Deep learning-based Dosimetry in Radionuclide Therapy: Is It Worth the Effort?


Abstract—We propose a novel unified framework to perform whole-body voxel-level dosimetry taking into account patient-specific tissue heterogeneity and activity distribution using Monte Carlo (MC) simulations and deep learning algorithms. We extended the core idea of the voxel-scale MIRD dosimetry formalism previously validated for positron emitters used in diagnostic imaging (\(^{18}\)F) to radionuclides with complex decay schemes used in therapy (\(^{177}\)Lu). In this context, we trained a model to predict the deposited energy distribution obtained from MC simulations (specific S-values), while two-paired input channels consist of density map and dose distribution kernel in soft-tissue (single S-value) are fed into the network. Transfer learning was applied using our previous \(^{18}\)F model fine-tuned on \(^{177}\)Lu dataset. Accordingly, whole-body dose maps were constructed through convolving specific S-values into time-integrated activity distribution obtained from SPECT images. The Deep Neural Network (DNN) predicted dose map was compared with the reference (Monte Carlo-based) and two MIRD-based methods, including single-voxel S-value (SSV) and multiple voxel S-value (MSV) approaches. The results demonstrated that DNN, MSV and SSV show a comparable performance against the MC approach in soft tissue. However, in small size heterogeneous boundaries (lumbar region), DNN outperformed other approaches achieving lower bias (4%) compared to MSV (26%) and SSV (30%) tech.

Index Terms—Internal dosimetry, deep learning, radionuclide therapy, Monte Carlo.

I. INTRODUCTION

Direct Monte Carlo (MC) calculations is deemed the gold standard technique for reliable dosimetry estimation in clinical and research settings [1]. Though MC simulation addresses the simplifications of other internal dosimetry calculation techniques, e.g. MIRD formalism, including single-voxel S-value (SSV) and multiple voxel S-value (MSV) approaches, it is prohibitive for daily clinical usage owing to its heavy computational burden [2, 3]. Deep learning algorithms have been recently employed in radiation dosimetry [4]. Lee et al. [5] used a U-Net deep neural architecture for internal dosimetry. Gotz et al. [6] set out a pipeline to reconstruct voxel-wise dose distribution for \(^{177}\)Lu-PSMA radiotherapy.

In the current study, we extended our previous deep learning-guided dosimetry model for diagnostic positron emitters (\(^{18}\)F) to therapeutic agents (\(^{177}\)Lu-Dotatate) suitable for neuroendocrine tumor (NET) patients. A detailed description of the proposed methodology was previously reported in [7].

II. MATERIAL AND METHODS

A. Data preparation

The dosimetry framework consists of the following steps:

1. Post-injection quantitative SPECT image acquisition,
2. Serial SPECT/CT image registration,
3. Volume-of-interest (VOI) segmentation,
4. Tim-activity curve generation,
5. Voxel-level dosimetry (MC, DNN, MSV, SSV).

A set of hybrid SPECT/CT images of NET patients was acquired to prescribe multiphase \(^{177}\)Lu-Dotatate radionuclide therapy. Two to three different time point post-injection images were available for each patient. SPECT images at different time points were registered by means of non-rigid transformations based on normalized correlation cost function. Kidneys, liver, spleen (contoured on CT images) and tumors (contoured on SPECT images) were segmented for calculation of VOI-effective half-lives (\(T_{1/2}\)). Time-activity curves were created based as described in [8]. Integrated time activity distribution was fed into different voxel-dosimetry methods to construct patient-specific 3D dose maps.

B. Network training

Our previously trained model on 12,000 \(^{18}\)F kernels was transferred for tuning with a total of 1300 density kernels randomly sampled from 24 CT images to provide \(^{177}\)Lu-specific S-values from MC simulations. The kernel size was about 31 cm\(^2\) with a resolution of 4.8 mm. The dose maps generated by J. M. Beauregard is with Cancer Research Centre and Department of Radiology and Nuclear Medicine, Université Laval, Quebec City, Quebec, Canada. H. Zaidi is also with Geneva University Neurocenter, Geneva University, CH-1205 Geneva, Switzerland; Department of Nuclear Medicine and Molecular Imaging, University of Groningen; University Medical Center Groningen, 9700 RB Groningen, Netherlands; and Department of Nuclear Medicine, University of Southern Denmark, DK-500, Odense, Denmark (e-mail: habib.zaidi@hcu.ge.ch).

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DNN, MSV, SSV were evaluated quantitatively using metrics, including the Normalized Root Mean Square Error (NRMSE), Normalized Absolute Error (NMAE) and dose-volume-histograms (DVHs) with those corresponding to the ground truth (MC).

III. RESULTS

The calculated NRMSE and NMAE between predicted kernels against MC kernels were about 5.1±0.2% and 1.7±0.07%, respectively (Fig. 1). The joint histogram analysis between DNN and MC-based dose kernels demonstrated a strong agreement ($R^2 = 0.98$). Fig 2. compares the bias map in lesions and OARs of a patient along with line profile crossing the calcified liver and lumbar regions. The absorbed dose to the

![Dose difference plot](image)

Fig. 1. NMAE (%) and NRMSE (%) (left) obtained within dose kernels when using DNN against MC-based approaches. Joint histogram analysis displaying the correlation between predicted dose kernel against corresponding MC-based counterparts.

![Bias map and line profile](image)

Fig. 2. Case study of a NET patient prescribed with 10 GBq 177-Lu-Dotatate.

CT and MC-based dose map (top), bias map between DNN, MSV and SSV with respect to MC dose map in units of Gy (middle) along with line profile crossing a calcified region and lumbar vertebrae. DVH plot obtained from MC simulation for tumor and OARs.

![Absorbed dose plot](image)

Fig. 3. Absorbed doses in tumors and OARs from a single-round of $^{177}$Lu-Dotatate injection.

The qualitative and quantitative assessment proved that DNN, MSV and SSV show a consistent agreement against MC in soft-tissue ROIs (maximum SSV error ~2%). However, in heterogeneous boundaries and small size inhomogeneities such as lung-liver interface and bone metastases, DNN addresses successfully the simplifications of MSV and SSV approaches.

IV. DISCUSSION

The calculated NRMSE and NMAE between predicted kernels against MC kernels were about 5.1±0.2% and 1.7±0.07%, respectively (Fig. 1). The joint histogram analysis between DNN and MC-based dose kernels demonstrated a strong agreement ($R^2 = 0.98$). Fig 2. compares the bias map in lesions and OARs of a patient along with line profile crossing the calcified liver and lumbar regions. The absorbed dose to the tumor and OARs obtained from MC simulations for three patients are presented in Fig 3. Mean absorbed dose difference between DNN, MSV and SSV against MC ground truth were calculated up to 0.7%, 1.3% and 2.7%, respectively.

V. CONCLUSION

We proposed a unified methodology for patient-specific dosimetry-guided radionuclide therapy planning using deep learning algorithms. It was observed that MC-based dosimetry calculation is a must for radiopharmaceuticals with complex decay schemes including a large fraction of gamma decay, that has a significant impact on cross-fire dose from hot regions within the patient.

REFERENCES