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A SIMULATED ANNEALING APPROACH TO LEFT VENTRICLE 3D RECONSTRUCTION FROM TWO ANGIOGRAPHIC VIEWS

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ABSTRACT -- In this paper, a simulated annealing approach is used to solve the left ventricle, tridimensional reconstruction problem based on two angiographic views. The algorithm works under the assumption of having parallel projections and a homogeneous mixture of blood and contrast agent filling the ventricular cavity. Those assumptions allow to decompose the original 3D object into a stack of bidimensional slices, in order to simplify the reconstruction process. Each slice is modeled as a bidimensional Markov-Gibbs random field and the reconstruction process is started with an initial approximation, which is appropriately deformed by using a simulated annealing optimization procedure in order to minimize an energy function that includes projection compatibility and spatial regularity constraints. The results obtained by reconstructing a 3D binary database of the ventricle from two synthesized projections, as well as the reconstruction obtained from two orthogonal angiographic images show a low reconstruction error and the shapes of the reconstructed slices are highly correlated with the original database.

Key-words: 3D Reconstruction from Projections, Simulated Annealing, Markov Random Field.

INTRODUCTION

Assessment of the ventricular function allows to determine several parameters defining the physiological status of the ventricles. The estimation of those parameters is usually based on the analysis of angiographic images previously digitized and processed in order to enhance their information content. The analysis of the ventriculographic images allows to measure the ventricular volume, the ejection fraction, the wall stress, the ventricular synergy and other important parameters (Yang *et alii*, 1978). Many of these parameters are estimated by assuming an ellipsoidal tridimensional model for the ventricle shape (Kennedy *et alii*, 1970). This restrictive assumption could be released by the appropriate 3D reconstruction of the ventricle, in order to improve the precision of the estimation.

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The 3D ventricle shape reconstruction method described here is based on the work of Pellot *et alii* (1994), about the 3D reconstruction of coronary sections. In our case, it has been necessary to review some particular points in order to reconstruct the left ventricle shape from the information provided by only two orthogonal angiographic views. This constraint is imposed by the image acquisition technology that only considers mono-plane and bi-plane equipment. The reconstruction problem as stated is difficult because of its ill-posed nature and the possibility of having an infinite number of solutions fulfilling the given angiographic views. In order to reduce such indeterminacy, the solution must be regularized by including some a priori information about the ventricle shape.

The proposed method considers the ventricle shape as a closed set O in the Euclidean space, that is simply connected, bounded and can be constructed by stacking a set of bidimensional slices. This model allows to describe the ventricle shape at any instant of the cardiac cycle including several abnormal ventricle shapes as in the case of arteriosclerotic heart disease, or any other disease characterized by asynergic movements or wall hypertrophy. Considering the assumption of parallel projection geometry that implies placing the X-rays source at an infinite distance from the irradiated object, the 3D reconstruction process can be managed as solving several bidimensional slice reconstruction problems, where each slice O_z is reconstructed from two densitometric profiles taken from the angiographic views. This reconstruction process is aimed to obtain the interior and contour region of the ventricle in each considered slice under the additional constraint of having a homogeneous X-rays absorption coefficient in the ventricle in order to develop a binary reconstruction. Several solutions have been proposed for solving this binary reconstruction problem (Onnash, 1978) (Slump *et alia*, 1982), notwithstanding the existence of multiple solutions and the strong assumptions about the geometry of the acquisition system require further research in order to improve the results.

The proposed algorithm models the global and local spatial properties of the reconstructed slice as a Markov Random Field (Sigelle *et alia*, 1992). Additionally the equivalence between the Markov and Gibbs description is used (Besag, 1974) by writing the a priori probability of the reconstructed slice based on an energy function that groups the addition of several potential interaction functions, designed for penalizing the less probable configurations.

METHOD

Reconstruction slice model

Each ventricular slice O_z is expressed as:

$$O_z = \dot{O}_z \cup \partial O_z \tag{1}$$

where $\dot{O}_z$ is a connected open and bounded set that describes the interior region and ∂O_z is the contour region of the ventricle in each slice.

We work under the assumption that the contour ∂O_z is a smooth and continue curve derivable except in a finite number of points. Additionally, we assume the ventricle filled by a

homogeneous mixture of blood and contrast agent, in this way the constant absorption coefficient of the ventricle interior region, allows to consider each slice of the ventricle as a binary matrix where each element can take the zero or one value depending if the element belongs or not to the ventricle. The 2D reconstruction problem implies the searching for a 2D binary array of size $N_1 \times N_2$, denoted $\{x_{ij}\}$ based on two 1D projection arrays $f_x(i)$ and $f_y(j)$ with N_1 and N_2 elements respectively, corresponding to a pair of rows taken from the angiographic views. The binary array $\{x_{ij}\}$ must satisfy the given 1D projections:

$$\begin{aligned} \sum_{j=1}^{N_2} x_{ij} &= f_x(i) \qquad i = 1,\ldots,N_1 \\ \sum_{i=1}^{N_1} x_{ij} &= f_y(j) \qquad j = 1,\ldots,N_2 \end{aligned} \tag{2}$$

and

$$\sum_{i=1}^{N_1} f_x(i) = \sum_{j=1}^{N_2} f_y(j) \tag{3}$$

Due to the imperfections related to the image acquisition process, it is necessary to develop a pre-processing stage for the two angiographic views, including logarithmic subtraction, contrast enhancement, segmentation, alignment and densitometric equalization (Prause *et alia*, 1992) between the two projections in order to satisfy the equation (3).

The Markov Random Field -- Each 2D reconstruction slice is modeled as an image $x = \{x_{ij}\}$, represented by a matrix of size $N_1 \times N_2$, that corresponds to a realization of the random field denoted by X, associated to a finite lattice:

$$L = \left\{(i,j) \middle| 1 \le i \le N_1,\ 1 \le j \le N_2\right\} \tag{4}$$

including a collection of $N_1 \times N_2$ pixels or sites each of them placed at position (i,j). In this lattice it is possible to define a neighborhood system $\nu = \left\{\nu_{ij} \middle| (i,j) \in L\right\}$ where the neighborhood ν_{ij} is defined as a set of pixels such that:

$$(i,j) \notin \nu_{ij} \text{ and } (k,l) \in \nu_{ij} \iff (i,j) \in \nu_{kl} \tag{5}$$

In addition, one can consider a subset of L denoted as a clique c, that includes only one pixel (i,j), or any other set of pixels that satisfy the following condition: $(i,j) \neq (k,l)$, $(i,j) \in c$, and $(k,l) \in c$ implies that $(i,j) \in \nu_{ij}$. The collection of all possible cliques in (L,ν) is denoted C. The

Random Field X is binary as $x_{ij} \in \Lambda = \{0,1\}$ and x_{ij} takes the 1 value if the pixel belongs to the ventricle, and the 0 value otherwise for each pixel placed at $(i, j) \in L$. The set including all possible configuration for the slice is denoted $\Omega = \left\{X = \{x_{ij}\} \middle| x_{ij} \in \Lambda,\ (i, j) \in L\right\}$ where each configuration is a Markov Random Field realization in L (Geman *et alia*, 1984) (Pellot *et alii*, 1994).

According to the Hammersley-Clifford theorem (Besag, 1974), a Markov Random Field X defined in (L, ν), has a Gibbs distribution or equivalently, it is a Gibbs Random Field in relation to the neighborhood system ν if and only if its joint probability distribution is of the form:

$$P(X = x) = \frac{1}{Z} e^{\left\{-\frac{1}{T}E(x)\right\}} \tag{6}$$

this joint distribution is basically an exponential distribution, where T is a constant used in the simulated annealing optimization procedure and E is the energy function that is estimated from each realization of the random field X. The energy function $E(x)$ is defined as:

$$E(x) = \sum_{c \in C} V_c(x) \tag{7}$$

where $V_c(x)$ is the potential function associated with clique c, and Z is the partition function:

$$Z = \sum_{x \in \Omega} e^{-\frac{E(x)}{T}} \tag{8}$$

which can be considered as a normalization constant. The only constraint over the completely arbitrary potential functions $V_c(x)$ is that they should be a function of pixel values included in clique c (Besag , 1974) (Besag, 1972) (Heitz, 1991).

Energy function

The energy function was designed in order to provide the minimum energy value for the ideal reconstruction solution. This energy function includes several terms where each of them models a different attribute of the reconstructed slice, in such a way that the solution is the best compromise between terms of the energy function. The terms included are: the slice fidelity with respect to the given projections E_1^z, that can be estimated as the difference between the projection profiles $f'_x(i)$ and $f'_y(j)$ of the current reconstruction slice z, and the given projection profiles denoted $f_x(i)$ and $f_y(j)$, as follows:

$$E_1^z = \frac{1}{\Delta j} \sum_{i=i_{min}}^{i_{max}} \left[f'_x(i) - f_x(i)\right]^2 + \frac{1}{\Delta i} \sum_{j=j_{min}}^{j_{max}} \left[f'_y(k) - f_y(k)\right]^2 \tag{9}$$

where the profile $f_x(i)$ is non-zero between i_{min} and i_{max}, and $f_y(j)$ is non-zero between j_{min} and j_{max} therefore $\Delta i = i_{max} - i_{min}$ and $\Delta j = j_{max} - j_{min}$.

In this case each difference is weighted with the appropriated coefficients Δi or Δj in order to keep both terms in equation (9) equally important during the optimization process. The term E_2^z corresponds to the internal energy of the reconstructed slice as it considers the slice contour smooth and with only a small number of irregularities. This term estimates the interaction energy of pixels included in a second order neighborhood as:

$$E_2^z = \frac{1}{8}\sum_{i=1}^{N_1}\sum_{j=1}^{N_2}\left(8 - \sum_{l_1=i-1}^{i+1}\sum_{l_2=j-1}^{j+1}\delta\left(x_{ij}^z - x_{l_1 l_2}^z\right)\right) \tag{10}$$

where $\delta(\bullet)$ is the Kronecker delta function, which is equal to one if $x_{ij}^z = x_{l_1 l_2}^z$ and equal to zero if $x_{ij}^z \neq x_{l_1 l_2}^z$.

The last term E_3^z in the energy function models the degree of similarity between adjacent slices and can be expressed as the difference between the current solution for the reconstructed slice and the optimal solution for the adjacent previously reconstructed slice. The spatial similarity can be estimated as:

$$E_3^z = \sum_{i=1}^{N_1}\sum_{j=1}^{N_2}\left|x_{ij}^z - x_{ij}^{z-1}\right| \tag{11}$$

where x_{ij}^z represents the pixel value at position (i, j) for the reconstruction slice z and x_{ij}^{z-1} is the pixel value at position (i, j) for the previously reconstructed slice $z-1$.

The energy function is obtained as the linear combination of the previously described terms and defines the Gibbs distribution used in the optimization process. The general form of this linear combination is:

$$E^z = \alpha_1 E_1^z + \alpha_2 E_2^z + \alpha_3 E_3^z \tag{12}$$

where α_i are weighting coefficients whose values are selected according to the optimization procedure.

Those coefficients values were empirically obtained by considering several typical slices taken from a 3D heart binary database. The α_1 coefficient is kept constant during all annealing procedure and its value is fixed as $\alpha_1 = 10$. The α_2 coefficient is gradually lowered at each temperature stage k, in order to allow for the presence of small irregularities on the slice contour. A decreasing

function expressed as $\alpha_2 = 0.99^k \alpha_{2_o}$ was found as optimum, with an initial value $\alpha_{2_o} = 1$. The α_3 coefficient is also gradually lowered in order to allow for differences between the current reconstruction slice and the previously reconstructed slice. A decreasing function expressed as $\alpha_3 = 0.95^k \alpha_{3_o}$ was determined with the initial value $\alpha_{3_o} = 1$.

Algorithm implementation

The goal of the reconstruction process is the search for the most probable configuration corresponding to the slice realization that minimizes the energy function. In order to obtain an approximate solution for this problem, a simulated annealing algorithm is used.

The reconstruction process is developed on a slice basis considering as the input the rows of the two orthogonal angiographic views of the ventricle. The algorithm includes two stages, in the first stage, the optimal solution search, starts with an initial approximation for the reconstruction slice. This approximation can be an elliptic section estimated from the given projections, a previously reconstructed slice or an approximate reconstruction obtained by any other method. During this stage, the initial temperature T_0 is estimated. As the temperature parameter T controls the performance of simulated annealing algorithm, in our problem T_0 is fixed with a high value, in this way at the beginning of the reconstruction process almost all transitions are accepted. The heuristic rule for estimating the initial temperature value is based on Johnson *et alii* (1989), and it relies on an acceptation coefficient A_{c_o}, defined as the ratio between the number of accepted and proposed bad transitions that increase the energy function. In order to estimate the parameter, first a value A_{c_o} close to 1 is chosen and then the average energy change $\overline{\Delta E^z}$ is obtained by considering $N_1 + N_2$ random bad transitions. The initial temperature parameter T_0 is estimated by using the following relation:

$$T_0 = \frac{\overline{\Delta E^z}}{\ln\left(A_{c_o}^{-1}\right)} \tag{13}$$

The second stage for the slice reconstruction correspond to the simulated annealing algorithm in order to obtain the optimal solution. This solution is attained by progressive lowering of the temperature parameter. This lowering ratio is an important parameter that determines the simulated annealing execution time and the quality of results. In our case a lowering temperature function $T_k = g^k T_0$ is used, where g is the cooling constant that is heuristically fixed in 0.95 $(0 < g < 1)$. At each temperature stage k, new configurations for the reconstruction slice are generated, those configurations are accepted or rejected according to the transition acceptation criteria in order to optimize the energy function. The slice contour pixels are scanned on a random and without replacement basis. This contour is considered as the union set of an internal contour with pixels taking the 1 value and an external contour with pixels taking the 0 value. First a random scan for pixels belonging to the inner contour is developed and the new value for the chosen pixel, if accepted for transition, is the binary complement of the current value. When all pixels in the inner contour have been visited, an external contour is determined and its pixels are visited on the same

random basis. The acceptation criteria is based on the comparison between the occurrence probability of the current configuration, denoted as $P(x_a)$ and the probability of the new configuration denoted $P(x_n)$. The comparison between both probabilities is done by estimation of the energy change given by:

$$\Delta E^z = E^z(x_n) - E^z(x_a) \tag{14}$$

If the energy change is negative, the new configuration is unconditionally accepted as $P(x_n) > P(x_a)$ otherwise the new configuration is accepted based on the probability value $P_{ace}(\Delta E^z, T_k)$ given by:

$$P_{ace}(\Delta E^z, T_k) = \frac{P(x_n)}{P(x_a)} = e^{-\frac{\Delta E^z}{T_k}} \tag{15}$$

This value is a probability threshold that defines when the positive change in the energy function is accepted and it allows to avoid local minimums and to pursue the optimization process until attaining a possible global minimum. The procedure for acceptation implies the generation of a random number p_a in the interval $[0,1]$ picked from a uniform probability distribution, therefore if $P_{ace}(\Delta E^z, T_k) > p_a$ the transition is accepted, otherwise it is rejected.

The algorithm is stopped when the number of accepted transitions is lower than 7% of the internal contour pixels for a given temperature stage. The procedure is then repeated for another slice until all slices of the tridimensional object have been reconstructed.

RESULTS

Slice reconstruction

The reconstruction method was first tested on isolated 2D slices without considering the similarity term E_3^z in the energy function. The original 2D slices were taken from a 3D binary database obtained by segmenting and binary filling of a tomographic scanner (CT) 3D database of a dog heart. The slice reconstruction was performed from row and column additions (projection profiles) of the original binary slice. The reconstruction process was initialized with a slice taken from the original 3D database that is four slices apart from the current reconstruction slice.

The reconstruction error was computed by using the relative error criteria between the original slice x and the reconstructed slice $\hat{x}$, defined as:

$$\text{ERROR}\% = \frac{\sum_{i=1}^{N_1}\sum_{j=1}^{N_2}\left|x_{ij} - \hat{x}_{ij}\right|}{\sum_{i=1}^{N_1}\sum_{j=1}^{N_2} x_{ij}} \times 100 \qquad (16)$$

In Figure 1, the results for the reconstruction of several slices are shown. As the original database is known, the reconstruction error can be estimated for each reconstructed slice. The minimum reconstruction error for this database is 1.34% of the original slice. The parameters used in the Simulated Annealing algorithm were $A_{c_o} = 0.02$, $\alpha_1 = 10$, $\alpha_{2_o} = 1$ and $\alpha_{3_o} = 0$.

ORIGINAL						
RECONSTRUCTION						
ERROR %	4.35	2.44	1.55	1.54	1.34	3.06

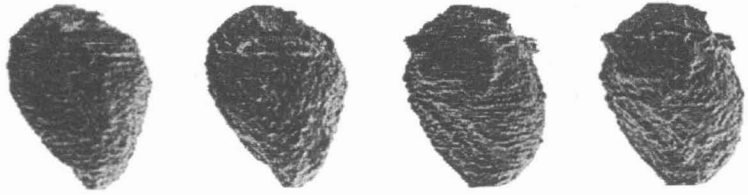
Figure 1. Obtained results for the slice reconstruction. In the upper row the original slices are shown, the reconstruction and the error are shown below.

3D reconstruction

For developing the 3D reconstruction, the energy model previously used for the slice reconstruction case was extended for considering the adjacent previously reconstructed slice with $\alpha_{3_o} = 1$. As initial reconstruction, an ellipse estimated from the given profiles is used for the first reconstructed slice, then the previously reconstructed slice is used as initial solution.

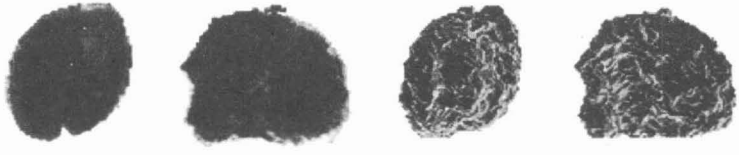
In Figure 2, the 3D reconstruction of the binary 3D database for the dog heart is shown, where one can appreciate both the reconstructed database and the original database visualized from the same viewpoint for two different views. In this case the reconstruction error is 5.5%. This error was estimated by using a 3D extension of equation (16).

In Figure 3, a 3D reconstructed object from two real and pre-processed ventricular angiographic views is shown. In figure 3a and 3b one can see the ventricular angiographic views LAO 60° and RAO 30°, respectively after logarithmic subtraction, median filtering, segmentation and densitometric equalization (Prause *et alia*, 1992). In figure 3c and 3d the binary 3D reconstructed object is shown, visualized from a similar viewpoint as the original angiographic views. In this case, even when the tridimensional reconstruction error cannot be estimated, we can see a good degree of match between the synthesized projections of the reconstructed object and the original angiographic projections with an error as low as 7%.



(a) (b) (c) (d)

Figure 2. Reconstruction for the 3D binary database of the dog heart. (a) and (c) two orthogonal views of the original 3D binary database, (b) and (d) two orthogonal views for the 3D binary reconstructed object.



(a) (b) (c) (d)

Figure 3. Tridimensional binary reconstruction from two orthogonal ventricle angiographic views: (a) and (b) left ventricle angiographic views LAO 60° and RAO 30°, (c) and (d) two views for the binary reconstructed object.

CONCLUSIONS

We have presented a Markov model based method for the binary 3D reconstruction of the ventricle shape from two angiographic views. The proposed algorithm works under the assumption of having a parallel projection geometry and a homogeneous mixture of blood and contrast agent. The first assumption is approximately valid as long as the input projections are corrected according to a magnification factor derived from the acquisition geometry. For the second assumption to be valid, the contrast agent must be injected at the right velocity and it is also recommended to average several projection frames. When this assumption is not valid, the reconstruction error is important as the shape appears deformed or with holes even when the actual ventricular shape is more regular. Any other noise or residual error avoiding the fulfilling of the equation (3) is attenuated according to the desintometric equalization procedure. This preprocessing stage upgrades the input data and makes the reconstruction process a feasible task even though further research is necessary in order to improve the projection data quality.

The probabilistic approach associated to the proposed method, allows to adequately solve the ambiguity related to the reconstruction problem. The results obtained with a binary 3D database show a high degree of correlation with the original database. The low reconstruction error obtained in this experiment shows that the algorithm is able to approach the optimal solution that matches the

real shape of the 3D object. When the reconstruction is performed from two real angiographic views the comparison of these views with the synthesized views obtained from the reconstructed object gives a low error value. The reconstructed tridimensonal object would match the actual ventricular shape as long as the initial solution has the right spatial orientation and the input projections are appropriately preprocessed in order to fulfill the required constrains. The reconstruction procedure is flexible for allowing the modification of the energy function in order to include additional factors that could intervene in the reconstruction process or for releasing some restrictive constraints as the parallel projection.

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