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Amphithéâtre Schittly – ENSISA-Lumière

DECIPHERING CELLULAR MORPHO-DYNAMICS USING BIOIMAGE INFORMATICS

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Cell deformation and migration are key factors involved in numerous aspects of cell development, immune responses, cancer and infectious diseases. Our team develops image analysis tools and software to extract quantitative information from multi-dimensional, multi-modal live microscopy, with the aim to derive mathematical models of cellular morpho-dynamics.

Throughout this talk, I shall describe some of our algorithmic developments to

a) automatically track multiple cells in 2D/3D microscopy in cluttered environments and low signal-to-noise conditions,
b) efficiently describe the 3D morphology of cells despite their natural shape variability,
c) extract biophysical quantities at the intra-cellular level directly from imaging data.

Finally, we shall emphasize the need for open-source tools and software by presenting the Icy platform:

http://icy.bioimageanalysis.org

a next-generation software dedicated to the bioimaging communities by providing the latest developments in image acquisition, visualisation, analysis and computational modeling.
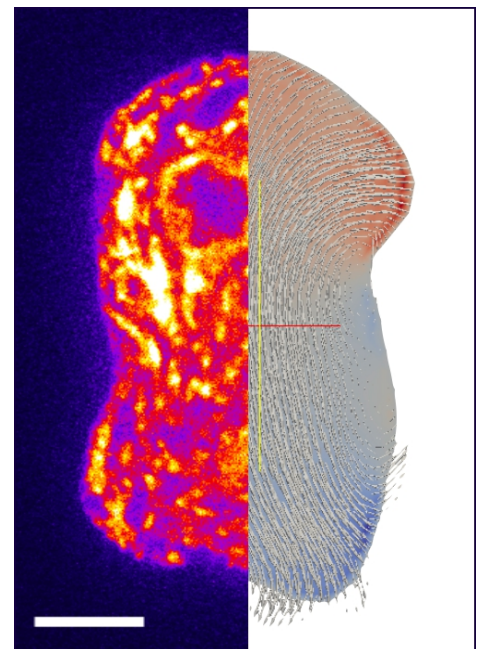
References :

[1] F. de Chaumont, S. Dallongeville, N. Chenouard, *et al.,* Icy: an open bioimage informatics platform for extended reproducible research, Nature Methods **9**, p. 690 (2012)

[2] A. Dufour, T.-Y. Liu, C. Ducroz, *et al.,* Signal Processing Challenges in Quantitative 3-D Cell Morphology: More than meets the eye, IEEE Signal Processing Magazine **32**, p. 30 (2015)