Semi-automatical Validation of SPECT/CT Scanners

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Abstract. Hybrid scanners, which enable the performance of single photon emission tomography (SPECT) and X-ray computerized tomography (CT) in one procedure, have considerable potential as an all-rounder in the nuclear medicine departments. However, challenges remain in validating the accuracy of such hybrid systems. In this paper, a systematic validation method with minimum user interaction is proposed, which has been successfully used on a data-set from a SPECT/Spiral-CT hybrid camera. This method focuses on measuring the distance between the centers of gravity of the SPECT hot spot and its counterpart in the CT image. A novel adaptive threshold method is proposed to automatically segment SPECT hot spots, while the corresponding CT structures are segmented by the semi-automatic random walk method, based on a fast multigrid solver. Accuracy and reproducibility of the validation method have been confirmed by experiments with 21 clinical data-sets.

1 Introduction

Hybrid scanners combining SPECT and CT offer physicians the opportunity to acquire correlated functional and morphological information from a patient in a single session. However, the anatomical accuracy of this hardware-based registration has not yet been sufficiently validated. Phantom studies are not suitable for the validation of the hybrid scanner because it is technically difficult for a phantom to simulate respiratory and cardiac movements, both of which play a key role in mismatching. In a recent study [1], the accuracy of a SPECT/CT system has been quantitatively evaluated by measuring the distance between the centers of gravity of corresponding lesions in two modalities. However, the reproducibility and the accuracy were still questioned, since the selection of centers of gravity was determined by the users. In this paper, we propose a more automatic and more reproducible validation scheme for SPECT/CT hybrid scanners.

2 Methods

We measure the degree of the matching of corresponding structures in SPECT and CT volumes to evaluate the accuracy of the SPECT/CT fusion. The pipeline

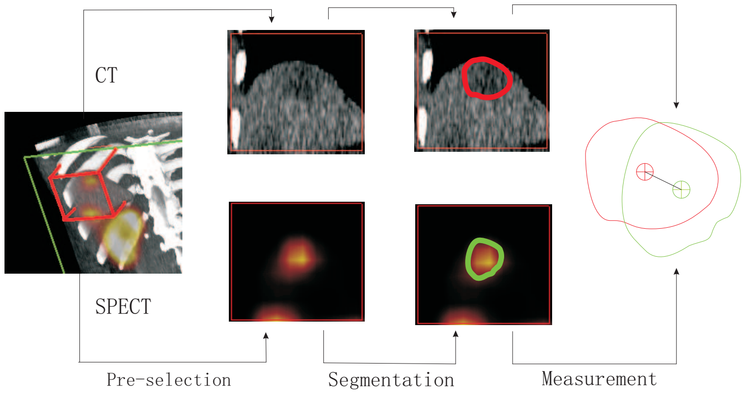

Fig. 1. The work flow of the validation. **Pre-selection:** User manually selects a cubic region that contains both SPECT/CT hot spots from the fused MPR view. Pre-selection of the computation region largely speeds up the following processing operations, but has no influence on the final validation results. **Segmentation:** Segmenting the three-dimensional SPECT hot spot using the adaptive thresholding method (full-automatic). Segmenting the corresponding object in the CT volume via the random walk method (semi-automatic). **Measurement:** Computing the centers of gravity of the segmented SPECT/CT objects. Measuring the distance of two centers to evaluate the quality of the SPECT/CT fusion.

of validation scheme is demonstrated in Figure 1. In this validation scheme, a hot spot in a SPECT volume and its corresponding structure in a CT volume can be segmented with minimum user interaction. a new fully automatic thresholding method is used to segment SPECT hot spot. The optimal threshold is chosen based on the maximally stable extremal region (MSER) [2–4] algorithm. The segmentation actually starts the connected thresholding from the given seed and seek a range of thresholds that leaves the peak of hot spot effectively unchanged. The corresponding CT structure is segmented by a semi-automatic random walk method [5], which allows users to select seeds to intuitively guide the algorithm to separate desired objects from the background. From our experience, drawing the seeds on the middle slice in the axial, sagittal and coronal views is sufficient. The quality of a SPECT/CT fusion is evaluated by the distances between the centers of gravity of the segmented SPECT/CT objects. The validation tool has been successfully integrated into a commercial software of medical image analysis (Syngo, Siemens Medical Solutions).

3 Results

To evaluate the validation tools, we select a set of 21 patients (13 female, 8 male; age range: 10-80 years; mean age: 59.55) examined by a SPECT/spiral CT scanner between November 2006 and March 2007. We choose adenomas of the parathyroid glands on 10 patients and the physiological accumulations of the submandibular gland on the other 11 patients for this study.

The accuracy of the validation tool is evaluated as follows: Two operators perform the validations independently. One operator directly uses the validation tool to measure the distances in X-, Y- and Z-direction (t_x, t_y, t_z) between the hot spot on SPECT and the structure on CT. In the same way, the second operator validates the SPECT/CT volumes, where the SPECT volume has been artificially shifted in X-, Y- and Z-directions. The shift parameters (s_x, s_y, s_z) are randomly generated between 5 mm and 10 mm or between -5 mm and -10 mm. We denote the distances measured by the second operator as $(\hat{t}_x, \hat{t}_y, \hat{t}_z)$. The extent to which the ground truth shift (s_x, s_y, s_z) and the measured shift $(d_x, d_y, d_z) := (\hat{t}_x - t_x, \hat{t}_y - t_y, \hat{t}_z - t_z)$ match, indicates the accuracy of the validation. The experiment yields a clear linear association between the ground truth and the measurement: The correlation coefficients are 0.9927, 0.9909 and 0.9853 in X-, Y- and Z-directions, respectively. The anatomical inaccuracies, measured by the mean $\pm$ standard deviation of the absolute error, are reported to be 0.7189 ± 0.6298 mm in X-direction, 0.9250 ± 0.4535 mm in Y-direction and 0.9544 ± 0.6981 mm in Z-direction.

To evaluate the intraobserver reproducibility, the distances between the SPECT hot spot and CT structure are measured twenty times in five different patients, yielding a mean standard deviation of 0.2177 mm in the X-direction, 0.3039 mm in the Y-direction and 0.3350 mm in the Z-direction. This indicates a high intraobserver reproducibility of the measurement of the X-, Y- and Z-distances. The mean time needed for a full validation process, including the time for data loading and user operation, is less than 2 minutes on a AMD Athlon 3200+ computer (2.20 GHz, 2.00 GB RAM).

4 Conclusion

The purpose of this paper is to introduce a novel way of validating the anatomical accuracy of the SPECT/CT hybrid scanner through the segmentation of hot spot on SPECT and the corresponding structure on CT. The experimental results show that the measurement of this validation tool is sufficiently accurate and reproducible for the clinical data. In our future work, we plan to apply this validation tool to analyse the variation of the accuracy of hybrid scanners with respect to different positions, tracers or acquisition protocols.

References

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