INFLUENCE OF MOTION-BLUR IN SINGLE CELL IMAGE ANALYSIS VIA MICROFLUIDIC MICROSCOPY

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Microfluidic-based microscopy platforms have been shown to be powerful technics for high throughput single cell imaging and analysis [1]. Such tools are critical to automatically isolate for instance, healthy from unhealthy cells. This was demonstrated in [2] where the feasibility of sorting steady single cells was obtained with sub resolved images, by using textural features. A noise, specific to microfluidic, not studied in [2], is the blur caused by the displacement of the cell during image acquisition. Here, we extend the work of [2] by adding such blur and we study the motion-blur influence on image quality and on the performance of cell classification; this is investigated for various cell velocities.

Realistic widefield microscopy simulated image sets with two resolutions are used in this study. Resolutions are defined by modifying the objective lens parameters used to compute the PSFs (see table 1). Motion-blur is simulated as a convolutional kernel applied to YZ image planes, where its size depends on the cell velocity ranging from 10 to 60 µm/sec. The deblurring of the images is proposed with two standard and complementary approaches: (i) classical deconvolution with Lucy-Richardson (LR) algorithm, well suited in this situation where the PSF of the microscope is known, (ii) pixel to pixel deep learning-based CARE algorithm [3]. For both denoising methods, hyperparameters, such as the deconvolution iterations number for LR and the trained model architecture for CARE were optimized. Finally, we used textural feature spaces (LBP, GLCM and scattering transform) and SVM classifier for cell classification similarly to the approach of [2].

Classical standard measures such as the structural similarity (SSIM) and the accuracy are used to evaluate deblurring and classification performances, respectively. As demonstrated in [3], CARE shows better denoising performance for moving cells with an average $SSIM_{CARE} \simeq 0.57$, versus $SSIM_{LR} \simeq 0.35$ with LR for all tested image resolutions and cell velocities. Concerning cell classification and as illustrated in table 1, CARE allows the enhancement of low-resolution image classification by comparison to LR. However, the impact of the microfluidic noise on higher image resolution is negligible where classification is even better for non-denoised images. In conclusion, motion-blur effect brought by the micro-fluidic could be reduced by applying post-processing based on deep learning denoising or by carefully pre-selecting the objective lens for the acquisition.

Resolutions	Features	Raw	LR	Care
Low (M=40, n=1, NA=0.75)	GLCM	71.8 ± 0.72 %	58.5 ± 1.6 %	**69.1 ± 1.3 %**
	LBP	55.7 ± 0.7 %	53.6 ± 1.2 %	**63.8 ± 0.9 %**
	Scatnet	66.5 ± 1.2 %	69.5 ± 1.1 %	**70.2 ± 1.2 %**
High (M=60, n=1.51, NA=1.4)	GLCM	**75.1 ± 0.9 %**	69.4 ± 0.8 %	76.3 ± 1.3 %
	LBP	**75.6 ± 0.7 %**	71.3 ± 1.7 %	74.4 ± 0.7 %
	Scatnet	**83.8 ± 0.7 %**	79.9 ± 0.4 %	80.2 ± 0.4%

Table 1: Classification results of raw, LR and CARE, for low and high resolutions for a cell speed of 20 µm/sec.

[1] F. Sala et al. "High-throughput 3D imaging of single cells with light-sheet fluorescence microscopy on chip." *Biomedical optics express*, **11**, 4397-4407 (2020).
[2] A. Ahmad et al. "Detecting differences of fluorescent markers distribution in single cell microscopy: textural or pointillist feature space?", *Frontiers in Robotics and AI*, **7**, 39 (2020).
[3] M. Weigert et al. "Content-aware image restoration: pushing the limits of fluorescence microscopy", *Nature methods*, **15**, 1090-1097 (2018).