CONVEX SPATIO-TEMPORAL SEGMENTATION OF THE ENDOCARDIUM IN ULTRASOUND DATA USING DISTRIBUTION AND SHAPE PRIORS

Mattias Hansson¹, Ketut Fundana¹, Sami S. Brandt² and Petri Gudmundsson³

¹ School of Technology, Malmö University, Sweden
² Laboratory of Computer Science and Engineering, Oulu University, Finland
³ Faculty of Health and Society, Malmö University, Sweden

ABSTRACT

We present a convex variational active contour model with shape priors, for spatio-temporal segmentation of the endocardium in 2D B-mode ultrasound sequences, which can be solved by Continuous Cuts. A four component (signal dropout, echocardiographic artifacts, blood and tissue) Rayleigh mixture model is proposed for modeling the inside and outside of the endocardium. The parameters of the mixture model are determined by Expectation Maximization, for the sequence. Annotated data is used to provide prior data, by which prior distributions for the inside and outside of the endocardium are constructed. Segmentation is then achieved by minimizing the Hellinger distance between prior and estimated distributions, under the constraints of a statistical shape prior built from principal eigenvectors of the annotated data. Since our model is convex, we can employ a fast optimization method: the Split-Bregman algorithm. Promising segmentation results and quantitative measures are provided.

Index Terms— Convex Segmentation, Continuous Cuts, Shape Prior, Distribution Prior, B-mode ultrasound, Endocardium, Rayleigh mixture model

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. However, ultrasound images suffer from speckle contamination, which is the result of interference between echoes, produced when the ultrasound beam is reflected from tissue. In addition to speckle, the presence of areas in the image where no echo is returned, so-called signal dropout, complicate segmentation. In this paper, we deal with the segmentation of the endocardium in B-mode ultrasound image sequences. Information about the location of the endocardial wall may be used for determining ejection fraction (by comparing systolic and diastolic volume) and assessment of regional wall abnormalities of the heart; measures used in diagnosis of ischaemic heart disease.

Dependent on the spacing in the image relative to the speckle size, different statistical models have been proposed to model the distribution of speckle in B-mode ultrasound images. These include Rician, pre-Rician K, and Generalized K-distribution, homodyned K-distribution and Rician Inverse of the Gaussian distribution, which are all highly complex distributions. Simpler distributions have been proposed, notably the Nakagami distribution, and the Rayleigh distribution, which is a special case of Nakagami. See [1] for an overview of proposed distributions for B-mode ultrasound images. Transformations, e.g. log-compression, are often used to construct B-mode images. Unless all parameters of the transformations are known, we cannot hope to reconstruct the signal. Because the exact construction of the B-mode image is often unknown, one has to model the B-mode data on a case-by-case basis. In this paper we have chosen to employ a Rayleigh mixture model for our B-mode data.

Inspired by the work of [2], we propose to use a segmentation model based on the Split-Bregman method. The segmentation model [2] consists of histogram/pdf competition, which works very well on images that have distinct distributions, an assumption mostly does not hold for ultrasound images. We therefore propose a segmentation model that consists of minimizing the distance between estimated and prior pdfs, estimated from annotated data. In [3] a prior histogram of the region of interest is used to perform segmentation, which is reminiscent of our method except we employ both estimated and training data in the construction of the prior pdfs.

An in depth overview of existing models for ultrasound segmentation is given in [1] and most recently in [4]. The models employing shape and distributional priors share the most analogy with our work, however, these models are non-convex, unlike the one proposed in this paper, and do not employ fast optimization algorithms like e.g. Split-Bregman.

Contributions: Our approach has the following novelties: the use of a convex active contour model in spatio-temporal cardiac segmentation using mixture modeling, the use of Split-Bregman optimization in this context and a novel shape prior formulation which preserves the convexity of the energy formulation.
2. THEORY

2.1. Mixture speckle model

In this paper we have chosen to employ the Rayleigh distribution to model the speckle in our ultrasound images. The Rayleigh probability density function is given by

\[ p_{\text{rayl}}(I|\sigma) = \frac{I}{\sigma} \exp\left(-\frac{I^2}{2\sigma^2}\right), \sigma > 0, \]

(1)

where \( I \) denotes intensity values. The inside and outside of the endocardium is modeled as a mixture of Rayleigh densities (to account for speckle), including a Dirac measure at zero (to account for signal dropout). Thus our proposed mixture model is defined as

\[ p(x|\alpha, \sigma) \propto \alpha_i \delta_0 + \sum_{i=2}^{n} \alpha_i p_{\text{rayl}}(x|\sigma_i) 1_{(x>0)}, \]

(2)

where \( \alpha_i > 0 \), s.t. \( \sum \alpha_i = 1 \), are the mixture weights, \( \delta_0 \) denotes the Dirac delta at zero, and \( 1 \) is the indicator function.

Empirically we have observed that the pixel intensities of ultrasound images can be divided into 4 categories: (1) signal dropout, (2) echocardiographic artifacts, (3) blood, and (4) tissue. Signal dropout implies no echo returned to the transducer, resulting in zero intensity. This may also be due to post-processing where very low intensities are quantized to zero. By artifacts we refer to areas with tissue-like intensity caused by chordae, papillary muscles, ribs or local increase in signal strength. The inside of the endocardium is assumed to consist of a mixture of categories (1), (2) and (3), while the outside is taken to be a mixture of the 4 categories.

Given an input sequence of \( N \) ultrasound images we wish to determine the mixing weights of each category on the inside and outside of the endocardium, respectively, denoted by \( \alpha_j^{\text{inp}} \) and \( \alpha_j^{\text{out}} \), \( j = 1, ..., 4 \). Let

\[ \alpha_j^{\text{inp}} = \alpha_j^{\text{out}} + \alpha_j^{\text{in}}, \]

(3)

where \( \alpha_j^{\text{inp}} \) is the weight, determined by Expectation Maximization (EM), for category \( j \) in the input sequence. We use annotated data to calculate \( \alpha_j^{\text{inp}}, j = 1, 2, 3 \). By assumption \( \alpha_j^{\text{in}} = 0 \). Let \( \alpha_j^{\text{inp}} \) be the fraction, estimated by EM, of category \( j \) on the inside of the endocardium of annotated sequence \( i \). Furthermore, let \( A_i^{\text{inp}} \) denote the number of pixels in annotated sequence \( i \), and \( A_i^{\text{in}} \) the number of pixels inside the endocardium in the same sequence. Then we get

\[ \alpha_j^{\text{in}} = \frac{1}{N} \sum_{i=1}^{N} \alpha_j^{\text{inp}} \frac{A_i^{\text{in}}}{A_i}, j = 1, ..., 3. \]

(4)

Finally \( \alpha_j^{\text{out}} \) is determined by (3).

2.2. Convex segmentation model with shape prior

Segmentation is achieved by minimizing the distance between the prior inside/outside distribution \( p_{\text{in}}/p_{\text{out}} \) and the corresponding estimated ones \( p_{\text{in}}/p_{\text{out}} \). The estimated pdf:s are given by Parzen’s window method [5],

\[ p_{\text{in}}(x, \chi_\Omega) = \frac{1}{|\Omega|} \int_D G_\sigma(x - I(y)) \chi_\Omega(y)dy, \]

\[ p_{\text{out}}(x, \chi_\Omega) = \frac{1}{|\Omega|} \int_D \chi_\Omega(y)dy, \]

(5)

where \( \Omega \) is the domain inside the segmenting contour, \( I(x) \) denotes image intensity at the point \( x \), \( \chi_\Omega \) is the characteristic function of the set \( \Omega \), and \( G_\sigma(x) = e^{-x^2/2\sigma^2} \) is defined similarly.

We use the Hellinger distance [6] to measure closeness between estimated and prior pdf:s, which has also been proposed in [3]. The symmetric Kullback-Leibler distance may also be used. The distance between the prior inside/outside distribution \( p_{\text{in}}/p_{\text{out}} \) and the corresponding Parzen estimated ones \( p_{\text{in}}/p_{\text{out}} \) is given by

\[ HL(\chi_\Omega, \chi(x)) = \int_{\mathbb{R}_+} \left( \sqrt{p_{\text{in}}(x)} - \sqrt{p_{\text{out}}(x, \chi_\Omega)} \right)^2 + \left( \sqrt{p_{\text{out}}(x)} - \sqrt{p_{\text{out}}(x, \chi_\Omega)} \right)^2 dx. \]

(6)

The energy functional consists of the Hellinger distance (6) and a boundary length term,

\[ E(\Omega) = \lambda HL + \mu \int_{\partial\Omega} ds, \]

(7)

where \( \Omega \) is a region in the sequence and \( \lambda, \mu > 0 \). We formulate the energy functional (7) as a convex minimization problem, by employing the methods of Chan, et. al. [7]. This approach is known as Continuous cuts. Following [2], to find the optimal region \( \Omega \) in the image domain \( \Omega_0 \), we solve the following convex minimization problem

\[ \min_{u \in [0,1]} \int_{\Omega_0} -\lambda V_{HL} u + \mu |\nabla u| dx, \]

(8)

where \( V_{HL} \) is the speed of the Hellinger distance (6) and \( |\nabla u| \) is the total variation of the function \( u \). In order to strengthen our segmentation functional we add a shape prior energy term to the convexified version of (7), similar to [8] although here a different formulation of shape prior is considered. Let \( \bar{u} \in [0,1]_{\Omega_0} \) be a shape prior. The shape prior energy is then

\[ E_{\text{shape}}(u) = \int_{\Omega_0} (1 - \bar{u}) u + (1 - u) \bar{u} dx = \int_{\Omega_0} (1 - 2\bar{u}) u dx. \]

(9)

The term \( \int_{\Omega_0} \bar{u} dx \) is constant w.r.t \( u \) and can thus be disregarded when minimizing over \( u \). Since \( \nabla E_{\text{shape}}(u) = 1 - 2\bar{u} \) we formulate the shape prior augmented version of (8) as

\[ \min_{u \in [0,1]} \left\{ \int_{\Omega_0} -\lambda (V_{HL} + \gamma (1 - 2\bar{u})) u + \mu |\nabla u| dx \right\}, \]

(10)
where $\gamma > 0$. Our shape prior term is integrated in such a way that the thresholding property, see [7], is upheld in (10). When solving (10) $\tilde{u}$ is kept fixed, and updated after finding a minimizer. Thus, finding the final segmentation $u$ consists of solving sequential minimization problems, with the prior $\tilde{u}$ being updated in between each of them.

In this paper we choose to employ binary maps using PCA to build our prior $u$, as first proposed in [9]. Let $X = \{x_1, \ldots, x_n\} \subset S$ be a set of transitionally registered binary training shapes where $S = \{0,1\}^m$ is our segmentation space, and $m$ is the length of shape vectors. The shapes are transitionally registered to a user-selected point. Furthermore, let $P = [P_1, \ldots, P_n]$ be the $n$ principal eigenvectors of the covariance matrix of $X$. A segmentation vector $u \in S$ is projected onto the feature space $F$ by $\phi(u) = P^T (u - \bar{x}) = y$, where $\bar{x}$ is the mean training shape. The shape prior $\tilde{u}$ is then obtained by reprojecting $y$ into $S$, i.e. $\tilde{u} = Py + \bar{x}$, and is the shape in the training set which is closest, under our assumptions, to our current segmentation $u$. See right column in Figure 1(c) and 1(d) for examples of $\tilde{u}$ corresponding to $u$.

3. IMPLEMENTATION AND RESULTS

Our algorithm for segmenting the endocardium in ultrasound sequences can be divided into three main parts. Firstly, mixture distribution parameters are estimated by the EM algorithm from the ultrasound sequence. Secondly, the estimated parameters are used to construct prior distributions for the inside and outside of the endocardium. In the final step, segmentation is achieved by minimizing the distance between the prior and online estimated pdf:s by a Continuous cut integrated with a statistical shape prior.

The ultrasound data used in this paper consists of cardiac cycles of two-chamber apical long-axis (LAX 2C) views of the heart, which were obtained using Philips Sonos 7500, Philips iE33 or GE Vivid 7, from consecutive adult patients referred to the echocardiography laboratory at Malmö University hospital in Sweden, which has a primary catchment area of 250,000 inhabitants. Expert segmentations of the endocardium have been provided by the same hospital. We divide our data, cardiac cycles from 25 distinct patients, into two sets: training set and validation set. The training set consists of 20 cardiac cycles. The training set is further divided into subsets, corresponding to parts of the cardiac cycle. The validation set consists of 5 cardiac cycles.

Training data from annotated ultrasound sequences is used both in constructing the prior distributions, and the statistical shape prior. The shape prior is transitionally registered to a user-selected point from an end-diastolic frame, which approximates the center of the endocardium, due to low chamber deformation at end-diastole.

The mixture parameters $\theta = \{\alpha_i, \sigma_i; i = 2,3,4\}$, corresponding to the categories (2) echocardiographic artifacts, (3) blood, and (4) tissue, are estimated by Expectation Maximization (EM) [10]. The mixture weight for signal dropout $\alpha_1$ is readily computed without EM, this is simply the proportion of zero intensity values in the sequence. In practice, we substitute the signal dropout intensities with random samples from the blood category, since regions of blood intensity return the least echo and are most subject to dropout.

We apply the fast Split-Bregman method to our convex minimization problem (10). The Split-Bregman method is a technique for minimization of $L_1$ regularized functionals and has been previously applied for segmentation and surface reconstruction [11], and shown to out-perform well-known methods, such as graph cuts and methods based on duality.

Given estimated mixture parameters, we compare our proposed convex segmentation method to an equivalent non-convex formulation implemented using Fast Marching Level Sets [12]. Average running time per frame for Convex/Non-Convex formulation was 10/120 sec on a Intel 2.4 GHz Duo processor. Both were implemented using C++. One of the main advantages of using the convex formulation is its robustness with respect to initialization. This is not the case for the non-convex formulation which depends highly on the initialization, in this case proximity to the endocardial wall.

Quantitative results for end-systole/diastole are shown in Table 2, and by images for 2 sequences in Figure 1. We use Average Distance (AD), employed by comparable works [1], to measure the distance between points on the endocardial wall in the expert contour and the one produced by our method. Points on the valve are excluded, since these are not clinically relevant. Authors Chen and Boukerroui work with Long Axis sequences, four (4C) and two chamber (2C) respectively, while Mikic, Chalana and Lin work on Short Axis (SAX) sequences and thus these results are somewhat less useful for comparison. See [1] for a summary of these works. Average distance is defined as follows, $AD = \frac{1}{2} \left\{ \frac{1}{n} \sum_{i=1}^{n} d(a_i, B) + \frac{1}{m} \sum_{j=1}^{m} d(b_j, A) \right\}$, where $A = \{a_1, a_2, \ldots, a_n\}$ and $B = \{b_1, b_2, \ldots, b_m\}$ are sets of contour points, and $d(a_i, B) = \min_j ||b_j - a_i||$. Our convex, and thus fast, algorithm produces results (Table 2) comparable to those in Table 1.
We made our convex prior formulation by PCA, but the model
is extendible to more complex shape priors, e.g. using mani-
fold learning of shapes. We choose a Rayleigh mixture model
for B-mode ultrasound as this fit our data well, see left col-
umn in Figure 1(c) and 1(d). However the shifting nature of
B-mode, due to the variability in their construction, can
make other speckle model assumptions, such as Nakagami,
more appropriate. In our future work we plan investigate the
numerical properties of the convex prior formulation, refine
the statistical prior model and extend the validation to include inter- and intra-expert studies.

5. CONCLUSIONS
We have proposed a convex method for segmentation of the
endocardium in ultrasound sequences using shape priors,
assuming a Rayleigh mixture model for the post-processed ul-
trasound data, and have obtained promising results. We have
formulated an energy functional, which measures the close-
ness between prior and estimate distributions of the inside and
outside of the endocardium, respectively. The energy func-
tional of the model is convex and can thus be minimized using fast algorithms, where Split-Bregman minimization was employed in this paper.

6. REFERENCES
[1] J. A. Noble and D. Boukerroui, “Ultrasound image seg-
au principe dequivalence distributionelle,” Revue de
for finding global minimizers of image segmentation
[8] K. Fundana, A. Heyden, C. Gosch, and C. Schnorr,
“Continuous graph cuts for prior-based object segmen-
shape-based approach to robust image segmentation,” in
likelihood form incomplete data via the EM algo-

lications of the split bregman method: Segmentation
and surface reconstruction,” Tech. Rep 09-06, Dept.
Methods Evolving Interfaces in Computational Geom-
etry, Fluid Mechanics, Computer Vision, and Materials