TANGO–A Customizable Tool for High Throughput for Images Analysis of Nuclear Signals

Jean Ollion¹, Philippe Andrey², Christophe Escudé¹, Thomas Boudier³

1. Muséum National d'Histoire Naturelle, Paris. France

2. IJPB, INRA, Versailles, France 3. Université Pierre et Marie Curie, Paris, France

ollion@mnhn.fr

http://tango.tuxfamily.org/

Abstract

The nucleus is a highly structured and organized cellular compartment. The genome is not randomly organized inside the nucleus, each chromosome occupies a particular space called the chromosomal territory (CT). Within CTs genes of particular interest may occupy particular localization and move during expression. Repeated DNA sequences located in the centromeric regions of mammalian chromosomes are thought to organize the genome by interacting with each other or with specific nuclear compartments such as the nucleolus or the lamina. In order to analyze nuclear organization, a statistical study needs to be run on a large population of cells. Modern microscopes allows to acquire a large amount of fields. Thanks to software such as ImageJ it is possible to automate analysis including filtering and quantitative measurements. Unfortunately in ImageJ available processing and measurements are only for 2D images. Furthermore since different users may need different settings for filtering and analyses, the use of macros has its limitation. We have developed TANGO (Tool for Analysis of Nuclear Genome Organization) to analyze thousands of nuclei in 3D. All images, settings and results are stored in a database (mongo-DB, powerful multi-platform object-oriented DB), a customizable processing chain can be set up for each different experiments using available plugin in ImageJ and new ones have been developed like 3D spatial statistics. The visualization of the 3D images and results benefits from the development of powerful 3D interfaces such as Image5D and 3D Viewer.

Keywords

ImageJ, database, 3D, nucleus, processing, analysis, measurements

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