

Segmentation of Bone Structures by Removal of Skin and using a Convex Relaxation Technique

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Abstract: In this paper an algorithm to extract the skin and obtain the segmentation of bones from patients in CT volumes is described. The skin is extracted using an adaptive region growing algorithm followed by morphological operations. The segmentation of bone structures is implemented by the minimization of an energy function and using a convex relaxation minimization algorithm to minimize the energy term. The cost terms in the energy function are computed using the distance between the mean and variance parameters within bone structures in a training set and the mean and variance parameters computed locally at each voxel position (x,y,z) in a test dataset. Several performance metrics have been computed to assess the algorithm. Comparisons with two techniques (thresholding and level sets) have been carried out and the results show that the algorithm proposed clearly outperform both techniques in terms of accuracy in the delimitation results.

1 INTRODUCTION

The analysis of bone structures is interesting for physicians, surgeons and radiologists in many applications, such as bone fractures, cancer, analysis of bone densities, diagnosis of some diseases (osteoporosis, rheum, arthrosis), etc. Usually, in these analysis, simple operations, such as thresholding, are performed to extract bone structures in CT 3D volumes. However, the thresholding technique is not valid when some of those diseases happen, as Hounsfield values within bones may have different values as those expected. Furthermore, Hounsfield values within bones vary due to the different components (mainly periosteum, compact (hard) bone, cancellous (spongy) bone and bone marrow), making the segmentation of these structures difficult. Fig. 1 shows a CT slice where these Hounsfield differences can be appreciated. Note that Hounsfield values in cancellous bone, for instance, are quite similar to those values in surrounding organs, making thresholding techniques fail as they select either only the boundaries of bones or some other soft tissues around the bone structures. Besides, even boundaries in bone structures (compact bone) can be difficult to be segmented due to some of the diseases above mentioned.

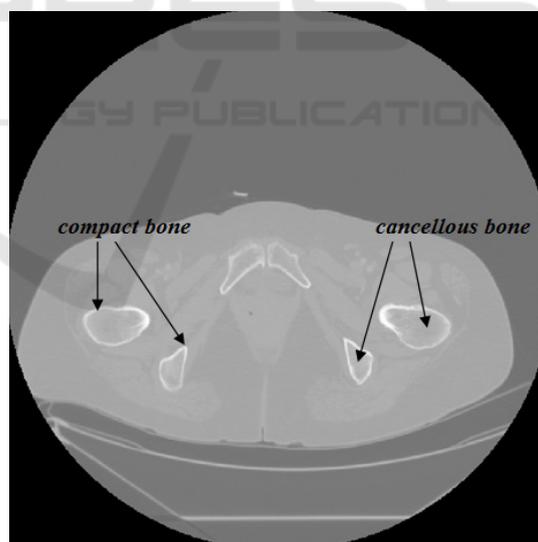


Figure 1: Different parts within bones in CT volumes.

Another problem that physicians have to face is the high computational cost when managing 3D CT volumes. Thus, automatic algorithms able to segment complete bone structures would be very useful for specialists in the field, decreasing the time in selecting them.

Many works have been presented to carry out the

segmentation of bone structures (Kang et al., 2003; Sebastian et al., 2003; Cheng et al., 2013; Cervinka et al., 2014; Aslan et al., 2009; Calder et al., 2011; Kratky et al., 2008; Perez et al., 2015), being graph cuts and level set algorithms (Kratky et al., 2008) considered as representative of the state-of-the-art methods. However, the main drawbacks in all these works is that either they are focused in one or two bone structures (hip, acetabulum, femoral head, vertebral bodies, etc.), thus losing generality, or they require high computational times or suffer from high sensitivity to initialization (Kratky et al., 2008).

In this paper an algorithm to segment bone structures is described. The procedure tries to be fast and general to any kind of bone structures. The paper is organized as follows: Section 2.1 describes the extraction of the skin surface in order to facilitate the selection of bone structures by removing artificial structures that may have high Hounsfield values outside the patient and reducing the areas within each slice to be analyzed. Although there are few works addressing the segmentation of skin in CT volumes (Kang et al., 2014; Xiangrong et al., 2004; Banik et al., 2010), the delimitation of the skin can be very useful in order to facilitate the segmentation of other organs or structures such as liver, heart, muscle tissues, lung etc. Section 2.2 describes the algorithm developed to perform the bone segmentation. Basically, the segmentation of bone structures is implemented applying the continuous max-flow algorithm by Yuan et al., (2010) building an energy function to be minimized. The cost terms in the energy function are obtained from distance images which are built by computing the distance between the local mean and variance in each CT voxel to the parameters mean and variance computed from all the voxels in bone structures within a training dataset. Section 3 shows the results and finally, the conclusions and future work are described.

2 METHODOLOGY

2.1 Skin Selection

In order to facilitate the segmentation of bone structures, the first stage of the algorithm extracts the surface skin of the patients in the CT volumes under analysis. The common techniques to delimitate the skin in CT volumes are based on the use of global thresholds and edge detection techniques (Kang et al., 2014; Zhou et al., 2004; Banik et al., 2010). However, global thresholds are

not valid in all the cases and edge detection techniques usually have problems with edge delimitation and connection. As indicated in the work by Zhou et al., (2004), skin has a depth of about 2mms. Considering that the CT volumes throughout this work have an xy spatial resolution of about 0.781mm/pixel, 2mms corresponds to approximately 3 pixels in the xy plane directions.

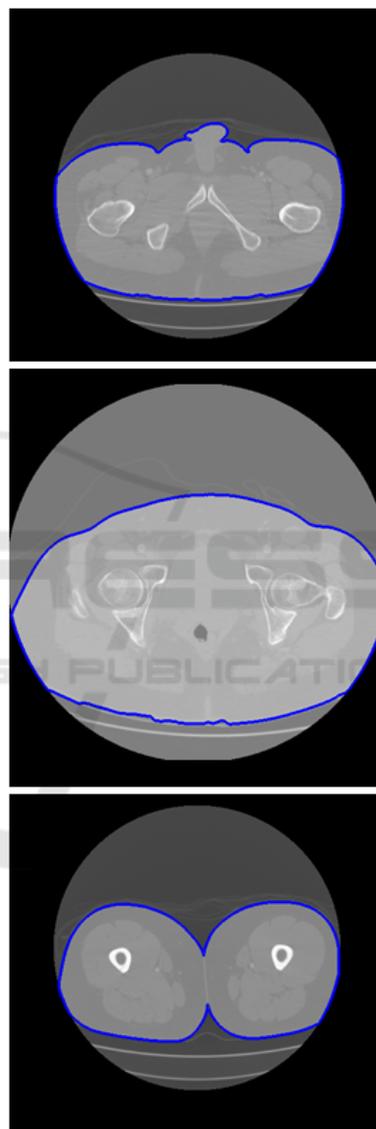


Figure 2: Skin (in blue) of three patients in different CT slices.

The skin selection stage is performed in two steps. In the first step, a neighbourhood-connected region growing algorithm is applied to select inner structures within the body. For this, some seeds within the patient are selected. These seeds are

selected randomly and automatically by selecting some voxels corresponding to bone (voxels with Hounsfield values over 1700). The inclusion criterion only takes into account Hounsfield values within a range specified by the user by means of two range values. Experimentally, the best lower and upper inclusion values were 800 and 2500, respectively. Only voxels with values within the range are selected if also their neighbouring voxels have Hounsfield values within the same range. With this algorithm, artifacts or air (like in lungs or outside the body) are discarded. The result is a binarized image.

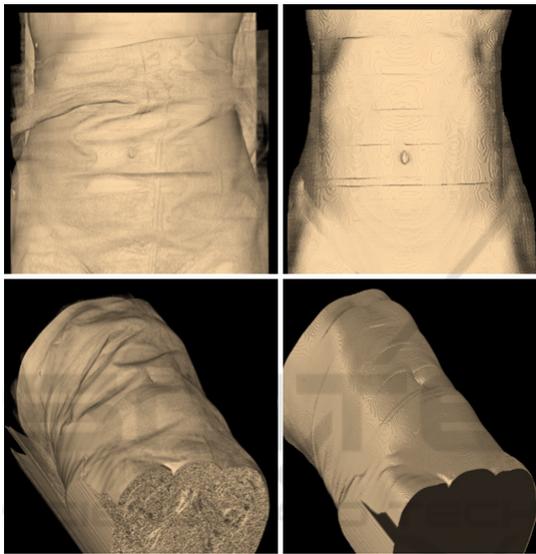


Figure 3: Examples of the 3D surface (skin) of a patient. Left figures correspond to the surface before the skin extraction operation. Right figures show the outer surface of the patient.

The outer boundary of the binarized image will correspond to the skin. Thus, in the second step, an structure element of 3 voxels in the xy axis and 1 voxel in the z axis is employed. Using a simple erosion morphological operation and subtracting the result to the original binarized image, the skin can be obtained.

Fig. 2 shows the skin boundaries of three CT slices corresponding to three different patients. Fig. 3 shows two examples of the 3D surface (skin) of a patient. Left figures correspond to the surface before the skin extraction operation. Right figures show the outer surface (skin) of the patient. Note in Fig. 2 and 3 how artificial artefacts, such as sheets or bed, have been removed.

2.2 Bone Segmentation

The algorithm for bone segmentation has three different stages.

2.2.1 Normalization

In the first stage, a thresholding operation is performed in order to remove soft tissue (such as fat or some organs) with Hounsfield values below those present in bones. To compute this threshold a set of training CT slices were analyzed to determine the minimum value present in all the bone structures. More particularly, the training set was composed by 10 CT slices extracted from CTs of different patients and different to those used in the test set. Subsequently, a threshold was chosen under this minimum value. The thresholding operation guarantees that all the bone structures are maintained in the CT slices while removing all those soft tissue structures which could interfere in the bone structure delimitation. The experimentally threshold obtained had a value of 900 HU (*Hounsfield Units*). With this thresholding operation all the bone structures are still clearly visible while many of the soft tissues have been removed.

Finally, the CT volumes are scaled with the following scaling operation:

$$\text{Scaled_Im} = \frac{\text{Thresh_Im}}{\max(\text{training_set})} \quad (1)$$

where Thresh_Im is the thresholded Image obtained in the previous step and Scaled_im is the Image obtained after the scaling operation. The maximum value within the training set is used also to scale the Dicom CT slices. Note that with this scaling operation the Dicom slices will have values in the range [0,1].

2.2.2 Computation of Statistical Distance Image

In the second stage, using all the voxels within bone structures in all the scaled CT slices belonging to the training set, the mean and variance parameters are extracted. This set of two parameters is denoted as *RSP* (*Reference Statistical Parameters*). Then, for each CT volume in the test dataset and at each voxel position (x,y,z) , the parameters mean and variance are computed using a 5×5 local neighborhood around the voxel position (x,y,z) . Then, the Euclidean distance from this computed set of parameters to the reference parameter set *RSP* (mean and variance) is obtained. This distance value is stored in the called

SDI (*Statistical Distance Image*) image at the same positions (x,y,z) .

Fig 4 shows two slices corresponding to two different patients (first row) and the corresponding two SDI images obtained (second row). Note that voxels belonging to bones have low values whereas voxels not corresponding to bones present high values.

2.2.3 Convex Relaxation to Implement Bone Segmentation

In the last stage, the convex relaxation technique proposed by Yuan et al. (Yuan et al, 2010) is used to perform the segmentation stage. Yuan et al. modified the classical discrete min-cut max-flow in graph-cut implementations by creating a continuous domain and allowing the labeling terms to be continuous. The fast max-flow implementation by Yuan et al. provided a convex solution and, as proved by Yuan et al., their implementation outperformed the classical graph-cut techniques both in terms of speed and accuracy. Yuan et al. demonstrated that their fast max-flow implementation is equivalent to the continuous s-t min-cut problem as follows:

$$\min_{u(x) \in [0,1]} \int_{\Omega} (u(x))C_s(x)dx + \int_{\Omega} (1-u(x))C_t(x)dx + \int_{\Omega} C(x)|\nabla u(x)|dx \quad (2)$$

where $u(x)$ is the continuous labeling function and C_s and C_t are the cost terms in the energy function. Note that according to Eq. (1), the cost term C_s should take low values inside bone structures and high outside them. On the contrary, C_t should take high values inside bone structures and low values outside them. In our experiments, C_s and C_t were computed as follows:

$$\begin{aligned} C_s &= (\text{Scaled_Im} + (1 - \text{SDI}))/2 \\ C_t &= 1 - C_s \end{aligned} \quad (3)$$

The most right term in Eq. (2) is a penalty term. $C(x)$ is a penalty function that penalizes voxels at boundaries with low gradients.

This $C(x)$ function is computed as follows:

$$C(x) = \frac{b}{1 + a \cdot |\nabla \text{Scaled_Im}(x)|} \quad (4)$$

where a and b are constants and were obtained empirically. The parameters a and b took the values 10 and 0.2 respectively. In the third row of Fig. 4 the cost terms C_s corresponding to two slices of two different cases are shown.

The energy term described in Eq. (2) is minimized using the algorithm described by Yuan et al. in (Yuan et al., 2010).

3 RESULTS

Bone structures in 45 slices belonging to 15 different CT volumes (and different to those in the training set) were manually segmented by an expert and used as groundtruth to assess the algorithm. The CT volumes were composed on average of 250 CT slices. The same CT slices were processed as described in the previous section and several evaluation metrics were computed. These metrics have been computed in terms of TP (*true positive voxels*), FP (*False positive voxels*), TN (*true negative voxels*) and FN (*False negative voxels*). TP are those voxels classified by the algorithm as bone and also by the expert in their manual segmentation. FP are those voxels classified as bone by the algorithm but not by the expert. TN correspond to voxels classified as not belonging to bones both by the algorithm and by the groundtruth segmentation. Finally, FN are those voxes classified as not belonging to bones by the algorithm but they correspond to bones according to the groundtruth. The metrics used for the evaluation are DICE, Jaccard, Sensitivity, Specificity, PPV and are computed as follows:

$$\text{Dice} = \frac{2 \cdot TP}{2 \cdot TP + FP + FN} \quad (5)$$

$$\text{Jaccard} = \frac{TP}{TP + FP + FN} \quad (6)$$

$$\text{Sensitivity} = \frac{TP}{TP + FN} \quad (7)$$

$$\text{Specificity} = \frac{TN}{FP + TN} \quad (8)$$

$$\text{PPV} = \frac{TP}{TP + FP} \quad (9)$$

A conventional PC (Intel ® Core™ i7-2670QM, CPU @ 2,20GHz, 6GB RAM) was used in all of these evaluations.

In order to compare the results obtained by the algorithm with other state-of-the-art methodologies, comparisons using the same evaluation metrics with a level set implementation and with the classical thresholding technique have been carried out. Particularly, the level set methodology adopted in the experiments is the Distance Regularized Level Set Evolution (DRLSE) implementation (Li et al, 2010). The same test dataset was used to perform the comparisons.

In the Level-Set implementation some configurable parameters are selected to perform the segmentation. Particularly, the parameter values

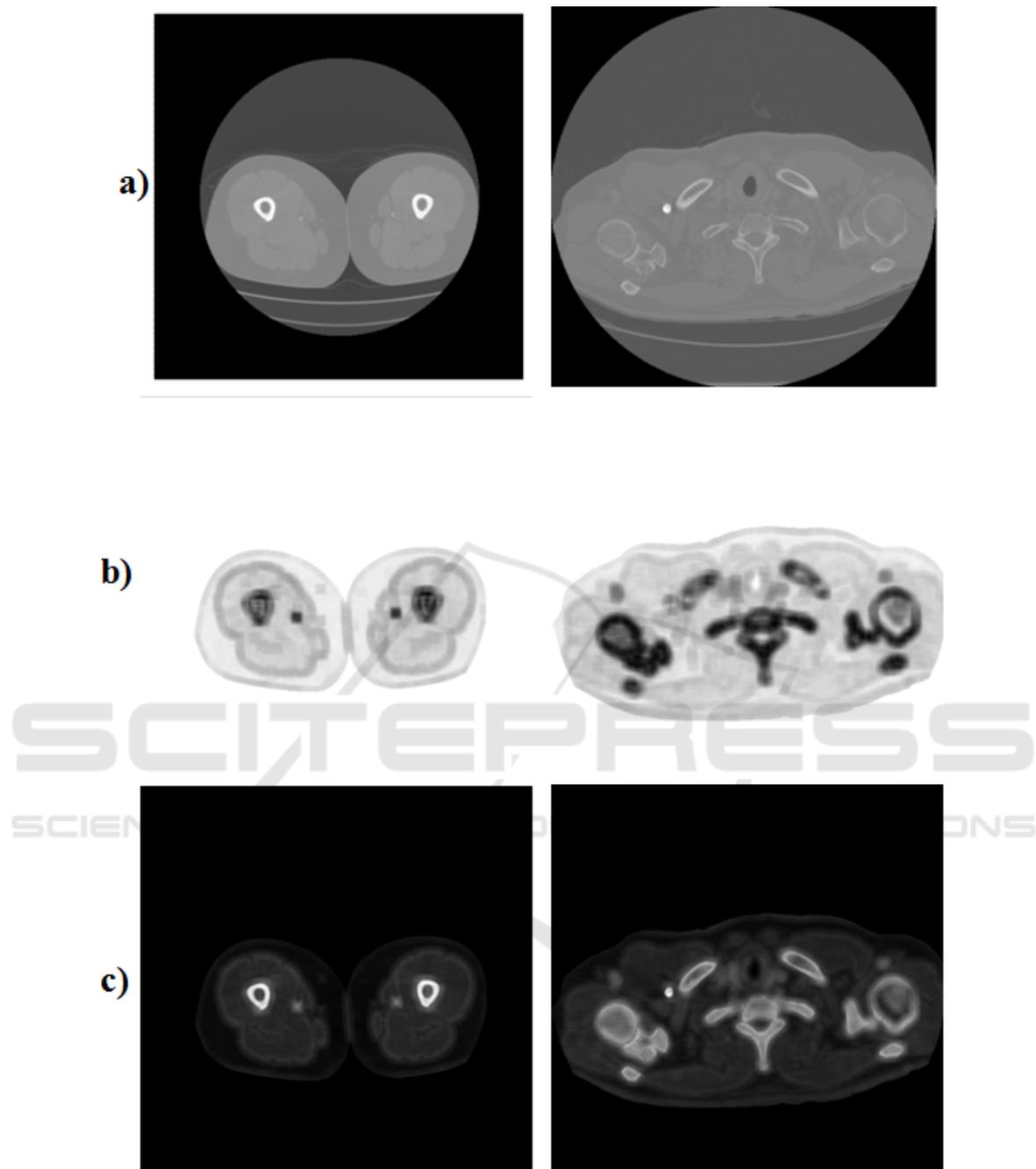


Figure 4: First row (a): Original CT slices. Second row (b): SDI images corresponding to the slices in the first row. Third row (c): Cost Image terms used as input in the convex relaxation algorithm.

$\lambda = 20$, timestep $\Delta t = 5$, $\varepsilon = 1.5$ and $\alpha = 1$ required by the algorithm were used in our experiments. The DRLSE algorithm was applied to the 45 scaled dicoms (*Scaled_Im*) described in the previous section.

Regarding to the thresholding implementation, a threshold is selected and all Hounsfield values under

that threshold are set to zero. In our experiments the threshold selected was that providing the best results. Experimentally, using the training set, the threshold value obtained was 1100.

Table 1 shows the evaluation metrics for the algorithm described throughout this paper and the two segmentation techniques above indicated. The

average computational time required to segment one slice for every algorithm is also indicated. Note that the algorithm described throughout this paper was the only providing good results, followed by the thresholding implementation. The level set implementation had difficulties when several bone structures are present or when some bone structures had diffuse boundaries or low gradient values. In many of these cases the DRLSE algorithm required a very high computational time (high number of iterations) to provide acceptable results. Note, according to Table 1, that the standard deviation obtained in the different metrics when using the DRLSE algorithm are high, thus showing that the method performed very well in some slices (Dice Coefficient of 0.94 in the best case), whereas it was incapable of performing the segmentation in others (Dice Coefficient of 0.04 in the worst case).

In terms of computational times, the thresholding technique was the fastest one requiring only about 0.023 seconds to segment one slice. Considering a CT volume composed of about 100 slices, this would imply a processing time of only 2 seconds.

Table 1: Metrics obtained in the different experiments. The values in the table represent the mean value of each metric \pm its standard deviation.

	Thresholding	DRLSE	Algorithm proposed
Dice	0.79 \pm 0.09	0.59 \pm 0.35	0.9\pm0.053
Jaccard	0.66 \pm 0.13	0.49 \pm 0.34	0.83\pm0.087
PPV	0.80 \pm 0.13	0.52 \pm 0.37	0.86\pm0.085
Sensitivity	0.80 \pm 0.16	0.94 \pm 0.21	0.97\pm0.049
Specificity	0.99 \pm 0.01	0.88 \pm 0.13	0.99\pm0.005
Computational Time (<i>seconds per slice</i>)	0.11\pm0.05	2752 \pm 657	89 \pm 6.73

In Fig. 5 the results obtained using the three different methodologies are shown. Only some slices are shown for visualization purposes. The red contours correspond to the groundtruth segmentation provided by the expert. Blue regions correspond to the segmentation results obtained with each algorithm. Note that the thresholding technique is not able to select all the voxels within bones as they present Hounsfield values under the specified threshold. It can be also appreciated that the level set technique had difficulties when the number of bone structures is very high (second row, first column) or selected non bone tissue if it was enclosed within a bone structure (third row, first column).

4 CONCLUSIONS

In this paper a technique to implement the selection of bone structures in CT volumes is described. The first stage consists in the delimitation of the skin (outer surface of the patient) in order to facilitate the segmentation of the bone structures by reducing the computational cost required. Note that the computation of the *Statistical Distance Image* has a considerable computational cost. Thus, discarding the outer elements in the patient together with the application of a threshold to discard soft tissues decreases significantly the number of voxels to be processed. Therefore, the computational time to implement the segmentation is considerably reduced.

A convex relaxation technique is applied using the Histogram Distance Image as input. The convex relaxation technique employed is the fast continuous max-flow implementation by Yuan et al., (2010) using the previously computed SDI image as cost term in the energy function.

Comparison with an state-of-the-art algorithm (DRLSE implementation) (Li et al., 2010) and the thresholding technique, which is the preferred and fastest technique in most of the tools used in the clinical practice, show that the algorithm proposed clearly outperform both techniques in terms of accuracy in the delimitation results.

In future implementations, comparisons with other techniques will be carried out. Note that the performance results provided by the DRLSE implementation were low and maybe other techniques could be more suitable in the segmentation of bone structures.

Besides, in future works, the two-label algorithm described will be modified in order to identify a high number of labels thus allowing the identification of other kind of structures.

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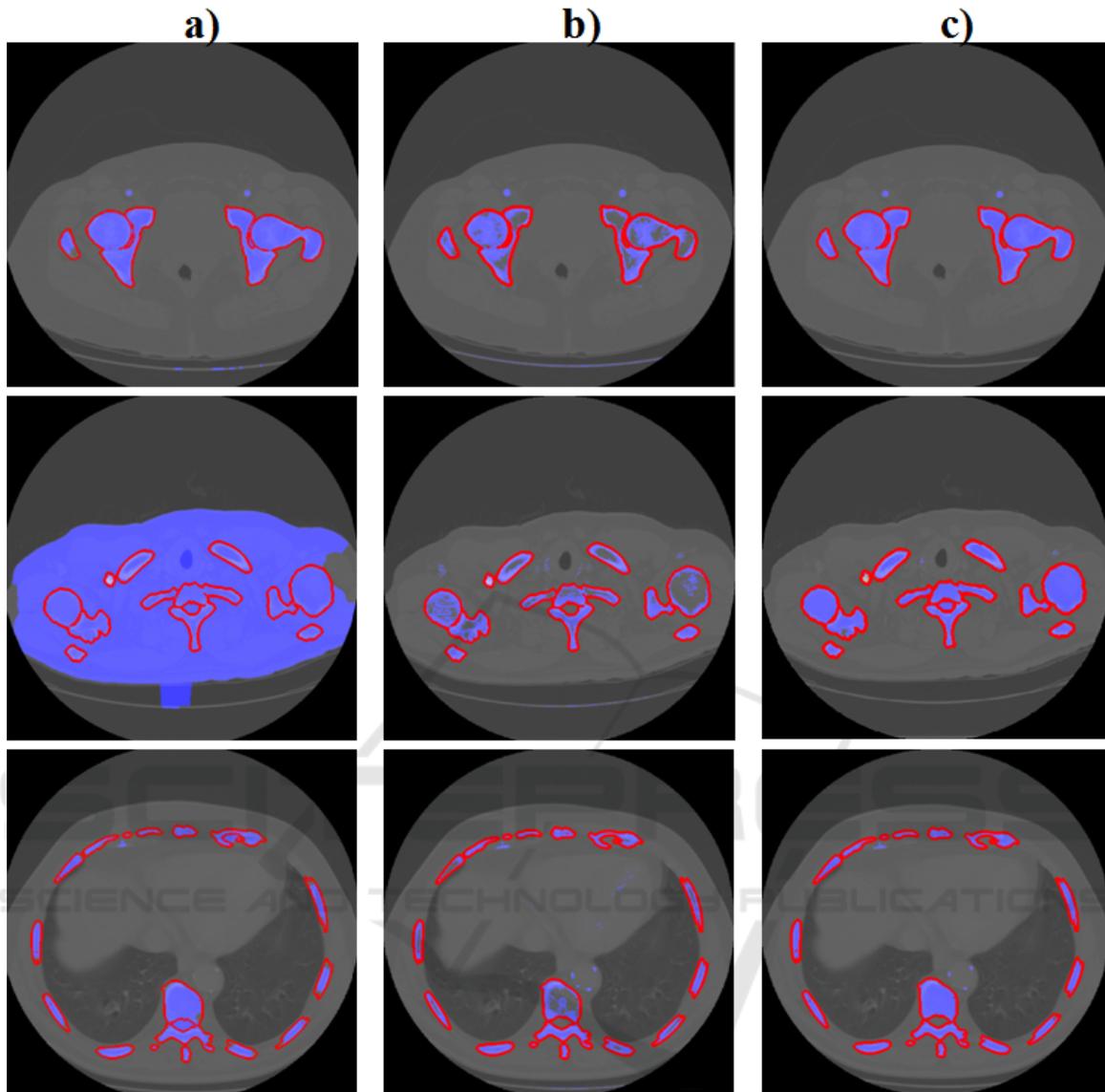


Figure 5: First Column (a) shows the results (blue regions) provided by the DRLSE algorithm. Central column (b) shows the results (blue regions) provided by the thresholding implementation. Right column shows the results provided by the algorithm described (blue regions). The groundtruth segmentations are contoured in red.

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