

## TANGO II: an integrated framework for 3D bioimage analysis of cell nuclei

The study of nuclear architecture has become an important field of cellular biology. Extracting quantitative data from large sets of 3D fluorescence images helps understanding how the genome is functionally organized within different nuclear compartments. We present here Tango II, a new image analysis tool for studying nuclear architecture from fluorescence microscopy images. It is based on the Bacmman plugin in ImageJ for processing and extracting quantitative data from 3D stacks. Tango II intuitive interface enables users to define compartments, perform segmentation, and analyze multiple nuclei in microscopy fields. It integrates the most common quantitative measurements, including colocalization and shell analysis. Statistical processing and analysis of subpopulations is facilitated by a Python library that enables interactions between statistical analysis and image datasets. We illustrate here the capabilities of Tango II by investigating the impact of the cell cycle on heterochromatin distribution.

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