A Method of Rapid Quantification of Patient-Specific Organ Dose for CT Using Coupled Deep Multi-Organ Segmentation Algorithms and GPU-accelerated Monte Carlo Dose Computing Code

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ABSTRACT

**Purpose:** Information about patient-specific organ doses from CT scans can open the door for many new applications such as customized scan planning and person-specific risk assessment leading to the ultimate goal of achieving low-dose and optimized CT imaging. One technical barrier has been the lack of computational tool for automatic multi-organ segmentation for CT images, followed by rapid organ dose calculations. – This paper describes a new method to apply deep-learning algorithms for automatic segmentation of radiosensitive organs from 3D tomographic CT images before computing organ doses using a GPU-based Monte Carlo code.

**Methods:** A deep convolutional neural network (CNN) for organ segmentation is trained to automatically delineate radiosensitive organs from CT. Dice Similarity Coefficient (DSC) is used to evaluate the segmentation performance of our network against the gold standard. With a GPU-based Monte Carlo dose engine (ARCHER) to derive CT dose of a phantom made from a subject’s CT scan, we are then able to compute the patient-specific CT dose for each of the segmented organs. The developed tool is validated by using Relative Dose Error (RDE) against the organ doses calculated by ARCHER with manual segmentation performed by radiologists. The dose computation results are also compared against organ doses from population-average phantoms to demonstrate the improvement achieved by using the developed tool. In this study, two datasets were used: The Lung CT Segmentation Challenge 2017 (LCTSC) dataset, which contains 60 thoracic CT scan patients each with 5 segmented organs, and the Pancreas-CT (PCT) dataset, which contains 43 abdominal CT scan patients each with 8 segmented organs. A five-fold cross-validation of the new method is performed on both datasets.

**Results:** For the 60 patients from LCTSC dataset, the median DSCs are 0.97 (right lung), 0.96 (left lung), 0.93 (heart), 0.88 (spinal cord) and 0.78 (esophagus). For the 43 patients from PCT dataset, the median DSCs are 0.96 (spleen), 0.96 (liver), 0.95 (left kidney), 0.89 (stomach), 0.87 (gall bladder), 0.79 (pancreas), 0.74 (esophagus), and 0.64 (duodenum). Comparing with the traditional organ dose evaluation method that based on population-average phantom, our proposed method achieved the smaller RDE range on all organs with -4.3%~1.5% vs -31.5%~33.9% (lung), -7.0%~2.3% vs -15.2%~125.1% (heart), -18.8%~40.2% vs -10.3%~124.1% (esophagus) in the LCTSC dataset and -5.6%~1.6% vs -20.3%~57.4% (spleen), -4.5%~4.6% vs -19.5%~61.0% (pancreas), -2.3%~4.4% vs -37.8%~75.8% (left kidney), -14.9%~5.4% vs -39.9%~14.6% (gall bladder), -0.9%~1.6% vs -30.1%~72.5% (liver), and -23.0%~11.1% vs -52.5%~1.3% (stomach) in the PCT dataset.

**Conclusion:** It is feasible to evaluate the multi-organ doses from CT scan by using GPU-based Monte Carlo dose engine and the patient-specific phantom with the automatically segmented organs from CNN, which achieves significant improvement compared with the traditional method based on population-average phantom.

**Keywords:** Convolutional neural network, multi-organ segmentation, Monte Carlo, CT organ dose
1. INTRODUCTION

In the United States, the number of diagnostic x-ray CT examinations had increased 20 folds between the 1980s and 2010s, owing to rapidly improving multi-detector CT (MDCT) technologies [1-3]. CT is replacing conventional radiography as the initial diagnostic exam in emergency rooms and CT scanners are also integrated with modalities in nuclear medicine (PET/CT) as well as in image-guided radiotherapy where a patient can receive multiple scans [4]. The American College of Radiology (ACR) urgently calls for more effective methods to evaluate and manage such imaging doses [1], citing that existing dose computational tools were insufficient for patient-specific dose quantification, scanner optimization, and protocol comparison.

Today, CT scanners are designed to supply only CTDI (Computed Tomography Dose Index) data that are not based on patient-specific anatomical and organ dose information [5]. However, for risk assessment and procedure/equipment comparison purposes, organ doses are often needed. Currently, the most widely used CT organ dose assessment methods rely on off-line software, such as VirtualDose [6], to report organ doses using pre-calculated data from population-averaged anatomical phantoms [7]. If organ volumes can be segmented from patient-specific CT images, then it is feasible to derive organ doses using a Monte Carlo code. In fact, GPU-based Monte Carlo dose computing codes, such as ARCHER, can achieve acceptable statistical uncertainty in a few seconds [8].

CT image segmentation for radiosensitive organs has been a challenging task. Manual organ segmentation of 3D CT images is labor-intensive and user-dependent, making the approach impractical for clinical applications. Automatic segmentation of organs is thus of great significance to solve the problem. Traditional methods for the segmentation of organs rely on low-level image features, which are often time-consuming and tedious. For example, thresholding, Hough transform and atlas-registration based methods [8] have been used for segmenting organs with different attributes, but those methods require strong prior knowledge about the anatomical structures and have relatively insufficient performance for the clinical trial. Recently, deep learning methods involving the so-called convolutional neural network (CNN) have made impressive progress in automatic organ segmentation [9-12]. The state-of-the-art models in organ segmentation are variants of encoder-decoder architecture such as Fully Convolutional Networks (FCN) [13] and U-Net [14]. However, these methods are usually trained for specific organs and cannot be easily extended to multi-organ segmentation needed for organ dose from CT. Recently, Trullo et al. [15] used a modified 2D FCN to segment four organs at risks from CT images and apply Conditional Random Fields (CRF) to further improve the segmentation performance. Gibson et al. [16] applied a 3D Dense V-Network to segment eight organs from CT images that are relevant for navigation in endoscopic pancreatic and biliary procedures. However, they did not perform organ dose calculation. To our knowledge, this paper is the first time a study coupling deep CNN for multi-organ segmentation and rapid organ dose Monte Carlo calculation for CT is reported.

The purpose of this paper [17] is to demonstrate the feasibility of a fast patient-specific CT organ dose assessment method that first performs segmentation of multiple organs from patient-specific CT scan using CNN algorithms, followed by GPU-accelerated Monte Carlo dose calculations using the ARCHER code. Fig. 1 illustrates the overall computational process of this method.
2. MATERIALS AND METHODS

2.A Organ segmentation

2.A.1 Datasets and image preprocessing

In this study, two datasets were used: (1) The Lung CT Segmentation Challenge 2017 (LCTSC) [18-20], which contains 60 thoracic CT scan patients with 5 segmented organs, including left lung, right lung, heart, spinal cord, and esophagus. (2) Pancreas-CT (PCT), which contains 43 abdominal CT scan patients with 8 segmented organs, including the spleen, left kidney, gallbladder, esophagus, liver, stomach, pancreas and duodenum [11, 16, 20, 21].

For each patient in the two datasets, the Hounsfield Unit (HU) values were processed using a minimum threshold of -200 and a maximum threshold of 300, before the data were normalized between 0 and 1. In order to pay more attention to the organs, we cropped the foreground as training data according to the body contour in the original CT images. Finally, to circumvent the computer memory limitation, data downsampling was performed using linear interpolation for CT images and using nearest interpolation for the labels. The image resolution in the LCTSC datasets was resampled to 2 mm x 2 mm x 2.5 mm. To further improve the segmentation performance of the esophagus and spinal cord, the volumes of these two organs were cropped separately for fine segmentation. The image resolution of these two organs was resampled to 1 mm x 1 mm x 2.5 mm. In the PCT dataset, the size of CT images was resampled to 144 x 144 x 144 pixels, which was found to generate better segmentation performance than the resolution of 1mm x 1mm x 2.5mm. The experiments in this dataset are as a supplementary proof to our proposed method in CT organ dose evaluation, the fine segmentation for small organs is omitted to simply the process of segmentation.

2.A.2 Network architecture

The proposed network in this study is based on the 3D U-Net [14]. As shown in Fig. 2, the network consists of an encoder and a decoder. The encoder extracts image features, while the decoder performs a voxel-level classification to achieve organ segmentation. The encoder contains 4 repeated residual blocks. Each block consists of 4 convolutional modules and each convolutional module is composed by a convolution layer with the kernel of 3x3x3, an instance normalization, and a leaky rectified linear unit. For each residual block, the stride of convolution layer in the convolutional modules is 1x1x1 except for the last convolutional module in which the stride is 2x2x2 to achieve the purpose of downsampling, and there is a spatial dropout layer between the early two convolutional modules to prevent the network from overfitting. The decoder contains 4 repeated segmentation
blocks. Each block consists of 2 convolutional modules and 1 deconvolutional module. Four dashed arrows in the figure indicate four skipping connections that copy and reuse early feature-maps as the input to later layers having the same feature-map size by a concatenation operation to preserve high-resolution features. In the final 3 segmentation blocks, a 1×1×1 convolution layer is used to map the feature tensor to the probability tensor with the channels of the desired number of classes, n, before all results are merged by the upsampling operation to enhance the precision of segmentation results. Finally, a SoftMax activation is used to output a probability of each class for every voxel [22].

2.A.3 Training

The network architecture and training strategies are the same for both datasets, but the network is trained separately. For the LCTSC dataset, the 60 patients are divided into 5 groups with 12 patients per group. For the PCT dataset, the 43 patients are divided into 5 groups with 8 or 9 patients per group. Then the 5-fold cross-validation is performed.

At the training stage, we first randomly extract the patches from the resampled CT images for data to achieve diversity and to prevent overfitting. The size of patch is 96x96x96 in the LCTSC and 128x128x128 in the PCT. As noted earlier, the size of patch is 32x32x32 for the fine segmentation of the esophagus and spinal cord in LCTSC. Then, the network is trained by the patch and its corresponding label. The loss function is a weighted dice similarity coefficient defined as:

\[
\text{Loss} = -\frac{1}{N \times K} \sum_{i=1}^{N} \sum_{k=1}^{K} \frac{2 \times \sum_{v=1}^{V} (p_{i,k,v} \cdot y_{i,k,v}) + \epsilon}{\sum_{v=1}^{V} p_{i,k,v} + \sum_{v=1}^{V} y_{i,k,v} + \epsilon},
\]

where \(p_{i,k,v}\) is the predicted probability of the voxel \(v\) of the sample \(i\) belonging to the class \(k\), \(y_{i,k,v}\) is the ground truth label (0 or 1), \(N\) is the number of samples, \(K\) is the number of classes, \(V\) is the number of voxels in one sample, and \(\epsilon\) is a smooth factor (set to be 1 in this study). The initial learning rate is 0.0005, and the Adam algorithm [23] is used to update the parameters of the network. The validation loss was calculated for every epoch, and the learning rate is halved.
when the validation loss no longer decreases after 30 consecutive epochs. The training process is terminated when the validation loss no longer decreases after 50 consecutive epochs.

2.A.4 Testing

In the testing stage, we first extract the patches from each CT images with a moving window with size of 96x96x96 in the LCTSC and 128x128x128 in the PCT. The stride is 24 in the LCTSC and 16 in the PCT. In other words, we extract multiple patches from one patient and feed them into the network. The output of the network is a probability tensor for each patch. Then we merge all the probability tensors from the same patient with a mean operator in the overlapping area to obtain the final probability tensor. Next, the class of each voxel is determined by the largest probability, which is the preliminary organs segmentation results and the value of each voxel is the class number. Last, using the nearest neighbor interpolation, we resample the preliminary segmentation results to the size of original CT images to obtain the final organs segmentation results. It is worth noting that, for the fine segmentation of esophagus and spinal cord in the LCTSC, we first crop their own volume according to the multi-organ segmentation results, and then the volume is resampled to 1mm x 1mm x 2.5mm. Next, similar to the previous multi-organ segmentation, we extract the patches of 32x32x32 with a moving stride being 8x8x8 and separately feed them into their own networks. Finally, the fine segmentation of the esophagus and spinal cord were filled into the initial multi-organ segmentation results.

All experiments were performed on a Linux operation system. Keras was used to design and train our neural network, the backend is TensorFlow [24]. The hardware includes (1) GPU: Nvidia GeForce Titan X Graphics Card with 12GB memories, and (2) CPU: Intel Xeon Processor X5650 with 16GB memories.

2.B Organ dose calculations

A GPU-accelerated MC code, ARCHER, previously developed by us was used to calculate the organ dose in the radiotherapy [25]. Designed to work with both Nvidia and AMD GPU hardware devices, ARCHER is an accurate and fast MC simulation tool that, for this study, simulates the transport of low-energy (1~140keV) photons in heterogeneous media where photoelectric effect, Compton scattering, and Rayleigh scattering can take place. A series of CT scan protocols are predefined, including a combination of scan mode (helical or axial), beam collimation (5, 10, or 20 mm) and kVp (80, 100, 120 or 140). Fig. 3 illustrates one of the simulation cases involving a patient in a helical CT scan.

![FIG. 3. Illustration of a patient in a helical CT scan for the purposes of dose simulations.](image)
This study uses a model representing a GE Lightspeed Pro 16 multi-detector CT that has been validated in our previous studies [26, 27]. The simulated scanning protocol includes 120 kVp, 20 mm beam collimation, axial body scan at a constant 100 mAs. CT scanner’s continuous rotational motion is simulated using the step-and-shoot pattern, with each rotation approximated by 16 discrete positions [26]. Using patient-specific CT images that have been segmented for organs of interest, ARCHER to calculate the average absorbed dose for each organ.

To show the potential clinical impact of the new method, patient-specific organ dose results are compared against organ doses derived from the method used at Massachusetts General Hospital using the VirtualDose software that is based on population-average phantoms. Fig. 4 shows the population-average phantoms in the VirtualDose software, RPI-Adult Male and RPI-Adult Female phantoms, having 73 kg and 63 kg in weight, respectively [28].

**FIG. 4.** The population-averaged RPI-Adult Male (left) phantom and RPI-Adult Female (right) phantom in VirtualDose are used for organ dose comparison in this study to show the clinical impact of the new method [23]

2.C Segmentation and organ dose evaluation criteria

The Dice Similarity Coefficient (DSC) used to evaluate the performance of organ segmentation [29] is defined as:

\[ DSC = 2 \times \frac{A \cap B}{A + B} \]

where \( A \) is the area of manual segmented organ and \( B \) is the area of the predicted segmented organ by the network. The DSC ranges from 0 to 1 with the latter indicating a perfect performance.

The Relative Dose Error (RDE) used to evaluate the accuracy of dose calculation for each organ is defined as:

\[ RDE = \frac{D - D_r}{D_r} \times 100\% \]

where \( D_r \) is the reference organ dose calculated by ARCHER using patient-specific phantom and manually segmented organ which is regarded as the criterion. \( D \) is the organ dose calculated by ARCHER using patient-specific phantom and the organ segmented from the network (i.e., our method) or the organ dose using the population-average phantom.

3. Results

3.A Organs segmentation

The performance of our network in organ segmentation is evaluated in terms of the DSC. As shown in Fig. 5, the segmentation results of all organs are summarized in these two box plots. For 60 patients from LCTSC, we achieved the median DSCs of 0.97 (right lung), 0.96 (left lung), 0.93 (heart), 0.88 (spinal cord), and 0.78 (esophagus) as can be seen in Fig. 5 (a). For 43 patients from PCT, we achieved the median DSCs of 0.96 (spleen), 0.96 (liver), 0.95 (left
kidney), 0.89 (stomach), 0.87 (gall bladder), 0.79 (pancreas), 0.74 (esophagus), and 0.64 (duodenum) as can be seen in Fig. 5 (b). In both Fig. 6 (a) and (b), we show a segmentation example from LCTSC and PCT, respectively. The segmentation results of manual delineation and our network for the organs are visualized in axial, sagittal, coronal, and 3D views.

**FIG. 5.** Evaluation of organ segmentation performance in terms of DSC. (a) Comparison with 60 patients from the LCTSC database. (b) Comparison with 43 patients from PCT database.

**FIG. 6.** Visual comparison of organ segmentation between manual methods from LCTSC or PCT database (showed in the upper row in each panel) and our automatic method (showed in the upper row in each panel), in terms of axial, sagittal, coronal, and 3D views (from left to right). (a) LCTSC database showing left lung (yellow), right lung (cyan), heart (blue), spinal cord (green), and esophagus (red). (b) PCT database showing spleen (green), pancreas (navy), left kidney
(yellow), gallbladder (blue), esophagus (red), liver (bisque), stomach (magenta), and duodenum (purple).

We further compared our automatic segmentation performance with the other methods using 12 test patients provided by the LCTSC. Table 1 lists the organs segmentation performances of the seven methods in the contest as well as the interrater variability (denoting the segmentation performance for three raters on three training cases for these organs) [19] together with these results from our method. Comparing with the seven methods in the contest, our method has achieved the better segmentation performance than all other methods for the heart and esophagus. For other organs, the segmentation performance is comparable with the best results by other methods. Furthermore, our method contained the same level of interrater variability in the segmentation of all organs except for esophagus. These results suggest that our automatic organ segmentation method is accurate and acceptable for the purposes of organ dose calculations for CT.

**TABLE 1.** Comparison of our automatic segmentation performance using 12 test patients from LCTSC database against results of seven methods in the contest database and the interrater variability [19]. The results are expressed in terms of mean ± standard deviation for the DSC.

| Methods | Left lung | Right lung | Heart  | Esophagus | Spinal cord |
|---------|-----------|------------|--------|-----------|-------------|
| Interrater variability | 0.96±0.02 | 0.96±0.02 | 0.93±0.02 | 0.82±0.04 | 0.86±0.04 |
| Method 1 | 0.97±0.02 | 0.97±0.02 | 0.93±0.02 | 0.72±0.10 | 0.88±0.04 |
| Method 2 | 0.98±0.01 | 0.97±0.02 | 0.92±0.02 | 0.64±0.20 | 0.89±0.04 |
| Method 3 | 0.98±0.02 | 0.97±0.02 | 0.91±0.02 | 0.71±0.12 | 0.87±0.11 |
| Method 4 | 0.97±0.01 | 0.97±0.02 | 0.90±0.03 | 0.64±0.11 | 0.88±0.05 |
| Method 5 | 0.96±0.03 | 0.95±0.05 | 0.92±0.02 | 0.61±0.11 | 0.85±0.04 |
| Method 6 | 0.96±0.01 | 0.96±0.02 | 0.90±0.02 | 0.58±0.11 | 0.87±0.02 |
| Method 7 | 0.95±0.03 | 0.96±0.02 | 0.85±0.04 | 0.55±0.20 | 0.83±0.08 |
| Our method | 0.96±0.01 | 0.96±0.02 | 0.93±0.02 | 0.75±0.10 | 0.88±0.04 |

3.B Organ dose calculations

The accuracy of organ dose calculations is evaluated in terms of RDE. In the dataset from LCTSC, we calculated the organs doses of 60 patients in total, including lung, heart, and esophagus. The left lung and right lung are regarded as one organ, and the RDE of the spinal cord was not shown because it is not segmented in the population-average phantom. In the dataset from PCT, we calculated the organs doses of 43 patients in total, including the spleen, left kidney, gallbladder, liver, stomach, and pancreas. The duodenum is not segmented in the population-average phantom, and the esophagus in the specific patient is just a part of the real esophagus due to abdominal CT scanning, so the RDEs of duodenum and esophagus were not shown. Comparing with the phantom-based method, our proposed method achieved the smaller RDE range on all organs with -4.3%~1.5% vs -31.5%~33.9% (lung), -7.0%~2.3% vs -15.2%~125.1% (heart), -18.8%~40.2% vs -10.3%~124.1% (esophagus), -5.6%~1.6% vs -20.3%~57.4% (spleen), -4.5%~4.6% vs -19.5%~61.0% (pancreas), -2.3%~4.4% vs -37.8%~75.8% (left kidney), -14.9%~5.4% vs -39.9%~14.6% (gallbladder), -0.9%~1.6% vs -30.1%~72.5% (liver), and -23.0%~11.1% vs -52.5%~1.3% (stomach), which means that our proposed method had a great improvement in the organs dose evaluation of CT scan. As shown in Fig. 7 (a) and (b), we showed the box plot of RDEs for each organ in these two datasets, respectively. The reference organ dose is
calculated on the specific patient using manual segmentation. The label “proposed method” represents the RDE between organ dose from automatic segmentation and reference organ dose, the label named “phantom-based method” represents the RDE between organ dose from the population-average phantom and reference organ dose.

**FIG. 7.** The box plot of Relative Dose Error (RDE) of organs for (a) the 60 patients from LCTSC and (b) the 43 patients from PCT. The reference organ doses are calculated on the specific patient using manual segmentation. The label named “proposed method” represents the RDE between organ doses from automatic segmentation and reference organ doses, the label named “phantom-based method” represents the RDE between organ doses from the population-average phantom and reference organ doses.

The time of organ dose calculation includes two parts. One is the time of automatic organ segmentation by CNN, which is about 5 seconds for each patient. The other is the time of dose calculation by ARCHER, which is about 10 minutes for each patient. At present, we rebuild the patient-specific phantom with the same resolution with CT images to calculate the dose distribution maps by ARCHER using just one GPU. In fact, it is not necessary to use such high resolution. In the next study, we can use lower resolution in the condition of ensuring acceptable accuracy, which will save time significantly. At the same time, we can also use more GPU. Therefore, it is very hopeful to further reduce the time of organ dose calculation.

4. DISCUSSION

In this study, we designed a 3D convolutional neural network to segmented the thoracic and abdominal organs in the two CT datasets, respectively. Especially, we had a fine segmentation for esophagus and spinal cord in the dataset from LCTSC, and the median DCS is from 0.75 to 0.78 for esophagus and from 0.84 to 0.88 for spinal cord, which showed that it is a good method to further improve the segmentation performance for small organs by performing fine segmentation based on initial coarse segmentation. In the duodenum, the segmentation performance of our network was relatively poor, the reason may be that the organ and its surrounding tissues have similar pixel value in CT image, which makes the network hardly recognize the real boundary, and it is possible to improve its segmentation performances if the network is able to use prior knowledge like radiologists. Even though, the results have shown that our network is advanced and effective enough in the multi-organ segmentation task. Note that the purpose of this study is not the organs segmentation, so we did not compare our network with other organs segmentation methods in detail.

In a CT scan, the height, weight, and anatomy of a patient can influence the dose of the organs. There is no doubt that it will introduce some errors using the population-average phantom replacing the specific patient for organ dose calculation. In this study, we proposed a patient-specific CT organ dose assessment method combining the organ automatic segmentation technique by CNN and GPU-accelerated Monte Carlo dose calculations technique. The results
suggested our proposed method is feasible and effective, and it is a great improvement in the accuracy of organ dose calculation comparing with the traditional method based on the population-average phantom. The limitation of this study is that the data we used is from open source dataset online, where the number of segmented organs is not enough. Next, we will further apply the proposed method to clinical data with enough segmented organs.

5. CONCLUSION

In this study, we first achieved the automatic organs segmentation in the two CT datasets using a convolutional neural network model. Then the organs doses were calculated by ARCHER using the patient-specific phantom and the segmented organs from the network. The RDEs of our proposed method are very low in all organs. Comparing with the traditional method based on the population-average phantom, our proposed method has a great improvement. It means that our method is feasible and efficient for the multi-organ doses calculation in the CT scan.

CONFLICT OF INTEREST DISCLOSURE

X.G. Xu is co-founder of Virtual Phantoms, Inc (Albany, New York) that commercializes software technologies—VirtualDose for medical dose reporting and ARCHER for real-time Monte Carlo dose engine through STTR grants from NIH/NIBIB (R42EB010404 and R42EB019265-01A1).

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