


Fast assembling of neuron fragments in serial 3D sections

Hanbo Chen  · Daniel Maxim Iascone ·
Nuno Maçarico da Costa · Ed S. Lein ·
Tianming Liu · Hanchuan Peng

Received: 19 January 2017 / Accepted: 16 March 2017 / Published online: 1 April 2017
© The Author(s) 2017. This article is an open access publication

Abstract Reconstructing neurons from 3D image-stacks of serial sections of thick brain tissue is very time-consuming and often becomes a bottleneck in high-throughput brain mapping projects. We developed NeuronStitcher, a software suite for stitching non-overlapping neuron fragments reconstructed in serial 3D image sections. With its efficient algorithm and user-friendly interface, NeuronStitcher has been used successfully to reconstruct very large and complex human and mouse neurons.

Keywords Neuron · Stitch · Neuron stitcher · Reconstruct morphology · Alignment · Vaa3D

Digital reconstructions of neurons from very large three-dimensional (3D) brain images are crucial for modern neuroscience [1–3]. Despite recent great advances in neuron labeling, brain clearing, and high-resolution 3D tissue-imaging [4, 5] to study mammalian brains, many

neuroscientists still rely on physical sectioning of brains followed by imaging such sections using either light microscopy in 3D or electron microscopy in 2D. The acquired images of serial sections are then stacked and aligned to generate a very big image volume, from which neurons are reconstructed and quantified (e.g., Fig. 1a–d). Dendrites and axons severed at the section boundaries will need to be stitched. This is often a challenging bottleneck for proper reconstruction of locally dense dendritic and axonal trees.

It is quite labor intensive to stitch neuron segments manually over multiple sections. Automated methods may provide a significant increase in the throughput to neuronal reconstruction. However, this is a non-trivial task for algorithms because there could be missing tissues as well as distortions during sectioning, making stitching neuronal segments across multiple sections much more challenging in comparison with stitching overlapping tiles within single sections [6, 7] (Fig. 1c). Several studies [8–12] aimed at aligning traced neuron fragments (Supplement, Section 1) because a neuron reconstruction often gives a concise and less noisy description of neuron morphology than the respective raw image. These methods demonstrated various levels of suitability in identifying an alignment. Yet, most of these tools are not readily available in their Open Source form, and thus a thorough evaluation is difficult. Moreover, none of the existing methods was explicitly designed to handle the artifacts such as tissue loss or noise. Hence, their performance is sensitive to the quality of neuron reconstruction (Supplement, Section 4).

To address these challenges, we developed NeuronStitcher, a software package that automatically assembles complicated neuron fragments reconstructed from adjacent serial sections. NeuronStitcher utilizes a triangle-

Electronic supplementary material The online version of this article (doi:10.1007/s40708-017-0063-9) contains supplementary material, which is available to authorized users.

H. Chen · N. M. da Costa · E. S. Lein · H. Peng (✉)
Allen Institute for Brain Science, Seattle, WA, USA
e-mail: hanchuanp@alleninstitute.org

H. Chen
e-mail: cojoc.chen@gmail.com

H. Chen · T. Liu
Cortical Architecture Imaging and Discovery Laboratory,
Department of Computer Science and Bioimaging Research
Center, The University of Georgia, Athens, GA, USA

D. M. Iascone
Department of Neuroscience, Columbia University, New York,
NY, USA

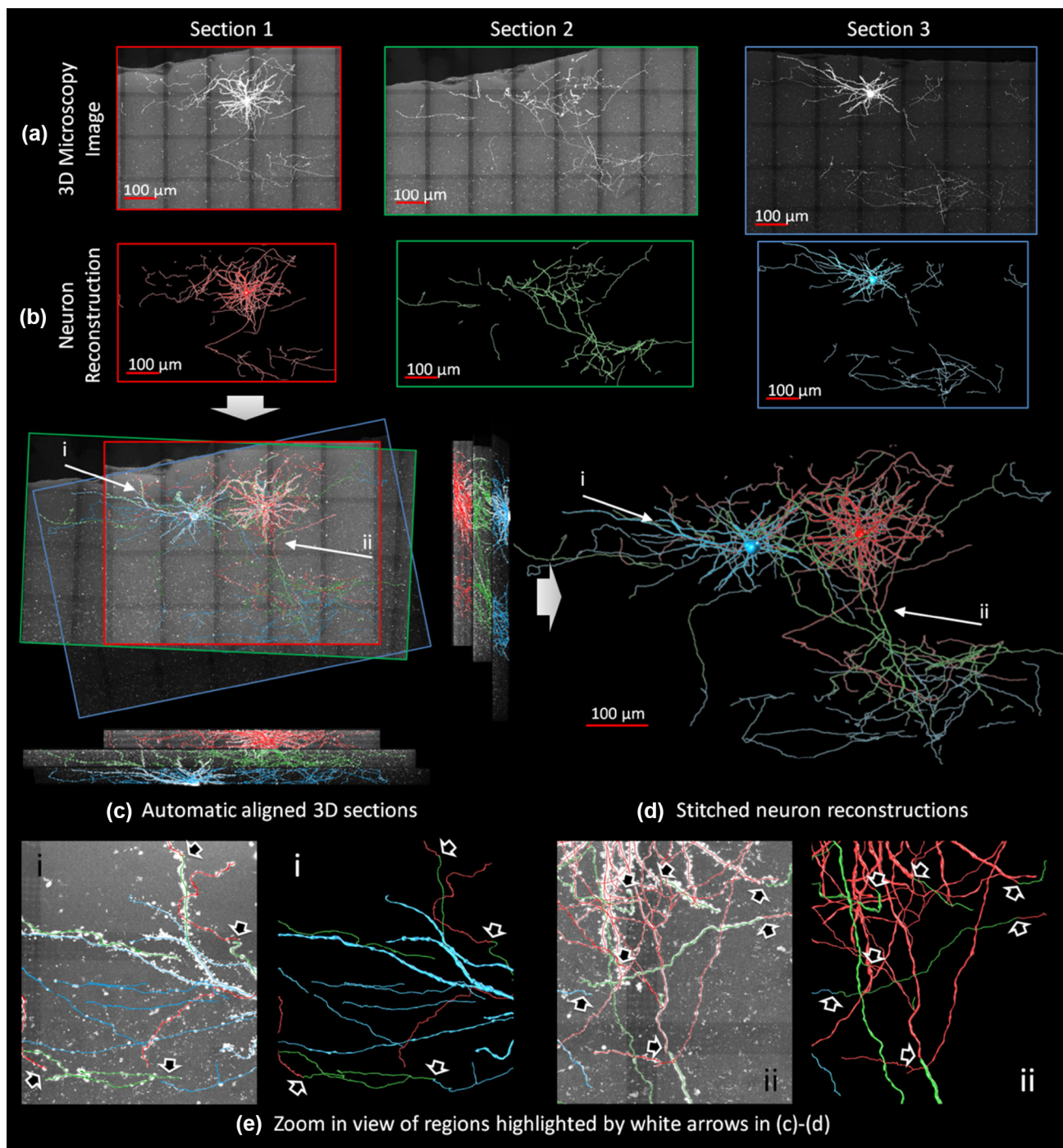


Fig. 1 Illustration of the 3D neuron stitching problem and results. Three continuous sections containing 2 neurons in a mouse brain are shown. The objective was to align neuron reconstructions (b) from adjacent 3D sections (a) and stitch them into complete neuron reconstructions (c, d). Different colors (red, green, and blue) were

assigned to the reconstructions in each section. All the snapshots were generated from a view perpendicular to the section plane except the two side-view pictures shown on the right and bottom of (c). (e) Zoom-in views of two regions in (c) and (d) with the stitched neurites highlighted by arrows. (Color figure online)

matching algorithm to estimate the initial match of severed neurites on the sectioning plane based on their relative location and branch orientations (Supplement, Section 2.3). Then, the reconstruction alignment process is iterated until the final matched neurites are smoothly

stitched (Supplement, Section 2.4). To make NeuronStitcher perform well for neurites that have varying quality, we have also developed three methods to remove noise when determining severed neurites (Supplement, Section 2.2).

We evaluated the accuracy of NeuronStitcher using carefully generated “ground truth” reconstructions from a piece of mouse brain tissue containing a labeled pyramidal neuron within the hippocampal CA1 region (Supplement, Section 4.1). Specifically, the whole neuron was first imaged and thereafter semi-automatically reconstructed in 3D by an expert as the ground truth reconstruction (Figure S 10(a)). Then, we evenly sliced the neuron into three serial sections in the z direction, each of which was imaged individually. The reconstructions of neuron fragments from all individual sections were generated by an expert and then stitched together using NeuronStitcher (Figure S 10(b)). A careful comparison of the ground truth reconstruction to the stitched reconstruction showed that 98% bifurcations of the 3D reconstructed, tree-like neuron morphology in the ground truth had their correspondence in the stitched reconstruction (Supplement, Section 4.1), and the minor amount (2%) of missing correspondence happened at the section interfaces and was due to the sectioning process.

We also considered an alternative way to produce the “ground truth” to evaluate the accuracy of NeuronStitcher (Supplement, Section 4.3). We chose 5 densely arborized reconstructions from mouse visual cortex. To generate the simulated data, each reconstruction was digitally “sectioned” into two halves. One half was then randomly rotated and shifted in parallel with the sectioning plane. Several different gaps (1, 2, 4, and 8 μm) were added to simulate the different levels of tissue loss during sectioning. Both the vertices and edges within the sectioning gaps were removed (Figure S 17). To test NeuronStitcher, it was used to stitch the two portions of data back together. Our automatic matching found the correct matching and alignment in most cases (Figure S 18). Even when a considerable amount of tissue was lost (8 μm gap), the alignment was still close to the ground truth (10.4 μm). In such a case, most of the severed neurites were correctly matched (75% precision, 62% sensitivity) by using the default parameters. Notably, the errors due to the substantial information loss in the big gaps should be anticipated (Figure S 18(c)-(e)). We also tested NeuronStitcher with different parameter configurations, which showed that NeuronStitcher was robust to varying parameters. For instance, when the gap size was 1 μm , the distance to the truth was $1.3 \pm 0.4 \mu\text{m}$, the precision was $90 \pm 6\%$, and the sensitivity was $87 \pm 15\%$ on average for all the 58 sets of parameters tested.

In our experiments, we applied NeuronStitcher to stitch two images of a mouse V1 neuron from confocal microscopy and another two biocytin-filled human neurons imaged by bright field microscopy (Supplement, Section 4.2, Table S 2). In total, 16 pairs of sections were stitched (the results of 3 adjacent pairs in Fig. 1 and more results in Figures S 11-15). Among all automatically

matched neurites, 356 (86.6%) were accepted by an expert (Table S 3). NeuronStitcher typically finished the computation within seconds, requiring less than 100 Mb memory. The time for a user to visually check and adjust results depended on the complexity of the reconstruction. For our testing datasets, the average time for stitching (including automated computation, visual inspection, parameter fine-tuning, and manually adjustment of the result) an adjacent pair of serial sections was 13'08" (median: 9'41", minimum: 0'13", and maximum: 36'31") (Table S 3).

The quality of neuron reconstructions and the selected parameters might influence the performance of NeuronStitcher. To broaden the utility of NeuronStitcher to work with a variety of data acquisition processes, we designed an interactive graphical user interface to (1) allow a visual evaluation on the stitching results and live adjustments of matching parameters; and (2) enable manual corrections of incorrect matching results (Supplement, Section 3). The software was implemented in C/C++ as a plugin of Vaa3D [13, 14], which is a publicly available Open Source platform with a user-friendly interface for 3D+ image analysis and visualization (<http://www.vaa3d.org>). The screenshot of the GUI and the guidance of the tool can be found in Supplement, Section 3, Figures S 6–9, and Videos S 1–4.

Acknowledgements This work was sponsored by the Allen Institute for Brain Science. The authors wish to thank the Allen Institute founders, P. G. Allen and J. Patton, for their vision, encouragement, and support. We thank Zhi Zhou, Staci Sorensen, Lu Li, and Hongkui Zeng for assistance in providing data and discussion of the usability of the software.

Conflict of interest On behalf of all authors, the corresponding author states that there is no conflict of interest.

Open Access This article is distributed under the terms of the Creative Commons Attribution 4.0 International License (<http://creativecommons.org/licenses/by/4.0/>), which permits unrestricted use, distribution, and reproduction in any medium, provided you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons license, and indicate if changes were made.

References

- Helmstaedter M, Mitra PP (2012) Computational methods and challenges for large-scale circuit mapping. *Curr Opin Neurobiol* 22:162–169
- Parekh R, Ascoli GA (2013) Neuronal morphology goes digital: a research hub for cellular and system neuroscience. *Neuron* 77:1017–1038
- Meijering E (2010) Neuron tracing in perspective. *Cytom A* 77:693–704
- Chung K et al (2013) Structural and molecular interrogation of intact biological systems. *Nature* 497:332–337

5. Hama H et al (2011) Scale: a chemical approach for fluorescence imaging and reconstruction of transparent mouse brain. *Nat Neurosci* 14:1481–1488
6. Preibisch S, Saalfeld S, Tomancak P (2009) Globally optimal stitching of tiled 3D microscopic image acquisitions. *Bioinformatics* 25:1463–1465
7. Bria A, Iannello G (2012) TeraStitcher—a tool for fast automatic 3D-stitching of teravoxel-sized microscopy images. *BMC Bioinform* 13:316
8. Weber B et al (2014) Automated stitching of microtubule centerlines across serial electron tomograms. *PLoS ONE* 9:e113222
9. Dercksen VJ et al (2009) Automatic alignment of stacks of filament data. In: 2009 IEEE International Symposium on Biomedical Imaging: From Nano to Macro 971–974 (IEEE). doi: [10.1109/ISBI.2009.5193216](https://doi.org/10.1109/ISBI.2009.5193216)
10. Dercksen VJ, Hege H-C, Oberlaender M (2014) The Filament Editor: an interactive software environment for visualization, proof-editing and analysis of 3D neuron morphology. *Neuroinformatics* 12:325–339
11. Hoglebe L et al. (2011) Trace driven registration of neuron confocal microscopy stacks. In 2011 IEEE international symposium on biomedical imaging: from nano to macro 1345–1348 (IEEE). doi: [10.1109/ISBI.2011.5872649](https://doi.org/10.1109/ISBI.2011.5872649)
12. Luzzati F, Fasolo A, Peretto P (2011) Combining confocal laser scanning microscopy with serial section reconstruction in the study of adult neurogenesis. *Front Neurosci* 5:70
13. Peng H, Bria A, Zhou Z, Iannello G, Long F (2014) Extensible visualization and analysis for multidimensional images using Vaa3D. *Nat Protoc* 9:193–208
14. Peng H, Ruan Z, Long F, Simpson JH, Myers EW (2010) V3D enables real-time 3D visualization and quantitative analysis of large-scale biological image data sets. *Nat Biotechnol* 28:348–353

Hanbo Chen obtained his Ph.D. degree in computer science at The University of Georgia. His research interest lies in studying brain network and developing method for high-dimensional big data analysis which includes multi-scale, multi-modal, multi-subject, and across-species brain image data.

Daniel Maxim Iascone is a graduate student in Dr. Franck Polleux's lab at Columbia. He is studying how the human-specific duplication of SRGAP2 helped drive human brain evolution. His project focuses on assessing how SRGAP2C coordinates synaptic development across whole cortical neurons and determining how this impacts neuronal activity. Before that, he was as an undergraduate student in Dr. Jeannie Chin's lab at Thomas Jefferson University, where his research focused on determining how seizure activity in Alzheimer's disease alters neural stem cell division in the adult hippocampus. His long-term research goal is to combine molecular tools for genome editing and advanced imaging techniques to study cellular control of neural circuit development in vivo.

Nuno Maçarico da Costa joined the Allen Institute in 2013 as an Assistant Investigator in the Neural Coding department. He leads the Network Anatomy group in its efforts to map the wiring diagram of the mouse neocortex and its functional connectivity. He graduated in Biology from the Faculty of Science of the University of Lisbon. Afterwards, he moved north to Copenhagen, Denmark, where he studied the interactions between the hippocampus and prefrontal cortex in rats. After this period with the charming Danes, he returned to Portugal and joined the Doctoral Program in Biology and Medicine

of the Gulbenkian Foundation. He performed his doctoral research in the Institute of Neuroinformatics in Zurich and obtained a PhD degree in Natural Sciences from the Swiss Federal Institute of Technology. During his PhD, he described the fine structural details of the thalamocortical pathway to cat visual cortex using correlated light and electron microscopy. He stayed in Zurich as a Post-Doc fellow and later as a Junior Group Leader investigating the network anatomy of the neocortex in several mammalian species.

Ed S. Lein joined the Allen Institute in 2004 and provides scientific guidance and oversight for the creation of large-scale gene expression atlases of the mammalian brain as online resources for the scientific community. He was part of the team that generated the inaugural Allen Mouse Brain Atlas and now leads efforts to extend these anatomical and gene expression atlasing efforts to the developing human and nonhuman primate brain. Particular interests of his work at the Allen Institute include the use of large-scale gene expression data to map functional brain divisions, define specific neuronal subtypes, and compare cellular-level gene expression patterns from rodents to humans to identify molecular pathways unique to humans. He received his B.S. degree in biochemistry from Purdue University and his Ph.D. in neurobiology from the University of California at Berkeley. His postdoctoral work at the Salk Institute for Biological Studies focused on molecular profiling of specific hippocampal and neocortical cell types and the generation of molecular genetic tools for functional manipulation of specific neuronal subtypes. He is also an Affiliate Assistant Professor in the Department of Physiology and Biophysics at the University of Washington.

Tianming Liu is a Professor of Computer Science at The University of Georgia. His research in recent 15 years has been focused on brain imaging and computational neuroscience, and he has published over 240 papers on these topics. He received the NIH K01 Career Award and the NSF CAREER Award on his research areas.

Hanchuan Peng leads a group of computational neuroanatomy and smart imaging at the Allen Institute for Brain Science. His current research focuses on bioimage analysis and large-scale informatics, as well as computational biology. Before joining the Allen Institute, he was the head of a computational bioimage analysis lab at Howard Hughes Medical Institute, Janelia Farm Research Campus. He is also an adjunct or affiliate professor with several USA and China universities. He is the inventor of a number of algorithms and software/hardware systems, including Vaa3D, BrainAligner, NeuronTracers, SmartScope, mRMR, and 3D Virtual Finger. His recent work includes developing novel and very efficient algorithms for 3D and high-dimensional image analysis and data mining, building single-neuron whole-brain level 3D digital atlases for model animals, and Vaa3D (<http://vaa3d.org>), which is a high-performance visualization-assisted analysis system for large 3D/multi-dimensional biological and biomedical image datasets. He built the first neuron stereotypy map of a fruit fly brain, co-developed the first single-cell-resolution 3D digital maps of *C. elegans*, and led one of the largest studies to date on 3D brain image registration and standardization. He was also the inventor of the widely cited minimum Redundancy Maximum Relevance (mRMR) feature/variable selection methods in machine learning and data mining. He was a recipient of Cozzarelli Prize (2013) and DIADEM Challenge award (2010). He was the founder of the annual Bioimage Informatics conferences (<http://bioimageinformatics.org>) and has taken various leading roles in several other journals.