Speckle blind SIM with calibration targets

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In fluorescence microscopy, the unknown sample ρ is related to a series of low-resolution acquisitions $\{y_m\}_{m=1}^M$ *via* the convolution model $y_m = h \otimes (\rho \times I_m) + \epsilon_m$, with h the microscope point spread function that exhibits a bounded Fourier support $\mathcal{D}_{\text{PSF}}$, I_m the m-th illumination pattern and ϵ_m an additive noise component. When I_m is homogeneous, the sample frequencies inside $\mathcal{D}_{\text{PSF}}$ are the only ones that can be retrieved from the dataset, hence limiting the image resolution. Following [1], a super-resolved estimate of ρ can nevertheless be achieved with speckle illuminations. Thanks to a mathematical refoundation of this technique [2], the super-resolution mechanism of this technique is now understood and a very fast numerical implementation has been derived and recently tested with real data. More specifically, some ArgoLight test patterns imaged with a home-made fastSIM setup [3] leads to a super-resolution factor higher than 1.8 after reconstruction.

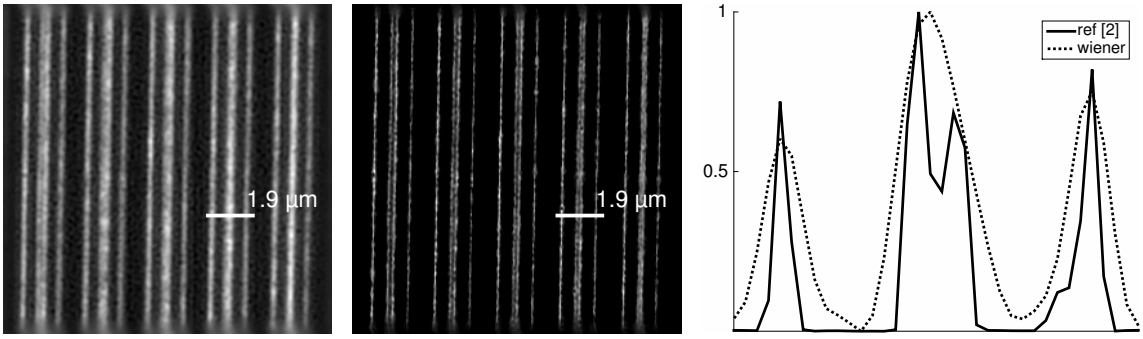

Figure 1: Reconstruction of the Argolight test pattern L from a series of 100 speckle illuminations: (left) Deconvolution of the mean of the dataset; (center) Blind-SIM reconstruction; (right) Line section plot extracted from both reconstructions.

References

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