Fast wavelet-based deconvolution of fluorescence micrographs

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ABSTRACT

Modern biology depends crucially on two research modalities:[1] fluorescent markers and high-resolution microscopy. The need to track biological compounds down to molecular scales poses considerable challenges to the instrumentation. In this context, deconvolution microscopy is becoming a key-element in the experimental process.

Wavelet-based deconvolution methods are a recent and promising development.[2] However, they have not been considered as a serious alternative to existing deconvolution methods so far, mainly due to their computational cost. Our contribution shows the feasibility of wavelet-regularized deconvolution at a cost comparable to a few tens of iterations of a standard algorithm. This can be considered the present tolerance limit, given the size of usual biomicroscopy data sets.

Wavelets have proven to be a very successful tool for the estimation of signals that are corrupted by noise. Denoising methods based on a thresholding of the wavelet coefficients were first introduced and justified in a statistical framework.[3] They were later reinterpreted in a variational framework,[4] which can be extended to more general inverse problems such as deconvolution.

Let us denote by $\mathbf{y}$ a vector containing noisy and blurred measurements of some original signal $\mathbf{x}_{\text{orig}}$. To estimate this signal, several research groups[2,5,6] have proposed to minimize the cost function

$$J(\mathbf{x}) = \|\mathbf{y} - \mathbf{H}\mathbf{x}\|_2^2 + \lambda\|\mathbf{W}\mathbf{x}\|_1. \tag{1}$$

Here, $\mathbf{H}$ is a matrix that models the linear distortions introduced by the measurement device. In the case of deconvolution, $\mathbf{H}$ is the block-circulant matrix corresponding to the impulse response of the microscope. The Euclidian norm $\|\mathbf{y} - \mathbf{H}\mathbf{x}\|_2$ measures the "mismatch" between the measured signal $\mathbf{y}$ and the prediction corresponding to the estimate $\mathbf{x}$. $\mathbf{W}$ is a transform matrix such that $\mathbf{W}\mathbf{x}$ contains the wavelet coefficients of $\mathbf{x}$, and $\|\mathbf{W}\mathbf{x}\|_1$ represents the sum of the absolute values of these coefficients. This term, whose influence can be controlled by the scalar λ, favors estimates with a sparse wavelet extension. This constraint makes sense because many "natural signals" exhibit this property.

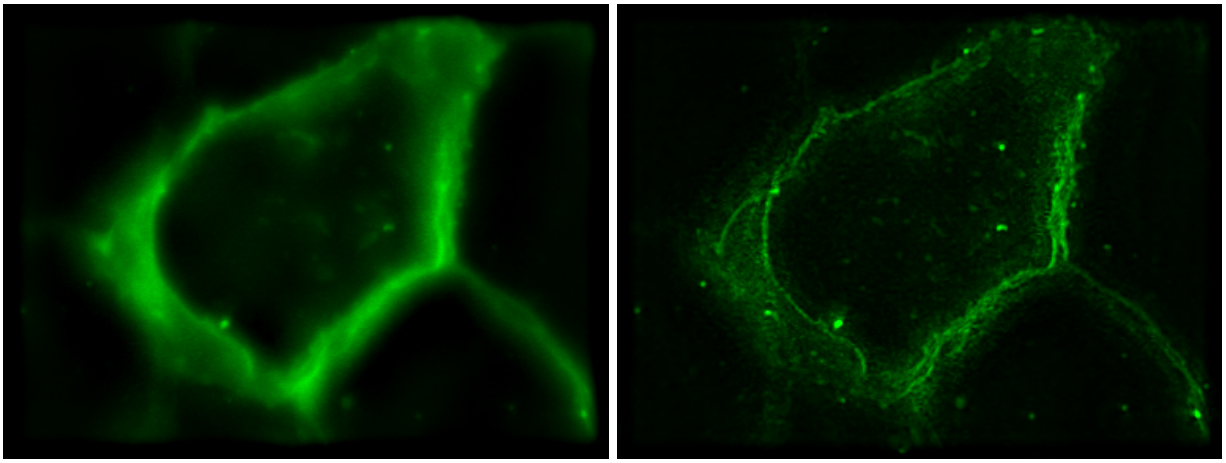
In the case of an orthonormal wavelet basis, it has been shown[5] that (1) can be minimized by iterating the mapping

$$\mathcal{M}\{\mathbf{x}\} = \mathbf{W}^T\mathcal{T}_{\lambda\tau/2}\{\mathbf{W}[\mathbf{x} + \tau\mathbf{H}^T(\mathbf{y} - \mathbf{H}\mathbf{x}]\}.$$

This is essentially a Landweber iteration (with step size τ) followed by a wavelet-domain soft-thresholding operation (with threshold $\lambda\tau/2$). Unfortunately, this algorithm displays slow convergence in experimental situations.[2]

We propose to use Shannon wavelets for regularization. This allows us to separate the expression of the cost function (1) into subband-specific terms. By adapting the derivation of Daubechies et al.,[5] we introduce subband-dependent step sizes an threshold levels. Because our subband-dependent parameters are much larger than in the standard algorithm, we achieve an acceleration of roughly one order of magnitude.

The potential of this acceleration is illustrated in the images below. They show maximum intensity projections of a 3D stack of a fluorescence-labeled fibroblast cell, with fluorescent microbeads inserted in the sample medium. The left-hand image is the result of 10 iterations of the existing deconvolution algorithm, while the right-hand image was obtained using 10 iterations of our accelerated algorithm. The left-hand image cannot be distinguished visually from the acquired widefield image, due to the slow convergence of the original algorithm. Our algorithm rapidly produces an image where the cell membrane is better defined and the microbeads are significantly brighter.



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