Automatic Segmentation of Lung Parenchyma using Fuzzy Clustering

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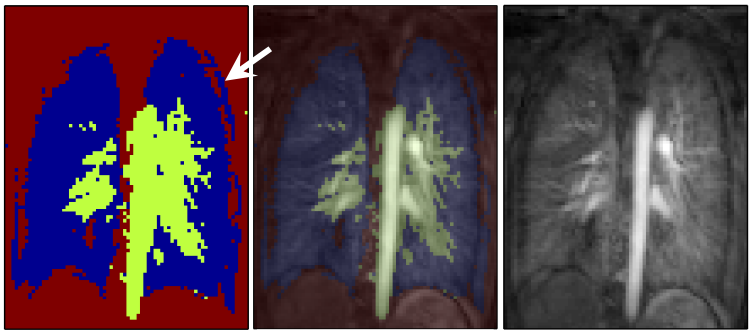

Figure 1: *FCM clusters of a partition containing the Aorta Descendens and large pulmonary vessels. Left: Clusters (red: Tissue; blue: Parenchyma; yellow: Vessels); Middle: Overlay of clusters with the anatomic reference; Right: Anatomic reference (maximum intensity projection (MIP) over time of the respective partition). The arrow indicates voxels falsely distributed to the parenchymal cluster.*

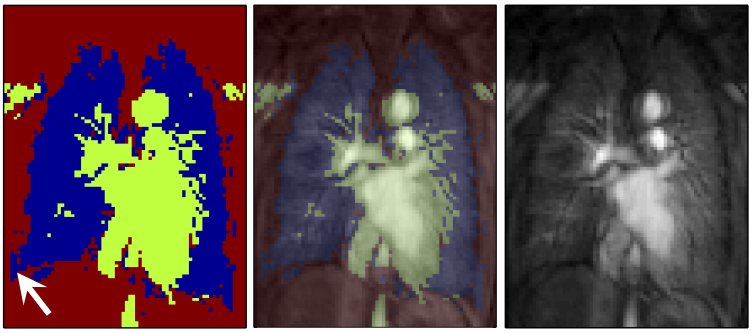

Figure 2: *FCM clusters of a partition containing the heart and large pulmonary vessels. Left: Clusters (colours alike Figure 1); Middle: Overlay of clusters with the anatomic reference; Right: Anatomic reference (MIP over time of the respective partition). The arrow indicates voxels falsely distributed to the parenchymal cluster.*

Introduction

Segmentation of lung parenchyma is required in quantitative dynamic contrast-enhanced (DCE) lung imaging to determine functional parameters like pulmonary perfusion, mean transit time or regional pulmonary volume. The lungs are permeated by many larger blood vessels. Pulmonary arteries show larger signal enhancement during the contrast agent (CA) passage compared to pulmonary parenchyma. Thus, drawing regions of interest (ROIs) in the parenchyma which incorporate (partial volume) voxels of larger pulmonary blood vessels leads to an overestimation of pulmonary perfusion. Manually drawing ROIs is always affected by user subjectivity. In this context, in slices containing the heart, cardiac motion influences the depiction of the CA passage. This is hard to notice in manual segmentation and, therefore, leads to erroneous quantified perfusion rates. Hence, it would be desirable to automatically segment the lung parenchyma from pulmonary vessels and cardiac structures. Different approaches to achieve automatic segmentation have been reported [1,2], however many studies are performed with manual segmentation of the parenchyma (e.g., [3,4]). We propose to utilize Fuzzy C-Means (FCM) clustering to automatically segment the lung parenchyma from large blood vessels and cardiac structures. FCM clustering was originally introduced to DCE-MRI to select voxels for accurate arterial input function (AIF) determination [5]. A similar approach was presented using a combination of Kohonen clustering network and subsequent FCM clustering [2]. This work demonstrates that FCM clustering can distinguish lung parenchyma from vessels, the heart, and the surrounding tissue.

Methods

FCM clustering classifies multidimensional data such that samples with similar characteristics are grouped within a cluster. In DCE lung MRI each lung voxel shows a particular temporal signal course. FCM clustering groups voxels with similar temporal characteristics (onset and amplitude of signal enhancement, shape of the signal curve). For example, voxels in the pulmonary arteries exhibit an early onset and large amplitude of signal enhancement. Pulmonary parenchyma signal increases moderately after the CA has traversed the pulmonary arteries. Finally, the CA is washed out through the thoracic aorta, leading to high signal enhancement therein (compare Figure 3). In light of this, automatic segmentation of pulmonary parenchyma should be feasible. To prove this hypothesis, a 3D DCE-MRI dataset was acquired. Imaging parameters: Siemens Trio 3.0 T (Siemens Healthcare, Erlangen, Germany), 32 channel coil (In Vivo, Gainesville/FL, USA), FLASH, α=19°, T_R=1.69ms, T_E=0.64ms (asymmetric echo), af=3 (GRAPPA), FOV 480x435x140mm³, 252x128x28, Gadovist® 1.0 mmol 4ml (Bayer Healthcare, Leverkusen, Germany). The FCM clustering algorithm was implemented according to [5] with 40 instead of 10 clusters to properly segment the large 3D volume. A volume of interest was selected to restrict the clustering to the thorax. The finally obtained 40 clusters of the 3D volume were combined to three final clusters: Pulmonary parenchyma, surrounding tissue, and blood vessels/heart.

Results

Figures 1 and 2 demonstrate the capability of the FCM clustering to distinguish lung parenchyma, large (pulmonary) vessels and surrounding tissue even if the partition includes the heart. However, as indicated by arrows, voxels which obviously do not belong to the parenchyma are also included. Figure 3 explains this observation: These falsely distributed voxels exhibit the same temporal enhancement as lung parenchyma. This is caused by truncations artifacts along the phase encoding direction, leading to signal enhancement outside the lung boundaries.

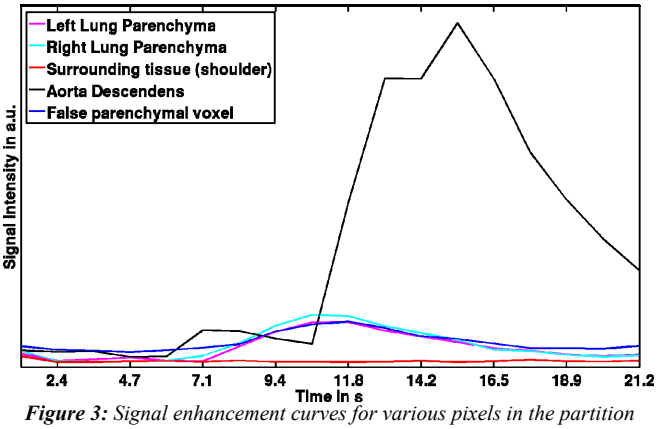

Figure 3: *Signal enhancement curves for various pixels in the partition shown in Figure 1. The falsely clustered voxel exhibits a similar signal enhancement as parenchymal voxels. The aorta and the surrounding tissue differ both in amplitude and occurrence of the CA induced signal enhancement from parenchymal voxels.*

Discussion and Conclusion

In this work, FCM clustering was successfully applied to automatically segment the lung parenchyma from surrounding tissue, the heart and (pulmonary) vessels. User interaction is significantly reduced, thereby lowering the subjective bias in data analysis. However, if voxels are obviously falsely distributed to the parenchymal cluster, they can be manually removed. Alternatively, the ROI restricting the clustering to the thorax can be drawn more accurately to fit the pulmonary anatomy. Another way to circumvent misaligning voxels is to reduced truncation artifacts by increasing spatial resolution. However, this comes at the cost of reduced temporal resolution, which can not always be tolerated.

References

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