because particles are subject to a perspective transformation. The visual quality of reconstructions directly rendered from Octree compressed data appears to be higher than that derived from raycast.

Early results of x-ray reconstructions from direct projection of Octree compressed volumes suggest that this approach may be able to deliver performance and image quality necessary for real-time 2D-3D registration.

TubeTK: an open-source toolkit of algorithms operating on images of tubes

D. Pace[1], A. Enquobahrie[1], P. Reynolds[1], J. Jomier[2], E. Bullitt[3], S. Aylward[1]
[1]Kitware Inc, Carrboro, United States
[2]Kitware SAS, Villeurbanne, France
[3]Neurosurgeon, Chapel Hill, United States

Keywords Medical imaging · Tubular structures · Image processing and analysis · Open-source software

Purpose

Tubes are a common geometrical structure that occur at multiple scales throughout the body and are visible in a variety of medical imaging modalities. Examples of anatomical tubular structures include blood vessels, nerves, bile ducts and bronchi. Quantifying tubular structures extracted from medical images provides a way of measuring anatomical response to disease status. We have shown, for example, that vascular tortuosity can be used to grade both tumor response to treatment [1] and the progression of retinopathy of prematurity. Also, preservation of vasculature structures is a common treatment goal that also motivates tube segmentation. Furthermore, the geometry of tubes equates to image features that are insensitive to noise, contrast, and imaging modality [2], and therefore not only support anatomic quantification but also provide a basis for image registration [3]. We have shown, for example, that tubes in computed tomography, magnetic resonance imaging and ultrasound support image registration for longitudinal change detection, image-guided interventions and statistical atlases formation to distinguish populations.

With these applications in mind, our goal is to develop a software toolkit of algorithms for images depicting tubular structures. Driving clinical applications for our toolkit include using vascular features to (1) align intra-operative ultrasound with pre-operative images during image-guided brain tumor resection and abdominal ablation interventions, (2) achieve image-based quantification of retinal diseases and of tumor progression, and (3) parameterize populations to identify biomarkers for stroke and schizophrenia.

Methods

We have developed an open-source software library "TubeTK" for segmentation, registration and analysis of images depicting tubular structures (www.tubetk.org). TubeTK currently includes software for:

- Tube segmentation based on centerline extraction and radius estimation, which operates on 2D and 3D images acquired from multiple modalities such as MR angiograms, X-ray CT, and B-mode ultrasound [2].
- Vessel and surface enhancing diffusion filtering, based on local image geometry measures [4].
- Tube tortuosity metrics, which have been shown to be predictive of vascular abnormalities in the brain [1] and retina.
- Vascular network model-to-image registration that operates across modalities [3].

TubeTK also provides implementation of several medical imaging algorithms that take advantage of other image geometrical constructs (e.g., points and surfaces), in addition to some that are generally applicable, including:

- Image registration that aligns images of sliding anatomy, such as respiration-induced sliding of the lungs and abdominal organs against the chest wall [5].
- Probability density function (PDF)-based image segmentation, which inputs a rough initial segmentation and incorporates interactive refinement.
- Fundamental image processing algorithms, such as edge-enhancing, coherence-enhancing and hybrid anisotropic diffusion filtering.
- "ImageMath": an easy-to-use command line interface to many of ITK's basic image processing capabilities, such as histogram-based filtering, thresholding, blurring, resampling, image-fusion and image statistics.
- "tubeImageViewer": a light-weight application for 3D image viewing.

TubeTK's algorithms are implemented in C++ with extensive use of ITK (www.itk.org) and VTK (www.vtk.org), and also using CTK (www.commontk.org) and Qt. TubeTK provides both a command line interface and integration with the 3D Slicer open-source medical imaging application (www.slicer.org). The project undergoes nightly regression testing with online dashboard reporting using CMake/CTest/CDash (www.cmake.org), representing high-quality software engineering practices. The source code is distributed within an online git repository (www.tubetk.org/tubetk.git) under the Apache 2.0 license, and thus is freely available for use by both non-commercial and commercial organizations.

Results

Example results of image processing and analysis using TubeTK are shown in Figure 1. Figure 2 shows screenshots of TubeTK's software in operation.

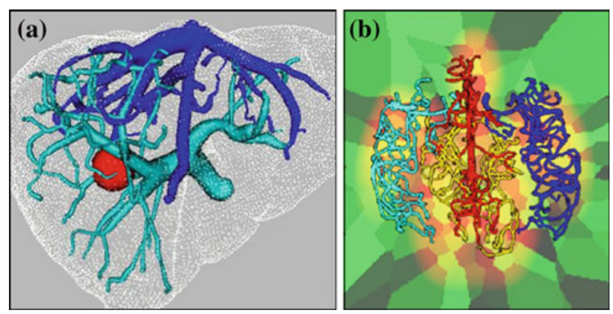

Fig. 1 **a** Vessels, liver and tumor models extracted from multiple, registered CT scans taken at different phases of contrast progression. **b** A 3D model of a patient's intracranial arteries, colored by connectivity, and overlaid on one slice of visualization of a vascular atlas that depicts expected vessel locations (*red cloud*) and regions having equal probability of containing a vessel segment (*green* parcellation of space)

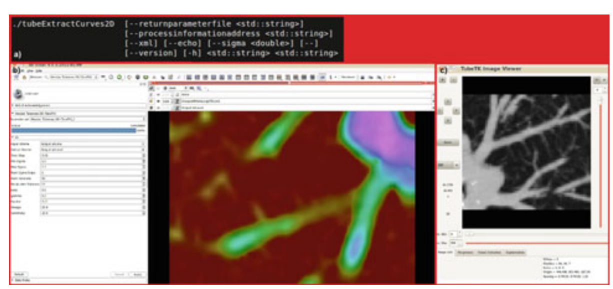

Fig. 2 Screenshots of TubeTK's (**a**) command-line interface, **b** integration in 3D Slicer, **c** tubeImageViewer

Conclusion

The development of algorithms specially designed for image-based analysis of tubular structures has wide implications for image-guided diagnosis, interventions, and disease monitoring. We have presented TubeTK, an open-source software toolkit that distributes a variety of medical imaging algorithms for images depicting tubular structures, with the aim of accelerating research, development and clinical translation in the field.

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Small bowel segmentation on high-resolution CT scans using the mesenteric vasculature as a roadmap

W. Zhang[1], J. Liu[1], T. Nguyen[1], J. Yao[1], A. Louie[2], S. Wank[2], R. Summers[1]

[1]National Institutes of Health, Radiology and Imaging Sciences, Bethesda, United States

[2]National Institute of Diabetes and Digestive and Kidney Diseases, Bethesda, United States

Keywords Medical image segmentation · Mesenteric vasculature · Small bowel · Computed tomography

Purpose

To develop a method to segment the small bowel on high-resolution contrast-enhanced CT scans using the mesenteric vasculature as a roadmap.

Methods

The method is motivated by the strong anatomic relationships between the mesenteric vasculature and the small bowel, and the fact that the segmentation of the mesenteric vasculature is easier than that of the small bowel on contrast-enhanced CT scans. The method consists of three steps.

First, to reduce the effect of line-like structures in fat and occlusions of bones, the internal abdomen region of the body is automatically identified. The subcutaneous fat, spine and pelvic bones are removed from the outside in using region growing, morphological techniques and adaptive thresholding [1, 2].

Second, the mesenteric vasculature is automatically extracted to create a map. In this step, multi-view multi-scale Frangi's line-structure filters [3] are used on maximum intensity projection (MIP) images to detect vessels, where the MIP image slabs are generated by rotating and resampling the 3D coronal volume. Then, non-vessel lines (false positives) located at the edges of abdominal organs and tissues are detected and deleted. In this step, we use the expected Gaussian distribution of vessel profiles and the Kullback-Leibler distance [4] measurement between candidate distribution and the reference, where the lines detected by the filter are the candidates while the true vessels are the references. Vessels which supply the large bowel and organs other than the small bowel are excluded based on a local distance map, where scale-based thresholds of membership values are used.

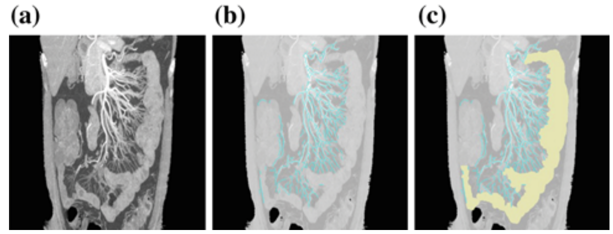

Fig. 1 Small bowel segmentation procedure. **a** Abdominal CT MIP image built after excluding subcutaneous fat and bones. **b** Mesenteric vessel segmentation. Vessel centerlines (*light blue*) are overlaid on the MIP image. **c** Small bowel segmentation (*yellow*)

Third, the small bowel region is segmented using the mesenteric vasculature map. A connected component method is used to detect the vessel bifurcations in MIP images and construct chains of bifurcation points to make it easier to map the structure of the mesenteric vasculature. Then, the extrema points of the mesenteric vasculature map are detected. These extrema points are connected to the last points in each bifurcation chain and identify the mesenteric side of the small bowel wall. From the mesenteric side of the small bowel wall, fuzzy-connectedness [5] is used to identify the opposite side of the small bowel wall (the "anti-mesenteric" side).

To evaluate the performance of our system, high-resolution contrast-enhanced abdominal CT scans of six patients suspected of having small bowel carcinoid tumors were acquired at 1 mm thickness and 0.5 mm reconstruction interval, following oral administration of Volumen and intravenous administration of Isovue-300. The mesenteric vasculature of one case and small bowels of six cases were manually labeled as the standard-of-reference for evaluation.

Results

An example of the small bowel segmentation is shown in Fig. 1. The method could automatically detect mesenteric vessels with diameters as small as 1 mm. The average point-to-point volume overlap (segmentation accuracy) for the vessels was 82.3 % with a 3.6 % false positive rate. The small bowel segmentation accuracy was 79.3 % with 3.8 % standard deviation, and the false positive rate was 21.2 % with 4.5 % standard deviation. False positives were mainly located on nearby solid organs and soft tissues with intensity similar to small bowel. False negatives were mainly a consequence of having missed small mesenteric vessels.

Conclusions

We proposed a novel mesenteric vessel map-guided framework for segmenting the small bowel. The preliminary results show that the mesenteric vasculature can be used as a roadmap to accurately locate the small bowel. The small bowel segmentation may have application for automated detection of small bowel tumors such as carcinoid.

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