Automated Segmentation of Oriented Branching Structures through Dilation Shells using Dynamic Programing

Submitted, January 10, 2019
Computer Aided Radiology and Surgery (CARS) 2019
Rennes France

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The authors have no conflicts of interest and all human studies have been approved and performed in accordance with ethical standards and informed consent.

Abstract

Purpose: We present a new algorithm for finding branching paths of maximum connectivity through 3D images. Our immediate application is segmenting small veins in cerebral white matter in high-field susceptibility-weighted magnetic resonance images, to parameterize their number, tortuosity, and branching patterns in small vessel disease.

Methods: Our algorithm finds continuous paths with maximum connectivity. Since the veins branch outward from the lateral ventricles, we use the dilation operator from mathematical morphology to create a stack of one-voxel-thick shells outward from the ventricles. We then simultaneously explore paths between every possible starting and ending voxel in these shells, stepping through successive shells along continuous paths and using dynamic programming to efficiently eliminate inferior paths at each step. Multiple paths with the same starting voxel and but different ending voxels indicate branching.

Results: Initial results demonstrate effective and rapid 3D segmentation of small veins and identification of branch points. The paths accommodate local discontinuities and are thus readily parameterized as continuous functions.

Conclusion: Our new algorithm holds promise for identifying and parameterizing oriented branching structures of high connectivity in 3D images. It has numerous potential applications, including understanding vascular and neurological anatomy. Validation against manual segmentation and further development is planned.

Introduction

We have developed a new automated algorithm to segment small veins recently identified in susceptibility weighted images (SWI) from ultra-high field (7T) magnetic resonance (MR) images. In SWI, the veins appear darker than the surrounding tissue due to the magnetic properties of deoxygenated hemoglobin [1]. The veins branch outward from the lateral ventricles into the surrounding white matter (the blood actually drains the other way, towards the ventricle). There is compelling evidence that changes in these small cerebral vessels, including those due to small vessel disease (SVD), represent early pre-clinical markers of brain pathology across mental health disorders (e.g., [2][3]). Better characterization of these vessels may serve as an important marker for prevention and treatment studies. Previously, manual tracing methods have primarily been used to identify and parameterize these veins [4]. Here we describe a new general algorithm that takes advantage of the known draining orientation of the vessels. Our requirements are that the algorithm be fast and automated, due to the potentially large number of 3D images and the tedious and time-consuming nature of manually segmenting the numerous small veins. An automated algorithm would also be expected to decrease variability in determining parameters, especially given the difficulty in accurately tracing tortuous linear objects in 3D. The ultimate goal is to provide rapid and reliable determination of parameters for these veins, including density, tortuosity, degree of branching, etc. We next describe the basic algorithm and preliminary results.

Methods

To identify the veins within the cerebral white matter, we explore a large space of possible paths and find those paths with greatest *connectivity* in intensity, that is to say, paths whose voxels maintain a similar intensity from voxel to voxel. Then from these paths we select those with the lowest average intensity, characteristic of veins in our SWI images.

Our algorithm has evolved from a prior 2D algorithm developed for cardiac segmentation [5-7], subsequently extended to N dimensions and contributed to the National Library of Medicine Insight Toolkit (ITK)[1] as part of its infrastructure supporting chain-codes [8,9]. Chain-codes are representations of parametric curves that connect neighboring voxels into a linear chain, specifying the direction at each step from a given voxel to one of its neighbors [10]. Neighbors in our case are defined as being within a 3×3×3 cube of the central voxel. Chain codes are well suited as a basis for parameterizing linear objects such as veins, while providing a convenient platform for voxel-level image analysis algorithms.

[1] https://itk.org

Building on this previous work, we have further introduced a new ability to incorporate an expected direction using *dilation*. Dilation is a standard technique in *mathematical morphology* [11] in which a shape is expanded using a *structuring element*. In our case, the structuring element is a 3×3×3 cube of voxels around a central voxel, from which repeated dilation produces a concentric set of shells, each one voxel thick, around the original shape. To establish the expected direction of the veins, we place the initial shape at the surface of the ventricle, and from there we dilate our one-voxel-thick shells outward into the white matter. A chain-code having just a single voxel in each shell should then be capable of following a given vein by connecting to a voxel in the next shell, in particular, that voxel whose intensity most resembles its own. Building chain-codes in this manner follows the expected direction of the veins. Multiple paths can inhabit a single vein, allowing branch points as the paths extend away from the ventricle.

Consider a reasonable example for our application: a volume with 50 dilation shells each containing 1000 voxels (the actual number of voxels will typically vary from shell to shell). The number of possible paths crossing this volume is clearly astronomical, even with the constraints put on our chain-codes. However, we know that all possible paths begin with a particular voxel in the first shell and end with at a particular voxel in the 50th shell. So, we restrict our search to keeping track of the optimal solution for each possible starting/ending voxel pair. In the case of our example, this limits our search space to $1000\times1000 = 1$ million paths, a large but manageable number. At each dilation step we exclude inferior candidates, updating the optimal path for each starting/ending voxel pair by connecting to the neighboring voxel in the previous shell with an intensity most similar to our own. This is an example of *dynamic programing* [12], which divides an optimization problem into independently solvable steps, thereby permitting the traversal of an otherwise intractably large search-space. In our example, it produces the million top candidates for paths with high connectivity, excluding inferior solutions along the way.

Since the veins are branching outward through the dilations shells, we know that each voxel in the final shell can represent only one branch. Thus, we may look at all the paths reaching a given voxel in the ending shell and select the one with the lowest mean intensity, thereby identifying a set of just 1000 paths (in our example) that should contain all the veins, since the veins have the lowest intensity of any tissue in the SWI images.

Whereas each voxel in the final shell can represent only one branch, each voxel in the first shell can represent a trunk with multiple branches. Branch points may thus readily be identified by finding voxels in the first shell that connect to more than one voxel in the last shell, since multiple paths from a starting voxel can inhabit the trunk of a vein that branches to multiple voxels in the ending shell. Thus it may be seen that the dilation shells organize the image analysis of our application to find the veins in their expected orientation and branching direction.

Our algorithm presently uses routines from the ITK and the Visualization Toolkit (VTK)[2], as well as custom C++ functions operating directly on arrays for maximum efficiency. It operates in both the OSX and Windows environments. For the results described below, we used an Apple 3.1 GHz PowerBook.

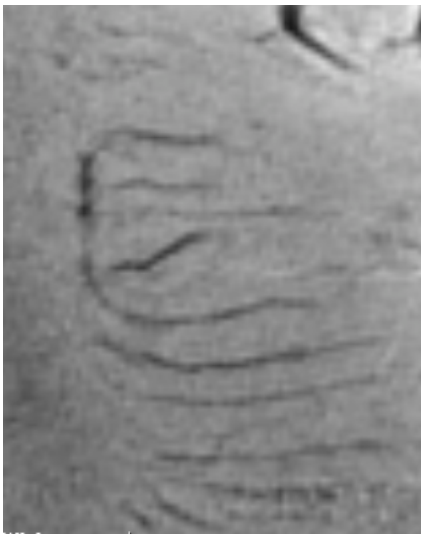

Fig. 1. Susceptibility weighted MRI of veins in the cerebral white matter branching out from the ventricle (see text).

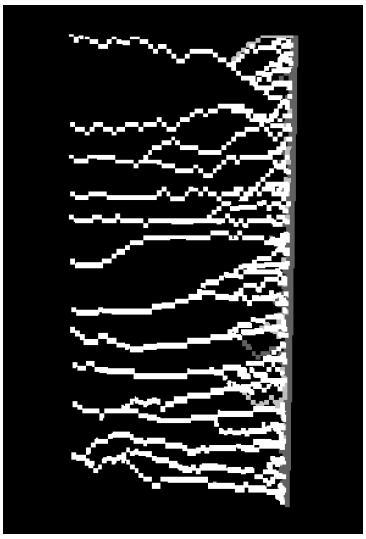

Fig. 2. Sum of paths (equally weighted) resulting from application of algorithm to image in Fig. 1.

Results

An image of the brain was obtained using a 7-Tesla MRI scanner and the SWI protocol. The data was cropped to

[2] https://www.vtk.org

a volume containing $80\times105\times5$ voxels, a slice through which is shown in Fig. 1. Veins are evident extending toward the right from the ventricle (the ventricle is not well differentiated from the white mater in this image, but occupies the relatively homogenous region in the left portion of the image). An initial shape with a face roughly at the surface of the ventricle was used for the dilation of 50 shells, each of which containing $105\times5 = 525$ voxels. Thus, roughly a quarter of a million paths (525×525) were maintained as the algorithm proceeded through the 50 shells from left to right.

The 525 paths with the lowest average intensity that reached each ending voxel were summed into an image whose Maximum Intensity Projection (MIP) is shown in Fig. 2. The individual paths were equally weighted, so that pixel intensity serves as a histogram of the number of paths passing through each voxel. Comparing Figs. 1 and 2, it is clear that the significant veins have been identified, keeping in mind that Fig. 1 is only a slice through the volume, while Fig. 2 is a projection of the entire volume. Branch points are clearly evident in Fig. 2. Total time for the algorithm was approximately 2 seconds.

One artifact is evident at the far-right side of Fig. 2. Since we are displaying one path reaching each of the voxels in the ending shell, multiple tiny branches appear that do not necessarily correspond to veins. These could be eliminated by introducing various parameters, such as intensity, connectivity, or expected branching pattern. However, we are looking for a way to eliminate them without introducing such a parameter, since a strength of the algorithm is its lack of parameters.

Conclusions

We have presented a new algorithm for identifying oriented branching structures of high connectivity in 3D images, which builds chain-codes through dilation shells to follow the expected direction of the veins and their branching structure. The algorithm appears to work well, identifying the significant veins visible in a test image. Validation against manual segmentation is planned. We expect to develop the algorithm further to provide rapid and reliable determination of parameters for the small veins, including number, tortuosity, and degree of branching. The algorithm may have other applications, including segmentation of other vascular or neurological anatomy.

Acknowledgements

We wish to thank Tamer Ibrahim, PhD, for supplying the SWI image used in our initial development. We further acknowledge funding from NIH grant R01 MH111265, the Department of Bioengineering at the University of Pittsburgh, and the Coulter Foundation.

References

1. Haacke EM, Mittal S, Wu Z, Neelavalli J and Cheng Y-CN, Susceptibility-Weighted Imaging: Technical Aspects and Clinical Applications, Part 1, American Journal of Neuroradiology January 2009, 30 (1) 19-30; DOI: https://doi.org/10.3174/ajnr.A1400
2. Pugh KG, Lipsitz LA. The microvascular frontal-subcortical syndrome of aging. Neurobiology of aging. 2002;23(3):421-31. PubMed PMID: 11959405
3. Taylor WD, Aizenstein HJ, Alexopoulos GS. The vascular depression hypothesis: mechanisms linking vascular disease with depression. Molecular Psychiatry. 2013;18(9):963. doi: 10.1038/mp.2013.20.
4. Shaaban CE, Aizenstein HJ, Jorgensen DR, MacCloud RL, Meckes NA, Erickson KI, Glynn NW, Mettenburg J, Guralnik J, Newman AB, Ibrahim TS, Laurienti PJ, Vallejo AN, Rosano C. In Vivo Imaging of Venous Side Cerebral Small-Vessel Disease in Older Adults: An MRI Method at 7T. American Journal of Neuroradiology. 2017;38(10):1923-8. doi: 10.3174/ajnr.A5327.
5. Stetten G., Drezek, R.,Active Fourier Contour Applied to Real Time 3D Ultrasound of the Heart, International Journal of Image and Graphics, vol. 1, no. 4, pp. 647-658, 2001.

6. Ota T., Fleishman C., Strub M., Stetten G., Ohazama C., von Ramm O., Kisslo J., Real-Time Three-Dimensional Echocardiography: Feasibility of Dynamic Right Ventricular Volume Measurement Using Saline Contrast, American Heart Journal, vol. 137, pp 958-66, 1999.

7. Collins M., Hsieh A., Ohazama C., Ota T., Stetten G., Donovan C., Kisslo , Ryan T., Assessment of Regional Wall Motion Abnormalities with Real-Time 3-Dimensional Echocardiography, Journal of the American Society of Echocardiography, vol. 12, no. 1, pp. 7-14, January, 1999.

8. Galeotti J., Stetten G., Creation and Demonstration of a Framework for Handling Paths in ITK, MICCAI Workshop on Open-Source Software issue of The Insight Journal. 2005

9. Galeotti J., Stetten G., N-Dimensional Path Optimization: The Implementation of a Novel Algorithm in ITK, MICCAI Workshop on Open-Source Software issue of The Insight Journal, 2005.

10. Freeman H, On the Encoding of Arbitrary Geometric Configurations, IRE Transactions on Electronic Computers, Volume: EC-10, Issue 2, pp. 260 – 268, June 1961, 10.1109/TEC.1961.5219197.

11. Dougherty, ER, An introduction to morphological image processing, Bellingham, Washington USA: SPIE Optical Engineering Press, 1992.

12. Bellman R, Dynamic Programming, Princeton University Press (1957). Dover paperback edition (2003), ISBN 0-486-42809-5