Automatic anatomy partitioning of the torso region on CT images by using multiple organ localizations with a group-wise calibration technique

Xiangrong Zhou*[a], Syoichi Morita[a], Xinin Zhou[b], Huayue Chen[c], Takeshi Hara[a], Ryujiro Yokoyama[a], Masayuki Kanematsu[d,e], Hiroaki Hoshi[f] and Hiroshi Fujita[a]

[a] Department of Intelligent Image Information, Division of Regeneration and Advanced Medical Sciences, Graduate School of Medicine, Gifu University, Gifu-shi, 501-1194 Japan
[b] School of Information Culture, Nagoya Bunri University, 365 Maeda, Inazawa-cho, Inazawa-shi, 492-8520 Japan
[c] Department of Anatomy, Division of Disease Control, Graduate School of Medicine, Gifu University, Gifu-shi, 501-1194 Japan
[d] Radiology Services, Gifu University Hospital, Gifu-shi, 501-1194 Japan
[e] Department of Radiology, Gifu University Hospital, Gifu-shi, 501-1194 Japan
[f] Department of Radiology, Graduate School of Medicine, Gifu University, Gifu-shi, 501-1194 Japan

ABSTRACT

This paper describes an automatic approach for anatomy partitioning on three-dimensional (3D) computed-tomography (CT) images that divide the human torso into several volume-of-interesting (VOI) images based on anatomical definition. The proposed approach combines several individual detections of organ-location with a group-wise organ-location calibration and correction to achieve an automatic and robust multiple-organ localization task. The essence of the proposed method is to jointly detect the 3D minimum bounding box for each type of organ shown on CT images based on intra-organ-image-textures and inter-organ-spatial-relationship in the anatomy. Machine-learning-based template matching and generalized Hough transform-based point-distribution estimation are used in the detection and calibration processes. We apply this approach to the automatic partitioning of a torso region on CT images, which are divided into 35 VOIs presenting major organ regions and tissues required by routine diagnosis in clinical medicine. A database containing 4,300 patient cases of high-resolution 3D torso CT images is used for training and performance evaluations. We confirmed that the proposed method was successful in target organ localization on more than 95% of CT cases. Only two organs (gallbladder and pancreas) showed a lower success rate: 71 and 78% respectively. In addition, we applied this approach to another database that included 287 patient cases of whole-body CT images scanned for positron emission tomography (PET) studies and used for additional performance evaluation. The experimental results showed that no significant difference between the anatomy partitioning results from those two databases except regarding the spleen. All experimental results showed that the proposed approach was efficient and useful in accomplishing localization tasks for major organs and tissues on CT images scanned using different protocols.

Keywords: 3D CT images, anatomy partitioning; organ localization; generalized Hough transform.

1. INTRODUCTION

Anatomy partitioning of the human body that aims to identify the scope of different organ and tissue regions on computed-tomography (CT) images. It is an essential step in recognizing anatomical structures necessary to develop computer-aided diagnostics and surgical systems. Successful anatomy partitioning can considerably simplify established image-processing algorithms such as organ segmentation, image registration, and lesion detection. In addition, it enables us to use the data-mining and image-retrieval concepts and techniques to discover knowledge based on big datasets of medical images.

The essence of anatomy partitioning is to localize all organs and tissues on a CT scan. The technical difficulty of the partitioning process concerns using a single approach or scheme to solve many different organ localization tasks. The

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most important criterion for evaluating the performance of the partitioning process is its accuracy in adapting to inter-patient variation on extensive CT cases scanned using different protocols. Many studies have been reported on organ localizations on CT images based on machine-learning approaches [1,2]. For example, Zheng et al. proposed a marginal space learning approach to locate heart, liver, and other organs on CT and magnetic resonance imaging [3,4]. Dikmen et al. presented a learning method to detect the anatomical landmarkers on CT images [5]. Criminisi et al. used decision forests to locate several major organs on whole-body CT images [6]. These previous studies showed the acceptable performance of multiple organ localization on 3D medical images. However, the targets in these studies were limited to a few major organs and were easy for recognition. The remaining challenge is to localize other targets such as the uterus, gallbladder, and different vertebrae, which is commonly required in the anatomy partitioning process. Furthermore, most performance evaluations in previous studies were based on a handful of patient cases that failed to show the robustness of localization methods.

In this study, we propose an approach to realize automatic partitioning of the torso region on CT images. The target organ partitions include 35 VOIs defined as the minimum bounding boxes of major organs and tissues in routine diagnosis. This approach combines an independent organ localization method [7–9] and a group-wise calibration and correction technique. Machine-learning-based object detection and generalized Hough transform-based point-distribution estimation is used in the localization and calibration processes. These are described in the following section.

2. METHODS

2.1 Outline

The proposed approach is constructed according to two major processing steps: (1) single target-organ localization that finds the bounding box of the target organs based on window sliding and pattern matching on the feature space; (2) group-wise calibration and correction based on the spatial relations among multiple organ locations. The first step focuses on identifying local image similarity of a target organ and output likelihood values of the target organ location on each pixel of a CT scan. The second step emphasizes validating the spatial relationships of the detected organ locations based on human anatomy. We determine the final locations of CT scanned organs by balancing the local image similarity (likelihood value) and global spatial relationship of the multiple organ locations (prior probability) obtained in Step 1 and 2, respectively. The flowchart of the proposed approach is shown in Fig.1. Details of each processing step are described as follows.

2.2 Single organ localization

The basic unit of anatomical partitioning is an organ location defined by a 3D box that bounds the target organ region tightly and accurately. The goal of this processing step is to detect a candidate list of this bounding box for each target organ on a CT scan respectively. The list's order of priority for each candidate is ranked by the likelihood value (similarity to the target organ) of a detected box. Our approach for organ localization includes two stages. In an offline training stage, we search the discriminative features of species of organs by using a trial-and-error approach based on many training CT scans in which the target-organ location has been sketched manually. We then build an ad-hoc feature space with a classifier to distinguish the target organ from the remaining regions. In the testing stage, a sliding window is used to scan all pixels on an imputed CT scan to classify on the corresponding feature space (i.e., determine whether the current location is the target organ).

In our previous research [7], we proposed a universal method for detecting organ locations on 3D CT scans. Instead of sliding a window directly on a 3D-image space, our method trained three independent 2D detectors to capture the different sections of a 3D target's appearance in three bodily directions, multiple image scales and orientations by using ensemble-learning approach. The outputs of our 2D detectors were integrated based on a collaborative majority voting in 3D to enhance the robustness of the final localization result. We established the 2D detectors as "weak" so that they only needed to detect a part of the organ region. In addition, we allowed several false positives in the results. Majority voting of multiple 2D candidates from three independent directions can combine all weak 2D detectors into a "strong" 3D detector, which can then indicate the bounding box of the target organ stably and accurately.

The output of organ localization is a list of candidates (3D boxes) that passed the majority voting process. A candidate was defined as a 3D box that met the condition in which more than one section of the 3D box in each 2D direction is detected by the 2D detectors. Candidate priority is defined as the sum of the numbers of 2D sections detected by all 2D detectors. The likelihood value of the candidate is calculated by normalizing the priority based on the volume of a

detected 3D box. All candidates are ranked by their likelihood values showing the intra-organ-image-similarity to the same type of organ regions in the training dataset.

2.3 Group-wise calibration and correction of multiple organ locations

The localization process described in Section 2.2 can correctly detect the locations of organ regions (e.g., kidney, liver, and lung) that have unique image appearances compared to the remaining regions on a CT scan. However, in the case of certain targets such as the gallbladder and pancreas that have similar appearances to that of other tissues, the detectors may be confused in distinguishing between the target organ and background. In addition, they may not always output the correct organ locations. In such cases, the spatial relationships to the other organs (e.g., liver, stomach) are useful to improve the correctness of the organ localization process. In general, requiring the trained detectors to output the correct locations of all kinds of organs on all unknown CT scans is unrealistic. However, ensuring that the locations

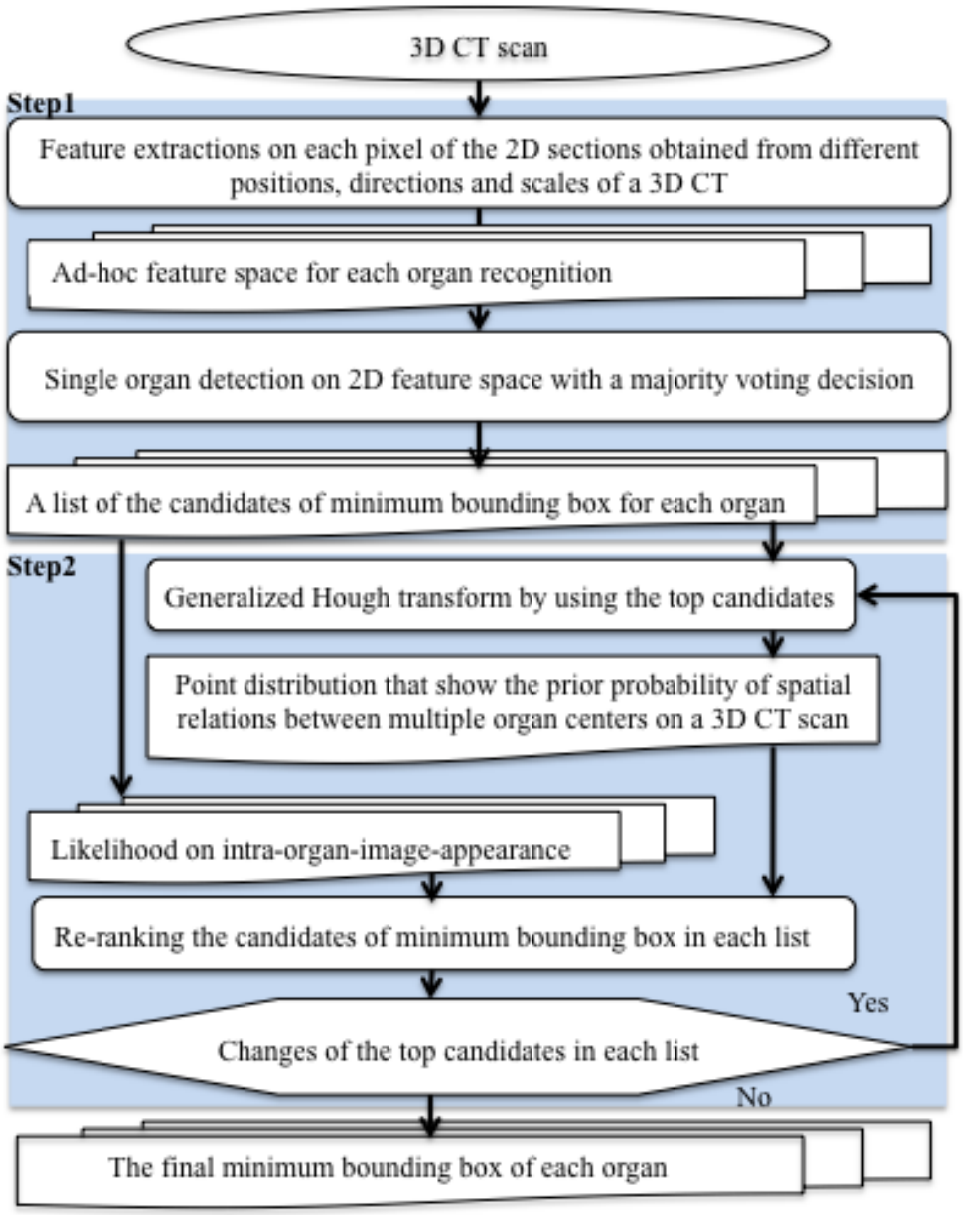

Fig. 1 Processing flow of anatomical partitioning on 3D CT scans. (*MBR: minimum bounding rectangle)

of most organ types can be detected correctly on a CT scan is possible. The purpose of this processing step is to identify a few outliers in the detected organ locations on a CT scan. The solution is to use the spatial relationships among the multiple organs to constrain all candidates of the detected organ locations on a CT scan. This method employs generalized Hough transform to conduct a group-wise calibration based on detected candidates of the multiple organ locations. It also estimates the reasonable locations of the outliers based on prior anatomical knowledge derived from the training dataset.

The process involved in this step is designed as an iteration to update and sort the candidate list of each organ location obtained from Step 1. The goal of this step is to ensure the final list of top candidates properly represent all target organ locations. We define a global cost function based on the sum of likelihood values of current top candidates with the condition (constraint) that the spatial relations between the top candidates are valid. This validation is based on the minimum distance of each selected top candidate to a point distribution of organ centers obtained from a training dataset. In fact, the generalized Hough transform is used to realize the validation process. Here, the detection of a single organ casts probabilistic votes for locations of the other organs in a CT scan. We used the top candidate of each organ to vote the potential central locations (point cloud) of the other organs. We consider the point distribution as a prior probability of the multiple organ center positions on a CT scan. We use a K-nearest neighbor search within the candidates list to renew and select the top candidate by maximizing the global cost function defined by the likelihood values.

These processing steps are repeated, thereby generating the point cloud to show the prior center position of each organ and re-ranking the top candidate for organ locations. These iterations are performed until the top candidate in each list has no change (see Fig. 1). A maximum number of iterations was established to terminate this process, thereby avoiding an infinite loop.

3. EXPERIMENT AND RESULTS

Two datasets that included 4,300 cases of high-resolution 3D volumetric CT scans and 287 low-resolution PET-CT scans were used in our experiment. We used two kinds of multi-slice CT scanners (one from GE Healthcare and another from Philips Medical Systems) to scan high-resolution CT images. Each CT scan used a common protocol and covered the entire human torso region by approximately 800–1200 axial CT slices with an isotopic spatial resolution of approximately 0.6–0.7 mm and 12-bits density (CT number) resolution. The low-resolution CT images were scans produced for PET examinations with 1.2 mm spatial resolution in the axial section and 5.0 mm slice spacing. The age of the patients from which these CT scans derived ranged from 25 to 92 years. All CT scans were from patients having specific real or suspicious abnormalities.

Thirty-five major organs and tissues were selected as targets for evaluating the performance of the organ localization method. These included: heart, liver, gallbladder, spleen, pancreas, stomach, bladder, left and right lungs, left and right kidneys, left and right femur-heads, left and right psoas major muscles, uterus and rectum, abdominal rectus muscle, inferior vena cava (IVC) with ventral aorta, and bodies of vertebrae (12 thoracic and 5 lumbar). We manually marked the 3D locations of these targets in 300 3D high-resolution CT scans in order to train the 2D detectors. This resulted in 4,000–10,000 positive and 40,000–100,000 negative 2D training samples used to train the 2D detectors for organs of each sagittal, coronal, and axial direction. The detectors for each target were trained separately except for those detecting vertebrae that shared the same three 2D detectors for both thoracic and lumbar spines. The trained detectors were applied to localize the 35 target organs and tissues in the other 4,000 3D high-resolution CT and 287 low-resolution PET-CT scans.

We first conducted subjective evaluations of the anatomical partitioning on the multiple organ localization results. We then randomly selected several CT scans for quantitative evaluations. The authors of our study manually labeled the ground-truth of each target organ location (3D box) and measured the volume variance and center shift between the detected organ location and ground truth. An example of the detected organ locations in 3D CT scans is shown in Fig. 2. A typical computing time was 16 s per CT scan and was accomplished using a computer equipped with an Intel Core2Duo 2.23 GHz CPU.

4. DISCUSSION AND CONCLUSION

We considered the detected organ location to be successful if the majority parts (two-thirds of the volume) of the detected 3D box and the ground-truth MBR overlap. Our subjective evaluation based on test samples (4,000 high-resolution CT cases) showed that the successful rates were distributed from 95–100% for 31 organs (lung, heart, liver, left/right kidney, left/right psoas major muscle, IVC & ventral aorta, left/right femur head, bladder, abdominal rectus muscles, uterus & rectum, spleen, stomach, bodies of vertebrae). The rates of pancreas and gallbladder were 72 and 80%, respectively. These results showed that the proposed approach accomplished the localization tasks for most organ and tissue types in more than 95% CT cases, except for localization of the two organs mentioned. Failure regarding pancreas and gallbladder were because of the poor performance of the trained 2D detectors. Specifically, a smaller sample number (smaller volume in 3D) and greater variances in those two organs were present compared to those of other organs examined during the training stage. Furthermore, the image appearances of these two organ were not sufficiently unique

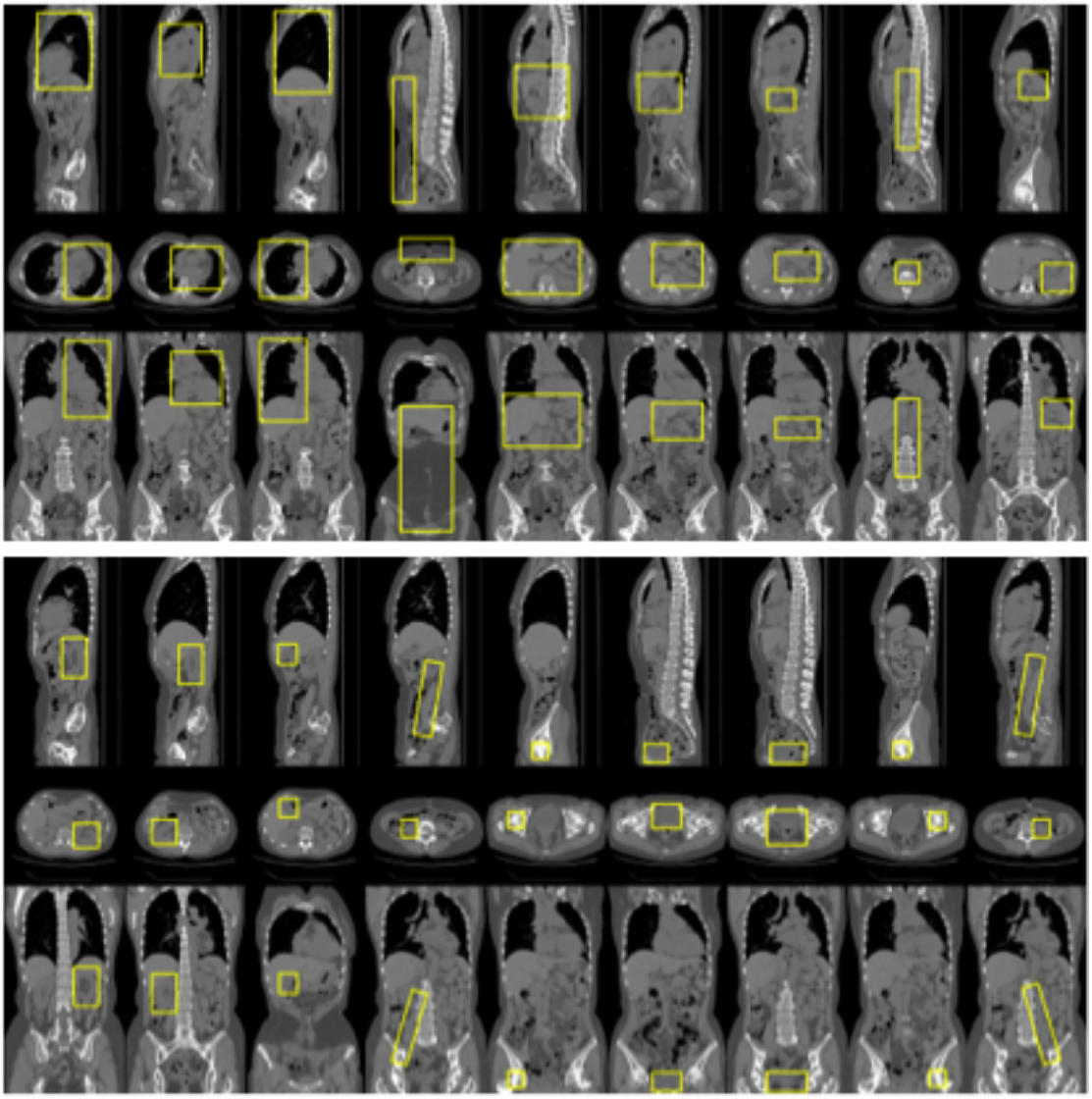

Fig. 2. Example of the localization results for major organ and tissues in a 3D CT scan. Three slices that pass through the detected center position of the target organ are shown. The rectangle indicates the detected organ location (bounding rectangles from upper-left side: left lung, heart, right lung, abdominal rectus muscles, liver, stomach, pancreas, IVC & ventral aorta, spleen; and from lower-left side: left kidney, right kidney, gallbladder, right psoas major muscle, right femur head, bladder, uterus & rectum, left femur head, and left psoas major muscle).

compared to those of the remainder regions in the CT images. We determined that the group-wise calibration and correction process considerably enhanced the robustness in these cases in which the trained 2D detectors were not sufficiently strong. For example, in the case of gallbladder localization, the success rate improved by 10% after group-wise calibration and correction. For our quantitative evaluation, the center-shift distances between the localization result and gold standard were less than 50 voxels in most CT cases, with the modes ranging from 10 to 20 voxels. The histograms of volume variance in most organs were distributed between -20 and 20% with modes near zero, except with respect to the bladder and liver. These evaluation results showed that the proposed approach located the center position approximately and determined the size of the bounding box of the target organ regions. However, in cases in which the target organ has a large variance in volume (bladder) or asymmetrical shape (liver), the accuracy of the detected bounding rectangle must be improved.

Experimental results of localizations on PET-CT scans showed that the performance of 2D detectors had considerable degradations because of the worse image quality and lower spatial resolution of the PET-CT scans compared to the high-resolution CT images used in training. However, we found that the final success rates of localization for those organs did not change considerably except with respect to the spleen (down from 95 to 88%) and pancreas (up from 72 to 99%). These results showed that the group-wise calibration and correction were efficient to enhance the robustness of the 2D detectors. From the quantitative evaluations, we confirmed that the accuracy of the detected box was degraded to 4–29 voxels on center distance and from -50 to 10% on volume variance compared to the gold standards [9]. These results showed that organ location accuracy was fundamentally dependent on the performance of 2D detectors assessed during the training process. Group-wise calibration can enhance the robustness of the localization process. However, it is not very helpful as a means to improve the accuracy (center location and volume) of the detected 3D bounding box.

In conclusion, we proposed a universal approach that can be used to partition the human torso region automatically by localizing major organs and tissues on 3D CT scans. This approach was applied to 35 organ and tissue regions. The efficiency and accuracy of the proposed approach were validated and satisfactory performance was proven on more than 4,000 real clinical CT scans.

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REFERENCES

1. P. Viola and M. J. Jones: Rapid object detection using a boosted cascade of simple features, IEEE CVPR, 2001.
2. R. Lienhart and J. Maydt: An extended set of Haar-like features for rapid object detection, IEEE ICIP 2002, vol. 1, pp. 900-903, 2002.
3. Y.Zheng, B.Adrian, G.Bogdan, S.Michael, and C.Dorin: Four-chamber heart modeling and automatic segmentation for 3-D cardiac CT volumes using marginal space learning and steerable features, IEEE TMI, vol.27, pp.1668-1681, 2008.
4. H.Ling, S.K.Zhou, Y.Zheng, B.Georgescu, M.Suehling, and C.Dorin: Hierarchical, learning-based automatic liver segmentation, IEEE CVPR, 2008.
5. M.Dikmen, Y.Zhan, and X.S.Zhou: Joint detection and localization of multiple anatomical landmarks through learning, SPIE Medical Imaging 2008, vol.6915, 2008.
6. A.Criminisi, J.Shotton, and S.Bucciarelli: Decision forests with long-range spatial context for organ localization in CT volumes, in MICCAI workshop on Probabilistic Models for Medical Image Analysis (MICCAI-PMMIA), 2009.
7. X. Zhou, S. Wang, H. Chen, T. Hara, R. Yokoyama, M. Kanematsu, H. Hoshi, and H. Fujita: Automatic localization of solid organs on 3D CT images by a collaborative majority voting decision based on ensemble learning, Computerized Medical Imaging and Graphics, vol.36, 4, pp. 304-313, 2012 .
8. X.Zhou, A.Yamaguti, X.Zhou, T.Hara, R.Yokoyam, M.Kanematsu, and H.Fujita: Automatic organ localizations on 3D CT images by using majority-voting of multiple 2D detections based on local binary patterns and Haar-like features, Proc. of SPIE Medical Imaging 2013: Computer-Aided Diagnosis, 8670, 86703A-1 - 86703A-7, (2013).
9. M. Shimizu, T. Hara, X. Zhou, C. Muramatsu, S. Ito, S. Kumita, K. Ishihara, T. Katafuchi, H. Fujita: Evaluation of automatic segmentation results of organ regions on torso CT images of FDG-PET/CT, International Forum on Medical Imaging in Asia, PS.1, No.480, (2015).