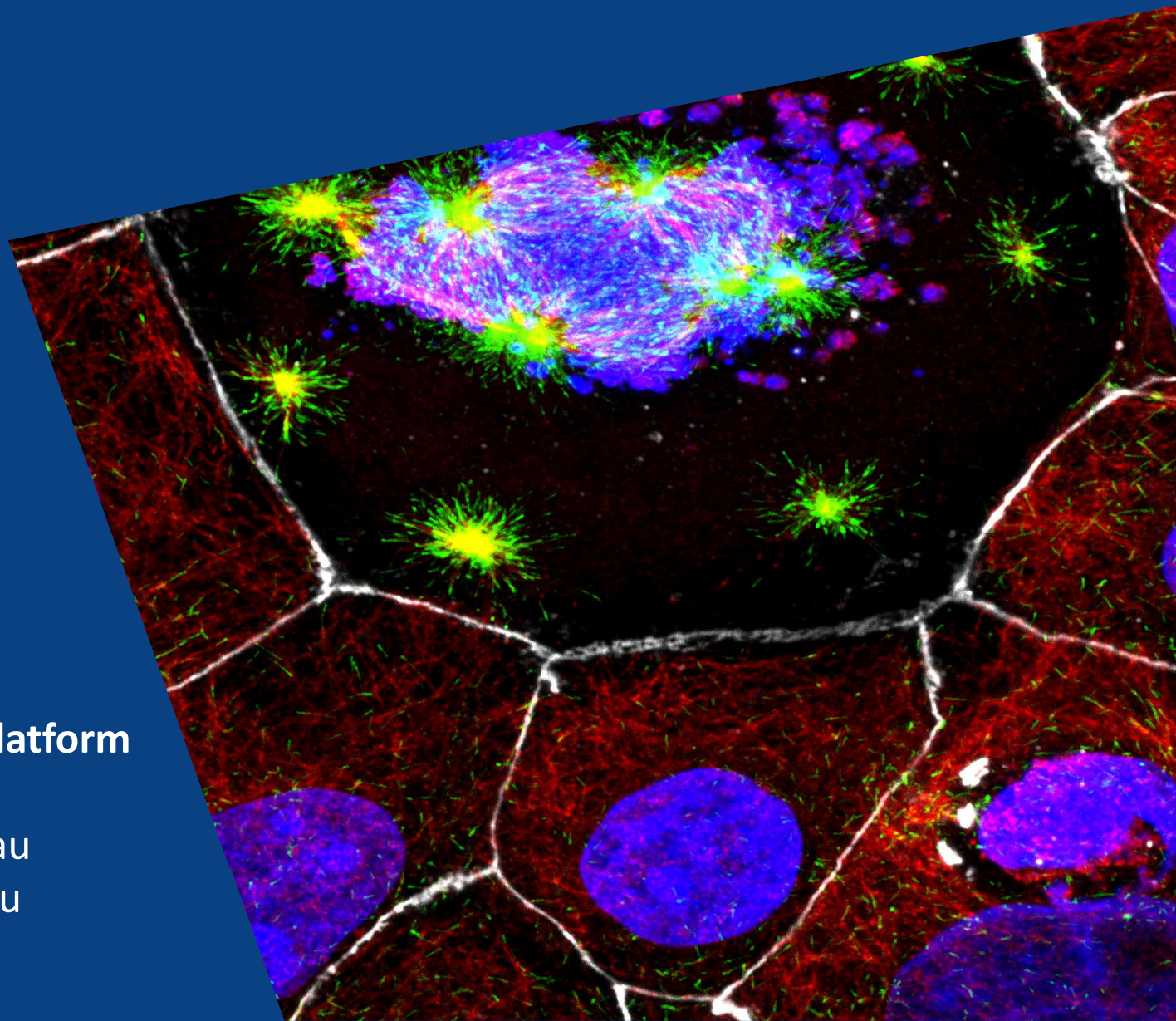
ImageJ learn https://imagej.net/Introduction

Cell Profiler https://cellprofiler.org/

NEUBIAS academy https://neubiasacademy.org/

THE UNIVERSITY OF MELBOURNE

Thank you



Biological Optical Microscopy Platform

bomp-enquiries@unimelb.edu.au
www.microscopy.unimelb.edu.au

BOMP Workshop Schedule

Date	Day	Format	Time	Event	Type
7th March	Tuesday	1hr	11-12pm	Launching Seminar : Stellaris 5	Seminars
14th March	Tuesday	1hr	10-11am	**Introduction to**: Bio-image Analysis	Seminars
15h March	Wednesday	1hr	10-11am	Launching Seminar : LSM980	Seminars
28th March	Tuesday	1day	10-12pm & 2-4pm	**BOMP workshop series:** FIJI/ImageJ for Beginners	Workshop
30th March	Thursday	1day	10-12pm & 2-4pm	**BOMP workshop series**: FIJI/ImageJ for Quantification	Workshop
27th April	Tuesday	1day	9-1pm	**BOMP workshop series:** Cell Profiler	Workshop
Early May		1hr x 2	10-12pm	**Introduction to:** Fluorescence Microscopy	Seminars
29th June	Thursday	1day	10-12pm & 2-4pm	**BOMP workshop series:** Huygens deconvolution	Workshop
25th July	Tuesday	1day	9-12pm & 1-4pm	**BOMP workshop series:** IMARIS 3D image analysis - Basic	Workshop
27th July	Thursday	1day	9-12pm & 1-4pm	**BOMP workshop series:** IMARIS 3D image analysis - Advanced	Workshop
15th Aug	Tuesday	1hr	10-11am	**Focus on:** Lightsheet Microscopy	Seminar & Demo
29th Aug	Tuesday	1hr	10-11am	**Focus on:** High Content Imaging	Seminar & Demo
5th Sep	Tuesday	0.5day	9-12pm	**BOMP workshop series:** Zen Intellesis	Workshop
12th Sep	Tuesday	1hr	10-11am	**Focus on:** Super-Resolution Microscopy	Seminar & Demo
26th Sep	Tuesday	1day	10-12pm & 2-4pm	**BOMP workshop series:** Colocalisation	Workshop
11th Oct	Tuesday	1day	10-12pm & 2-4pm	**BOMP workshop series:** QuPath - Fluorescence	Workshop
24th Oct	Tuesday	0.5 day	9-12pm	**BOMP workshop series:** FIJI/ImageJ Macro writing for biologists - Day1	Workshop
26th Oct	Thursday	0.5 day	9-12pm	**BOMP workshop series:** FIJI/ImageJ Macro writing for biologists - Day2	Workshop
28th Nov	Tuesday	1day	10-12pm & 2-4pm	**BOMP workshop series:** Image Segmentation	Workshop