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Automatic Alignment of Myocardial Perfusion Images with Contrast Cardiac Tomography

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Abstract

Explicit fusion of perfusion data from Positron Emission Tomography (PET) or Single Photon Emission Computed Tomography (SPECT) with coronary artery anatomy from Computed Tomographic Coronary Angiography (CTCA) has been shown to improve the diagnostic yield for coronary artery disease (CAD) compared to either modality alone. However, most clinically available methods were developed for multimodal scanners or require interactive alignment prior to display and analysis. A new approach was developed to register and display the two distributions obtained either from a single multimodal imager or from separate scanners, and a preliminary validation was undertaken using interactive alignment by experts.

I. Introduction

Integration of anatomical data from contrast cardiac CT performed for angiography (CTA) with physiological information from nuclear myocardial perfusion images (MPI) has been shown to be more accurate than either alone for diagnosing coronary artery disease[1]. However, most implementations presume that the images are already in close alignment, as happens with a dual modality scanner, or require that the images be aligned manually. An automatic algorithm has been recently described, but it only the left ventricle (LV). As the

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LV may be very rotationally symmetric, ignoring the right ventricle (RV) may be less accurate [2]. A robust automatic alignment method is needed.

II. Methods

The basic approach is to identify the LV in both datasets, as well as the RV in the CTA. Next an initial alignment on binary images of the LV chamber is performed, a dilated version of the CTA boundaries is used to mask out the transformed MPI, and a final alignment on the CTA and the masked MPI is performed.

Perfusion quantitation on the short axis MPIs provides an estimate of LV endocardial boundaries which are used to create a mask of the LV chamber. Hand segmentation is used to separate ventricular myocardium and chambers. This segmented CTA is automatically labeled as either myocardium, LV chamber, RV chamber, and background. based on size and location. The CT LV is then automatically reoriented into short axis slices using an adaptation of the method previously outlined by Faber et al.[3].

The reoriented LV chamber from the CTA is rigidly aligned with the binary LV chamber created from the MPI using an iterative optimization technique with a sum of squared difference function; this transform is used to reslice the original MPI. This aligned MPI is masked with a dilated and smoothed version of the full CTA mask, (including myocardium and LV and RV chambers), to eliminate background structures and preclude matching the CT heart with extracardiac objects in the MPI.

Finally, the masked MPI is aligned with a smoothed version of the CTA myocardial mask. This smoothing creates a CT image that is closer to the resolution of the MPI. Again, mutual information is maximized using an iterative optimization technique to find the best rigid transform for the MPI. This transform is used to reslice the original MPI into the space of the reoriented short axis space of the CTA.

Twenty four patients from a previous study were used for validation [1]. These included both SPECT and PET and abnormal and normal studies. Transaxial CTAs were interpolated to a voxel size of $1 \times 1 \times 2$ mm, and our own software was used to hand trace the epicardial and endocardial boundaries in each. Note that these boundaries were closed, so that the in and outflow tracts of the ventricles were capped. The end result of this interactive tracing was binary images with 1's inside the myocardium (including the cap) and 0's everywhere else. Short axis MPIs were also traced, in their original resolution, for the sole purpose of validation. Note that these boundaries were not used for alignment. The binary images from both the hand traced MPI and CTAs were converted into a triangulated set of boundary points, in order to be able to more accurately measure the distance between them.

The MPIs were aligned to their corresponding segmented CTAs using the methods described above. The final transform was used to transform the surface points generated from the binary MPI masks. The distance between the CTA and MPI surfaces after automatic alignment was measured.

The gold standard for aligning MPI and CT images is interactive expertise. To evaluate how automatic alignment compared with interactive, two experts interactively translated and rotated the short axis MPIs to match short axis CTAs, where the short axis CTA images were obtained as described above. This rigid transform was also used to transform the MPI surfaces, and again, distances between the interactively aligned MPI and CTA surfaces were computed for both experts' alignments.

The difference between the MPI surface points from the two interactive alignments was also computed, in order to determine the interobserver variation in interactive alignment. For comparison, the difference between MPI surface points obtained after automatic alignment and those obtained after the two interactive alignments was also measured.

III Results

Overall, the distance between MPI and CTA surfaces was 4.42 ± 3.46 mm for the automatic method. Distances for the two expert alignments were 4.64 ± 3.64 and 4.30 ± 3.33 mm. These are not significantly different from each other. A direct comparison between the points after expert alignment vs. after automatic alignment showed a difference of 5.10 ± 2.87 for the first expert and 5.72 ± 2.94 for the second expert. The difference between corresponding points when the two expert alignments were compared was 5.45 ± 3.17 mm. Two explicit examples are shown in Fig. 1.

There was no significant difference between alignment accuracy for normal and abnormal studies; however, PET alignments were significantly more accurate than SPECT alignments for both expert and automatic alignments. Average distance was 4.20mm between PET vs CT but 5.04mm between SPECT vs CTA for the experts' alignments. For the automatic alignment, average distance was 4.04mm for PET vs CTA but 4.84mm for SPECT vs CTA.

IV. Conclusion

Automatic registration between segmented CTAs and masked MPIs is similarly accurate and not significantly different to the gold standard of interactive alignment.

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Fig 1.

A. An abnormal SPECT image in which alignment was poorest. The difference between SPECT and CT surfaces were 5.96, 7.34, and 5.92mm for the automatic method and experts 1 and 2, respectively. This figure shows overlays of the SPECT on the CT for the automatic alignment and the two expert alignments. B. A normal PET image in which the alignment worked best. The distances between the normal PET surface and CT surface were 3.78, 3.22, and 3.22mm for the automatic method, expert 1, and expert2, respectively.