Expert-Model Based 3D Reconstruction of the Left Ventricle Using Transthorasic Echographic Images *

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Abstract

Using a rotating probe combined with a ECG gating technique we acquire transthorasic datasets (20 Images per ECG Cycle for 9-18 rotations). The aim of this research is the automated Left Ventricle (LV) reconstruction (3D+t) for later diagnoses. One of the main stages during the reconstruction process is the detection of the wall boundaries. Here we propose an approach based on a pre-calculated model of the displacement field of the heart to guide the detection process in combination with active contours. The numerical model obtained during a learning phase can later be used for diagnoses as well.

1 Introduction

The interpretation of echographic images is one of the most difficult tasks in biomedical image interpretation, because of the low image quality of the data sets. The task of finding and following the ventricle boundaries in Echocardiology is recently done using approaches, based on snakes [5] or active contours (see for example [7]).

Although snakes are a powerful tool in image interpretation and object recognition, they have some restrictions and disadvantages.

- If the external forces are too small (Gradient energies) snakes tend to shrink.
- The method of search is local and blind that means, if an image feature is too far away it will not be found.
- If a contour contains holes and if there is more than one gradient in a region the contour will get attached to the highest gradient.

Because of these drawbacks snakes can not be used "as is" to detect the ventricle. Gradient information obtained from echographic images is always incomplete because of drop outs. Sometimes even whole boundary sections are missing.

In addition to the active contours we work with statistical knowlage of the heart movement. A statistical model is created during a learning phase. During the search process this model is used to guide the identification process. The combination of snakes and statistical knowledge is called "Expert Model based Search" [4] [3] [1].

The paper is organised as follows: First the registration and the modelling process is described. Then the initialisation and detection process is introduced. We finish with the presentation of our results and our conclusions.

2 Model Description and Creation

For our acquisition we use a rotating scanner. As a result of each acquisition we get for each rotation angle a time serious of images. Each series contains 10- 20 images of the LV. Start- and end-point of the series are aligned using the ECG-Trigger mechanism [6].

In our research we want to predict the displacement of the contour points. That means if we have

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found a point i of the contour in the image frame t, we want to predict where this point are likely to be found in image frame $t+1$ and to determine a region where the point has to be found. For practical reasons the model has to be flexible and easy to update.

Our modelling approach is similar to that of Cootes/Taylor [4]. But instead of modelling the form or the model shape, we model the displacement field. Therefore we use the average displacement and its standard deviations. The displacement is calculated for 60 points of the contour. This points are found by projecting a grid onto the contour and saving the contour points lying on the grid (see Fig. 1).

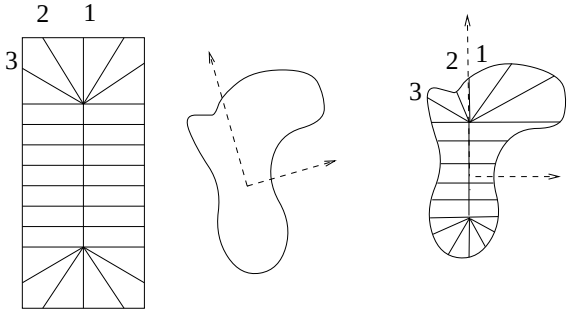

Figure 1: (a) Model Grid, (b) Model trace, (c) Selected points

Calculations are done in 2D+t and then transformed into 3D+t space. In the following the model building process is explained. The model is created as follows (overview):

- Traces are manually extracted by a medical professional [6] and stored in a database (1).
- The model is initialised with the data and the velocity field of the first object. The variations for each point are set to zero (2).
  - Therefore 40 - 60 points per trace are extracted using our "heart grid" (Fig. 1a (3).
  - The velocity for each contour point is calculated and stored (4).
- New objects are added to the model (5).
  - 40 - 60 points per trace are extracted using our "heart grid" .
  - The average velocity is updated (6).
  - The standard deviation is updated (7).

(1) During a first phase an expert traces manually the heart borders of our example datasets. Therefore a 4D editing and visualising tool was developed [6]. As a result we get a trace for each frame of the patient data set.

(2) To get the same number of labeled points for each frame, we search for the main axis of the closed contour (see [2]). Then a grid is projected on the contour. The points lying on the grid are stored. The grid is positioned in such a way that the middle axis lies on the main ventricle axis. As the middle length of the grid half of the length of the ventricle contour was chosen. The middle point of the grid lies on the centre point of mass of the contour 1b.

(3) The displacement $(v_i(t) = p_i(t) - p_i(t-1))$ for the i^{th} point p_i of a contour is calculated using the grid of trace $i(t)$ with trace $i(t+1)$. All displacement vectors are stored in the average velocity vector of the model and the standard deviations are set to zero.(see Fig. 2b)

We calculate the displacement vectors for all points and traces of our model. The points and the displacement field are stored in our model.

(4) During the following steps new displacement vectors are added to the model. This phase is called the learning phase. During this phase the mean displacement and its standard deviation are updated (mechanism of adaption). We only store the number of examples n that have contributed to the current model, the mean displacement and the standard deviation for each point of the traces.

Before we can add new displacement vectors to the model, model and trainings set have to be aligned with respect to a set of axis. Aligning means transforming the traces that model and training example have the same scale and spacial position (Fig. 2a).

To do this the matching method of Umeyama [8] is used. The idea is to minimise the distance vector between the two point sets using a singular value decomposition method. P_1 is the point set of the first trace of the trainings set and P_2 the first trace of the model set with N points $p^1(x,y)$ and $p^2(x,y)$. Between the two sets a relation can be formulated as follows:

$$p_i^1 = c * R * p_i^2 + t + S_i \quad (1)$$

with the rotation matrix R, a scaling factor c and a translation vector t. S_i represents a noise factor that has to be introduced because in medical images a perfect match is almost impossible. The aim of further computations is to find the transformation values so that the difference between contour P_1 and contour P_2 gets minimal. Therefore p_i^1 is subtracted in equation 1 and the quadrated sum of squared differences is minimised.

$$S^2 = \frac{1}{N} * \sum_{i=1}^{N} \| p_i^1 - (c * R * p_i^2 + t) \|^2 \quad (2)$$

In our case we solve this "global Orientation Problem" using a single value decomposition method of the Covarianz matrix H which was proposed by Umeyama [8]. As a result transformation parameters are received (rotation R, scaling s and translation t) that give an optimal transformation of the point sets (see Fig. 2). We apply the calculated parameters to all traces of the patient in the same spacial position.

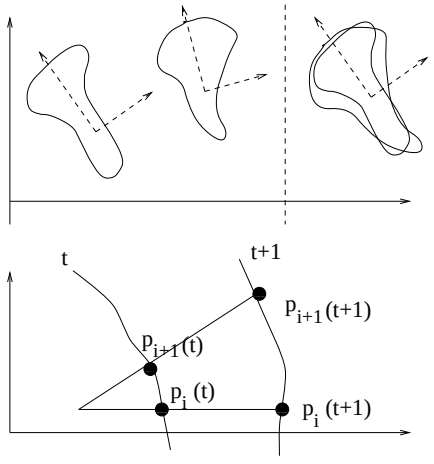

Figure 2: (a) Model and Contour before Registration, (b) Contour and Model after Registration

(5) After we have aligned the trainings set and model, we calculate the displacement vector v_i for each point of the trainings set. Then the model is updated:

$$\bar{v}_{i,n+1} = (v_i + n * \bar{v}_{i,n}) * \frac{1}{(n+1)} \quad (3)$$

with $v_i = (p_i(t) - p_i(t+1))$

as the displacement in point i and $\bar{v}_{i,n+1}$ the updated average and $\bar{v}_{i,n}$ the old average displacement and n the number of the added example.

$$\bar{s}_{i,n+1} = (s_i + n * \bar{s}_{i,n}) * \frac{1}{(n+1)} \quad (4)$$

where $s_i = (v_i - \bar{v}_{i,n+1}) * (v_i - \bar{v}_{i,n+1})$ is the displacement variations at point i

As a result we get the average displacement field for each point p_i and the standard derivations of the displacement field. This model is then used as a guide during the detection process.

3 Initialisation and Detection Process

During the detection phase the model is used to predict new positions of the boundaries in the next image frame.

In the following paragraph the steps during the detection phase are described (overview) :

- Initialisation of the first contour in the first image of dataset for a given patient (1).
- Alignment of the model and patient data (2).
- Replacement of the contour - points using the pre- calculated displacement values.

$$p_i(t) = p_i(t-1) + v_i\bar{(}t) \quad (5)$$

  Snake based search and examination of the results (3).

  - If the contour point is within the region predefined by the model. The point is saved (3a).
  - If it is not we suspect the model has matched a wrong edge and the point is left unchanged (3b).

- The found contour in frame t is used as an initialisation of the next search in frame $t+1$. (goto 3)

(1) First the expert initialises the first contour of our dataset. We find the model points using the heart grid.

(2) Then the model is fitted into the trace. We use the above described method (Umeyama) to align model and current contour. The global transformations are applied to all model traces of a spacial position.

(3) We then use the first trace as an initialisation in the following image frame, add the pre- calculated displacement values and search using the classical snakes. Snakes are first introduced by Kass/Witkins [5]. The idea is to define one energy holding the contour together and another one attracting the contour to image features. Using an iterative shema this Energy is minimised.

$$E_{snake} = \int_0^1 (E_{int}(v(s)) + E_{image}(v(s)))ds \quad (6)$$

For the minimisation the iterative Euler Method is used. After the searching process the grid is applied to the contour and the distance vectors are calculated.

(3a) If the newly calculated point lies within a 3* σ region of the displacement field ($\sigma_i = \sqrt{s_i/n}$. The point is saved.

(3b) Otherwise the point is not saved instead the point is replaced by the average point (see equation 3).

4 Results

The above method using this a priori knowledge was compared to a detection method only using snakes. Both times the traces of the physician served as a reference. As an error estimation the least squared error between calculated and manually traced objects was taken.

$$er = \frac{1}{n}\sum_1^n \frac{(p^{calc}(i) - p^{trace}(i)}{p^{trace}(i)} \quad (7)$$

with $p^{calc}(i)$ the calculated point at position i and $p^{trace}(i)$ the point predicted by the phsician in position i.

	Sets	Mean Error
Snakes	10	20 %
Expert Model	10	10 %

5 Conclusion and Future Work

In this paper we presented a first approach using a numerical 2D+t model for the extraction of the left ventricle in transthorasic images. Although such an approach can help detecting and following the LV boundaries the search always has to be controlled by a physician. Especially phatological LVs will be missinterpretated.

In our future work we will optimise our model and modelise the displacement fields of phatologic hearts as well.

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