

Toward a generic approach for dose distribution recovery by using Deep Learning and GPU-based Geant4 simulations

A. Touil¹, H-P. Dang¹, D. Benoit¹,
D. Visvikis¹, J. Bert¹

¹Laboratory of Medical Information Processing (LaTIM), INSERM-UMR 1101, Brest, (France).

Background: Monte Carlo Simulations (MCS) play a key role in medical image applications, especially in the field of radiotherapy and dosimetry distributions. The main drawback of MCS is the need for a long computational time to obtain a result with a sufficient statistic. Recently, many Deep Learning (DL) systems have shown a significant progress to improve MC simulation speeds and qualities. For example, several DL-based approaches have been proposed to improve the statistical quality of MCS starting from the low sampling dose distributions [1, 2]. Despite their effectiveness, their performance is highly dependent on the setup of the MC simulation. Indeed, they are learned from maps of dose data sets generated from the same configuration (source energy characteristics, anatomical region, etc).

Materials and Methods: The main goal of this work is to propose a generic method which is able to generate dose maps with higher statistical quality from lower one, independently of their types and configurations. The used network architecture is based on the U-Net [3] structure that have seen significant efficiency in the medical imaging field over the last years [4]. Here, our preliminary work consists in considering both the patient's anatomy (CT) and the low sampling dose map as input data for the network. We start our work by building two training datasets to be used for the learning stage. They are generated from a publicly available dataset of 82 CT scans [5]. A voxelized phantom and a photon cone-beam source are placed behind the patient. To perform different MC simulation setups, randomly sampled energy, beam aperture, beam position and viewing angle values were used. The beam aperture and the viewing angle sampled values, for the two generated datasets, were uniformly distributed over the interval of [0.5, 4.99] and [-180, +180] degrees, respectively. However, the energy sampled values were uniformly distributed over the interval [50, 999] keV, which leads to medical and also therapy applications, for the first dataset (called *Dataset1*) and [50, 150] keV for the second dataset (called *Dataset2*). Each of the above-mentioned setup simulations was performed twice, on the same CT, with two different levels of statistical precision: one with 5×10^5 photons (low sampling) and one with 5×10^8 (high sampling). The Open-Source GPU-based Geant4 MC platform

GGEMS [6] were used to perform the different simulations. The GPU card used for the MC simulations was a NVIDIA GTX3090. A total of 10000 and 1534 pairs of 2D image samples were generated for *Dataset1* and *Dataset2*, respectively. Each of them was divided into two subsets: a training subset with 80% of the samples and a validation subset with 20% of the samples. We adopted the Adam algorithm with a learning rate of 10^{-4} for optimization and the Mean Squared Error (MSE) as the loss function. The U-Net training process learns to predict the high sampling dose maps, with their fine details, from the low sampling dose maps and the corresponding CT slices considered as inputs and it was trained twice. The first training model (called *System1*) was performed on *Dataset1*, for 200 epochs and 10 batches. However, the second training model (called *System2*) was performed on *Dataset2*, for 500 epochs and 10 batches. The two systems were trained on the same GPU NVIDIA GeForce GTX 1080 card.

Preliminary results: The running time for the low and high sampling MC simulations was about 0.6 ± 0.1 s and 23 ± 1 s with a mean uncertainty of $2 \pm 0.7\%$ and $60 \pm 30\%$, respectively. The training stages took about 6 and 1.5 hours for the *System1* and *System2*, respectively.

Figure 1 shows the result, using the *System1*, for two low sampling dose maps with different energy values: 92 keV (*Sample1*) and 690 keV (*Sample2*). The absolute error maps prove that this trained model was able to improve the overall low sampling statistical quality maps. However, the fine details in the background were not properly recovered for the sample with the low energy value (*Sample1*). The MSE values for these samples were 1.8×10^{-4} for *Sample1* and 8.6×10^{-3} for *Sample2*.

Figure 2 shows the results obtained by applying the two systems (*System1* and *System2*) for the same sample (*Sample2*). The obtained absolute error map obtained by *System2*, compared to that obtained by *System1* shows an improvement in terms of recovering the fine details, in the generated dose map, and thus leads to a result statistically equivalent to a higher sampling dose map. The MSE value for this case, with the learned *System2*, was 9.2×10^{-4} compared to the previous 8.6×10^{-3} value obtained with *System1*.

Discussion & Conclusions: These preliminary results are promising. They show the ability to enhance the statistical MC simulation speeds and qualities. However, they highlight the impact of considering a large of energy values' interval in decreasing the model's performances. To handle with this encountered problem of unbalanced dataset, our main idea, which is our work in progress, consists of encoding the energy information to the trained model. Such strategies avoid increasing the computing time's problem with additional training and condition the model to

accurately recover the fine details even with small energy values.

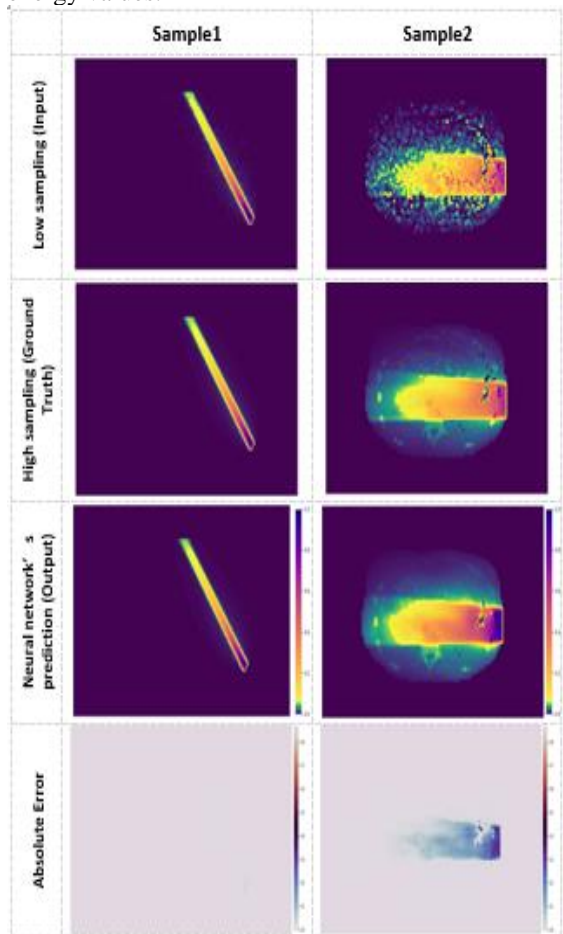


Figure 1: A representative result for two low sampling MCS, with different energy values, from the validation set. The rows, from top to bottom: the low sampling MCS (network input), the high sampling MCS (Ground Truth), the predictions of the network, and the absolute error maps between the Ground Truth and the network prediction.

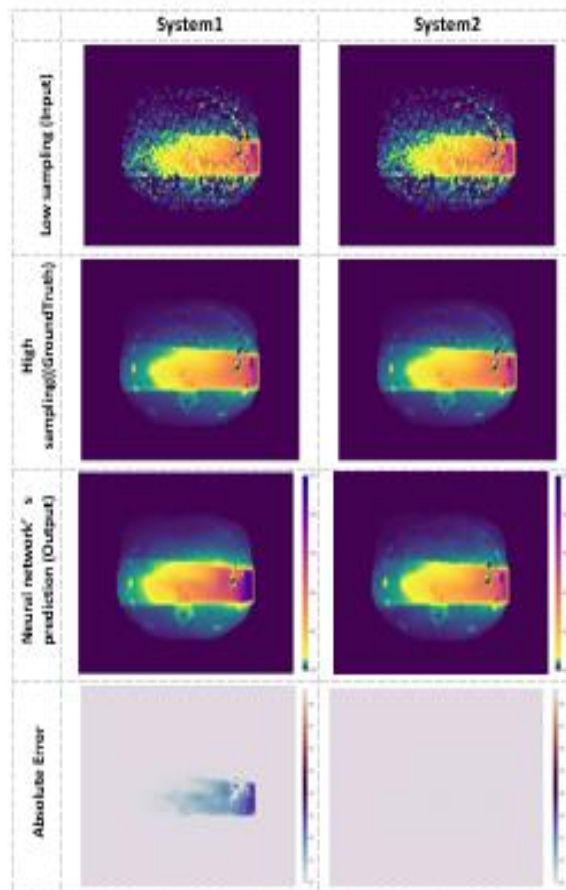


Figure 2: Representative result from the validation set, using the two trained systems (first line for System1 and second line for System2). The rows, from top to bottom: the low sampling MCS (network input), the high sampling MCS (Ground Truth), the predictions of the network, and the absolute error maps between the Ground Truth and the network prediction.

References:

- [1] T. Bai *et al.*, "Deep dose plugin: towards real-time Monte Carlo dose calculation through a deep learning-based denoising algorithm," *Mach. Learn. Sci. Technol.*, vol. 2, no. 2, p. 025033, 2021.
- [2] S. Martinot *et al.*, "High-Particle Simulation of Monte-Carlo Dose Distribution with 3D ConvLSTMs," in *MICCAI* 2021.
- [3] O. Ronneberger, P. Fischer, and T. Brox, "U-Net: Convolutional Networks for Biomedical Image Segmentation," in *MICCAI* 2015.
- [4] D. Nguyen, *et al.*, "3D radiotherapy dose prediction on head and neck cancer patients with a hierarchically densely connected U-net deep learning architecture," *Physics in medicine & Biology*, 64(6), 2019.
- [5] H.R. Roth *et al.* "Data from pancreas-ct. the cancer imaging archive." *IEEE Transactions on Image Processing* (2016).
- [6] D. Benoit, J. Bert and D. Visvikis, <https://ggems.fr>