Geometric modeling of aortic dissections through convolution surfaces

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SPIE. MEDICAL IMAGING

INTRODUCTION

This work revisits a successful modeling technique, called convolution surfaces, to visualize the three-dimensional structure of aortic dissections by considering computed tomography angiography (CTA) images. This pathology occurs when the aortic duct splits into two blood streams, the true lumen (TL) and false lumen (FL), as shown in Fig.1. The morphological characteristics of the aorta are therefore crucial for a clinician and provide vital support since they can be used to extract significant information for surgery and treatment planning. Convolution surfaces are a kind of implicit surfaces, and they were used for visualizing vascular tree structures which adhere to the skeleton and local vessel radius [1], while producing smooth transitions and surfaces and are considered as input information. In fact, they are used to represent the true and the false lumen through the convolution of local segments. The choice of filter to approximate the vascular structure is limited. The fundamental characteristics of the filter function make sure that it is continuous and monotonous and that at a certain distance it has a zero or close to zero gradient. Low pass filters, such as Gauss, have similar characteristics. The utilized filters prevent irritating bulges and, in some cases, represent the course of the vessel diameter faithfully. Additionally, we introduce an optimization strategy based on a genetic algorithm to create the separation caused by the dissection flap.
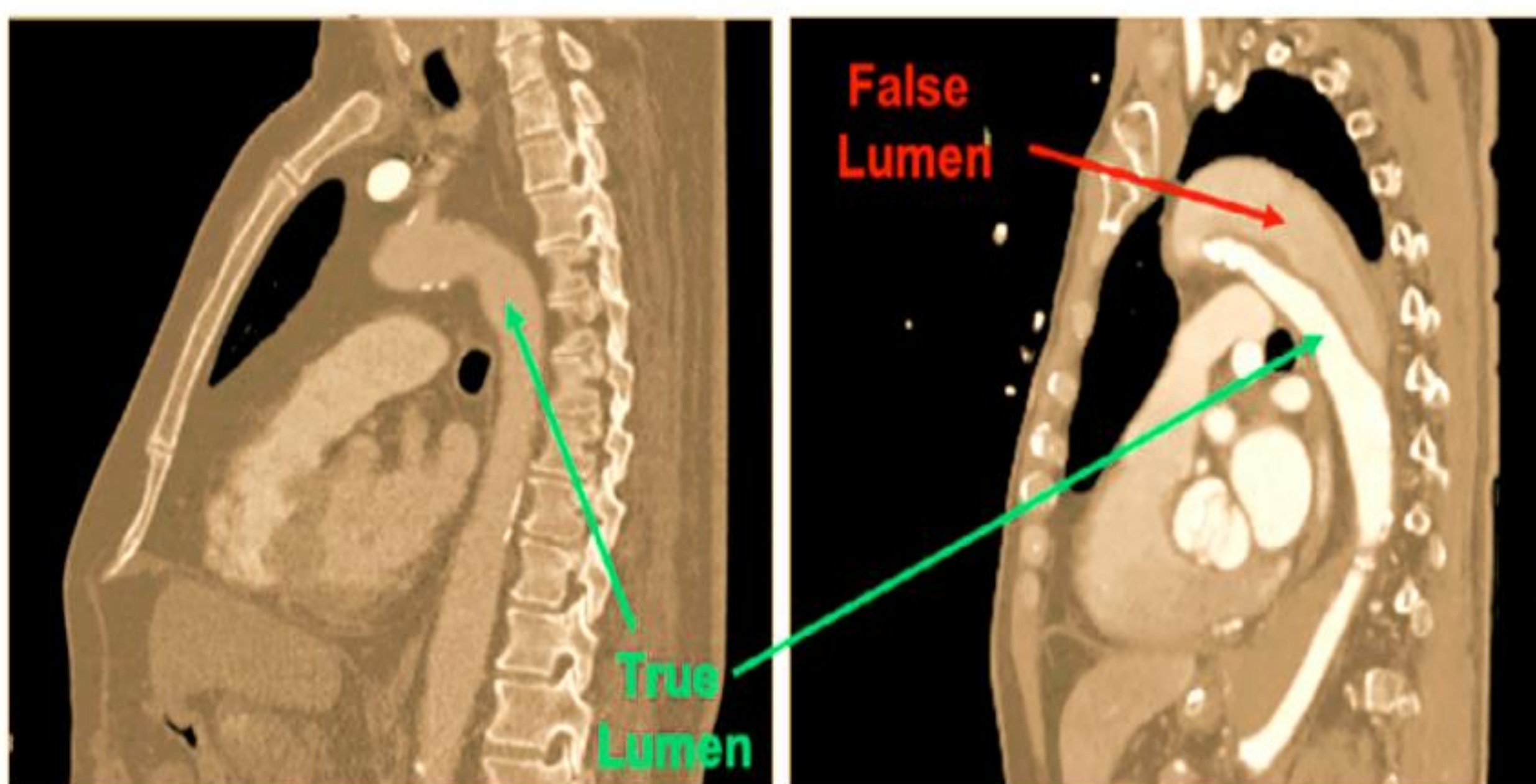

Fig. 1. Computed tomography angiography of a healthy subject (left), where only one lumen is visible in the aorta; an aortic dissection case, where the false and true ylumina are clearly distinguishable (right).
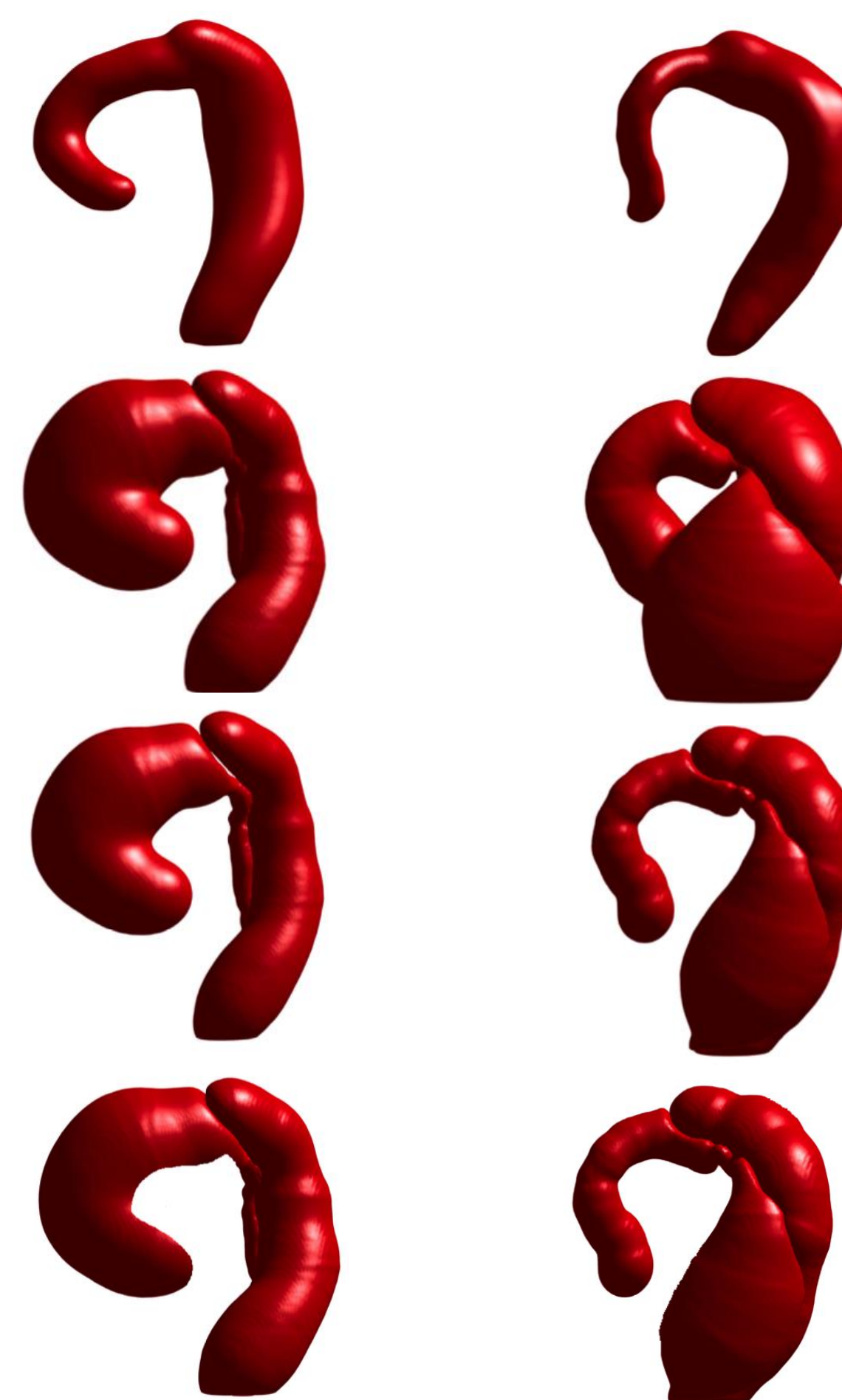
METHODS

Fig. 2. Convolution surfaces in the two patients using different filter functions: for the first raw, the radius values are fixed; for the second, there are a uniform distributions of the radius when $\omega = \ln 2$; for the third, it is used the same method of the second raw, but $\omega = 5 \ln 2$. The last row is obtained with the genetic algorithm.

We used CTA images of two Type B AD datasets from the ImageTBAD collection [3]. 3D skeletons of TL and FL segmentations are extracted in Slicer 3D. For each skeleton point, the corresponding radius values for each point of centerlines are extracted. The implementation of our pipeline produces a different three-dimensional structure of aortic dissections, as in Fig.2. For an initial representation as in Oeltze and Preim [1], the convolution surface along a line segment has a fixed radius with an appropriate convolution kernel. In the second representation, we used a continuous and monotonic filter function, as Gauss filter. In this case, the filter depends on the radius and to generate a uniform radius along each skeleton segment belonging to the centerlines, an interpolation is performed between the radii at the endpoints. Because two separate centerlines are employed in both filtering functions, that produce two meshes, one for true lumen and one for false lumen, an equation is applied that adds the two lumens through a linear combination, producing the final structure of the aortic dissection. Then, the genetic algorithm is introduced to improve the segmentation of the three-dimensional structure of the aortic dissection.
For each 3D structure of the aorta, different isovalue is considered.

RESULTS

To quantitatively analyze the differences between the results achieved, for Patient 1 and Patient 2 (Table 1) the Sørensen-Dice similarity coefficient is exploited between the segmentation masks and each 3D structure of the aortic dissection obtained in this work. The values highlighted in yellow represent the best results obtained, as predicted by the second fitness function given as input to the genetic algorithm that produces the convolution surfaces reported in Fig.3.

Sørensen-Dice similarity coefficient	Patient 1	Patient 2
Results of the first filter function	0.67	0.48
Results of the filter function when $\omega = \ln 2$	0.52	0.43
Results of the filter function when $\omega = 5 \ln 2$	0.77	0.57
Results of the filter function when $\omega = 5 \ln 2$ and weight coefficients are imposed	0.73	0.54
Results of the first fitness function of genetic algorithm	0.796	0.665
Results of the second fitness function of genetic algorithm	0.826	0.806

Table 1. Results of the Sørensen-Dice similarity coefficient applied to the various methods in both patients.

Fig. 3. Comparison between the results of second fitness function and real segmentation masks for the first patient (above) and for the second patient (below).

REFERENCES

[1] S. Oeltze, B. Preim. Visualization of Vasculature With Convolution Surfaces: Method, Validation and Evaluation. IEEE TMI. 2005, Vol. 24.
[2] G. Mistelbauer et al.. Implicit Modeling of Patient-Specific Aortic Dissections with Elliptic Fourier Descriptors. Computer Graphics Forum. 2021, Vol. 40, 3.
[3] Yao Z. et al.. ImageTBAD: A 3D Computed Tomography Angiography Image Dataset for Automatic Segmentation of Type-B Aortic Dissection. Frontiers in Physiology. 2021, Vol. 12.

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