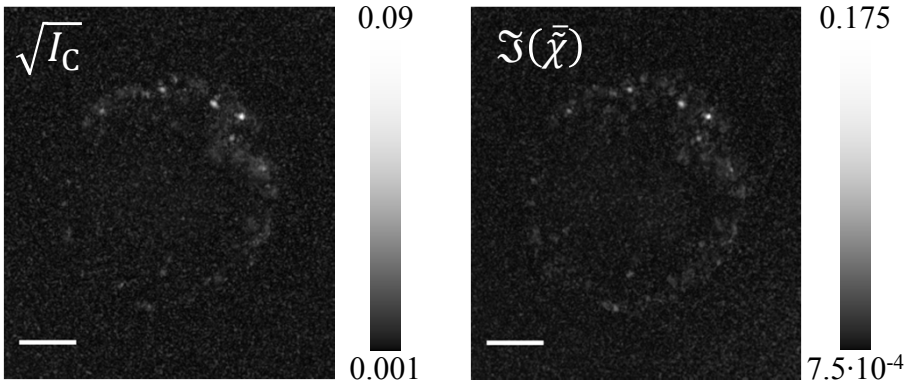

Fig. 4. Spectral error E_S of the $\sqrt{I_C}$ and $\Im(\bar{\tilde{\chi}})$ due to reconstruction from sparse sample data a linear grayscales as shown. The scale bar represents 5 μm.

speed by a factor $(S_{\max}/S+\rho)^{-1}$ where $\rho = P'/P$ is the fraction of spatial positions in dataset A compared to B, For the example shown here we have $S_{\max} = 8$, $S = 261$, $\rho = 0.01$ resulting in a 25 fold increase in acquisition speed. In our analysis it is required that $\rho P \gg S$ for a correct SVD-based noise filtering procedure. In typical situations where samples of a given chemical variety are imaged over a large set of replica, such as in high throughput screening, dataset A needs to be acquired only once, such that the speedup is effectively only limited by S/S', which is 33 in the present case. In absolute terms it is typically sufficient to measure at 5-10 spectral points to reconstruct most of the chemical information obtainable in a full spectral scan.

4. Conclusion

We have developed and demonstrated a sparse sampling method to reduce the acquisition time in CARS hyperspectral imaging. The method employs an adapted factorization of a large hyperspectral data matrix $(S \times P)$ into two smaller matrices of $(S \times P')$ and $(S' \times P)$, with $S' \ll S$ and $P' \ll P$. We demonstrated that the acquisition time for a human osteosarcoma U2OS cell was reduced by a factor of 25 without significant loss of information. This method, combined with state of the art CARS microscopes, is expected to enable real-time chemical imaging and high-throughput high-content label-free microscopy. The method is suited also for other coherent vibrational microscopy techniques such as stimulated Raman scattering, and in general for hyperspectral imaging techniques with sequential spectral acquisition.

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