

Questions and Answers

Chapter 9

Questions

- (Q1) *What is arterial remodeling? (Lancet, Vol. 353, pp. SII5–SII9, 1999)*
- (Q2) *What are the main challenges in lumen quantification process?*
- (Q3) *Discuss the three types of algorithms used in this chapter for lumen estimation?*
- (Q4) *What brings the low error and why?*
- (Q5) *Compare the error performance using three different systems?*

Answers

- (A1) Fuster *et al.* discussed the biological events that lead to acute coronary syndromes (ACS). Plaques of types IV and V (vulnerable) and type VI (complicated) were most likely lead to ACS. The beginning of an atherosclerotic lesion began with lipoprotein transport and development of the extracellular matrix. The disruption of plaques was made up of passive and active phenomenon. Inflammatory cells at the plaque site would weaken the fibrous cap through lytic processes, which was a step in arterial remodeling. Tissue factor (TF) was associated with *macrophages* and was involved in *coagulation, haemostasis, and thrombosis*. It was recognized that MRI is a promising tool for noninvasive plaque characterization.

(A2) Following are the challenges for lumen wall (inner) and vessel wall (outer) estimation processes:

- (a) *Multiple classes in the lumen region*: The lumen region consists of multiple classes. Core class (central part of the lumen), adjoining class (due to slow moving blood flow) and some times border pixels in the fibrous cap region giving different class. So, the lumen region can be C1, C1 + C2, and C1 + C2 + C3 class regions.
- (b) *Lumen shape variation*: The shape of the crosssection of the artery lumen is “circular” for some slices and near the bifurcation; it is “elliptical”. So, the ROI can change from slice to slice also. If one is taking the elliptical region to be circular, then large number of pixels will be missed along the major axis of the elliptical region. The elliptical region can be seen on slices before the bifurcation zone, while the circular regions can be seen on slices far from the bifurcation zone.
- (c) *Over-shooting of the human tracings*: Another difficult which can bring large error is when the human trace tracing the ideal boundary over shoots the lumen region and draws in the vessel wall area or even outer of vessel wall area. This “overshoot” tracing can bring large error between the computer estimated boundary and “ideal boundary.”
- (d) *Bleeding region of the lumen*: The bleeding issue is a serious problem. Sometimes lumen class C1 or C2 or C3 are not isolated. These class regions tunnel into the neighboring region and bleed, creating break in the wall boundary or bring missing boundary region.
- (e) *Partial volume effect*: The partial volume effect in the edge of the lumen can lead to misleading lumen wall boundary estimation.

(A3) **MRF**: Recently,¹ Suri developed the regional scale-space technique for segmentation of vessels in 2-D MIP images. The algorithm consisted of running the pixel classification approach using Markov random field with mean field (see Zhang, *IEEE Trans. Signal Process.*, Vol. 40, 1992). Here, the image segmentation was posed as a classification problem where each

¹Other examples of the fusion of region with boundary-based approaches are given by Suri (Int. Conf. in Appl. in Pattern Recogn. (ICAPR), Rio de Janeiro, Brazil, March 11–14, 2001).

pixel is assigned to one of K image classes. Suppose the input image was $\mathbf{y} = \{\mathbf{y}_{i,j}, (i, j) \in \mathbf{L}\}$, where $\mathbf{y}_{i,j}$ is a pixel, i.e. a 3-D vector, and \mathbf{L} was a square lattice. Denote the segmentation as $\mathbf{z} = \{\mathbf{z}_{i,j}, (i, j) \in \mathbf{L}\}$. Here, $\mathbf{z}_{i,j}$ is a binary *indicator vector* of dimension K , with only one component being 1 and the others being 0. For example, when $K = 3$, $\mathbf{z}_{i,j} = [0, 1, 0]^T$ means we assign the pixel at (i, j) to class 2.

Using the notation introduced above, the segmentation problem can be formulated as the following MAP (maximum a posteriori) inference problem:

$$\hat{\mathbf{z}} = \arg \max_{\mathbf{z}} [\log p(\mathbf{y}|\mathbf{z}, \Phi) + \log p(\mathbf{z}|\Theta)], \quad (1)$$

where Φ and Θ were model parameters. In this work, we assume that the pixels in \mathbf{y} are conditionally independent given \mathbf{z} , i.e.,

$$\log p(\mathbf{y}|\mathbf{z}, \Phi) = \sum_{i,j} \log p(\mathbf{y}_{i,j}|\mathbf{z}_{i,j}, \Phi). \quad (2)$$

Furthermore, we assume that conditioned on $\mathbf{z}_{i,j}$, the pixel $\mathbf{y}_{i,j}$ has a multivariate Gaussian density, i.e., for $k = 1, 2, \dots, K$,

$$p(\mathbf{y}_{i,j}|\mathbf{z}_{i,j} = \mathbf{e}_k, \Phi) = \frac{e^{-\frac{1}{2}(\mathbf{y}_{i,j} - \mathbf{m}_k)^T \mathbf{C}_k^{-1} (\mathbf{y}_{i,j} - \mathbf{m}_k)}}{(2\pi)^{3/2} |\mathbf{C}_k|^{1/2}}, \quad (3)$$

where \mathbf{e}_k was a K -dimensional binary indicator vector with the k th component being 1. From this, $\Phi = \{\mathbf{m}_k, \mathbf{C}_k\}_{k=1}^K$ contained the mean vectors and covariance matrices for the K image classes. For \mathbf{z} , we have adopted an MRF model with a Gibbs' distribution (Zhang, *IEEE Trans. Signal Process.*, Vol. 40, 1992):

$$p(\mathbf{z}|\Theta) = \frac{1}{Z} e^{-\beta E(\mathbf{z})}, \quad (4)$$

where

$$E(\mathbf{z}) = \frac{1}{2} \sum_{i,j} \sum_{(k,l) \in \mathbf{N}_{i,j}} (1 - 2\mathbf{z}_{i,j}^t \mathbf{z}_{k,l}) \quad (5)$$

is the energy function which decreased (causing $p(\mathbf{z}|\Theta)$ to increase) when neighboring pixels were classified into the same class (the set of the neighbors of (i, j) is denoted as $\mathbf{N}_{i,j}$).

Since Θ was generally not sensitive to particular images, it was set manually here. Φ , on the other hand, was directly dependent on the input

image and hence had to be estimated during the segmentation process. In this work, as in (Zhang, *IEEE Trans. Signal Process.*, Vol. 40, 1992), this was achieved by using the EM algorithm (Dempster *et al.*, *J. R. Stat. Soc.*, Vol. 39, pp. 1–37, 1977), which amounts to iterating between the following two steps:

(1) *E-step*: Compute:

$$Q(\Phi|\hat{\Phi}^{(p)}) = \langle \log p(\mathbf{y}|\mathbf{z}, \Phi) + \log p(\mathbf{z}|\Theta)|\mathbf{y}, \hat{\Phi}^{(p)} \rangle.$$

(2) *M-step*: Update parameter estimate:

$$\Phi^{(p+1)} = \arg \max_{\Phi} Q(\Phi|\Phi^{(p)}).$$

Here, $\langle \cdot \rangle$ represented the expectation, or mean, and the superscript p denoted the p th iteration. This translated into the following formulas for updating the parameter estimates:

$$\langle \mathbf{z}_{i,j}^{(p)} \rangle = \sum_{\mathbf{z}_{i,j}} \mathbf{z}_{i,j} f(\mathbf{z}_{i,j}) \quad (6)$$

$$\begin{aligned} \hat{\mathbf{m}}_k^{(p+1)} &= \frac{\sum_{i,j} \langle \mathbf{z}_{i,jk}^{(p)} \rangle \mathbf{y}_{i,j}}{\sum_{i,j} \langle \mathbf{z}_{i,jk}^{(p)} \rangle}, \\ \hat{\mathbf{C}}_k^{(p+1)} &= \frac{\sum_{i,j} \langle \mathbf{z}_{i,jk}^{(p)} \rangle [\mathbf{y}_{i,j} - \hat{\mathbf{m}}_k^{(p+1)}][\mathbf{y}_{i,j} - \hat{\mathbf{m}}_k^{(p+1)}]^T}{\sum_{i,j} \langle \mathbf{z}_{i,jk}^{(p)} \rangle}, \end{aligned} \quad (7)$$

where $k = 1, 2, \dots, K$, $\mathbf{z}_{i,jk}$ was the k th component of $\mathbf{z}_{i,j}$, and $f(\mathbf{z}_{i,j})$ was a “mean field” probability distribution (see Zhang, *IEEE Trans. Signal Process.*, Vol. 40, 1992).

These formulas, in addition to providing the estimate of Φ , also produced a segmentation. Specifically, at each iteration, $\langle \mathbf{z}_{i,jk}^{(p)} \rangle$ was interpreted as the probability that $\mathbf{y}_{i,j}$ was assigned to class k . Hence, after a sufficient number of iterations, we can obtain the segmentation \mathbf{z} for each $(i, j) \in \mathbf{L}$ by

$$\mathbf{z}_{i,j} = \mathbf{e}_{k_0}, \quad \text{if } k_0 = \arg \max_{1 \leq k \leq K} \langle \mathbf{z}_{i,jk}^{(p)} \rangle. \quad (8)$$

In this way, the EM procedure described above generated the segmentation as a by-product and therefore provided an alternative to the MAP solution of Eq. (1). For those interested in the application of MRF in medical imaging, see Kapur (Ph.D. Thesis, Artificial Intelligence Laboratory, MIT, Cambridge, MA, 1999), who recently developed a brain segmentation

technique which was an extension to the EM work of Wells *et al.* (*IEEE Trans. Med. Imag.*, Vol. 15, pp. 429–442, 1992) by adding the Gibbs' model to the spatial structure of the tissues in conjunction with a mean-field (MF) solution technique, called Markov random field (MRF) technique (for details on MRF, see Li (*Markov Random Field Modeling in Computer Vision*, Springer Verlag, 1995) and Geman *et al.* (*IEEE Trans. Pattern Anal. Mach. Intell.*, Vol. 6, pp. 721–741, 1984)). Thus the technique was named expectation maximization–mean field (EM-MF) technique. By Gibbs' modeling of the homogeneity of the tissue, resistance to thermal noise in the images was obtained. The image data and intensity correction were coupled by an external field to an Ising-like tissue model, and the MF equations were used to obtain posterior estimates of tissue probabilities. This method was more general to the EM-based method and is computationally simple and an inexpensive relaxation-like update. Other work in the area of MRF for brain segmentation can be seen by Held *et al.* (*IEEE Trans. Med. Imag.*, Vol. 16, pp. 878–887, 1998).

FCM: In this step, we classified each pixel. Usually, the classification algorithm expects one to know how many classes (roughly) the image would have. The number of classes in the image would be the same as the number of tissue types. A pixel could belong to more than one class, and therefore we used the fuzzy membership function to associate with each pixel in the image. There are several algorithms used to compute membership functions, and one of the most efficient ones is Fuzzy C mean (FCM) based on the clustering technique. Because of its ease of implementation for spectral data, it is preferred over other pixel classification techniques. Mathematically, we expressed the FCM algorithm below but for complete details, readers are advised to see Bezdek *et al.* (*Med. Phys.*, Vol. 20, pp. 1033–1048, 1993) and Hall *et al.* (*IEEE Trans. Neural Networks*, Vol. 3, pp. 672–682, 1992). The FCM algorithm computed the measure of membership termed as the *fuzzy membership function*. Suppose the observed pixel intensities in a multispectral image at a pixel location j was given as

$$\mathbf{y}_j = [y_{j1} \ y_{j2} \ \dots \ y_{jN}]^T, \quad (9)$$

where j takes the pixel location, and N is the total number of pixels in the data set. In FCM, the algorithm iterates between computing the *fuzzy membership function* and the centroid of each class. This membership

function is the pixel location for each class (tissue type), and the value of the membership function lies between the range of 0 and 1. This membership function actually represents the degree of similarity between the pixel vector at a pixel location and the centroid of the class (tissue type); for example, if the membership function has a value close to 1, then the pixel at the pixel location is close to the centroid of the pixel vector for that particular class. The algorithm can be presented in the following four steps. If $u_{jk}^{(p)}$ is the membership value at location j for class k at iteration p , then $\sum_{k=1}^3 u_{jk} = 1$. As defined before, \mathbf{y}_j is the observed pixel vector at location j and $\mathbf{v}_k^{(p)}$ is the centroid of class k at iteration p , thus, the FCM steps for computing the fuzzy membership values are

- i. Choose the number of classes (K) and the error threshold ϵ_{th} , and set the initial guess for the centroids $\mathbf{v}_k^{(0)}$ where the iteration number $p = 0$.
- ii. Compute the fuzzy membership function, given by the equation

$$u_{jk}^{(p)} = \frac{\|\mathbf{y}_j - \mathbf{v}_k^{(p)}\|^{-2}}{\sum_{l=1}^K \|\mathbf{y}_j - \mathbf{v}_l^{(p)}\|^{-2}} \quad (10)$$

where $j = 1, \dots, M$ and $k = 1, \dots, K$.

- iii. Compute the new centroids, using the equation

$$\mathbf{v}^{(p+1)} = \frac{\sum_{j=1}^N (u_{jk}^{(p)})^2 \mathbf{y}_j}{\sum_{j=1}^N (u_{jk}^{(p)})^2}. \quad (11)$$

- iv. Convergence was checked by computing the error between the previous and current centroids ($\|\mathbf{v}^{(p+1)} - \mathbf{v}^{(p)}\|$). If the algorithm had converged, an exit would be required; otherwise, one would increment p and go to step 2 for computing the fuzzy membership function again. The output of the FCM algorithm was K sets of fuzzy membership functions. We were interested in the membership value at each pixel for each class. Thus, if there were K classes, then we threw out K number of images and K number of matrices for the membership functions to be used in computing the final speed terms.

GSM The graph segmentation method (GSM) segments an image by treating it as a graph $G = (V, E)$ where V the set of vertices are the pixels and E the set of edges are pairs of pixels. Using a weight function $w(e)$, where

e is an edge (v_i, v_j) , the weights of the edges are computed and the edges are sorted by weight in a non-decreasing order. Initially, each pixel v_i is segmented into its own component C_i .

For each edge (v_i, v_j) in the list, a decision criterion D is applied and a decision is made whether or not to merge the components C_i and C_j . After this decision is made on each edge in the list, the result is a list of the final components of the segmented image.

The input image is first smoothed by a given smoothing parameter σ . Input constant k determines the size preference of the components by changing the *threshold function* $\tau(C)$.

The decision criteria D is a comparison between the *difference* between components C_i and C_j and the *minimum internal difference* among C_i and C_j . The difference between two components is defined as the minimum weight of the edges that connect the two components:

$$Dif(C_i, C_j) = \min_{v_i \in C_i, v_j \in C_j, (v_i, v_j) \in E} w((v_i, v_j)). \quad (12)$$

The minimum internal difference among two components C_i and C_j is defined as the minimum of the sum of the *internal difference* and the threshold function of each component:

$$MInt(C_i, C_j) = \min(Int(C_i) + \tau(C_i), Int(C_j) + \tau(C_j)), \quad (13)$$

where the internal difference $Int(C)$ of a component C is defined as the maximum weight in the minimum spanning tree $MST(C, E)$ of the component:

$$Int(C) = \max_{e \in MST(C, E)} w(e), \quad (14)$$

and where the threshold function $\tau(C)$ is defined as

$$\tau(C) = \frac{k}{|C|}, \quad (15)$$

where k is the input constant and $|C|$ is the size of the component C .

If the difference between the two components is greater than the minimum internal difference among the two components, then the two components are not merged. Otherwise, the two components are merged into one component.

- (A4) The low error is achieved when the ROI is changed from circular to elliptical in shape. The equations used for rotation of the ellipse about its center with an angle α is given by the new coordinates in Eq. (16)

$$x'_i = (x_i - x_0) \cos(\alpha) - (y_i - y_0) \sin(\alpha) \quad (16)$$

$$y'_i = (x_i - x_0) \sin(\alpha) + (y_i - y_0) \cos(\alpha) \quad (17)$$

- (A5) We ran the system using each of the three different classifying methods on real patient data. Ground truth boundaries of the walls of the carotid artery were traced for 15 patients. Overall the number of boundary points was roughly 22,500 points. A pixel was equivalent to 0.25 mm. Using MRF, the average error was **0.61** pixels; using FCM, the average error was **0.62** pixels; using GSM, the average error was **0.74** pixels.