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Automatic Detection of Left and Right Ventricles from CTA Enables Efficient Alignment of Anatomy with Myocardial Perfusion Data

Marina Piccinelli¹, Tracy L. Faber^{1,†}, Chesnal D. Arepalli¹, Vikram Appia², Jakob Vinten-Johansen³, Susan L. Schmarkey³, Russell D. Folks¹, Ernest V. Garcia¹, and Anthony Yezzi²

¹Department of Radiology and Imaging Sciences, Emory University, Atlanta, GA, US

²Electrical Engineering, Georgia Institute of Technology, Atlanta, GA, US

³Division of Cardiothoracic Surgery, Emory University, Atlanta, GA, US

Abstract

Background—Accurate alignment between cardiac CT angiographic studies (CTA) and nuclear perfusion images is crucial for improved diagnosis of coronary artery disease. This study evaluated in an animal model the accuracy of a CTA fully automated biventricular segmentation algorithm, a necessary step for automatic and thus efficient PET/CT alignment.

Methods and Results—Twelve pigs with acute infarcts were imaged using Rb-82 PET and 64-slice CTA. Post-mortem myocardium mass measurements were obtained. Endocardial and epicardial myocardial boundaries were manually and automatically detected on the CTA and both segmentations used to perform PET/CT alignment. To assess the segmentation performance, image-based myocardial masses were compared to experimental data; the hand-traced profiles were used as a reference standard to assess the global and slice-by-slice robustness of the automated algorithm in extracting myocardium, LV and RV. Mean distances between the automated and the manual 3D segmented surfaces were computed. Finally, differences in rotations and translations between the manual and automatic surfaces were estimated post PET/CT alignment. The largest, smallest, and median distances between interactive and automatic surfaces averaged 1.2 ± 2.1 , 0.2 ± 1.6 , and 0.7 ± 1.9 mm. The average angular and translational differences in CT/PET alignments were 0.4° , -0.6° and -2.3° about x, y and z axes, and 1.8, -2.1 , and 2.0 mm in x, y and z directions.

Corresponding Author: Marina Piccinelli, PhD, Department of Radiology and Imaging Sciences, 101 Woodruff Circle, Room 1203C, Emory University, Atlanta 30322, Georgia, US, mpiccin@emory.edu, Telephone: +1 404.727.6113, Fax: +1 404.727.3488.

[†]Dr. Tracy L. Faber, this project's principal investigator, passed away on March 24, 2012.

NEW KNOWLEDGE GAINED

The automated segmentation of the myocardium from CTA acquisitions allows in a single display reliable fusion of anatomical CTA information and physiological myocardial perfusion information.

Conflicts of Interest

Some of the authors (EG, RF, TF) receive royalties from the sale of the Emory Cardiac Toolbox and have equity positions with Syntermed, Inc., which markets ECTb. The terms of these arrangements have been reviewed and approved by Emory University in accordance with its conflict of interest policies.

The remaining authors do not have any conflicts of interest.

Conclusions—Our automatic myocardial boundary detection algorithm creates surfaces from CTA that are similar in accuracy and provide similar alignments with PET as those obtained from interactive tracing. Specific difficulties in a reliable segmentation of the apex and base regions will require further improvements in the automated technique.

INTRODUCTION

In recent years, three-dimensional (3D) fusion of multislice CT angiography (CTA) and myocardial perfusion imaging (MPI) for the assessment of coronary artery disease (CAD) has proven its incremental diagnostic value over the two modalities separately considered (1–5). Myocardial perfusion imaging (MPI) with either PET or SPECT is an established method for the assessment of the functional significance of coronary stenosis (6,7), while CTA provides the complementary *morpho-anatomical* information on the heart structure, the coronary tree configuration and the location of stenosis, information that is otherwise unavailable to the physician (8,9). By visually fusing these two types of knowledge, clinicians are provided with tools to better interpret complex situations of multiple perfusion defects, to identify the direct cause of abnormalities and conversely, to spare patients unnecessary invasive exams in case of non-critical lesions (4,5,10).

A number of technical issues have to be addressed for this integration to become a reliable and efficient tool for everyday use in a clinical environment. In a previous work published by our group (11), an algorithm for the automated alignment of MPI and CTA images obtained from different scanners was presented. Both left (LV) and right (RV) ventricles were manually identified on the two datasets, binary images were created and successively aligned using mutual information principles (12). Since the reference standard remains manual registration, a comparison of automated versus interactive alignments was conducted and no significant differences were observed.

A crucial prerequisite for the proposed alignment algorithm is the availability of myocardial tomograms from the CTA and MPI images. Manual tracings are considered the reference standard, but exhibit the fundamental drawback of being time-consuming and more importantly operator-dependent. While tools for automated quantitative MPI are readily available (6,7,13), researchers have been working for decades on efficient methods to segment cardiac CT (or MR) (14,15,16). Promising methodologies for the automated extraction of complex anatomical structures rely on the use of model-based segmentation algorithms and on their capability of incorporating prior information about the features of the object to be delineated (17,18). Following this approach, a level set region-based algorithm for the automated detection of LV and RV edges was developed (19,20). The segmentation is constrained by local shape priors retrieved from the statistical analysis of a training datasets and was successfully tested on synthetic images as well as on cardiac acquisitions for myocardium extraction in both 3 and 4D.

With the final rationale of proposing a completely automated procedure for 3D image fusion, the aim of this work was two-fold: first the accuracy of the proposed automated edge detection algorithm was assessed in an animal model on a set of contrast-enhanced CTA images; manual segmentation was also performed by an expert user and considered as the

reference standard for the myocardium delineation of both LV and RV. Secondly, perfusion images were aligned to the CTA acquisitions by means of our published second-generation biventricular fusion technique (11) using both the automatically segmented and the manually traced myocardial contours. Differences in translations and rotations between the two resulting alignments were estimated, with the registration of the manual tracings taken as the reference standard.

MATERIAL AND METHODS

Animal Selection and Preparation

Twelve female Yorkshire cross farm-bred pigs were obtained from North Carolina; their average weight ranged 35–40 kg. Before image acquisitions acute myocardial infarcts were created in either the left anterior descending artery (LAD) or left circumflex artery (LCX) vascular territories of each animal by means of a previously described angiographic technique (21). The animals were transported to the scanner room and intubated. Appropriate animal care was provided according to norms/standard protocols approved at our Institution, i.e. Institutional Animal care and Use Committee (IACUC) of Emory University. Vascular accesses at the femoral artery and the femoral vein were created and the perfusion defects produced by administering a predefined number of 25µm sterile microspheres to embolize the target microvasculature (21). After the intervention, the animals were first stabilized and successively imaged by both positron emission tomography (PET) for perfusion analysis and CTA for morpho-anatomical assessment.

Imaging Acquisitions

PET Imaging—PET imaging was performed before the CT study. The animal was placed on the table in the supine position. A transmission scan was performed using the CT portion of a CT/PET scanner. Immediately afterwards, a resting IV injection of 50mCi Rb-82 was given. Each animal was then scanned using the acquisition protocols described for patients in the PET guidelines of the American Society of Nuclear Cardiology (22). All PET images were reconstructed using iterative techniques with attenuation correction.

CTA Imaging—Immediately after PET, the animal was taken for a CTA examination. According to our institutional protocol, the animal was placed in a supine position, head-first position on the scanner gantry. A three-lead ECG was used and no heart rate controlling medications or nitroglycerin were used during the examination. For injection of contrast, an IV access was secured through the existing catheter in the femoral vein and a bi-phasic injection protocol with dual-head power injector was used. Non-ionic iodinated contrast (Isovue 370 mg·mL⁻¹, Bracco) was used for both bolus test and angiographic examination. For bolus test, pure contrast of about 20 ml was injected at a rate of 5 mL·second⁻¹ followed by contrast-saline mix (30% contrast + 70% saline) of about 30 mL. For the CTA study, the amount of undiluted contrast to be administered at the rate of 5 mL·second⁻¹ was calculated on the base of the peak enhancement obtained by the previous bolus test technique. Thereafter a saline flush of 30 mL of contrast-saline mix for 6 seconds at 5 mL·second⁻¹ was given. Time to peak enhancement ranged between 9 and 11 seconds, accounting for a total amount of contrast injected ranging between 70 and 90 mL.

A retrospective ECG triggered dual-source CT (Somaton Definition, Siemens Medical Systems, Forchheim, Germany) was used to perform the cardiac CT examinations with tube modulation technique. CTA began with respiratory termination with a cranio-caudal acquisition and the following parameters: gantry rotation time of 0.33 second; tube voltage of 120 Kvp; tube current of 400–500 mAs; adaptable pitch based on the animal heart rate; detector collimation 2×32 ; image slice thickness of 0.75 mm with reconstruction increment of 0.4 mm single-segment reconstruction algorithm, which would result in a temporal resolution of 83 ms medium-to-smooth (B26f) kernel. All CTA datasets were reconstructed at best diastole and best systole; a different phase was selected if motion artifacts were noticed. In plane image resolution ranged between 0.19×0.19 to 0.49×0.49 mm. Image datasets were finally processed on a separate workstation (ADW 4.2 General Electric Medical System, Milwaukee, WI).

CTA Myocardial Segmentation

As a proof of concept and since no ventricular function was performed on the base of the CTA images, only one dataset between the acquired best systole and best diastole phase was chosen and used to test the performance of the algorithms, including comparing automatic to manually extracted volumes in this non-standard phase. All selected CTA datasets were resampled to obtain isotropic voxel dimensions of $1.0 \times 1.0 \times 1.0$ mm.

Interactive manual tracings of the epicardium and endocardium were carried out for all the animals by means of in-house developed software for each CTA acquisition. LV and RV were both delineated by an expert user.

Automatic myocardial segmentation was also performed in each case according to the level set model-based algorithm developed by our collaborators (19,20). The mathematical and technical details of the algorithms can be retrieved in the referenced papers and do not represent the focus of the present manuscript; here, we only briefly describe the main steps of this automated procedure. A set of the same 12 pigs CTA studies were used as training images and were manually segmented by expert users in order to identify myocardial edges and characterize their shape variations. The *leave-one-out method* of training was then implemented in processing each of the pigs' studies prospectively. This process consisted in training the automatic segmentation algorithm with 11 animal studies and applying the training to extract the contours of the 12th pig not included in the training set. This design was repeated for each pig. A crucial task of the level set model-based approach was also to identify and accordingly label different regions of the object to be segmented, i.e. the myocardium, depending on the amount of useful information contained in these regions. As low contrast issues may prevent a clear delineation of the edges separating the myocardium from surrounding tissues or, for some acquisitions, from the blood pool, the definition of these target masks allows the algorithm to differently weight during the segmentation the areas with fuzzy or corrupted boundaries from those with greater reliability (e.g. the RV myocardium is more difficult to segment than the LV one). A level set formulation (17) was used to represent both the training shapes and the reliability masks, and local Principal Component Analysis (PCA) was performed on both sets to obtain shape priors and mask priors within each image region. The actual segmentation was eventually achieved in two

steps. First the segmenting curve was evolved under the effects of a linear combination of local shape and mask priors in each region; successively the resulting curves were combined to obtain a global hybrid segmentation curve that evolved on the entire image domain.

From this automatic process 3D meshes were generated representative of the biventricular myocardium. Similar 3D meshes were generated from the hand-traced data. Figure 1 illustrates an example of a mesh generated from the hand traced procedure and compares it to the automated mesh for one of the analyzed CT image sets.

PET Myocardial Segmentation

In a separate independent process, the LV chamber was identified from the PET images using endocardial and epicardial boundaries generated by our previously published automated methods, which are part of the Emory Cardiac Toolbox (ECTb) (13, 23). Briefly, mid-myocardial LV points are obtained from the maximal count quantification algorithm and endo/epi LV surfaces are modeled at a fixed distance from these locations.

Myocardial Mass and Ventricle Volumes Extraction

Experimental Mass Measures—After the imaging procedures were completed, post-mortem ventricular mass measures were obtained separately for LV and RV in 8 out of 12 pigs to validate the automatic and manual CT boundaries detection. In 4 cases the measurements were not available: 2 pigs died on the scanning table and in the remaining 2 the area of infarct was either not large enough to be accurately measured or not visible at all. Their hearts were consequently not excised and mass measurements were not included in the present study.

Image-Based Measures—For each case two 3D binary mask images were created, one representing the heart manual segmentation and one the automated. The masks covered the same volume of interest, had the same dimensions and spatial resolution and were consequently directly comparable. Myocardium total volumes and masses were computed for the two segmentation modalities, the mass being calculated as the volume multiplied by a density factor of $1.05 \text{ g}\cdot\text{mL}^{-1}$ (13). Since both epicardial and endocardial boundaries were extracted, LV and RV total volumes were also computed to assess the algorithm robustness with respect to blood pools identification. In addition to global masses and volumes, slice-by-slice measures of myocardium mass, RV and LV volumes were computed

Comparison of Segmentation Techniques—The performance of the two segmentation techniques was assessed for the 8 available cases by comparing total myocardial image-based masses to experimental measures. For each couple of comparisons – true versus interactive and true versus automated – paired Student's t test, Pearson correlation, Bland-Altman analysis and standard estimation error (SEE) computation were performed. The image-based results were also compared to each other in terms of total myocardium masses as well as of LV and RV volumes with the same statistical techniques. Slice-by-slice agreement of myocardium mass and ventricles volume was assessed by means of Pearson's correlation within each case and for all the slices. Whenever applied a P value = 0.5 was used as threshold for statistical significance.

To further evaluate the accuracy of the automatically detected mesh with respect to hand-traced ones, a boundary error was defined as the point-to-point distance between the two 3D surface meshes created on the basis of the planar profiles (23). Particularly, the largest, the smallest and the median distances between interactive and automatic endocardial and epicardial surfaces were calculated.

PET/CT Automatic Alignment

Our automatic technique for CT and MPI fusion has been previously described and tested (11). Briefly, once the LV/RV endo/epi structure was segmented on CTA acquisitions, a binary mask was created, the left and right ventricles separated and the short axis identified on the CTA acquisition based on the LV chamber symmetry axis. PET LV short-axis binary images were also provided by the ECTb techniques and an initial rigid alignment performed between the LV CTA and LV PET masks. The re-oriented CTA mask with both left and right ventricles was then used to mask the original MPI and eliminate bright extracardiac objects. The resulting MPI was finally aligned to the short-axis CT according to mutual information principles. In Figure 2 the case example used in Figure 1 is displayed to exhibit the final result of PET/CT alignment according to the proposed algorithms; the manually segmented mask was employed.

The fusion of the CT to the PET acquisition was completed twice for each animal, once using the hand-traced profiles and once with the automatically extracted ones. Since the manual segmentation is considered the reference standard, the PET/CT alignment performed with the hand-traced mask was considered as the reference as well (11). Differences in alignment due to the use of the automatically segmented CTA myocardium instead of the manual ones were evaluated in terms of rotations around x, y and z axes and translations in the x, y and z directions between the two aligned CTs.

RESULTS

CT Automatic versus Manual Segmentation

Manual and automated segmentations were performed for all 12 CTA acquisitions. In most of the cases the best systolic phase was selected for the subsequent image processing steps after evaluation of a CTA expert. From the binary images, 3D triangulated meshes were created so that two endocardial and two epicardial surfaces were available for each case. The boundary distance error between automated and hand-traced meshes after alignment in all 12 animals exhibited maximum, minimum and median values of 1.2 ± 2.1 , 0.2 ± 1.6 , and 0.7 ± 1.9 mm, respectively.

Experimental measures for the myocardial mass were available in 8 cases, while image-based myocardial mass and ventricular volumes were computed for all 12 cases. In Table 1 all the measurements are reported. In Figure 3, left scatter plots and linear regression lines are displayed for the comparisons between true measures versus image-based and for the automatic versus interactive correlation for the myocardial mass determination. Pearson's coefficients and *P* values were as follows: $R_{\text{True vs Interactive}} = 0.029$, *P* value = 0.93, SEE = 7.20; $R_{\text{True vs Automated}} = 0.52$, *P* value < 0.05, SEE = 9.08; $R_{\text{Interactive vs Automated}} = 0.32$; *P*

value < 0.05 , SEE = 15.85. Figure 4 (left) displays scatter plots and correlation for right and left ventricular volume identification between the two segmentation modalities. For the LV measurements $R_{\text{Interactive vs Automated}} = 0.96$, P value < 0.05 , SEE = 5.59, while for the RV, $R_{\text{Interactive vs Automated}} = 0.72$, P value = 0.17, SEE = 9.59. Bland-Altman analysis was performed to further assess to level of agreement of image-based results with experimental measures and between the two segmentation modalities (Figure 3 (right for myocardial mass) and Figure 4 (right for ventricular volumes)).

Stronger correlations between image-based measures were determined when slice-by-slice comparisons were considered. In Figure 5A–C (top) myocardial mass and ventricular volumes are plotted by pooling together all image slices for all cases. Pearson's coefficients were for the myocardial mass, the LV and RV volumes respectively 0.88, 0.98 and 0.85; SEEs were respectively 0.48, 0.14 and 0.24. Qualitative and quantitative comparison of slice-by-slice agreement also showed that major discrepancies between interactive and automated profiles were present at the hearts' base and apex. Each couple of masks was separated in two domains: one for slices associated with the heart base and apex, and one for the central portion of the organ; apex and base segments were identified as 10% of total heart slices at the bottom and 10% at the top of the images. In Figure 5A–C, the apex and base slices (middle) and the central slices (bottom) are plotted separately. Pearson's coefficients were for the myocardial mass $R_{\text{central}} = 0.73$, SEE = 0.39 and $R_{\text{apex/base}} = 0.23$, SEE = 0.64; for the LV volume $R_{\text{central}} = 0.96$, SEE = 0.16 and $R_{\text{apex/base}} = 0.27$, SEE = 0.12; for the RV volume $R_{\text{central}} = 0.83$, SEE = 0.26 and $R_{\text{apex/base}} = 0.34$, SEE = 0.50.

Slice-by-slice comparisons were performed also within each case. Table 2 provides the Pearson's coefficients for myocardium, LV and RV for each case. In Figure 6 for some of the analyzed cases, automated versus interactive profiles extracted from different segments of the heart extension, i.e. from the apex, the central portion and the base, are displayed as examples: in Figure 6A, B different levels of agreement are shown at the apex, commonly good in the middle and rather poor at the base; Figure 6C shows case #5 for which the agreement was rather poor along the whole image extension. In this particular case, image artifacts were in fact visible along the whole CT acquisition affecting the automated algorithm performance.

PET/CT Alignment with Automatic versus Manual Segmentation

The alignment of PET and CT images was successfully performed for each case using both the automatically detected myocardial mesh and the hand-traced mesh. Figure 7 qualitatively compares for one of the analyzed cases oblique angle tomographic orientations of the results of aligning the PET cardiac count distribution with the hand-traced (top) CT mesh and with the automatically detected CT myocardial mesh. For a more quantitative assessment, Table 3 reports the differences in terms of rotations around the X, Y and Z and translation in X, Y and Z directions between the two alignments for all 12 animals.

DISCUSSION

Despite the continuous improvement in non-invasive imaging techniques, the reference standard for the clinical assessment of CAD still relies on invasive testing such as coronary

arteriography. The usefulness of image fusion of CTA and nuclear perfusion for the creation of a more complete picture of the patient's heart condition that could avoid invasive procedure may be widely accepted and recognized, but due to the lack of automation for some of the necessary image processing steps, the clinical application of multimodality image frameworks is still limited and requires additional efforts towards robustness and accuracy.

In this study, we determined in an animal model the favorable accuracy of the automated detection of biventricular myocardial surfaces from CTA acquisitions (20) as compared to manual tracings taken as reference standard. and their usage for the automated alignment of CT myocardial images with PET myocardial perfusion by way of our previously developed algorithms for multimodality image registration (11). The reliability of the automatic segmentation was determined by comparing the radial boundary differences between the automatically extracted myocardial surfaces to those hand-traced by an expert, while the accuracy of the registration of the automatic segmentation was assessed in terms of rotation and translation between these CT surfaces after alignment with PET studies.

Different sets of comparisons were performed. The use of an animal model allowed us to obtain myocardial masses from the animal excised organs and to directly compare them to the image-based results. The comparison of the image-based myocardial masses with the true values eventually exhibited rather poor correlations (Figure 3) as compared also with published literature particularly when CT is compared to MRI [24, 25]. A number of reasons may have contributed to these results: the limited number of cases affecting the power of the performed statistical analysis and particularly the objective difficulty of defining a clear cut through the base of the heart that would match the same VOI on the images. This hypothesis is supported by the markedly improved slice-by-slice comparison of automated vs interactive results (Figure 5) over total myocardial or ventricular results for both mass and volumes (Figures 3,4). Automated versus interactive total myocardial masses also did not strongly correlate; a deeper analysis of the results showed a strong effect of the base location as independently determined by the user and the automated algorithm on the total masses (Figure 3). However, higher accuracy was observed in the extraction of LV and RV borders - in this case the manual segmentation was used as "truth" - with higher correlations between the computed volumes, particularly for the LV (Figure 4), which is also a crucial feature in the alignment procedure.

To further investigate the agreement between image-based results single corresponding slices' segmentation were compared. Figure 5 (top) displays the higher correlation between the masses and volumes extracted by the two image-based modalities when all the slices are pooled together for the myocardium, the LV and the RV respectively. Figure 6 shows examples to substantiate the observation of a higher discrepancy in the segmentation results at the base and the apex of the heart that can greatly affect the total mass measures. Figure 5 (middle and bottom) also exemplifies these results in distinct correlation plots for apex/base and central image portions. Analogously, slice-by-slice comparisons showed higher correlation also within each case (Table 2).

From the results obtained it is clear that this automatic CT segmentation algorithm is not ready for clinical applications where an accurate measurement of myocardial mass is needed. The accurate measurement of myocardial mass is quite challenging because of the requirement that LV-endo, LV epi, RV-endo and RV-epi contours are accurately defined from apex to base. Our results show that the segmentation algorithm in the present formulation is very sensitive to locations such as the base and the apex where partial volume effects or irregularities in the anatomical structures are crucial. The degree of difficulties of the automated algorithm in accurately segmenting the apex and the base of the heart were not anticipated before this study and improvement of this task will be the subject of further development.

Nevertheless, our results indicate that this automatic CT segmentation algorithm is as ready for the fusion of PET/CT imagery as the manual segmentation of CT cardiac images. This is particularly true since the definition of reliable myocardial masks used in the global segmentation procedure uses the *a priori* information that accounts for giving more weight to the more reliable regions during the alignment process. Our results show (Fig. 7) excellent correlations for the LV volumes and thus the LV endocardial boundary definition, followed by good correlations of myocardial mass not including the base or apex, followed by good correlation for RV volumes and thus the RV endocardial boundary. The relative reliability of these regions is very similar to those obtained by our collaborators when validating other automatic myocardial delineation algorithms using shape segmentation with region growing and PCA (24). Moreover, the small errors in rotation and translation between the manual and automatic methods post PET/CTA alignment shown in Table 3 confirm the appropriateness of replacing the manual CT contours with the automatic ones for PET/CT alignment applications. These registration errors are comparable to the errors reported by other techniques (26,27).

A limitation of this work is that it used the alignment of the interactively hand-traced CTA biventricular mesh as a reference standard. Although these surfaces were defined by an expert in pig CT anatomy [TF], manual methods are subjective. Previously, we determined and reported in a study using six patients that the error difference between two interactive alignments was similar to the error difference between the automatic and interactive alignments (11). We could have chosen to compare our automatic CT contours to those from other automated methods (28,29). This was not done for a number of reasons. A large number of different segmentation solutions have indeed been proposed through the years to extract myocardial profiles from both CT and MR acquisitions. Still no methodology has emerged as a definitive reference for comparisons' sake; moreover, none of them have been validated to detect contours from pigs' hearts. But more importantly, the long-term goal of this project is automatic nuclear/CT cardiac fusion and thus the determination of the alignment error of our automatic CT surfaces was of paramount importance. Nevertheless, the comparison of the LV and RV mass determined from hand-traced CT, automatic CT mesh generation and post-mortem mass measurement served as an independent measure of the accuracy of the automatically determined biventricular myocardium from CTA.

Another limitation, as we have previously pointed out (11), is that this validation was performed using only static, motion-blurred perfusion images rather than a gated MPI study

extracted from the same R-R time interval as in the contrast CT image set. This limitation contributes to the error of the automatic alignment. Part of the reason for using the static perfusion distribution is that the alignment method requires the RV information that is often poorly resolved in the gated MPI individual frames. Analogously, only one phase between best systole and best diastole acquisitions commonly acquired was used to validate the segmentation algorithms and the fusion procedure. Nevertheless, the use of multimodality alignment using the same R-R time interval in the aligned modalities is a subject of continuing research by our team. The process of gated information from both MPI and CTA will additionally benefit from the availability of automated segmentation algorithms.

Finally, although the automatic alignment algorithm only requires an average of 42 seconds on a standard PC to register the MPI and CTA, the manual tracing of the biventricular myocardium from a contrast CT image set required approximately 25 minutes depending on the study and the experience of the user. This manual-operation has made the routine clinical use of this type of image fusion impractical. The results from this animal study offers promise that the coupling of our automatic contrast CT edge detection technique and our automatic alignment procedure may eventually allow the creation of a single framework for a completely automated fusion of CTA and MPI, from the identification of the heart to the final fusion and display of images and surfaces. Although we recognize that the fusion procedure can only be applied to those cases for which both MPI and a CT with contrast are available, a significant portion of patients with dubious or unclear diagnosis can benefit from these techniques and possibly avoid unnecessary invasive treatments or dangerous misdiagnosis. This work is indeed an important step in making the availability of the diagnostically rich fused cardiac PET/CTA or SPECT/CTA routinely available in the clinical practice.

CONCLUSIONS

Our automatic myocardial boundary detection algorithm created left and right ventricular, endocardial and epicardial surfaces from CTA cardiac images that are similar in accuracy compared to corresponding hand-traced surfaces. Moreover, the automated alignment of these automatically detected CTA surfaces with the PET surfaces are similar in accuracy to the automated alignment using hand-traced CTA surfaces. Further improvements to the automated segmentation algorithm will be implemented and tested in a follow-up study involving a larger patient cohort.

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Figure 1. Three-dimensional views of cardiac meshes generated from hand-traced (top) and automatically detected (bottom) CT myocardial boundaries from one of the animal experiments.

Figure 2. Results of PET/CT alignment of images from a pig with infarct in the left circumflex (LCX) vascular territory. Representative aligned oblique slices are shown side-by-side (top right panel) and superimposed (remaining three panels).

Figure 3. Left column, display of scatter plot, linear regression line and Pearson correlation coefficient for true versus interactive (top), true versus automated (middle) and interactive versus automated (bottom) myocardial mass measures; right column, Bland-Altman plots for the assessment of measurements agreement for true versus interactive (top), true versus automated (middle) and interactive versus automated myocardial masses.

Figure 4. Left column, comparison of image-based measures for LV and RV volumes; regression line and Pearson correlation coefficients also reported. Right column, Bland-Altman plots for measurements agreement assessment.

Figure 5.

Slice-by-slice comparison of interactive versus automated myocardial mass (A), LV (B) and RV (C) volumes. Top: all slices from all cases plotted; Middle: bottom 10% of total slices representing the heart apex and top 10% of total slices representing the heart base; Bottom: slices from the central portion. Linear regression lines also reported.

Figure 6.

Examples of interactive (red) versus automated (blue) segmented profiles for selected slice in the apex (top), at the center (middle) and at the base (bottom) of the heart with corresponding CTA slice. Various degrees of agreement are evidenced at the apex; usually good agreement on the center portion of the VOI and relatively poor consistency at the base.

Results of aligning the PET with handtraced CT myocardial boundaries

Results of aligning the PET with automatically detected CT myocardial boundaries

Figure 7. Oblique angle tomograms showing representative short axis (SA), horizontal long axis (HLA) and vertical long axis (VLA) orientations of the results of aligning the PET cardiac count distribution with the hand-traced (top) and automatically detected (bottom) CT myocardial meshes from the results shown in figures 1 and 2.

Table 1

Experimental and image-based measurements for the analyzed cases: myocardial mass and ventricular volumes (only image-based).

Case	TRUE MEASUREMENTS		IMAGE-BASED MEASUREMENTS					
			INTERACTIVE			AUTOMATED		
	MYOCARDIAL MASS (g)	MYOCARDIAL MASS (g)	LV VOLUME (cc)	RV VOLUME (cc)	MYOCARDIAL MASS (g)	LV VOLUME (cc)	RV VOLUME (cc)	RV VOLUME (cc)
1	na	88.31	49.20	19.29	139.52	44.87	10.16	
2	na	102.72	79.97	41.78	149.67	75.74	42.72	
3	na	122.50	58.78	30.78	127.18	50.43	44.12	
4	na	116.99	79.74	41.48	140.70	78.70	36.54	
5	100.90	96.30	29.13	22.91	95.32	11.93	3.95	
6	82.74	98.03	65.79	51.43	111.97	52.94	32.68	
7	109.52	105.83	64.55	51.11	119.64	58.78	43.95	
8	118.60	90.69	85.72	45.27	115.60	88.27	47.14	
9	103.40	89.74	60.02	25.31	114.66	61.95	34.41	
10	82.54	90.64	50.19	28.72	104.93	31.81	17.44	
11	86.00	103.75	47.56	26.26	95.14	46.66	18.98	
12	105.33	109.91	57.25	33.73	127.17	49.00	35.21	

na = value not available

Table 2

Pearson's correlation coefficients for image-based slice-by-slice comparisons of myocardial mass, LV and RV volumes.

Case	Myocardium	Left Ventricle	Right Ventricle
1	0.94	0.99	0.67
2	0.87	0.98	0.95
3	0.93	1.00	0.92
4	0.94	1.00	0.96
5	0.84	0.87	0.52
6	0.87	0.97	0.88
7	0.95	1.00	0.96
8	0.79	0.99	0.86
9	0.87	0.99	0.84
10	0.89	0.96	0.74
11	0.89	0.99	0.84
12	0.91	0.99	0.94

Table 3

PET/CTA alignment differences. Hand-traced versus automatic CTA profiles.

n=12	X	Y	Z
Rotation (°)	0.4	-0.6	-2.3
Translation (mm)	1.8	-2.1	2.0