Deconvolution increases the accuracy of measurements by image analysis in a model of trimethyltin-induced reactive gliosis of the rat entorhinal cortex

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Digital images were used in applications such as astronomy, medicine, physics and biology, to record and analyze results from experiments Due to the features of the imaging system, the recorded images can be degraded by blurring and noise. Image deconvolution, or image deblurring, is the process of reconstructing or estimating the true image from the degraded one [1]. In order to optimize morphometrical analysis of Glial Fibrillary Acidic protein (GFAp)-immunoreactive astrocyte of the whole rat entorhinal cortex of both trimethyltin hydrochloride- and saline treated rats, large images of it (about 30 000 x 20 000 pixels) were digitized by a microscope with a X – Y motorized computer-managed stage and an autofocusing system, using an objective 40x, a digital camera 2560x1920 RGB. Moreover it has been optimized a procedure of deconvolution and segmentation under the NIH ImageJ system. Such large images were first deblurred, by Modified Residual Norm Steepest Descent (MRNSD) and Wiener Filter Preconditioned Landweber (WPL) algoritms, and segmented, then analyzed, to measure the % of the area (in μ m2) occupied by GFApimmunoreactive cell bodies and processes, and classical morphometrical parameters. Statistical analysis was performed to describe obtained data and to point out differences between segmented only versus deblurred-segmented images. Our results can be summarized as follows. 1. Large images can be an useful tool to identify precisely the distribution of reactive astrocytes in the rat entorhinal cortex. 2. Deconvolution avoid an overestimation of the area of immunoreative astrocytes of about 10-15%. Segmentation allow a measurement with improved accuracy, precision and uncertainty. 3. This approach is time consuming and requires a multi-core hardware with a large amount of available RAM.

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References

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Keywords

Deconvolution; rat; entorhinal cortex; glial fibrillary acidic protein.