CYTOPACQ: A WEB-BASED TOOLBOX FOR GENERATION OF DIGITAL PHANTOMS AND SIMULATION OF IMAGE FORMATION IN 3D CELL IMAGING

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KEY WORDS: digital phantom, synthetic image, fluorescence microscopy, 3D cell imaging

Fluorescence microscopy still faces the problem of the quality of cell image analysis results. Degradations caused by cell preparation, optics and electronics considerably affect most 2D and 3D cell image data acquired using optical microscopy. That is why image processing algorithms applied to these data typically offer imprecise and unreliable results. As the ground truth for given image data is not available in most experiments, the outputs of different image analysis methods can be neither verified nor compared to each other.

Some papers solve this problem partially with estimates of ground truth by experts in the field (biologists or physicians). However, in many cases, such a ground truth estimate is very subjective and strongly varies between different experts.

In order to overcome these difficulties, we have created a toolbox [1] that can generate 3D digital phantoms of specific cellular components along with their corresponding images degraded by specific optics and electronics. The user can then apply image analysis methods to such simulated image data. The analysis results (such as segmentation or measurement results) can be compared with ground truth derived from input object digital phantoms (or measurements on them). In this way, image analysis methods can be compared to each other and their quality (based on the difference from ground truth) can be computed.

The present version of the simulation toolbox can generate cell nuclei in 3D using deformation of simple shapes and adding texture to the cell interior. Further, it can simulate optical degradations using convolution with supplied point spread function as well as electronic artifacts such as impulse hot pixel noise, additive readout-noise or Poisson photon-shot noise. We have also evaluated the plausibility of the synthetic images, measured by their similarity to real image data. We have tested several similarity criteria such as visual comparison, intensity histograms, central moments, frequency analysis, entropy and 3D Haralick features. The results indicate a high degree of similarity between real and simulated image data.

The work was supported by the Czech Ministry of Education (Grants No. 2B06052 and LC535).

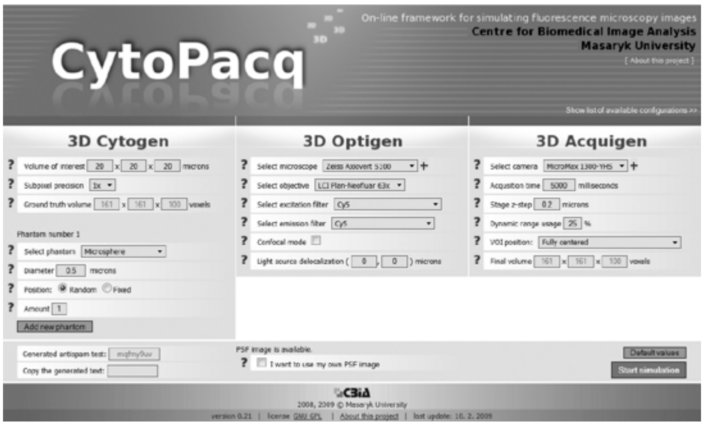

Figure 1: The simulation toolbox is freely available via simple web interface at **`http://cbia.fi.muni.cz/simulator/`**

[1] D. Svoboda; M. Kozubek, and S. Stejskal, “Generation of Digital Phantoms of Cell Nuclei and Simulation of Image Formation in 3D Image Cytometry,” *Cytometry Part A*, in press.