

MULTI-SCALE VESSEL BOUNDARY DETECTION

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ABBREVIATIONS

CT	: Computed Tomography
MR	: Magnetic Resonance
CE-CTA	: Contrast Enhanced - Computed Tomography Angiography
MRA	: Magnetic Resonance Angiography
MPR	: Multi Planar Reformat

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DAMAR ÇEVİRİTİNİN ÇOK-ÖLÇEKLİ TESPİTİ

ÖZET

Bu çalışmada, CTA ve MRA görüntülerinde bulunan damarların bölütlenmesine yönelik oldukça kararlı ve başarılı bir algoritma önerilmiştir. Önerilen algoritma, öncelikle ortalama kaydırma analizini[1] kullanarak bir boyutlu ışınlar boyunca ayrıtları bulur. Tıbbi veriler üzerinde çalışılırken sıklıkla karşılaşılan problemleri aşmak için ortalama kaydırma analizinde çok ölçekli uzamsal süzgeçler ve uyarlamalı erim süzgeçleri kullanılmıştır. Çok-ölçekli doğası yüzünden saptanan pek çok hatalı ayrit da yine bu aşama sırasında önerilen algoritmalarla silinir. İkinci aşamada ise farklı ölçeklerden gelen tüm ayrıtlar doğru ve verimli bir şekilde ortalama kaydırma metodunun özellikleri kullanılarak birleştirilir. Üçüncü aşamada ise yerel ve evrensel gruplama teknikleri kullanılarak gruplanan ayrıtlardan aday damar çevritleri oluşturulur ve gerçek damar çevriti aday çevritlerinin elipse benzerliğinden yola çıkılarak bulunur. Bu aşamada benzerliği ölçmek için Fourier betimleyicilerinden faydalanılır. Önerilen algoritma (i) damarların başka damarlar veya yüksek kontrasta sahip yapılarla çevrildiği durumlara, (ii) damar içindeki kontrast değişimlerine, ve (iii) damar boyutundaki ve şeklindeki değişimlere karşı oldukça kararlıdır. Yöntemin doğruluğu bazı MRA ve CTA örnekleri üzerinde gösterilmiştir.

Buna ek olarak, bu bölütlenme algoritmasını temel alan basit bir damar izleme algoritması geliştirilmiştir. Bu algoritma kullanılarak dolaşım sistemi hastalıkları olan daralma ve anevrizma modellenmiştir.

MULTI-SCALE VESSEL BOUNDARY DETECTION

SUMMARY

In this work, I present a robust and accurate method for the segmentation of cross-sectional boundaries of vessels found in contrast-enhanced (CE) CTA and MRA images. The proposed algorithm first detects the edges along 1D rays by using mean-shift analysis [1]. To overcome the problems associated with medical data, multiple spatial scale and adaptive range scale are employed to detect edges. Furthermore, most of the incorrect edges are deleted in this step. Second, edges from different scales are accurately and efficiently combined by using the properties of mean-shift clustering. Third, multi-scale edges are grouped using local and global perceptual edge grouping to form candidate boundaries and the final vessel cross-sectional boundary is selected based on elliptical shape verification. Fourier descriptors are employed to measure the similarity of a boundary to an ellipse. The proposed algorithm is stable to (i) the case where the vessel is surrounded by other vessels or other high contrast structures, (ii) contrast variations in vessel boundary, and (iii) variations in the vessel size and shape. The accuracy of the algorithm is shown on several MRA and CTA examples.

In addition to the segmentation algorithm, a naïve tracking algorithm is developed as a generalization of this algorithm. It is used to model the pathologies; stenosis and aneurysm.

1. INTRODUCTION

Medical Imaging is the process of visualizing a region of the human body which is not externally visible. The output of a medical imaging system could either be a two dimensional (2D) image or a three dimensional (3D) volume. It is clinically employed for diagnosis and evaluation of diseases. Once the pathology is detected on the image, quantitative and qualitative assessments could be done easily. Furthermore, it can be utilized for a better understanding of processes in living organisms.

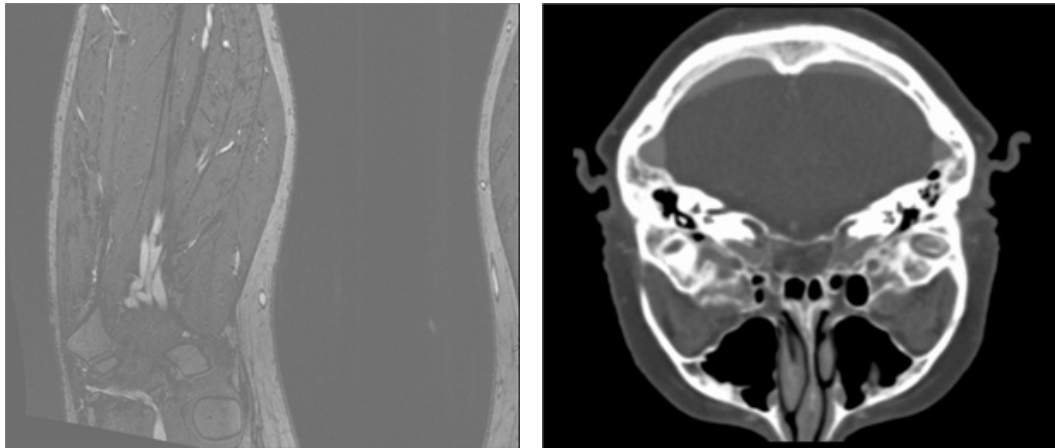


Figure 1.1: This figure illustrates two slices from a MR and a CT image.

1.1 History of Medical Imaging and Techniques

Cho et al. classifies medical imaging technologies into two rough groups based on their timeline: classical and modern methods [2]. Classical medical imaging began in 1895 with Röntgen's discoveries of X-rays and their subsequent utilization for the visualization of bones and other structures within the body [3]. On the other side, modern medical imaging began in the 1970's with the invention of computed tomography [4, 5]. G.N. Hounsfield developed the first device capable of producing true reconstructed images. Modern methods reconstruct medical images from tissue/radiation interaction database. Simply, CT imaging is based on a mathematical formulation that

states that the cross-sectional image of an object can be reconstructed if it is viewed from different number of angles. It is note worthy to mention that modern imaging is only the generalization of classical imaging and classical imaging can be classified as a special case of the modern methods [2].

In this work, the objective technologies are CT and MR. All of the experiments are implemented on three dimensional volumes generated by these methods. Figure 1.1 presents two slices from a MR and a CT image. Note that the most significant difference is the presence of bones with high intensity values in the CT image.

1.2 Medical Data

Most of the modern medical imaging technologies provide 3D images for diagnosis purposes. The basic element of a 3D digital image is called voxel and a 3D medical image is a lattice of voxel, Figure 1.2. However, in some cases, sampling rates could differ in x, y or z direction, so the uniformity of the lattice would be lost. This point should not be ignored while designing visualization and image analysis techniques.

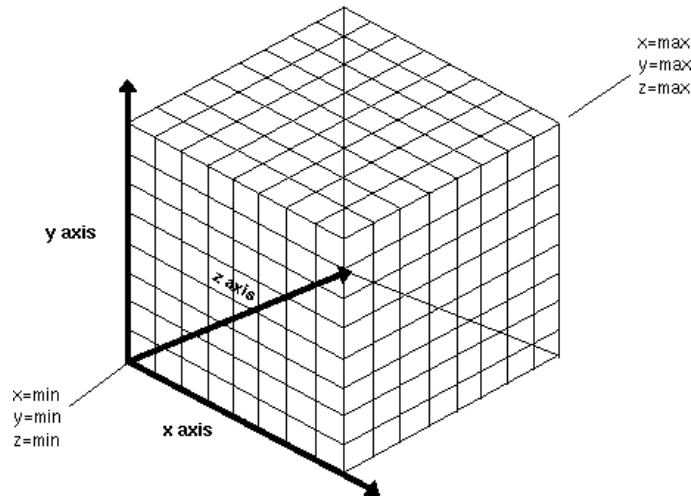


Figure 1.2: Representation of a 3D uniform lattice

The intensity value of a voxel varies from 0 to 4095 (4096 distinct colors), suggesting that 12 bits is used for coding. However, in most of the visualization techniques, intensity values are passed through a color transfer function to visualize medical data properly.

Although the proposed algorithm in this work is applied on 2D images, 3D medical images are used during our study. Each 2D image is generated from 3D volumes by cutting them with a plane whose normal is the vessel direction. The 2D images that are produced at a specific position and orientation in volume are called multi planar reformat (MPR) images.

1.3 DICOM

Storage and transmission of the medical images is addressed by the Digital Imaging and Communications in Medicine (DICOM) Standard [6]. American College of Radiology and the National Electrical Manufacturers Association proposed it in 1993 as an extension to their previous effort in 1988.

The DICOM Standard describes multiple levels of the ISO OSI network model and provides support for the exchange of information on interchange media. It defines an upper layer protocol that is working over TCP/IP (independent of the physical network), messages, services, information objects and an association negotiation mechanism [6]. This structure ensures that any two system implementations with compatible set of services and objects can effectively communicate between each other. Furthermore, independence from the underlying network technology allows DICOM to be deployed in many network architectures. At the application layer, the services address five primary areas of functionality:

- Transmission and persistence of complete objects (such as images, waveforms and documents),
- Query and retrieval of objects,
- Performance of specific actions,
- Workflow management (support of work lists and status information) and
- Quality and consistency of image appearance (both for display and print).

DICOM does not offer an architecture for the medical system; nor does it specify requirements, beyond the behavior defined for specific services. It can be considered as a standard of communications between disparate applications, devices and systems [6].

1.4 Medical Image Analysis

Image analysis is the extraction of meaningful information from images. It has a vast area of application. Specifically, in medical image analysis, problems mostly focus on the segmentation of structures and the registration of images.

In image analysis, segmentation is the partitioning of the image into homogenous regions according to a criterion. This criterion could be texture, color or even motion. The goal of this process is to depict the object of interest. In medical image analysis, segmentation is one of the main problems, because diagnosis and evaluation of pathologies mostly rely on the analysis of the object of interest and it should be segmented accurately for a proper analysis. In this work, the objective structures are the blood vessels.

1.5 Vessel Segmentation

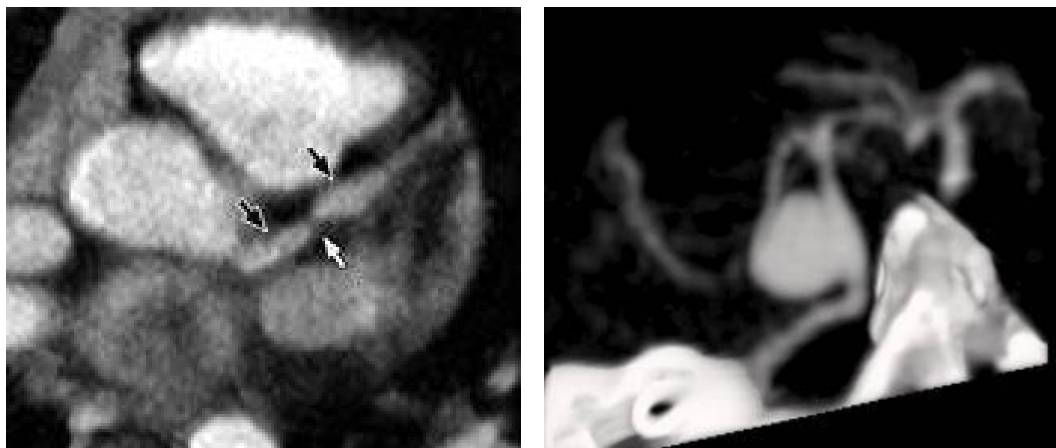


Figure 1.3: (left) coronary artery stenosis, (right) aneurysm

Angiography or arteriography is a medical imaging technique in which blood filled ncomes from the Greek words angeion, "vessel", and graphien, "to write or record". The image taken with this technique is called angiogram or angiograph. The main goal of the

majority of CE-CTA/MRA examinations is diagnosis and qualitative or quantitative assessment of pathologies in the circulatory system. The most common pathologies are aneurysms and stenosis caused by arterial plaques. Stenosis can simply be explained as the abnormal narrowing of a blood vessel or another tubular structure. The coronary artery (blood vessels that supply blood to the heart) stenosis is one of the most common and dangerous type of this disease. The most well-known syndrome based on this pathology is heart-attack. In Figure 1.3, narrowing of the coronary artery can be observed clearly. The other common pathology is a localized ballooning of a blood vessel, Figure 1.3. They are commonly observed at the junction points of the vessels. It is very dangerous because this bulge on the blood vessels carries the risk of bursting, which may lead to internal bleeding.

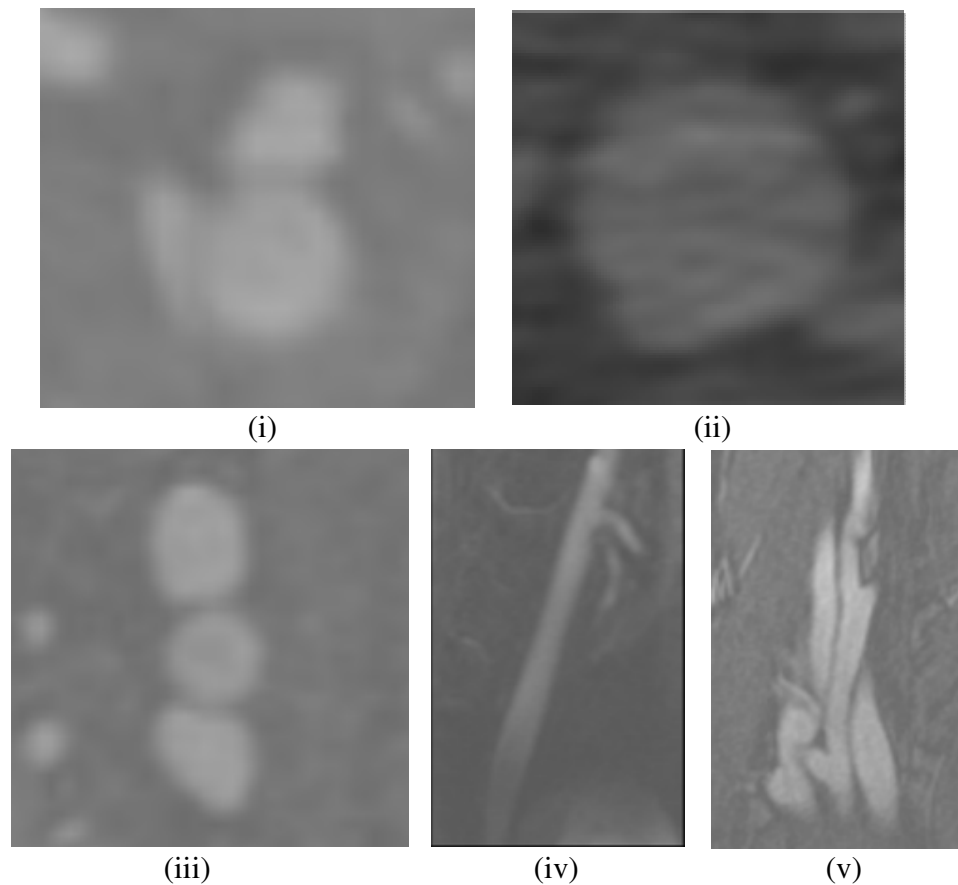


Figure 1.4: Difficulties of detection of cross sectional boundaries.

It is clear that the segmentation and modeling of vessels are very important during diagnosis and evaluation of these pathologies. Once the location of the pathology is determined, quantitative measurements can be made on the original 2D slice data produced at user-selected positions and orientations in the volume.

The objective of this work is the detection of cross sectional boundaries of vessels in CE-CTA and MRA images robustly and accurately. However, this is often a challenging task, Figure 1.4. Specifically, (i) Intensity profile would be diffused at one side while a very shallow one is present on the other sides of the vessel because of other nearby bright structures. (ii) Presence of significant noise levels in CT and MR images often forms strong edges in vessel. (iii) Local deviations from circular shape at vessel cross sectional boundary could occur because of nearby structures or presence of vascular pathologies locally. (iv) Contrast would change significantly through vessel in MR images. (v) Other bright structures would be present next to the vessel of interest. The proposed algorithm overcomes these difficulties while detecting vessel boundary.

In this study, a new segmentation technique is proposed based on multi-scale edge detection, local edge grouping, curve grouping and elliptical shape fit [7]. Specifically, first, edges along a ray are computed in several scales by using mean shift analysis [1]. Second, incorrect edges obtained from multiple scales are eliminated. Third, prominent edges are obtained by selecting edges based on their strengths, and the assumption that vessels are not nested structures. Fourth, smooth and long curve segments are constructed from prominent edges by a local grouping algorithm. Finally, the curve segments that best describes the vessel boundary are determined from the elliptic shape priors. This new algorithm is capable of segmenting vessel boundaries in great detail even in the extreme conditions illustrated in Figure 1.4. In addition, it is proposed that 2D cross-sectional vessel boundaries can be successfully used to model 3D vessels very accurately by a centerline tracking algorithm similar to one in [8]. The accuracy and robustness of the 2D cross-sectional boundary detection algorithm and the 3D vessel tracking algorithm is shown on several CTA and MRA data.

2. RELATED WORK

Previously, Hernandez-Hoyos et al. [9] presented a snake model for segmenting vessel boundaries in the planes orthogonal to the vessel centerline. Wink et al. [10] proposed a ray propagation method based on the intensity gradients for the segmentation of vessels and detection of their centerline.

Similarly, Tek et. al. [11] proposed a segmentation method for the cross-sectional vessel boundaries based on explicit front propagation via rays, which combines smoothness constraints with the mean-shift filtering. Specifically, they considered the curve evolution equation $\partial C(s,t)/\partial t = S(x,y)\vec{N}$ for the segmentation of vessel boundaries where $C(s,t)$ is a contour, $S(x,y)$ is the speed of evolving contour and N is the vector normal to $C(s,t)$. In this proposed approach, the contour $C(s,t)$ is sampled and the evolution of each sample is followed in time by rewriting the curve evolution equation in vector form [11]. The speed of rays $S(x,y)$ depends on image information and shape priors. They proposed to use $S(x,y) = S_0(x,y) + \beta S_1(x,y)$ where $S_0(x,y)$ measures image discontinuities, $S_1(x,y)$ represents shape priors, and β balances these two terms. In this approach, image discontinuities are detected via mean-shift analysis [1] along the rays. Comaniciu and Meer showed that mean-shift analysis, which operates in the joint spatial-range domain where the space of the 2-dimensional lattice represents the spatial domain and the space of intensity values constitutes the range domain, is a powerful method for robustly detecting object boundaries in images. Specifically, the strength of displacement vectors which measures the spatial movement of each spatial point are used for detecting the discontinuities. A point whose neighbor points moves toward distinct directions is called divergence point and a divergence point corresponds to discontinuity points. This algorithm works well in certain applications especially when vessel boundaries are well isolated. However, it faces difficulties when vessel boundaries become very diffused due to nearby vessels or other bright structures and

significant noise is present inside vessels. In addition, for the robust segmentation of vessels, it is very difficult to estimate parameters i.e., spatial, range kernel filter sizes, amount of smoothness constraints. In fact, vessel boundaries are often present in many different scales, which cannot be handled by the use of a single scale proposed by Tek [11]. In addition, curvature based smoothness constraints are not enough to impose shape constraints in many cases. Instead, elliptical shape descriptors are often needed for robust results. The presented approach in this work robustly handles all these difficulties.

3. MULTI-SCALE EDGE DETECTION

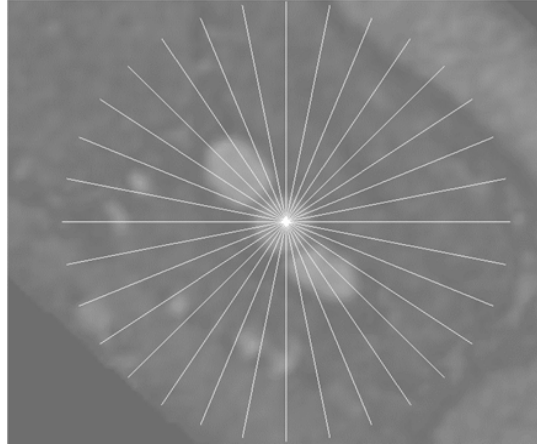


Figure 3.1: This figure illustrates the rays.

To detect a vessel boundary, first edges should be extracted. Instead of 2-D edge detection, rays are propagated from a point that is set within the vessel towards the vessel surface and the edge detection algorithm is then applied to these generated rays. By this way, the problem is reduced to 1-D edge detection instead of 2-D and definitely, it is computationally more efficient. Observe the Figure 3.1 illustrating the rays shot from an initial set point.

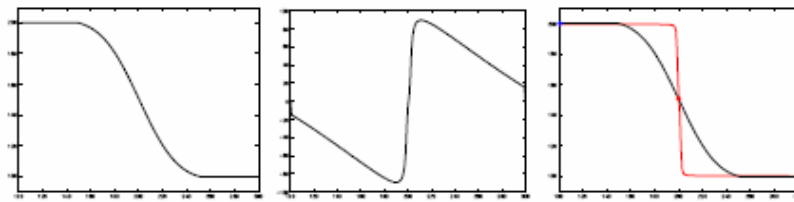


Figure 3.2: This figure illustrates the mean-shift filtering of a typical edge. Left: original intensity profile. Middle: Displacement vectors. Divergence of displacement vectors corresponds to the location of the edge. Right: Smoothed intensity and original intensity together and the two local mode of intensity around the edge.

One of the main problems in medical image segmentation is the accurate edge localization in the presence of noise. Most CT and MR images have significant noise

levels. When proper parameters are used, noise along these rays is eliminated while edges are preserved with mean shift analysis. This is the main reason behind the selection mean-shift analysis [1] for edge detection. As an output of mean-shift analysis, divergence points on the displacement vector sequence correspond to the discontinuity points on the ray. The drawback of other techniques using conventional smoothing methods is such a smoothing can shift or entirely eliminate low-contrast boundaries. Observe the Figure 3.2 which is explaining the mean shift filtering.

3.1 Mean Shift Analysis

Given the set $\{x_i\}_{i=1,\dots,n}$ of d dimensional points, the mean shift vector computed at location x is given by [1]

$$M_h(x) = \frac{\sum_{i=1}^n x_i K\left(\frac{x - x_i}{h}\right)}{\sum_{i=1}^n K\left(\frac{x - x_i}{h}\right)} - x \quad (3.1)$$

where K represent the kernel with a monotonically decreasing profile and h is the bandwidth of the kernel.

The mean shift vector is an estimate of the density gradient computed at point x [1]. This means the mean shift vector point towards the direction of the maximum increase in the density. As a result, successive iterations of Equation 3.1, defines a path from x to the local maximum of the density. In each step, the point x should be moved by $M_h(x)$.

This procedure can be applied on the joint spatial-range domain [1]. While the 2-dimensional lattice constitutes the spatial domain, range domain covers the intensity value space. At the end of the procedure, described above, point x is assigned a convergence point which represents the local mode of the density. The difference between the convergence point and the original point can be named as displacement vector. The algorithm produces discontinuity preserving smoothing. Conceptually, this process is similar to the anisotropic diffusion, nonlinear filtering, or bilateral filtering [12]. Figure 3.3 illustrates 2-D mean shift smoothing and convergence of the points.

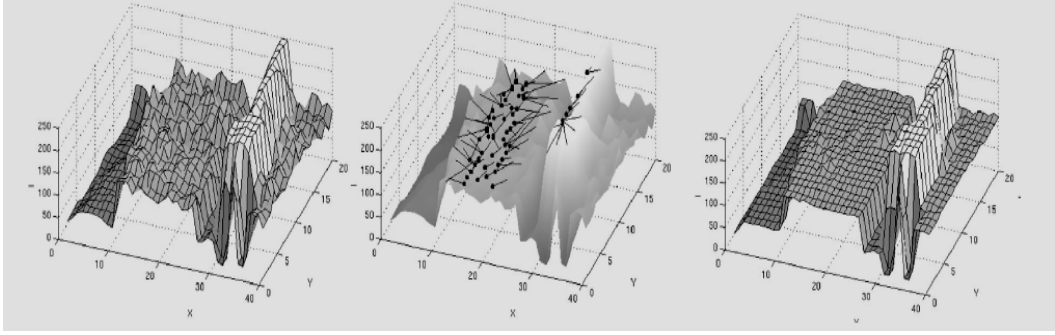


Figure 3.3: This figure illustrates the 2D mean shift analysis. (Left) Original signal (Middle) Displacement vectors (Right) smoothed signal [1]

3.2 Mean Shift Analysis Along a Ray

In this section, mean shift analysis applied on a 1-dimensional intensity profile which is obtained from a 2D grayscale image will be described. Specifically, let $\{x_i, I_i\}_{i=1, \dots, N}$ and $\{x_i^*, I_i^*\}_{i=1, \dots, N}$ are the original and filtered N points in the spatial-range domain. In addition to the smoothed signal, mean-shift analysis constructs the displacement vector sequence $\{d_i\}_{i=1, \dots, N}$, which measures the spatial movement of each point in the input sequence. Mean shift analysis is applied on the each point until they converges to a mode point.

Specifically, algorithm consists of three steps:

For each $i = 1, \dots, N$

1. Initialize $k = 1$ and $(x_i^{*k}, I_i^{*k}, d_i) = (x_i, I_i, 0)$
2. Compute the iterationz

$$x_i^{*k+1} = \frac{\sum_{j=1}^M x_j e^{-\frac{(x_i^{*k} - x_j)^2}{2\sigma_x^2}} e^{-\frac{(I_i^{*k} - I_j)^2}{2\sigma_I^2}}}{\sum_{j=1}^M e^{-\frac{(x_i^{*k} - x_j)^2}{2\sigma_x^2}} e^{-\frac{(I_i^{*k} - I_j)^2}{2\sigma_I^2}}} \quad (3.2)$$

$$I_i^{*k+1} = \frac{\sum_{j=1}^M I_j e^{-\frac{(x_i^{*k} - x_j)^2}{2\sigma_x^2}} e^{-\frac{(I_i^{*k} - I_j)^2}{2\sigma_I^2}}}{\sum_{j=1}^M e^{-\frac{(x_i^{*k} - x_j)^2}{2\sigma_x^2}} e^{-\frac{(I_i^{*k} - I_j)^2}{2\sigma_I^2}}} \quad (3.3)$$

until the displacement of the points are small enough, i.e. $|x_i^{*k+1} - x_i^{*k}| < \epsilon$

3. Assign $d_i = x_i^{*k+1} - x_i$

where σ_x and σ_I refer to Gaussian spatial kernel scale and range kernel scale, respectively.

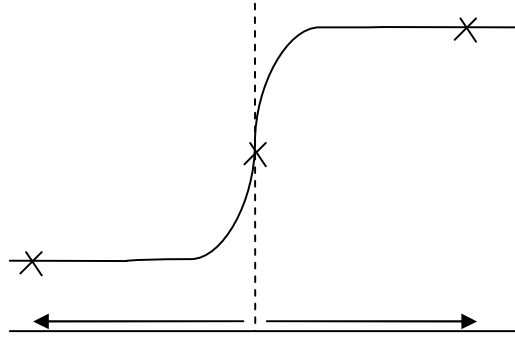


Figure 3.4: This figure presents the direction of displacement vector of the points around the edge point.

As stated before, divergence points on the displacement vector sequence correspond to discontinuities on the input sequence while convergence points correspond to the modes, Figure 3.4. Although the purpose is edge detection and divergence points are enough for locating the position of the edge, we still need convergence points. They are utilized for calculating edge strength and edge confidence which are used to remove the spurious edges. This elimination procedure will be explained in the next section.

Figure 3.5 illustrates an example where 1-dimensional intensity data is obtained from a slice of a CT image. Figure 3.5b and 3.5c illustrate the original intensity profile and the smoothed intensity profile, respectively. Observe that the mean shift procedure smooths the intensity data while preserving and sharpening its discontinuities. Similarly, Figure 3.5d depicts the displacement vectors along this 1-dimensional signal. As stated above, the edge detection step exploits the information contained in these displacement vectors.

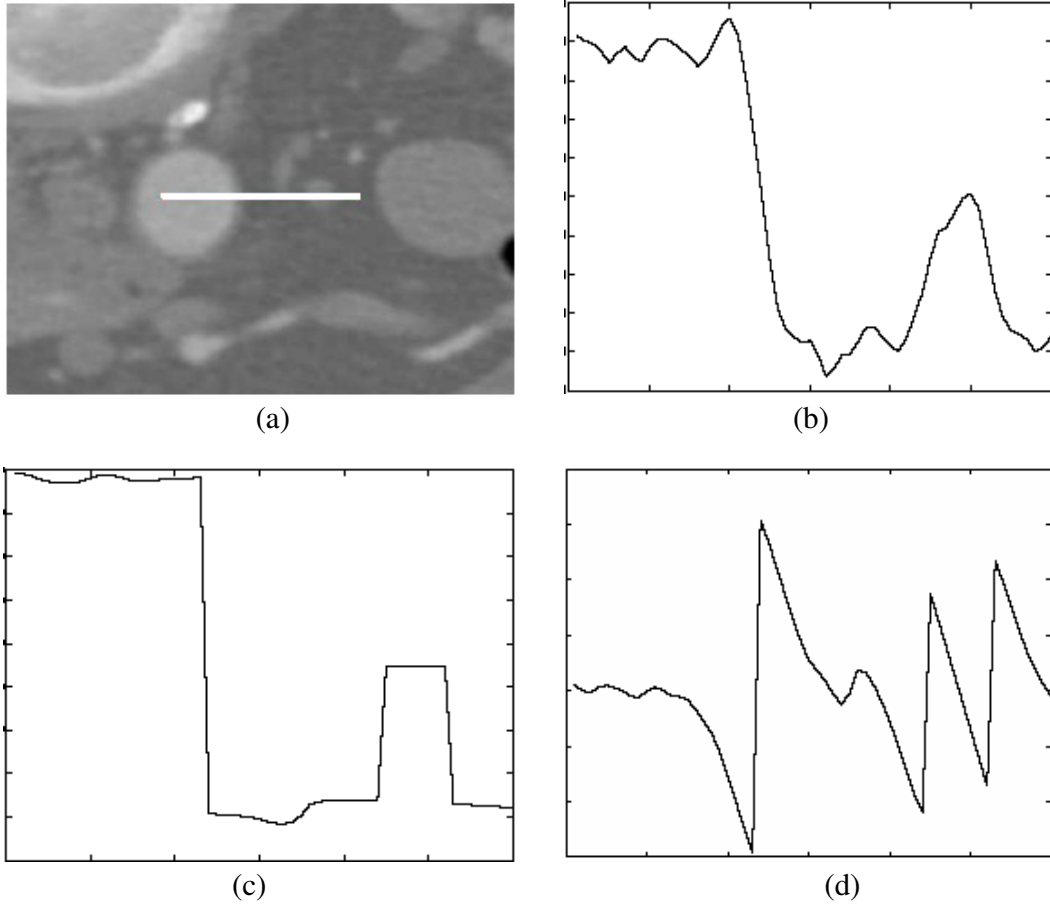


Figure 3.5: (a) A 1-dimensional intensity profile is obtained along the red line from a CT image containing the aorta. The left-end point of the red line is the beginning of data and right-end point is the end of data. (b) Original intensity profile (c) Smoothed intensity profile (d) The displacement vectors of each spatial point.

3.2.1 Multi-Scale Edge Detection with Mean Shift Analysis

As explained in the previous section, the robustness and accuracy of results heavily depend on the selection of spatial (σ_x) and range (σ_r) scale parameters of mean-shift analysis, because the vessel boundary are often in many spatial and range scales.

In many medical imaging applications, it is often assumed that boundary can be represented by high contrast step edges. However, in reality, diffuse edges, low contrast edges and gap edges occur frequently even in single cross-sectional vessel boundary. The robust and accurate detection of edges from these profiles requires edge detection in many scales [7]. However, integration of edge responses from different scales is not an easy task. It is also possible to apply the filtering in several range scales. However,

optimal range kernel size can be obtained directly from the intensity data. Specifically, we experimentally determined that the mean intensity difference between the right and left side of the spatial filters corresponds to the optimal range scales, which is verified in our experiments. In addition, it is assumed that the size of largest diffuse edge is known a priori to set the range of spatial kernels.

There are two main difficulties with obtaining the correct edge from multi-scale edges: First, multiple edge responses often present around the vicinity of the semantically correct edge due to the multi-scale nature of the algorithm. It is clear that localization of the edge changes with respect to the kernel size. Only the edge with correct position should be kept, and the others should be deleted. Second, there are often several edges along a ray corresponding to the structures of the boundaries. The edge corresponding to the boundary of a vessel can be determined from the geometric properties of the vessels and perceptual edge organization, which is explained in the next section. This section mainly deals with the first problem and describes how to remove incorrect edges based on edge confidence and edge strength.

Consider a typical intensity data containing a single edge. While the divergence of displacement vectors defines the location of the edge, the convergence of displacement vectors corresponds to the local mode of intensity, i.e. clustering of intensity data. The intensity data can be locally clustered around the edge by mean shift, if the proper scale, (σ_x) is chosen. We use this fact, i.e., local clustering, to define the edge confidence which measures the validity of an edge by checking the presence of local clustering. Specifically, the edge confidence for scale (σ_{xk}) at location i is given by [7]

$$E_{ci}(\sigma_{xk}) = \frac{\sum_{j=1}^M \frac{|I_j^* - I_i|}{|I_c - I_i|}}{M} \quad (3.4)$$

where M is the kernel size, I_j^* is the smoothed intensity at point j , and I_c is the intensity value of the convergence point. Observe that this measure is close to one if a local clustering forms around the edge, otherwise, it is close to zero. It is proposed to delete the edges with small confidence.

While the removal of low confidence edges is important, it cannot solely eliminate all incorrect edges. In fact, several high confidence edges form in the vicinity of a correct edge. To eliminate these incorrect edges, edge strength is defined as the intensity difference between convergence points. Specifically, the edge strength of an edge location i is given by $E_s(i) = |I_{c1} - I_{c2}|$ where I_{c1} and I_{c2} are the intensity values of the convergence points.

To eliminate incorrect edges, the following proposition is based on their edge and local mode. After elimination of incorrect edges, one edge stays for each real edge.

Proposition 1: An edge is a correct edge if it is not located under the local mode of another edge. If it falls inside the local mode of another edge, it must have higher edge strength [7].

4. VESSEL BOUNDARY EXTRACTION FROM MULTI-SCALE EDGES

In this section, an algorithm that selects the edges corresponding to the cross sectional boundary of the vessel will be presented. Specifically, it is a three stage algorithm. These stages are listed in the following;

1. Prominent edge selection
2. Local edge grouping to form curve segments
3. Curve grouping based on elliptical shape prior

Final stage constructs a complete curve that corresponds to the vessel boundary.

4.1 Prominent Edge Selection

The objective of prominent edge selection can be explained as the elimination of most of the edges that do not correspond to a vessel boundary. The algorithm developed for this stage, determines prominent edges using the no nested structure assumption [7]. This assumption is based on the fact that vessels, found in CE-MRA/CTA data, are not embedded in any other bright structure. However, in reality, the vessels would be partially surrounded by other bright structures as in Figure 4.1, and our algorithm is designed to overcome this case.

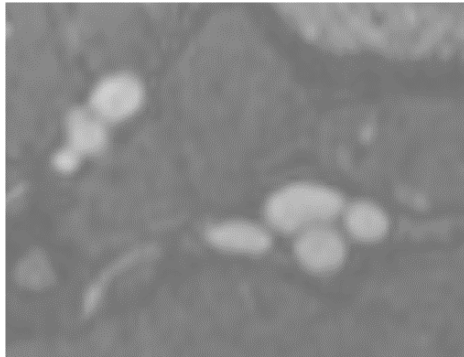


Figure 4.1: A cross-sectional cut from peripherals data.

Specifically, under no nested structure assumption, the first significant edge, encountered during propagating along a ray from the seed point towards the surface of the vessel, often corresponds to the vessel boundary. When the significant edge is determined, the rest of the edges on the ray are deleted. This operation could be explained mathematically, as the edge E_i is deleted if $E_{si} < k_1 E_{sj}$ where $j > i \geq 0$ or if $k_1 E_{si} < E_{sj}$ where $i > j \geq 0$, and k_1 is a parameter which specifies relative strength of edges.

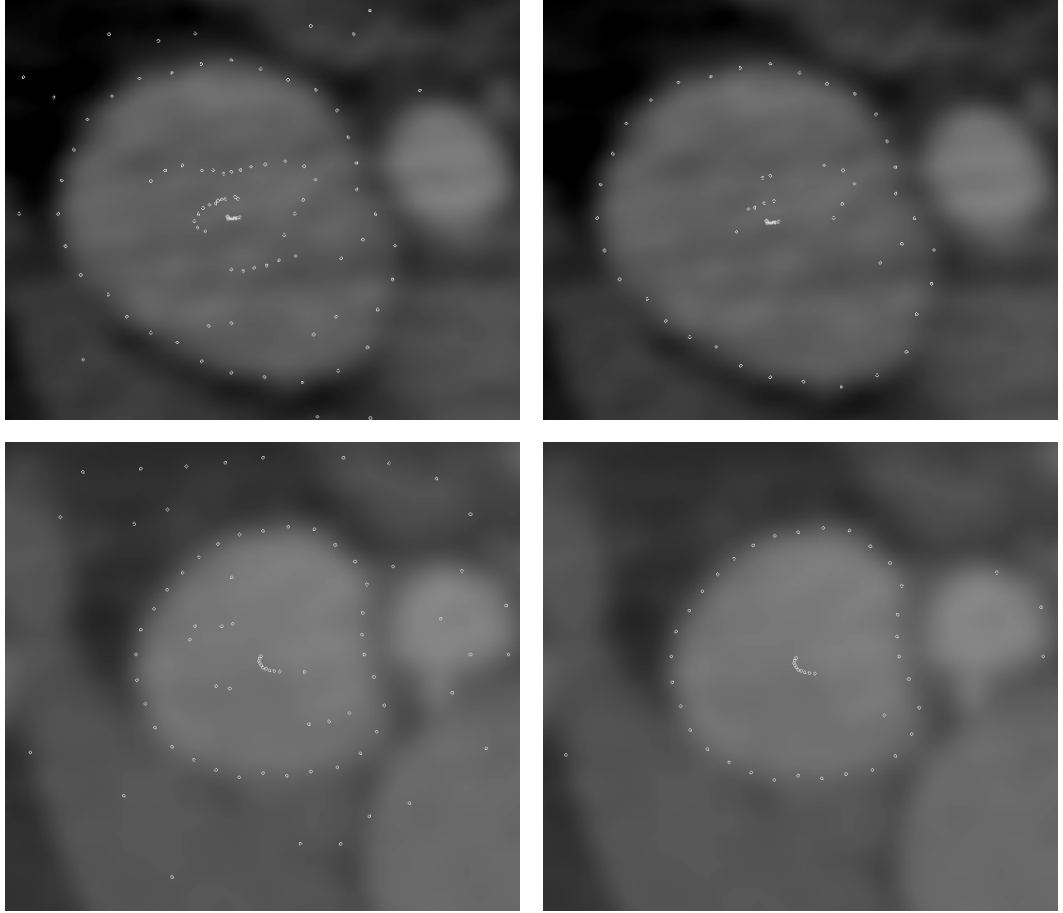


Figure 4.2: This figure illustrates the results of prominent edge selection on two different examples; (left) multi-scale edges, (right) prominent edges.

Although it is expected that a proper k_1 value is enough to extract the vessel boundary, in many cases, edges of the other surrounding bright structures and significant in-vessel noise do not allow this. On the other side, it is very difficult to estimate a proper value

for k_1 . Under these circumstances, it is proposed to use multiple k_1 values to select prominent edges from multi-scales. Each prominent edge map that corresponds to a different k_1 value is combined on an edge map. In our experiments, all prominent edges are obtained by setting k_1 to 0.1, 0.2, 0.3, 0.5, 0.7, 0.9 respectively. Figure 4.2 demonstrates the prominent edge selection algorithm on two real examples. Observe that this method reduces the number of edges significantly while preserving the ones that are crucial.

4.2 Local Edge Grouping to Form Curve Segments

In the previous stage, edge elements which are not a part of the vessel are eliminated. After removing these irrelevant edges, the local edge grouping problem becomes relatively easy. In this stage, our goal is to organize edges into curve segments via perceptual edge grouping.

Previously, Gestalt psychologists proposed that the human visual system selects those that depict regularities such as good continuation, proximity, symmetry, closure, etc. for the organization of visual data [13]. Law of prägnanz says that humans try to experience things in as good a Gestalt way as possible. In this sense, "good" can mean several things, such as regular, orderly, simplistic, symmetrical, etc. Other supporting laws are;

- Law of Closure - Our mind adds missing elements to complete a figure (Figure 4.3).
- Law of Similarity - Our mind groups similar elements to an entity. The similarity depends on form, color, size and brightness of the elements.
- Law of Proximity - Regional or chronological closeness of elements are grouped by our mind and seen as belonging together (Figure 4.3).
- Law of Symmetry - Symmetrical images are seen as belonging together regardless of their distance.
- Law of Continuity - The mind continues a pattern, even after it stops (Figure 4.3).

- Law of Common Fate - Elements with the same moving direction are seen as a unit

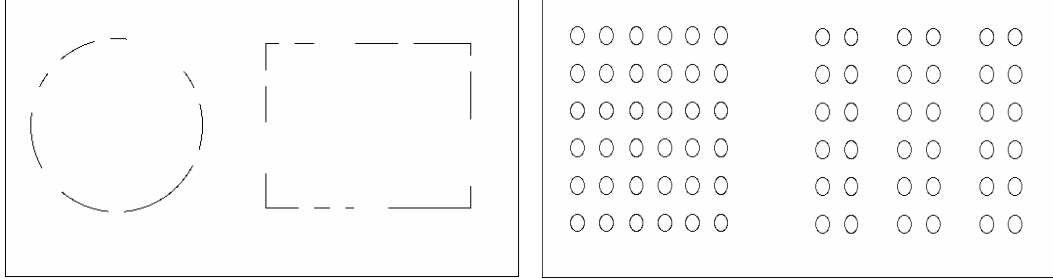


Figure 4.3: These figures illustrate (left) law of continuity, closure and (right) proximity.

These ideas have motivated approaches in computational vision where sets of edge elements, forming long smooth curves with few interruptions, are grouped together [14, 15, 11]. The selection process as to which nearby edge is most suitable for adding to the curve depends on statistics of the curve and effect of addition of a new edge. If addition of an edge does not affect the statistics of the curve, that edge could be noted as the perfect candidate.

The goal of obtaining smooth curve segments in our problem is relatively easy compared to the general edge grouping problem because

1. Edge elements are implicitly ordered by rays
2. Very few gaps are present
3. Spurious edges are almost non-existent.

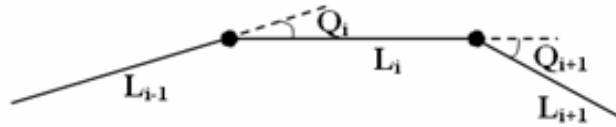


Figure 4.4: This figure illustrates the main idea of local grouping.

This algorithm exploits the angle θ_i and the distance L_i between edge elements to obtain long smooth curves, Figure 4.4. Specifically, edge grouping starts from three edge elements, which forms a smooth curve, i.e. small θ_i . It is easy to see that to form an angle, we need three edge points. It then expands in two directions (clock-wise and

counter clock-wise) by adding more edge elements. To decide on which edge element will be selected in the direction of expansion, first, an upper bound and a lower bound is computed depending on the angle and distance statistics of the curve segment. Second, if the properties of the candidate edge stay are within this interval, it is marked as suitable for expansion. Often, there is only one suitable edge, but if there is more than one suitable edge for expansion, then that point is marked as a branch point, and new curve segments are initialized from this branch point. On the other side, expansion of the curve stops in the direction of the branch point. When expansion of the curve segment stops in both directions, it is added to the curve segment set and the procedure starts again with a new edge group. This procedure continues until there are three neighboring edges that forms a smooth curve. This grouping algorithm converts edges into a set of curve segments. Figure 4.5 demonstrates the result of the algorithm on two real examples.

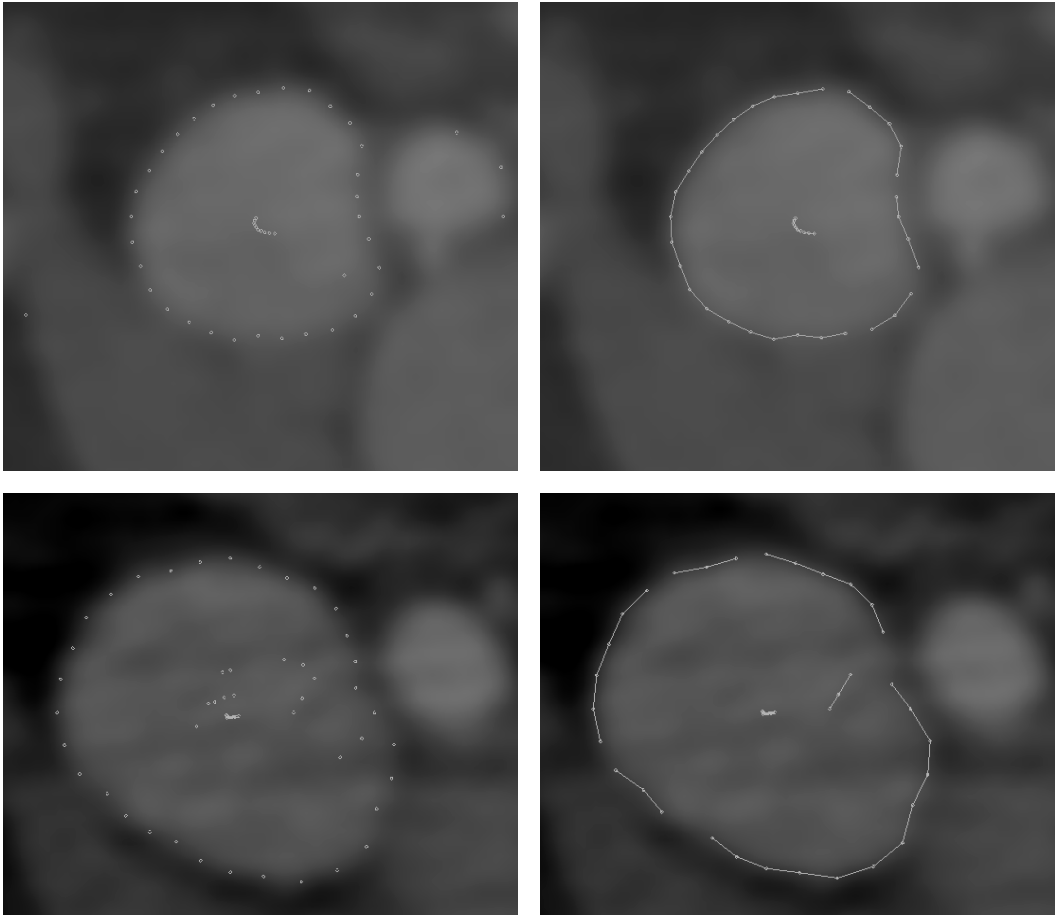


Figure 4.5: This figure illustrates the results of local edge grouping on two different examples; (left) prominent edges, (right) curve segments.

4.3 Curve Grouping Based on Elliptical Shape Prior

The previous stage constructs a set of curves from prominent edges. In this stage, our goal is to select a subset of k curves that correspond to the cross-sectional vessel boundary. Assuming that the final boundary will be ellipse-like leads us to the correct vessel boundary. The subset of the curves, forming a shape most similar to an ellipse when combined, should be considered as the boundary of the vessel.

4.3.1 Construction of Curve Subsets

Number of the subsets of a set is 2^k , when the number of the elements is k and it is clear that even a little increase in the number of curves will result in a dramatic increase in the number of subsets. Therefore, analyzing every subset of the set would be computationally inefficient. To solve this problem, only the curve segment subsets whose elements form a complete curve when combined together are marked as the candidate subset.

4.3.2 Gap completion

Another problem at this point is the gaps between curve segments. There are two factors behind a gap, ungrouped edges usually cause just small gaps, and absence of edges due to the presence of nearby bright structures. For example, when arteries touch veins in MS-325 contrast enhanced MRA; there is no boundary between them. Similarly, in CTA, no boundary between bone and the adjacent vessel may be present due to intensity similarities. Those gaps should be completed with the best “completion curve” to form a complete vessel boundary. These completion curves for gaps between curve segments or edge elements are often constructed from circular arcs [16], elastica [17] or Euler-Spiral [18]. In this work, cubic splines are proposed to complete gaps. Computational efficiency of the method and easiness of implementation were the major factors behind this decision.

A cubic spline is a spline constructed of piecewise third-order polynomials. These piecewise polynomials pass through a set of m control points [19], Figure 4.5. In our application, edges on the curve segments are our control points. To constitute piecewise polynomials, the fact that polynomials should satisfy the continuity property at control

points could be used. First and second order derivatives of the polynomials should match at the overlapping points (common control point).

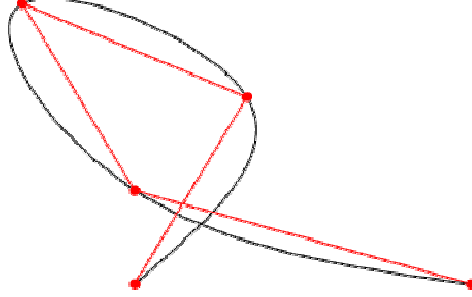


Figure 4.6: Cubic spline fit to five control points

Consider 1-dimensional spline for a set of $n+1$ points $(y_0, y_1, \dots, y_n)$. Let the i -th piece of the spline be presented by

$$Y_i(t) = a_i + b_i t + c_i t^2 + d_i t^3 \quad (4.1)$$

where t is a parameter $t \in [0, 1]$ and $i = 0, 1, \dots, n-1$. Then

$$Y_i(0) = y_i = a_i \quad (4.2)$$

$$Y_i(1) = y_{i+1} = a_i + b_i + c_i + d_i \quad (4.3)$$

Taking the derivative of $y_i(t)$ in each interval then gives

$$Y'_i(0) = D_i = b_i \quad (4.4)$$

$$Y'_i(1) = D_{i+1} = b_i + 2c_i + 3d_i \quad (4.5)$$

Solving previous equations for a_i, b_i, c_i, d_i gives

$$\begin{aligned} a_i &= y_i \\ b_i &= D_i \\ c_i &= 3(y_{i+1} - y_i) - 2D_i - D_{i+1} \\ d_i &= 2(y_i - y_{i+1}) + D_i + D_{i+1} \end{aligned} \quad (4.6)$$

Now require that the second derivatives also match at the points, so

$$\begin{aligned}
Y_{i-1}(1) &= y_i \\
Y'_{i-1}(1) &= Y'_i(0) \\
Y_i(0) &= y_i \\
Y''_{i-1}(1) &= Y''_i(0)
\end{aligned} \tag{4.7}$$

for interior points, as well as that the endpoints satisfy

$$\begin{aligned}
Y_0(0) &= y_0 \\
Y_{n-1}(1) &= y_n
\end{aligned} \tag{4.8}$$

This gives a total of $4n-2$ equations. To obtain two more equations, require that the second derivatives at the endpoints be zero, so

$$\begin{aligned}
Y''_0(0) &= 0 \\
Y''_{n-1}(1) &= 0
\end{aligned} \tag{4.9}$$

Rearranging all these equations leads to the following beautifully symmetric tridiagonal system [20]

$$\begin{bmatrix} 2 & 1 & & & \\ 1 & 4 & 1 & & \\ & \cdot & \cdot & \cdot & \\ & & \cdot & \cdot & \cdot \\ & & & 1 & 4 & 1 \\ & & & & 1 & 2 \end{bmatrix} \begin{bmatrix} D_0 \\ D_1 \\ \cdot \\ \cdot \\ D_{n-1} \\ D_n \end{bmatrix} = \begin{bmatrix} 3(y_1 - y_n) \\ 3(y_2 - y_0) \\ \cdot \\ \cdot \\ 3(y_n - y_{n-2}) \\ 3(y_0 - y_{n-1}) \end{bmatrix} \tag{4.10}$$

If the curve is instead closed, the system becomes

$$\begin{bmatrix} 4 & 1 & & & \\ 1 & 4 & 1 & & \\ & \cdot & \cdot & \cdot & \\ & & \cdot & \cdot & \cdot \\ & & & 1 & 4 & 1 \\ & & & & 1 & 4 \end{bmatrix} \begin{bmatrix} D_0 \\ D_1 \\ \cdot \\ \cdot \\ D_{n-1} \\ D_n \end{bmatrix} = \begin{bmatrix} 3(y_1 - y_n) \\ 3(y_2 - y_0) \\ \cdot \\ \cdot \\ 3(y_n - y_{n-2}) \\ 3(y_0 - y_{n-1}) \end{bmatrix} \tag{4.11}$$

In our algorithm, the Equation (4.11) is used, because vessel boundaries are closed curves. Observe the result of cubic spline completion in Figure 4.6.

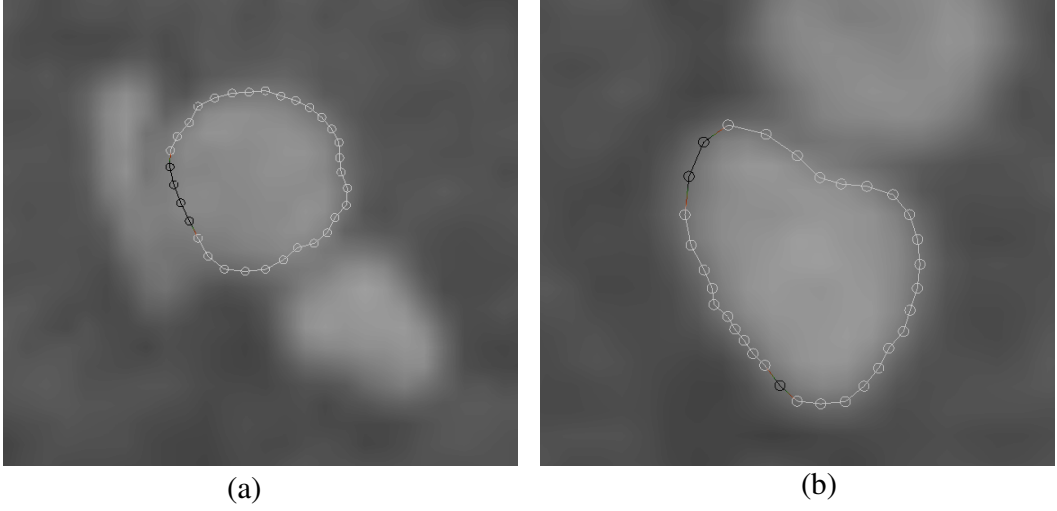


Figure 4.7: Real examples illustrating the curve completion with cubic splines. Black curve segments are the completed parts.

4.3.3 Curve Grouping Based on Elliptical Shape Prior

The curve segment subset representing the vessel boundary, is selected based on an elliptical fit measure. Specifically, while global shape of the vessel resembles an ellipse, it often exhibits local variations. Generally, these variations occur because of other nearby structures. In this work, Fourier Descriptors are proposed for an accurate shape representation which preserves local deformations while representing an ellipse globally. Specifically, an elliptical fit measure is computed based on Fourier Descriptors for each candidate subset. Among them, a subset of curve segments with best fit an ellipse is selected as the final vessel boundary.

4.3.3.1 Fourier Descriptors

Fourier representation is the expression of the curve in terms of an orthonormal basis. It allows us to express any object as a weighted sum of a set of known functions. An orthonormal set is preferred to avoid redundancy.

The main advantage of Fourier representation is its compactness. In terms of shape analysis, when an object is transformed to the frequency domain, low frequency components capture the rough shape information, while high frequency components

keep the details. This can be experimentally observed if an object is reconstructed with a few coefficients. This property is very important for classification algorithms because in this way, the objects with similar shapes cluster in the shape space.

However, in our algorithm, we need to evaluate the similarity of the objective vessel boundary to an ellipse. To achieve this goal, first we transform the vessel boundary to frequency domain and reconstruct the curve with a few Fourier coefficients. If fairly small number of Fourier coefficients is used, the new curve is expected to have an ellipse-like shape because of the characteristics of the basis functions. The proposed measure uses this fact. The simple idea behind our measure says that if the input boundary is similar to an ellipse, the distance between the input boundary and its reconstructed counterpart will be very small while the reconstructed one is expected to have a shape very close to ellipse. In other words, this method measures the amount of high frequency components.

To apply the Fourier transformation on a closed curve, it should be treated as a signal. While a closed curve is a 1-manifold and its elements are ordered, the points on the boundary could form a 1-D signal. $x(s) + iy(s)$ representation is suitable for this purpose while $s \in [0,1]$ and $x(0) = x(1)$.

Discrete Fourier Transformation and Inverse Discrete Transformation are defined as

$$a(k) = \frac{1}{N} \sum_{n=0}^{N-1} u(n) e^{-j2\pi kn/N} \quad k = -N/2, \dots, N/2-1 \quad (4.12)$$

$$u(n) = \frac{1}{N} \sum_{k=0}^{N-1} a(k) e^{j2\pi kn/N} \quad n = -N/2, \dots, N/2-1 \quad (4.13)$$

As stated before, number of Fourier coefficients determines the amount of detail kept during reconstruction process. Observe the Figure 4.7 presenting the difference between the curves reconstructed with different number of coefficients.

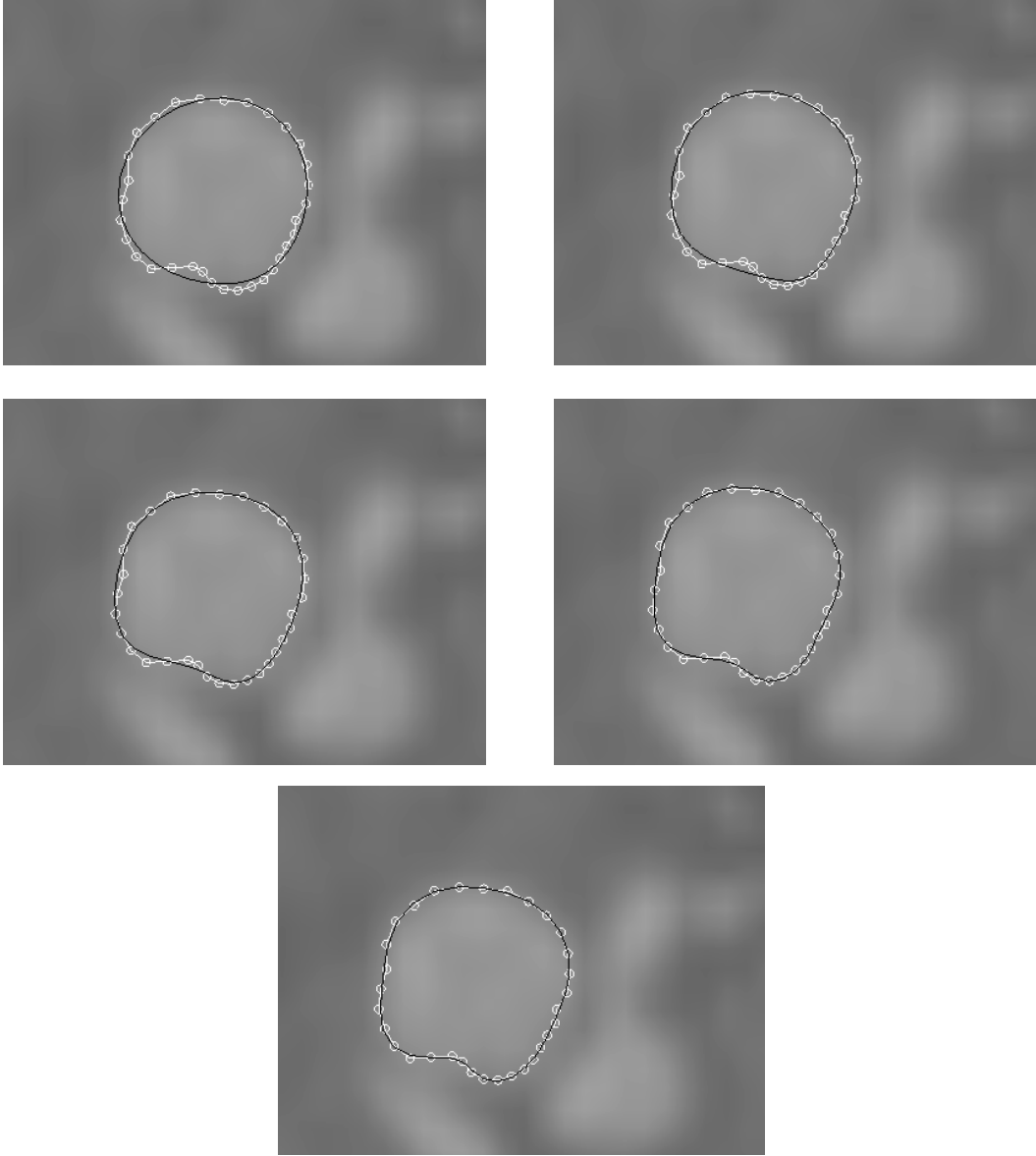


Figure 4.8: This figure illustrates the difference between the curves reconstructed with different number of coefficients (5, 7, 9, 11, 13).

4.3.3.2 Elliptical fit measure

Elliptical fit measure is simply computed as;

$$M = \frac{1}{d(C_{in}, C_{reconstructed})} \quad (4.14)$$

while C_{in} is the input boundary, $C_{reconstructed}$ is the closed curve reconstructed with Fourier coefficients of the input boundary and $d(.)$ is the distance function. Clearly, while distance between curves decreases, elliptical fit measure increases, and vice versa.

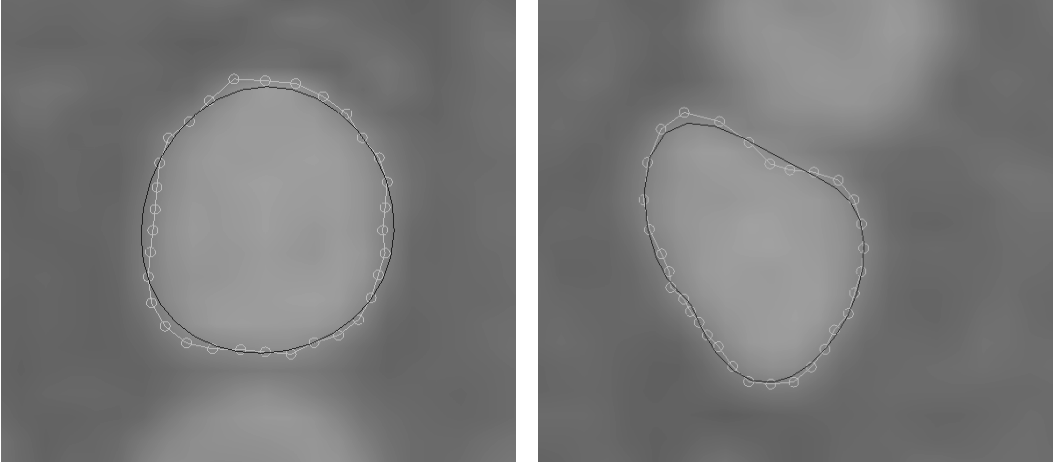


Figure 4.9: Real examples illustrating the curve reconstruction step. White curves are the real vessel boundary while black ones are the reconstruction results. 7 Fourier coefficients are used in both examples.

In our experiments, we used 7 Fourier coefficients since low number of coefficients (less than 5) does not capture local deformations of boundary and high number of coefficients (greater than 11) allows too much local deformation. Figure 4.8 shows the results of boundary reconstruction with 7 Fourier coefficients. We experimentally observed that these elliptical descriptors are very accurate in capturing vessel boundaries in great accuracy and robustness.

5. RESULTS AND VALIDATION

The performance of the proposed algorithm is tested on several CT and MR images. In this section, segmentation results, mostly covering the problems mentioned in the introduction section will be presented. Furthermore, validation results based on “ground truth” segmentation created by an expert will be demonstrated.

During our experiments, all parameters are constant. Thus, no change in the parameters is required to obtain accurate results robustly. In addition, results do not depend on the location of the seed point. Current implementation of the algorithm takes 150 ms for a slice on a personal computer with Pentium IV 1.8 GHz processor.

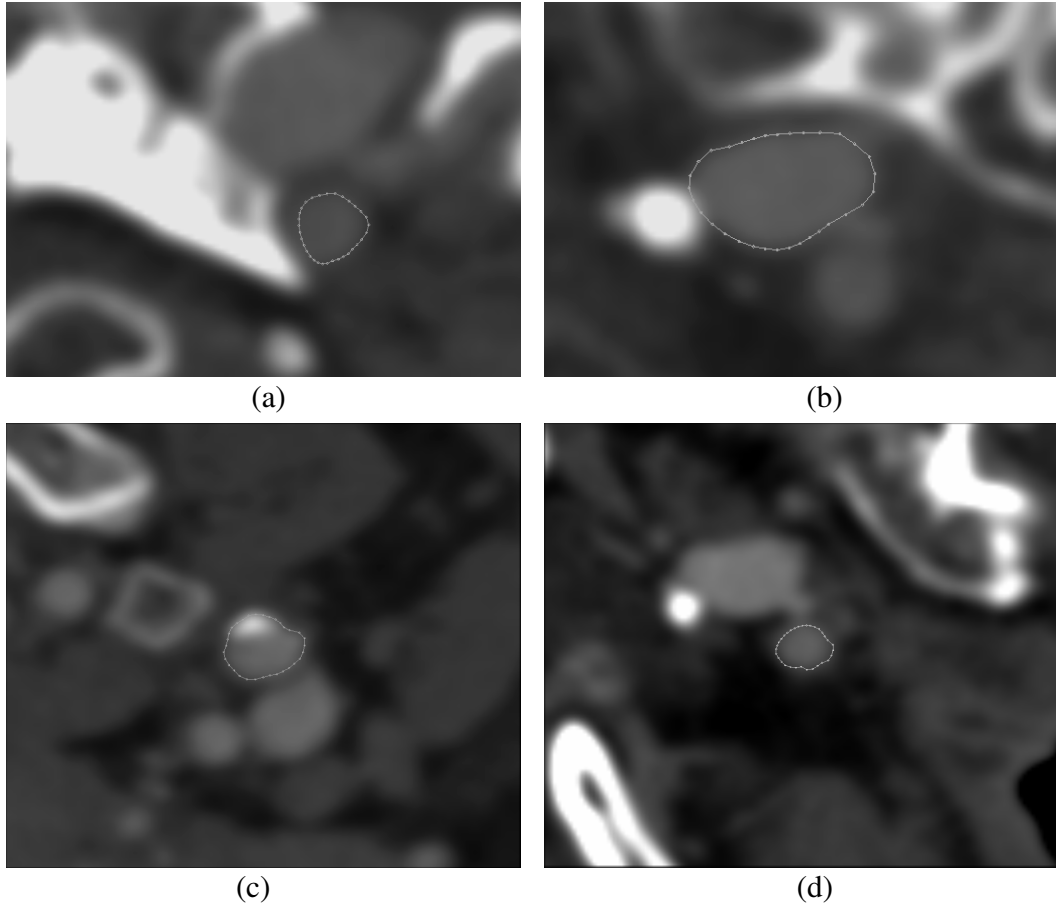


Figure 5.1: This figure presents the results of the algorithm on a CT carotid data.

Figure 5.1 presents the results of the algorithm on a CT carotid data. The most significant difference between CT images and MR images is the presence of bones with very high intensity values. Furthermore, the intensity value of their outermost layer is generally very close to the intensity value of vessels, and this property may lead to problems during segmentation. Clearly, our algorithm overcomes the problem of presence of other bright structures (bone) next to the vessel by using shape prior, Figure 5.1a and Figure 5.1b. In addition, in Figure 5.1d calcification is segmented as a part of the vessel despite of its high intensity profile, because shape prior forces the algorithm to choose an elliptical vessel boundary.

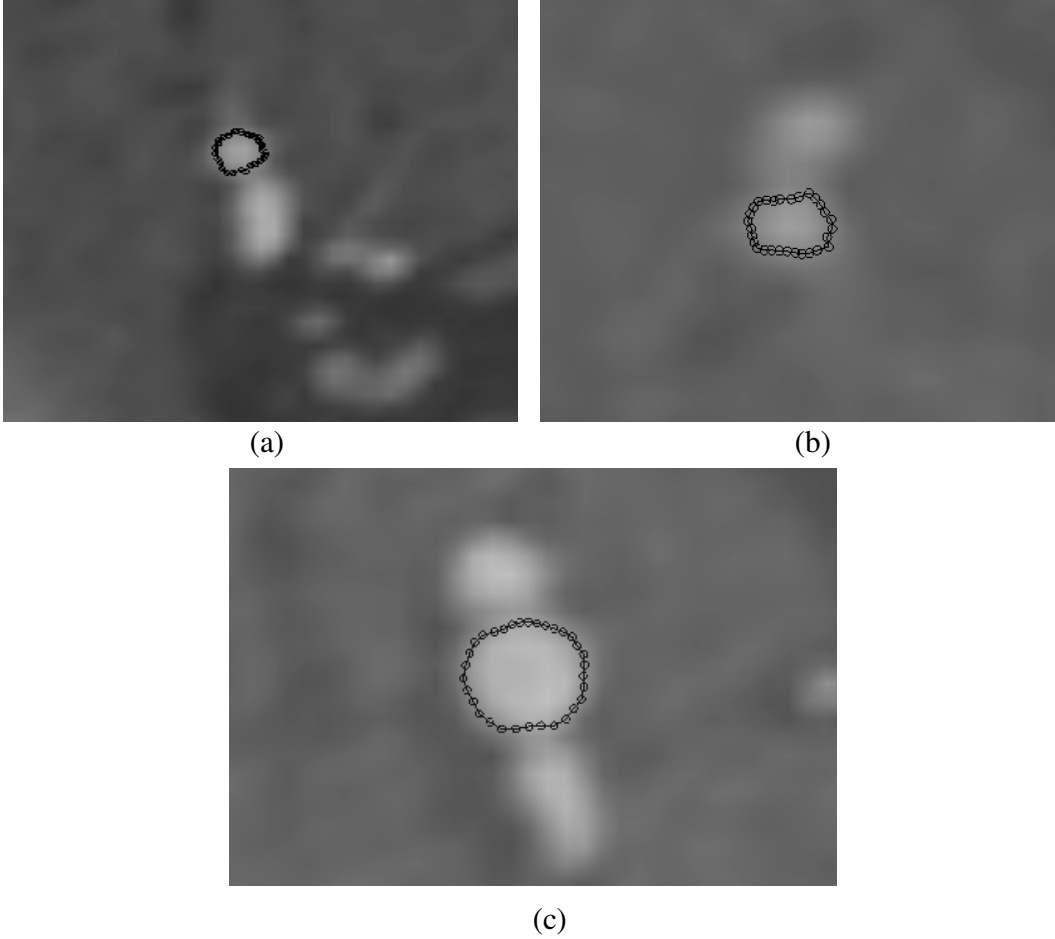


Figure 5.2: This figure presents the results of the algorithm on small vessels found in a MR peripherals data.

Figure 5.2 presents the results of the algorithm on small vessels found in a MR peripherals data. Our proposed algorithm handles this kind of vessels successfully, while

most of the algorithms fail to segment them. To have sub-voxel accuracy at the localization of the boundary, we up-sample the intensity profiles and this leads to an accurate and robust segmentation of small vessels.

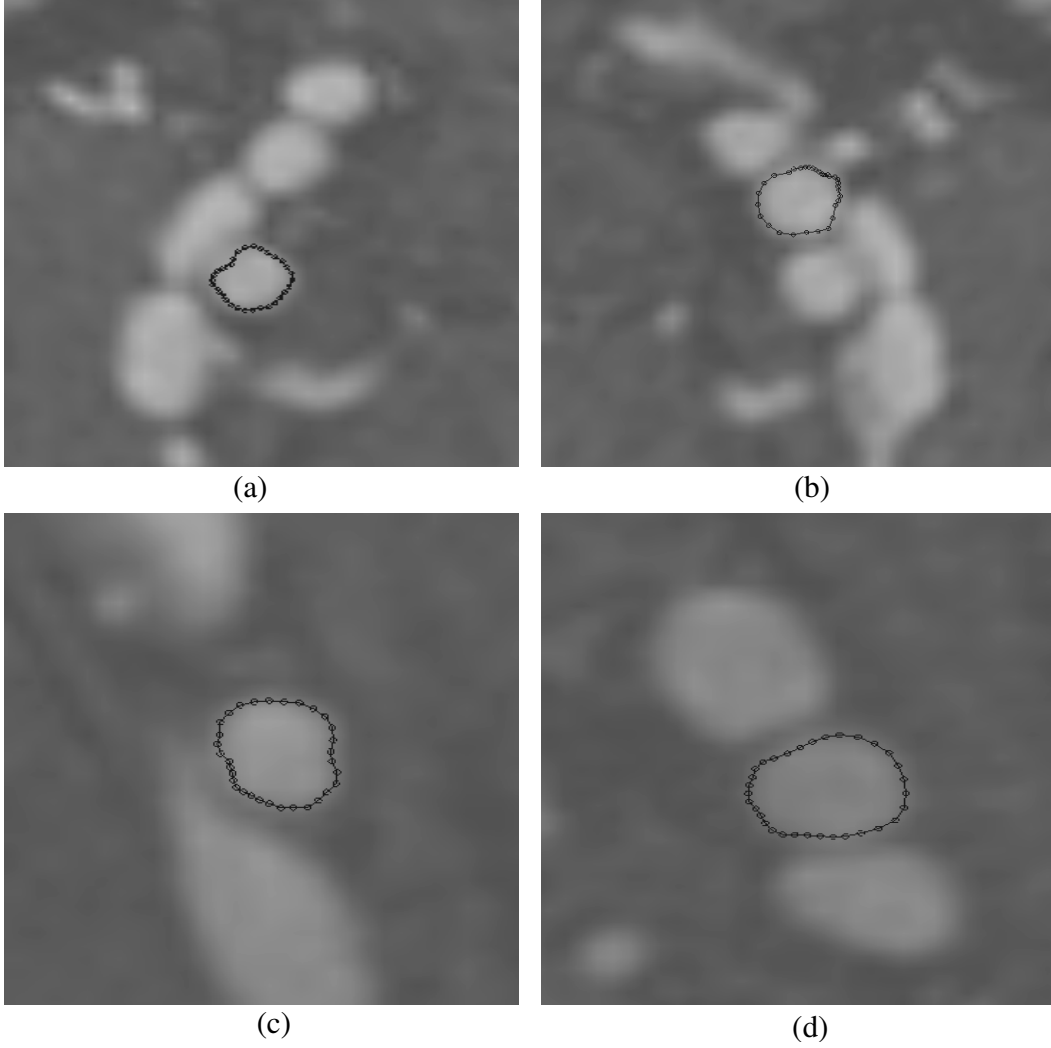


Figure 5.3: This figure presents the results of the algorithm on vessels found in a MR peripherals data. They are partially surrounded by other vessels.

Figure 5.3 shows how our algorithm is successful at segmenting vessel boundaries in case of the vessel is partially surrounded by other vessels, especially, observe Figure 5.3a and 5.3b. Handling the cases presented above shows that our algorithm overcomes the problem that the intensity profile would be diffused at one side while a very shallow one is present on the other sides because of other nearby vessels.

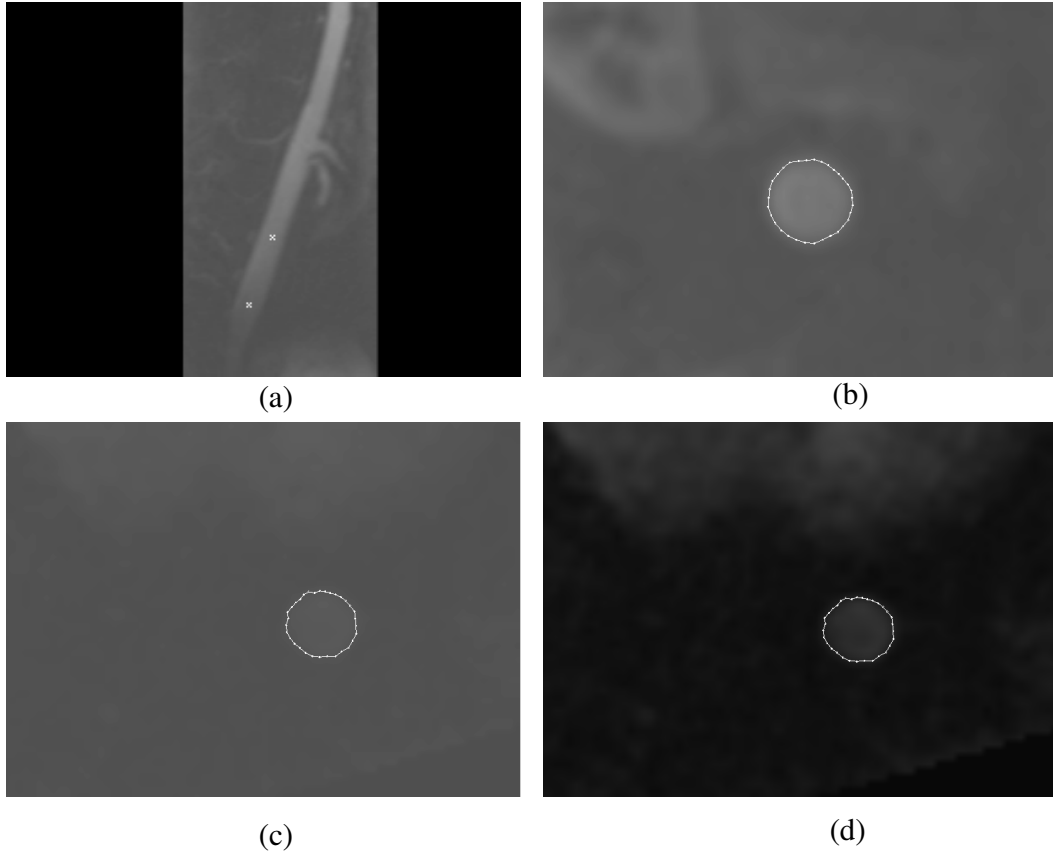


Figure 5.4: This figure presents the results of the algorithm on a vessel in which contrast changes significantly.

Figure 5.4 presents the results of the algorithm on a vessel in which contrast changes significantly, Figure 5.4a. Figure 5.4b (upper point) and Figure 5.4c (lower point) are segmentation of the vessel boundary around the points marked on Figure 5.4a. Note that vessels, found in Figure 5.4b and Figure 5.4c, are passed through the same color transfer function, but it is almost impossible to visualize the vessel in second figure unless the color transfer function is changed significantly, Figure 5.4d.

Figure 5.5 presents the results of the algorithm on noisy data. All examples are taken from a CT image. Although our algorithm performs quite well on noisy data, it fails in some cases when in-vessel noise creates a wrong boundary.

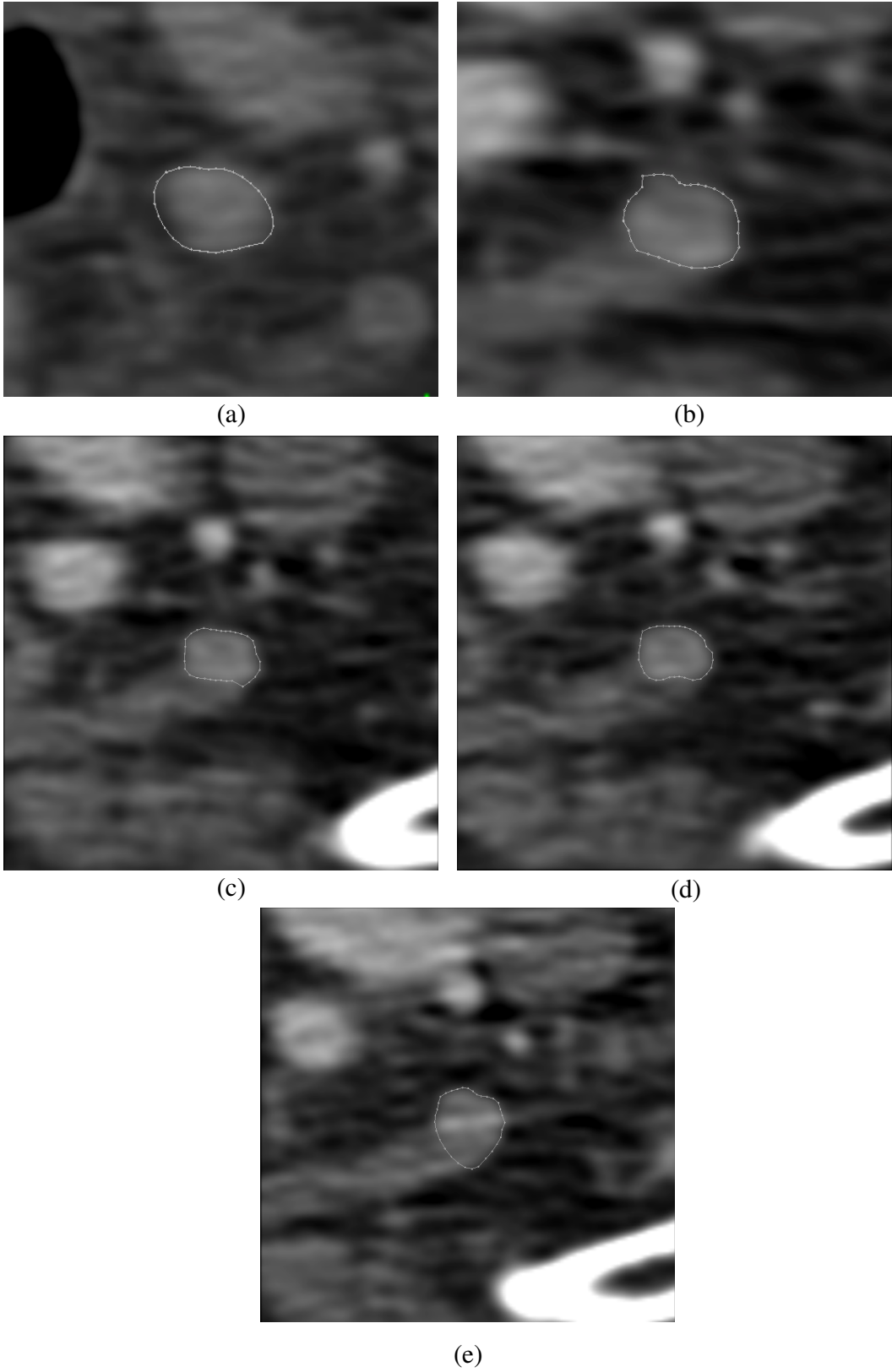


Figure 5.5: This figure presents the results of the algorithm on noisy data.

Table 5.1: This table illustrates the distance differences between computed and expert constructed vessel cross-sectional boundaries in percentage (%) for 8 different locations. The $(x \pm y); z$ representation describes: x (the average distance difference), y (the standard deviation of this difference) and z (the maximum distance difference between two contours in percentage).

	Patient-1	Patient-2	Patient-3	Patient-4
Contour-1	$(2.98 \pm 1.77); 6.93$	$(3.95 \pm 3.02); 13.12$	$(7.45 \pm 5.28); 21.83$	$(9.82 \pm 5.44); 21.71$
Contour-2	$(2.02 \pm 1.28); 5.37$	$(3.60 \pm 2.23); 11.19$	$(1.69 \pm 0.96); 5.01$	$(11.35 \pm 4.00); 19.42$
Contour-3	$(2.40 \pm 2.07); 9.54$	$(4.29 \pm 3.62); 14.82$	$(1.87 \pm 1.37); 5.96$	$(13.07 \pm 3.75); 19.76$
Contour-4	$(3.36 \pm 2.54); 8.78$	$(2.24 \pm 1.40); 5.63$	$(2.78 \pm 1.68); 6.04$	$(16.72 \pm 5.13); 24.76$
Contour-5	$(4.64 \pm 5.03); 19.05$	$(3.48 \pm 3.90); 13.75$	$(3.73 \pm 3.17); 12.69$	$(14.51 \pm 4.85); 21.69$
Contour-6	$(3.46 \pm 3.32); 15.53$	$(2.58 \pm 2.27); 7.07$	$(3.19 \pm 3.03); 12.61$	$(13.22 \pm 6.34); 25.31$
Contour-7	$(3.19 \pm 4.40); 17.99$	$(4.90 \pm 3.40); 10.69$	$(3.89 \pm 4.17); 14.22$	$(13.25 \pm 3.74); 21.49$
Contour-8	$(3.00 \pm .56); 12.04$	$(4.35 \pm 2.44); 10.23$	$(5.80 \pm 4.49); 15.58$	$(13.27 \pm 5.45); 23.87$

The accuracy of results is validated by comparing them against “ground-truth” results created by an expert on 4 data sets. Specifically, the 2D cross-sectional vessel boundaries were detected via the proposed algorithm at the user selected locations. These results were then compared to the expert generated results in Table 5.1. We present average error, standard deviation and maximum error between each contour in percentage. Each contour is described by 48 contour points. Let C_i represent a point on the expert-created contour. Similarly, let its corresponding point on the computed contour be represented by $\widehat{C}_i$. Since each contour differs in size, percentage errors are used in our validation instead of actual distance in mm. In order to find the percentage difference between two points, we performed a radial comparison using the ratio of the diameter of the user constructed contour to the difference, $|C_i - \widehat{C}_i|$. The proposed algorithm performs very well on many data sets. Especially, observe that for the first three data sets mean distance and standard deviations are very low. For the Patient-4 the

difference is between computed and ground-truth data is relatively high compared to the other data sets. However, the expert is satisfied with the accuracy of the results on Patient-4 because maximum diameter of vessel in that data set was 5 pixels. Thus, maximum error was often less than one pixel.

6. VESSEL TRACKING

Accurate detection and modeling of vessels is an important task in medical image applications [21, 12, 22]. While the main goal of this paper is the accurate and robust detection of vessel cross-sectional boundary, the 2D cross-sectional vessel boundaries can be successfully used in vessel modeling algorithms [7]. Specifically, we implemented a naïve vessel tracking algorithm that is similar to the one described in [8].

For each step

- Detect the vessel direction with Hessian matrix analysis [22]
- Extracts cross-sectional boundary of vessel.
- Moves to the centroid of the cross-sectional boundary
- Moves towards the vessel direction.

In each step, algorithm moves along the vessel centerline while extracting the cross sectional vessel boundary. It gives an accurate model of the vessel. However, it cannot track multiple braches of the vessel when it comes to a bifurcation (branching point of vessels) point and this is the main drawback of it. On the other side, it can be successfully used modeling stenosis and aneurysm very accurately.

6.1 Hessian Matrix Analysis

Modeling vessels directly from images by the eigenvalue analysis of Hessian matrix has been very popular in vascular image analysis [22]. In this work, only vessel direction detection part of that algorithm is used.

Specifically, the Hessian matrix of image I is given by

$$H(x, y, z) = \begin{bmatrix} I_{xx} & I_{xy} & I_{xz} \\ I_{yx} & I_{yy} & I_{yz} \\ I_{zx} & I_{zy} & I_{zz} \end{bmatrix} \quad (6.1)$$

and describes the local intensity variations of a voxel in a 3D image. Typically, a 3D image is filtered with a normalized second order Gaussian derivative to compute the Hessian matrix at each location. It is well-known that eigenvalues, $\lambda_1, \lambda_2, \lambda_3$ corresponds to the derivatives along the eigenvectors, e_1, e_2, e_3 . The eigenvectors of Hessian matrix represents the local tubular structures. In other words, the eigenvector e_1 corresponding to the smallest eigenvalue is in the direction of tube and the other eigenvectors e_2 and e_3 defines the cross-sectional plane, thus forming an orthonormal coordinate system, Figure 6.1.

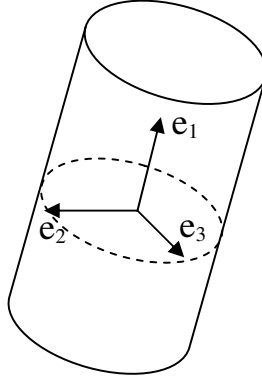


Figure 6.1: This figure illustrates the cross-sectional coordinate system of the vessel.

6.2 Results

6.2.1 Peripherals Data

The algorithm is tested on a MR peripheral data and the result is presented in Figure 6.2. As stated before, juxtaposed vessels are problematic cases for both segmentation and tracking algorithms. However, we claim that our segmentation algorithm overcomes these challenging problems. Observe that the proposed tracking algorithm tracks the vessel successfully until it encounters a bifurcation point.

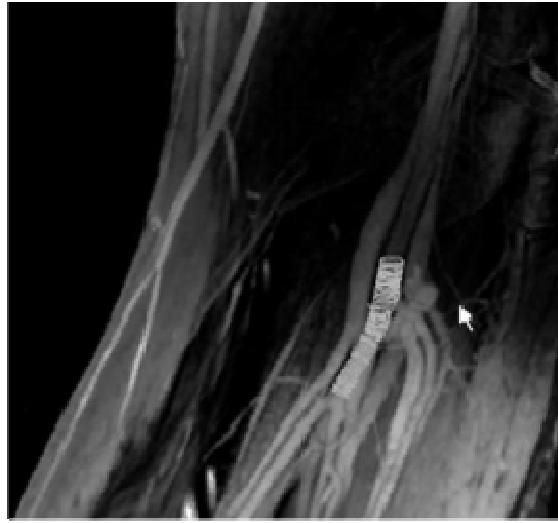


Figure 6.2: Result of the tracking algorithm on a MR peripheral data.

6.2.2 Carotid Data

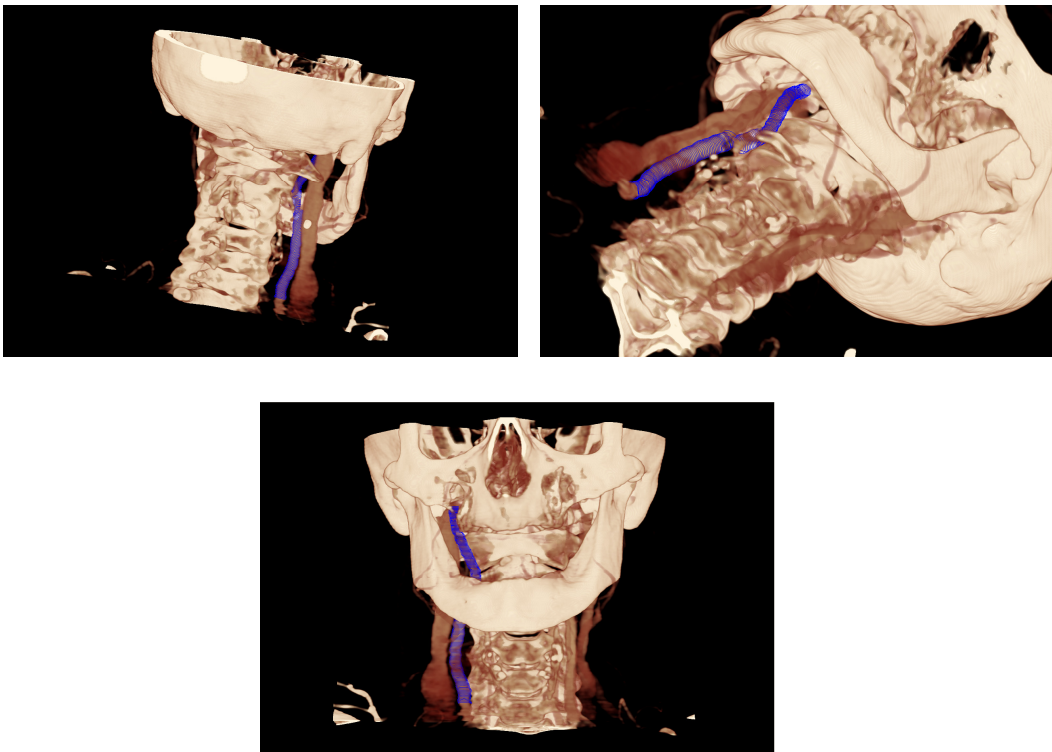


Figure 6.3: This figure illustrates the result of the tracking algorithm on a CT carotid image.

The algorithm is tested on a CT carotid data and the result is presented in Figure 6.3. As stated before, the main problem in CT images is the high intensity structures (bones). Our algorithm accurately and robustly tracks the vessel.

6.2.3 Aneurysm Modeling

In this section, the tracking algorithm is employed to model the vessels carrying an aneurysm, Figure 6.5



Figure 6.4: This figure illustrates the vessels carrying an aneurysm and the result of the tracking algorithm.

6.2.4 Stenosis Modeling

The tracking algorithm is experimented on a coronary artery (blood vessels that supply blood to the heart) stenosis. A cross-sectional area/radius profile would be very useful during quantification of the stenosis. In Figure 6.4, observe the cross-sectional vessel boundaries detected while moving through the coronary vessel. As you see, vessel narrows after a while and enlarges again after a few steps.

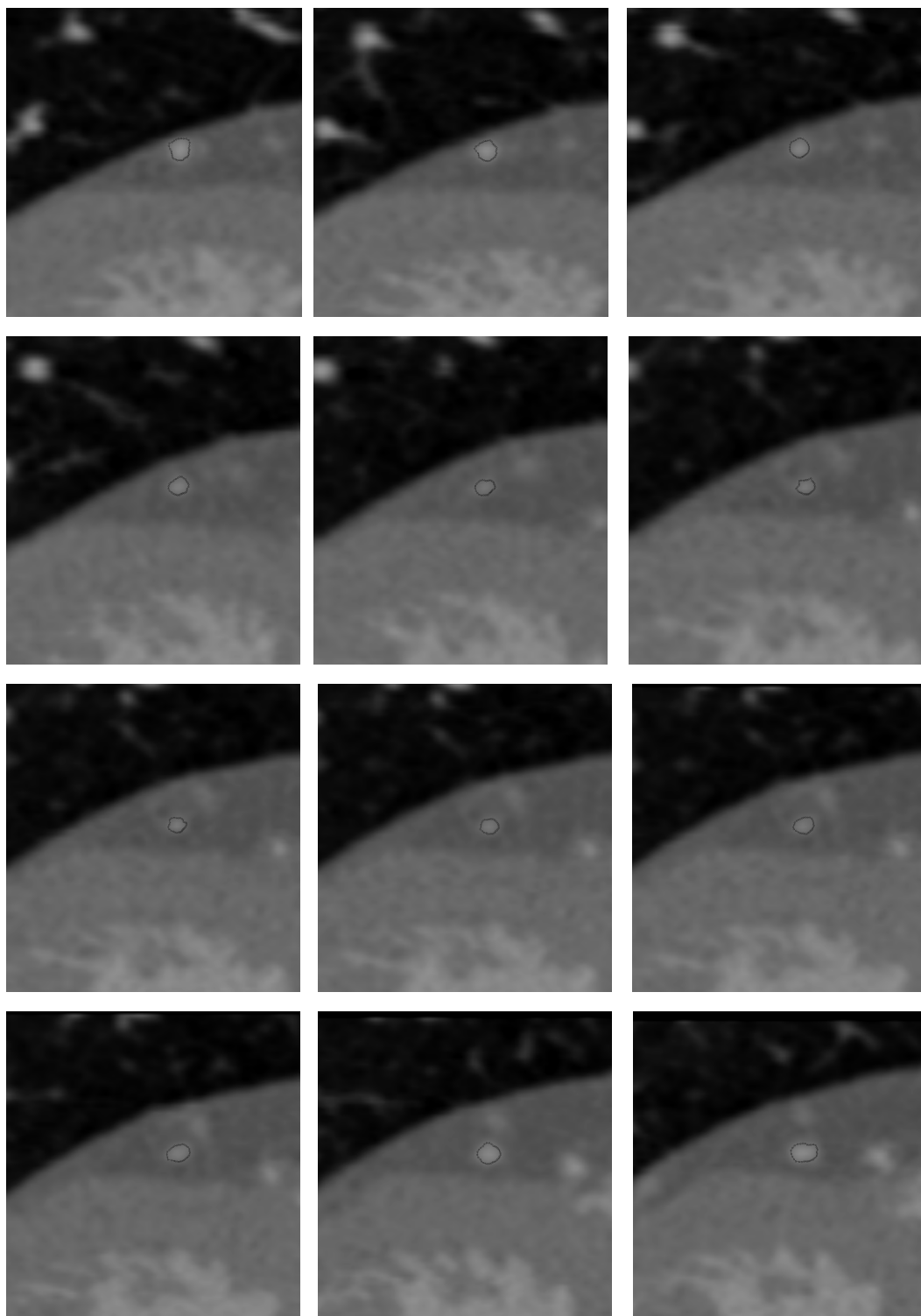


Figure 6.5: This figure illustrates the narrowing at the cross-sectional vessel boundaries, detected while moving through the coronary vessel

7. CONCLUSION

In this work, a method for detecting vessel boundaries accurately and robustly is proposed. The proposed algorithm is accurate and stable even where the vessels are surrounded by other vessels or other high contrast structures, contrast variations are present along vessels, and variations in the vessel size and shape are common. Furthermore, this segmentation algorithm is generalized to a tracking algorithm to model vessels accurately which is very important for diagnosis of circulatory system pathologies, i.e. stenosis and aneurysm.

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