Regional Multiscale Motion Representation for Cardiac Disease Prediction

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***Abstract*—Heart characterization is a challenging task due to the non-linear dynamic performance and the strong shape deformation during the cardiac cycle. This work presents a regional multiscale motion representation of cardiac structures that is able to recognize pathologies on cine-MRI sequences. Firstly, a dense optical flow that considers large displacements was computed to obtain a velocity field representation. Then, regional dynamic patterns are coded into a multiscale scheme, from coarse to fine, emerging the most relevant cardiac patterns that remain along the different scales. The resulting motion descriptor is then formed by a set of flow orientation occurrences computed in whole multiscale regions. This descriptor is mapped to a previously trained Random forest classifier to obtain a prediction of the cardiac condition. The proposed strategy was evaluated over a set of 45 cine-MRI volumes achieving an average F1-score of 77.83% on the task of binary classification of among fourth cardiac conditions.**

cine-MRI, Cardiac disease classification, Multiscale analysis, Optical Flow

I. INTRODUCTION

Cardiovascular diseases are the leading cause of death around the world that amounts in 2016, more than 17.9 millions of deaths, according to World Heart Organization (WHO) [1]. The understanding of cardiac motion patterns results fundamental to treat, prognoses and follow heart diseases. Cine-MRI sequences are ideal medical sequences that provide heart anatomic and dynamic visualization over the cardiac cycle, allowing to cardiologist analyze particular conditions and support diagnose [2]. Despite current advantages from cine-MRI sequences, clinical heart diagnosis is a challenging task due to the very complex shape and motion behavior of ventricles. Likewise, non-linear cardiac motions are captured in low temporal resolution and represented as strong position changes, which difficult the analysis of dynamic patterns.

In the state of the art has been reported several computational strategies to model cardiac shapes and motions, that help with quantitative diagnosis support. For instance, automatic filtering of large cine-MRI collections, regarding the acquisition plane, is valuable to support diagnosis w.r.t other similar volumes. In such line, Margeta *et. al.* [3], [4] proposed several strategies based on convolutional neuronal network (CNN) and forest classifiers to predict chambers regarding acquisition views. Such an approach is interesting as the first step of classification but remain limited to global cine-MRI modeling. Also, several approaches have been developed to code cardiac structures and motions, which result useful to predict and correlate diseases. For instance, Zuluaga *et. al.* [5] proposed a multi-atlas approach to assisted diagnosis, in which synthetic representative images are generated from particular pathology populations. Then, the label of the most similar representative image is propagated to the target image. However, this method only considers morphological heart features, losing a motion cardiac characterization. Other approaches have segmented ventricles and estimated the cardiac disease condition from obtained shapes on diastole and systole states [6]–[9]. These approaches achieve promising results but depend on the segmentation task of ventricles and also lost motion information into the analysis.

Also, Goksel *et. al.* [10] introduced a left ventricle (LV) myocardium classification strategy using tagged MRI sequences. In this work, normal vs abnormal classification was achieved by analyzing predominant motion curves as a descriptor of heart dynamics. The validation shows coherent results but remains restricted to the use of tagged sequences that lost anatomic heart information. In Sarmiento *et. al.* [11] was proposed a dense Hough Transform to track heart and a motion histogram at different heart segments to code motion. The resulting descriptor is mapped a Support Vector Machine Classifier (SVM) to predict the volume class. This approach, however, takes much of the computation time to localize the heart center from Hough transform and the descriptor is limited to a fixed split of heart, losing dynamic information.

The main contribution of this work is a spatio-temporal motion descriptor that coded regional dynamic patterns from a multiscale scheme. This regional analysis along cardiac cycle form a descriptor that serves as a signature of the particular heart condition. Firstly, a dense motion field is obtained from an optical flow considering large displacements, a typical condition of heart dynamic. Then, several spatial scales are obtained to analyze ventricles along motion from coarse to fine motion scheme. Each of the computed regions is summarized with motion histograms that coded the most common occurrences of orientation. The set of histograms form the motion descriptor that is mapped to a Random forest classifier to obtain non-linear boundaries among pathologies,

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achieving an automatic prediction.

II. PROPOSED METHOD

This work introduces a new approach to regionally characterize profiles of apparent velocity, captured from a dense optical velocity field. For doing so, a spatial optical flow was implemented that is able to recover large heart displacement. Hence, heart regions are analyzed from a spatial multiscale approach, allowing to stand out the most significant patterns of motion. In such case, heart region is iterative split from coarse to fine segments. Each of these sub-regions is summarized by using a histogram of velocity orientations, that counts the main velocity occurrences on specific regions. The whole characterized regions are mapped to a random forest strategy for disease prediction. In the next subsections are described in detail the steps considered on the proposed approach.

A. Large Displacement Optical Flow

The principal challenge on cardiac motion characterization is to track and recover the non-linear behavior of heart chambers, during the diastole and systole process. In this work was implemented a dense optical flow, that considers large motion displacement, and allows to recover salient motion cardiac patterns [12]. This approach is able to describe motion/deformation of chambers, from several restrictions to represent the object of interest, between two consecutive cine-MRI frames: $I(\mathbf{x})_t$, $I(\mathbf{x})_{t+1}$. The resultant motion field $w := (u, v)^T$ recover displacement vectors for each pixel on each cine-MRI slice. This work assumes classical restrictions, such that the heart color ($E_c(w) = |I_t(x+w(x))-I_{t+1}(x)|^2)$) and the gradients ($E_g = (|\nabla I_t(x + w(x)) - \nabla I_{t+1}(x)|^2)$ remain the same in short intervals of time. Likewise, in this approach is included additional restrictions to lead with non-linear deformations by considering smoothness on captured field, computed on near regions, expressed as $E_s(w) = (|\nabla u(x)|^2 + |\nabla v(x)|^2)$. Interestingly enough, this approach is able to capture non-local coherent displacements of the heart by considering similar appearance velocity field patterns, calculated among consecutive regions using the matching of SIFT descriptors. This non-local restriction could be formalized such as: $E_d(w1) = |f_{t+1}(x + w_1(x)) - f_t(x)|^2$, where d is the descriptor vector and $(f_{(t)}, f_{(t+1)})$ are the computed velocity patterns in matched non-local regions. Hence, the resulting cardiac motion field is obtained by minimizing the described restriction at each couple of consecutive frames, following an optimization architecture: $E(w) = E_c(w)+\gamma E_g(w)+\alpha E_s(w) +\beta E_m(w, w1) + E_d(w1)$. According to this, we can quantify the movement of the cardiac cycle taking into account long displacements caused by diastole and systole in this periodic cycle. Examples of the computed cardiac motion field are illustrated in Figure 2. An additional advantage of implemented large displacement flow is the robustness against local noise produced by low resolution of images or which is naturally captured in such devices.

B. Regional Multiscale Analysis of cardiac structures

Dynamic heart patterns could be regionally identified according to different cardiac structures. In such sense, a proper spatial analysis results fundamental to emerge relevant cardiac descriptors that allow standing out heart kinematic structures. Nevertheless, tracking such patterns associated with cardiac regions is difficult because of the natural heart deformation during cycle. In this approach, a regional multi-scale analysis was adopted (see Figure 1), which consists of splitting the heart region from coarse to fine spatial scales. The dynamic patterns that remain along the spatial scales are the most significant for describing a particular heart.

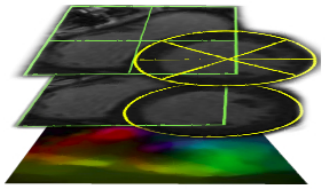


Fig. 1: Regional Multiscale heart analysis. Once the dense optical field is captured, a regional analysis is herein adopted

A set scales were computed at each time over basal slices, using short axis cine-MRIs and for the whole cardiac cycle. At each time, the computed motion field $[\mathbf{u_t}(\mathbf{x}), \mathbf{v_t}(\mathbf{x})]$ was split into three different scales, according to spatial reference of slice $I(x)$. In a coarse scale, the complete region of the heart s_g^0 is bounded to analyze the main average velocity patterns of heart (see on Figure 2-b). In a second scale, the heart region is vertically split to characterize ventricle motion patterns, individually: (s_l^1, s_r^1). Due to heart anatomy, the left ventricle region s_l^1 is bounded in a circular way, while for right ventricle region s_r^1 is defined as a rectangle (see on Figure 2-c). Finally, the finest scale is defined to capture localized pattern regions in both ventricles, expressed as $(s_{l_1}^2, \ldots, s_{l_k}^2), (s_{r_1}^2, \ldots, s_{r_j}^2)$. The left ventricle is radially split $s_{l_i}^2$ following the American Heart Association (AHA) protocol [13]. This protocol has been built from clinical experience and radially characterizes left ventricle patterns that could be associated with diseases (see on Figure 2-d). The main advantage of proposed work is from such scale, the expert could visualize left ventricle dynamic behaviors. Regarding the right ventricle, in most fine scale, the regions $s_{r_i}^2$ are obtained by proportionally splitting the high-level rectangle. Such configuration results the most appropriate because of the stationary performance of this ventricle, with strong local deformations.

The regional multiscale characterization enriches dynamical heart analysis and allows a better description of diseases [14]. Specifically, this redundant analysis over different spatial scales promotes that coherent and persisting motion patterns will be more significant as functional heart descriptor. Such multiscale approach is carried out at each time of the sequence,

recovering a complete description of whole heart dynamic. From such detailed description is possible to differentiate abnormal patterns, resulting useful for automatic predictions that serve as support of diagnosis. For instance, the cardiac hypertrophy is understood as increasing of ventricles with the consequence of slow velocity patterns on cardiac cycle. In such case, the global scale could be sufficient to characterize these examples from controls. In contrast, some heart failures are a consequence of poor capacity to pump blood as a consequence of wear in some localized regions. In such a case, the finest scale is demanding to better understand the diseases and also to find the proper difference with respect to control hearts.

C. Regional Velocity Histograms

Once the spatial partition is carried out at different scales s_i, a velocity descriptor is computed as oriented velocity histograms, which are weighted w.r.t the norm of the field in each region. Given the magnitude of each velocity vector, $\|\nabla W(x)\|$ and taking into account a set of orientation bins $p = \Delta\theta$ for each histogram, the histogram at each segment could be defined as:

$$h(p) = \sum_{i \in \theta \mathbf{W}(\mathbf{x})} R_i(x) \left\|\nabla W(x)\right\|, i = \left\{1, 2, ..., \frac{2\pi}{\Delta\theta}\right\} \tag{1}$$

$$R_i(x,y) = \begin{cases} 1 & \text{if } (i-1)\Delta\theta \leq \theta(x) < i(\Delta\theta) \\ 0 & \text{elsewhere} \end{cases}$$

Then, each region into the multiscale framework is characterized at each slice using the oriented velocity histograms, defined as $\mathbf{H_c} = [h_1, h_2, \dots h_k]$. The set of histograms $\mathbf{H_c}$, computed along the cardiac cycle constitutes the cardiac motion descriptor that represents the heart performance and could highly correlate the cardiac condition of each cine-MRI.

D. Forest Prediction of the Cardiac Disease

Classification and disease prediction from computed motion patterns were carried out using a supervised Random Forest algorithm (RaF). This algorithm is well known for the robust performance face to complex problems that require the definition of non-linear boundaries into feature space. In our particular case, motion histograms can exhibit such complex structures, requiring non-linear functions to split the feature space. In our approach is defined as a training set of motion descriptors $\mathbf{x_i} \in R^n$, where n is the dimension of concatenated bins, computed on a multiscale approach. Each $\mathbf{x_i}$ has associated a corresponding label y_i of the particular cardiac pathology. Then, from the defined training dataset $(\mathbf{x_i}, y_i)$ is defined a forest of decision trees, as: $h(\mathbf{x}, \Theta_k), k = 1, 2, ..., n$ where Θ_k is each i.i.d decision tree. Each tree Θ_k is formed by a uniform random selection of features. For each selected bin feature x_i is learned a particular threshold τ_i that builds node in the tree $\varrho(x_i, \tau_i)$ and produces a new left and right partition. The whole process of learning, i.e., the split each feature to form particular data structures, is carried out into a minimization impurity scheme using an entropy information gain.

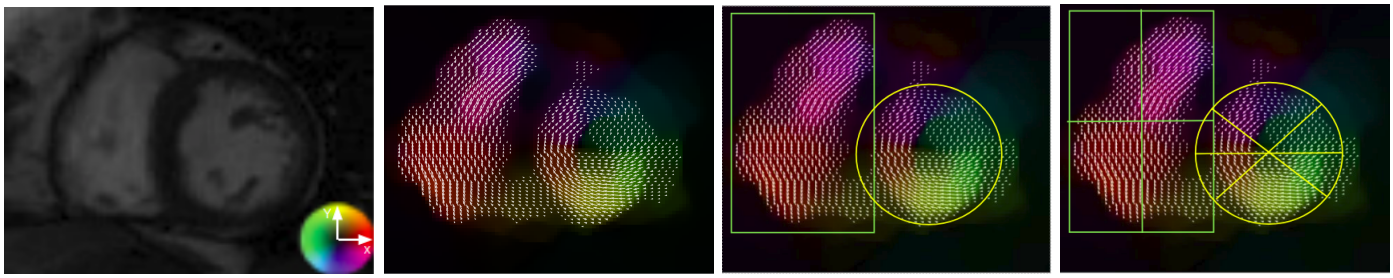
According to the random selection of features, different tree structure emerge from the same training dataset. The set of trees are called "estimators" and each of them gives an independent pathology prediction vote. Due to the estimation of decision trees is done under a uniform random process, the voting process follows the law of large numbers, *i.e.,* the votes of the trees will converge to the same result [15]. In our particular work, each tree is codified on binary classification or multi-classification according to the subset of training.

E. Dataset Description

The dataset used in this approach was the Cardiac cine-MRI, proposed in a MICCAI challenge, called SunnyBrook Cardiac Data (SCD) [16]. The SCD contains 45 cine-MRI images with the following diseases: Heart failure with infarction (HF-I) having an ejection fraction (EF) $< 40\%$, Heart failure without infarction (HF) with EF $< 40\%$, Hypertrophy (HYP) having a normal EF $> 55\%$ and Normal patients (N) with EF $> 55\%$. The dataset has 32 male and 13 women patients cases with an average of 61 years. The cine MRI volumes could vary spatially between [10 - 20] slices, with a temporal sampling of 30 frames to represent the whole cardiac cycle. Each of the slices has a spatial size of 255×255.The original use of this dataset is segmentation of left ventricle on short axis cardiac sequences. Nevertheless, in this approach, we take advantage of the annotation and extra meta-data to use on disease prediction problem. For doing so, the disease label was included in a supervised learning problem. In this work, it was only used the cardiac basal slice because of the better cardiac structure representation. The whole cardiac cycle was herein considered for this basal structure.

III. RESULTS

The proposed descriptor is very fast on computation terms, since only histograms of taking into account from fixed cardiac windows. Some delay is reported regarding the computation of large displacement flow, but the strategy could be adapted to more efficient optical flow approaches. Experiments of proposed approach were carried using the following motion descriptor configuration: 3 scales, 156 spatial regions, and 12 bins for each orientation velocity histogram. The final motion descriptor size was 2964 scalar values. Each volume was manually selected basal slice, at first frame, in which left and right ventricle are well defined. The whole cardiac cycle was captured, allowing to track heart motion patterns spatially and over time. Once the motion descriptor was computed, a previously trained random forest strategy was used for the automatic disease prediction task. As baseline was used a Support Vector Machine, with a radial base function, and operating as a binary classifier [17]. The disease labels are only available on training public dataset. Then, quantitative results were only obtained from such sub-set, under a leave-out-cross validation, in which an isolated sample is used for testing while the rest form the training data. This one folding is performed for whole samples on the sub-set. An example of the dense optical flow computed over cine-MRI



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

Fig. 2: Motion Magnitudes of the Heart. A) Image of interest (MRI). B)First Scale Window. C)Second Scale Window. D) Third Scale Window

sequences is illustrated in Figure 2. As observed in this plot, the motion field effectively computes heart velocity patterns, with a proper description of left and right ventricle motion characterization. Then, a dense field is then represented on a YCrCb color map (see Figure 2-a), the channels (Cr, Cb) being the respective (u, v) components, and the luminance code Y the norm for each velocity vector. Consequently, the left ventricle shows radial motion patterns because of the natural contraction/expansion during diastole/systole moments. For right ventricle can be observed a more smooth gradient of the velocity field, that will be changed locally during the cardiac cycle.

Quantitative results were computed using a Random Forest of only two depth levels in each decision tree, being computationally efficient, a critical issue to support diagnosis in clinical scenarios. Two different metrics were used to evaluate the proposed strategy: the accuracy (number of true positive, over the total of samples), and the F1-score that represent a harmonic mean between precision and recall. Table 1 summarizes the quantitative results achieved by the proposed strategy, with an average accuracy of 77.83%. As observed in the table, the proposed strategy achieve almost perfect classification between classes N and the rest of diseases. Some limitations are reported between $HF - IvsHF$ because of the close dynamic pattern similarities, that is even challenging for experts. In contrast, the baseline using the SVM strategy achieved an average accuracy of 61.9. In such case, the classification strategy properly classifies $HF - IvsN$, $HFvsHYP$ and $HFvsN$ classes but fail on the differentiation among $HF - IvsHF$ and $HYPvsN$. In almost all cases, the F1-score shows a proper performance of recall that increases the score of harmonic mean prediction.

Regarding the classification strategy, in Table 1 could be observed that random forest outperform the results quantified from a radial kernel coded by a support vector machine. These results could be associated w.r.t the way to define boundaries by the random forest, which better adapt non-linearities in feature space, while the voting strategy guaranty a convergence to the mean.

In literature, a similar work proposed motion descriptor in [11] being our baseline, based on motion field quantification and the Hough transformation. Nevertheless, the proposed approach achieves an increasing score prediction of around 6.9%, over the same dataset. Such fact could be justified because the multiscale nature that allows to stand out more persistent motion patterns among the different scales.

Cardiac Disease	SVM(%)		RF(%)		
	Accuracy	F1	Accuracy	F1	Estim
HF- I vs HF	34.9	51.6	62.6	60.9	6
HF-I vs HYP	52.2	68.6	65.2	65.2	100
HF-I vs N	90.0	94.7	80.0	80.0	7
HF vs HYP	70.8	82.9	79.4	79.2	20
HF vs N	85.7	92.3	90.5	90.5	6
HYP vs N	38.1	55.2	89.3	85.7	4
AVERAGE	61.9	74.2	77.83	76.92	6(1:100)

Table 1. Support Vector Machine and Random Forest Classifier Results of Binary Classifier.
*F1: F1-Score, Estim: Estimators

A second experiment was carried out to evaluate the performance of the proposed strategy into a multi-classifier approach. In such sense, whole motion descriptor of four pathologies are put into the same space, and the classifier tries to define boundaries for different diseases. In Table 2 is summarized the obtained results using the proposed motion descriptor and a RaF strategy. As expected, the classification rate is reduced because of the complexity to try to classify several classes at the same time. Interestingly enough, in such a strategy, the classification of normal cardiac samples achieve a score of 100%. This results could be interesting to discard control cardiac patterns from abnormal ones. The proposed descriptor is very fast on computation terms, since only histograms of taking into account from fixed cardiac windows. Some delay is reported regarding the computation of large displacement flow, but the strategy could be adapted to more efficient optical flow approaches.

Cardiac Disease	Accuracy (%)	F1-Score (%)	Estim	Depth
HF-I	37.5	31.6	3	2
H F	44.4	53.3	3	2
HYP	35.3	41.4	3	2
N	100	20.0	3	2
AVERAGE	51.6	37.8	3	2

Table 2. Random Forest Classifier Results of Multi-classifier
*Estim: Estimators

In general, the proposed strategy achieves a proper performance to identify and classify different cardiac pathologies by only motion information. This involves a time-efficient strategy that can be used directly in clinical settings. Even, in multi-class scenarios, the proposed strategy for filtering out normal cases of abnormal cases could be suggested. Because of the complexity of cardiac patterns, as reported in Tables 1 and 2, the best results are obtained by splitting up the problem on binary classifications.

IV. CONCLUSIONS

In this paper was introduced as an approach to describe and characterize heart motion patterns along the cardiac cycle. We obtain a motion pattern descriptor capturing large displacement fields, achieving a good tracking of cardiac structures. Such velocity patterns are able to capture the non-linear motion of cardiac dynamic. The cardiac velocity field is quantified taking into account motion histograms computed at several spatial scales. Such analysis allowed a detailed sub-region description, where persisting motion patterns stand out across the computed scales. For left ventricle in a second spatial scale, the sub-regions were taken following an AHA segmentation model, which permits an association with typical clinical analysis. The proposed descriptor is robust due to the information captured through the multiple scales is able to properly quantify the movements of the heart during the cardiac cycle, achieving a good prediction of heart disease. In future works will be evaluated the proposed approach with larger datasets, that include new cardiac pathologies. New geometrical primitives and local coding are expected to be included in the model to perform better heart tracking.

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