Automatic EAT Segmentation in Computed Tomography Images

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Abstract

Recent research indicates a connection between epicardial adipose tissue (EAT) and Coronary Artery Disease (CAD). EAT is a type of fat situated within the pericardium, a thin membrane sac that covers the heart. Hence, its segmentation and quantification could prove valuable for investigating its potential as a CAD risk stratification tool. However, manually segmenting these structures proves to be a demanding and time-consuming task, making it unsuitable for clinical settings. This has driven the development of automated segmentation methods. This study introduces an automated method for segmenting EAT in CT scans. A U-Net framework is thus used to segment the pericardium, which then allows to segment the EAT through thresholding. The quantification metrics resulted in a bias of 0.98 ± 15.351 cm³ and a Pearson Correlation Coefficient (PCC) of 0.924. In terms of segmentation metrics, the values for DSC, recall, and precision were 0.749 ± 0.051, 0.766 ± 0.069, and 0.748 ± 0.085, respectively. The results indicate that satisfactory performance can be attained on an external dataset encompassing diverse anatomical variations, using solely public datasets for training. However, incorporating more data will enhance the robustness of this approach, particularly in outlier cases. Future approaches should prioritize refining the integration of 3D information to achieve a more precise segmentation, mainly on the lower pericardium.

1 Introduction

Coronary Artery Disease (CAD) is the most prevalent type of heart condition and a leading global cause of death [3]. It occurs when deposits of calcium, fatty lipids, and inflammatory cells narrow and harden the coronary arteries, reducing blood flow to the heart muscle. This deprivation of oxygen and blood can result in symptoms like chest pain (angina) and even a myocardial infarction.

Recent studies suggest that changes in epicardial adipose tissue (EAT) might have a significant role in the development of CAD, introducing a valuable factor for evaluating cardiovascular risk [6]. The standard practice for assessing EAT involves initially segmenting the pericardium, a thin double-layered membrane sac that envelops the heart, followed by the application of a Hounsfield Units (HU) threshold that isolates adipose tissue. Nevertheless, accurately identifying the pericardium is extremely challenging, resulting in significant segmentation discrepancies among experts. This task remains laborious and unsuited for clinical application, emerging the need to enhance the repeatability [2].

Over the past years, numerous research investigations have explored the use of machine and deep learning algorithms to automatically segment the pericardium and EAT in CT scans. In 2016, Rodrigues et al. [4] explored a method for segmenting the EAT. Their approach combined feature extraction, intersubjective atlas-based registration, and classification. They yielded a remarkable Dice similarity score (DSC) of 97.9% for EAT segmentation. However, it's worth noting the performance of atlas-based techniques heavily relies on registration accuracy [2].

Zhang et al. [7] introduced an approach utilizing the U-Net framework, employing dual U-Nets on CT scans. The initial U-Net identifies the pericardium, while the second focuses on locating and segmenting EAT within the pericardium. The proposed method achieves a mean DSC of 91.19%.

While numerous studies display encouraging outcomes, the efficacy of these tools in large populations remains unproven. Furthermore, most studies use data from a single cohort with similar properties, not providing good generalization for the model. The work presented in this report is a study towards the automatic segmentation of the EAT in CT imaging. A state of the art architecture is trained for this purpose using publicly available data. Furthermore, a generalization analysis of the considered segmentation solution is performed using a private external dataset.

2 Methods

2.1 Datasets

Three datasets were used in this study: Cardiac Fat, OSIC and Centro Hospital de Vila Nova de Gaia e Espinho (CHVNGE). Three examples of the CT slice and the corresponding manual segmentation for each one of the datasets are shown in Figure 1. The Cardiac Fat dataset[1] was acquired in Rio de Janeiro and released publicly by Rodrigues et al. [4]. The dataset includes 20 CT scans with 878 slices belonging to 20 patients as DICOM images (512×512 pixels). The original ground truth was obtained via manual segmentation by a physician and a computer scientist who labeled the EAT and pericardium. The OSIC dataset[2] was created from the OSIC Pulmonary Fibrosis Competition hosted on Kaggle. This dataset consists of 85 CT scans with 12,133 slices whose scans were conducted using six distinct scanners. The manual pericardial segmentation were performed by an experienced radiologist. Finally, the CHVNGE dataset is a subset of 190 patients randomly selected from the EPICHEART (The influence of EPICardial adipose tissue in HEART diseases) Study (ClinicalTrials.gov: NCT03280433), collected at the CHVNGE in Vila Nova de Gaia, Portugal. The dataset includes 190 CT scans with 8661 slices as DICOM images (512×512 pixels). The pericardial segmentation was obtained via manual segmentation by a medicine student.

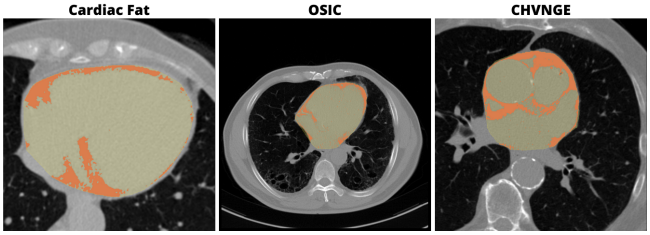

Figure 1: Datasets overview. EAT (red) and Pericardial (yellow) labels, overlapped with DICOM images. The EAT label was obtained by applying the fat HU range inside the pericardium label.

[1] http://visual.ic.uff.br/en/cardio/ctfat/index.php
[2] https://www.kaggle.com/sandorkonya/ct-lung-heart-trachea-segmentation

2.2 EAT Segmentation

First, an automatic method was developed to accurately segment the pericardium. Before training the network, the CT slices were clipped to [-1000, 1000] HU and then normalized to a range between 0 and 1. The input images were resized to 256×256 and data augmentation techniques such as rotations, zoom, flips and shifts were employed. Besides that, calcifications were artificially generated using a Gaussian distribution to make the model robust to the presence of extensive calcifications and medical devices.

A U-Net was then trained for pericardial segmentation [5], provided with three consecutive axial slices: the one to be segmented (k), as well as the previous (k - 1) and next (k + 1). The Cardiac Fat and OSIC datasets were randomly divided as follows: 60% of the CT scans for training, 20% for validation, and the remaining 20% for testing. The model was trained with the Dice loss function and using the adaptive moment estimation (Adam) optimizer.

A post-processing technique was utilized in three key steps to enhance the quality of the 3D image segmentation. Initially, only the largest connected component in the 3D space was retained, discarding disconnected parts. To ensure continuity, a 3D approach was implemented, incorporating pixels from adjacent slices when present in both upper and lower slices. Lastly, a 2D convex hull operation was applied to individual slices, addressing holes and refining the segmentation's appearance.

Once the pericardium was accurately segmented, the fat HU range [-150,-50] was applied within the pericardium to isolate the EAT.

All the external validation was conducted using the 190 patients from the CHVNGE dataset. Evaluation of EAT segmentation performance was done on the external CHVNGE dataset using the DSC [1], precision and recall. Subsequently, the quantification of EAT volume was performed. The assessment of agreement between the readers was conducted using the Pearson Correlation Coefficient (PCC) and the bias.

3 Results and Discussion

Following the validation process on the CHVNGE dataset, the quantification metrics yielded a bias of 0.98 $\pm$ 15.351 cm^3 and a PCC of 0.924. As for the segmentation metrics, the values for DSC, recall, and precision were 0.749 $\pm$ 0.051, 0.766 $\pm$ 0.069, and 0.748 $\pm$ 0.085, respectively. These results demonstrate favorable agreement between manual quantification and the automated approach, characterized by a high PCC and a minimal bias. Among the segmentation metrics, recall achieved the highest value, implying that the model's strongest capability lies in accurately segmenting EAT. However, the lower precision value of approximately 0.02 in comparison to the recall suggests occasional instances where the model misidentifies other fats as EAT.

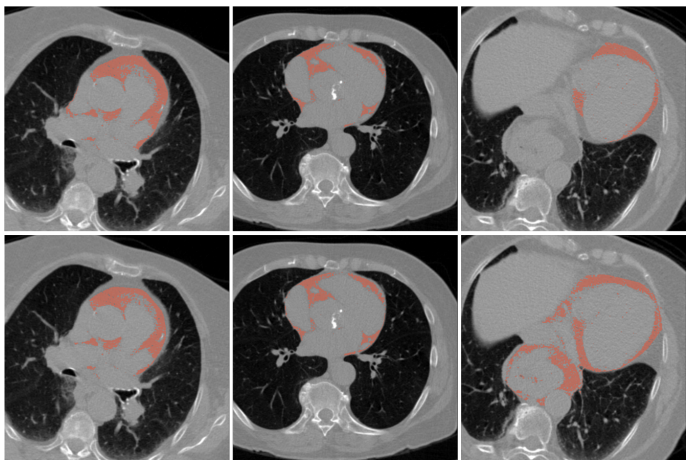

Figure 2: Examples of EAT segmentation from the manual (top row) and automatic (bottom row) approach.

Figure 2 showcases three examples of EAT segmentation from different patients. In the first scenario, there is general agreement among segmentations, although a slightly larger EAT volume was identified by the human reader. The second instance illustrates the accuracy of the automatic model to deal with huge calcifications, presenting an almost perfect EAT segmentation. Additionally, the minimal impact of zoom and rotation on the model in these two cases underscores the efficacy of data augmentation methods. The third example exposes a deficiency in the automated approach, inaccurately segmenting EAT due to anatomical variations, being this a reason for the lower precision values. These variations are primarily observed in the lower slices where other organs might be present, and they occasionally appear in higher regions than usual due to certain medical conditions. This can lead the model to misidentify them as the pericardium. Therefore, this instance emphasizes the need for broader training data, encompassing diverse anatomical variations that conventional augmentation techniques cannot simulate.

4 Conclusions

In conclusion, upon assessing the model's performance in 190 patients from the CHVNGE dataset, it was observed that the automated approach achieved satisfactory outcomes. A good correlation was observed between the manual and automatic EAT volume quantification and the segmentation metrics exhibited promising outcomes. The incorporation of artificial calcifications and augmentation techniques during the model's training demonstrated their effectiveness. However, there is a need for additional data variability in training to enhance the performance in patients with significant anatomical variability. Considering the difficulty and computational demands of training a 3D network, a possible future direction could involve incorporating more slices beyond the usual three axial slices or providing the model with coronal, axial, and sagittal views. It's worth highlighting that the main contribution of this work is to explore the potential of using publicly available data exclusively for training the model. The model's performance is evaluated on an external private dataset containing numerous patients with diverse anatomical variations. Consequently, the observed performance values are lower compared to those reported in the literature.

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