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Left ventricle 3D reconstruction using Gibbs Random Fields and Simulated Annealing

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Abstract

This paper proposes a left ventricle tridimensional reconstruction method from two orthogonal X-rays angiographic projections. The algorithm works under the assumption of having two segmented parallel projections and an homogeneous mixture of blood and contrast agent, in order to develop a binary reconstruction based on a Markov Random Field model and Simulated Annealing. The 3D ventricular object is considered as a stacked bidimensional slice set and each slice is reconstructed from the two one-dimensional profiles corresponding to a pair of rows obtained from the segmented projections.

Each bidimensional slice is described in a polar coordinate reference system as a function $r_i = R(\theta_i)$ that describes each point in the slice contour. This discrete one-dimensional function describing the two-dimensional slice is modeled as a non-causal Markov Random Field, where the conditional probability of one point given the rest of points is equivalent to the conditional probability of the same point given the points belonging to a neighborhood. The slice joint probability distribution is deduced by considering the equivalence between the Gibbs and Markov Random Fields. This joint probability is defined by an energy function including the local potential interaction between the sites included in a neighborhood. The energy function depends on the projections errors of the reconstructed slice, its connexity and the 3D spatial regularity.

The proposed algorithm starts with a provided initial approximate reconstruction that is then appropriately deformed to obtain the most probable slice form. Such deformation process is performed by using the probabilistic Gibbs model and the Simulated Annealing in order to minimize the energy function.

Performance of the reconstruction method was evaluated with preprocessed ventricular angiographic images and a 3D binary database. The results are promising as the reconstruction error is less than 7%.

1 Introduction

The ventricular function is defined by a parameter set describing the mechanical and electrical activity of this cavity. This parameter set is an important attribute necessary for determining the right therapeutic procedure used in patients with cardiac diseases. Many of those parameters, as the ventricular volume, the ejection fraction and the ventricular synergy, are estimated by the assumption of an elliptical tridimensional model for the left ventricle shape as is presented in Yang et al.[1]. This assumption can lead to important estimation errors. The tridimensional reconstruction of the ventricular shape, has as a goal to remove this restriction. In this way, it is possible to improve the assessment of the ventricular function.

The proposed reconstruction algorithm starts with the provided information from two preprocessed angiographic views, acquired simultaneously according to two mutually orthogonal directions (for example the conventional LAO 60° and RAO 30° views). For simplicity it is considered that the contrast agent is homogeneously mixed with the blood in the ventricular cavity, in this way, the binary reconstruction is performed instead of a gray level reconstruction. It is also assumed that the angiographic images were acquired according to a parallel projection model. Consequently, it is possible to consider the 3D object as a stack of 2D parallel slices in order to decompose the original tridimensional reconstruction problem in a set of bidimensional reconstruction problems, where each 2D slice is reconstructed from its two unidimensional projection profiles taken from the angiographic views. In the binary case, each slice is completely defined by its contour which is a boundary separating the ventricular cavity from the background.

In general, the reconstruction problem from only the provided information from two orthogonal projections is an ill defined inverse problem, because it is not possible to assure the existence, uniqueness and stability of the solution without including additional restrictions. Consequently, the solution must be regularized as proposed by Terzopoulos[2] based on a priori information about the ventricular shape. The Markov Random Field description, is a probabilistic model that allows to consider this information for solving the reconstruction problem as is shown in Toro et al.[3].

2 Method

The proposed reconstruction method works under the assumption that the acquired angiograms contain only information about the left ventricle. This is possible by performing the logarithmic subtraction and the segmentation of the angiographic image. The intensity gray level of each pixel in the input images is related to the depth information in the left ventricle. This information is

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grouped into a matrix form for each image and they are denoted as $\boldsymbol{I}_y$ and $\boldsymbol{I}_x$ of size $N_1 \times N_3$ and $N_2 \times N_3$ respectively.

2.1 The left ventricle model

Based on the a priori knowledge about the left ventricular shape as was reported in Chen et al.[4], it can be considered as a closed set in R^3, bounded and with simple connexity, that can be expressed as:

$$\boldsymbol{O} = \overset{\bullet}{\boldsymbol{O}} \cup \partial \boldsymbol{O} \tag{1}$$

where $\overset{\bullet}{\boldsymbol{O}}$ is a connected set, open and bounded representing the interior region of the object and $\partial \boldsymbol{O}$ is the contour boundary. Under this 3D object tridimensional representation, each slice can be defined as the intersection of the object with an horizontal plane $\boldsymbol{H}_m$ at height m, $(1 \le m \le N_3)$. Each slice can be expressed as:

$$\boldsymbol{O}_m = \boldsymbol{O} \cap \boldsymbol{H}_m = \overset{\bullet}{\boldsymbol{O}} \cup \partial\, \boldsymbol{O}_m \tag{2}$$

in particular, the planar contour $\partial\, \boldsymbol{O}_m$ is considered as continue, except for a finite number of points. The tridimensional object is decomposed in a finite set of slices $\boldsymbol{O}_m$ with $m \in [m_{min}, m_{max}]$, each one associated to a pair of 1-D projection profiles denoted as $f_y(k)$ and $f_x(l)$ corresponding to the gray level information of two rows taken from the given angiographic images.

The slice contour is represented in a polar coordinate system with origin o_m. Each contour point is represented by a scalar function $r_i = R(\theta_i)$, where r_i represents the distance from the given contour point to the origin o_m and θ_i is the angle in the polar coordinate representation. The slice contour can be represented as a set of points:

$$R = \left\{ r_i = R(\theta_i) \middle| i = 1,2,\ldots,M \text{ and } \theta_i = \frac{2\pi}{M-1} \right\} \tag{3}$$

This slice contour representation is convenient as the number of possible solutions is restricted to the contours with the simple connexity propriety. The reconstruction slice represented by the binary matrix $\boldsymbol{X}$ of size $N_1 \times N_2$, is obtained by polygon filling of the given contour points in (3).

The considered problem is how to reconstruct the slice contour $\partial\, \boldsymbol{O}_m$ from the slice projection profiles $f_y(k)$ and $f_x(l)$ in such a way that the binary reconstructed pattern $\boldsymbol{X}$ fulfill the given projections:

$$\sum_{l=1}^{N_2} x_{kl} = f_y(k) \qquad \sum_{k=1}^{N_1} x_{kl} = f_x(l) \tag{4}$$

subject to the constraint:

$$\sum_{k=1}^{N_1} f_y(k) = \sum_{l=1}^{N_2} f_x(l) \tag{5}$$

2.2 The Random Field Markov Model

Each slice contour $\boldsymbol{R}$ is modeled as a one dimensional Random Field $\boldsymbol{R} = \{R_1, R_2, \ldots, R_M\}$ associated to a set $\boldsymbol{L} = \{i \mid 1 \le i \le M\}$ including M sites, where each random variable R_i takes a value $r_i \in \Lambda$ and $i \in \boldsymbol{L}$, where Λ is a set including all possible values for the random variable. The set $\boldsymbol{R}$ is defined as a Markov Random Field in relation to a neighborhood system:

$$\eta = \{\eta_i \mid \forall i \in \boldsymbol{L},\ \eta_i \subseteq \boldsymbol{L}\} \tag{6}$$

where η_i is a neighborhood of site i such that $i \notin \eta_i$ and if $j \in \eta_i$ then $i \in \eta_j$, for any $i \in \boldsymbol{L}$. As a Random Markov Field the local and global conditional probabilities are related as:

$$P(r_i \mid r_{L-\{i\}}) = P(r_i \mid r_{\eta_i}) \tag{7}$$

where r_{η_i} are the values for the neighbors of site i and $r_{L-\{i\}}$ are the set of values in the sites included in $\boldsymbol{L} - \{i\}$. This Markovian property of the Random Field allows to model its local and global characteristics, notwithstanding, there is not a feasible direct method for estimating the joint probability distribution of the slice contour from the associated conditional probability distribution. The estimation in this case is made by using the hammersley-Clifford theorem, in Besag[5] that states the equivalence between a Random Markov Field and a Random Gibbs Field in relation to a neighborhood system η, if and only if the joint probability distribution is of the form:

$$P(\boldsymbol{r}) = \frac{1}{Z} e^{-\frac{1}{T}E(r)} \tag{8}$$

where Z is a normalization constant that allows $P(\boldsymbol{r})$ to fulfill the conditions to be considered a probability distribution function, $\boldsymbol{r}$ is a realization of the

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Random Field $\boldsymbol{R}$ and $E(\boldsymbol{r})$ is the energy function that can be expressed as $E(\boldsymbol{r}) = \boldsymbol{a}\boldsymbol{U}^T(\boldsymbol{r})$, where the vector $\boldsymbol{U}(\boldsymbol{r}) = [U_1(\boldsymbol{r}) \quad U_2(\boldsymbol{r}) \quad U_3(\boldsymbol{r})]$ includes three potential functions and $\boldsymbol{a}$ is a vector including three weighting parameters $\boldsymbol{a} = [\alpha_1 \quad \alpha_2 \quad \alpha_3]$. The parameter T is usually known as temperature and it is used in the optimization algorithm.

The energy function is constructed from some potential functions derived from the local contour characteristics, and it is defined as:

$$U_s(\boldsymbol{r}) = \sum_{c \in C} V_c(\boldsymbol{r}) \qquad s = 1,2,3 \tag{9}$$

where c is a subset of $\boldsymbol{L}$ known as a clique, that includes only one site or any other set of pixels that satisfy the following condition, $i \neq j$, $i \in c$ and $j \in c$ implies that $i \in \eta_j$ and $\boldsymbol{C}$ is the collection of all possible cliques in the neighborhood.

2.3 The energy function

The energy function was designed in such a way that the solution for the slice contour provides the minimum energy value in order to maximize the joint probability distribution giving by equation (8). It was chosen an energy component that measures the degree of match between the given projections and the current slice reconstruction projections. If the given projections are $f_y(k)$, $f_x(l)$ and the current slice projections are denoted as $f_y^p(k)$ and $f_x^p(l)$ the first energy component U_1 for the slice m is estimated as:

$$U_1^m = \frac{1}{\Delta l}\sum_{k=1}^{N_1}\left(f_y(k) - f_y^p(k)\right)^2 + \frac{1}{\Delta k}\sum_{l=1}^{N_2}\left(f_x(l) - f_x^p(l)\right)^2 \tag{10}$$

where the profile $f_x(l)$ takes values greater than zero in the range $l_{min} \leq l \leq l_{max}$ and $f_y(k)$ in the range $k_{min} \leq k \leq k_{max}$ consequently Δk, Δl are the number of non zero samples in each profile, that are used to weight the square error in order to keep both terms equally important during the optimization process.

The second energy component is a regularization term that constraints the number of plausible solutions to the smooth slice contours. This component takes into account the fact that the ventricular contour is with high probability a smooth contour. In our case, we have used the following second order derivative approximation :

$$U_2^m = \sum_{i=1}^{M}\left(r_{i-1} - 2r_i + r_{i+1}\right)^2 \tag{11}$$

This potential energy term is defined on a second order neighborhood $\eta = \{\eta_i = \{i-2, i-1, i+1, i+2\} | \, i = 1,2,\ldots, M\}$ where only the sites included in the clique $c_1^2 = \{i-1, i, i+1\}$ are used.

The third component considers the regularity constraint of spatial smoothing between adjacent slices. This smoothing constraint is very useful specially when the slice contour has only slight modifications from one slide to the other. This term is obtained as the difference between the current contour and the previously reconstructed slice contour:

$$U_3^m = \sum_{i=1}^{M} \left(r_i^m - r_i^{m-1} \right)^2 \tag{12}$$

where r_i^m is the current contour radial length and r_i^{m-1} is the contour radial length of the previously reconstructed contour after translation to the current origin o_m.

2.4 Optimal solution search

The Simulated Annealing algorithm works on an iterative basis by searching for the configuration that minimizes the energy function. The algorithm starts with an approximate initial solution (usually an elliptical or approximate reconstruction that considers the a priori knowledge about the slice) that is then deformed or modified. The new possible configuration candidate $\boldsymbol{r}_n$ is generated by slight modifications of the current configuration $\boldsymbol{r}_a$, those modifications are performed by a random visitation procedure, where each radial element is modified in a random and without replacement basis. For each radial element visited, the new radial value r_{ni} is generated according to the following relation:

$$r_{ni} = r_i + rr \tag{13}$$

where rr is a random number picked from a uniform distribution in the real interval $[-ru/2, ru/2]$ and ru is a threshold defining the radial variation range that is estimated as:

$$ru = 1 + \frac{\bar{r}\,\beta^k}{10} \qquad \text{with} \qquad \bar{r} = \frac{\sum_{i=0}^{M} r_i}{M} \qquad \text{and} \qquad \beta = 0.95 \tag{14}$$

The modification of only one radial element gives rises to a new possible configuration. This configuration is chosen according to the probability relation $P(\boldsymbol{r}_n)/P(\boldsymbol{r}_a)$, in this way the normalization constant Z does not intervene in the process. If $P(\boldsymbol{r}_n) > P(\boldsymbol{r}_a)$ the new configuration is unconditionally accepted, otherwise it is accepted if $P(r_n)/P(r_a)$ is greater than a random number p_a generated in the range (0,1) according to a uniform probability distribution. This procedure allows to attain a global minimum for the objective function without getting stuck on any local minimum.

The performance of the Simulated Annealing is affected by the initial choice of the temperature parameter and also by the decreasing law of this parameter. If the initial temperature value is high, the optimization algorithm would take a great number of iterations in order to reach the optimal solution. Otherwise if this value is very low, the final solution would show an important error level. The initial temperature is estimated according to the heuristic method proposed by Jhonson et al.[6]. The temperature decreasing ratio was chosen as $T_k = g^k T_0$, where g is a cooling constant that is heuristically fixed as 0.95.

The optimal solution search is performed by contour scanning cycles at each temperature value k, where all M sites of the contour are visited and modified. The optimal searching procedure is stopped when the number of accepted transitions is lower than 4% of M.

3 Results

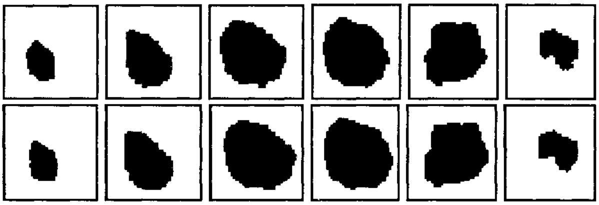
In order to evaluate the reconstruction method, several tests were performed, including the slice reconstruction without considering the adjacent slice information. The method was also tested by reconstructing a known 3D binary object, and by performing the reconstruction from two real angiographic views appropriately preprocessed.

3.1 Isolated slice reconstruction

The slices to be reconstructed were taken from a 3D binary database, obtained by segmentation and binarization of a tomographic scanning database of a dog heart. The reconstruction was performed from the orthogonal projection corresponding to the row and column addition of several slices of the binary database. In this test, we use 60 radial elements for describing the contour. The weighting parameters of the energy function components were taken as $\alpha_1 = 100$, $\alpha_2 = 1$ and $\alpha_3 = 0$. The information of the adjacent slice was not considered and the reconstruction method was started with an elliptical initial approximation that has its mayor axis placed between the second and four quadrant. The algorithm showed a good performance, with results that have a form very close to the original one, as shown in figure 1. The reconstruction errors are less than 6% and we can obtain error levels as low as 1.28% .

3.2 Tridimensional Reconstruction

In this test, 60 radial elements were used for representing each slice contour. The weighting parameters of the energy function were taken as $\alpha_1 = 100$, $\alpha_2 = 1$ and $\alpha_3 = 0.95^k$, where the last parameter is gradually reduced at each temperature state in order to allow for differences between the current slice and the neighbor previously reconstructed slice. An elliptical approximation is used to start the reconstruction method. This approximation has the mayor axis in the second and fourth quadrant. In figure 2, it is shown the 3D binary database and the reconstructed tridimensional object, visualized from the same viewpoint. In this case the reconstruction error is 7.02%.



3.34%	2.31%	1.28%	2.12%	1.48%	6.23%

Figure 1: Obtained results for the isolated slice reconstruction. In the first row, the original slices are shown. In the second and third row the reconstructed slices are shown as well as the reconstruction error for each slice.

In figure 3a it is shown two angiographic views, RAO 30° and LAO 60° respectively, after logarithmic subtraction, median filtering, segmentation and densitometric equalization as recommended by Prause & Onnash[7]. The two angiographic views are used for performing the left ventricle 3D reconstruction, using the same parameters that were used in the previous tests. In this case, as the original tridimensional object is unknown, the performance of the reconstruction method is estimated by comparison between the projections of the reconstructed object and the original angiographic views. The projections errors are 12.74% and 11.05%. These errors are the consequence of several factors, including the presence of noise in the angiographic images, the selection of a possible wrong orientation for the initial approximate reconstruction and the limitation of the polar coordinate representation for modeling complex slice forms that could be present in the left ventricle. Even when this error is present, the reconstruction algorithm is able to recover a tridimensional object shown on figure 3b, with a smooth surface that matches the a priori medical knowledge about the real left ventricle shape.

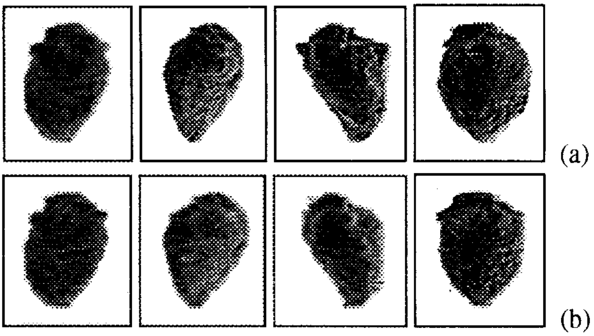


Figure 2: Tridimensional reconstruction from two orthogonal projections of a 3D binary database of a dog heart. a) Four views of the original database, b) Four views of the tridimensional reconstructed object.

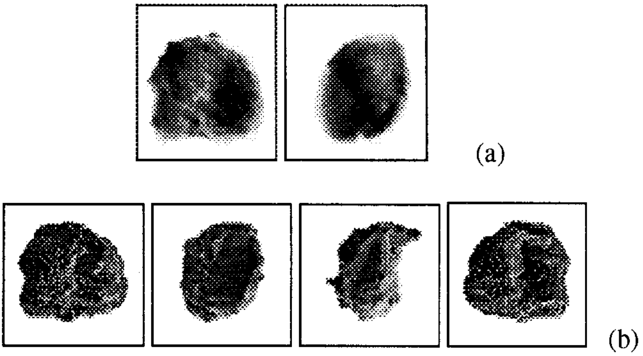


Figure 3: a) Left ventricle angiographic views RAO 30° and LAO 60°. b) Several views of the tridimensional reconstructed object obtained from the two real angiographic views shown in (a).

4 Conclusions

The probabilistic Markovian model for the slice contour allows the reconstruction of the left ventricle tridimensional shape from the information provided by two angiographic projections, taken according to mutually orthogonal directions. The model allows to solve the ambiguity of the problem by including a priori information in the form of constraints and any initial approximate reconstruction.

The Simulated Annealing algorithm allows to attain a useful global minimum corresponding to the binary reconstruction, that minimizes the projection error, and satisfies the rest of constraints.

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