Available Online at www.ijcsmc.com

International Journal of Computer Science and Mobile Computing

A Monthly Journal of Computer Science and Information Technology

ISSN 2320–088X

IJCSMC, Vol. 2, Issue. 7, July 2013, pg.356 – 364

RESEARCH ARTICLE

METHODS FOR SEGMENTATION OF IVUS ATHEROSCLEROSIS IMAGES

R. Ravindraiah[1], K. Tejaswini[2]
[1]Assistant professor, Dept. of ECE, Madanapalle Institute of Technology & Science, Andhra Pradesh, India
[2]Student, Dept. of ECE, Madanapalle Institute of Technology & Science, Andhra Pradesh, India
[1] ravindra.ranga@gmail.com; [2] tejaswini4b7@gmail.com

Abstract----- ***Segmentation is an important aspect of medical image processing. Segmentation of coronary arteries of atherosclerosis is one important process prior to many analyses and visualization tasks for intravascular ultrasound (IVUS) images. It is also helpful in the finding of the disease and its progressive treatment. Different methods are used for medical image segmentation such as Clustering methods, Thresholding method, Classifier, Region Growing, Deformable Model, Markov Random Model etc. The main purpose of this survey is to provide a comprehensive reference source for the researchers involved in Expectation-Maximization based medical image processing. There are different types of Expectation-Maximization algorithms for medical image. Their advantages and disadvantages are discussed.***

Keywords----- Medical Imaging; Segmentation; Expectation-Maximization

INTRODUCTION

Image segmentation is an effort to classify similar colors of image in the same group. It clusters colors into several groups based on the closeness of color intensities inside an image. The objective of the image segmentation is to extract the dominant colors. The image segmentation is very important to simplify an information extraction from images, such as color, texture, shape, and structure. The applications of image segmentation are diversely in many fields such as image compression, image retrieval, object detection, image enhancement, and medical image processing. Several approaches have been already introduced for image segmentation. Here we used different algorithms based on Expectation Maximization. Image segmentation can also use for analysis of the image and further pre-processing of the image. After a segmentation process each phase of image treated differently. Now we are going through about medical images like Ultrasound Images (US) which is widely used today.

Atherosclerosis (or arteriosclerotic vascular disease) is a condition where the arteries become narrowed and hardened due to an excessive buildup of plaque around the artery wall. The disease disrupts the flow of blood around the body, posing serious cardiovascular complications like heart attack or stroke. The following figure 1 shows a normal elastic artery. The walls of arteries (endothelium) are composed of three concentric zones: Tunica adventitia (outer), tunica media (middle), and tunica intima (inner layer).

© 2013, IJCSMC All Rights Reserved

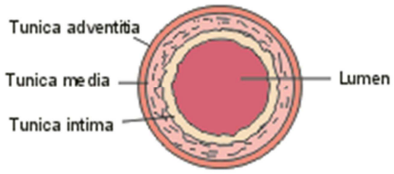

Figure 1: Cross section of coronary artery

ATHERSCLEROSIS IMAGING TECHNICQUES

Raman Spectroscopy:

Spectroscopy is an optical technique which uses the reflected light from the plaques to determine the chemical composition of the tissue. Different chemical compositions scatter different wavelengths (and energies) so each tissue, due to its chemical composition (lipid, collagen, calcium, etc.), has a unique pattern of light absorbance. To apply this property and detect the chemical composition, many approaches are under development. Raman spectroscopy collects light scattered by tissue when illuminated with high-energy laser. While most of this scattered light is at the same wavelength as the incident light, some are at different wavelengths. The amount of the wavelength shift which is called Raman shift depends on the characteristics of the molecule. Using this wavelength difference, Raman spectroscopy has a high molecular sensitivity but its tissue penetration is as low as 0.3 mm.

Thermography:

Thermography is a catheter-based technique which detects heat released by the cells of atherosclerotic plaques. Atherosclerosis is an inflammatory disease and any temperature difference in activated inflammatory cells may reflect and predict plaque disruption and thrombosis. The idea behind Thermography is the fact that vulnerable plaque is a very active metabolic area and higher temperature could be found, due to the heat released by activated macrophages either on the plaque surface or under a thin cap. While in many researches most atherosclerotic plaques showed higher temperatures compared to healthy vessel wall, the independent role of thermography is limited because the structural definition obtained from high resolution imaging techniques is required. The necessity of a proximal balloon to provide a blood-free field is one of the limitations of this new technique. Also, plaque temperature may be affected by inflammation and variable blood flow in the lumen making the results unreliable. Another limitation to this technique is being unable to provide information on eroded but non-inflamed lesions.

Intravascular Angioscopy:

Intracoronary angioscopy, as the first intravascular imaging device, is based on a fiber optic transmission of visible light. It facilitates direct visualization of the plaque surface, color of the luminal surface, presence of thrombus, and macroscopic features of the arterial wall. Angioscopy is able to detect vulnerable plaque features, such as ruptured caps and red discoloration (intra-plaque hemorrhage). Using this technique, the old thrombus or the normal appearance of the vessel surface is reflected as white. A red surface may indicates a fibrin or erythrocyte-rich thrombus and lipid-rich core and the thin fibrous cap is yellow in color. These yellow plaques are not detectable by angiography. However, this technique has several drawbacks, one being the limited part of the vessel tree, angioscopy is able to investigate and that is due to the size of its device. One of the limitations of angioscopy is that the inability to examine the different layers within the arterial wall remains. Also, to make the visualization clear, the vessel has to be occluded and the remaining blood flushed away with saline.

Optical Coherence Tomography (OCT):

Optical coherence tomography (OCT) is a useful technique which can provide images with ultra-high resolution. It measures the intensity of reflected light and compares it with a reference. The reference is obtained by a mirror reflection on an arm. The mirror is dynamically translated in order to achieve cross correlation at incremental penetration depths in the tissue. The measured intensity represents backscattering at a corresponding depth [1]. OCT results in high resolution images for future diagnosis. The axial resolution of OCT is dependent on the bandwidth of the source or the range of wavelengths within the beam. Based on histology, the OCT image interpretation is as follows: A lipid pool generates decreased signal areas with poorly delineated borders, a fibro-calcific plaque which shows a sharply delineated region with a signal-poor interior and a fibrous

© 2013, IJCSMC All Rights Reserved

which plaque produces a homogenous signal rich lesion. It also provides useful information about structural details like thin caps or tissue proliferation [2].

Intravascular Ultrasound (IVUS):

Over the past few years, intravascular ultrasound (IVUS) technology has become very useful for studying atherosclerotic disease. IVUS is a catheter-based imaging technique providing real-time high-resolution images of the vessel wall and lumen. IVUS is useful in the evaluation of coronary disease due its characteristics. Sound waves bounce back with varying intensity and different time delays according to the density of the plaques they have encountered, and hence, grant the identification of plaque composition - fibrous, fibro - fatty, calcified or mixed (see figure 2). The time delay of reflected ultrasound waves is translated into spatial image information while, the intensity is converted to an intensity map encoded by a gray-scale. The displayed intensity for each target object is proportional to the amount of sound energy returned. Dense targets such as calcified plaques are bright white in the IVUS image and the least dense plaques such as the medical layer in the vessel appear black. The 2D image is then obtained from the variation of the angular position of the imaged line over 360 degrees. Its features are detected based on the echogenecity and the thickness of the vessel. Depending on the distance from the catheter the axial resolution is approximately 150 microns and the lateral is 300 microns.

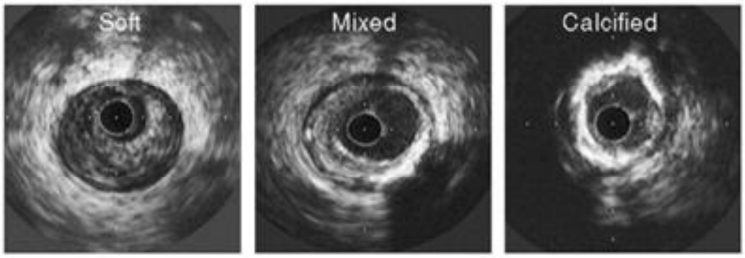

Figure 2: Soft, mixed fibrous and calcified and calcified plaques identified using IVUS images

Different types of Expectation-Maximization Algorithms

1. Expectation Maximization
2. Gaussian Mixer Model Expectation maximization
3. Diffused Expectation Maximization
4. Adaptive Distance Expectation Maximization
5. Multiresolution Diffused Expectation Maximization
6. Neighborhood Expectation Maximization
7. Variational Expectation Maximization
8. Structural Expectation Maximization
9. Semi-supervised Expectation Maximization

2. EXPECTATION-MAXIMIZATION (EM)

The EM (expectation-maximization) algorithm is an iterative approach to compute maximum-likelihood estimates when the observations are incomplete. Expectation Maximization (EM) is one of the most common algorithms used for density estimation of data points in an unsupervised setting. The expectation maximization (EM) algorithm introduced by Dempster (1977) for maximization likelihood functions with missing data. This algorithm is a popular tool for simplifying difficult maximum likelihood problems. It has two steps; in E-step we compute the expectation and in M-step the maximization of the last step is done and iteration EM-steps continue until convergence occur. The EM algorithm is used for the research of the parameter achieving the maximum likelihood. The criteria of stop of the algorithm, is either a maximum number of iterations to limit the time of calculation, either a lower mistake. It is put easily in application because it leans on the calculation of the complete data.

1. Initialize

$$\theta^{(0)} = (p_1^{(0)}, \ldots, p_k^{(0)}, m_1^{(0)}, \ldots, m_k^{(0)}, D_1^{(0)}, \ldots, D_k^{(0)}) \quad (1)$$

© 2013, IJCSMC All Rights Reserved

2. (E-step) Compute

$$P^{(r+1)}(i|x_s) = \frac{p_i^{(r)} N(x_s | m_i^{(r)}, D_i^{(r)})}{\sum_{i=1}^{k} p_i^{(r)} N(x_s | m_i^{(r)}, D_i^{(r)})} \quad (2)$$

3. (M-step) Compute

$$\hat{m}_i^{(r+1)} = \frac{\sum_{s=1}^{n} P^{(r+1)}(i|x_s) x_s}{\sum_{s=1}^{n} p^{(r+1)}(i|x_s)} \quad (3)$$

$$\hat{D}_i^{2(r+1)} = \frac{\sum_{s=1}^{n} P^{(r+1)}(i|x_s)(x_s - \hat{m}_i^{(r+1)})^2}{\sum_{s=1}^{n} P^{(r+1)}(i|x_s)} \quad (4)$$

$$\hat{p}_i^{(r+1)} = \frac{1}{n} \sum_{s=1}^{n} p^{(r+1)}(i|x_s) \quad (5)$$

4. Iterate steps 2 and 3 until convergence.

The drawback of EM is, it does not directly incorporate spatial modeling and can therefore be sensitive to noise and intensity in homogeneities.

2.1 GAUSSIAN MIXER MODEL EXPECTATION-MAXIMIZATION (GMM-EM)

The application of standard GMM (using a grey level as a single feature of pixel) yields a good segmentation of pixels inside regions and pixels of contours. However, it includes a bad clustering of noisy pixels of white region. This clustering drawback is essentially due to the only utilization of the intrinsic feature of pixel to be classified (gray level) without take into account the information relative to spatial position in the image. This information turns out to be important in the segmentation context. Image is a matrix within which each element is a pixel. The value of the pixel is a number that shows intensity or color of the image. Let X be a random variable that takes these values. For a probability model determination, we can suppose to have mixture of Gaussian distribution as the following form:

$$f(x) = \sum_{i=1}^{k} p_i N(x | \mu_i, \sigma_i^2) \quad (6)$$

Where k is the number of components or regions and $p_i > 0$ are weights such that $\sum_{i=1}^{k} p_i = 1$,

$$N(\mu_i, \sigma_i^2) = \frac{1}{\sigma\sqrt{2\pi}} \exp\left(\frac{-(x-\mu_i)^2}{2\sigma^2}\right) \quad (7)$$

Where μ_i, σ_i^2 are mean and standard deviation of class i. For a given image X, the lattice data are the values of pixels. However, the parameters are $= (p_1, \dots, p_k, \mu_1, \dots, \mu_k, \sigma_1^2, \dots, \sigma_k^2)$.

The application of the GMM segmentation algorithm can generate a good classification of the internal pixels to the regions as well as the noisy pixels, but produces a deterioration of the contours between the two regions. Of this study the advantage and the inconvenient of the use of the grey level and the spatial feature for the noise and the contours classification.

2.2 DIFFUSED EXPECTATION-MAXIMIZATION (DEM)

The DEM algorithm is different from previously proposed methods. Several methods have tried to incorporate within the EM algorithm a prior term in order to maximise a log posterior probability instead of log-likelihood, thus leading to quite complex EM steps [3]. Alternatively, Haker et al. [4] compute an initial posterior probability map, through some kind of classification (e.g., clustering), followed by anisotropic diffusion on such map in order to account for spatial constraints among sites; clearly, in this way final results strictly depend upon the goodness of the initial labeling. Here, we follow a different approach: we operate on the maximisation of the log-likelihood function, and spatial context is implicitly accounted for via label diffusion along maximisation. As a result we obtain a quite simple but effective segmentation algorithm, which can be easily interpreted in terms of a competition/cooperation scheme on the *k* label probability planes: the E and M steps implement a competition among the different labels at site *i*, while the D-step can be considered as a cooperation step among sites on the

© 2013, IJCSMC All Rights Reserved

same plane. Its flexibility makes it suitable for any type of application. The DEM algorithm generally uses to measure the similarity between an individual and a class given by its center, a distance that grants the same importance to the different attributes took in account in the process of classification. To introduce the adaptive effect as for the selection of the attributes, we propose to use a dynamic distance and weighted derivative of the Euclidian distance. This new distance is given by the equation:

$$D(xj, vj) = (1 - pj)(xj^{NG} - vj^{NG})^2 + pj(xj^{spatial} - vj^{spatial})^2 \quad (8)$$

D is a bi-dimensional distance based on the two NG and Spatial attributes. In this equation, the weight pj permits to control the importance of every attribute for the classification of the pixel xj. So if the pj is thigh we privileges the spatial attribute otherwise one privileges the gray level. The term pj must be calculated for every pixel to classify according to its spatial configuration in the image. , we can deduct that the weight $p_j$must be maximized (tender verse 1) when the pixel to classify is a PR or a PB, because the decision of its adherence to the different classes must be taken only on the basis of the spatial attribute. However this p_j must be minimized (tender verse 0) in case of a PC or a NNP because the gray level in these cases is going to constitute a good criteria of classification. Advantage of the DEM is the regions to be segmented usually resides at different scales. The drawback of DEM is for e.g. points in almost uniform regions have longer interaction range than those in weak texture, and, moreover such range depends on the scale on which the analysis is performed [5]. Then the problem arises on which is the optimal scale at which segmentation must be carried out: a low resolution might result in a too coarse segmentation, with different regions merged together, whereas a high resolution, on the contrary could result in many fragmented images and involves a heavy computational load.

2.3 ADAPTIVE DISTANCE EXPECTATION-MAXIMIZATION (ADEM)

The complementarity of the level of gray and the average of the gray levels with regard to the classification can let consider an use joined of these two describers in the image segmentation with the help of the EM method. In this section we present a new version of the EM baptized Adaptive Distance EM (ADEM) that enrolls in this direction. This version tried to take advantage of the advantages of the two aforesaid features while avoiding their inconveniences and this while using an adaptive manner one or the other according to the spatial configuration of the pixel to classify. In the setting of our work, we distinguished four possible spatial configurations for the pixels asking for each a specific choice of the criteria of classification. These configurations are the following:

- PR : Pixel which belongs to a region
- PC : Pixel which belongs to a contour,
- NP : Noisy pixel,
- NNP : Neighbour of Noisy Pixel.

Formally, the different spatial configurations are characterized by the two statistical descriptors presented as follows:
The standard deviation (σ) characterizes the dynamics of distribution around the pixel to be classified. This attribute is calculated as follows:

$$\sigma(xj) = \sqrt{\frac{1}{N}\sum_{k=1}^{N}\big(xk - \mu(xj)\big)^2} \quad (9)$$

The NCN: represents the closest neighbours number in term of grey level regarding the considered pixel. It's defined as follows:

$$\mathrm{NCN}(x_j) = \mathrm{card}\{x_p \in neighborhood(x_j) / |x_p - x_j| \square S\} \quad (10)$$

S designates a threshold which is generally chosen in year empiric manner. From thesis two descriptors we can characterize the different spatial configurations possible of the pixels. In case of a PR the standard deviation is generally low, it is null for the constant regions. However the becomes high for gthe PC, NP and NNP. The distinction between these three configurations is made by using the NCN feature, which is generally low for a NP, moderate for a PC and high for a NNP. The classification of a PR or a PB must privilege the spatial attribute because the decision must be taken on the basis of the information of its neighborhood. On the other hand the classification of a PC or a NCN must privilege the level of gray of the pixel (NG) respectively to preserve the contours and to avoid the influence of the noise. The choice of the criteria of classification as well

© 2013, IJCSMC All Rights Reserved

as the characterizations of the spatial configurations are summarized .The segmentation consists in delimiting the three cerebral structures: gray matter (MG), white matter (WM) and the cerebrospinal fluid (CSF).

2.4 MULTIRESOLUTION DIFFUSED EXPECTATION-MAXIMIZATION (MDEM)

MDEM is a novel scheme that results in a simple but effective segmentation algorithm for color images that: 1) retains the appealing characteristics of a feature clustering based approach; 2) takes into account spatial constraints while avoiding complex schemes such as MRFs; 3) it operates within a Multiresolution framework, in order to reliably define regions of interest and efficiently perform required computations.

The MDEM algorithm is different from previously proposed methods. For instance, different approaches have tried to incorporate within the EM algorithm a prior term in order to maximize a log-posterior probability instead of log-likelihood, thus leading to quite complex EM steps [5],[6]. On the other hand, Haker et al. [7], have suggested to compute an initial posterior probability map, through some kind of preliminary classification (e.g., clustering), followed by anisotropic diffusion performed on such initial map in order to diffuse spatial constraints among probability sites; clearly, in this way final results strictly depend upon the goodness of the initial labeling. Here, we follow a different approach: we operate on the maximization of the log-likelihood function, and spatial context is implicitly accounted for along maximization via diffusion. Further, in order to take advantage of the structure of the image as represented at different scales, this methods has been carried out in a multiscale framework, thus yielding an accurate segmentation, without unduly increasing the computational load.

Here it has been assumed *K* fixed, in that we are not concerned with the problem of model selection. In general, this problem could be tackled by resorting to BIC or Akaike's information criteria [8]. However, this may not be necessary for biomedical images, since, depending on the application, the value of *K* is often assumed to be provided by prior knowledge of the anatomy being considered.

As a result we obtain a simple iterative segmentation algorithm which can be easily interpreted in terms of a multiresolution competition/cooperation scheme: at each resolution level of the pyramid, the E and M steps can be seen as an individual site competition between the *k* different label planes, while the interleaved diffusion step can be considered as a cooperation step within sites on the same plane. With respect to the computational load, the whole algorithm is slightly slower than the EM procedure. Currently, it takes 30 seconds for a 256 *x* 256 2-D image, using an Intel P*IV* 3*:*4 GHz processor, equipped with 2 GHz RAM, under Windows XP operating system. Finally, simulations show that the method performs quite well on a variety of medical images either with respect to more standard methods or also techniques specifically designed for an application (for instance, our skin lesion segmentation results can be compared with examples provided by Xu et al. [9] and it is flexible enough to be used in a wide range of applications.

2.5 NEIGHBORHOOD EXPECTATION-MAXIMIZATION (NEM)

In order to incorporate the spatial dependence into the objects, a modified version of the conventional expectation maximization (EM) [10] algorithm has been proposed in [11]. In this approach, the maximum likelihood criterion is penalized by a term that quantifies the degree of spatial contiguity of the pixels supporting the respective components of the probability density function (pdf) model. The spatial structure of a given data set is defined by using matrix $W=(w_{jk})$:

$$(w_{jk}) = \begin{cases} 1 \text{ if } x_j \text{and} x_k \text{are neighbours and } j \neq k, \\ 0 \text{ otherwise.} \end{cases} \quad (11)$$

The following term is then used for regularizing the maximum likelihood criterion

$$G(c) = \frac{1}{2}\sum_{j=1}^{n}\sum_{i=1}^{n}\sum_{k=1}^{c} c_{ij}c_{ik}w_{jk} \quad (12)$$

Where c is the number of classes and c_{ij} is the probability that x_j belongs to class i.This term characterizes the homogeneity level of the partition. The more the classes contain adjacent elements, the greater this term is. The new criterion of the NEM algorithm is obtained by optimizing the weighted sum of two terms

$$U(c,\varphi) = D(c,\varphi) + \beta G(c) \ , \quad (13)$$

Where $D(c,\varphi)$ is the log-likelihood function of EM algorithm , $\beta > 0$ is a fixed coefficient. Details about NEM can be found in [9]. This algorithm is maximized to get the optimum results just as the same structure as the PersonNameProductIDEM algorithm. Successful EM algorithm. Successful results have been reported for image segmentation using this algorithm.

© 2013, IJCSMC All Rights Reserved

2.6 VARIATIONAL EXPECTATION-MAXIMIZATION (VEM)

In this paper we use a deterministic Bayesian approach such as the VEM algorithm. The number of mixture components is decided by using the Bayesian Information Criterion (BIC), which corresponds to the Minimum Description Length (MDL) [12].Integrating over the entire parameter space would amount to a very heavy computational task, involving multidimensional integration. Variational Bayes algorithm has been used for estimating hyperparameters of mixture models [2, 9]. In our approach we use the initialisation provided by the maximum log-likelihood as described in previous Section. The proposed algorithm is called variational expectation-maximization (VEM) algorithm.

The VEM algorithm is iterative and consists of two steps at each iteration: variational expectation (V-E) and variational maximization (V-M).

In the first step we compute the a posteriori probabilities, given the hidden variable distributions and their hyperparameters.

In the V-M step we find the hyperparameters that maximise the log-likelihood, given the observed data and their a posteriori probabilities.

In the V-E step we calculate the a posteriori probabilities for each data sample **x** j, depending on the hyperparameters:

$$\hat{p}(i|x_j) = \exp\left[\frac{-1}{2}\log|S_i| + \frac{1}{2}d\log 2 + \frac{1}{2}\sum_{k=1}^{d}\Psi\left(\frac{v_i+1-k}{2}\right) + \Psi(\lambda_i) - \Psi(\sum_{k=1}^{N}\lambda_k) - \frac{v_i}{2}(X_j - m_i)^T\beta_i s_i^{-1}(X_j - m_i) - \frac{d}{2\beta_i}\right] \quad (14)$$

In the V-M step we perform an intermediary calculation of the mean parameter as in the EM algorithm, but considering the a posteriori probabilities from (14):

$$v_k = \left\{X_j \,|\, k = \underset{i=1}{\overset{N}{\operatorname{argmax}}}\hat{P}(i \,|\, X_j)\right\} \quad (15)$$

where $\hat{P}(i \,|\, X_j)$ are the a posteriori probabilities obtained at the convergence of VEM algorithm. An important issue in colour image segmentation is the selection of an appropriate colour space and that of a representative set of colours. Image respresentation in the L*u*v* colour space has been found as appropriate to be modelled by Gaussian mixtures[13,14].

2.7 STRUCTURAL EXPECTATION-MAXIMIZATION (SEM)

We can also learn structure from incomplete data by applying the structural EM (SEM) algorithm of Friedman (1997) to our setting. We start with some initial graph structureG^0, initial parametersq^0, θ^0 , and dataset D. At each iteration, as with SEM for Bayesian networks, we choose between taking a step to update the parameters and taking a step to modify the structure.

Parameter Update Step: Run the EM algorithm, computing new expected sufficient statistics and updating the parameters as following equation

$$q_{z|u}^{k+1} = \frac{\bar{M}[x|u]}{\bar{T}[x|u]}; \quad \theta_{xx'|u}^{k+1} = \frac{\bar{M}[x,x'|u]}{\bar{M}[x|u]} \quad (16)$$

Structure Modification Step: Using the current parameterization and expected sufficient statistics, choose a structure modification that increases the score. SEM is used with a variety of scores, most commonly the BIC score or the Bayesian score with expected sufficient statistics as if real. In both cases, the score can be written in terms of expected sufficient statistics, allowing SEM to be used with our algorithm above. SEM leaves unspecified the issue of how many greedy search steps one takes before recomputing the expected sufficient statistics and parameters. Nodelman et al. (2003) showed that, for CTBNs, structure search for a fixed number of parents per node can be done in polynomial time. Thus, it is possible, in this setting, to find the globally optimal structure given the current parameterization in the structure modification step. If one does this, SEM for CTBNs becomes an iterated optimization algorithm with a full maximization step for both structure and parameters.

© 2013, IJCSMC All Rights Reserved

2.8 SEMI-SUPERVISED EXPECTATION-MAXIMIZATION

The iterations for the proposed semi-supervised algorithm are started using the update equations described in 1, 2 and 3. As it can be seen from the previous section, all the update equations have a supervised and an unsupervised part that are integrated in the same expressions.

E-step: Estimation of the Gaussian mode posteriors $p(x_i \mid y_j, \Theta_i)$ using the last maximisation step.

M-step: Update parameters μ, R and ρ using the posteriors estimated in the E step in expressions 1, 2 and 3.

The objective of the semi-supervised EM algorithm is to iteratively optimise the parameters. The process stops when the change for the log-likelihood between two consecutive steps is less than certain ϵ. The threshold value used is set as follows:

$$\epsilon = \frac{1}{100}\left(1 + D + \frac{(D+1)D}{2}\right)\log(ND) \tag{17}$$

Where N is the number of samples and D is the dimension of each sample.

REFERENCES

[1] P. Agostoni, J.A. Schaar, and P.W. Serruys. The challenge of vulnerable plaque detection in the cardiac catheterization laboratory. Cardiovascular Medicine, 7:349–358, 2004.

[2] J.A. Ambrose, S.L. Winters, R.R. Arora, A. Eng, A. Riccio, R. Gorlin, and V. Fuster. Angiographic evolution of coronary artery morphology in unstable angina. The American Journal of Cardiology, 7:472–478, 1986.

[3] SANJAY-GOPAL, S. and HEBERT, T.J.: 'Bayesian pixel classification using spatially variant finite mixtures and the Generalized EM algorithm', IEEE Trans. Image Proc., 1998, 7, pp.1014-1028

[4] HAKER, S., SAPIRO, G. and TANNENBAUM, A.: 'Knowledge-based segmentation of SAR data with learned priors', IEEE Trans. Image Proc., 2000, 9, pp.299-301

[5] G. Boccignone, M. Ferraro, An Information-theoretic Approach to Interactions in Images, Spatial Vision 12 (1999) 345-362.

[6] S. Sanjay-Gopal, T.J. Hebert, Bayesian pixel classification using spatially variant finite mixtures and the generalized EM algorithm, IEEE Trans. Image Proc. 7 (1998) 1014-1028.

[7] Y. Zhang, M. Brady, and S. Smith, Segmentation of Brain MR Images Through a Hidden Markov Random Field Model and the Expectation-Maximization Algorithm, IEEE Transactions on Medical Imaging 20(1) (2001) 45-57.

[8] S. Haker, G. Sapiro, A. Tannenbaum, Knowledge-based segmentation of SAR data with learned priors, IEEE Trans. Image Proc. 9 (2000) 299-301.

[9] D.J.C. MacKay, Information Theory, Inference, and Learning Algorithms, Cambridge University Press, UK, 2003.

[10] L. Xu, M. Jackowski, A. Goshtasby, D. Roseman, S. Bines ,C. Yu, A. Dhawan, A. Huntley, Segmentation of skin cancer images, Image and Vision Computing 17(1999) 65-74.

[11] Dempster, A.P.—Laird, N.M.—Rubin, D.B.: Maximum-Likelihood from Incomplete Data Via the EM Algorithm. J. Roy. Statist. Soc., Vol. B39, 1077, pp. 1–38.

[12] Ambroise, C.—Govaert, G.: Convergence of an EM-Type Algorithm for Spatial Clustering. Pattern Recognition Letters, Vol. 19, 1998, pp. 919–927.

[13] J. Rissanen. Stochastic Complexity in Statistical Inquiry. World Scientific, 1989.

[14] D. Comaniciu. An algorithm for data-driven bandwidth selection. IEEE Trans. On Pattern Analysis and Machine Intelligence, 25(2):281–288, 2003.

[15] Z.H. Zhang, C.B. Chen, J. Sun, and K.L. Chan. EM algorithms for Gaussian mixtures with split-and-merge operation. Pattern Recognition, 36(9):1973–1983, 2003.

© 2013, IJCSMC All Rights Reserved

Authors Bibliography

Mr. R. Ravindraiah received his B.Tech degree from G.Pullareddy Engineering College, Kurnool, India in 2008 and M.Tech from AITS, Rajampet, India in 2011. He is doing research work in Bio-Medical Image Processing and presented some papers in reputed journals, IEEE & ELSEVIER Conferences. His research work includes analysis and processing of images of pathologies like Atherosclerosis, Retinopathy and Leukemia. Currently he is the Assistant Professor in department of Electronics and Communication Engineering, Madanapalle institute of technology and science, Madanapalle. Under his guidance many UG and PG students have completed their projects.

Ms. K. Tejaswini received her B.Tech degree in Electronics and Communication Engineering from Mekapati Rajamohan Reddy Institute of Technolgy and Science, Udayagiri, India in 2011.Currently she is pursuing M.Tech degree Digital Electronics and Communication Systems in Madanapalle institute of technology and science, Madanapalle, India.

© 2013, IJCSMC All Rights Reserved