NANOJ: HIGH-PERFORMANCE OPEN-SOURCE SUPER-RESOLUTION MICROSCOPY ANALYSIS IN IMAGEJ

Romain Laine$^{1,2}$, Kalina Tosheva$^{1,2}$, Robert D. M. Gray$^{1,2}$, Pedro Almada$^{1,2}$, David Albrecht$^{1,2}$, Jason Mercer$^{1,2}$, Christophe Leterrier$^3$, Pedro M. Pereira$^{1,2}$, Siân Culley$^{1,2}$, Ricardo Henriques$^{1,2}$

$^1$MRC Laboratory for Molecular Cell Biology, University College London, Gower Street, London, WC1E 6BT, UK
$^2$Department of Cell and Molecular Biology, University College London, Gower Street, London, WC1E 6BT, UK
$^3$Aix Marseille Université, CNRS, NICN UMR7259, 13344 cedex 15, Marseille, France
E-mail: r.henriques@ucl.ac.uk

KEY WORDS: ImageJ, Fiji, Super-resolution microscopy, Image analysis, Image quality assessment, Fluidics, Quantitative imaging, Modelling

Super-resolution microscopy has become essential for the study of nanoscale biological processes. This type of imaging often requires the use of specialised image analysis tools to process a large volume of recorded data and extract quantitative information. In recent years, our team has built an open-source image analysis framework for super-resolution microscopy designed to combine high performance and ease of use. We named it NanoJ - a reference to the popular ImageJ software it was developed for. In this talk I will highlight the current capabilities of NanoJ$^1$ for several essential processing steps including super-resolution image reconstruction (NanoJ-SRRF)$^2$, image quality assessment (NanoJ-SQUIRREL)$^3$, structural modelling (NanoJ-VirusMapper)$^4$ and control of the sample environment (NanoJ-Fluidics)$^5$.

References: