**Abstract**

Thanks to the development of improved microscopy imaging techniques and the advent of highly selective fluorescent dyes, fluorescence microscopy imaging has allowed the precise identification of tagged molecules in biological specimen. Of particular interest are the visualization and the study of living cells, which induce tight constraints on the imaging process. To avoid the alteration of the sample and to achieve a high temporal resolution, low fluorophore concentration, low-power illumination and short exposure time need to be used in practice. These stringent imaging conditions generate undesirable random distortions, called noise, that have a negative impact on the signal-to-noise ratio (SNR) of the resulting images. We have thus developed PureDenoise, an ImageJ plugin for the efficient, fast, and automatic denoising of multidimensional fluorescence microscopy images. This Java plugin is based on the Poisson Unbiased Risk Estimate-Linear Expansion of Thresholds (PURE-LET) denoising approach. Assuming a mixed Poisson-Gaussian noise model, an unbiased estimate of the mean-square error (MSE) is used to optimize the parameters of a linear expansion of Haar wavelet-domain thresholding functions. These data-adaptive thresholding rules take into account the high redundancy between neighboring slices (resp. frames) in 3D (resp. 2D-timelapse) fluorescence microscopy images. The proposed plugin features an automatic noise parameters estimator and two cursors for balancing the denoising quality and the computation time. A multithreaded implementation allows to denoise several slices or frames in parallel, which drastically reduces the overall execution time. For instance, a 400x400x10 data set can be efficiently denoised within a couple of seconds.

**Keywords**

Fluorescence microscopy, denoising, risk estimation, ImageJ, Java, multithreading, Haar wavelet, Poisson-Gaussian noise