

Regional Motion Patterns for the Left Ventricle Function Assessment

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Abstract

Regional scores (e.g. strain, perfusion) of the Left Ventricle (LV) functionality are playing an increasing role in the diagnosis of cardiac diseases. A main limitation is the lack of normality models for complementary scores oriented to assessment of the LV integrity. This paper introduces an original framework based on a parametrization of the LV domain, which allows comparison across subjects of local physiological measures of different nature. We compute regional normality patterns in a feature space characterizing the LV function. We show the consistency of the model for the regional motion on healthy and hypokinetic pathological cases.

1. Introduction

The presence of a myocardial scar, as well as the decrease of coronary blood flow supply at a given territory, induce a variation of the (normal) regional patterns of myocardial contractility and impair global myocardial function [8]. In order to describe myocardial function, two issues should be addressed:

- **Define one or several parameters characterizing the myocardial function and which can be obtained for any patient in a reproducible manner.** Several global indicators such as cardiac output, ventricular volume or ejection fraction have been widely used in clinical routine to evaluate heart function [6]. Nevertheless, these indicators are not able to localize injured zones. Regional parameters, such as strains or perfusion, have arisen as more precise indicators for cardiac function assessment [2]. Regional parameters require estima-

tion of the motion that the myocardial tissue undergoes along the cardiac cycle. Tagged MR (TMR) [1] is the reference imaging modality for intramural tissue motion visualization. The 2D motion maps provided by any of the (many) existing methods [4, 7, 9] are the input data for computing local function scores.

- **Create a pattern of normality (parameter ranges) from a healthy population and define a measure in the parameter space discriminating pathological cases.** There is a lack of statistical analysis on the expected parameter ranges and normality patterns for assessment of the LV function. Existing approaches [10, 3] register all frames to a reference one to account for inter and intra patient variability. In [10] the authors use average motion models for improvement of motion estimation in TMR sequences. The work in [3] uses functional component analysis to extract statistical models of a single strain. Statistical models of complementary regional data extracted from different image modalities has not been deeply addressed, so far.

In this paper we define a general comparison framework, the Normalized Parametric Domain (NPD), which allows moving over the left ventricular domain (\mathcal{LV}) in (natural) radial and circumferential coordinates based on anatomical features at any time of the cardiac cycle. In this manner, the NPD allows the fusion of clinical parameters of different natures (scalar and vectorial), their comparison across patients and, thus, definition of normality models. Principal component analysis serves to define the variation model of a vector describing LV integrity in the NPD domain. Our framework is used to compute regional patterns of the LV motion observed in TMR sequences from 17 volunteers. The validation is done in healthy volunteers and patients with

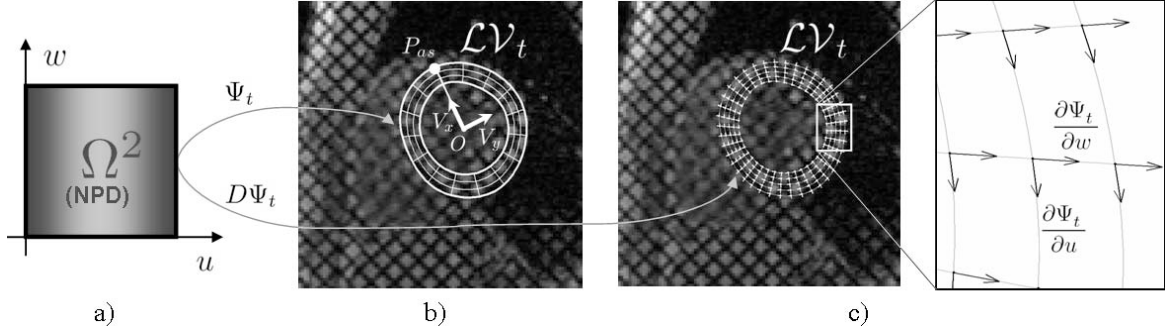


Figure 1. NPD Framework. a) Normalized Parametric Domain. b) Anatomical reference and parametrization of \mathcal{LV}_t . c) Local reference (and detail) for vectorial data mapping.

several degrees of hypokineses.

The paper is organized as follows: Section 2 defines the NPD framework, Section 3 constructs the statistical models of regional functionality and Section 4 presents the results obtained for analysis of the regional motion.

2 Normalized Parametric Domain

Comparing data extracted from different subjects requires coping with two main issues:

- Intra-patient variability related to the change of LV geometry due to cardiac motion.
- Inter-patient variability related to heart's anatomical differences among subjects.

Existing approaches [10, 3] address both issues by registering all frames to a reference one. Although they serve to compare across patients, they do not provide intuitive coordinates. Provided that analysis and extraction of LV scores requires a further segmentation step to define the LV domain, we [5] parameterize the LV domain by its angular and radial coordinates. This registers the LV to its normalized parametric domain, $\Omega^2 = [0, 1] \times [0, 1]$, via the parametric diffeomorphism [11]. We will note by \mathcal{LV}_t the LV domain in the image at a given systolic time, t , and by $\Psi_t(u, w) : \Omega^2 \rightarrow \mathcal{LV}_t$, its parametrization. The map $\Psi_t(u, w)$ is defined using B-splines and taking into account anatomical landmarks in a two-fold process:

- **STEP1: Initial parametrization.** First we define a new coordinate system based on anatomical landmarks in order to account for affine differences among subjects. An affine coordinate system is given by means of an origin of coordinates, O , and two independent axis, V_x, V_y . The new origin is

defined as the center of mass of a set of points segmenting the myocardial borders (endocardium and epicardium). The new axis V_x is a unitary vector starting at O and pointing to the point, P_{as} , joining the right and left ventricles and separating the septum and the anterior walls. Finally the vector V_y is also unitary, orthogonal to V_x and pointing oppositely to the septal wall. The parametrization at time zero, is given by fitting a B-Spline to a uniform sampling (in the new affine coordinate system) of the region enclosed between endocardium and epicardium.

- **STEP2: Parametrization at positive times.** Image points in \mathcal{LV}_0 boundaries are evolved according to the heart motion estimated by applying the Harmonic Phase Flow method [4] to Tagged MRI sequences. Keeping the same parametric values than at $t = 0$, we adjust a B-spline to the updated \mathcal{LV} domain.

The above procedure ensures that, regardless of the patient and imaging modality, a given parameter (u, w) always corresponds to the same anatomical location in the \mathcal{LV} . Figures 1 (a) and (b) illustrate the main steps involved in the definition of NPD and the map $\Psi_t(u, w)$. Figure 1 (b) shows the affine reference of STEP1 and a uniform sampling (square regions) of the approximation by B-splines of the \mathcal{LV} domain enclosed between myocardial walls.

2.1 Mapping Data to the NPD

In order to compare measurements across different patients, data must be mapped to the NPD. Local scores of the LV function can be either scalar (e.g. strain) or vectorial (e.g. motion). Scalar data is mapped to Ω^2 by simply computing it at the points, $\Psi_t(u, w)$, given

by the parametrization. For vectors one should use the Jacobian of the inverse of the parametrization, which computation is not straightforward. As alternate we decompose [11] the vectors into their circumferential (corresponding to the u coordinate) and radial (corresponding to the w coordinate) components. This local reference (see fig.1(c)) is obtained by normalizing the vectors given by the parametrization partial derivatives:

$$E_{circ}(p) = \frac{\partial \Psi_t}{\partial u}(u, w), \quad E_{rad}(p) = \frac{\partial \Psi_t}{\partial w}(u, w)$$

The coordinates of vectorial scores in the above local reference system are mapped back to Ω^2 as scalar quantities for comparison across subjects.

3 Regional Function Patterns

The mapping to Ω^2 of several clinical scores, each of them emphasizing a functional aspect, gives, for each point $\Psi_t^n(u, w) \in \mathcal{LV}_t$, a Q -dimensional feature vector, $\Phi_t(u, w) = (\phi_t^1(u, w), \dots, \phi_t^Q(u, w))$, characterizing LV functionality. We define regional function patterns by dividing \mathcal{LV} into several spatio-temporal regions.

Regions are obtained by splitting Ω^2 into $N_L \times N_S$ rectangular regions, $\omega_{l,s}$, with $l = 1 \div N_L$ and $s = 1 \div N_S$. The mapping of such regions into \mathcal{LV} give a partition into N_L layers and N_S sectors. The functional behavior at a given region (l, s) and systolic time t is defined by the average of the descriptors of a set of points uniformly sampled in that region:

$$\Phi_{l,s,t} = \frac{1}{N_u N_w} \sum_{i=1}^{N_u} \sum_{j=1}^{N_w} \Phi_t(u_i, w_j) \quad (u_i, w_j) \in \omega_{l,s}$$

Normality patterns follow from the statistical analysis of the values obtained for healthy volunteers. We apply principal component analysis to each region in order to obtain the orthogonal basis that best explains the correlations among functional parameters. The eigenvectors of the covariance matrix of the observations, $\Sigma_{l,s,t}$, give the modes of variation and the eigenvalues their normal expected ranges around the average value of all samples $\mu_{l,s,t}$.

3.1 Regional Function Assessment

Given a new incoming subject, we evaluate its regional LV function by computing the deviation of its regional descriptor, $\Phi_{l,s,t}$, from the average normal model. We use the Mahalanobis distance given by:

$$dM_{l,s,t} = \sqrt{(\Phi_{l,s,t} - \mu_{l,s,t})^T \Sigma_{l,s,t}^{-1} (\Phi_{l,s,t} - \mu_{l,s,t})}$$

to quantify such deviation at a given systolic time t . The average of $dM_{l,s,t}$ for all times gives a compact description of the region integrity:

$$\overline{dM}_{l,s} = \frac{1}{N_P} \sum_{t=1}^{N_P} d\Phi_{l,s,t}$$

for N_P the number of sequence frames (systolic phases). For a wide clinical use, we will describe the degree of functional abnormality as "moderately", "mildly" or "severely" abnormal. Under the assumption of normally distributed data, we might classify values according to the area of a cumulative normal distribution of covariance matrix $\Sigma_{l,s,t}$ and mean $\mu_{l,s,t}$. We consider that normal population covers 95% of the area (≤ 2 standard deviations) and that values outside 99.9% of the area should be considered "severely" abnormal. This gives the following rule:

$$RF_{l,s} = \begin{cases} Normal & \text{if } \overline{dM}_{l,s} \leq 2 \\ Moderate Ab. & \text{if } 2 < \overline{dM}_{l,s} \leq 3 \\ Mild Ab. & \text{if } 3 < \overline{dM}_{l,s} \leq 4 \\ Severe Ab. & \text{if } 4 < \overline{dM}_{l,s} \end{cases}$$

4. Experiments and Results

We applied our NPD framework to characterizing and assessing the regional motion observed in TMR sequences. Our data set consists of 17 healthy volunteers and 4 patients with several degrees of hypokinesia. For each subject, TMR sequences at basal, mid and apical myocardial levels were recorded in breath-hold with a Siemens Avanto 1.5 T. (Erlangen, Germany) equipment. The 2D tissue motion extracted with the HPF [4] method constitutes the feature space. For each level, we computed regional models for 3×15 regions in 9 systolic phases. Two experiments were performed:

- **Consistency of the statistical model.** We have computed the leave-one-out error for the volunteers data set. Table 1 summarizes the results: the 1st column ($\overline{dM}_{l,s} \leq 2$) gives statistics for well classified regions and the 2nd column ($\overline{dM}_{l,s} > 2$) for wrong classified ones. For all three levels, we achieve an average accuracy rate over 90% and a similar range in the Mahalanobis distance (below 2.43 in average) for wrong classified sectors. It is worth mentioning that all regions were classified as normal in 5 basal, 8 mid and 8 apical sequences.
- **Clinical potential.** Physicians were asked to visually identify those regions moving abnormally. The classification given by $RF_{l,s}$ computed using

Table 1. Leave-one-out Error

	$\overline{dM}_{ls} \leq 2$		$\overline{dM}_{ls} > 2$
	<i>Acc.Rate</i>	\overline{dM}_{ls}	\overline{dM}_{ls}
<i>Base</i>	90% \pm 8%	1.35 \pm 0.34	2.34 \pm 0.27
<i>Mid</i>	92% \pm 9%	1.26 \pm 0.36	2.39 \pm 0.35
<i>Apex</i>	91% \pm 8%	1.22 \pm 0.35	2.43 \pm 0.37

the 17 volunteers for normality models was compared to the manual labelling. Figure 2 shows, in bulls eye charts, the output of RF_{ls} with the abnormal regions manually identified (with dots) for 3 of the patients considered. We obtained a 5% of false negatives (regions that physicians considered to behave abnormally, not recognized by our classifier) for base, 9% for mid and 5% for apex.

5. Conclusions and Future Work

We presented a general framework, the NPD, allowing comparison across patients of data coming from different image modalities. NPD is used to create normality patterns of complementary descriptors of the regional function of the LV. We illustrate its clinical potential by creating normality patterns of the LV motion in TMR sequences from 17 volunteers. Model consistency is shown by average leave-one-out accuracies over 90%. We obtained encouraging results in assessing the regional integrity of the LV in 4 hypokinetic pathological cases.

Given the difficulty of manually labelling pathological cases, in this work we focused on motion patterns of a healthy population. We plan extending results to characterization of specific pathologies using further clinical scores, such as strains and perfusion.

Acknowledgements

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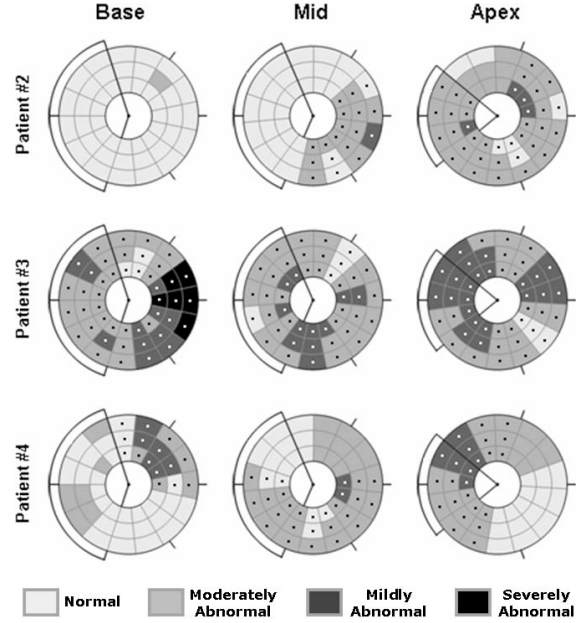


Figure 2. LV Motion Assessment in Pathological Cases

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