

# Real-time Voxel-Wise Patient-specific Monte Carlo dose reconstruction in whole-body CT images using Deep Neural Networks



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## INTRODUCTION

Computed Tomography (CT) has an undeniably important role in medical imaging as a tool for diagnosing and following a wide range of pathologies. On the other hand, CT, as a high-dose imaging modality, is responsible for a considerable part of the population's medical radiation per capita[1]. There are multiple quantities in a range of accuracy and availability for reporting the radiation dose in CT and comparing its radiation risk with other modalities. Computed tomography dose index (CTDI), the most available metric, has nothing to do with radiation risk. Monte Carlo (MC) patient-specific radiation dose calculation is considered the gold standard for organ dose evaluation in CT. However, The expensive computational burden has limited its application in routine clinical practice. The GPU-accelerated platforms made MC closer to real-time dose calculations and less time-consuming[2]. Deep learning has proved to outperform available methods in various tasks, including dosimetry [3, 4], image segmentation, and protocol optimization[5] in medical imaging. The aim of this study was to develop a deep learning method to generate a real-time dose map associated with CT examination in a much shorter time and with comparable accuracy to MC as a step toward dose optimization in total body CT (TBCT) imaging.

## METHODS

A total of 48 (25 male and 23 female) TBCT images were included. CT images were converted to a density map with a 5 mm resolution. Essential components are incorporated into the MC simulations, including the source model, and protocol-related parameters were directly adopted from our previous work[6]. All acquisitions were in 120 kVp and 2mm slice thickness. The output of MC simulation, which was a dose map per single mAs, was (DP) used to construct a voxel dose map by the implementation of X-Ray tube current. The DP maps and their corresponding CT image were normalized, cropped to 94×144×208 and fed into the neural network (Figure 1).

A 3D deep residual neural network was trained to generate a dose map per mA from CT images using the niftynet platform. Data were randomly split into training & validation (38 cases) and external test sets (10 cases). The network output, deep DP map, was used to generate voxel dose maps by implementing the corrections mentioned earlier. Two Deep and ground truth voxel dose maps were compared by calculating quantitative parameters of structural similarity index (SSIM), percent relative error (RE), percent relative absolute error (RAE), and gamma pass rate[7]. Multiple organs of the liver, cardiac, pancreas, Bones, kidneys, spleen, bladder, and lungs were segmented on the images, and the dose differences between the organ segments calculated on the deep and ground truth dose maps were calculated.

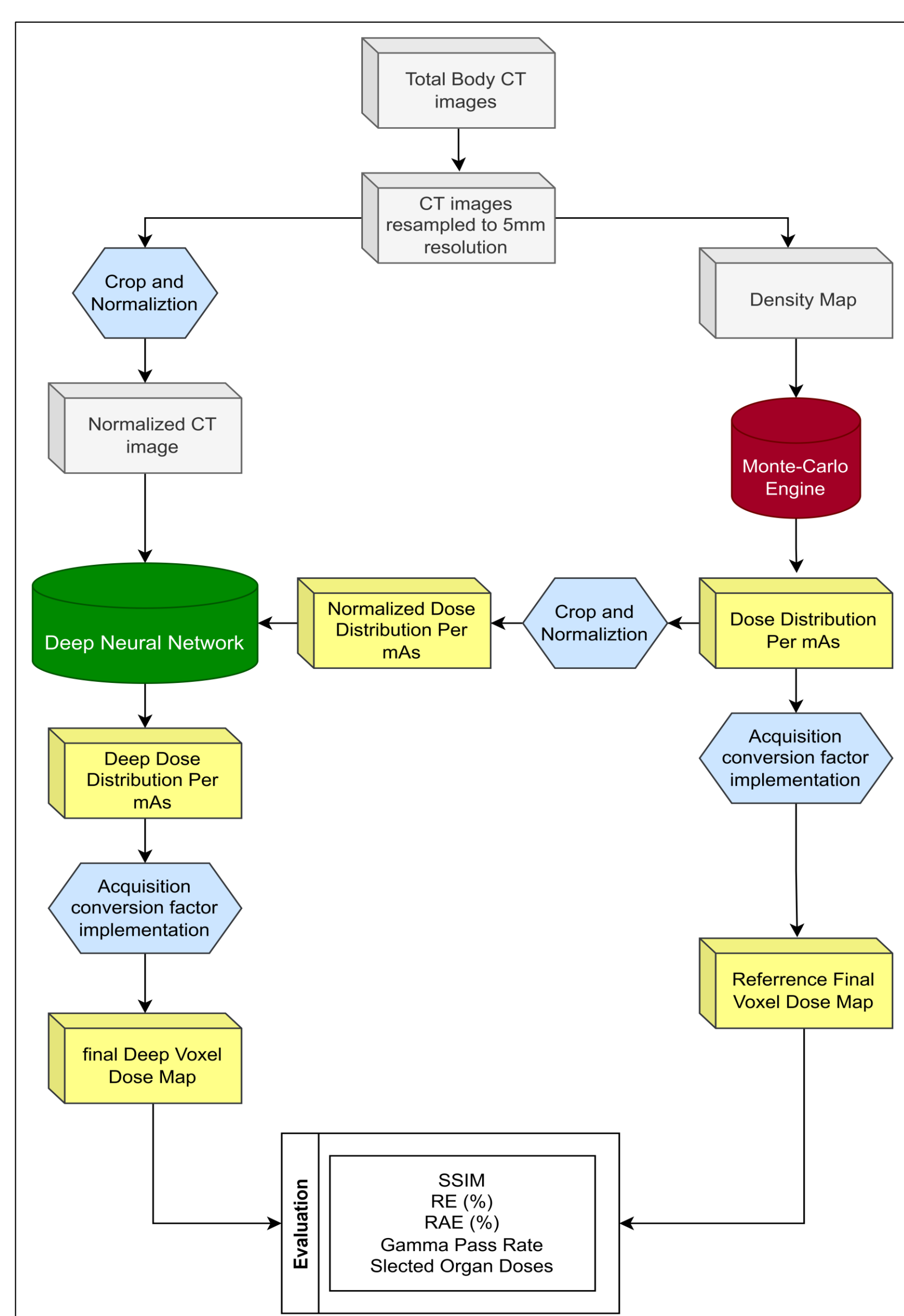


Fig 1. Flowchart of steps followed in this study protocol.

## RESULTS

The average patient weight, age, and height were  $73.5 \pm 16$  (Kg),  $58.4 \pm 18.1$  (years), and  $168 \pm 12$  (cm), respectively. The average and standard deviation of SSIM, RE, RAE, and gamma pass rate were  $0.96 \pm 0.01$ ,  $3.43 \pm 3.29$ ,  $5.17 \pm 2.73$ , and  $91.4 \pm 3.4$ , respectively. Figure 2 shows the box plot of the organ dose differences for selected organs, the most significant error was for the lung, while the lowest was for bladder segmentation. The average absolute error in organs was 6.8%. Figure 3 shows an example of a coronal slice from the deep dose map compared with the ground truth. As visible in figure 3, the most significant difference is in regions with a high gradient of density, such as bone/soft tissue or lung/silver interfaces.

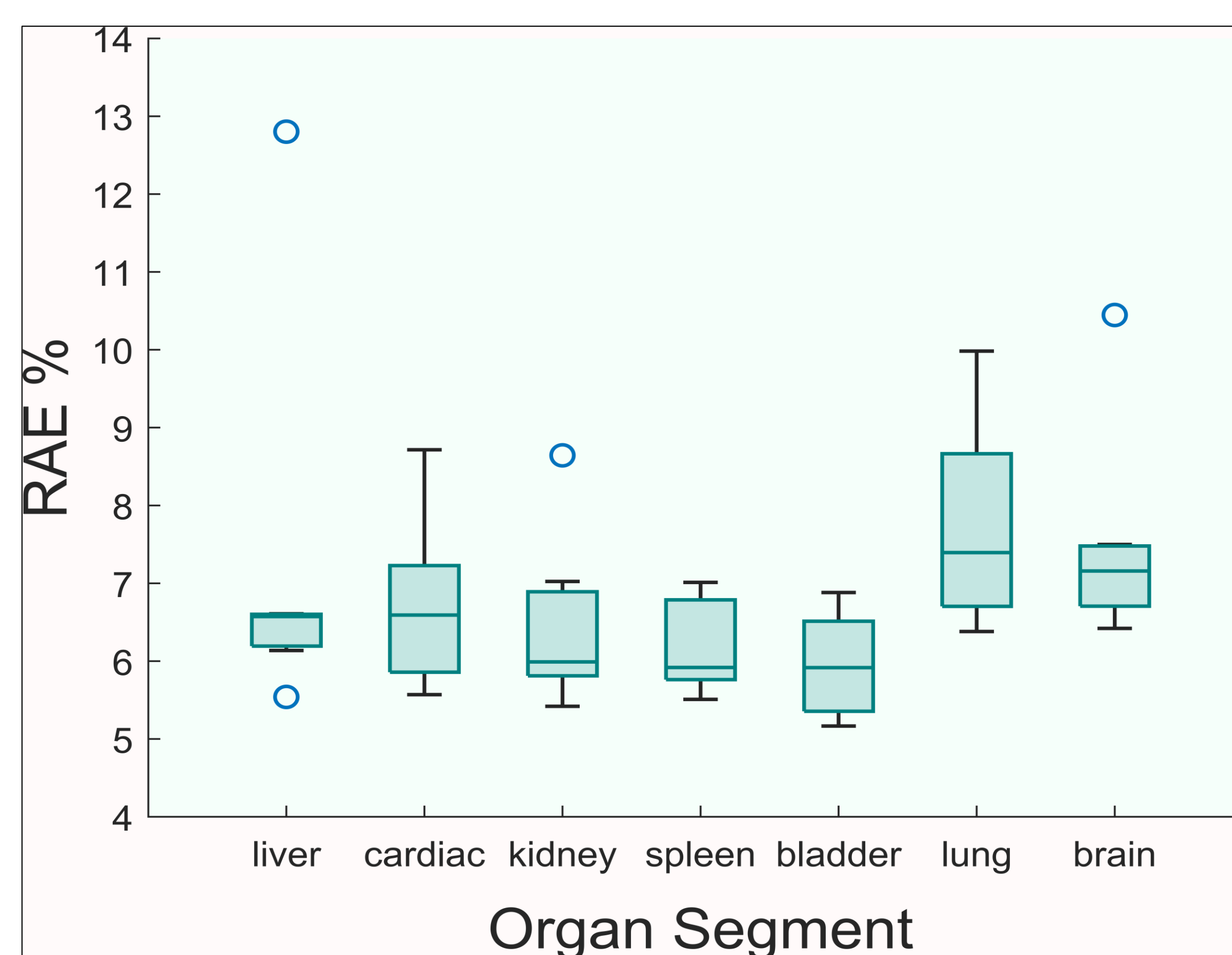


Fig 2. Boxplots of percent relative absolute error in organ doses calculated on deep dose maps.

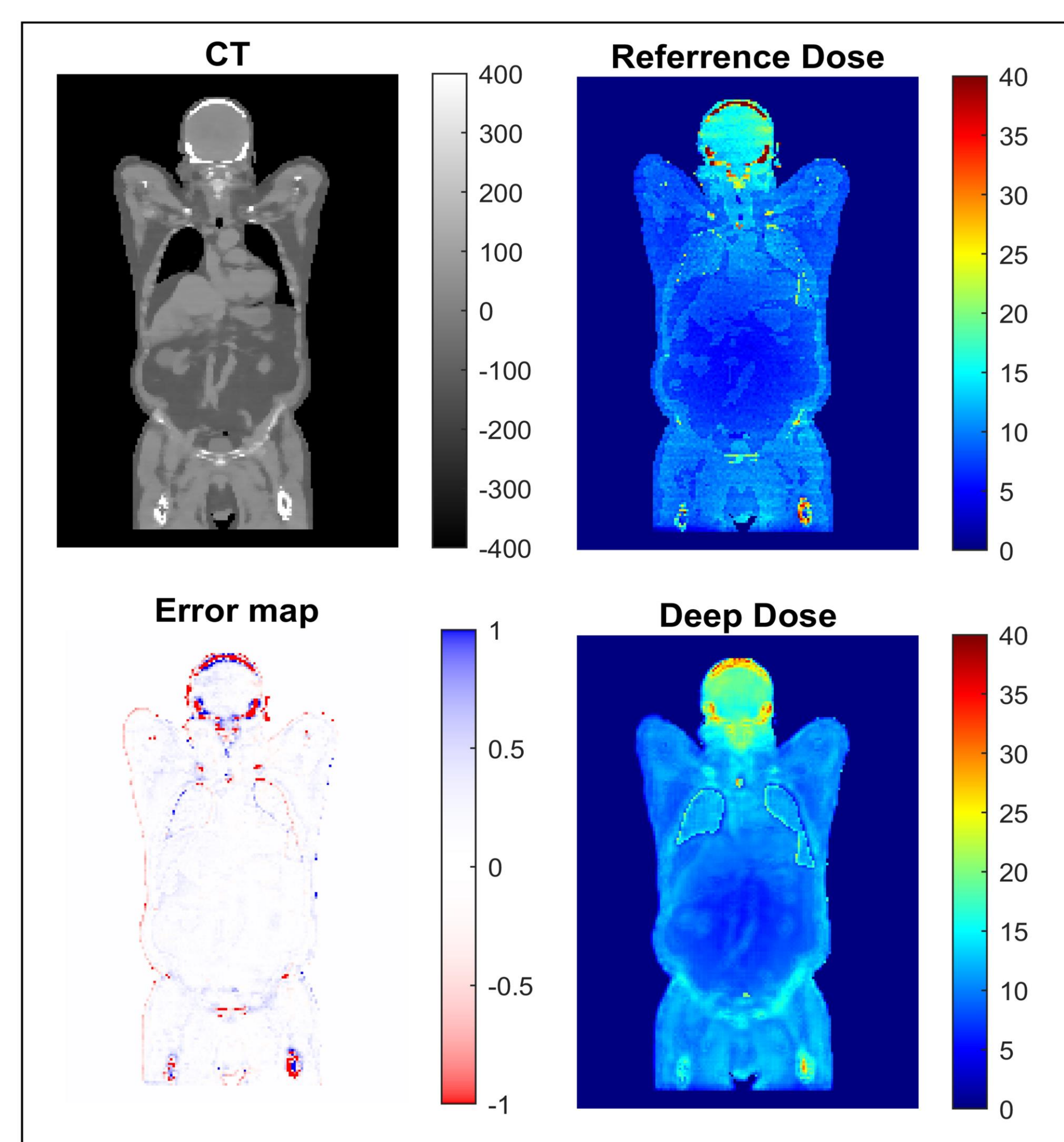


Fig 3. An example of a coronal slice from the CT image (top left, HU), the ground truth MC dose map (top right, mGy), the deep predicted dose map (bottom right, mGy), and the error map (bottom left, mGy). The color bar is shown for all images.

## CONCLUSION

This study proposed a DL-based method to directly generate the radiation dose distribution associated with total body CT examinations. We evaluated our proposed method by comparing the dose maps at voxel and organ dose levels and achieved excellent accuracy in organ doses, overall errors, and gamma pass rate. The performance of our method is much better than pre-tabulated software[8] and comparable with the recently published paper by Maier et al. [4]. It should be mentioned that compared to their method, our model uses only CT images as input. The whole process of pre-processing, deep network inference, and post-processing can be done in less than a few seconds. Besides, there is no need for programming skills as it is necessary for MC calculations. These mentioned features make this method feasible and practical to measure accurate doses in clinical practice. The main limitation of this study was using a single scanner; further evaluation is needed to check the generalizability.