EFFICIENT BAYESIAN-BASED MULTI-VIEW DECONVOLUTION

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Modern light sheet fluorescence microscopy (LSFM) is able to acquire developing specimen with high spatial and temporal resolution throughout their entire development. LSFM allows the acquisition of several large high-resolution three-dimensional stacks (*views*) from different orientations every few seconds that cover the entire sample volume. The resulting massive datasets have the potential for reconstruction of complete lineage trees of all cells in large developing organisms like *Drosophila* or Zebrafish. Segmentation and tracking in those datasets requires an initial reconstruction of the data that typically consists of a multi-view registration and a multi-view fusion step.

Multi-view registration is typically solved using external landmarks like fluorescent beads embedded into the agarose [1] or by precise calibration of the microscopy setup, while most practical multi-view fusion steps involve a weighted average in order to fuse the overlapping views. Multi-view deconvolution has been previously proposed as an alternative as it significantly improves contrast and resolution in the reconstructed dataset. Due to the computational complexity of deconvolution it was, however, too inefficient in order to be applied to datasets that can easily range up to several terabytes.

We present an efficient derivation of Bayesian-based multi-view deconvolution (also known as Richardson/Lucy deconvolution). We take into account conditional dependencies between the overlapping views that contribute to a single time-point of a LSFM time-series. We achieve an up to 40-fold decrease in convergence time compared to previous derivations of Bayesian-based deconvolution of multiple views. This significant increase in performance allows the multi-view deconvolution of entire time-acquisitions on a single workstation computer in reasonable time. We demonstrate the performance and quality on simulated datasets as well as long-term time-lapse LSFM acquisitions and illustrate the increase in quality compared to classical optical sectioning microscopy. We provide efficient implementations based on ImgLib2 [2] for CPU and GPU processing, which are integrated into Fiji [3] and its bead-based LSFM multi-view registration & fusion framework.

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