

Local Quantitative Measurements for Cardiac Motion Analysis

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Abstract. We design for this work a new practical tool for computation of non-rigid motion in sequences of 2D heart images. The implementation of our approach allows us to integrate several constraints in the computation of motion : optical flow, matching of different kinds of shape-based landmarks and regularity assumption. Based on the determination of spatio-temporal trajectories, we next propose several measurements to analyze quantitatively the local motion of the left ventricle wall. Some experimental results on cardiac images issued from clinical cases illustrate our approach.

1 Introduction

Cardiac motion analysis has received these last years a great attention from the computer vision community [2, 3, 5, 9, 11, 12]. Since it is a non-rigid organ, the recovery of quantitative parameters featuring heart deformations is a very difficult problem. New medical imagery modalities like Computed Tomography (Fast-CT) or Magnetic Resonance Imagery (MRI) produce now 3D sequences of the beating heart, the second method having the major advantage to be non invasive, while requiring post-synchronization to reconstruct a complete cardiac cycle. More sophisticated imagery techniques like Tagged MRI [1] or Phase Velocity MRI [6] give now direct physical information about the motion. But, until now, these techniques are not often clinically used for a number of reasons. First, the cost of such machines is relatively high. Secondly, sophisticated post-processing tools are necessary to take advantage of these data, like 3D visualization or 3D motion analysis. These tools are not widespread at the moment.

On the other side, cardiologists very often use modalities like Cardiac Ultrasonography, Doppler echocardiography, Angiography or Ventriculography which produce real-time sequences of heart cross-sections or 2D projections. It is clear that the heart deforms in the 3D space and consequently, an accurate study of its deformations must be done with 3D acquisitions. Nevertheless, at this time, it seems that computer vision techniques can be very helpful for cardiologists to give local quantitative measurements on 2D data. These local measurements, combined with global cardiac parameters and the "visual" experience of heart specialists, could help them to improve evaluation, comparison and classification of sequence data. For this study, we designed a simple and fast tool for computing motion in sequences of 2D images.

In our approach we track closed curves which are representative of the anatomical deformations through the time sequence. Several works have already been done on this subject, in particular *Cohen et al.* [5] who match closed 2D *snakes* by minimizing a couple of energies. One energy measures the difference of curvatures between matched points. The second measures the regularity of the correspondence function. For high curvature points, they privilege the first energy. *McEachen et al.* [9] use parametric deformable curves. The matching is also based on curvature with a particular attention to high curvature points, but also integrates information provided by Phase Velocity MRI. Our approach has the following particularities : (i) we perform matching between iso-intensity curves, (ii) we use two kinds of shape-based landmarks : curvature extrema and curvature zero-crossings. This approach can be generalized to 3D images and we plan to do so in the future.

This paper is organized as follows. We first present the method we used to compute motion field between 2D curves (section 2). Based on the determination of spatio-temporal trajectories, we next propose different kinds of local quantitative measurements for assessing myocardial function (section 3). Finally, we illustrate our study with some experimental results issued from clinical cases (section 4).

2 Motion Computation

In this section, we present the different steps of the method for computing motion fields. We first consider a particular curve on each frame (section 2.1), we next extract shape-based landmarks on these curves (section 2.2) and we finally use these landmarks to perform curve matching (section 2.3).

2.1 Isolines

In medical imaging the grey level (or *intensity*) of a pixel is often representative of the tissue which is imaged. These curves are generally called *iso-intensity curves* or *isolines*. Actually, an isoline may be not everywhere significant and it may be necessary to consider only its relevant parts.

Considering a time sequence of images $(I_t)_{t=1,N}$, we first smooth them with a recursive gaussian filter [10]. The width of the filter (about 4 pixels) was chosen in order to preserve accuracy while having smooth curves. Next we extract an isoline (L_t) on each image. We assume that the set $(L_t)_{t=1,N}$ represent the evolution of the same physical boundary during time. The intensity of isolines is chosen manually and is the same for the whole sequence. By construction, these curves are closed, ordered and defined in the real 2D space, i.e. they are defined at a sub-pixel resolution. The problem now amounts to compute the local motion between two successive isolines.

The intensity of the pixel is also often used to do tracking in a time sequence. Optical flow is now a well-known technique for recovering motion, it is based on the assumption that the intensity of a particular point is constant. First used on

sequences of 2D images like in [7], it has been next generalized for 3D images [12]. Thus, by matching isolines with same iso-intensity, one integrates implicitly the optical flow assumption.

2.2 Shape-based Landmarks

The most common way for recovering curve nonrigid motion consists in tracking some particular points in the curve. These points are generally called *landmarks*. A landmark may have several characteristics. One of them is that they must be trackable in a time sequence. Another is that they must well characterize the overall motion. In fact, it means that one may compute the motion just by propagating the values computed on these landmarks. There are different kinds of landmarks : implanted markers, physical landmarks and shape-based landmarks.

Implanted markers are distinctive points physically put in the organ and can thus be tracked easily during the motion [9]. Unfortunately this method is only used for research purpose and can not be clinically generalized.

Tagged MRI is a new technique which provides physical landmarks during the cardiac cycle. It generates a magnetization grid superimposed on the MRI data. Next this grid moves with the heart tissue as the heart moves [1]. Then one has just to compute the displacement of the grid nodes (or intersect points between tag lines and anatomical structures) to obtain the right motion of some points. This method has been successfully used for example to track a volumetric deformable model of the left ventricle [11].

Shape-based landmarks are directly computed from the images. Unlike preceding categories, these landmarks have not always anatomically meaningfull although some works proved their relevance for tracking cardiac motion [9]. In our case, we work on 2D curves and we use two kinds of landmarks : (i) *curvature extrema points* which have been widely used to track left ventricle wall in ultra-sound images [5] or MRI cross-sections [9] (ii) *curvature zero-crossing points* which also are trackable and representative of the anatomical shape.

The estimation of curvature along the isoline is based on the computation of angles between three successive points in the curve. One may compute this curvature at different scales by considering different distances between these successive points. We used here a scale of 20 pixels.

2.3 Curves Matching

The landmarks matching procedure uses the assumption that time resolution is sufficiently fine. This assumption is common for more sophisticated techniques as well. We use a two-step method :

- For each landmark detected in an isoline, we search the closest landmark in the following isoline. If this landmark is sufficiently close and if the difference of curvature of this couple of points is sufficiently small, we accept the match. In this first step, the distance between points is computed in the 2D space.

To add robustness, we keep only *symmetric* matches, i.e. for which the result is identical if we consider the curves in reverse order.

- In the second step, the distance is computed along the curves, i.e. we consider the difference of arclength. For computing arclength, the closest match obtained in the first step gives us the two *starting points*.

This method runs successively with curvature extrema points and curvature zero-crossing points.

In order to obtain a dense motion field between the two curves, we perform linear interpolation between each couple of adjacent displacement vectors given by the landmarks matching algorithm. Next we smooth the resulting motion field by iterative local averaging. All these computations are done at a sub-pixel resolution. We have also taken into account the *starting point problem* by considering at each step of our process the 2D curves as closed *loops* [5].

3 Local Quantitative Measurements

In order to detect cardiac diseases, it is important to make the distinction between global and local quantitative measurements. For example, *ejection fraction* which measures the relative variation of the heart volume between end-of-diastole and end-of-systole is a global parameter. Its normal value is comprised between 0.5 and 0.8. If the computed value is for example less than 0.5, it means that the heart is diseased but it can not help to determine accurately the location of the pathology. Another example concerns mathematical analysis of motion fields with modal analysis which gives a compact but global description of the field [3]. In this work we try to determine local quantitative measurements because they can prove more useful for the cardiologist to locate and quantify a pathology.

3.1 Spatio-temporal Trajectories

trajectories computation To consider a single point motion, we define a *spatio-temporal trajectory* as a list of points $(P_t)_{t=1,N}$ for which each point P_t belongs to the isoline (L_t) in a time sequence and represents the position of the same physical point P a time t . Like for motion estimation, the trajectory is computed at a sub-pixel resolution.

periodicity constraint It is logical to compute periodic trajectories because of the periodic nature of the heart beats. The method we used is described in [6]. We first compute two trajectories, one in the forward direction and the other in the backward direction. Next we compute an averaged trajectory by combining these two trajectories. The averaged points are computed along the curves. The weighting of each trajectory depends on the temporal position of the point. If it is far from the starting point, the weight will be low and vice versa. Thus, by construction, the averaged trajectory will be periodic.

temporal smoothing The periodicity constraint integrates the temporal dimension in the motion computation. However it is desirable to add an other temporal constraint in order to further regularize the spatio-temporal trajectory. Such a result can be obtained just by smoothing the curvature along the trajectory. One convenient way to do this consists in minimizing the trajectory length. In order to preserve the original shape of the trajectory, the smoothing is performed only if the local length of the trajectory can be substantially decreased, it means for most unregular pathes. This processing is iterated until the trajectory does not change anymore. Figure 1 shows the trajectory of a point with all the isolines.

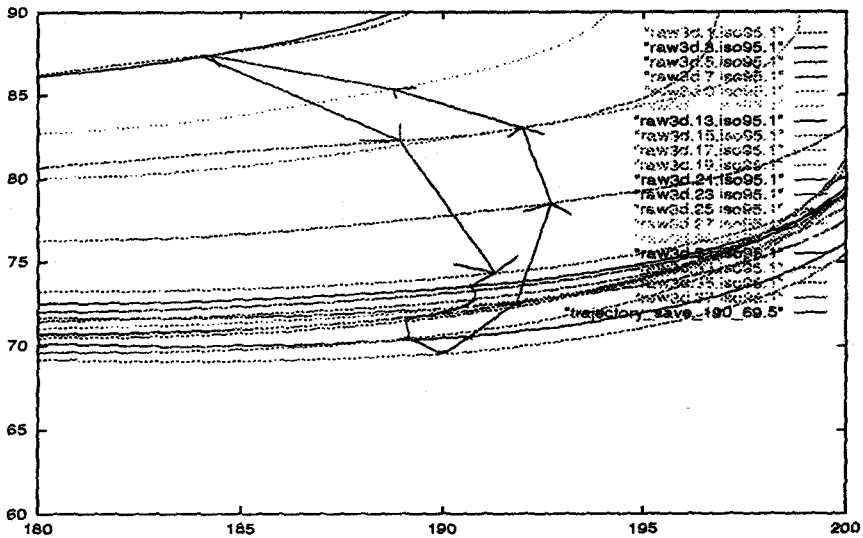


Fig. 1. Spatio-temporal trajectory : this result integrates motion field computation, periodicity constraint and temporal smoothing

trajectory kynesis Velocity of a point $\frac{\partial P}{\partial t}$ and its acceleration $\frac{\partial^2 P}{\partial t^2}$ may be useful for cardiologists in particular to check the regularity of the motion which helps to quantify the local physical characteristics of the heart muscle.

3.2 Segments Time Evolution

If we consider the trajectories of two neighbor points along the isoline, they describe the time evolution of the left ventricular wall segment between them. Thus we may calculate during time some measurements to characterize it : (i) *length* which gives an index of local elasticity of the curve segment (ii) *bending energy* which is equal to the sum of squared curvature along the segment, gives information about its local deformability.

4 Experimental Results

4.1 Ventriculography with Catheterization

Angiography is an imaging technique which consists in introducing an X-ray contrast agent in the arteries with a catheter. By this mean, one can inspect the interior of the arteries, and, in pathologic cases, detect artherosclerotic or fibromuscular stenoses inside an artery which can lead to disturbances in blood flow. In some cases, the little balloon at the top of the catheter may be next used to open stenotic coronary blood vessels [4].

Ventriculography is a similar examination but, this time, the catheter is directly introduced inside the left ventricle. So, with the contrast agent, it becomes possible to evaluate the motion of the left ventricle wall. Figure 2 shows an image produced by this examination.

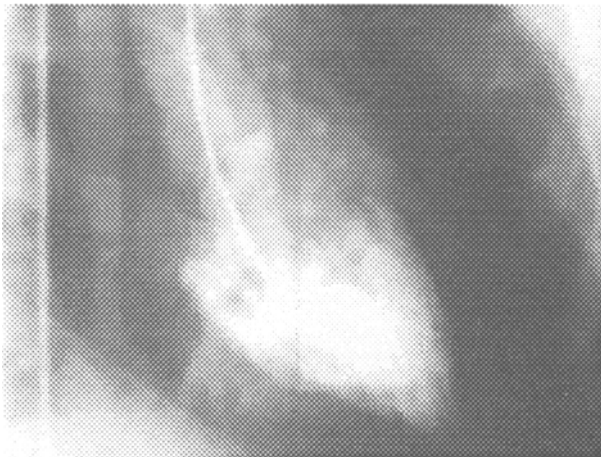


Fig. 2. Ventriculography with catheterization data (courtesy of Bikur Holim Hospital)

Generally, distinction is made between four kinds of kinesis [8] : (i) normal kinesis (ii) hypokinesis : the motion is less than normal (iii) akinesis : some

parts of the wall do not move (iv) dyskynesis : some parts of the wall do not move in the normal direction. An accurate evaluation of the wall motion can point to a certain problem in the heart muscle or in the coronary arteries.

4.2 Clinical Cases Analysis

We did experiments on clinical cases provided by the cardiology department of the *Bikur Holim* hospital, at Jerusalem. Ventriculography is done routinely in this hospital. Nevertheless, our processing requires some preliminar conditions : (i) the quantity of injected contrast product must be sufficient in order that all the ventricle wall may be apparent (ii) the structures appearing in the image background may not perturb the isoline extraction first stage. Under these conditions, we perform the following chain of computations for each sequence :

- compute all the motion fields
- consider the relevant part of the isoline and divide it into N segments of equal arclength
- for each segment, compute the following features
 - **Midpoint Motion** : trajectory length (TOT), maximal displacement between two frames (MAX), minimal displacement (MIN), mean displacement (MEAN), standard deviation (SD) and amplitude (AMP) which corresponds to the maximal distance between two positions in the trajectory.
 - **Segment Length** : maximal length (MAX), minimal length (MIN), length fraction ($\text{FRAC} = \frac{\text{MAX} - \text{MIN}}{\text{MAX}}$), mean length (MEAN) and standard deviation (SD).
 - **Segment Bending** : maximal bending (MAX), minimal bending (MIN), bending fraction (FRAC) , mean bending (MEAN) and standard deviation (SD).

These parameters are based on the currently used cardiological techniques for the evaluation of the heart muscle [4] and the doctors demands. Other characteristic measurements of the heart muscle function are being considered.

CASE 1 We present now results obtained on a clinical case. By a cardiologist diagnosis, it is a case of normal kynesis. For the first example, we considered 10 segments. Figure 3 presents the evolution of the segments length and bending during time. Table 1 presents the evolution of each segment midpoint motion, overall length, and bending, which gives some quantification of the heart muscle behavior at that segment.

CASE 2 By a cardiologist diagnosis, this second example is a case of slight hypokynesis near the heart apex. Figure 3 presents the evolution of the segments length and bending during time. Table 2 presents the same features as table 1 computed on each segment. The hypokynesis is confirmed by the low amplitude

Table 1. Features computed on the segments (CASE 1)

Segment Number		1	2	3	4	5	6	7	8	9	10
Midpoint Trajectory	TOT	79.5	100.8	107.3	163.6	154.9	177.3	130.5	104.0	92.0	98.7
	MAX	8.9	17.4	17.4	23.1	21.6	24.8	30.0	28.1	23.4	19.1
	MIN	0.4	0.2	0.3	0.2	0.7	1.0	0.3	0.5	0.5	0.1
	MEAN	4.7	5.9	6.3	9.6	9.1	10.4	7.7	6.1	5.4	5.8
	SD	2.4	3.7	4.5	5.7	5.2	5.9	7.0	5.9	5.1	4.8
	AMP	30.5	43.4	48.8	65.1	72.0	82.6	58.0	43.4	34.6	34.0
Length	MAX	56.2	50.6	67.8	59.0	59.2	55.8	57.2	48.4	55.5	47.5
	MIN	28.5	30.1	32.9	39.5	32.0	21.1	18.3	23.5	29.6	25.9
	FRAC	0.5	0.4	0.5	0.3	0.5	0.6	0.7	0.5	0.5	0.5
	MEAN	41.8	38.6	44.8	45.8	46.4	42.1	40.3	38.0	41.3	33.7
	SD	8.0	6.2	9.9	6.3	9.0	8.9	12.1	9.6	7.3	7.0
Bending	MAX	16.4	7.7	9.0	11.4	1.2	24.3	13.2	2.4	1.2	5.7
	MIN	6.0	0.1	0.5	0.0	0.0	12.9	2.1	0.2	0.1	0.0
	FRAC	0.6	1.0	0.9	1.0	1.0	0.5	0.8	0.9	0.9	1.0
	MEAN	11.7	1.8	2.8	3.3	0.5	18.7	5.5	0.9	0.4	2.1
	SD	3.1	2.0	2.6	3.4	0.3	3.6	3.3	0.6	0.3	2.0

in segments 4, 5, 6, 7 (near the heart apex) relative to case 1. We are currently working on a statistical model of heart kinesis with a large number of cases.

Conclusion

We have presented a fast and practical tool for computing motion field on sequence of 2D cardiac data. Based on the determination of spatio-temporal trajectories, this tool allowed us to compute local quantitative measurements representative of the heart activity during the whole cardiac cycle. These measurements may be useful for cardiologists to evaluate more accurately some cardiovascular diseases, like coronary arteries disease. The next step will consist of doing clinical validation on a large number of cases. We hope to present such results at the time of the conference. Future work includes definition of standard local parameters in order to reduce the heart deformations to a minimal number of representative values. Another direction concerns the developpement of the user-interface for a practical use. Finally we intend to extend these measurements for other kinds of modalities, like cardiac ultrasonography and also sequences of 3D data.

Acknowledgments

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Table 2. Features computed on the segments (CASE 2)

Segment Number		1	2	3	4	5	6	7	8	9
Midpoint Trajectory	TOT	160.4	146.0	112.1	108.1	107.7	81.7	85.1	165.9	209.8
	MAX	37.9	33.2	25.0	27.6	27.9	22.9	25.2	40.3	46.6
	MIN	1.0	0.4	1.1	0.6	0.2	0.6	0.8	0.1	0.3
	MEAN	10.7	9.7	7.5	7.2	7.2	5.4	5.7	11.1	14.0
	SD	8.5	8.1	5.9	6.0	6.3	5.0	5.9	11.4	13.5
	AMP	70.5	68.6	47.5	41.9	41.7	32.3	37.4	50.0	64.6
Length	MAX	62.2	55.6	44.9	47.0	57.1	44.8	57.9	43.5	43.5
	MIN	43.5	31.6	22.1	14.4	28.4	28.8	27.4	13.0	16.9
	FRAC	0.3	0.4	0.5	0.7	0.5	0.4	0.5	0.7	0.6
	MEAN	53.2	40.6	34.6	31.9	43.1	37.3	37.6	31.0	31.3
	SD	6.4	5.6	8.5	9.4	8.2	5.7	8.5	10.7	9.1
Bending	MAX	5.8	20.5	4.0	16.9	18.7	1.8	1.6	3.2	5.0
	MIN	0.2	2.3	0.4	1.6	3.0	0.1	0.1	0.3	0.2
	FRAC	1.0	0.9	0.9	0.9	0.8	0.9	0.9	0.9	1.0
	MEAN	2.5	13.4	2.3	11.1	8.4	0.7	0.6	1.8	2.0
	SD	1.5	6.5	1.0	4.2	4.5	0.5	0.5	0.9	1.5

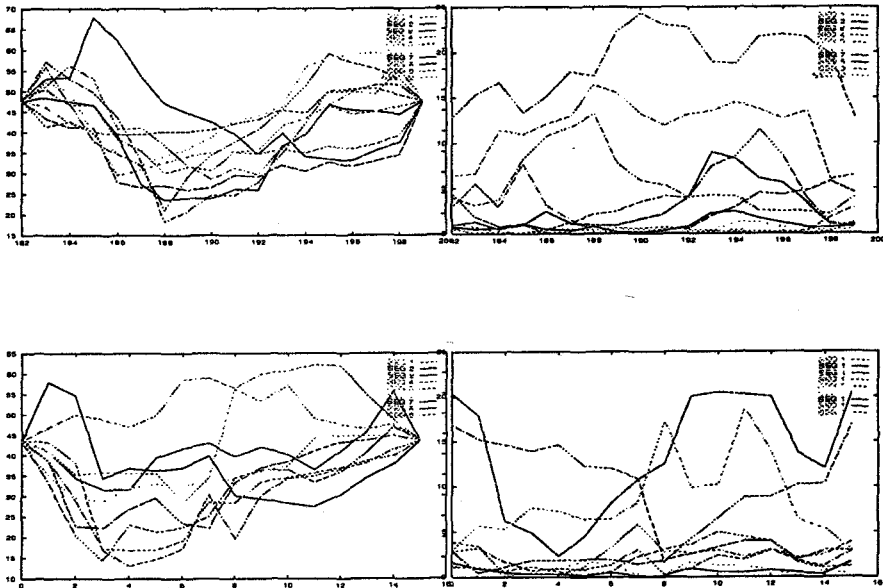


Fig. 3. Evolution of length (left) and bending (right) for each segment. On up, CASE 1 and on bottom, CASE 2

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