



SPITFIR(e): a supermaneuverable image restoration algorithm for 2D, 3D and 3D+Time microscopy images

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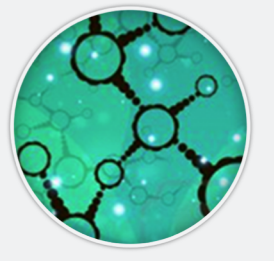
SPITFIR(e): a supermaneuverable image restoration algorithm for 2D, 3D and 3D+Time microscopy images

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SPITFIR(e) method

Variational model for image restoration

$$\hat{u} = \arg \min_{u \in \mathbb{R}^{\Omega}} F(f, u; h, \mathcal{T}) + \lambda R_{\rho}(u)$$

Data fidelity term (Poisson-Gaussian noise)

$$V_{noise}(\mathbf{x}) \triangleq \mathbb{E}[(f(\mathbf{x}) - (h * U)(\mathbf{x}))^2] = \alpha u(\mathbf{x}) + \sigma^2$$

Sparsity-promoting regularizer

$$SHV_{\rho}(u) = \int_{\Omega} \sqrt{\rho^2 \|\mathcal{H}u(\mathbf{x})\|_F^2 + (1 - \rho)^2 u(\mathbf{x})^2} d\mathbf{x}$$

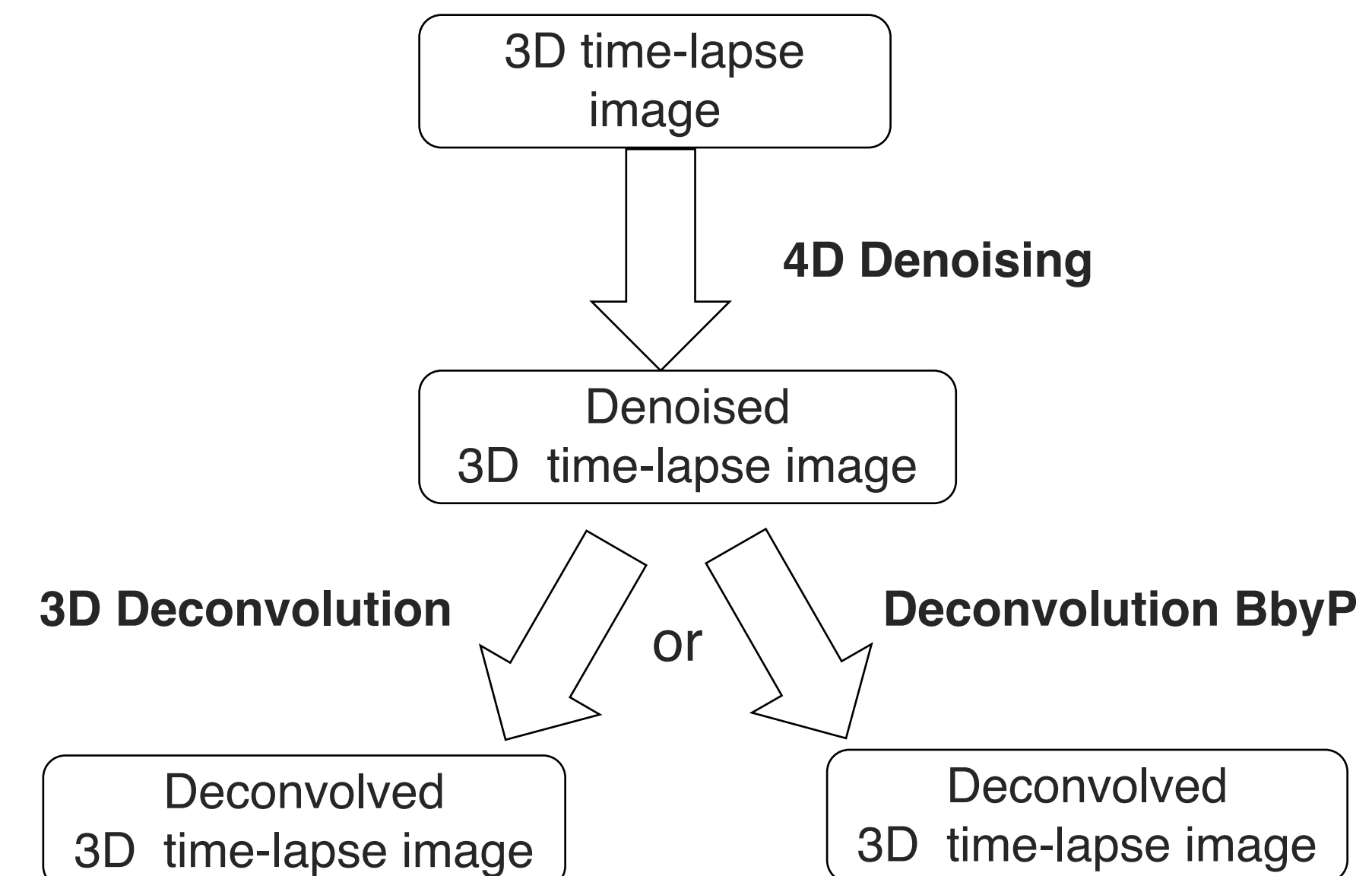
Optimization

The optimization problem is **convex but not smooth**, and is solved with a **first-order method** to minimize the sum of convex functions, based on the **proximal splitting approaches** [1].

SPITFIR(e) Denoising: Dirac PSF for denoising 2D-3D-4D images

SPITFIR(e) Deconvolution:

- PSF is known: 3D deconvolution
- PSF is not well known: Deconvolution "plane-by-plane" (PbyP)



LLSM

Lattice Light Sheet Microscopy [3]

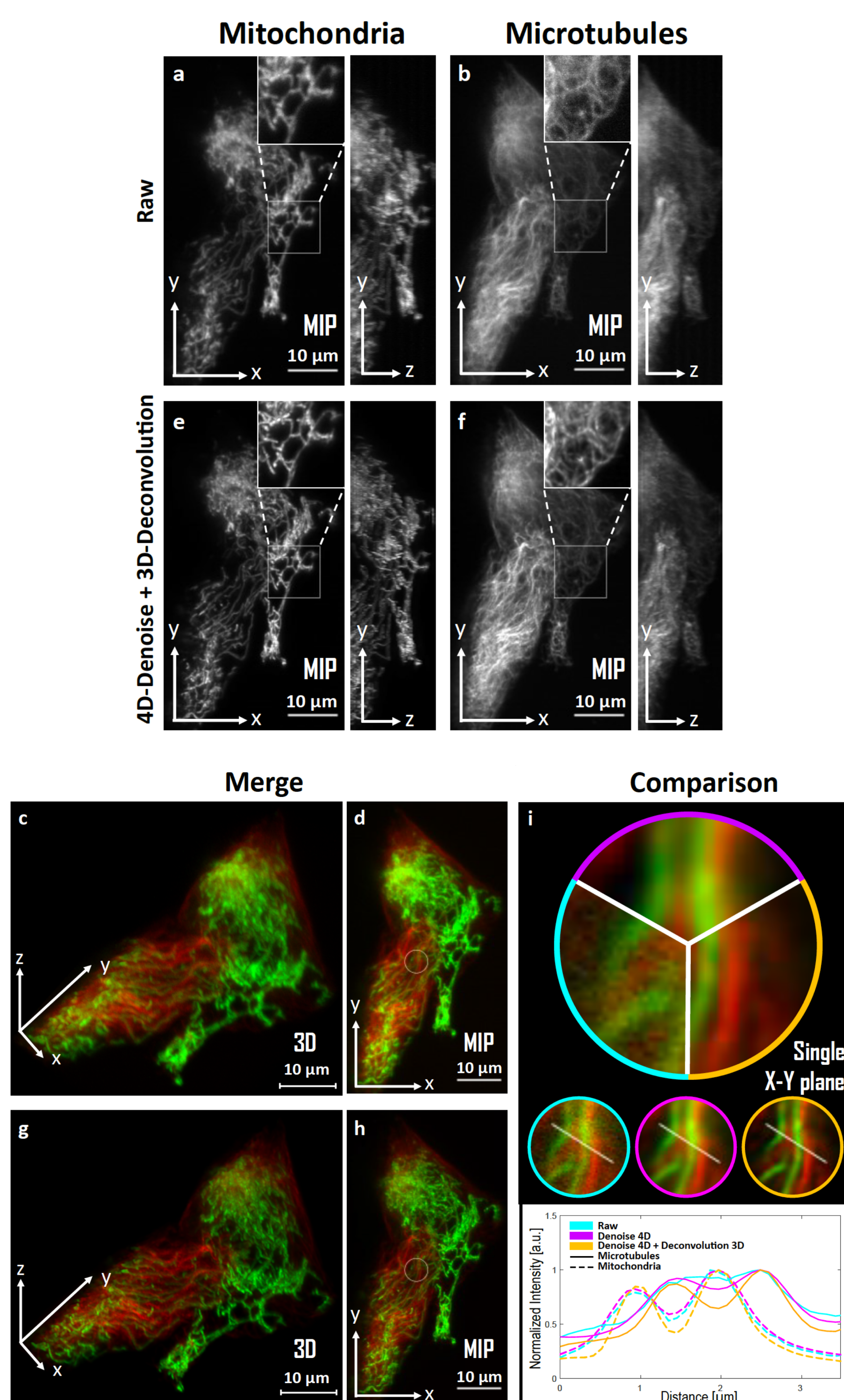


Fig 1. SPITFIR(e) for 4D-denoising, background subtraction, and 3D-deconvolution in LLSM. 60 planes 3D volumes of live RPE1 cells double stained with PKMR for Mitochondria (a,e) and with Tubulin TrackerTM Deep Red for Microtubules (b,f) were acquired within 2:2s per stack using lattice light-sheet microscopy. MIP of representative raw images for Mitochondria and Microtubules, respectively, before (a,b) and after (e, f) SPITFIR(e) 3D+Time denoising and 3D deconvolution. Merged results are shown in (c, d) and (g, h) maximum intensity projections, and intensity profiles in (i)

STED

Stimulated Emission Depletion [4]

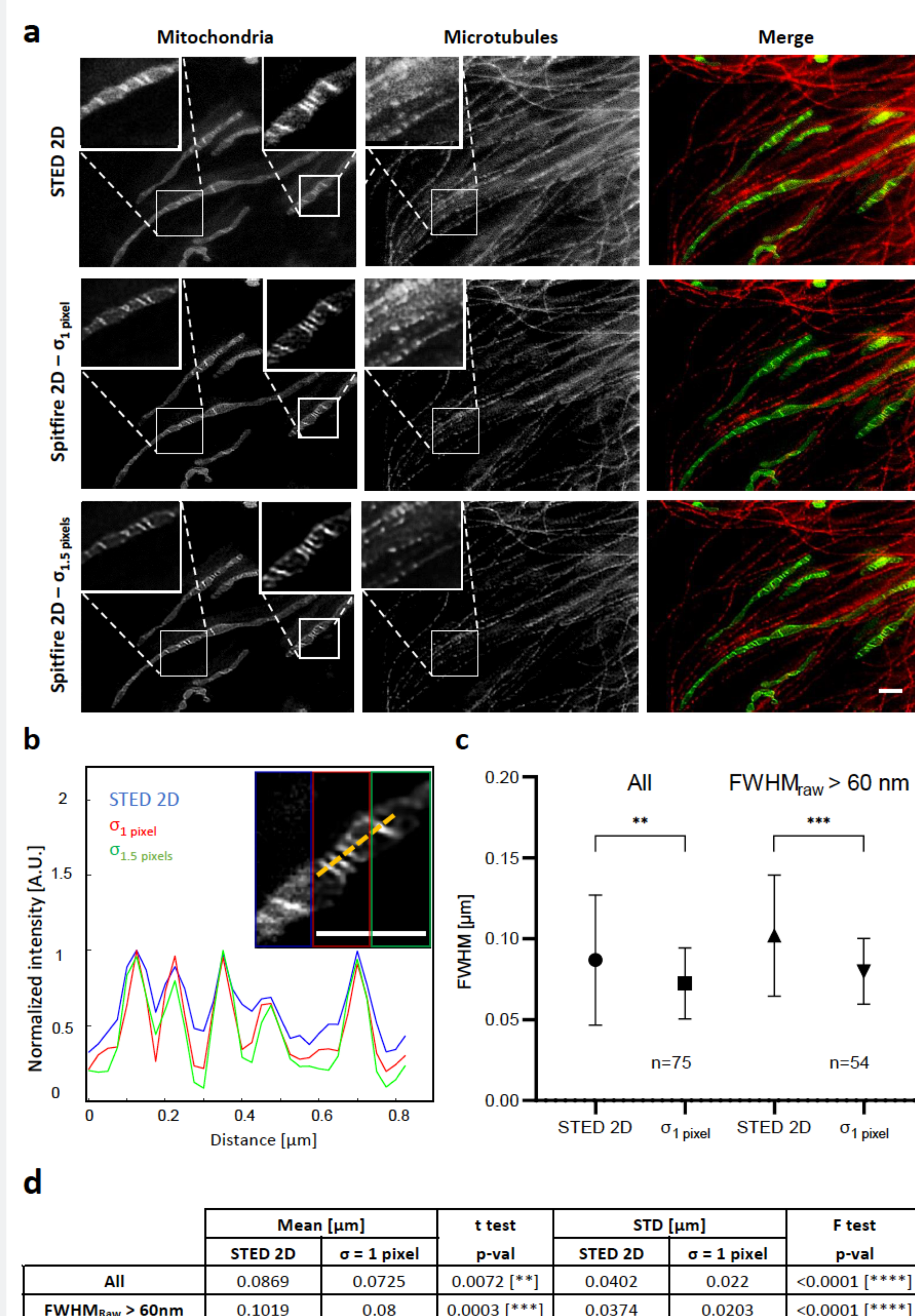


Fig 2. SPITFIR(e) increases the signal-to-noise of low-light images in STED imaging. Live RPE1 cells double stained with PKMR (mitochondria) and Tubulin TrackerTM Deep Red (microtubules) were imaged by STED nanoscopy before and after being processed by SPITFIR(e) (a). Partial overview of 2D STED raw data of RPE1 cells for mitochondria, microtubules and their superimposed images are shown from left to right (a, upper panel). 2D STED images were improved by SPITFIR(e) using two different 2D Gaussian model $\sigma_{xy} = 1$ pixel (a, middle panel) and $\sigma_{xy} = 1.5$ pixels (a, lower panel). (b) Normalized intensity line profiles were measured in the insets (b) for cristae regions. Statistics analysis is including in (d).

MFM

MultiFocus Microscopy [5]

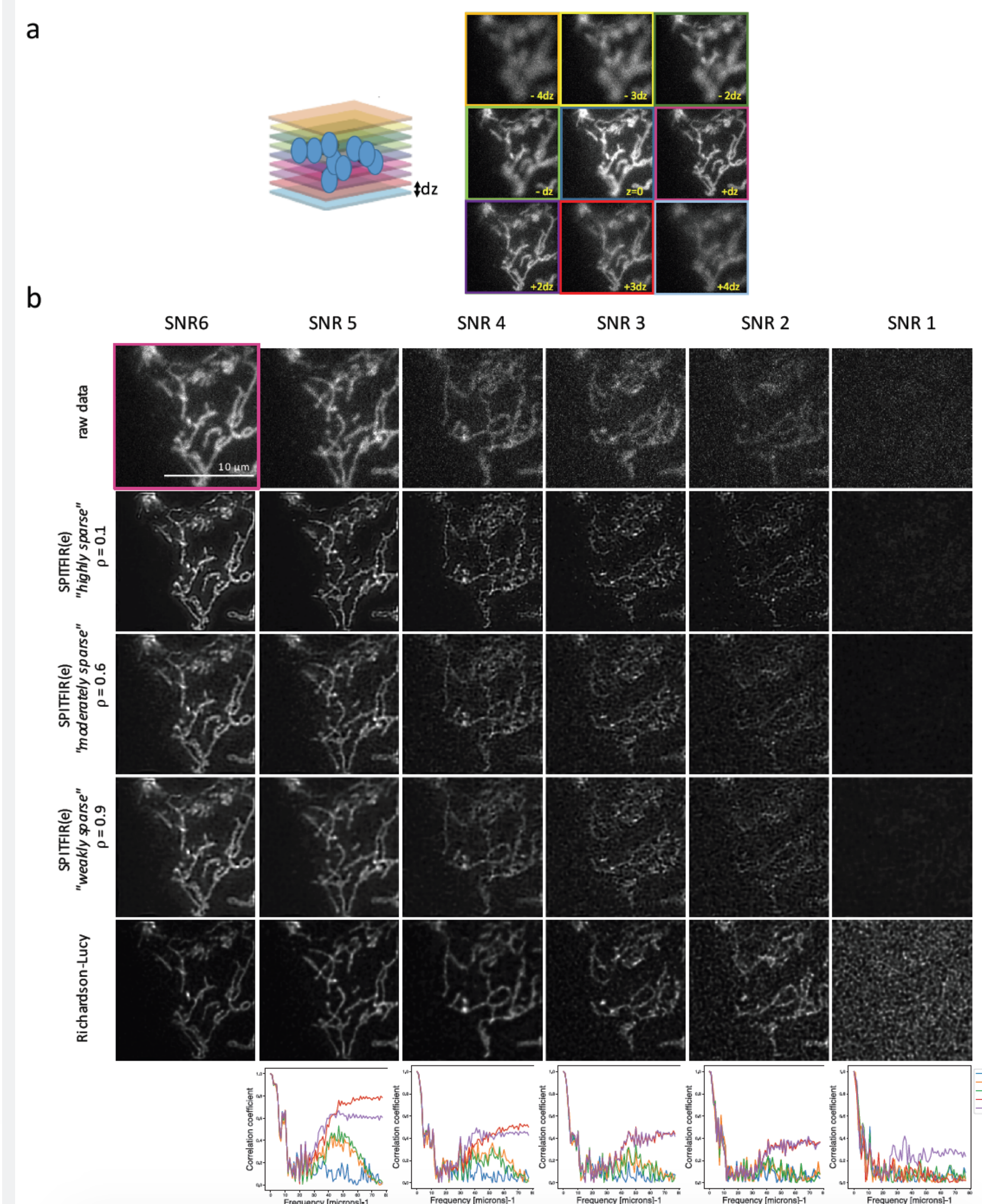
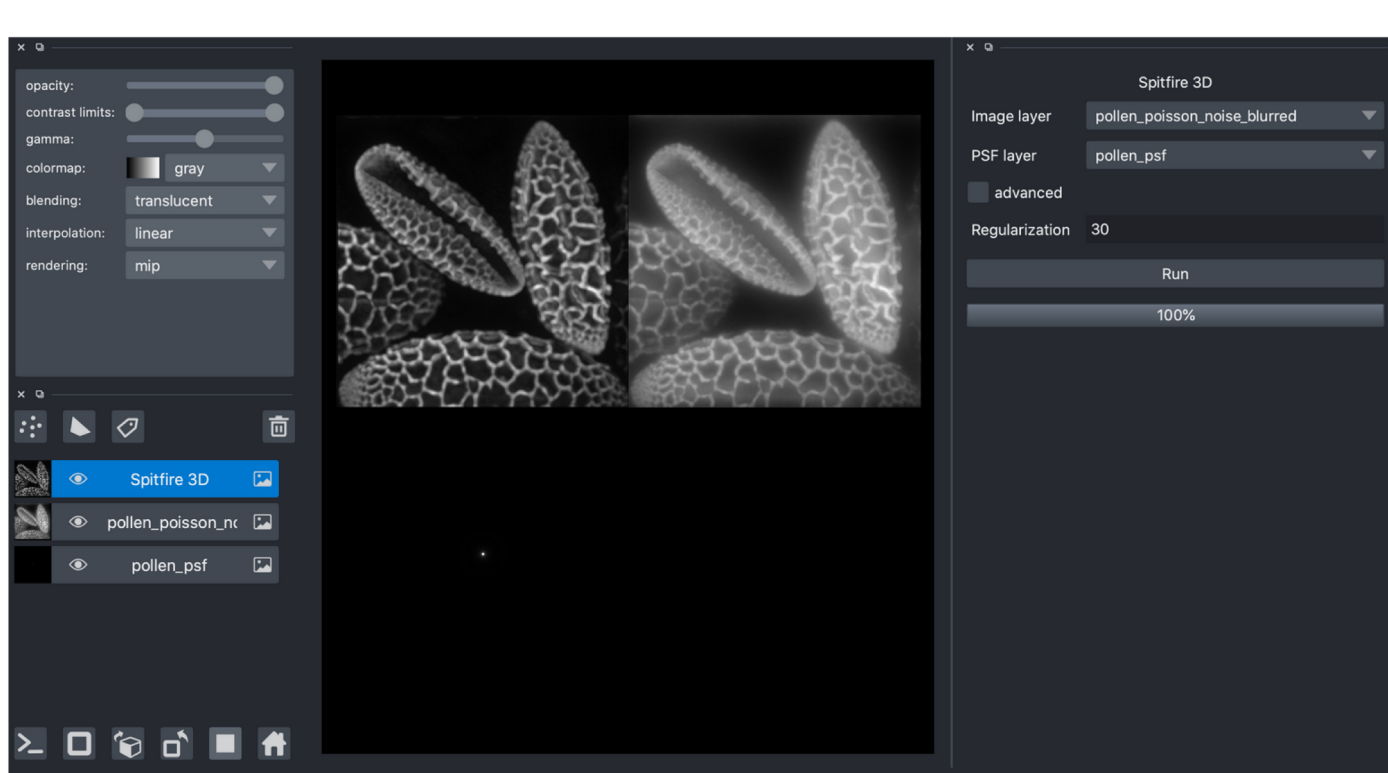


Fig 3. A comparison of Multi-Focus microscopy image reconstruction with different amounts of sparsity and SNR values. (a) MFM allows simultaneous acquisition of a 3D stack of nine equally spaced focal 2D images at low-illumination with a frame rate of 100 images per second, thus covering the whole volume of mitochondria in a single 3D image. The set-up is based on a diffraction grating to form multiple focus-shifted images followed by aberration-free focusing. (b) The image grid display the deconvolution results on the 6th plane in (+dz in a)) of the MFM stack for each SNR value

Resources

Napari plugin: napari-sdeconv



Source code:

- ✓ github.com/sylvainprigent/simglib
- ✓ C++ parallel implementation
- ✓ GPU (Cuda) implementation
- ✓ Conda package



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