

TANGO Tools for Analysis of Nuclear Genome Organization

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TANGO (Tools for Analysis of Nuclear Genome Organization) is an image analysis framework dedicated to the study of nuclear architecture (Ollion et al., 2013, Bioinformatics, 29-1840). This generic software includes tools to (1) process various types of signals, (2) quantify several features on signals, and (3) assist statistical analysis of quantifications.

The user interface allows to manage large datasets of images, visualize them in 3D and rapidly assess the quality of processing. Moreover, TANGO is interfaced with the statistical processing software R, which allows to easily apply all R tools to data generated by TANGO, and to define and access subpopulations of nuclei both in R and TANGO.

We will present the software through the description of a practical case in order to give an overview of its different concepts and functionalities.