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scanR: TruAI Assisted Quantitative Image-Based Cytometry

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Abstract

Keywords

High content analysis, Quantitative Image-based cytometry, cytology, artificial intelligence, AI, deep learning, qIBC, cell analysis, TruAI, scanR

scanR: TruAI Assisted Quantitative Image-Based Cytometry

With the variety of sample preparation protocols, fluorescent markers, experimental assays, and cell lines used in research labs, it is difficult and time consuming for individual researchers to create robust and/or flexible acquisition and analysis workflows for high content applications. Commercially it is also complicated to provide robust, ready-to-go, analysis protocols that are still sufficiently flexible to cover the required variety of assays and analyses, such as apoptosis, autophagy, cell count, cell differentiation, mitotic index, protein expression, or transmigration, performed in many laboratories.

To make generation of workflows and analysis faster and easier, scanR from Olympus is designed to allow quick generation of custom assays which are both very flexible and robust, and at the same time allows for very rapid testing and tweaking of parameters. With a logical structure and workflow inspired by flow cytometry, detected objects are displayed in parameter scatter plots, where clouds of populations, isolated by user defined parameters and gates, can emerge, revealing phenotypes that can be displayed in galleries for visual inspection or statistically quantified (Figure 1). The analysis parameters can easily be tuned to extract quantitative data for a very wide range of applications, including kinetic assays.

This image-based cytometry approach is very powerful for high content imaging and analysis and is further enhanced by the integration of oru TruAI deep learning module which allows for segmentation and analysis of targets that can otherwise be extremely difficult to isolate or identify using classical

methods (Figure 2.). In scanR, classical analysis, assisted by user-trained neural networks, can extract the real data while guaranteeing robustness and giving easily verifiable results.

After a general introduction to the scanR HCS system, I will demonstrate our image-based cytometry workflow, and how we have integrated deep learning to make previously complex and labour intensive tasks quick and easy.

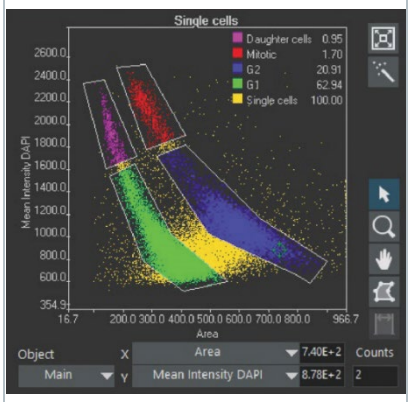

Figure 1. Cytometry-Gated cell populations

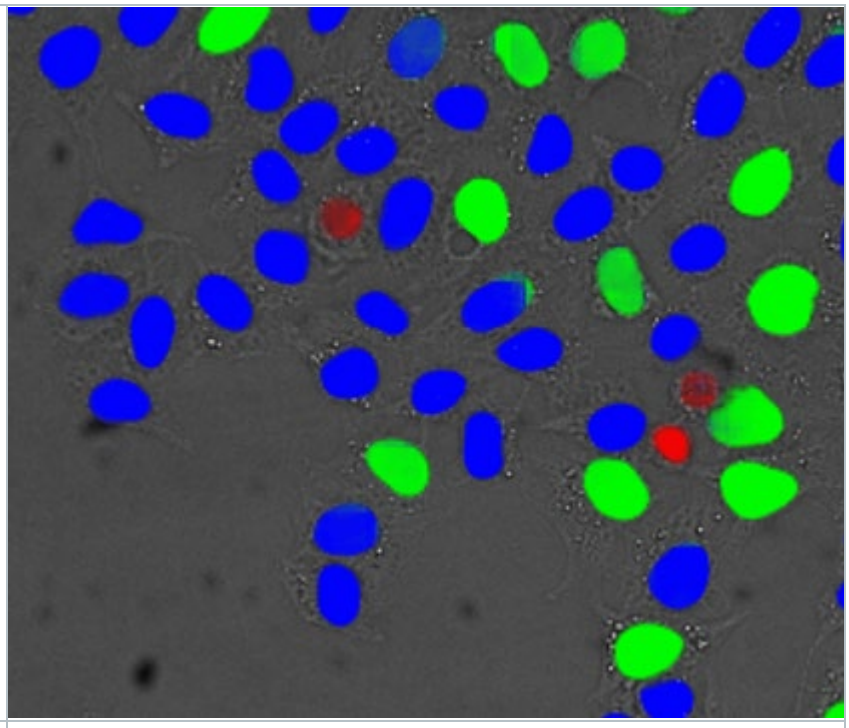

Figure 2. Cell cycle classification in Bright Field based on Deep Learning