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UNIVERSITÀ DEGLI STUDI DI TORINO



# From microtubules tracking to cell nuclear volume evaluation: swapping from T to Z axis in confocal microscopy

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## Introduction

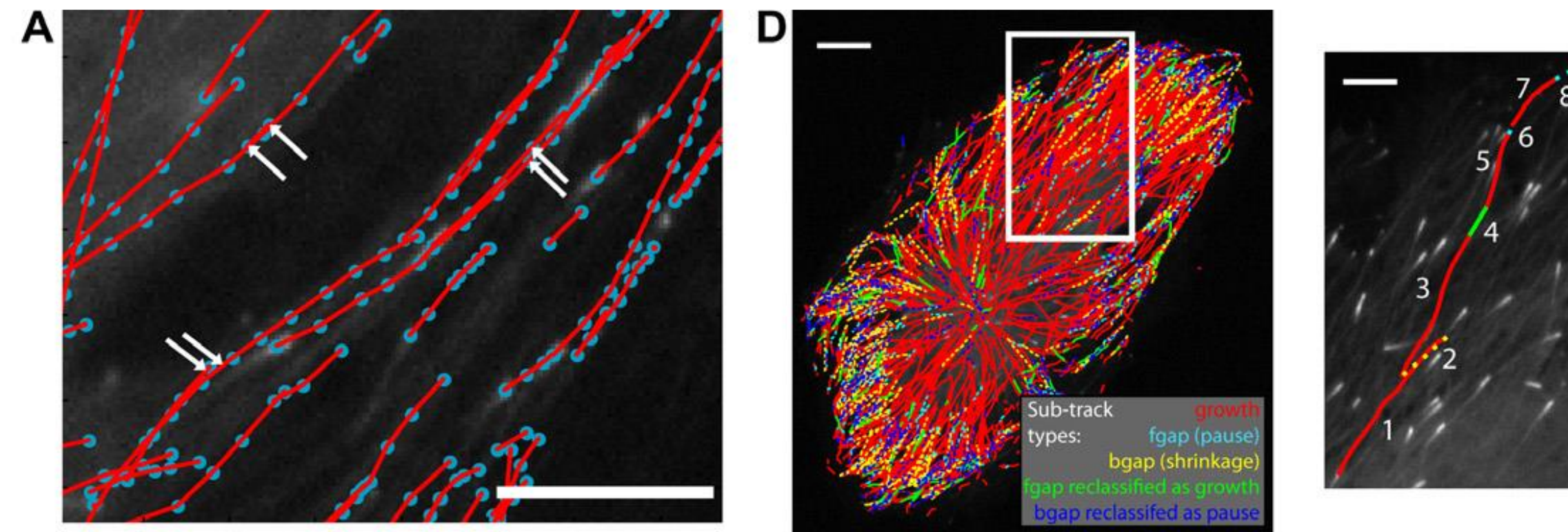
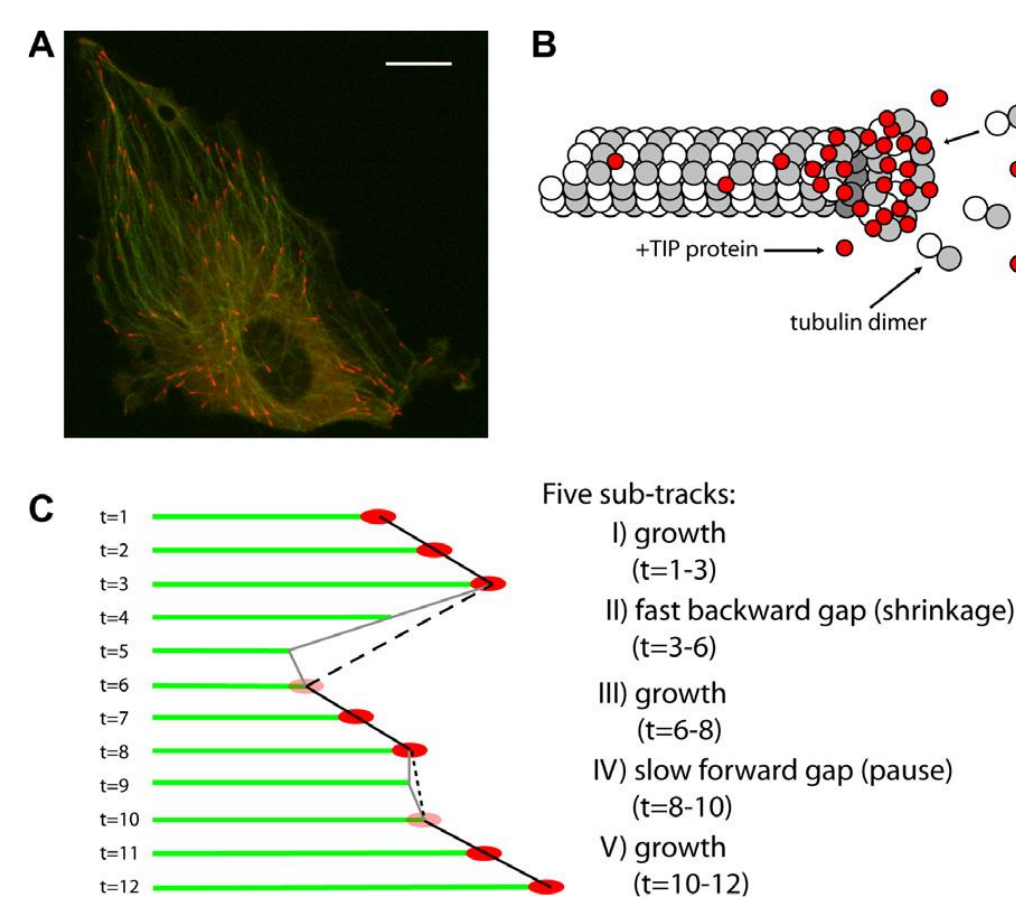
Image post processing with Matlab and ImageJ: microtubules dynamics, endoreduplicated nuclei size

- Microtubules dynamics measurements: growth rate, shrinkage. Time series images in confocal microscopy, post processing imaging with Matlab PlusTipTracker

- Endoreduplication: size of the nuclei which double DNA content without dividing. Z series images in confocal microscopy, post processing imaging with three compared methods: Our designed plugin in ImageJ, 3D Object counter in ImageJ, TrackMate in ImageJ.

## T Axis

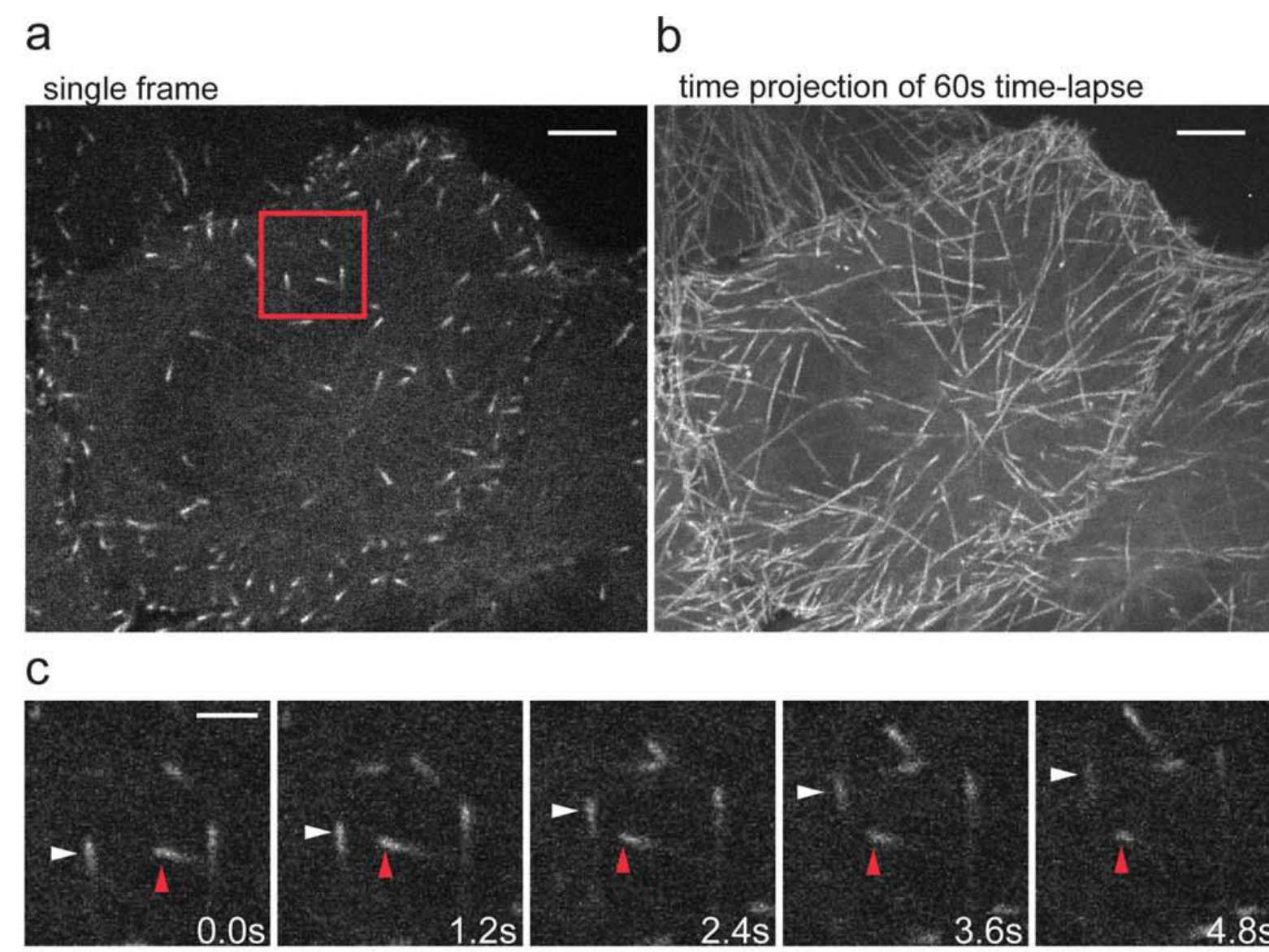
Microtubules dynamics can be evaluated analyzing time-series images of fluorescently labeled microtubule plus end binding proteins.



Matlab

PlusTipTracker

Kathryn T. Applegate, Sebastien Besson, Alexandre Matov, Maria H. Bagonis, Khuloud Jaqaman, Gaudenz Danuser (2011) plusTipTracker: Quantitative image analysis software for the measurement of microtubule dynamics Journal of Structural Biology 176, 168-184



Anne Straube (2011) How to measure microtubule dynamics? Anne Straube (ed.), *Microtubule Dynamics: Methods and Protocols*, Methods in Molecular Biology, vol. 777, 2011, pp 1-14

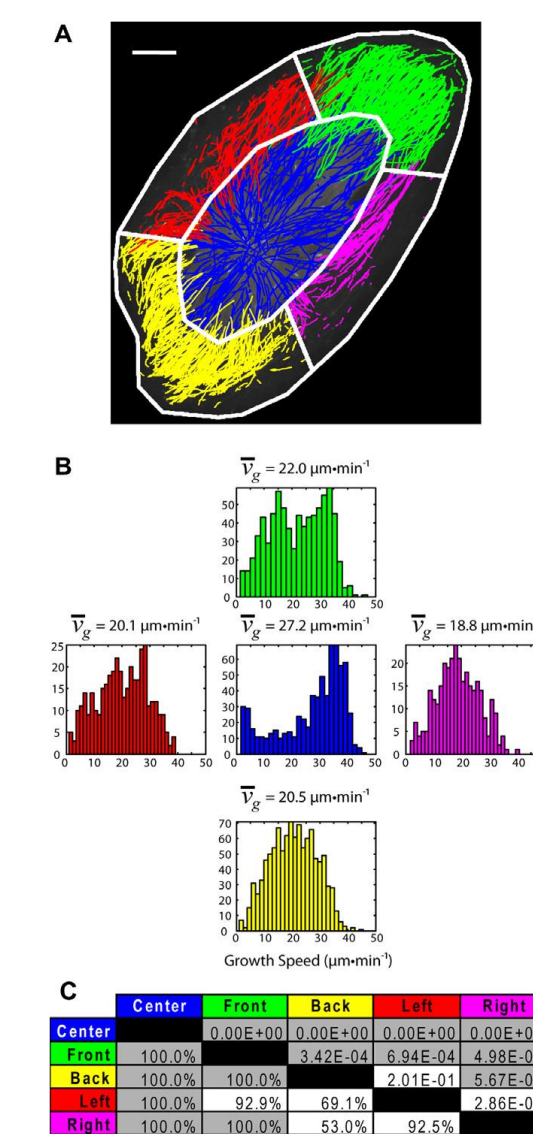


Table 2. Detected comets and velocities automatically calculated

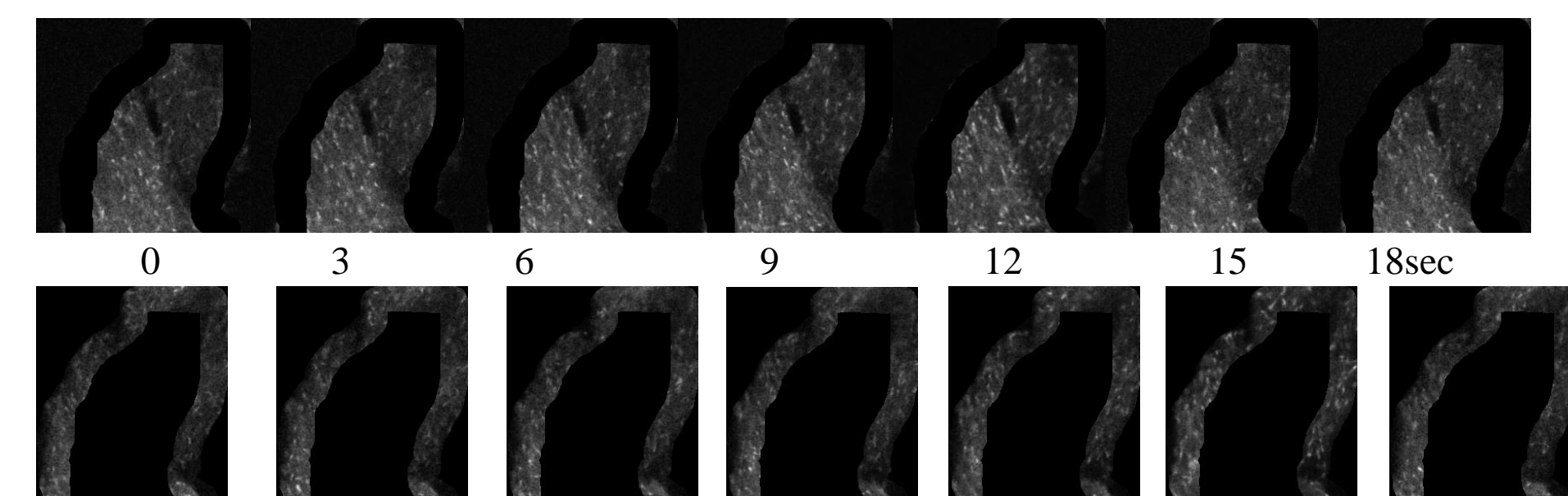
Movie	Minimize1	Minimize2	Series124
Boundary	515	417	282
Inside	578	484	280

Table 3. t Student test on two samples H0: does not exist differences between velocities on boundary and inside cell

Movie	Minimize1	Minimize2	Series124
P t-test	0.0058	0.55	0.08

Table 4. t Student test: population vs samples of comets really near to cell boundary

Minimize1	Velocity ( $\mu\text{m min}^{-1}$ )	P t-test
Population	7.66756	0.030
Sample	4.01092	



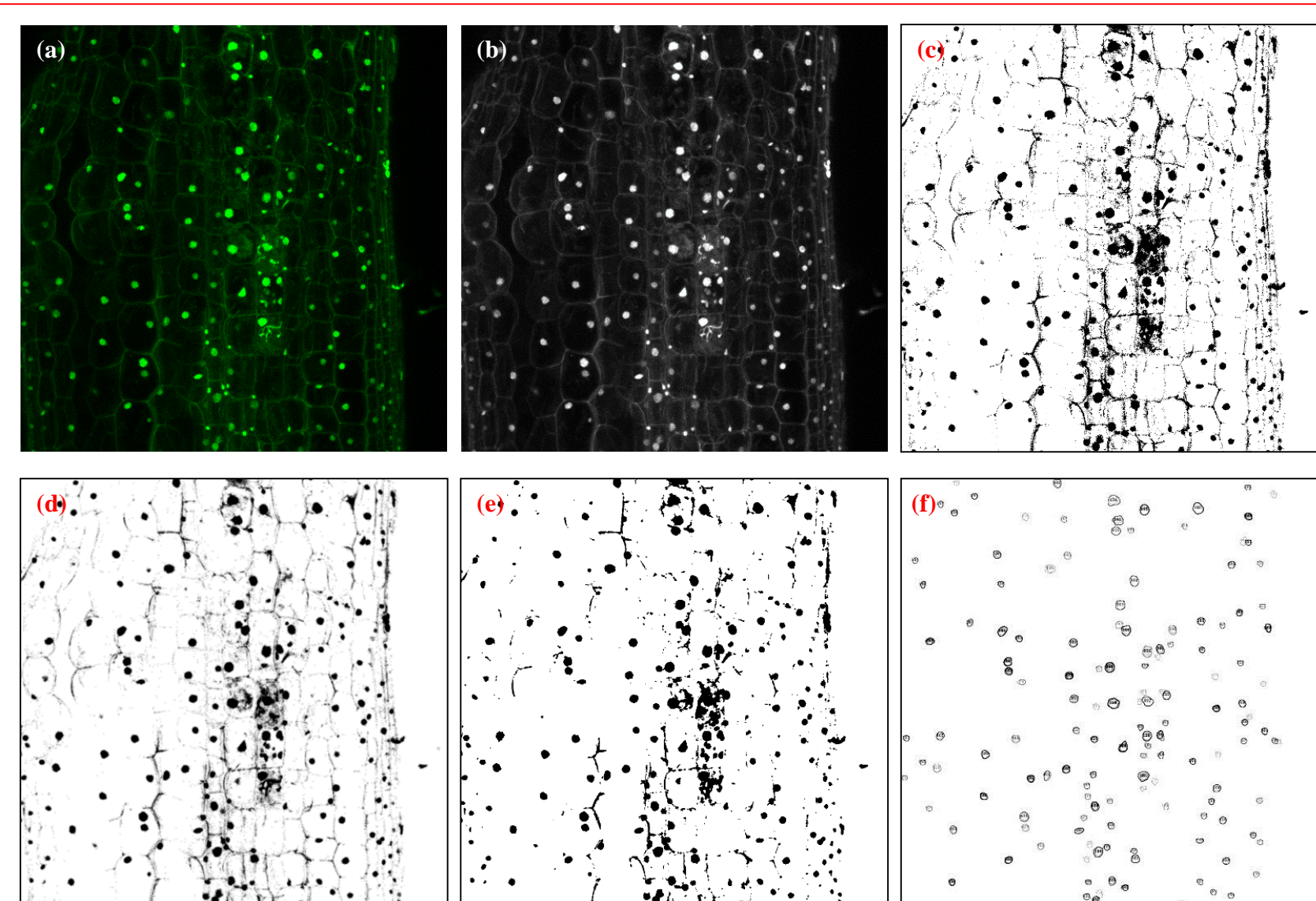
## Z Axis

ImageJ

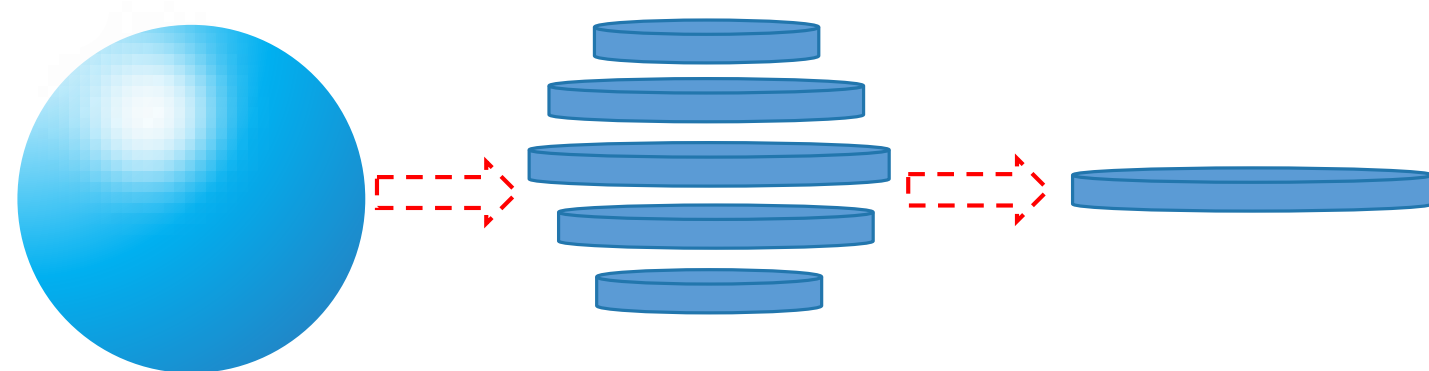
Designed detection macro

3D Object counter

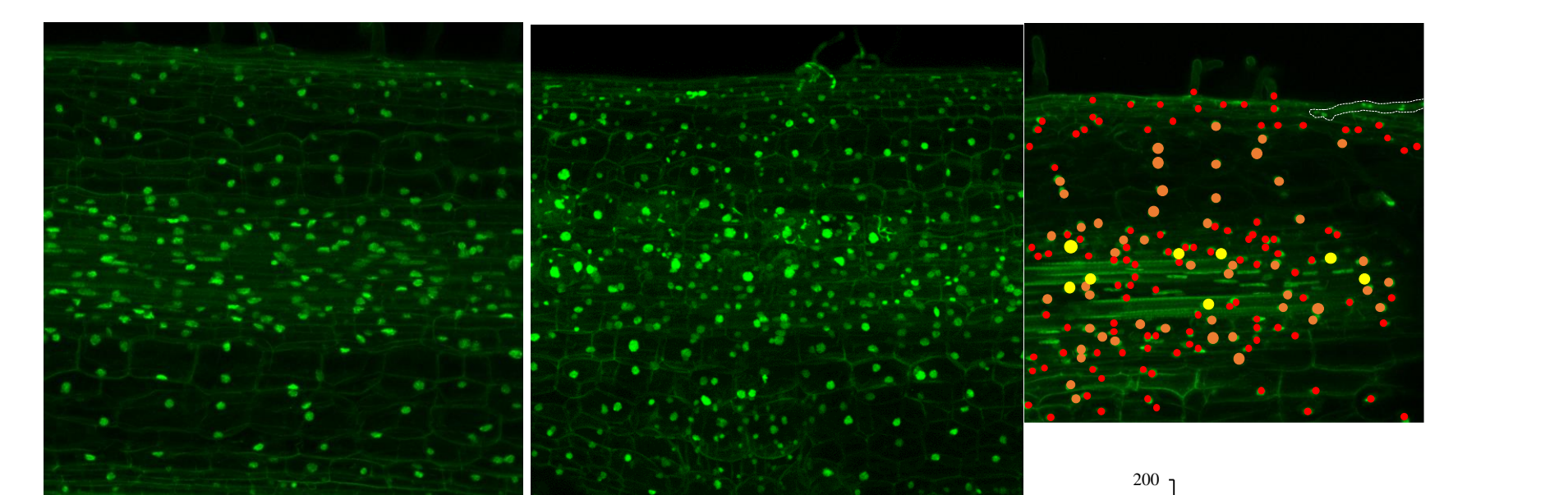
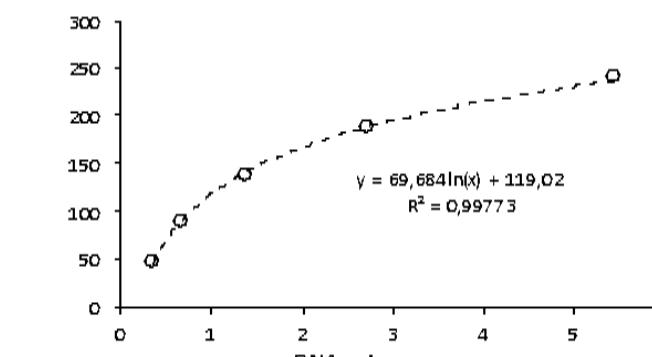
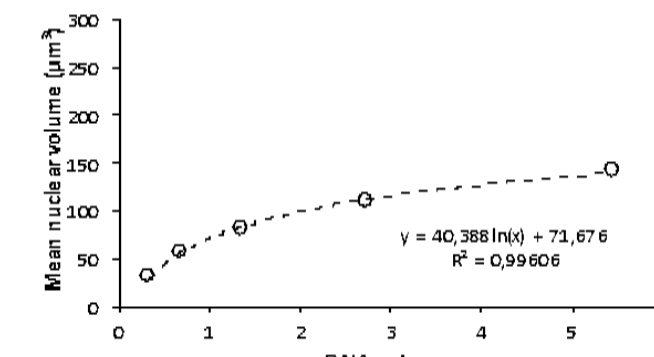
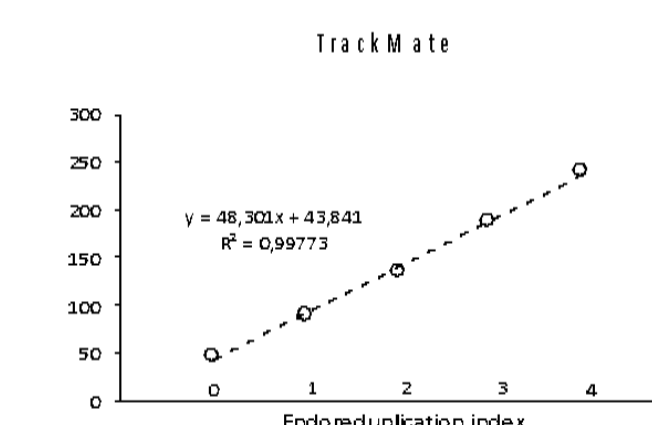
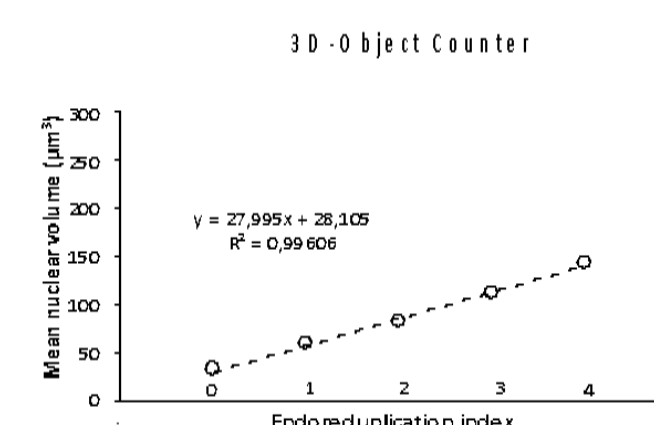
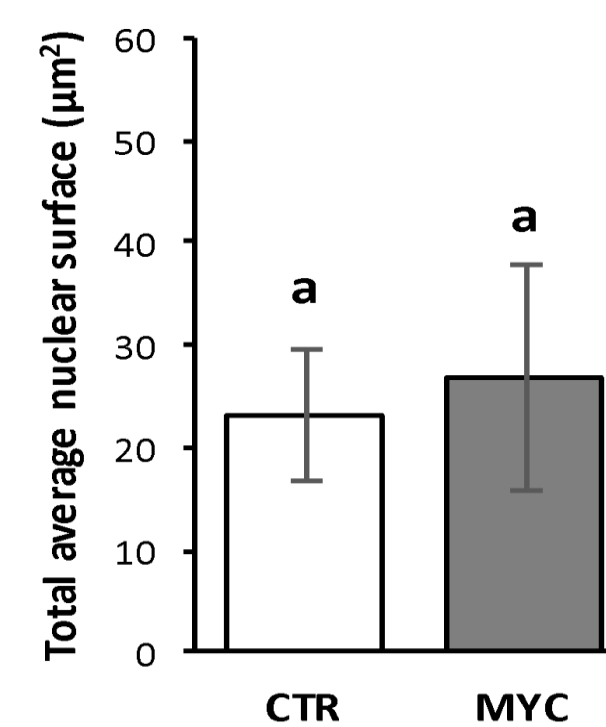
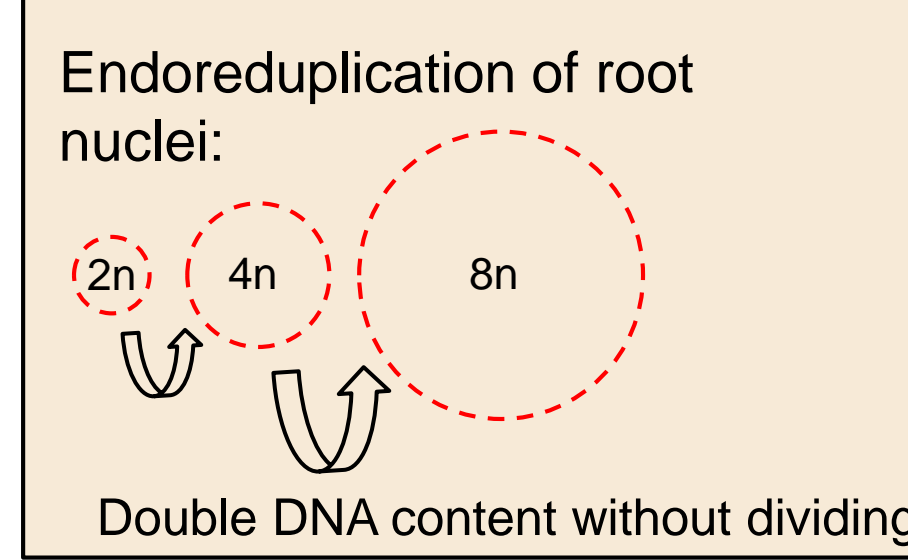
Track mate



Swapping from T to Z axis we detected and associated all sections from each nucleus



Lingua G, Fusconi A, Berta G. The nucleus of differentiated root plant cells: modifications induced by arbuscular mycorrhizal fungi. *Eur J Histochem.* 2001;45(1):9-20.



EI	Mean values (3-00)	K-means (TrackMate)	DNA (picograms)	DNA volume (μm³)	Volume ratio [VR] (DNA volume / measured nuclear volume)
2C	0	30.37 ± 7.35	38.99	1.09	0.34
4C	1	55.92 ± 7.09	73.71	2.18	0.68
8C	2	82.85 ± 7.15	104.11	4.36	1.36
16C	3	108.38 ± 6.06	136.1	8.72	2.72
32C	4	134 ± 7.44	167.27	17.44	5.44
64C	5	157.63 ± 5.87	199.42	34.88	10.88
128C	6	186 ± 9.81	237.26	69.76	21.76
256C	7	213 ± 8.08	278.34	139.52	43.52

Jovtchev G, Schubert V, Meister A, Barow M, Schubert I. (2006) Nuclear DNA content and nuclear and cell volume are positively correlated in angiosperms. *Cytogenet Genome Res.* 2006;114(1):77-82.

## Results

T-Axis Automatic detection and tracking methods are computational tool useful to follow thousand of particles in each cell: we can compare mean velocities of cellular regions: we divide the ROI in two SUB-ROI: boundary region and inside region to test differences in mean velocities

Z-Axis All volume estimation methods converged on the same conclusion:

- Nuclear size increased in mycorrhizal roots
  - Compatible with predicted changes related to different ploidy levels
- Full support to flow cytometry and gene expression analyses, with the advantage of localizing endoreduplicated nuclei in the root sections, showing that endoreduplication occurs in the colonized area

