Knowledge-based Quantification of Pericardial Fat in Non-Contrast CT Data

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ABSTRACT

Recent studies show that pericardial fat is associated with vascular calcification and cardiovascular risk. The fat is imaged with Computed Tomography (CT) as part of coronary calcium scoring but it is not included in routine clinical analysis due to the lack of automatic tools for fat quantification. Previous attempts to create such an automated tool have the limitations of either assuming a preset threshold or a Gaussian distribution for fat. In order to overcome these limitations, we present a novel approach using a classification-based method to discriminate fat from other tissues. The classifier is constructed from three binary SVM classifiers trained separately for multiple tissues (fat, muscle/blood and calcium), and a specific code is assigned to each tissue type based on the number of classifiers. The decisions of these binary classifiers are combined and compared with previously determined codes using a minimum Hamming decoding distance to identify fat. We also present an improved method for detection of a compact region-of-interest around the heart to reduce the number of false positives due to neighboring organs. The proposed method UH-PFAT attained a maximum overlap of 87%, and an average overlap of 76% with expert annotations when tested on unseen data from 36 subjects. Our method can be improved by identifying additional discriminative features for fat and muscle/blood separation, or by using more advanced classification approaches such as cascaded classifiers to reduce the number of false detections.

Keywords: pericardial fat, non-contrast CT, classification, SVM

1. INTRODUCTION

Recent studies have shown that pericardial fat is associated with vascular calcification, adiposity and cardiovascular risk.\textsuperscript{1} Currently, pericardial fat is not routinely used to assess cardiovascular risk in clinical practice. Computed tomography (CT) is currently the standard imaging modality to measure abdominal fat,\textsuperscript{2} however, abdominal CT imaging is not routinely performed for cardiovascular risk assessment. Pericardial fat has shown excellent correlation with abdominal visceral fat,\textsuperscript{3} a known cardiovascular risk factor. Although pericardial fat is routinely imaged during CT scans for coronary calcium scoring, it is currently ignored in the analysis of CT images due to the unavailability of computational tools for automatic detection and quantification. With an increasing number of patients going through cardiac CT imaging for coronary calcium scoring, these cardiac CT scans are readily available for the quantification of pericardial fat.

Previous studies on pericardial fat imaging were limited to manually outlined regions-of-interest and preset fat attenuation thresholds. The average CT attenuation for fat tissue varies across subjects, and also depends on the CT scanner.\textsuperscript{4} Recently, Dey \textit{et al.}\textsuperscript{5,6} developed a fat quantification tool that attempts to reduce the manual burden by detecting the cardiac region-of-interest. However, this method uses preset fat attenuation thresholds to compute fat. Bandekar \textit{et al.}\textsuperscript{7} proposed an affinity-based pericardial fat detection method using various texture features in addition to the intensity values. The distribution of these features was assumed to be Gaussian, which may not be true in practice. To overcome these limitations, we present a novel approach for pericardial fat detection and quantification from non-contrast cardiac CT scans acquired for routine calcium scoring. The key contributions of this work are: i) a support vector machines (SVM) classification model\textsuperscript{8} for pericardial fat tissue detection, and ii) an improved method for detection of a compact region-of-interest around the heart, reducing the number of false positives due to neighboring organs.
2. METHODS

Owing to the presence of multiple tissue types (i.e., fat, muscle/blood and calcium) within the heart region, the problem of pericardial fat detection can be formulated as a multi-tissue multi-class (segmentation) problem. Our approach to solve such a multi-class separation problem involves construction of classifiers for each interface between any two tissue types (i.e., fat vs. muscle/blood, fat vs. calcium, and calcium vs. muscle/blood). We use SVM-based classifiers which have been proven to be robust and effective. Additionally, SVM classifiers do not assume any kind of distribution of the training data, and hence are suitable for our purpose. The outline of the current method is presented in Algorithm 1.

<table>
<thead>
<tr>
<th>Algorithm 1</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Training Phase</strong></td>
</tr>
<tr>
<td>Step 1: Computation of features from samples</td>
</tr>
<tr>
<td>Step 2: Feature selection</td>
</tr>
<tr>
<td>Step 3: Parameter estimation using grid search</td>
</tr>
<tr>
<td>Step 4: Training binary classifiers</td>
</tr>
<tr>
<td><strong>Testing Phase</strong></td>
</tr>
<tr>
<td>Step 5: Heart cavity segmentation</td>
</tr>
<tr>
<td>Step 6: Fat classification</td>
</tr>
</tbody>
</table>

2.1 Training Phase

For training purposes, the samples for fat tissue were obtained through manual annotations provided by an expert radiologist. The standard fat attenuation thresholds as used as fat HU range to assist the observer. The blood samples were obtained within the HU range of mean ± standard deviation from a manually annotated blood region of interest (ROI). The calcium samples were extracted using a standard threshold of 130 HU.

**Step 1:** After obtaining the samples for different tissue types the next important step was to represent each sample in terms of a feature vector. Each individual sample was considered as a two-dimensional point in a given transverse plane. Based on this two-dimensional property of samples we computed image features based on appearance and texture. However, location based features were not used in the current framework due to high variations in anatomical location of the heart region across patients. The following list depicts the set of features extracted for each sample:

1. We used the HU intensity value of a sample as a measure of closeness of the sample to a specific tissue type. Apart from that we computed the gradient magnitude value which captures the high frequency information available at the sample.

2. In order to include the neighborhood information into the feature set, we extracted three statistical based features computed around a $3 \times 3$ neighborhood of each sample. We used entropy, standard deviation, and HU intensity range as statistical measures.

3. We computed 15 Laws\textsuperscript{9} texture energy features at each sample. These texture energy features are computed by applying two dimensional convolution kernels to an image and then performing a window operation. These two-dimensional convolution kernels are computed by convoluting two one-dimensional kernels which are sensitive to the level, edge, spot, wave, and ripple characteristics at each sample. Finally, similar pattern characteristic features computed in different directions are combined to remove directional dependence resulting in total of 15 features.

4. We computed 16 Gabor\textsuperscript{10} based texture features. These features are computed by convoluting the image with Gabor filters designed to capture local frequency descriptors of a sample in four different scales and four different orientations.
In total the feature set contains 36 features which are computed for each sample. Moreover, all the features computed were normalized to unit variance using a linear scaling transformation.\textsuperscript{11}

**Step 2**: In order to determine the best subset of features for fat detection using the SVM, we used a wrapper-based forward feature selection method tailored to the support vector machines. In forward feature selection, features are incorporated into progressively larger subsets while computing a classification performance measure of each subset. In the current classifier model, the input data for each classifier is unbalanced due to the different number of samples acquired for each tissue type. In the case of unbalanced data, classifier accuracy does not reflect the actual performance of classification. Hence, we choose F-measure as a performance metric which considers the number of samples in each class. The F-measure is computed as a harmonic mean of precision and recall. The F-measure of each subset is computed using four-fold cross validation in which data is divided into four subsets where one set is alternatively used for validation while the other three are used for training. The subset in which the F-measure is above a certain threshold and no longer improves with the addition of more features is considered as an optimal subset.

**Steps 3-4**: The SVM classifier model works on the principle that there exists an optimal linear hyper plane in a higher-dimensional feature space that maximally separates the two classes. For a given set of training samples \( x_i \in \mathbb{R}^n \) and class labels \( y_i \in \{-1, 1\} \), where \( i = 1, 2, \ldots, l \) and \( l \) is the number of samples, the SVM optimization problem with slack variable \( \xi_i \) and normal to hyper plane \( \omega \) is given by:

\[
\min_{\omega, b, \xi} \frac{1}{2} \omega^T \omega + C \sum_{i=1}^{l} \xi_i \\
\text{subject to } y_i (\omega^T \phi(x_i) + b) \geq 1 - \xi_i, \quad \xi_i \geq 0.
\]

Here, \( \sum_{i=1}^{l} \xi_i \) represents the amount of misclassification by training samples \( x_i \). The parameter \( C \) is used as a penalty value to allow the amount of misclassification for a classifier model. In practice a small value for \( C \) is preferred as it allows the classifier model to rely more on the separation of training samples in the feature space. \( \phi(x_i) \) represents the mapping of input data \( x_i \) into high dimensional space using the transformation \( \phi \) from kernel function \( K(x_i, x_j) \), where \( K(x_i, x_j) \equiv \phi(x_i)^T \phi(x_j) \). We used a radial basis kernel function \( K(x_i, x_j) = \exp(-\gamma \|x_i-x_j\|^2) \) for feature mapping, with \( \gamma \) as a kernel width parameter.

The penalty parameter \( C \) and the kernel parameter \( \gamma \) for each of the three classifiers are determined using a grid search technique. Three binary SVM classifiers are trained, each classifying specific tissue types from fat, blood/muscle and calcium using the features and parameters from the steps above. For each classifier, the SVM parameters are computed using four-fold cross validation. To compute result of the combined classifier model, a code word of all classes. Here zero entries in the matrix indicate that a particular class has no significance to a given classifier.

<table>
<thead>
<tr>
<th>Table 1. Code Matrix M</th>
<th>Fat vs. Muscle/Blood</th>
<th>Fat vs. Bone</th>
<th>Muscle/Blood vs. Bone</th>
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<tbody>
<tr>
<td>Fat</td>
<td>1</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>Muscle/Blood</td>
<td>-1</td>
<td>0</td>
<td>1</td>
</tr>
<tr>
<td>Bone</td>
<td>0</td>
<td>-1</td>
<td>-1</td>
</tr>
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**2.2 Testing Phase**

**Step 5**: The heart cavity in a cardiac CT scan is defined as a region enclosed between the lungs and bounded by the inferior and superior limits of heart. These heart limits are identified using anatomical information. The limits of the heart cavity region are defined in the transverse direction with the top slice as where the pulmonary
We initiate segmentation of the heart cavity region between the inferior and superior limits of the heart by identifying the human body. We determine the human body region using thresholding, connected-component labeling, and hole-filling operations. The resultant human body contour is depicted in Fig. 1(b). Next, we segment the lung using an upper threshold of -250 HU within the body contour; the left and right lungs, if connected, are separated horizontally from the smallest connected vertical column. Additionally, we perform a morphological closing operation on the lung mask to include the pulmonary vessels. In Fig. 2(a), the resultant lung region is shown overlayed on a CT slice.

To determine the anterior limit of the heart cavity, we segment the inner thoracic cavity by formulating it as an optimal surface detection problem. A global optimal boundary surface is computed by solving a node-weighted directed graph in a cylindrical coordinate system. The optimal surface is further refined to be locally optimal by recomputing the surface in a narrow band around the globally optimal surface. Figure 2(b) depicts the thoracic mask overlayed on the original dicom image. The heart cavity is obtained by excluding the lung region from the inner thoracic cavity. To exclude the descending aorta and other organs on the posterior side, the posterior boundary limit of the heart cavity is determined to be the shortest path between the two lung regions below the lung center and above the segmented descending aorta. Figures 2(c) and 2(d) depict the detected descending aorta and the heart cavity overlayed on a CT slice, respectively. This step is repeated for all slices from the superior limit of the heart into the diaphragm appears. For the remaining slices, the heart cavity region from the previous slice is projected until the inferior limit.

**Step 6:** The selected optimal subset of features are computed for the unseen case. The heart cavity computed in the previous step is used to localize the search region for the SVM classifiers. The binary output of each classifier is used to construct a code for each sample. This code is compared with the base code words for each class defined in the matrix M, and the sample is assigned to the tissue class with the closest code word using the minimum Hamming decoding distance. Figures 3(a) and 3(b) depict the fat region detected manually and by UH-PFAT overlayed on a CT slice, respectively.
3. RESULTS

The non-contrast cardiac CT scans were acquired at the Department of Imaging, Cedars-Sinai Medical Center; the acquisition protocol has been described in detail in Dey et al. Each CT scan has 50 to 60 axial slices with a resolution of $0.68 \text{ mm} \times 0.68 \text{ mm}$ and slice thickness of $3 \text{ mm}$. We selected 46 sequential subjects for experiment and validation. Our method was implemented in MATLAB and we used LIBSVM to train the individual SVMs using a nonlinear Gaussian radial basis kernel function.

The CT data were divided into two groups: 10 subjects for training and 36 subjects for testing. For training, the samples were extracted from axial slices between the initial slice and diaphragm slice. To compare the performance of classifiers, we used F-measure as an accuracy metric. The F-measure obtained for the three classifiers at various stages of the feature selection process is depicted in Fig. 4. We selected 13, 2, and 4 features for fat-blood, fat-calcium, and blood-calcium classifiers, respectively; the higher number of features in fat-blood shows the significance of their overlap.
The performance of the method is measured by the Dice-similarity coefficient (DSC), which is computed as the ratio of the number of overlapping voxels to the total number of voxels identified in fat regions detected by the proposed method and the expert-annotated fat regions. Table 2 shows the spatial overlap between the two fat volumes from superior limit to diaphragm appearance, and from superior limit to inferior limit. Our method acquired a maximum DSC value of 0.92 and 0.87, respectively, for the two comparisons mentioned with respect to the manual annotations. Such a similarity coefficient indicates the strength of our approach to detect pericardial fat with high overlap.

Table 2. Dice similarity coefficient statistics in testing dataset

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<tr>
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<th>DSC (mean ± std)</th>
<th>DSC Range [min, max]</th>
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<tbody>
<tr>
<td>Superior to Diaphragm Limit</td>
<td>0.82 ± 0.04</td>
<td>[0.71, 0.92]</td>
</tr>
<tr>
<td>Superior to Inferior Limit</td>
<td>0.76 ± 0.05</td>
<td>[0.64, 0.87]</td>
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</table>

4. CONCLUSION

In this paper, we presented a classification-based framework to detect pericardial fat tissue in cardiac CT scans. We also described a new method to compute a compact heart region-of-interest to reduce the number of false pericardial fat detections in the neighboring organs. Our initial results are promising: maximum overlaps of 0.92 and 0.87 indicate that a classification-based method could be more appropriate than preset threshold-based and affinity-based methods. Misclassification occurs mainly for the voxels with HU values at the interface of fat and blood attenuation values. Thus, there is significant overlap in the attenuation of fat and blood, which requires further investigation. Currently, we are investigating additional discriminating features for fat/blood separation. We are also exploring more advanced classification approaches, such as cascaded classifiers to reduce the number of false detections.

ACKNOWLEDGMENTS

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Figure 4. Feature selection plots depicting the F-measure of the three classifiers: (a) fat-blood, (b) blood-calcium, and (c) fat-calcium, obtained for various feature subsets selected incrementally through a forward feature selection method.

REFERENCES


