Quality of biological images, reconstructed using localization microscopy data.

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Fluorescence localization microscopy is extensively used to gain insights into spatial architecture of subcellular compartments. This modality relies of determination of spatial positions of fluorophores labelling an extended biological structure, with precision exceeding the diffraction limit. Several established models describe influence of pixel size, signal-to-noise ratio and optical resolution on the localization precision. The labelling density has been also recognized as important factor affecting reconstruction fidelity the imaged biological structure. However, quantitative data on the influence of both sampling and localization errors on the fidelity of reconstruction of biological structure are scarce. It should be noted that processing localization microscopy data is similar reconstruction of a continuous (extended) non-periodic signal from a non-uniform noisy point samples. Typically, such tasks are realized with numeric optimization as few analytical solutions exist. In two dimensions the problem may be formulated within framework of matrix completion. However, no systematic approach has been adopted in microscopy, where images are typically rendered by representing localized molecules with Gaussian distributions (widths determined by localization precision).
Here we analyze the process of two-dimensional reconstruction of extended biological structures as a function of the density of registered emitters, signal-to-noise ratio and the area occupied by the rendered localized molecule. We quantify overall reconstruction fidelity with different established image similarity measures. Furthermore, we analyze the recovered spatial frequency spectrum (optical transfer function) for different reconstruction arrangements.