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Left atrial appendage segmentation and quantitative assisted diagnosis of atrial fibrillation based on fusion of temporal-spatial information

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ABSTRACT

In this paper, we present an approach for left atrial appendage (LAA) multi-phase fast segmentation and quantitative assisted diagnosis of atrial fibrillation (AF) based on 4D-CT data.

We take full advantage of the temporal dimension information to segment the living, flailed LAA based on a parametric max-flow method and graph-cut approach to build 3-D model of each phase. To assist the diagnosis of AF, we calculate the volumes of 3-D models, and then generate a "volume-phase" curve to calculate the important dynamic metrics: ejection fraction, filling flux, and emptying flux of the LAA's blood by volume. This approach demonstrates more precise results than the conventional approaches that calculate metrics by area, and allows for the quick analysis of LAA-volume pattern changes of in a cardiac cycle. It may also provide insight into the individual differences in the lesions of the LAA. Furthermore, we apply support vector machines (SVMs) to achieve a quantitative auto-diagnosis of the AF by exploiting seven features from volume change ratios of the LAA, and perform multivariate logistic regression analysis for the risk of LAA thrombosis.

The 100 cases utilized in this research were taken from the Philips 256-iCT. The experimental results demonstrate that our approach can construct the 3-D LAA geometries robustly compared to manual annotations, and reasonably infer that the LAA undergoes filling, emptying and re-filling, re-emptying in a cardiac cycle. This research provides a potential for exploring various physiological functions of the LAA and quantitatively estimating the risk of stroke in patients with AF.

1. Introduction

Thrombotic diseases have become a serious threat to human life and health. About 80% of the cardiogenic thrombi navigate to the brain with the coursing blood, which causes strokes [1]. The cardiogenic thrombi (Fig. 1 a–c) occur mainly in the left atrial appendage (LAA). In the case of atrial fibrillation (AF), the volume of LAA increases and its systolic function does not work properly, which leads to outlet obstruction and blood stasis, and eventually induces thrombosis [1]. The LAA is a cardiac substructure that is above the left ventricle (LV) and connected to the left atrium (LA). Its shape is highly variable, often tubular, hooked and with a few lobes. Its size varies from 1 to 19 cm^3 [2]. The LAA also has many physiological functions, such as the secretion of atrial natriuretic peptides (ANP).

Computed tomography (CT) is one of the most advanced medical imaging diagnosis tools. For cardiovascular disease, it can greatly assist clinicians to obtain the anatomical information of the LAA and predict the risk of thrombosis [3] (Fig. 1 c).

Owning to the LAA's small and variable structure, it is both challenging and rewarding to study it based on CT data (Fig. 1), and few researchers have focused on LAA in the image processing domain. Most existing segmentation algorithms are applied to the analysis of a single phase instead of the entire cardiac cycle. There is no automated LAA segmentation approach for 4-D CT data. In order to systematically describe the morphological structure of the LAA, we need to study the entire cardiac cycle. To this end, this research proposes a series of approaches for multi-phase segmentation. Then, we calculate the volume of non-rigid LAA based on the segmentation result. Furthermore, some important metrics are calculated for the diagnosis of AF. Specifically, we leverage the left atrial appendage ejection fraction (LAA-EF), left atrial appendage peak emptying flux (LAA-PEF), and left atrial appendage peak filling flux (LAA-PFF) as indicators of LAA abnormity and AF [4].

The main steps and contributions of our proposed approach are the following:

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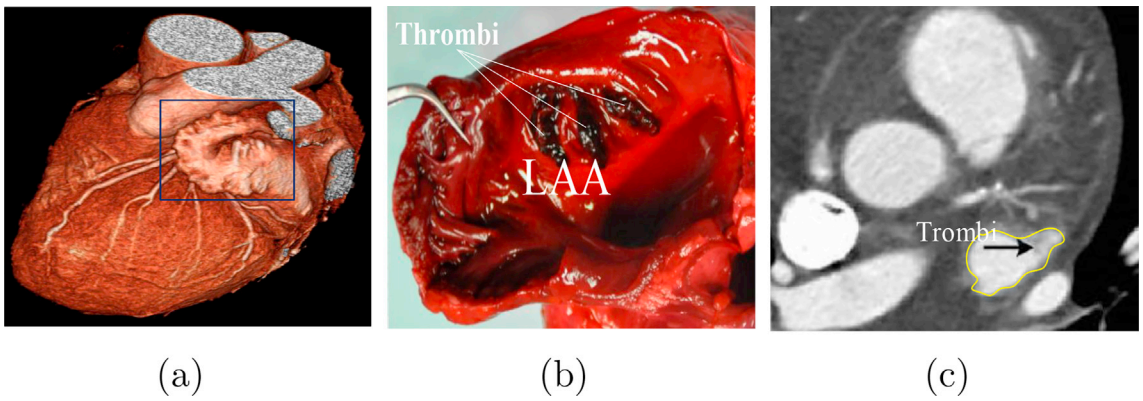

Fig. 1. The LAA, LAA thrombi and an axial CT slice with the LAA. (a) Volume rendering of a heart with the LAA marked by a rectangle, (b) LAA thrombi, (c) An axial CT slice with the LAA marked by a yellow border. (For interpretation of the references to color in this figure legend, the reader is referred to the Web version of this article.)

- We propose a new approach for single phase LAA segmentation without using explicit shape models. Our approach can detect the tips and lobes of the LAA precisely which are missed in most previous research [5–7].
- We propose a fast multi-phase LAA segmentation approach based on 4-D CT data to obtain motion information, which has not been discussed in previous studies. In the patient's CT examination, we find that there is no radical change in the size and position of the LAA between adjacent phases, which we call temporal continuity. We segment the images of all scan sequences iteratively using a graph-cut with the initial seed generated by the previous phase segmentation result. In particular, after the LAA phase with the biggest volume (45% phase) segmented, we generate the initial seed points for its adjacent phases by checking the prior segmentation mask and the image intensity. We determine that the seed points are adequate such that the graph-cut can achieve competitive performance for our multi-phase segmentation task. This process is carried out iteratively until all scan sequences are segmented.
- We calculate the LAA volume of each phase and generate the "volume-phase" curve, which clearly demonstrates that the LAA undergoes filling, emptying, and then re-filling, re-emptying in the entire cardiac cycle. We also screen out the individual differences in lesions of LAA, such as the LAA "stunning" [8].
- We calculate the important dynamic metrics quickly and non-invasively as indicators of LAA abnormity and AF: LAA-EF, LAA-PEF, LAA-PFF. These metrics are calculated by volume, instead of area, which is frequently used in clinical medicine [9]. Furthermore, we apply support vector machine (SVM) to achieve quantitative auto-diagnostics of AF by exploiting seven features of patients' data, and perform multivariate logistic regression analysis for LAA thrombi. This can be a new application of 4-D CT.

The 100 cases utilized in this research were taken from the Philips 256-iCT. The experimental results demonstrate that our approach can construct muti-phase 3-D LAA geometries robustly compared to manual annotations, and generate the "volume-phase" curve to calculate the key function metrics of the LAA. This research provides a potential for studying various physiological functions of the LAA and quantitatively estimating the risk of stroke in patients with AF.

2. Related work

The current work focuses on single phase LAA segmentation using generative model-based approaches. Researchers generally consider the LAA as a part of the left atrium (LA). Zheng *et al.* [5] segmented the entire LA using a multi-part model. They only used a smooth mesh to encase the LAA roughly, but the C-arm CT data they used did not embody the details of LAA, such as the lobes on LAA. Grasland-Mongrain *et al* [6,7]. segmented the LAA by shape-constraints [10]. In this study, the researchers encountered a problem in segmenting the tips of the LAA [6,7] owing to the vagueness of the shape model.

The generative model-based approaches [5,10] cannot deal with the lobes on LAA which are of great clinical significance. A non-model approach is preferred because it is generally driven by the image itself without explicit shape constraints. We could have applied 3-D region-growing [11] to segment the LAA in the bounding box which is simpler and faster, however the segmentation results (Fig. 2 a, b) are not satisfactory because of:

- The interference of the left superior pulmonary vein (LSPV) and the left circumflex branch (LCX) which are adjacent to the LAA;
- The crimping and adhesion of lobes on LAA.

In comparison, our approach solves these problems because it takes full advantage of the continuity of the topological relationships between slices and between phases (Fig. 2 c).

Graph-cut [12] is also a widely used approach. However, this approach is cumbersome because the user needs to mark the seeds of the foreground and background. In addition, it is challenging to determine the value of the parametric λ which has a strong impact on the final result. In fact, a single λ value can not guarantee competitive results under all image conditions. Instead of finding the optimal λ, some work in computer vision [13,14] generated a pool of segmentation proposals using parametric max-flow/min-cut solver [15]. Parametric max-flow can solve the max-flow/min-cut problem with a set of λ values while max-flow in graph-cut solves the problem with a single λ value. By ranking all proposals in the pool, they have achieved competitive performance in vision tasks such as object segmentation.

Inspired by this work based on parametric max-flow, we have proposed a new discriminative model-based approach for single phase LAA segmentation on computed tomography angiography (CTA) data in our previous study [16]. It is a three-step process. After obtaining a bounding box containing the LAA, we first generate a segmentation pool for each slice by setting different seed hypotheses and different λ values. Then, we rank all proposals in each pool and select the best one. Finally, we merge all selected 2-D results using spatial continuity and build the 3-D model. This method can handle large shape variations and almost all image conditions, while it segments only a single phase when the LAA has the largest volume [16].

We segment the LAA slice by slice when dealing with single phase volume. There are two reasons. First, the 3-D combination of relations of seeds is cumbersome, based on the entire 3-D volume and cannot be processed in parallel, which slows down the calculation speed; second, the 2-D preliminary segmented results can be cross-checked according to