Morphological restoration:
A fast alternative to deconvolution of 3D images of cells

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Abstract

Two-photon microscopy (TPM) is a powerful tool for intra-vital imaging and is widely employed in a lot of biomedical applications [1]. Any microscopy image represents a convolution of the actual sample with the point spread function (PSF) of the microscope, which depends on both the microscope characteristics and the sample properties. The shape of a PSF from TPM is close to a Gaussian, which is elongated along the optical axis relative to the lateral axes, resulting in an elongated shape of the visualized cells. For the analysis of cell shape or detection of interactions, it is crucial to first restore the original cell shape. For this, a number of image deconvolution techniques exist [2], but most of them require enormous computational resources in terms of computation time and memory.

Often, the quantitative analysis of cells employs only binary cell masks obtained in the process of image segmentation. For such cases, we propose a novel fast morphological restoration approach, where first cell segmentation is performed, and then the cell boundaries are shifted towards the cell center by the distance, by which the cell image has enlarged due to the PSF. We propose two approaches for estimating this enlargement: an approach based on PSF parameters and a "blind" approach based on computing the eccentricity of the "average cell" in an ensemble of cells.

We validated our restoration technique in comparison with the "Iterative Deconvolve 3D" plugin of the Fiji software [3] using (i) synthetic cell images and (ii) experimental TPM images of mast cells in murine ear skin. Both PSF-based and blind versions of our approach yielded similar restoration results with respect to the Fiji implementation (Fig. 1), however, at the benefit of reducing the computation time by two orders of magnitude.

[1] V. Konjufca and M. J. Miller, "Two-photon microscopy of host-pathogen interactions: acquiring a dynamic picture of infection *in vivo*," *Cell. Microbiol.*, vol. 11, no. 4, pp. 551–559, Apr. 2009.

[2] P. Sarder and A. Nehorai, "Deconvolution methods for 3-D fluorescence microscopy images," *Signal Process. Mag. IEEE*, vol. 23, no. 3, pp. 32–45, 2006.
[3] R. Dougherty, "Extensions of DAMAS and Benefits and Limitations of Deconvolution in Beamforming," 2005.

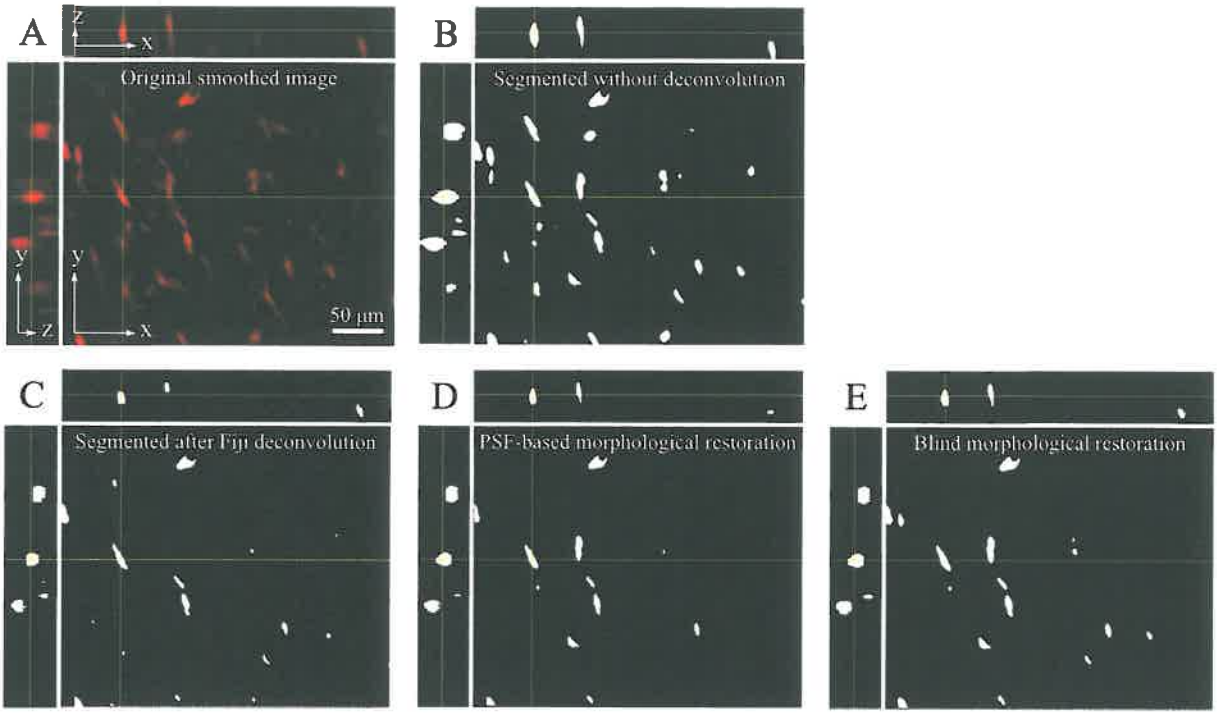

Figure 1: TPM images of mast cells in murine ear skin (A) segmented without deconvolution (B), and after applying different restoration approaches: Fiji iterative deconvolution (C), PSF-based (D) and blind (E) morphological restoration.