



Introduction to image processing and analysis with ImageJ / Fiji.

Part 6

Colocalisation, cell tracking,
other software

Course by Dale Moulding



Session 6

15 minute lecture

Learning objectives:

- Correct background for better analysis
- Develop multiple strategies for image analysis
- Use filters to pre-process images
- Cell counting. Manually and automatic
- Thresholding to generate binary images and masks
- Identifying double / triple stained cells
- **Explain the difference between colocalization and co-expression**
- **Track moving objects**
- **Access other useful (free) software**



Colocalisation v co-expression

https://imagej.net/Colocalization_Analysis

- Identifying double stained cells is not measuring colocalisation
- Double stained cells are identified as overlapping objects
- Colocalisation analysis is a measure of the degree of overlap & the relationship in intensity between two channels.
- It is often measured as Pearson's correlation coefficient and Manders split coefficients.



Colocalisation v co-expression

https://imagej.net/Colocalization_Analysis

- Pearson's gives a measure of the intensity relationship between 2 channels.
1 = perfect correlation, 0 = n correlation, -1 = perfect exclusion
- Measured in every pixel (or voxel) of an image. Perfect colocalisation may be expected between 2 subunits of a protein complex.
- SubUnit-A & SubUnit-B are always found together in cells. If there is a lot of A in a particular pixel, there will be an equivalent amount of B. As the intensity of one Subunit rises or falls, the other does so to exactly the same degree.



Colocalisation v co-expression

https://imagej.net/Colocalization_Analysis

- Manders gives an indication of the amount of fluorescence (above a pre-defined background level) in each of 2 channels that is found in the same place as the other channel.
- It does not measure the relative amounts of each channel, rather it gives a value from 0 to 1 indicating the fraction of Channel A signal that overlaps with Channel B & vice versa. The values for each channel are likely to be different.
- The value given is not a statistical measure. You need to measure multiple images for a statistical analysis.



Colocalisation v co-expression

https://imagej.net/Colocalization_Analysis

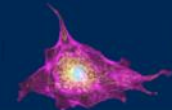
- ImageJ / Fiji plugins Coloc 2 & JaCoP can be used for both Manders and Pearsons analysis.
- Great care must be taken in these measurements. Image noise, resolution, background, intensity (too bright / too dim) etc etc can all have a massive impact on the analysis.
- Get expert help!
- Read the link above very carefully.



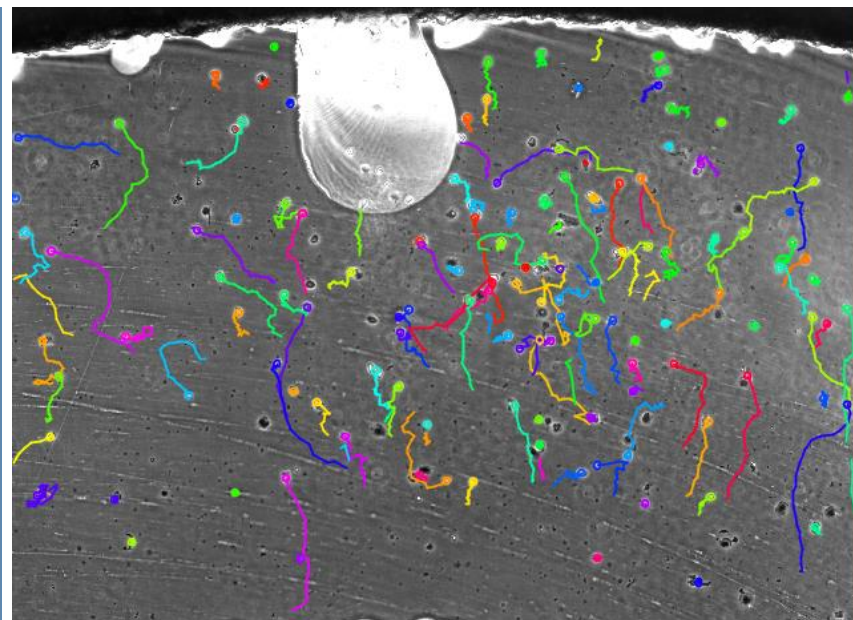
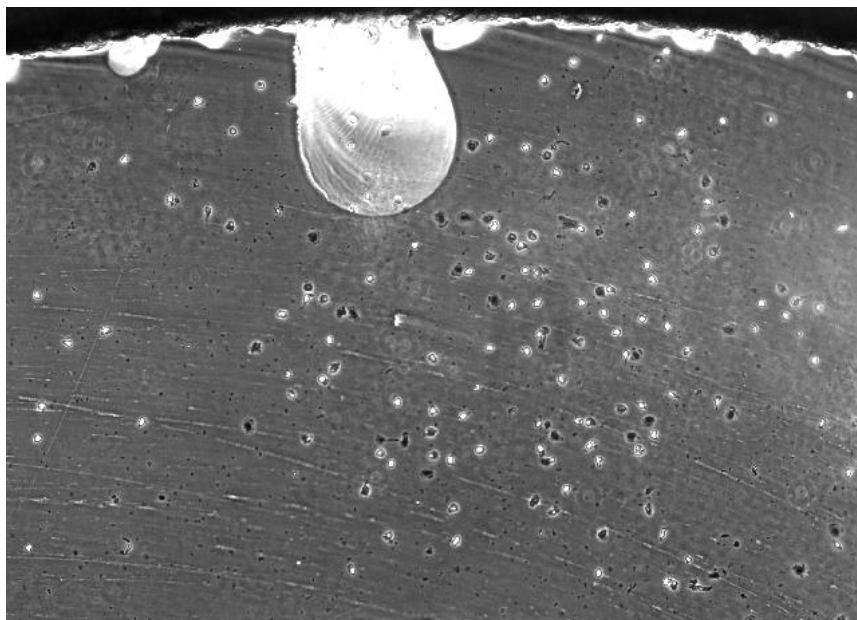
Colocalisation v co-expression

https://imagej.net/Colocalization_Analysis

- Co-expression: you get a count of the proportion of objects that overlap between two different channels
- Colocalisation: you get an indication of the interaction between two channels, either as the degree of agreement between the intensity in each channel (Pearson's) or the degree of overlap in signal between two channels (Manders).



Object tracking in time-lapse imaging



Objects (cells, organelles etc) can be tracked over time, to measure their movement.

- Speed – steady? variable?
- Direction
- Tortuosity



Object tracking in time-lapse imaging – Image registration

- Multi-point time-lapse imaging may have image drift. The stage / sample may move slightly between positions.

- This can be corrected: Image registration

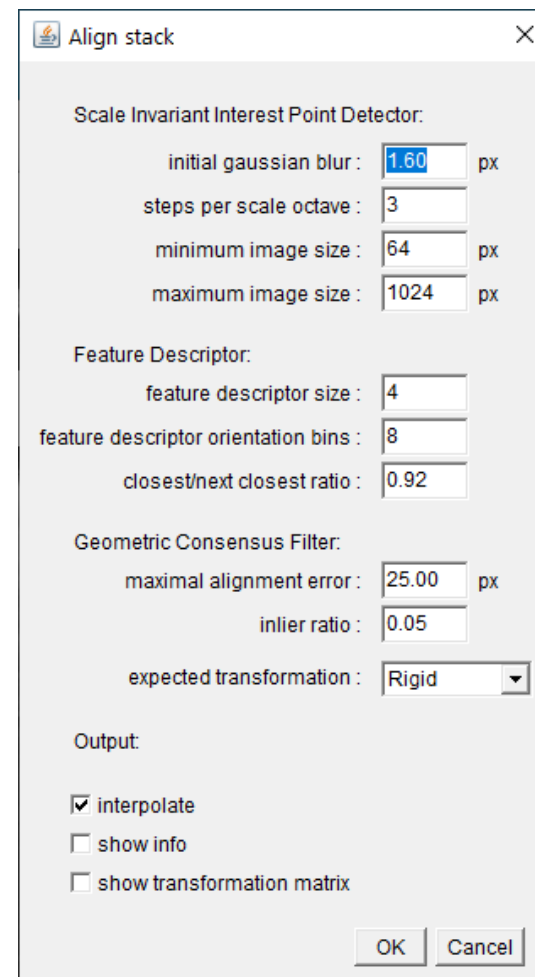
Plugins / registration >

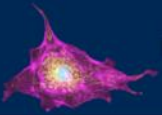
Linear Stack Alignment with SIFT

Or

Plugins / registration > StackReg

(Big-EPFL update site)





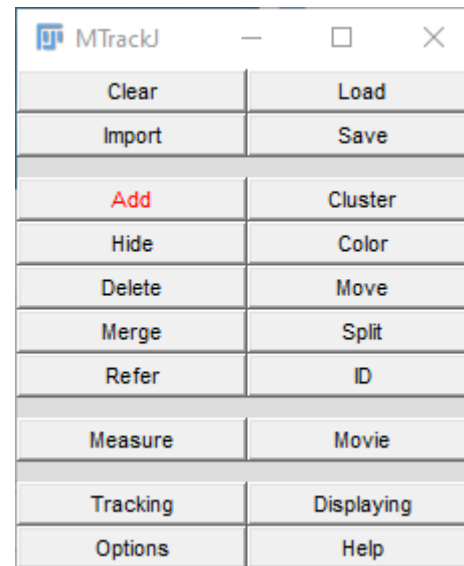
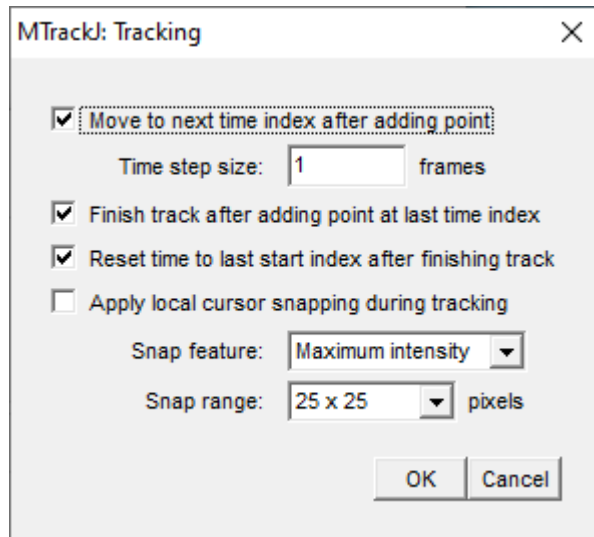
Object tracking in time-lapse imaging

<https://image.science.org/meijering/software/mtrackj/>

Plugins / MTrackJ

(requires ImageScience update site in Fiji)

Extremely well documented on the website.



Manual tracking. Click an object, the image advances one frame click again, etc etc...



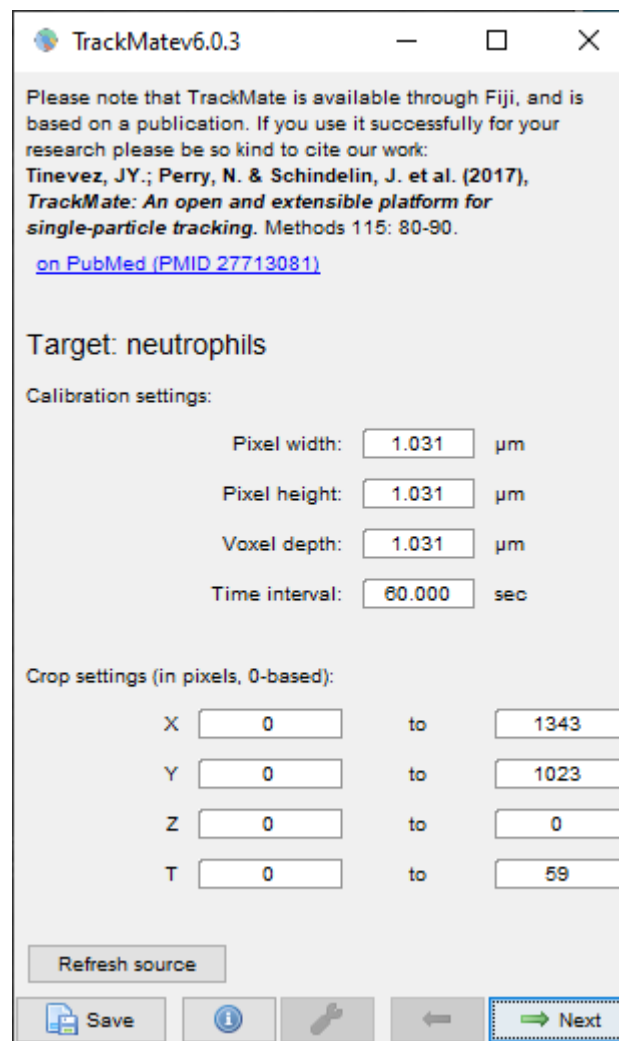
Object tracking in time-lapse imaging

<https://imagej.net/TrackMate>

Plugins / Tracking / TrackMate

Extremely well documented on the website.

Automatic tracking. Follow the step by step interface, fine tune the parameters to detect objects.



TrackMatev6.0.3

Please note that TrackMate is available through Fiji, and is based on a publication. If you use it successfully for your research please be so kind to cite our work:
Tinevez, JY.; Perry, N. & Schindelin, J. et al. (2017), *TrackMate: An open and extensible platform for single-particle tracking*. Methods 115: 80-90.
[on PubMed \(PMID 27713081\)](https://pubmed.ncbi.nlm.nih.gov/27713081/)

Target: neutrophils

Calibration settings:

Pixel width:	<input type="text" value="1.031"/>	µm
Pixel height:	<input type="text" value="1.031"/>	µm
Voxel depth:	<input type="text" value="1.031"/>	µm
Time interval:	<input type="text" value="60.000"/>	sec

Crop settings (in pixels, 0-based):

X	<input type="text" value="0"/>	to	<input type="text" value="1343"/>
Y	<input type="text" value="0"/>	to	<input type="text" value="1023"/>
Z	<input type="text" value="0"/>	to	<input type="text" value="0"/>
T	<input type="text" value="0"/>	to	<input type="text" value="59"/>

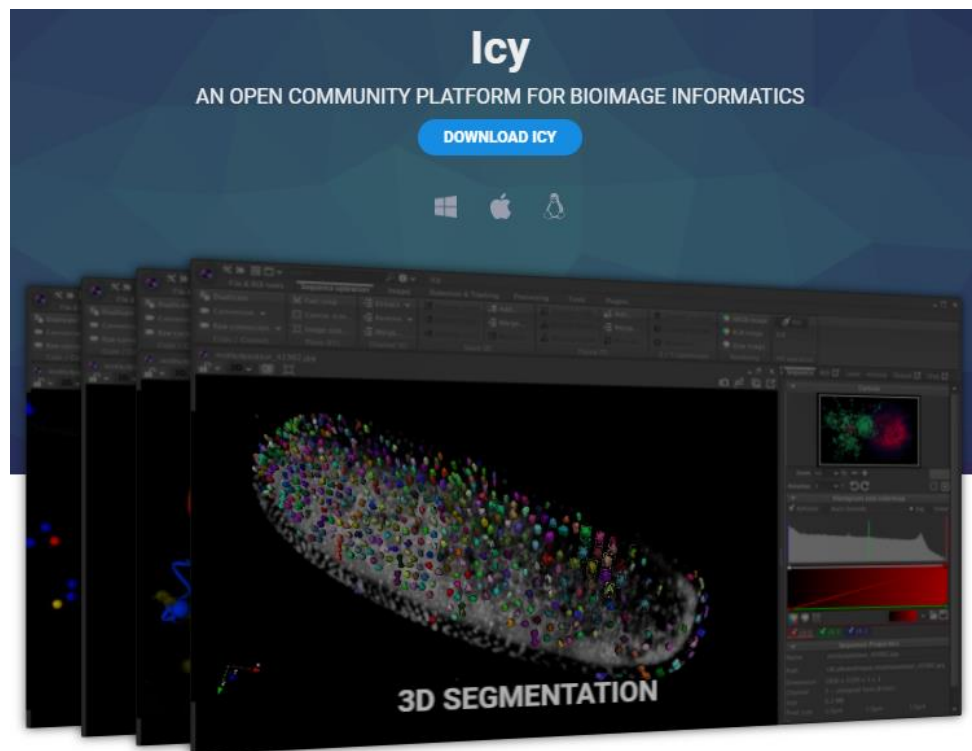
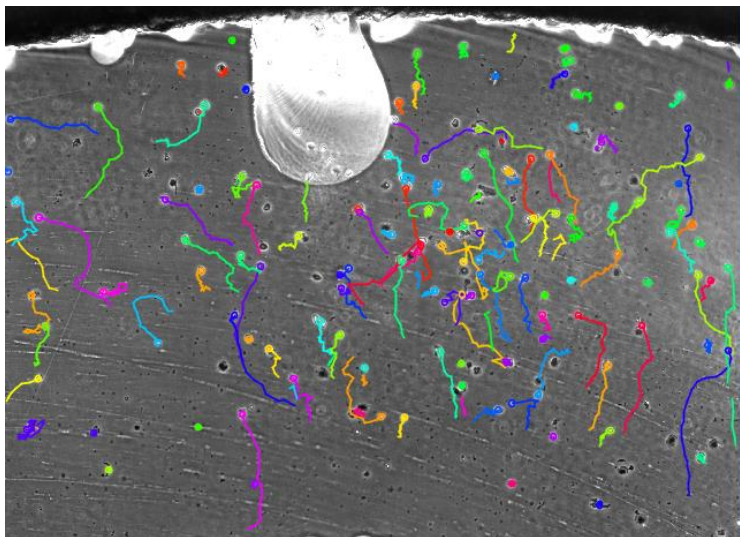


Object tracking in time-lapse imaging

<http://icy.bioimageanalysis.org/plugin/spot-tracking/>

Automatic tracking.

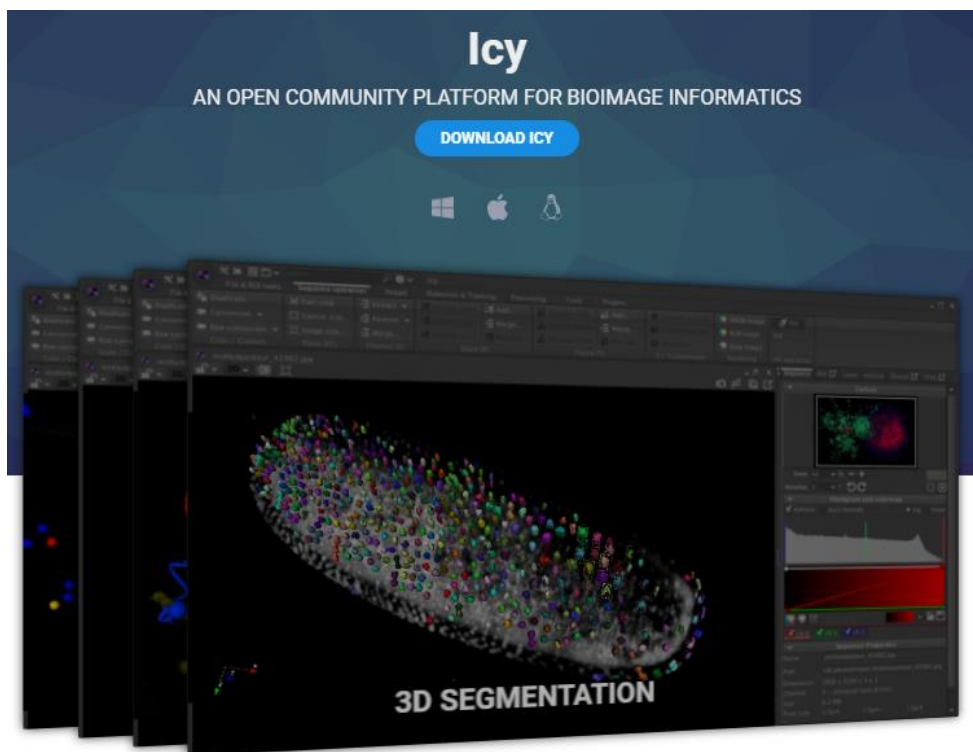
Well documented on the website.





Other open source, free Image Analysis software

<http://icy.bioimageanalysis.org/>



- Great companion to Fiji
- 3D image analysis
- 3D visualisation
- Object tracking
- Segmentation etc
- Automation via scripts & protocols

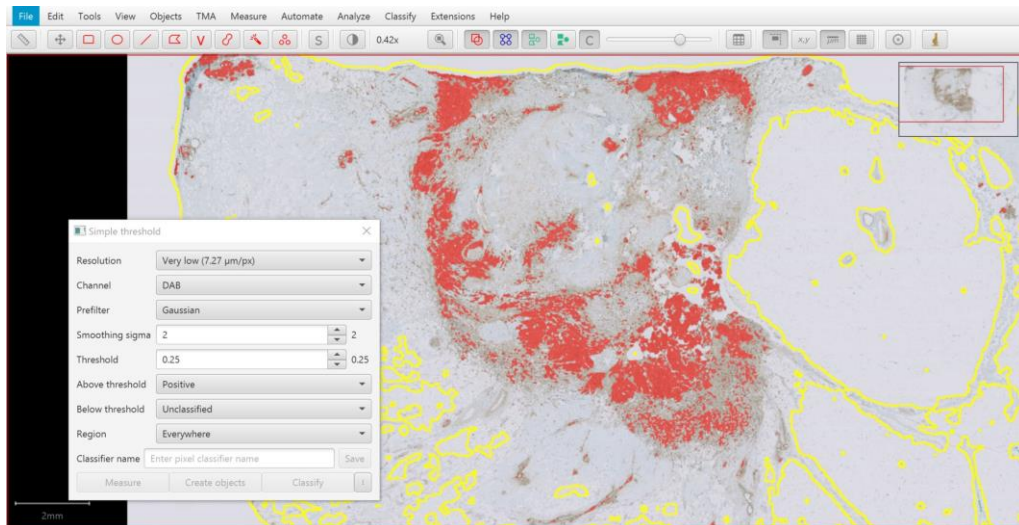


Other open source, free Image Analysis software

<https://qupath.github.io/>



- Fantastic histopathology analysis
- H&E, DAB etc
- Segmentation, counting, machine learning
- Fluorescence
- User guides, videos etc make learning the software very easy





Other open source, free Image Analysis software

<https://cellprofiler.org/>



CellProfiler™
cell image analysis software

- High content screen
- Designed to analyse massive data sets
- Well documented
- Templates for many standard analysis protocols
- Templates relatively easily adapted to your own analysis

