

## Improvement of DNN Model Performance for External Exposure Dose Estimate

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\***Keywords** : External exposure, Dose estimate, DNN, AI performance

### 1. Introduction

For the safety management of radiation workers in nuclear power plants, it is necessary to estimate the radiation exposure dose to workers during work planning or after an accident. We aimed to develop an AI model that can predict the exposure dose similar to the results of Monte Carlo simulation for quick and accurate dose assessment in the situation of external exposure to the human body. Before creating a database to train the AI model, we first developed an AI model for whole-body doses that can quickly collect results with small uncertainties to understand the requirements for creating an AI prediction model with adequate performance. There was an attempt to apply the DNN model to estimate the whole-body dose values by point source location [1, 2]. However, it was found that the relative errors for points in specific spaces, such as nearby human phantoms, were larger than the maximum value found on the test data. For a DNN model to be a good substitute for Monte Carlo simulation, the difference between the simulation computational results and the DNN model predictions must be small enough in all cases. In this study, we attempted to improve the performance of the model by reducing the maximum relative error over the entire data domain.

### 2. Methods and Results

This section describes the process of building a DNN-based dose prediction model and how the relative error distribution of the entire data changes when the model training influencing factors are altered. Based on the model structure that performed best in the previous study [2], the maximum relative error distributions of the predictions changed as the factors for training were varied. The factors considered are the data included in the training and the loss function.

#### 2.1 Model Building Algorithm

Whole-body dose data for the human phantom by point source location were calculated with an uncertainty of less than 1% from Monte Carlo simulations using GEANT4. The exposed subject was the standing MRCP

Male Phantom (55.77 cm × 29.13 cm × 176 cm), and the radiation type was 1.0 MeV gamma-ray. The collected data consisted of about 55,000 grid points spaced 5 cm or 10 cm apart within a 2 m × 2 m × 2 m space centered at the origin. 10% of the total data was randomly sampled as test data and the rest of the data was split into training and validation data in an 8:2 ratio. The Cartesian and spherical coordinates of radiation point sources and whole-body dose values were extracted from each output file. Since the dose is inversely proportional to the square of the distance from the source, the inverse of the square of the distance between the point source and the origin was included as an input variable. For the selected input variables (x, y, z, r, theta, phi, 1/r<sup>2</sup>) and output variables (whole-body absorbed dose), the hyper-parameters of DNN model were optimized using Keras-Tuner's hyperband tuning algorithm. The tuning targets were the number of layers, the number of nodes in each layer, and learning rate. The optimizer was selected as Adam, and the loss function was fixed as the mean absolute error (MAE).

Figure 1 shows a scatter plot of the whole-body dose prediction error for each source location in the test data.

The scatter plot on the left shows all source locations in the test data, while the scatter plot on the right shows only those cases where the error is greater than 1%.

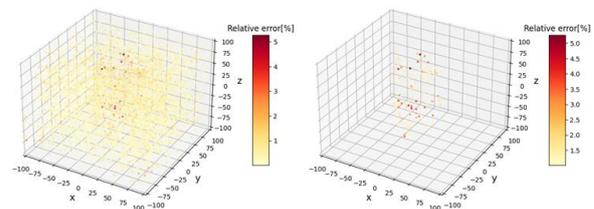


Fig. 1. Scatter plots showing the whole-body dose prediction error of the DNN model by source location in the test data. (left : all test data, right : data with an error of 1% or more)

Overall, the dose predictions have less than 1% error from the Monte Carlo simulation results, but the maximum error can exceed 5%. While this model can still be used for dose prediction with some uncertainty in certain areas depending on the intended use, improvements have been attempted to the model to

further reduce the difference with the computational simulation results.

## 2.2 Improving Data Imbalance

When checking the distribution of predicted value errors during the model tuning process, the errors exceeding 1% were mainly distributed around the surface of the phantom and at the corners of the total source distribution area. This is presumed to be due to two reasons. One is that the pattern of the relationship between location and dose changes dramatically when located very close to the phantom surface. Figure 2 shows the relative positions of several points in relation to the human phantom.

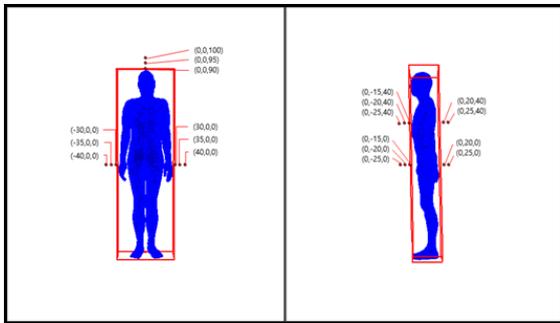


Fig. 2. Illustration of the location of points around the human phantom by coordinates

It is observed that points with x-coordinate of -30, y-coordinate of -15 or z-coordinate of 90 are located very close to the human phantom surface. This can lead to a sharp increase in the dose gradient with distance. There is also a tendency for the edges of the data region to have larger errors than elsewhere. Therefore, for this model, the decision was made not to consider surface contamination. We set a margin space of about 5 cm thick from each surface of the human phantom box (red line in Figure 2) and excluded sources located within that area from the data. Next, it was thought that the output variable (whole-body dose) was highly unbalanced, resulting in large errors in areas with low data frequency. The best approach would be to add data in areas where data is relatively sparse, but there are limitations on the time and cost of generating data. So, it is necessary to find a way to develop a model that performs acceptably with as little data as possible. To mitigate the data imbalance without adding data, the dose values were log-transformed using the equation (1) to reduce the absolute value of the skewness of the data distribution, as shown in Figure 3.

$$(1) y_t = \log(10^{-n} \times y + 1)$$

To account for the scale of the dose values, n was set

to 18. To increase the range of the distribution of y values,  $y_t$  was multiplied to 10,000 to increase the range of the distribution of target values, as small differences can change significantly when the predicted values outputted by the log-transformed values are converted to doses.

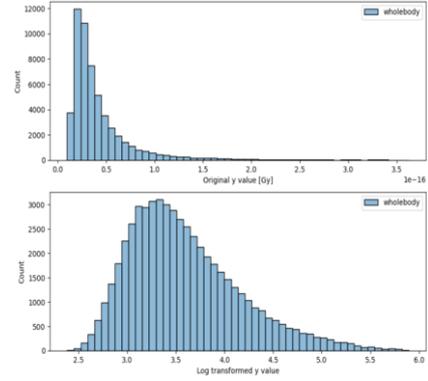


Fig. 3. Distribution of whole-body doses before and after log transformation (top : original data, bottom : log-transformed data)

As a result, the trained model produced predictions with relative errors within 5% for all data, including test data not included in training and train/validation data included in training.

## 2.3 Replacement of the Loss Function

The loss functions for regression models provided by Keras include mean squared error (MSE), mean absolute error (MAE), mean absolute percentage error (MAPE), mean squared logarithmic error (MSLE), cosine similarity, Huber, and logcosh[3]. Different types of loss functions can have different learning directions, such as reducing the impact of outliers or penalizing over- and underestimates differently. Since the data used in this study was obtained through simulation, there are no outliers, so the goal is to create a model that can reflect all of the data well. Therefore, we replaced the loss function with MSE, which reflects the influence of data with large errors to a greater extent. As a result, the dose prediction model has the smallest maximum relative error for all the data so far. Figure 4 shows the relative error of the predictions of the final selected model for all data. It is verified that the DNN model can be used to predict the dose with a relative error within about 3% for all considered source positions.

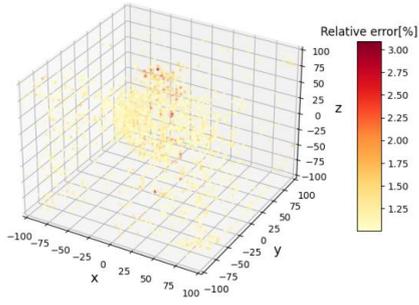


Fig. 4. Scatter plots showing the whole-body dose prediction error of the DNN model by source location in the full data. (DNN model was trained with log-transformed output variables)

#### 2.4 Validation of Dose Estimation in External Exposure Scenarios Using the DNN Model

To validate that the DNN model can be applied to predict whole body dose in scenarios of exposure to various types of radiation sources, dose estimation was performed for a planar radiation source at various locations. Using the GEANT4 code, the results calculated with  $nps\ 10^8$  were assumed to be the real value and compared with the predicted dose from the DNN model. In the base scenario, the radiation source was defined as a planar source with a  $10 \times 10$  cm square shape. Within the radiation source area, 1,000 locations were selected on a regularly spaced grid, and the final dose value was calculated by averaging the output of the DNN model for the selected locations. The DNN model's predicted dose and GEANT4 calculation results are shown in Table I. In all cases considered, the DNN model predictions agree with the GEANT4 calculations within 3%.

Table I: Dose prediction results from DNN model for planar source exposure scenario

Plane	Center location	GEANT4 calculation [Gy]	DNN model prediction [Gy]	Relative error
yz plane parallel	(-40,0,0)	1.16E-16	1.14E-16	-2%
	(-50,0,0)	7.71E-17	7.65E-17	-1%
	(40,0,0)	1.07E-16	1.06E-16	-1%
	(50,0,0)	7.27E-17	7.24E-17	0%
xz plane parallel	(0,-20,0)	2.25E-16	2.22E-16	-1%
	(0,-30,0)	1.48E-16	1.47E-16	-1%
	(0,-40,0)	1.05E-16	1.05E-16	0%
	(0,-50,0)	7.85E-17	7.81E-17	-1%
	(0,20,0)	3.20E-16	3.18E-16	-1%
	(0,30,0)	1.93E-16	1.93E-16	0%

	(0,40,0)	1.31E-16	1.30E-16	-1%
	(0,50,0)	9.43E-17	9.42E-17	0%
xy plane parallel	(0,0,95)	8.21E-17	8.00E-17	-3%
	(0,0,100)	5.27E-17	5.21E-17	-1%
	(0,-40,95)	4.20E-17	4.17E-17	-1%
	(0,-40,100)	3.70E-17	3.67E-17	-1%
	(0,40,95)	4.59E-17	4.58E-17	0%
	(0,40,100)	4.03E-17	4.02E-17	0%
	(0,-40,0)	1.06E-16	1.05E-16	-1%
	(0,40,0)	1.32E-16	1.31E-16	0%
	(0,-40,-85)	3.44E-17	3.42E-17	0%
	(0,40,-85)	4.05E-17	4.05E-17	0%

### 3. Conclusions

The prediction error of the DNN model developed to predict the whole-body dose of a human phantom exposed by a point source is mainly high when the point source location is close to the phantom surface or far from the phantom. This was assumed to be due to the unbalanced distribution of the output variable due to the gridded data sampling. To resolve the data imbalance, new data can be added or the data can be undersampled. However, adding new data is time-consuming and costly, and it requires deciding how much new data to add each time the target variable changes. Undersampling can lead to poorer predictive performance because it doesn't utilize the information in the data available. In this study, the log transformation of the output variable was performed to reduce the skewness of the distribution to train the DNN model, and MSE, which better reflects the impact of large errors, was used as the loss function. As a result, the prediction performance of the model was found to be better than before. In addition, it was verified that the developed model can be used to produce similar results to Monte Carlo simulation in the exposure scenarios for point source as well as plane source. Due to the complex geometry of the human phantom, Monte Carlo simulations take several minutes to run even on a server with 36 threads, while the DNN model can produce results in seconds on a regular desktop. It is expected that the developed DNN model can be utilized to perform whole body dose calculations in heterogeneous source distributions within a short time and easily by non-experts.

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### **ACKNOWLEDGEMENTS**

This research was supported by the National Research Foundation of Korea (NRF) grant funded by the Korea government (Ministry of Science and ICT) (RS-2022-00144350).