CTScanTool, a semi-automated organ segmentation tool for radiotherapy treatment planning

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Abstract. The goal of radiation therapy is to eradicate tumors while sparing normal tissues from radiation damage. Therefore, accurate definition of tumor and organ boundaries is important for achieving good treatment outcome. Segmentation of tumors and organs at risk is a standard procedure done by radiation oncologists for radiation therapy treatment planning, for which computed tomography (CT) images are commonly used. In this paper, we present the development of CTScanTool, the organ segmentation tool with a graphical user interface, allowing semi-automated and manual delineation. The proposed semi-automated segmentation method is based on the combined techniques of region growing, morphological reconstruction, and watershed transform algorithms. The semi-automated segmentation results of CT images were compared with those contoured by experienced radiation oncologists. In the experiment, we investigated the combined segmentation method on brain, lung and kidney tissues. In all cases, the true positive rate (sensitivity) was higher than 95%. Jaccard indices and positive predictive values (precision) were higher than 91% for brain and lung tissues and better than 81% for kidney tissues. In the near future, CTScanTool will be incorporated in the Proton pencil beam Scanning treatment PLANning system (PSPLAN) used for research and education in proton therapy.

1. Introduction
Radiation therapy is the use of ionizing radiation to eliminate tumors while preventing surrounding normal tissues from radiation damage. Segmentation of targets and organs of interest, typically based on computed tomography (CT) images, is the primarily important step in radiation therapy treatment planning to ensure the coverage and conformity of radiation dose in the target volume. Manual segmentation by radiation oncologists is currently the standard procedure in the clinical practice and considered as the ground truth of the segmentation while semi-automated and automated segmentation methods have gained increasing interest for time and workload reduction [1].
Semi-automated segmentation of medical images can be categorized into methods that require and do not require prior knowledge of the morphology of anatomical structures. Region growing is one of the segmentation methods that do not rely on prior knowledge. The method is relatively straightforward and widely used in 3D segmentation of medical images [2].

As a part of the development of Proton pencil beam Scanning treatment PLANning system (PSPLAN) for research and education [3], a semi-automated segmentation tool called CTScanTool has been developed in MATLAB with a graphical user interface (GUI). The algorithm used in CTScanTool is a combination of the seeded region growing algorithm [4], morphological reconstruction [5] and the watershed transform [6]. This paper focuses on the description of CTScanTool and the validation against contours drawn by radiation oncologists using the statistical validation method based on the spatial overlap between two sets of segmentations.

2. Materials and Methods

2.1 Development of CTScanTool

CTScanTool is a semi-automated organ segmentation tool developed in MATLAB (The MathWorks, Inc., USA) with the graphical user interface (GUI). Figure 1 shows the main GUI of CTScanTool. The program can be run with MATLAB command lines or the executable file compiled from the MATLAB codes. The flowchart of CTScanTool is shown in figure 2. First, it reads all image slices from a specified folder path at once. Users are able to segment the region of interest (ROI) manually by drawing polygons with mouse clicks (figure 3a) or semi-automatically by selecting a seed point in the ROI, as shown in figure 3b. The semi-automated segmentation method is based on the combined techniques of the seeded region growing segmentation [4], morphological reconstruction [7] and the watershed transform [6].

In the seeded region growing technique, the ROI is iteratively grown from the manually specified seed point by comparing the intensity values of neighboring pixels with the region’s mean intensity. Only pixels with the intensity difference not exceeding a pre-defined threshold level are added to the ROI. At this step, users manually determine a suitable threshold level depending on the characteristic of the segmented region. For example, if the ROI and surrounding regions have low contrast, the suitable threshold should be low and vice versa.

![Figure 1. The graphical user interface (GUI) of CTScanTool.](image-url)
Figure 2. Flowchart of CTScanTool.

Figure 3. Manual segmentation by polygon drawing (a) and semi-automated segmentation based on the seeded region growing technique (b).

Small holes may occur inside the ROI derived from region growing. Morphological reconstruction [5] is applied to fill these holes automatically, as shown in figure 4. Holes are considered as background pixels (pixel value 0) that are not adjacent to the edge of the ROI. The operation starts by changing background pixels inside the ROI to foreground pixels (pixel value 1) until the boundary of the ROI is reached. If the segmented region does not cover the entire ROI, it is possible to merge remaining regions to the ROI by positioning seed points in the remaining regions and starting the semi-automated segmentation, as illustrated in figure 5. When the boundaries between regions are unclear, over segmentation may occur. To overcome this problem, the watershed transform based on topological structure of the image is applied to confine the ROI to the region around the seed point automatically [6], as shown in figure 6. After segmentation is completed, the coordinate pixels of delineation can be saved in .txt file format and these coordinate pixels can be retrieved and displayed on the corresponding CT image.
Figure 4. Morphological reconstruction to fill holes inside the ROI.

Figure 5. Merging of two semi-automated regions: Region 1 is initially segmented but does not cover the entire ROI (a) while Region 2 is the entire ROI after merging Region 1 with the remaining region (b).

Figure 6. Oversegmentation (a) and automatic selection of the ROI around the seed point using the watershed transform (b).

2.2 Statistical validation of CTScanTool

To validate CTScanTool, comparison of segmented ROIs with ROIs drawn by radiation oncologists, considered as the ground truth segmentation, were examined based on the elements of the confusion matrix [8] including the true positives (TP), the false positives (FP), the true negatives (TN) and the false negatives (FN), as shown in figure 7. The ground truth segmentation was obtained from retrospective data of the treatment plans for two patients treated with radiotherapy by two different radiation oncologists at Ramathibodi Hospital, independently of this study. The retrospective study was approved.
Results and Discussion

Figure 8 shows the comparison of ROIs drawn by CTScanTool and manually by radiation oncologists. The summary of the metrics used for evaluating the quality of segmentation is given in table 1. For all investigated cases, true positive rates (sensitivity) were higher than 95% while Jaccard indices and positive predictive values (precision) were above 91% for brain and lung tissues and above 81% for kidney tissues. This implies that target coverage (sensitivity) was relatively good while the segmentation quality may deteriorate by the false positives of surrounding tissues for low-contrast images such as those of the abdomen and pelvic region. Similar results for kidney segmentation have been obtained by three commercial softwares that are based on automated (atlas-based) segmentation methods with the average Jaccard indices of 81% [9]. Compared to manual segmentation that needs manual specification of ROI contours, the semi-automated method used in CTScanTool requires selection of a single seed point in most cases, thus reducing time and workload for the segmentation process.
Figure 8. ROIs drawn by CTScanTool (green) and radiation oncologists (red): (a) brain, (b) lung and (c) kidney.

Table 1. Metrics for evaluating CTScanTool.

| ROI             | Number of tested images | Jaccard index (%) | True positive rate (sensitivity) (%) | Positive predictive value (precision) (%) |
|-----------------|-------------------------|-------------------|--------------------------------------|------------------------------------------|
| Brain           | 101                     | 94.7±2.6          | 98.5±1.5                             | 96.1±3.0                                 |
| Lung            | 27                      | 91.7±4.9          | 95.1±4.5                             | 96.3±1.9                                 |
| Left kidney     | 33                      | 86.3±3.7          | 98.5±2.0                             | 87.5±3.5                                 |
| Right kidney    | 32                      | 81.6±4.3          | 97.6±2.9                             | 83.4±4.4                                 |

4. Conclusions
CTScanTool, the semi-automated segmentation tool for target and organ delineation in radiation therapy was developed as a part of the development of the Proton pencil beam Scanning treatment PLANning system (PSPLAN) for research and education. The segmentation method used in CTScanTool is based on the combined techniques of seeded region growing, morphological reconstruction and watershed transform methods. The semi-automated segmentation tool was validated against the ground truth, giving reasonable agreement to the manual segmentation by radiation oncologists.

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