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Multi atlas-based muscle segmentation in abdominal CT images with varying field of view

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Abstract

The development of automatic techniques for the analysis of abdominal CT images is a topic of large interest. By using automatic techniques, objective diagnostic support can be provided to physicians and organ segmentation can eliminate time-consuming manual procedures such as delineation. Automatic kidney segmentation has been achieved for healthy cases but is unsuccessful in cases with diseased kidney. In this paper we propose an automatic system to assist the segmentation of abdominal organs, using the medially positioned psoas major muscles’ shape and location along with previously accomplished segmentations of the liver and spleen. A framework is employed to segment the vertebral column and rib bones, and the left and right psoas major muscles are segmented using a multi-atlas-based segmentation with weighted decision fusion and non-rigid registration. Due to a varying field of view (FOV) in each dataset and the requirement of an equal FOV for registration, an adjustment is made between pairs of datasets using an automatic vertebra identification framework created in this paper. The vertebra identification shows desired results in 88% of 68 datasets. The psoas major segmentation accuracy is inspected using a cross-validation among 21 datasets, showing a median Jaccard similarity coefficient (JSC) of 63.4% and 68.6% for the left and right muscles respectively. Future work will focus on adapting the kidney segmentation framework to include the shape and position of the psoas major muscle in the processing.

Keywords: automatic segmentation, abdominal X-ray CT images, vertebrae identification, field of view correction

1 Introduction

Abdominal computed tomography (CT) images used in medical screening are generally not utilized to the full extent. Knowledge of examination heuristics, patient history and common sense are needed along with the expertise of inspecting CT images in order to come to a diagnosis. Medical imaging systems can provide a wealth of information, which may not be presented in an organized form, and overwhelm a practicing physician. Computer-aided diagnosis (CAD) can provide automatic objective diagnostic support to physicians with limited experience and improve the accuracy and speed of the diagnosis. Using CAD, time-consuming tasks such as manual tracing of muscle outlines can be eliminated, thus providing objective tracing results and removing inter-physician variability.

A prerequisite for these automatic techniques is automatic organ segmentation. In previous work, automatic kidney segmentation was achieved for healthy cases, based on the use of a probabilistic atlas and a multi-level statistical shape model [1]. However the results for diseased kidneys were unsatisfactory, due to difficulties in global localization of the organ and subsequently the detection of the correct organ outlines. In Figure 1 the abdominal region is shown containing the kidneys, liver, spleen and psoas major muscles. In Figure 1b the kidney is diseased due to cancer which results in dark areas in the CT image, marked by the arrows. Automatic kidney segmentation has difficulties detecting the outlines of the kidney as shown in Figure 1b due to the deviation in intensity compared to healthy kidney tissue. A physician may require these outlines for the estimation of tumor volume.
Figure 1: Overview of abdominal organs in close proximity to the kidneys. These organs are partially in direct contact with the kidney. a) Healthy patient case. b) Patient with diseased kidney

Approximately 23% of all malignant tumors in adults develop in the kidney [2]. The two most common types are renal cell carcinoma (RCC) and urothelial cell carcinoma (UCC). RCC originates in the lining of the proximal convoluted tubule which are very small tubes in the kidney that filter blood and waste products [3]. In the Netherlands, the annual incidence of this, since recently, second most common urological tumor is about 11 per 100,000 inhabitants. Men are twice as often affected as women, most often in the ages ranging from 50 to 70. For patients with metastatic disease, two-year survival is between 0% and 20%.

It is assumed that nearby abdominal organs to the kidneys such as the liver and spleen, as well as the psoas major muscles, are constrained in their shape and location, allowing stable and accurate segmentation results. Segmentations of the liver and spleen have previously been accomplished [1]. Using the relations of the kidney to these organs in shape and position, a region of interest (ROI) can be specified in which the kidney may be present. The ROI thus allows for the improvement of kidney segmentation through global positioning and outline correction. The approach discussed can be considered general, as it’s application is not strictly limited to kidney segmentation: the application can be made any structure in the human body that is surrounded by other structures that can be accurately segmented.

The target in this paper is psoas major muscle segmentation in abdominal X-ray CT images through automatic techniques. In other work by Kamiya et al. [4] the segmentation of the psoas major had been accomplished. The psoas major muscles are directly attached to the vertebral column through tendons, and this known relation was used as a basis for segmentation. However due to this approach, the method is strictly suitable for psoas major segmentation. The method for segmentation in this paper is more general as it can be applied to other organs in the abdominal region.

A method called label fusion is employed which was implemented originally for the segmentation of muscle in the hip and leg region [5, 6]. The framework that uses this method is limited to using a fixed field of view, i.e. each dataset contains the same region of the human body. After a normalization process, each dataset has equal spatial dimensions in $\mathbb{R}^3$. The novelty in this paper is the application of the label fusion method to the abdominal region with datasets of a variable field of view.
2 Materials and methods

2.1 Overview

Figure 3 presents a overview of the segmentation of the psoas major. A division is made between phases in the processing line named common, training and application. The two types of datasets that are used are the training datasets and the patient CT dataset, which are both abdominal X-ray CT datasets.

In the common phase, an original CT image is processed by segmenting the vertebral column and the rib bones. The vertebral column is partitioned by recognizing and separating each vertebra. Subsequently, each vertebra is identified with a corresponding anatomical label. Unique colors are given to identified vertebra for clarity.

In the training phase the output of the common phase is further processed. A ground-truth label is created of the left and right psoas major muscles through manual delineation. One dataset is A target dataset is chosen among the training datasets and the remaining datasets are used as atlases. Using the priorly identified vertebrae, the field of view between a target-atlas pair is made equal. A process of label fusion is applied to segment the psoas major muscle in the atlas datasets, by using the ground truth muscle labels from the atlas datasets.

2.2 Segmentation and partitioning of vertebral column and ribs

A framework created by the National Institutes of Health (NIH, USA) was employed to automatically segment and partition the vertebral column and rib bones in abdominal CT images [7]. The processing steps are outlined in the overview in Figure 3b and Figure 3c. The spine is one of the most prominent and stable structures for anatomical representation making it suitable as a landmark for image registration algorithms. Furthermore, it can provide a reference coordinate system for other organs in the chest and abdomen, aiding localization and segmentation.

The framework applies an image thresholding to obtain the initial spine segmentation. A hybrid method based on the watershed algorithm and directed graph search is applied to extract the spinal canal. After that, a four-part vertebra model consisting of the vertebral body, spinous process, and left/right transverse processes is fitted to segment the vertebral region and separate it from adjacent ribs and other structures. The resulting output of the framework is an image with labeled parts for e.g. cortical bone, spongy bone, rib bone and the spinal cord. In addition, the result of the vertebral column partition is available as geometric planes, positioned inter-vertebrally, spanned by two linearly independent vectors and bound in size. In Figure 2 the geometric planes are shown in green, along with the path of the spinal cord in red and the outer vertebra edges in blue.

Several modifications were made to the NIH framework, which is made in C++ and compiled using Visual Studio 2008 [Microsoft Corporation], in order to export the results of the geometric planes and spinal cord path. Other corrections were necessary in order to alleviate memory allocation errors which occurred when processing a certain type of dataset. The framework has proven to be suitable for non-contrast abdominal CT images.

2.3 Vertebrae identification

In this paper a method has been developed for the identification of vertebra, shown in the overview in Figure 3d. Each vertebra is automatically identified with an anatomical vertebral label through the use of rib bone detection.

According to anatomical knowledge, humans have 12 sets of ribs of which the first seven sets are attached to the sternum through the costal cartilage [8]. The remaining five sets are known as false ribs where the first three sets are indirectly attached to the sternum and the last two sets are known as floating ribs and are attached to the vertebrae only.
Figure 3: Overview of the processing pipeline used for the segmentation of the psoas major muscles. It shows the common phase, training phase and application phase. Training and patient CT datasets enter the common phase. The training datasets are further processed in the training phase, and enter the application phase. The various frameworks or programs or contributions are color coded.
The lowest floating rib bone is known to be attached to the vertebra labeled as T12. Vertebrae identification can be achieved by identifying the lowest floating rib bone and subsequently finding the connected T12 vertebra. This identification is used to derive the anatomical labels for other vertebrae.

The volume data of each vertebra is selected through use of a bounding box set between the intervertebral geometric planes from Section 2.2 above and below the vertebra.

The lowest floating rib bone detection proceeds as follows. Individual rib bones are extracted from the label image from Section 2.2 and given unique identification tags. A region is selected that contains the whole vertebral column as well as containing the nearby rib bones partially. The volume data outside this region is discarded. The previously extracted individual rib bones are processed to compute the volume, which is the total amount of voxels in a bounded region. The found volume of a rib bone $V_r$ is compared against the volume of the spinal cord $V_s$ within the middle vertebra of the dataset. Through a selection criterion the rib bones of interest are included for further analysis: a minimal volume fraction $V_r/V_s$ of 0.125 is required for selection. The selection criterion is found empirically through extensive testing. The selected rib bones of interest are sorted spatially from superior to inferior. The center of mass $X \in \mathbb{R}^3$ of each rib bone is computed through a weighted-average as follows

$$X = \frac{1}{V_r} \sum x_i.$$  \hspace{1cm} (1)

Subsequently, processing is done from superior to inferior. The average z-spatial distance between a pair of rib bones’ center of mass is computed. A large z-spatial distance is expected between T12 and hip bone, if available in the dataset, which makes it possible to exclude the hip bone and prevent it from being detected as the T12 rib bone. If no lower rib bones are available, the lowest rib bone is marked as the lowest floating rib bones. The T12 vertebra is found as being the closest to the center of mass of the lowest floating rib bones. The largest floating rib bone is used for this calculation. The corresponding second rib bone of the rib bone pair is then found, and the nearest vertebra to the rib bone is selected. The other vertebra labels are derived from the labeled T12 vertebra.

Figure 4: Identification of vertebrae is shown using color coding and anatomical labels. The lowest floating rib bones connected to the T12 vertebra are marked in white.

2.4 Visualization software

It is important to visually inspect the results of segmentations, partitioning and vertebrae identification for validation. A 3D volume rendering is shown in Figure 4 generated by an application created in this paper (ITK [9], VTK, Qt).

Volume isosurfaces are rendered after the generation of polygons using the marching cubes algorithm [10]. Inter-vertebral geometric planes were added in order to show the vertebral column partitioning. Separately identified rib bones are displayed in shades of green with the exception of the rib bone connected to the T12 vertebra which is marked in white. Vertebrae identification is displayed using unique color identification as well as text displaying the anatomical labeling. Furthermore, a line showing the path of the vertebral column is drawn which is the center of the spinal cord at each point in the axial plane.

Using Qt, an interface is implemented which allows for the selective viewing of separate parts in the scene.

2.5 Psoas major muscle ground truth labeling

A manual delineation of the left and right psoas major muscles is made using Vincent [Fuji Corp, Japan].
Figure 5: Overview of the segmentation process of the psoas major muscles. It shows the training phase and application phase.

Ground truth labeling is applied in the training phase and is shown in Figure 3e. The software allows the user to manually trace the muscle outlines, either by drawing freehand or using the drawing aiding system which automatically follows contours. Several slices throughout the axial plane are selected and outlines drawn manually. Information for slices between are interpolated. After completing the tracing, the coronal and sagittal planes are utilized for inspection and possible correction of the manual segmentation result. A resulting volume is obtained which is referred to as a ground truth label. In this study, manual tracing was performed on 21 CT datasets by a student without formal training in organ delineation.

2.6 Label fusion and field of view matching

A multi-atlas based segmentation with local decision fusion was employed, based on a framework that was originally used for musculoskeletal segmentation in the hip and leg area using a fixed field of view [5, 6]. In this framework, spatial normalization is first performed by registration of multiple atlas datasets to a target dataset. This reduces the inter-patient variability in body size, pose and positioning in the scanner. Using the deformation field found in the registration process, the ground truth labels of the segmented organ target are transformed along with the corresponding datasets. The ground truth labels are combined through a fusion process to form a segmentation in a target dataset. Fusion is applied by a spatially varying decision algorithm, where a probabilistic label is generated and compared against the intensity values in the target dataset.

In this paper, an application of this framework is made to the abdominal region and support is added for a varying field of view. Using a hierarchical strategy, initial normalization is performed with the Image Registration Toolkit (iRTK) [11] by using the previously segmented vertebrae labels in Section 2.2. The vertebrae labels are a stable structure and can be accurately segmented. An affine transformation along with a non-rigid transformation is used for the normalization process.

In order to arrive at a good result for spatial normalization, it is necessary to match the field of view between target and atlas pairs of datasets. In Figure 5 several datasets are shown with a varying field of view. Each of these datasets has several vertebrae in common. A field of view correction is made by selecting the common vertebra and cropping the datasets to the corresponding regions as shown in Figure 6. Vertebrae identification created in Section 2.3 allows for the range of vertebrae to be estimated in the target and atlas datasets. The most superiorly and inferiorly positioned vertebrae are identified and the overlapping regions are extracted from both datasets.

Unique labels are given to each identified vertebra in order to aid the normalization process as seen in Figure 6. This information is used for to match corresponding vertebrae and prevent extraneous warping to occur during the non-rigid transformations.

After the label-based spatial normalization is performed, the atlas image has identical dimensions as the target image. Further registration is done using intensity values in the original target CT image and
Figure 6: Overview of the segmentation process of the psoas major muscles. It shows the training phase and application phase.

The transformed atlas CT image in order to improve the result.

The label fusion is performed using a varying decision algorithm called weighted decision fusion (WDF). In this study, the left and right psoas major muscles are segmented in a target image using $N=20$ atlas datasets. First, the difference image $D_i$ between the transformed moving atlas and target image is computed

$$D_i(p) = \| A_i(u_i(p)) - U(p) \|, \forall i,$$

where each atlas $A_i$ has a transformation $u_i$ for normalization with the target image $U$. This image serves as an estimate of the registration success and is used as a decision factor for the inclusion of a label element in the fused label. Smoothing of $D_i$ is applied through the convolution with a Gaussian kernel $g_{\sigma_1}$. The inverse value of this operation $\lambda_i$ is defined as follows

$$\lambda_i(p) = \frac{1}{D_i(p) \ast g_{\sigma_1}(p) + \varepsilon} + \varepsilon,$$

where $\varepsilon$ is a small value to avoid zero divisions. $\lambda_i$ is used as a weighting factor for each element in a transformed ground truth label. Due to the inverse proportionality of $\lambda_i$ to the difference image $D_i$, large differences between the transformed moving atlas and the target image result in small weights, and vice versa.

The probabilistic label was determined by a weighted average of the transformed binary segmentations

$$S_p(p) = \frac{1}{N} \sum_{i=1}^{N} \lambda_i(p) S_i(u_i(p)).$$

The image is convolved with a Gaussian kernel $g_{\sigma_2}$ for smoothing

$$S_{\sigma_2}(p) = S_p(p) \ast g_{\sigma_2}(p),$$

and subsequently thresholding is applied at 0.7 in this study to create the binary image containing the fused label.

In the application phase, a muscle segmentation in the patient CT dataset is made using the previously created fused labels in the training phase. The same label fusion method is applied in order to arrive at a segmentation in the patient CT dataset.

2.7 Leave-one-out cross-validation

In order to assess the results of the label fusion method, leave-one-out cross-validation (LOOCV) is employed [12]. The datasets are partitioned such that a single sample of the training set is used for validation and the remaining samples are used for testing. Repetitions are performed with different partitions such that each sample in the training set is once used as the validation data, as shown in Figure 7. LOOCV allows for the prediction of how accurately the algorithm will perform in practice on a patient CT dataset.

![Figure 7](image_url)

**Figure 7:** Overview of the segmentation process of the psoas major muscles. It shows the training phase and application phase.
2.8 Measures of fused label success

The validity and accuracy of the fused label segmentation is inspected by comparing the generated fused label to the ground truth label. A description is made using the quantitative measures Jaccard similarity coefficient (JSC) [13], also called mean volume overlap (VO), and average distance error (AvgDist).

The Jaccard similarity coefficient represents the muscle regions of the ground truth standard as follows

\[
JSC = \frac{A \cap B}{A \cup B},
\]

where A and B represent the muscle regions in the ground truth standard and the fused label, respectively. The Jaccard similarity coefficient describes the ratio of the area of intersection to the area of union as shown in Figure 8a.

The average distance error is used as a second measure and is more suitable for small elongated shapes as opposed to the Jaccard similarity coefficient. On sampled points on the edge of the ground truth label, a perpendicular line to the surface is drawn which has the least distance to the surface of the fused label, as shown in Figure 8b. The measured distances are subsequently averaged.

\[\text{(a)}\quad \text{(b)}\]

Figure 8: Quantitative measurements used for the validation of the fused label result. a) Jaccard similarity coefficient. The blue area shows the overlap which is measured. b) Average distance error. The arrows show the minimum distance perpendicular vector from one shape to another which is measured on each point on the surface.

2.9 Application to a patient CT dataset

A segmentation of the psoas major muscle in a patient CT dataset starts with running the operations in common phase: segmentation of rib bone and vertebral column; vertebral column partitioning and lastly, vertebrae identification. A notable difference of a patient CT dataset when compared to a training dataset is the unavailability of ground truth labels of the psoas major muscles and thus the inability to describe the validate the results of the segmentation in quantitative numbers. The result of the final step in the training phase are the fused labels for the 21 training datasets. The same fusion label method can be re-applied to these fused labels of training step in order to create a fused label for the patient CT dataset. The advantage of this method is the highly stable result using only the best of the previously fused labels. In order to apply label fusion, field of view correction is once again necessary between each pair of patient CT dataset and training dataset.

3 Results

In this paper results have only been generated for the training dataset due to time restrictions. In this section, results of the vertebra identification shown in the overview as Figure 3d will be shown, as well as the segmented psoas major muscle results in Figure 3g.

3.1 Vertebra identification

Vertebrae identification results were inspected for correctness by comparing the identified T12 vertebra to its anatomically expected location. In Figure 9 results of the vertebrae identification are shown. As mentioned in Section 2.3, the T12 vertebra is connected to the lowest floating rib bone which in these results are colored white. Validation of vertebrae identification was performed on 68 datasets and showed expected results in 88% of all cases.

In the other 12% of the cases, often the T12 vertebra would be incorrectly identified as T11 or L1, resulting in a shift in anatomical labeling for each vertebra in the sample. Figure 10 shows a result with a shift in labeling: the T11 vertebra is incorrectly identified as T12 which results in the T12 vertebra being labeled L1.
Figure 9: Results of vertebrae identification for 4 samples. The T12 vertebra is connected to the rib bones marked in white. The anatomical numbering is displayed in text.
3.2 Fused label results

The fused labels generated in Section 2.6 are a volume that represents an approximation of the psoas major muscle. In Figure 11 the results of these fused labels are shown. The ground truth volume is displayed transparently and the opaque part of this muscle in the fused label result. A partial segmentation can be seen which extends up to the L5 vertebra in Figure 11.a and Figure 11.d. The ground truth label extends from L1 to below L6.

For each left and right psoas major fused labels, the measures of Jaccard similarity measures and average distance error are computed and shown in Figure 14 and Figure 15. From the results the left and right psoas major muscles have pairwise very similar results in Jaccard similarity index and average distance error. In average distance errors several outliers can be observed for samples 3, 15 and 18.

The median JSM are 63.4% and 68.6% for the left and right psoas major muscles respectively. Similarly, the median value for the average distance error was found to be 2.48 mm and 2.28 mm for the left and right muscles respectively. When comparing to other work [4] the VO was in the range of (0.683 - 0.904) with an average value of 0.723 which is higher than the values obtained in this paper.

The color maps shown in Figure 13 show the average distance error on each point of the surface in millimeter unit. The left and right muscles are shown in two sides of the volume. The ideal value of zero distance to the ground truth label is cyan colored and is shown on portions of the surface. Red and blue colors show are large negative and positive deviations respectively. A negative distance indicates that a portion of the fused label resides outside the ground truth label i.e. an overestimation in the segmenta-
tion is made. Vice versa for a positive distance, an underestimation is made. In the fused labels shown, the distance is largely red-shifted to the positive side indicating an oversegmentation.

Three of the datasets showed large deviations from the ideal shape as large outliers in average distance, numbers 3, 15 and 18 in Figure 15. In Figure 16 the color map results for 3 and 15 are shown. Evidently, the segmented muscle region has grown outside the psoas major. The strong red colors show are large negative distance to the psoas major ground truth label. Growing occurs mostly towards the nearby positioned kidney, which is largely in contact to the psoas major muscles.

Figure 12: Other results

Figure 13: Color map of the fused label results. On each point of the surface the average distance error (mm) is shown, mapped to a certain color.
Figure 14: Validation of the fused label results expressed in Jaccard similarity coefficient.

Figure 15: Validation of the fused label results expressed in average distance error.
4 Discussion

Vertebrae identification was unsuccessful in 12% of cases due to incorrectly recognized T12 vertebra, resulting in a shift in anatomical labeling for the remaining vertebrae. An incorrect detection such as in Figure 10 can have multiple reasons: underestimation of rib bone volume due to inaccurate segmentation of the rib bone and vertebral column by the framework discussed in Section 2.2, resulting in exclusion of target rib bones; a vertebra may contain a large traverse costal facet which is mistakenly detected as rib bone, further complicating the distinction between these structures and the smallest floating rib bones. In a small amount of cases problems occurred in the NIH framework step from Section 2.2 where due to memory allocation errors the segmentation could not be successfully made and subsequently the other steps in the processing pipeline could not be performed.

It is known that 8% of people have an extra lumbar rib called the thirteenth rib. The vertebrae identification algorithm may not be able to correctly identify the T12 vertebra in this case.

The fused label as obtained in the training data often showed a partial segmentation as result, as seen in Figure 11 and Figure 12. The main cause of this is the field of view correction step in Section 2.6, which crops the region between a target-atlas dataset that has common vertebrae. This step will always result in loss of psoas major volume as the muscle extends below L5 which is the maximum vertebra that can be detected (the L6 which is connected to the sternum cannot be detected in this framework). Furthermore, the psoas major extends below the vertebral column which inevitably gives a loss in volume. The size of the segmentation is dependent on the field of view of the target dataset, as all the atlas datasets are matched to fit the target dataset. In this study the size of the training dataset (N=21) allows a sufficiently large testing set for muscle segmentation.

As the kidney is generally positioned between the T11 and L3 vertebrae, and segmentations are usually achieved up to L4 or L5, the limited segmentation is considered to be a fully usable result for improving the kidney segmentation. However for improved reliability in edge cases, it should be attempted to segment the entire volume of both the left and right psoas major muscles. As mentioned in the introduction in Section 1, a ROI can be found using the organs nearby the kidney in order to aid the kidney segmentation through global positioning and outline correction. An improved segmentation of the psoas major muscles can aid in creating a larger ROI which is better able to contain the full kidney organ and lead to an improved kidney segmentation.

A phenomenon that became evident upon inspection of the fused labels was the growing of the fused label outside the psoas major shape. Growing usually occurred towards the kidney which is positioned close to the psoas major muscles and is partially in direct contact. The cause is due to the very similar intensity values between the psoas major muscle and the kidney. Both organs are soft tissues and during a CT scan these tissues will have a roughly equal attenuation, resulting in roughly equal Hounsfield units. A possible solution would be the use of contrast-dye which is intravenously injected into the patient and will accumulate in the liver, generating a higher signal. In this case, the liver will appear brighter which allows an improved separation of psoas major muscle and kidney.

Future work should first focus on creating a segmentation of the psoas major muscles in a target CT dataset, based on the results from the training phase, outlined in the application phase in Figure 3. Secondly, it should be attempted to adapt the kidney segmentation program to make use the ROI which can be calculated using the automatic segmentations of the psoas major muscles, liver and spleen. The shape, form and position of these organs is used for the correction of the segmentation results and for the initial search conditions.
References


