

ACCURATE ASSIGNMENT OF CYTOPLASMIC STRUCTURES TO INDIVIDUAL CELLS IN AUTOMATED, HIGH-VOLUME IMAGE CYTOMETRY

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In image cytometry, the 'cytoplasmic area' of cells is often identified by applying a polygonal or elliptical model around a central reference point, often the nucleus. This leads to biased measurement of cytoplasm and to assignment of objects or events at the cell perimeter to the nearest instead of the correct cell.

Multimode reading allows tracking multiple structures in individual cells in e.g. monolayer cultures. Fluorescent and brightfield multimode microscopic images were captured and analyzed with MIAS-2 microscopy readers. Using the eaZYX-IMAGING software, we applied novel shape detection principles that lead to dynamic cell perimeter identification and to accurate assignment of cytoplasmic structures to individual cells.

Examples will be given that show a robust performance in high and moderate intensity signals, but also in brightfield images with variable backgrounds and in 'high noise' low-light images from intensified cameras.