ROBUSTNESS OF AUTOMATIC QUANTITATIVE STUDY OF THE HEART FUNCTION VERSUS MANUAL ANALYSIS OF MRI TIME SEQUENCES

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Abstract : **The robustness of a segmentation method of the left ventricle on MR images and the accuracy of the computation of significant clinical parameters derived from the segmentation are shown. This is done by comparison with manual measurements performed by a cardiologist.**

I. INTRODUCTION

MRI appears today as a very promising investigation tool for cardiac studies, as it allows for fast acquisition of time sequences of the heart over a whole cardiac cycle, through gradient-echo technique [4]. MRI is non-invasive, provides good blood/tissue contrast regardless of the patient condition, and renders epicardium as well as endocardium. It is therefore better suited to cardiac analysis than angiography or echocardiography. The images used in this work are MRI time sequences acquired with a 1.5T Gyroscan (Philips), gated on the R-wave of the ECG, and with a repetition time TR = 27 ms providing from 19 to 32 images per cardiac cycle, depending on the patient heart rate.

Quantitative study of the left ventricle (LV) requires measuring endocardial volume for each image of the time sequence from a segmentation of the LV. Manual contour delineation has two major drawbacks : it is very time consuming and highly non-reproducible. This work aims at avoiding these drawbacks by providing automated measurements of parameters of clinical interest. The nearly automatic segmentation method has been previously described [2]. It is briefly recalled in section 2. In section 3, the measurements performed from the segmentation for quantitative analysis of the heart function are described. Section 4 details the validation step, which is the main contribution of this paper.

II. SEGMENTATION USING DEFORMABLE CONTOURS AND MATHEMATICAL MORPHOLOGY

The segmentation of endocardium is achieved using an active contour model called g-snake [3]. In this model, the contour is described as a C^2-continuous curve C, parametrized by an arc-length s, with mechanical properties specified by an internal energy expressed by :

$$E_{int}(C) = \int_0^1 \alpha(s) \| \vec{X}_s \|^2 ds + \int_0^1 \beta(s) \| \vec{X}_{ss} \|^2 ds + \int_0^1 \kappa \det(\vec{X}, \vec{X}_s) ds. \quad (1)$$

The first two terms in this energy refer to the classical snake model introduced in [1] and can be interpreted as stretching and bending energies, respectively. The third term in (1) is an isotropic pressure potential which controls the area of the region limited by C.

The initial contour C^0 is deformed until reaching the endocardial contours by applying an external energy derived from the image gradient $\nabla I(\vec{X})$:

$$E_{ext}(C,I) = -\lambda \int_0^1 \| \nabla I(\vec{X}) \|^2 ds. \quad (2)$$

In order to ensure consistency between contours in successive images, a coupling term is added to the total energy [2] which links together time adjacent contours. The resulting expression for E_{tot} is :

$$E_{tot} = \sum_{i=1}^{N} E^i{}_{int} + \sum_{i=1}^{N} E^i{}_{ext} + 2 \sum_{i=1}^{N-1} \sum_{j=i+1}^{N} E^{i,j}{}_{cpl} \quad (3)$$

where N is the number of images in the sequence and $E^{i,j}{}_{cpl}$ denotes the coupling energy calculated as :

$$E^{i,j}{}_{cpl} = \int_0^1 \rho \| \vec{X}^i - \vec{X}^j \|^2 ds \quad (4)$$

iff $i-j=1$ or $i=1$, $j=N$, otherwise $E^{i,j}{}_{cpl} = 0$. These conditions correspond to a nearest neighbor cyclic coupling.

Starting from an initial curve C^0, the segmentation is then performed by iteratively minimizing the total energy defined by (3). The initial contour is obtained via mathematical morphology. Since the LV appears as a non-uniform high intensity area, a marker of the LV is extracted as a regional maximum of the image obtained by filtering the original data by a morphological closing with a large dodecagonal structuring element [3]. This operation reduces noise while homogenizing intensity inside the LV and preserving roundness of the contours. The resulting marker is a good approximation of the LV, and initializing the active contour on its boundary allows the deformation process to converge rapidly.

III. QUANTITATIVE ANALYSIS OF THE HEART FUNCTION

The previously obtained segmentation allows volume measurements over the cardiac cycle from which parameters of clinical interest are calculated, either globally for the entire LV slice, or regionally by dividing the LV into radial sectors. Because of space requirements, this paper is restricted to global measurements. Cardiologists are interested in measuring LV volume and especially in studying, for a given patient, its variation under different conditions. Therefore, they need estimates of such quantitative parameters as ejection fraction (EF) - an usual parameter for estimating the LV function -, peak filling rate (PFR) and time to peak filling rate (TPFR) [4]. The EF is defined as the difference between end diastolic and end systolic volumes expressed as a percentage of end diastolic volume. The PFR is the maximum positive slope of the volume curve and represents the maximum blood flow during the rapid filling phase of diastole. The TPFR measures the time between the end of systole and the instant corresponding to PFR. PFR computation requires accurate calculation of slope. This is achieved

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by approximating the volume curve by retaining only the first four harmonics in the discrete Fourier transform of the volume measurements. Similar parameters can be computed for the ejection phase (peak ejection rate PER and time to peak ejection rate TPER with time origin at systole).

IV. VALIDATION

The weakness of the automatic method presented above lies in the number of parameters. Thus a validation step is needed to test the robustness of the parameters involved in the segmentation process. A good way to validate the method consists in comparing the measurements given by the algorithm with those obtained manually by a cardiologist. Since manual measurements are non-reproducible, the cardiologist was asked to segment each sequence twice. The algorithm, which is reproducible, is expected to give results consistent with the manual ones. In the following, comparisons are performed between the automated measurements and the best of the two manual contours, as well as between the two manual contours. It is difficult to find an objective criterion to compare the results. Since cardiologists are interested in relative rather than absolute values, following their suggestion we have chosen correlation between volume values as a comparison criterion. Table 1 shows the correlations obtained with various values of the parameters. The parameters vary within an interval I(p), providing a correlation varying within an interval I(c). These values can be compared with the 0.971 correlation between the two manual contours: the correlation values obtained with various parameters are always better than 0.971. Table 1 shows that all parameters can vary within a quite large interval without degrading the results, thus proving the robustness of the method. Similar results have been obtained for 6 normal and 4 pathological patients, for two different cardiac rates. These results also prove that the method can be used even by a cardiologist without any deep knowledge about image analysis and segmentation, by using default values: the results obtained this way are likely to be better than those given by a manual method.

parameter	I(p)	I(c)
SC	[1, 5]	[0.988, 0.998]
n	[20, 50]	[0.981, 0.986]
σ	[0.25, 2.5]	[0.979. 0.988]
β	[1.0, 11.0]	[0.988, 0.989]
ρ	[10.0, 50.0]	[0.983, 0.989]
λ	[1.0, 5.0]	[0.979, 0.988]
κ	[0.0, 10.0]	[0.983, 0.988]

Table 1 : correlation between algorithm and manual contours (SC denotes the size of closing, n the number of sampled points on the contour, σ the variance of the Gaussian used for gradient computation, β, ρ, λ, κ are presented in eq. (1) to (4)).

Table 2 illustrates the comparison between quantitative parameters computed by the algorithm (A) and those obtained from two manual contours (M1, M2). The two values given for PFR and PER correspond to absolute (ml/s) and normalized values with respect to the telediastolic volume (1/s). It can be observed from Table 2 that the bad reproducibility of manual measurements induces large variations in parameters. Values given by the algorithm are close, at least, from one of the manual results for all patients but the 4th. This this latter case is explained by poor image quality. In general, results are satisfactory and prove again that the method is at least as good as manual methods and more reliable. The same measurements have been performed for a second cardiac rate for each patient, induced by drug injection, and similar good results have been obtained. Thus, the method allows to compare significant clinical parameters of the heart function under various conditions.

patient	method	EF	PFR (ml/s)	PFR (1/s)	TPFR (ms)	PER (ml/s)	PER (1/s)	TPER (ms)
1	A	69.57	38.08	3.31	61.9	37.89	3.30	-241.1
	M1	70.83	45.93	3.92	273.6	42.72	3.65	-239.5
	M2	73.66	49.96	3.48	40.1	34.85	2.43	-116.4
2	A	61.49	29.27	2.51	98.0	28.76	2.47	-147.8
	M1	61.51	40.22	3.35	112.9	35.62	2.97	-187.8
	M2	62.06	28.53	2.41	138.0	36.71	3.10	-164.3
3	A	61.92	56.88	4.42	126.1	39.57	3.07	-175.4
	M1	69.01	56.36	3.43	108.9	50.60	3.08	-231.6
	M2	66.28	51.23	3.63	102.0	35.07	2.48	-106.3
4	A	47.50	31.57	2.59	118.6	40.27	3.30	-106.6
	M1	57.27	53.17	4.10	75.7	33.19	2.56	-96.7
	M2	64.01	51.57	3.19	100.8	44.62	2.76	-100.1
5	A	66.43	43.45	3.52	130.1	40.96	3.32	-210.1
	M1	67.49	48.39	3.94	59.9	45.56	3.71	-266.5
	M2	62.94	39.39	3.14	100.2	40.22	3.21	-222.2
6	A	62.61	19.16	2.11	144.2	29.97	3.30	-131.2
	M1	64.00	23.31	2.45	130.4	27.79	2.91	-130.4
	M2	61.12	24.71	2.52	106.1	30.80	3.14	-157.1

Table 2 : comparison of quantitative parameters.

The clinical parameters are significant when trying to assess for global abnormalities of the LV function in homogeneous diseases, such as hypertension or primitive cardiomyopathies. The same method applied to regional measurements allows to detect regional abnormalities which occur in ischemic disease or asymmetric LV hypertrophy.

V. CONCLUSION

The accuracy and robustness of an automatic method have been proved for quantitative analysis of heart function from temporal MRI sequences. When measuring values of clinical interest, good correlation with manual methods is obtained for algorithm parameters varying in large intervals. Therefore, precise optimization of parameters is not critical and cardiologists can use the method without a long training as default values provide results at least as good as those obtained with a time consuming manual way.

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