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Abstract:

Purpose: To provide an efficient method to extract useful information from the increasing amount of coronary CTA.

Methods: A quantitative coronary CTA analysis tool was built on OsiriX, which integrates both fully automatic and interactive methods for coronary artery extraction. The computational power of an ordinary PC is exploited by running the non-supervised coronary artery segmentation and centerline tracking in the background as soon as the images are received. When the user opens the data, the software provides a real-time interactive analysis environment.

Results: The average overlap between the centerline created in our software and the reference standard was 96.0%. The average distance between them was 0.38 mm. The automatic procedure runs for 3-5 min as a single-thread application in background. Interactive processing takes 3 min in average.

Conclusion: In preliminary experiments, the software achieved higher efficiency than the former interactive method, and reasonable accuracy compared to manual vessel extraction.

Integrating automatic and interactive methods for coronary artery segmentation: let the PACS workstation think ahead

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1. Introduction

Coronary artery disease (CAD) is one of the main causes of death in the world [1]. For the

assessment of coronary artery lesions like plaques, aneurysms and stenoses, computed

tomography angiography (CTA) has become a promising alternative to catheter coronary angiography (CA) for selected population, as it is non-invasive, faster and more cost-effective [2] compared to CA. During the last few years, coronary CTA has undergone rapid development. Both the spatial and the temporal resolution have increased considerably, which may improve the diagnostic accuracy. However, this also results in increasing amounts of image data generated by each examination. The typical number of images has increased from one optimal phase of around 100 slices to multiple useful phases of 300-500 slices. Finding an efficient method to extract useful information from this amount of data has become a focus of medical image processing researchers.

Interactive 3D volume rendering (VRT) or Maximum Intensity Projection (MIP) images and 2D curved multiplanar reformation (cMPR) reconstructed along vessels are generally believed to be a good way to facilitate the evaluation process and to enhance the quality of the assessment[]. The implementation of such visualization techniques eventually depends on coronary artery segmentation and centerline extraction. There is a large literature about vessel extraction in 2D and 3D medical images[3,4]. Basically, these methods can be divided into two groups: automatic/semi-automatic and interactive methods[4]. In general, automatic methods are more attractive for users because of time efficiency, but due to complexity and variability of the coronary anatomy and unpredictable artifacts, no available method can be sure to give correct results in all cases[3]. Most commercially available coronary CTA post-processing software, such as CTA software from Siemens Healthcare, TeraRecon Inc. and Vital Images Inc., therefore provides methods for user interaction, even in cases where automatic processing is the first step. As automatic methods are usually more computationally intensive, this approach will add some waiting time in the work-flow (typically varies from 30 seconds – 8min according to the algorithms []).

Building on our earlier work on "virtual contrast injection" visualization [5-7], this paper presents a quantitative coronary CTA analysis tool, built on the open-source PACS workstation software OsiriX [8], which integrates both fully automatic and interactive methods for coronary artery extraction. The computational power of an ordinary PC is exploited by running the non-supervised coronary artery segmentation and centerline tracking in the background as soon as the images are received. The software then provides a real-time interactive analysis procedure when the user opens the data. In preliminary experiments, the software achieved higher efficiency than our former interactive method [7], and reasonable accuracy compared to manual vessel extraction.

2. Method

The image processing in our software can be divided into three phases: Image reception and classification; automatic coronary artery tree extraction; and interactive coronary artery extraction and visualization. The workflow is summarized in Fig 1.
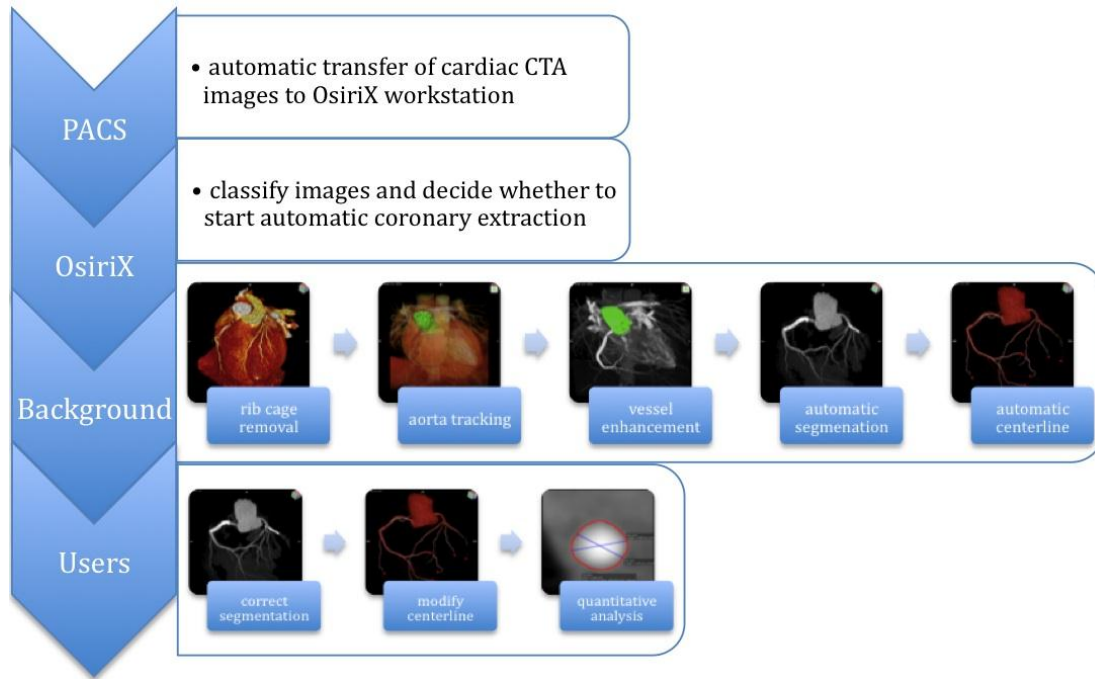

Figure 1. The workflow of the presented software

2.1 Image reception and classification

Our software is designed as a plug-in for the OsiriX system. Immediately after image acquisition, coronary CTA images are automatically sent to a workstation running OsiriX. Whenever OsiriX receives an image, it will send a message to our plug-in, where the series is classified as coronary CTA data needing automatic segmentation, if certain key words are found in the DICOM study description(0008,1030) (or in the fields Body Part Examined(0018,0015) and Contrast/Bolus Agent(0018,0010)). For examinations with multiple cardiac phases, several filters can be combined to select images acquired in a suitable part of the cardiac cycle depending on the heart rate, for example if the patient's heart rates is below 70 bpm the phase acquired around 70-80% RR period will be processed, if heart rate is above 80bmp the phase acquired around 30-40% RR period will be processed. The chosen images will be put in a queue, waiting for a system idle signal, and then fed into the automatic segmentation pipeline.

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2.2 Automatic coronary artery tree extraction

The automatic coronary tree extraction pipeline was modified from our earlier work [], there are four main steps: rib cage removal, aorta tracking, vessel enhancement and vessel segmentation with "virtual contrast injection" method.
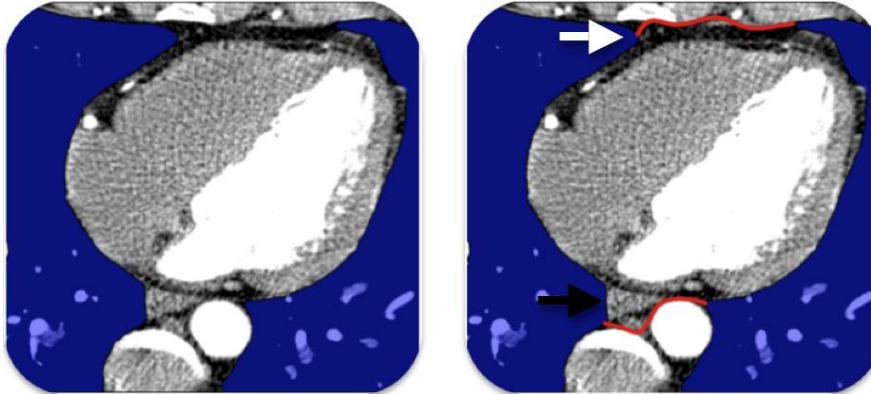
2.2.1 Rib Cage Removal

Figure 2: Left: Lung segmentation based on thresholding; Right: red line represents the 2D livewire connecting two lungs in anterior and posterior mediastinum (white arrow: retrosternal space; black arrow: azygoesophageal recess).

The method for removing the rib cage that we have used is based on a 2D livewire algorithm [9]. Based on the observation that in the upper axial sections through the heart, the heart is almost completely surrounded by the lungs (cf. Fig. 2, left), we have used 2D livewires to close the anterior and posterior mediastinum (cf. Fig. 2, right). The lung mask is created using thresholding(-300Hu) followed by binary morphological closing. The start and end points for livewires are automatically selected from the contours of the right and left lungs by scanning the contours using a ray projected from the center of the heart area (identified with a distance transform) and choosing the geometrically closest two points from each lung. In the end, all gaps in the lung contour will be bridged by the livewires. The cost function is designed to be able to attract the wire to the interior edge of the sternum and the azygoesophageal recess. Due to the nature of connectivity of the pericardia, an extra cost force related to the distance between the wires in adjacent slices is introduced, to prevent edges from jumping from slice to slice. Thanks to this force, the livewire can make reasonable cuts on the roots of pulmonary arteries and even in the lower slices through the heart, where there is less lung tissue in the image. The cost function used is described by:

$$C(x) = \times\exp(\frac{|f(x) \quad 100|}{10}) + \times\exp(\frac{50 \quad g(x)}{10}) + \times\exp(d(x))$$

Here, α, β and γ represent weight factors for the different forces, which were 1.0, 2.0 and 2.0, respectively, in our experiment. $f(x)$ is the intensity at x in the input image; 100 is the mean intensity of myocardium; $g(x)$ is the orientation-sensitive gradient magnitude at x, which is positive if the gradient is towards the center of the heart, otherwise negative; 50 is a noise balance factor which promotes the points with gradient higher than 50. $d(x)$ represents the distance from x to the segmented border in the preceding slice.
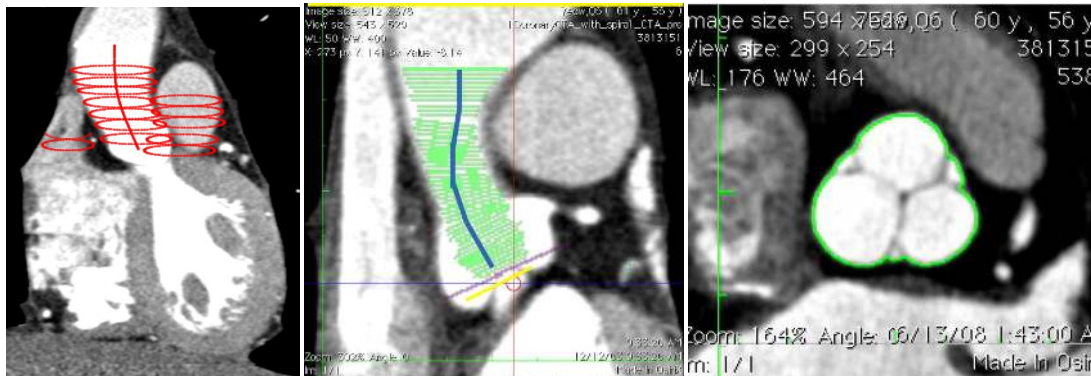
2.2.2 Aorta Tracking

Figure 3: Left: Circle Detection and Aorta Selection ; Middle: Aorta tracking and Automatic seeds created (Blue Lines: Direction of Cross-Section growing; Green: "Coronary Root" seeds; Yellow lines: seeds for unwanted structures; Purple line: barrier to separate aorta and left ventricle); Right: Stop slice where the aortic valve was found.

In order to segment the coronary arteries, ascending aorta that connect to coronary arteries need to be detected as a start point of the rest propagating step. Our aorta tracking algorithm consists of two steps, localization of aorta and 3D cross-section growing.

Localization of Aorta: Since the ribs and most of the descending aorta have been removed in the first step, we here use a simple 2D circle detection algorithm based on the Hough transform method [10] to search through the cranial third of the image volume. The assumed radii for the ascending aorta are 1-2.5cm. In each slice, the most prominent three circle-like shapes are recorded, and then all candidate circles are connected to each other if the overlap between circles is more than 90% and the distance between circle centers is less than 3 mm. The rough centerlines of the connected circles are scored based on the circle filter score of the Hough transform, the length and the location in the image (right or left relative to the other candidate centerlines). The longest centerline with highest circle score on the anatomical right half of the patient is considered to represent the ascending aorta (Fig. 3, left). However, only the cranial end of the centerline is actually used in the following aorta tracking.

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Three-Dimension Cross-section Growing: In the most cranial slice, a 2D threshold level-set algorithm (from Insight Toolkit, chapter 9 in [11]) is applied from the center of the aorta. The proper threshold is automatically calculated from two standard deviations below the mean intensity of all voxels above 100Hu in the aorta area found during the 2D circle detection. After the cross-section of the aorta in this slice has been segmented, another slice is chosen by a 1 mm increment in the z-direction of the vessel. The center of gravity from the last cross-section is then passed down to the new slice as a starting seed point for the level-set algorithm. The z-direction in the first slice is assumed to be equal to the z-direction of the patient (cf. Fig. 3, middle); later a correction is made every 10 mm in the z-direction by linear regression of the centers of the last ten cross-sections. The 3D cross-section growing will stop if the aortic valve is reached, as detected by an increased intensity variation in the center area of the cross-section (cf. Fig. 3, right). The center area is defined as the area within r/2 from the incircle center of the cross-section, where r is the radius of the incircle. An increased intensity variation is defined as a 4mm^2 circle area is found in which the mean intensity is 100Hu lower than the mean intensity of the cross-section.

2.2.3 Vessel Enhancement

Another preparation before starting the coronary artery segmenation is to enhance the connectedness between branches of the coronary tree, because the remaining segmentation step depends strongly on the grayscale connectedness of the vessel structure. We used here a multi-scale Hessian-matrix-based vesselness filter proposed by Sato et al. [12] (also from Insight Toolkit[11]) to enhance the input images, which gives high response (150~300 on ordinary CTA data) on vessel-like structure and rather low response (<30) on other parts like ventricles . To avoid the strong influence from calcium around the vessel which sometime can also be recognized as vessel-like structure by the vesselness filter, all voxels with intensity higher than 650 HU is set to 0 HU in this step. To speed up the processing, the rib-cage removed data is first resampled to lower resolution with 1 mm isotropic voxels, on which the line-structure filter is applied to detect bright tubular structures. The scale parameter for the vesselness computation is varied between 1.0 and 2.5 mm in steps of 0.5 mm.

The created vesselness map was then merged with the original CT data at original resolution using the formula

$$C(x) = I(x) + 3 \times V(x)$$

where $I(x)$ is the CT Value and $V(x)$ is the vesselness value.

2.2.4 Vessel Segmentation With "Virtual Contrast Injection" Method

In this step, we use a competing fuzzy connectedness tree algorithm, the so called "virtual contrast inject" method, to segment the segment the coronary artery trees and automatically extract centerlines from the tree structure.

In a 3D image, we define a path p joining two voxels, u and v, as a sequence of distinct voxels $u = w_0, w_1, \ldots w_{n-1}, w_n = v$, such that for each i, $0 \leq i \leq n$, w_{i+1} is a 26-neighbor of w_i. If $f(w_i)$ is the gray-scale value in voxel w_i, the strength of connectedness of p is determined by the darkest voxel along the path:

$$S(p) = \min_{w_i \ p}(f(w_i))$$

The connectedness between u and v is the strength of the strongest of all paths joining u and v:

$$C(u,v) = \max_{p(u,v)}(S(p))$$

In the virtual contrast injection algorithm, the grayscale connectedness computation is carried out as a competition between multiple seeds. Two or more seed regions, representing different vascular structures, are specified by the user, and the connectedness map from each seed region is calculated. At this stage, the membership of every voxel can be calculated by comparing its connectedness value to different seeds, assigning the voxel to the seed yielding the highest connectivity. Applying this strategy to all voxels in the image, a natural segmentation by "virtual contrast injection" is achieved [6]. The whole concept can be likened to contrast agents of different color being injected in the seed regions and circulating within the cardiovascular system while competing with each other. The propagation procedure for a seed is somewhat similar to Region Growing, but uses a non-local propagation criterion.

During the aorta tracing mentioned above, all voxels in the aortic cross-sections are marked as the "Coronary Root" seeds for the coronary arteries. Another set of seeds called "Other" seed is planted below the aortic valve and a barrier will be put in the aortic valve cross-section to stop the propagation from each side, (cf. Fig. 3, middle). During the processing, the "Coronary Root" seed at the real coronary ostium will start growing into coronary arteries, while the other seeds inside the aorta will be stopped by the vessel wall. On the other side, the "other" seeds in the heart chambers will finally occupy the heart

chambers and the front line between the two sets of seeds will converge on the weakest gray-scale linkage area, which usually is the edges of myocardia.

It should be pointed out that two extra sets of "other" seeds are planted in the top and bottom slices of the whole input volume, where coronary arteries should not appear according to the coronary CTA examination protocol. Those two sets of seeds will usually propagate to the pulmonary artery, liver and some other unwanted structures.

During the propagation of all the seeds, a fuzzy connectedness tree is constructed which records the propagating direction from each voxel to its neighbors. This competing fuzzy connectedness tree structure not only serves to solve an ambiguity problem that may arise when propagation from different seeds occurs along the same path [6], but also produces a path that follows the intensity ridge along the vessels as discussed in our previous report [6]. Notice that as the input image here used is a vessel-enhanced image, the intensity ridge actually represents the centerline of a vessel.

The distal ends of vessels can be automatically found by iteratively searching for the geometrically furthest point to the "coronary root" seeds or known centerlines in the tree structure.

After the automatic extraction of coronary arteries, the end points of the extracted centerlines, the connectedness tree structure and the low-resolution vesselness map are all saved on the user's hard disk for the interactive procedure.

2.3 Interactive Coronary Artery Extraction and Visualization
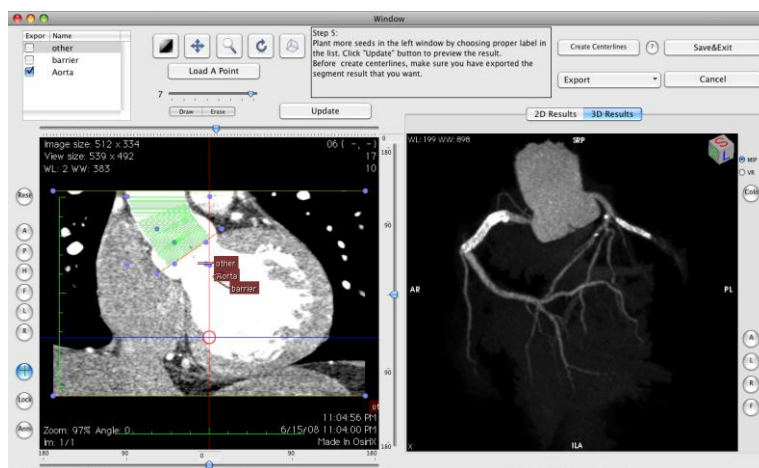

Figure 4. GUI for interactive segmentation. Left side showing original seeds; right side showing 3D result. In this case no new seeds have been planted yet, the 3D image showing the automatic segment results.

The interactive procedure will start when the user decides to open the CTA data with our plug-in in OsiriX. Using the connectedness tree structure created earlier, the segmentation

result can be presented as a 2D or MIP image in real-time to the user who can decide whether the results are satisfactory. If this is not the case, e.g., if some branches are missing, more seeds need to be specified. This is done in an MPR image. The "virtual contrast injection" algorithm is then restarted, using the newly planted seeds and the results from the automatic procedure as input. Thus the computation time is much shorter than in the initial segmentation. The segmentation results can be visualized in 2D or 3D and compared with MPR images of the input volume (Fig. 4), and the process iterated, if necessary. The MPR image can be placed through a particular point by clicking in the 3D window.
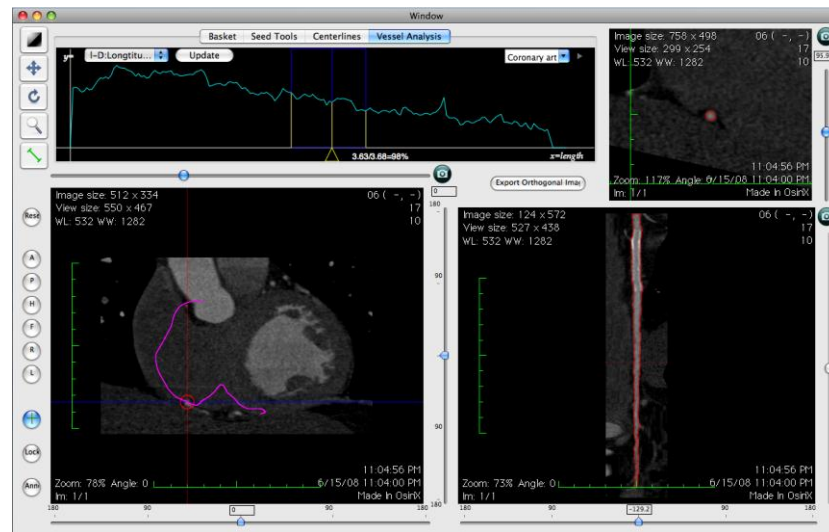

Figure 5. Quantitative Analysis GUI. The plot in the left upper corner shows the diameter changes along the centerline. In this case, the centerline was created automatically without any manual correction.

The user can also choose to visualize the automatically created centerlines. If the distal end of a desired branch is not in the right place, a new end-point can be manually added at an appropriate location in the segmented area. After a centerline has been selected, cMPR images can be produced to follow individual vessels or branches. Quantitative analysis tools are provided for stenosis evaluation as shown in Fig. 5. The contour of the vessel in the 2D cMPR images and cross-section images along the centerline are automatically segmented using a threshold-based level-set method (chapter 9 in [11]), which starts from the centerline of the vessel for each 2D image. A "repulsor" tool provided by OsiriX, which mimics a blacksmith's hammer, allows the user to correct manually any distortion of the segmentation results. A plot based on quantitatively analysis of these contours can be created showing the lumen changes along the vessel. The user can choose either to

compare the diameter of selected locations in the longitudinal cut plane along the vessel centerlines or to measure diameter or area in the corresponding cross-section images.

3.Evaluation

The newly developed software was tested on a Mac system with 2.2 GHz dual core Intel CPU and 4 Gb RAM. Standardized evaluation methodology and a reference database for evaluating coronary artery centerline extraction algorithms (publically available at http://coronary.bigr.nl) [4,13] were used for evaluating its performance. Thirty-two datasets acquired from two 64-slice scanners were randomly selected and included in this database, 20 cases from Sensation 64 and 12 cases fromm Somatom Definition (Siemens Medical Solutions, Forchheim, Germany). Image quality was scored as poor (defined as presence of image-degrading artifacts and evaluation only possible with low confidence, 6 cases), moderate (presence of artifacts but evaluation possible with moderate confidence, 11 cases) and good (absence of any image degrading artifacts related to motion and noise, 15 cases). The centerlines of 128 selected branches of the 32 datasets (4 from each case) were first annotated created by 3 observers independently, and the 128 reference centerlines were created by combining three centerlines from observers using a Mean Shift algorithm [4]. The whole procedure in total took the three observers approximately 300 hours. In this study, all 32 datasets were processed in our software, first without any user input and then complemented with manual correction. In each case, four branches were selected from all created centerlines by using 2 pre-defined points on each reference centerline, and compared with corresponding reference standard centerlines using the standardized evaluation software provided on the website [13]. The evaluation focuses on two main categories: the overlap between the automatically/interactively created centerline and the reference centerline and the average distance between those two centerlines. Both centerlines are resampled equidistantly using a sampling distance of 0.03 mm. A overlapping between two centerline points is defined if the distance between them is smaller than the radius defined at the reference centerline point by the three observers (detail explanation of the evaluation frameworks can be found in[4]). The average overlap between the centerline created in our software and the reference standard was 96.0%, and the average score of overlap was 70.8. The average distance between the created centerline and the reference standard centerline in the overlapping segments was 0.28 mm, which was close to the voxel size in most cases (The mean voxel size of the 32 datasets is $0.32\times0.32\times0.4$mm^3). More detailed evaluation parameters from the standardized

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methodology are listed in Table 1. Scores in table 1 were calculated by comparing the absolute overlap and accuracy values with the mean inter-observer variability, which is defined as 50. Further explanation can be found in [13]. Figure 6 provides a comparison of overlap evaluation before and after user's intervention. The automatic procedure took 1.4-2.5 minutes depending on the size of the input data. The interaction time ranged from 1 to 8 minutes (average 3.0 minutes). On average, 3 new seed regions, in addition to the automatically planted seeds, were used to achieve these results. Detailed results comparing the performance of fully automatic procedure and manually corrected results are listed in Table 2.

Table 1: Manually corrected results compared with the reference standard

Measure	min.	max.	avg.	average score**
Overlap*	76.3%	100.0%	96.7%	73.0
Overlap till first error*	5.6%	100.0%	74.5%	63.3
Overlap with diameter>1.5mm vessel*	76.7%	100.0%	96.9%	74.7
Average distance*	0.14 mm	0.91 mm	0.33 mm	40.6
Average distance inside vessel*	0.14 mm	0.53 mm	0.27 mm	41.6
Average distance within >1.5mm part*	0.14 mm	0.91 mm	0.33 mm	40.5

*) A detailed explanation of the definition of these parameters can be found in [13]. **) Scores were calculated by comparing the absolute overlap and accuracy values with the performance of the observers, which is defined as 50. Further explanation can be found in [13].

Table 2: Comparison of performance before and after manual correction

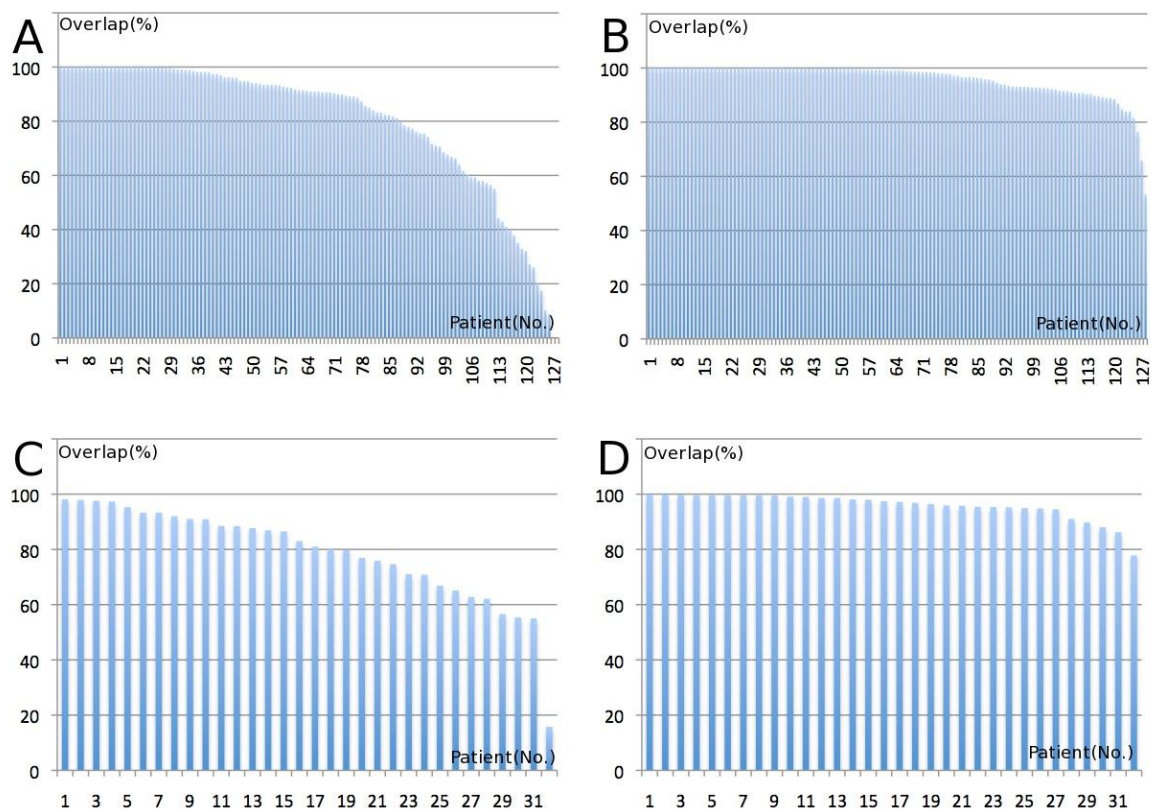|	Overlap	Overlap with diameter>1.5mm vessel	Average distance	Average distance inside vessel
Automatic Procedure	78.6%	80.8%	6.37 mm	0.31 mm
Interactive Procedure	96.0%	96.3%	0.38 mm	0.28 mm

Figure 6. The overlap between the centerlines created in our software and the reference standard (all sorted in a descending order). A,B: 128 centerlines created before and after user's intervention; C,D: average overlap of each patient before and after user's intervention

4. Discussion

In this study, we have evaluated a novel segmentation software, which combines automated and interactive processing, using standardized methodology and a reference database for evaluating coronary artery segmentation algorithms. As the purpose of the reference database is to explore the ability of different coronary artery centerline tracking methods, rather than clinical evaluation, the reference centerlines always extend to last distinguishable segment of the coronary arteries where the diameter of the vessel is usually less than 1 mm (3-4 voxels). Bearing this in mind, a 96.0% overlap with the standard centerline seems acceptable, in particular as the performance of our software remains better than the variation between the 3 observers, as judged by the average score of the overlap evaluation (cf. Table 1). Most errors in the created centerlines were located in the distal part of the vessel where its contrast to the noisy background is relatively poor. Although the diameter of the vessel might be larger than 1.5 mm, which is assumed as clinically relevant in the evaluation software, the clinical relevance would be relatively minor.

With the automatic processing method, about 80 percent of major coronary branches were detected without any user interaction. It should be pointed out that about one third of the total 128 branches achieved more than 99% overlap with the reference centerline in segments with diameter 1.5 mm or larger (which is believed to be clinically relevant), and two thirds achieved 90% overlap or higher (Fig. 6). The average interaction time of 3 minutes is considerably shorter than the previously reported 6 minutes average for the completely interactive procedure [7]. In the manual correction procedure, more than 80% of the branches needed none or only one extra seed region to achieve the results listed in Table 1. From our experience thus far, the automatic procedure can substantially speed up the review procedure in cases where there are no severe motion artifacts or stenoses present. This is a big proportion of the population undergoing coronary CTA examination, thanks to recent development of the acquisition technique, and as the examination is usually applied to patients with intermediate or low pre-test probability of CAD [14]. Compared to other automatic coronary artery segmentation or/and centerline tracking software[][], the uniqueness of the presented software is running the automatic processing step in the background whenever a coronary CTA series is received by the workstation. Letting the workstation software "think ahead" saves the users waiting time after they open the CTA exam. Because the automatic coronary artery extraction pipeline is designed as a single-thread program, the users can simultaneously carry out most 2D image viewing tasks without noticeable delay in performance on our dual-core Mac system. Further development will focus on pausing or stopping the automatic processing thread when computation-intensive tasks, like 3D rendering, are initiated. As the interval between two exams sent from the scanner is normally longer than 10 minutes, a workstation serving one CT scanner will still have ample time to perform the whole procedure. Although some commercial software can provide samilar automatic and interactive functions, and the processing time can be shorter than 1min with high-end hardware's supports, the users' experience with the processing speed will not precede their experience with our software as in our case the waiting time is only the time to load the data from harddisk. Moreover, the presented software is distributed as an open-source and free plugin together with OsiriX. We believe this software should be considered as an alternative post-processing tool on low-end hardware.

Another contribution of the paper is introducing a new automatic coronary artery segmentation pipeline, which is modified from our earlier work[]. Compare to other method regarding heart isolation [], our rib cage removal algorithm can not cut off the

top part of liver, however this method reduce the risk of truncating coronary arteries. Beside the 32 cases mentioned above, the rib cage removal has also been tested on other 44 cases of coronary CTA datasets, no coronary artery is missing after rib cage removal in those 6 cases. The typical processing time of 5-10seconds is superior over other method. The aorta tracking method was inspired by Hennemuth's work []. Unlike the original method, the direction of the cross-section plane is calibrated every 10 mm by linear regression of the centers of the last ten cross-sections. This design is based on the anatomical character of aortic valve and the fact that the ventricle can be very horizontal (like in Fig. 7). Compared to the original algorithms that use one-direction slice-by-slice region growing and apply a stop criterion if the size of this intersection area between the segmented region and the one in the preceding slice drops below a defined minimum, our method is more robust in certain extraordinary cases, as shown in Fig. 7.
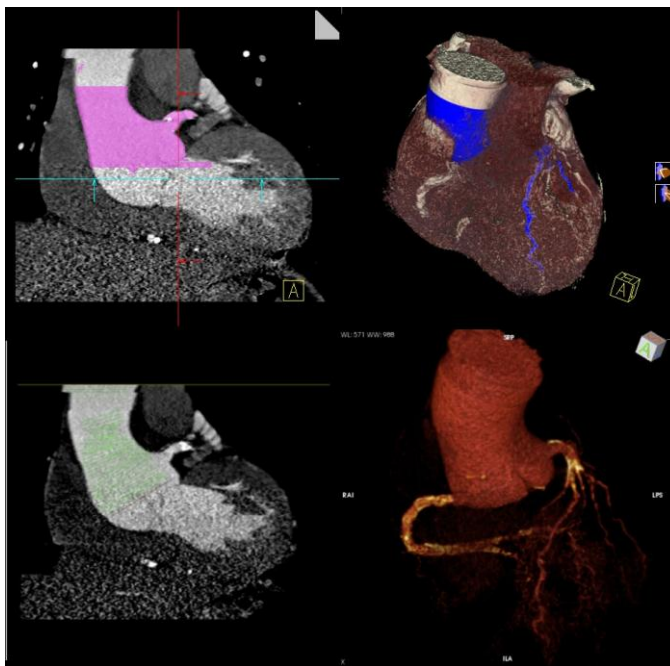

Figure 7. A special case on which the one-direction slice-by-slice region growing failed to find the right coronary ostium due to the unusual angle between the ascending aorta and left ventricle (the upper images). Our method can avoid this error by adjusting the growing direction (the bottom images).

The major difference between this new automatic segmentation pipeline and our earlier work is adding a step of vesselness enhancement, which not only strengthens the connectedness of the coronary vessel tree making the segmentation more robust, but also improves the centerline tracking accuracy by increasing the intensity difference from the center to edge of a linear structure. The average distance inside vessel has be improved from 0.39 from [] to 0.28mm on the same datasets.

A major limitation of the presented software is rather severe error of centerline tracking on the segments with severe calcifications, which were present in 20 of the 32 datasets. This is because the calcium usually has higher intensity value or even higher vesselness value. Although a threshold filter set at 650 HU is used to eliminate the influence from calcium, more sophisticated filters or segmentation algorithms are needed to correct the distorted segment, as the intensity of calcification varies much from patient to patient. It should be pointed out, although in other steps (section 2.2.1 and 2.2.2) thresholds are also used, they are rather stable on different exams from different patients and even from different scanners.

An advantage of the competing fuzzy connectedness tree algorithm is that it not only yields the centerlines of the coronary arteries, but also a segmentation of their branches. Although the segmentation was not directly evaluated in this experiment, it is noticeable that the centerline tracking in our algorithm is based on the segmentation result, which implies that the segmented arteries contain at least 96.0% of the reference centerlines of the 4 chosen branches. (In some cases, we have noticed errors in the extracted centerline even with a segmentation that includes the reference centerline.) As discussed in our previous report [7], this grayscale connectedness method does not yield the borders of a vessel, but rather gives the vessel surrounded by a certain amount of soft tissue (as shown in Fig 4). We believe that this segmentation reduces the probability of introducing false positive lesions during the segmentation step, compared to a conventional algorithm separating the vessel from the surrounding myocardium. Combined with proper 3D visualization (like MIP or VRT), the results should give physicians more reliable information about the coronary artery system and guide the user to inspecting more closely certain suspected locations in 2D images rather than going through every 2D slice. However, the clinical value of this technique needs to be further investigated.

Quantitative measurement has been introduced in some recent coronary CTA analysis software [15]. In the reported software, a semi-automatic 2D contour analysis function is included, which is complemented with the manual user correction function provided by the OsiriX system. This allows the user to get a quantitative estimate of stenoses rather than visually evaluating the presence or absence of stenosis. The accuracy of this function is still under investigation and will be reported in a different paper.

5. Conclusion

A new software module for coronary CTA analysis has been presented. The interactive processing is accelerated by non-supervised coronary artery extraction running in the background before the user opens the dataset. In this preliminary experiment, both accuracy and efficiency seem acceptable. Further work will include improved segmentation of calcifications and CPU time management of the automatic processing thread.

Acknowledgements.

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