Proceedings of 2017 IEEE 2nd International Conference on Control in Technical Systems, CTS 2017, 2017, pages 118-121

Two-step algorithm for the automated analysis of fluorescent microscopy data in biomedical applications

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Abstract

© 2017 IEEE. Measurement automation is essential in various biomedical and biotechnological applications become increasingly important with their intensification and wide utilization. Estimation of both pro- and eukaryotic cells subpopulations in different cultures, samples and tissues, including differentiation of live and dead bacterial cells, stem cells in eukaryotic cell culture and so on are essential in multiple biomedical and biotechnological applications. Fluorescent microscopy is a widely used methodology to obtain the above estimates. Wide utilization of biotechnologies increases the importance of automatic microscopic image processing tools design aiming at both qualitative and quantitative assessment of cells sub-populations. Existing methods are mostly based either on cell detection and counting or on the statistical analysis of image areas with similar staining. However, these methods exhibit known drawbacks including their inapplicability to the communities of cells adherent to each other and to external surfaces with biofilms being a prominent example. Another limitation of standard image processing tools in their high level of automation limiting the ability of the operator to adjust the algorithm parameters to particular microscopic imaging conditions as well as to specific features of the studied cells subpopulations. Here we present a two-step algorithm including preliminary adjustment of its parameters to the imaging conditions based on several representative images from the studied cohort in the first step and fully automated analysis of a large series of images with fixed algorithm parameters in the second step. Out results indicate that the suggested methodology is barely sensitive to the decision threshold value that allows to reduce the parameterization of the algorithm.

http://dx.doi.org/10.1109/CTSYS.2017.8109504

Keywords

cell staining, fluorescent microscopy, measurement automation, two-step algorithm

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