Bayesian Probability Maps For Evaluation Of Cardiac Ultrasound Data

Mattias Hansson¹, Sami Brandt¹,², and Petri Gudmundsson³

1 Center for Technological Studies, Malmö University, Sweden, mattias.hansson@mah.se.
2 Information Processing Laboratory, Oulu University, Finland.
3 Faculty of Health and Society, Malmö University, Sweden.

Abstract. In this paper we propose a Bayesian approach for describing the position distribution of the endocardium in cardiac ultrasound image sequences. The problem is formulated using a latent variable model, which represents the inside and outside of the endocardium, for which the posterior density is estimated. As the Rayleigh distribution has been previously shown to be a suitable model for blood and tissue in cardiac ultrasound image, we start our construction by assuming a Rayleigh mixture model and estimate its parameters by expectation maximization. The model is refined by incorporating priors for spatial and temporal smoothness, in the form of total variation, preferred shapes and position, by using the principal components and location distribution of manually segmented training shapes. The posterior density is sampled by a Gibbs method to estimate the expected latent variable image which we call the Bayesian Probability Map, since it describes the probability of pixels being classified as either heart tissue or within the endocardium. Our experiments showed promising results indicating the usefulness of the Bayesian Probability Maps for the clinician since, instead of producing a single segmenting curve, it highlights the uncertain areas and suggests possible segmentations.

1 Introduction

Echocardiography is more accessible, mobile and inexpensive compared to other imaging techniques and has become a widely used diagnostic method in cardiology in recent years. Unfortunately ultrasound images struggle with inherent problems which in large part stem from noise, and is often referred to as speckle contamination. Speckle is the result of interference between echoes, which are produced when the ultrasound beam is reflected from tissue, and has the properties of a random field, see [1, 2]. The use of the Rayleigh distribution in modeling model speckle in ultrasonic B-scan images is well-established through early works, such as [3, 1], and more recently [4].

There is much previous work done in the field of segmentation of cardiac ultrasound images, of which [5] provides an excellent overview. Here we will only mention those works which, like our algorithm, treat segmentation of blood and tissue as a pixel-classification or region-based problem. Our model makes a dependency assumption of neighboring pixels via total variation. A similar approach is employed in [6–10], where Markov random field (MRF) regularization is used. Like our model [7, 9–11]
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uses a Bayesian framework, although the construction of the posterior density function is different. Our approach uses priors on location and shape; of the forementioned, only [9] uses a shape prior. Also in [9] probabilistic pixel class prediction is used, which is reminiscent of the proposed Bayesian Probability Maps.

In this paper, we present a new method of determining the position of the endocardium in ultrasound sequences. This may be used for determining ejection fraction and assessment of regional wall abnormalities of the heart; measures used in diagnosis of ischaemic heart disease. The problem is formulated using a latent variable model, which represents the inside and outside of the endocardium. The method uses priors for spatial and temporal smoothness, in the form of total variation, preferred shapes and location, by using the principal components and location distribution of manually segmented training shapes. The main steps of the method are: 1) We assume a Rayleigh mixture model for the pixel intensities and estimate the parameters by expectation maximization. 2) The posterior distribution of the latent variables is sampled, using the estimated mixture parameters. 3) The mean of the posterior gives us the Bayesian probability map, which describes the position distribution of the endocardium. Instead of giving a single segmenting curve, the certainty of which may vary along the curve, our method provides a more versatile measure.

Our method shares some analogy with other region-based methods, but our approach of describing the position of the endocardium as the expected latent variable image and incorporating priors on location, shape and smoothness in space and time, is in its construction novel to our knowledge.

2 Model

Our goal is to determine the position of the endocardium in an ultrasound sequence. To accomplish this we represent the endocardium by the latent variable model with values one and zero for the inside and outside, respectively and estimate the posterior distribution of the latent variable model

\[ P(\mathbf{u}|\mathbf{z}, \theta) \propto p(\mathbf{z}|\mathbf{u}, \theta)P(\mathbf{u}|\theta) \]

(1)

where \( \mathbf{u} \) is the vector of latent variables, \( \mathbf{z} \) represent image intensities stacked into a single vector and \( \theta \) are parameters. The Rayleigh distribution has been reported to be an appropriate for modeling blood and tissue in cardiac ultrasound images, see [3, 1, 4]. Therefore to construct the likelihood \( p(\mathbf{z}|\mathbf{u}, \theta) \), we assume a Rayleigh mixture model for pixels intensities in the ultrasound images, as described in Section 2.1. In Section 2.2, we construct the prior distribution \( P(\mathbf{u}|\theta) \) by using prior knowledge such as temporal and spatial smoothness, shape and location.

2.1 Likelihood

We model the ultrasound data as a two component mixture model, one for the object intensities and zero for the background. Denoting the intensity value of pixel \( k \) in an ultrasound image by \( z_k \), we assume that

\[ p(z_k|\theta) = \alpha p_{\text{rayl}}(z_k|\sigma_1) + (1 - \alpha)p_{\text{rayl}}(z_k|\sigma_2), \]

(2)
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where \( \theta = \{ \alpha, \sigma_1, \sigma_2 \} \) are the mixture model parameters and 
\[ p_{\text{rayl}}(z|\sigma) = \frac{z}{\sigma} \exp(-\frac{z^2}{2\sigma^2}), \]
\( \sigma > 0 \) is the Rayleigh probability density function. Pixels are assumed to be independent in the mixture model. The likelihood is then defined as
\[
p(z|u, \theta) = \prod_j P(U_j \in \text{obj}|z_j, \sigma_1)^{u_j} P(U_j \in \text{backgr}|z_j, \sigma_2)^{1-u_j},
\]
where \( U_j \) and \( u_j \) are the random latent variable \( j \) and its realization, respectively, corresponding to \( z_j \) and 
\[ P(U_j \in \text{obj}|z_j, \theta) = \alpha p_{\text{rayl}}(z_j|\sigma_1)/(\alpha p_{\text{rayl}}(z_j|\sigma_1) + (1-\alpha)p_{\text{rayl}}(z_j|\sigma_2)) \] and 
\[ P(U_j \in \text{backgr}|\theta) = 1 - P(U_j \in \text{obj}|z_j, \theta). \]

2.2 Prior

Our prior model
\[
P(u|\theta) = P_B(u|\theta) P_{TV|B}(u|\theta) P_{\text{shape}|B, TV}(u|\theta) P_{\text{location}|B, TV, \text{shape}}(u|\theta)
\]
consists of four components, where each characterizes different kinds of properties preferred. The Bernoulli component \( P_B \) is the discrete latent variable distribution following from the Rayleigh mixture model. The total variation \( P_{TV|B} \) enforces spatial and temporal smoothness for latent variable images. Possible shape variations around the mean shape are characterized by trained eigenshapes of manually segmented images through \( P_{\text{shape}|B, TV} \). The sequence of ultrasound images is divided into subsequences, to take the temporal variations of the endocardium into account, and so for each part of the ultrasound sequence a corresponding set of eigenshapes and mean is used. The location prior \( P_{\text{location}|B, TV, \text{shape}} \) is constructed from the mean of the unregistered binary training shapes. The location prior describes the experimental probability value for each pixel location being either inside or outside of the endocardium, thus allowing only similar latent variable values as observed in the training data.

The Bernoulli prior is defined as
\[
P_B(u|\theta) = \prod_j \alpha^{u_j} (1-\alpha)^{1-u_j}
\]
and is thus a prior on the proportion of zeros and ones in \( u \) and \( j \in \{1, ..., N\} \), where \( N \) is the total number of latent variables in \( u \).

Let \( I_u(x; n) \) be a latent variable image, where \( x \) and its \( n \) are spatial and temporal coordinates, respectively. The total variation prior is then given by
\[
P_{TV|B}(u|\theta) \propto \exp\{-\lambda_{TV}||I_u(x; n) * h||_{L_1}\},
\]
where \( h \) is a three dimensional Laplacian kernel and \( * \) denotes convolution.

Let \( I_{u,r}(x; n) \) be the spatially registered latent variable image, corresponding to \( I_u(x; n) \), where the center of mass has been shifted to the origin; \( u^n_r \) and \( \bar{u}^n_r \) are the corresponding latent variable vectors. The shape prior is defined as
\[
P_{\text{shape}|B, TV}(u|\theta) \propto \prod_n \exp\{-\lambda_{\text{shape}}(u^n_r - \bar{u}^n_r)^T(C_n + \lambda_n I)^{-1}(u^n_r - \bar{u}^n_r)\},
\]
where $C_n$ represents the truncated covariance of the training shapes, whose center of mass has been shifted to the origin, and $\lambda_0 I$ is the Tikhonov regularizer [12]. The shape prior cannot strictly impose a shape which does not exist in the data, i.e. a shape which has a very low likelihood. However the shape prior can enhance structures which have low likelihood, which may be due to the effects of noise. The advantage of this is that structures which are e.g. tissue, will never be classified as endocardium.

The location prior is defined as

$$P_{\text{location}|\text{shape}, TV, B}(\mathbf{u}|\theta) \propto \begin{cases} 1 & \text{if } \frac{1}{\sum_j u_j} \sum_n \sum_x h (g \ast \bar{I}_{\text{train}}(x; n)) \bar{I}_{\text{u}}(x; n) = 1 \\ 0 & \text{otherwise} \end{cases} \quad (7)$$

where $\bar{I}_{\text{train}} = \frac{1}{K} \sum_k I_{\text{u}k}$ is the mean training image and $K$ is the number of training images. $g$ is a Gaussian kernel and $h$ is the step function s.t. $h(t) = 1$ for $t > 0$, otherwise $h(t) = 0$. This component has the effect that when sampling individual latent variables outside of the (smoothed) mean shape, the result of sampling will be that the latent variable is set to zero. Inside the (unregistered) mean shape the sampling is unaffected.

The three regularization parameters $\lambda_{TV}, \lambda_{\text{shape}}$ and $\lambda_0$ control the influence of the priors. Increasing $\lambda_{TV}$ makes the sample temporally and spatially smoother, while increasing $\lambda_{\text{shape}}$ makes the impact of the shape prior larger. Finally $\lambda_0$ controls the influence of the mean shape in the formation of the shape prior.

3 Algorithm

Our algorithm for generating Bayesian Probability Maps can be divided into three parts. First the mixture model parameters are estimated by the EM algorithm from our ultrasound data, as these parameters are needed to construct the posterior distribution of position of the endocardium. The posterior is then sampled by Gibbs sampling and the samples are used to compute the Bayesian probability map. The algorithm is summarized in Fig. 2.
3. ALGORITHM

Mixture Parameter Estimation → Sampling of the Posterior → Sample Mean → Bayesian Probability Map

3.1 Estimation of mixture model parameters

The complete data likelihood is represented according to the latent variable model as

\[ p(z, u|\theta) = \prod_j p_{\text{rayl}}(z_j|\sigma_1)^{u_j} p_{\text{rayl}}(z_j|\sigma_2)^{1-u_j}, \quad (8) \]

where \( z \) are the pixel intensity values and \( u = (u_1, \ldots, u_N) \) are interpreted as missing data, s.t \( u_j = 1 \) if \( x_j \) is inside the heart chamber, and otherwise \( u_j = 0 \). The mixture parameters \( \theta = \{\alpha, \sigma_1, \sigma_2\} \) are estimated by Expectation Maximization (EM) [13]. That is, on the E-step, we build the expected complete data loglikelihood, conditioned on the measured data and the previous parameter estimates, or

\[ \chi(\theta, \hat{\theta}^{(n-1)}) = E_{u|z,\hat{\theta}^{(n-1)}} \{ \log p(z, u|\theta) \} \]

\[ = \sum_{j=1}^{N} \left[ P(U_j \in \text{obj}|z_j, \hat{\theta}^{(n-1)}) \log p_{\text{rayl}}(z_j|\theta) + P(U_j \in \text{backgr}|z_j, \hat{\theta}^{(n-1)}) \log p_{\text{rayl}}(z_j|\theta) \right]. \quad (9) \]

On the M-step, the expected complete data loglikelihood is maximized to obtain an update for the parameters,

\[ \hat{\theta}^{(n)} = \arg\max_{\theta} \chi(\theta, \hat{\theta}^{(n-1)}) \quad (10) \]

and the steps are iterated until convergence.

3.2 Sampling of the Posterior

The sampling of the posterior (1) was performed by conventional Gibbs sampling [14, 15] i.e. drawing samples from

\[ P(u_j|u_1^{(i)}, \ldots, u_{j-1}^{(i)}, u_{j+1}^{(i-1)}, \ldots, u_N^{(i-1)}) \]

\[ = \left\{ P(u_j = k|u_1^{(i)}, \ldots, u_{j-1}^{(i)}, u_{j+1}^{(i-1)}, \ldots, u_N^{(i-1)}) \right\}_{k=0}^{1}, \quad j = 1, 2, \ldots, N. \quad (11) \]

After iteration the center of the heart is calculated, which determines the area of influence of the shape prior. \( I_{u_{\text{train}}} > 0.1 \) defines a region, which contains a large part of the endocardium, but without most of the blood present outside the endocardium. The center of mass of \( I_u(y; n) \) is calculated within this region and is used as an approximation of the center of the heart.
3.3 Sample Mean

To characterize the posterior distribution, we compute estimate conditional mean of the latent variable vector over the posterior

$$E\{u|z, \theta\} \approx \frac{1}{M} \sum_{i} u^{(i)} = \left(\hat{P}(U_k \in \text{obj})\right)_{k=1}^{N} \equiv \hat{u}_{CM}$$  

by the latent variable sample vectors $u^{(i)}$. By the strong law of large numbers $\hat{u}_{CM} \rightarrow E\{u|z, \theta\}$ when $n \rightarrow \infty$. The corresponding image $I_{\hat{u}_{CM}}$ represents the Bayesian probability map.

4 Experiments

4.1 Material

The ultrasound data used in this paper consists of cardiac cycles of two-chamber (2C) apical long-axis views of the heart. The sequences were obtained using the echocardiogram machines Philips Sonos 7500, Philips iE33 or GE Vivid 7, from consecutive adult patients referred to the echocardiography laboratory at the Department of Cardiology at Malmö University Hospital, Sweden, which has a primary catchment area of 250,000 inhabitants. Expert outlines of the endocardium in the sequences have been provided by the same hospital.

4.2 Initialization

We estimate mixture model parameters for pixels in our data lying within the non-zero region of the mean of all training images. This is a natural constraint since we do not sample latent variables outside this region. As an initial estimate of mixture model parameters we set $\alpha^{(0)}$ to the proportion of object pixels in the training images, and $\sigma_1$ and $\sigma_2$ are set to maximum likelihood estimate $\hat{\sigma} = \left(\frac{1}{2Q} \sum_{i=1}^{Q} x_i^2\right)^{\frac{1}{2}}$ of object and background pixels in the training data, where $Q$ is the number of pixels in the training set. Prior parameters $\lambda_{TV}$, $\lambda_{\text{shape}}$, $\lambda_0$ are set manually.

The Gibbs sampling algorithm is seeded by a sample obtained by Bayesian classification of the mean of the annotated images for each category of the heart cycle. The placement of these is determined by correlation of the sample, latent variable images, with masked log probability densities. Specifically, the position of $I_{\text{init}}(x; k)$, the initial latent variable image at time $k$, is determined by matching it and a masked log probability matrix $W$ by correlation. $W$ is the matrix resulting from termwise multiplication of the mask matrix $\bar{I}_{\text{train}}(x; n)$ and the probability matrix $p(Z_k|\sigma_1)$, which gives the object probability of each pixel $z_j$ in ultrasound image $Z_k$ in the sequence.

4.3 Evaluation

We divide our data into two sets: training set and validation set. The training set consists of 20 cardiac cycles. The training set is further divided into sets, corresponding to parts of the cardiac cycle. The validation set consists of 2 cardiac cycles.
5. CONCLUSION AND FUTURE WORK

As evaluation measure the expected misclassification $E_{mc}$ of a pixel, w.r.t the expert outline, is used. Let $I_{true}(x; n)$ be ground truth images corresponding to the data $z$. Then the expected misclassification of a pixel in the examined sequence is given by

$$E_{mc} = \frac{1}{N} \sum_n \sum_x (1 - I_{true}(x; n)) P(I_u(x; n) = 0) + I_{true}(x; n) P(I_u(x; n) = 1).$$

(13)

A low $E_{mc}$ guarantees that the Bayesian Probability Map is a true reflection of the entire heart cycle, not just a few selected images.

4.4 Results

In Figure (3) and (4) results from two validation sequences are displayed. Eight frames have been selected from each sequence, four from the systole and diastole phase of the cardiac cycle, respectively. Validation sequence A consists of 41 frames, and sequence B of 26.

The Bayesian Probability Map displayed, for both validation sequences, is formed from 50 samples. The probability map spans colors from red to blue with degree of probability of area being within the endocardium. Hence, red indicates the highest probability.

For sequence A we obtain $E_{mc} = 0.07$, while $E_{mc} = 0.11$ for sequence B. The higher expected misclassification for sequence B is clearly due to the fact that a large amount of blood is present outside the endocardium. However the probability map clearly captures the shape of the endocardium.

We compared our results with a Graph Cut method as described in [16–18]. We made this comparison since this method uses MRF, like [6, 7, 9–11]. In Figures (5) and (6) we observe that the Graph Cut method fails to identify the location as clearly as the proposed method.

5 Conclusion and future work

We have presented a novel approach to cardiac ultrasound segmentation, which consists of modeling the endocardium by latent variables. The latent variable distribution is then sampled which yields Bayesian Probability Map, which describes the location of the endocardium. In the future, we plan to introduce a connectivity prior for the latent variables, and to increase the sensitivity of categorization by refining the mixture model. Overall, the proposed Bayesian approach provides a framework into which such improvements can be easily incorporated and further evaluated. Furthermore we will introduce methods for optimizing the sampling process.
Fig. 3: Validation sequence A (41 frames). BPM with overlaid expert outline (white). Systole (A1-A4) and Diastole (A5-A8). $E_{mc}=0.07$, $\lambda_{TV}=0.75$, $\lambda_{shape}=38.5$, $\lambda_o=100$. 
5. CONCLUSION AND FUTURE WORK

Fig. 4: Validation sequences B (26 frames). BPM with overlaid expert outline (white). Systole (B1-B4) and Diastole (B5-B8). $E_{mc} = 0.11$, $\lambda_{TV} = 0.73$, $\lambda_{shape} = 40$, $\lambda_0 = 100$. 
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Fig. 5: Graph Cut (red) applied to Validation sequence A with expert outline (white). Systole (A1-A4) and Diastole (A5-A8).
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Fig. 6: Graph Cut (red) applied to Validation sequence A with expert outline (white). Systole (B1-B4) and Diastole (B5-B8).
5. CONCLUSION AND FUTURE WORK

References