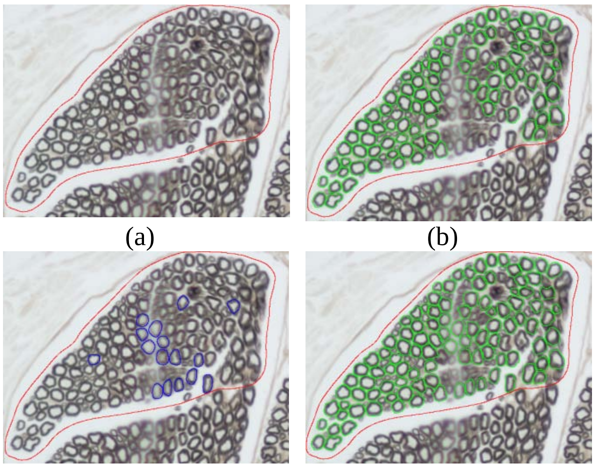

Figure 6: Performance evaluation of the proposed method: (a) MNFCs of a sub-fascicle in the original image; (b) the segmentation result for a purely 2D multi-scale watershed [4]; (c) the recovery results for MNFCs (blue) by using the proposed registration-based segmentation; (d) the final segmentation result for MNFCs.

5.Conclusion

In this paper we proposed an inter-frame registration-based segmentation method by which to obtain the 3D structure of nerve fiber from sequential microscopic cross-sectional images. The proposed method first segmented the MNFCs from each single image frame by using the multi-scale watershed hierarchical approach. Then we designed the spatially constrained registration (SCR) strategy, which takes image, geometric and biological structural features of MNFCs into account in order to register adjacent image frames and obtain the correspondences of inter-frame MNFCs. With the established connectivity, the proposed compensation mechanism efficiently recovered the missing MNFCs, certainly improving the segmentation results. The experimental results showed that the proposed method is more reliable on correspondence establishment than the ICP algorithm. Moreover, it achieved high segmentation accuracy with a detection rate of 91%. In the future, the proposed method can be applied to solve other image segmentation problems with a large number of cellular objects. Our system, which is near fully-automatic, can also help clinicians or researchers to efficiently collect reproducible data for investigating cell mechanics and evaluating neurological disorders.

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