Segmenting Descending Aorta using Machine Learning

1. Introduction

Atherosclerosis is one of primary causes of adverse cardiac events today. Plaque, a mixture of calcium, cholesterol fibrin and other substances accumulated in the vessel lumen causes stenosis or occlusion of the vessel. Depending on the location, atherosclerosis may result in strokes, heart attacks, aneurysms, and peripheral artery occlusion diseases.

The descending aorta is one of the most important vessel structures in the body. It is the largest artery in the body that runs down through the chest and the abdomen. The descending aorta begins below the arch of the aorta and ends by splitting into two great arteries (the common iliac arteries), which go to the legs. It has been observed that atherosclerosis of the descending aorta is a useful predictor of cardiovascular events[1].

With the advent of Multi Detector CT (MDCT) modality, Computer Tomography Angiography (CTA) is routinely used to image aortic vessels. CTA is ideal for preoperative evaluation of thoracic and abdominal aortic aneurysms, as it demonstrates their position, extent, and relationships to the renal and iliac arteries. CT is especially advantageous as it acquires information of the whole 3D volumetric data with high resolution rather than 2D projections in conventional angiography.

Geometric processing of CT vessel data has become increasingly more important for visualization, diagnosis and quantification of vascular diseases. The first step towards building patient-specific vessel geometry is reliable segmentation. However manual segmentation of a volumetric vessel is a very tedious task. The problem is exacerbated by the fact that CTA produces a huge number of tomographic slices of the aortic vessel. It has been shown in past studies that manual segmentations vary significantly between experts as well as when an expert segments the same image at different times[2].

The problems mentioned above underscore the need for reproducible and accurate automatic segmentation methods for the descending aorta in CT datasets. The aorta is complex in shape and appearance and varies significantly across individuals. In addition poor image contrast, noise, and missing or diffuse boundaries add to the complexity of the segmentation task. The goal of this project is to use machine learning algorithm(s) to build a probabilistic model, which can enable automatic segmentation of descending aorta in the CT volumetric datasets.

2. Methodology

The segmentation approach is based on the observation that blood filled regions are usually more easily recognizable in contrast-enhanced CT images[6]. If we can isolate the blood filled regions from the non-blood filled ones, the task of detecting the descending aorta becomes much simpler. Based on this observation, a machine learning algorithm is first used to estimate the probability distribution of three main classes of volumetric data. We then find the region filled with blood (which includes aorta, pulmonary trunk, heart chambers, and coronary arteries) using a Bayesian classification. We finally apply a level-set based active contour model to extract the descending aorta and obtain a 3D geometric model. All these steps of the methodology are explained in detail below.

The following notations have been used in describing the methodology:

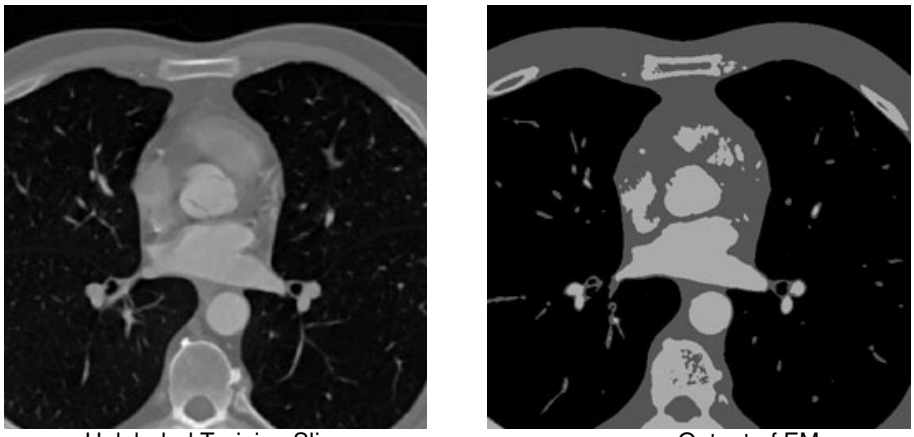
- I is the input image
- N is the number of voxels in I
- M is the number of classes of voxels
- $S = \{s \mid 1 \le s \le N\}$ is a set of integer indices into I
- $Y = \{Y_s \mid s \in S\}$ is the set of intensities of I. Y_s is the observed intensity at the s^{th} voxel of I
- W_{sc} is a binary indicator variable that indicates the membership of a voxel s to class j. W_{sc} =1 if voxel s belongs to class j otherwise it is 0.
- W_s is an M-dimensional indicator column vector whose c^{th} component is the indicator variable W_{sc}

2.1 Step 1: Estimating the probability densities

We assume that there are three classes of voxels in the CT Dataset (a) Blood-filled regions (b) Myocardium (c) Lung. Given a set of unlabeled training CT slices, we model the volume as a mixture of three Gaussians. If we

know the mean μ_c and standard deviation σ_c for each class where $c \in$ {blood-filled regions, myocardium, lung}, we can estimate the probability that the intensity of a voxel given that it belongs to a specific class. In other words we can find out $P(Y_s = v \mid W_{sc} = 1) = \frac{1}{\sigma_c \sqrt{2\pi}} \exp\left(- \frac{(v - \mu_c)^2}{2{\sigma_c}^2} \right)$

Two separate algorithms, K-Means and Expectation Maximization (EM) have been implemented to estimate the densities of the Gaussians. These two methods give us the mean μ_c and the standard deviation σ_c for each class. Step 1 of the methodology is executed offline on unlabeled training data once and the results (estimated densities) are stored for online usage.



Unlabeled Training Slice Output of EM

Figure 1: Result from EM

2.2 Step 2: Calculating the posterior probability using Bayes Rule

We can then use Bayes' rule to find out the probability that a voxel belongs to a specific class c given its voxel intensity. Thus $P(W_{sc} \mid Y_s = v) = \frac{P(Y_s = v \mid W_{sc}) P(c)}{\sum_{c'} P(Y_s = v \mid W_{sc'}) P(c')}$. Here we assume that the prior data $P(c)$ is uniformly distributed across all three classes. The classification of the voxels is then obtained by maximum a posteriori (MAP) estimation. In other words $W_{sj} = 1$ if $j = \arg\max_c \breve{P}(W_{sc} \mid Y_s)$. Here $\breve{P}(W_{sc} \mid Y_s)$ represents the result of applying an anisotropic diffusion filter on the posterior $P(W_{sc} \mid Y_s)$ before doing the MAP estimation. A gradient-based anisotropic diffusion filter is used to reduce noise (or unwanted detail) in the posterior probabilities while preserving specific image features.

2.3 Step 3: Extracting the aorta using level-set based active contour

Once we have classified each voxel as belonging to one of the three classes, we turn all non-blood filled voxels to zero and assign a non-zero value to all the blood-filled voxels. Now our job is to extract the descending aorta from these blood-filled voxels and discard other regions (such as coronary arteries, pulmonary trunks, heart-chambers etc). We employ a level set-based active contour model to detect the descending aorta. A detailed analysis of the level set model is available in literature[3]. Below we give a brief overview of the model.

The paradigm of the level set is that it is a numerical method for tracking the evolution of contours and surfaces. Instead of manipulating the contour directly, the contour is embedded as the zero level set of a higher dimensional function called the level-set function $\psi(X, t)$. The level-set function is then evolved under the

control of a differential equation. At any time, the evolving contour can be obtained by extracting the zero level-set $\Gamma((X),t) = \{\psi(X,t) = 0\}$ from the output. The main advantage of using level sets is that arbitrarily complex shapes can be modeled and topological changes such as merging and splitting are handled implicitly. The governing level set equation is

$\frac{d}{dt}\psi = -\alpha A(x).\nabla\psi - \beta P(x)|\nabla\psi| + \gamma Z(x)\kappa|\nabla\psi|$ where A is an advection term, P is a propagation term and Z is a spatial modifier for the mean curvature κ. The scalar coefficients α, β and γ weight the relative influence of each of the terms on the movement of the interface.

3. Implementation

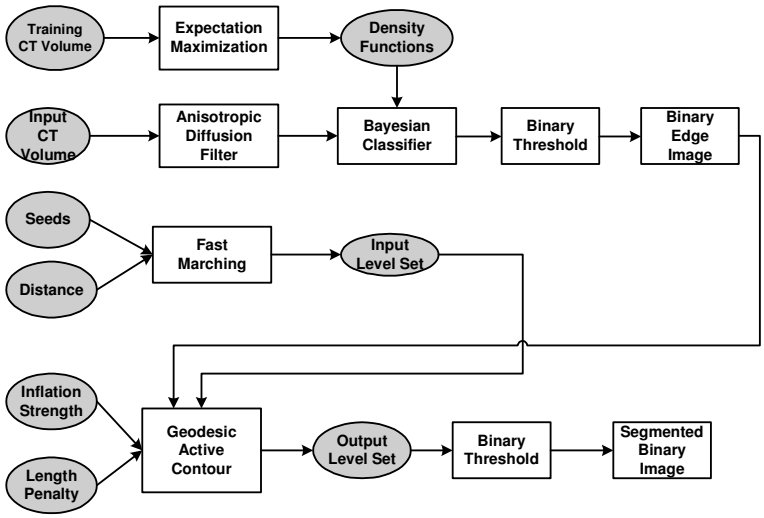


Figure 2: Implementation Pipeline

The above diagram presents how the methodology explained in section 2 was implemented using a pipeline approach. First we apply Expectation Maximization algorithm to the unlabeled training CT dataset to find the density functions of all the three groups of voxels mentioned earlier. These density functions are fed to the Bayesian classifier to classify the test CT volume. However before applying the Bayesian classifier, we first apply an anisotropic diffusion filter to smoothen the test CT volume while preserving the edge information. The smoothened image is passed as the input to a Bayesian Classifier to classify each voxel in one of three categories. This classified volume is then passed to a binary threshold filter, which sets all the non-blood-filled voxels to zero and assigns all the blood-filled voxels to the same non-zero number.

At this point we are ready to apply the geodesic active contour filter. This filter expects two inputs: the first is an initial level set and the second input is a feature image. The initial level set is computed by a Fast Marching Filter. A set of user-provided seeds is passed to a Fast Marching Image Filter in order to compute a distance map. A constant value is subtracted from this map in order to obtain a level set in which the zero set represents the initial contour. This level set as well the output of the Bayesian classifier are passed as inputs to the Geodesic Active Contour Level Set Image Filter. Finally, the level set generated by the Geodesic Active Contour Filter is passed to a Binary Threshold Image Filter in order to produce a binary mask representing the segmented object. For the Geodesic Active Contour Filter, several scaling parameters are used to trade off between the propagation (inflation), the curvature (smoothing) and the advection terms.

Microsoft's .NET technology and C++, C# language on Windows XP platform have been chosen to implement the methodology described above. MergeCOM3 toolkit from Merge-eMed has been used to load DICOM datasets[4]. ITK has been used for low-level image processing tasks[5]

4. Results

As explained in the methodology section, we run two different unsupervised learning algorithms to compute density functions of three groups of voxels (blood-filled regions, myocardium and lung). The training data for K-

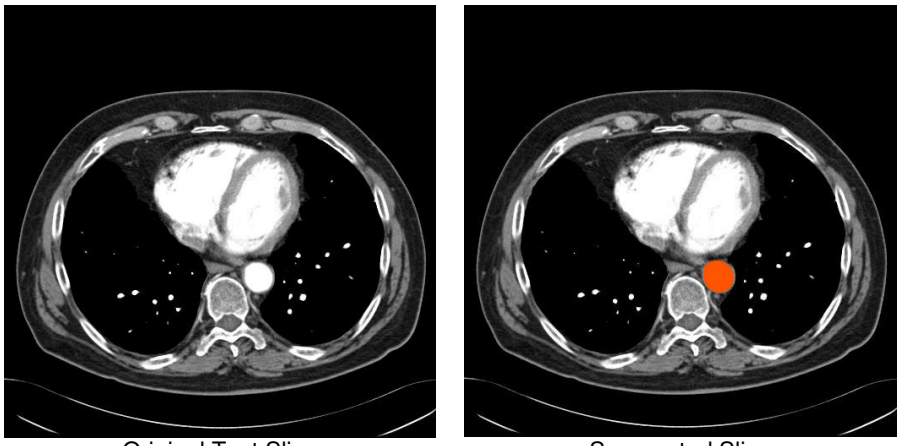
means and EM is a CT volume of Heart acquired with contrast agent from a single patient. There are 20 slices in the volume; each slice is 512 by 512. Each pixel is represented by 16 bits. A Modality Lookup transformation was applied to the original voxel data to convert them to Hounsfield Unit.

We found that both K-means and EM are dependent on the order in which the training image slices are presented, as well as on initialization points. We also found that as the bone (including rib-cages) voxels have a very similar intensity profile as that of blood-filled regions, both EM and K-Means usually cluster bones and blood-filled regions under one cluster.

For this application, we ended up using the density function results from EM as the k-means algorithm implicitly assumes that the data points in each cluster are spherically distributed around the center. Less restrictively, the EM algorithm assumes that the data points in each cluster have a multidimensional Gaussian distribution with a covariance matrix that may or may not be fixed, or shared. We run EM using different initial values and then used average means and standard deviations for three classes as inputs to the Bayesian Classifier. The final mean and variance for all the three density functions computed by EM are mentioned below (in Hounsfield unit):

	Mean	**Variance**
Myocardium	-50.25	14602.30
Lung	-896.22	6756.84
Blood-Filled Region	341.72	24304.81

The Bayesian Classification and geodesic active contour parts of the algorithm were executed online. We tested this part on a 3D CT data set of cardiac images. The images were acquired using a Siemens scanner with a slice spacing of 1 mm and an in-plane resolution of 0.742 mm. For the purpose of establishing ground-truth we manually identified the contour as well as marked all the pixels belonging to the descending aorta on each of the test slices. Because we applied the geodesic active contour to a binary volume, we found that the overall processing time for each slice is quite reasonable (~55 seconds). Below is an example of a single test slice and its corresponding segmentation result.



Original Test Slice Segmented Slice

Figure 3: Example of Segmented Slice

Several problems were discovered during the implementation of the geodesic active contour algorithm.

- We found that the Fast Marching filter is highly susceptible to the initial seed point as well as to the distance parameter used to specify distance from the seed point to the input level set. In the beginning we supplied only a single seed point (roughly at the center slice in the descending aorta) whose distance from the input level set contour was set to 5.0. With those parameters, we found that the algorithm provides best sensitivity at that center slice, but the sensitivity gradually decreases as we move away from the center to the two extreme ends of the aorta. To improve the overall sensitivity of the algorithm, we initialized the Fast Marching Level Set algorithm with multiple equidistant seed points in the volume. A distance of 15.0 was used for each one of the seed points. Below is a graph for the improved sensitivity plotted against slice position for a test volume of 20 slices.

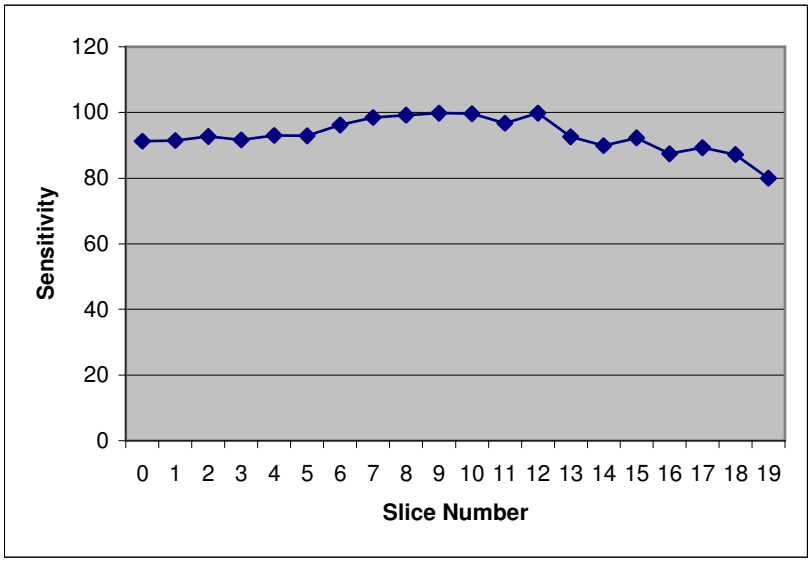


Figure 4: Sensitivity for each slice in the test data set

- We also found that the propagating surface leaks into the coronary artery, at the location where the left main (LM) coronary artery bifurcates from the aorta. We had to prevent this leakage by adjusting the weight between the curvature and the inflationary constant. One could also cut the linking sites of the left main coronary artery and the aorta in a few slices of the data where the linkage exists, and evolve the surface solely inside the descending aorta, however this technique necessitates manual intervention.

5. Conclusions and Future Work

We proposed a novel approach to segmenting and reconstructing the human descending aorta using machine learning. This method was tested on a data set of cardiac CT images. The application of our method results in a reconstructed geometric model of the descending aorta, which provides an improved comprehensive view of the vessels. This could potentially assist clinicians in achieving more accurate clinical diagnoses of atherosclerotic diseases in the descending aorta. Future work would involve the following items:

- Currently the user supplies the initial seed points for the Fast Marching Filter. We would like to automate the seed point selection process.
- For the Geodesic Active Contour Level Set Filter, currently the scaling parameters are found out by trial and error. In future we would like to learn these parameters by applying an appropriate machine-learning algorithm.
- We would like to test the overall algorithm for larger test datasets
- We would like to measure clinically significant parameters from the descending aorta model, such as the centerline and diameters of vessels.

6. References

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