Development of Dose Evaluation Algorithm for Boron Neutron Capture Therapy Using Convolution/Superposition Method

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1. Introduction

Monte Carlo techniques are the most favored tool for BNCT dose evaluation due to their accuracy in radiation dosimetry and applicability to various treatment conditions. Nevertheless, the Monte Carlo method is not the first choice for photon radiotherapy as it is still time-consuming and requires significant computational power. The convolution/superposition algorithm is widely used in conventional radiotherapy as it provides dose calculation results within a few minutes with reasonable accuracy, making it suitable for the clinical environment [1]. In this work, we applied the convolution/-superposition (C/S) technique to the neutron dose evaluation for a clinically practical BNCT treatment planning system.

2. Methods

The neutron C/S dose calculation method utilizes two distributions of physical quantity; the total energy generated per unit mass (TEGMA) by nuclear interaction and the energy deposition kernel. The released energy dissemination and deposition through the media can be predicted by convoluting TEGMA with the kernel. For each specific nuclear interaction, a corresponding TEGMA is defined as the product of mean energy released or generated per an interaction and the reaction rate per unit mass of the target medium. Three TEGMA libraries were constructed corresponding to the three main nuclear reactions that contribute to neutron dose in BNCT; which are $^{10}B(\mathrm{n},\alpha)\,^{7}Li$, $^{14}N(\mathrm{n},\mathrm{p})^{14}C$, and $^{1}H(\mathrm{n},\mathrm{n}')\,^{1}H$ reactions. In $^{10}B(\mathrm{n},\alpha)\,^{7}Li$ reaction, the Q-values are 2.33 MeV and 2.81 MeV accounts for 94% and 6% respectively. As for $^{14}N(\mathrm{n},\mathrm{p})^{14}C$ reaction, the Q-value is 0.626 MeV. The cross-sections of each element and energy were manually calculated by linear interpolation of microscopic cross-section data from ENDF/B-VII.1 library[2] and atomic number density of brain from ICRU report 46[3]. For $^{1}H(\mathrm{n},\mathrm{n}')\,^{1}H$ interaction, the hydrogen kerma factor[4] was adopted for hydrogen. The neutron flux in the medium by irradiation was simulated by MCNP 6.2[5] code. The calculated dose results from convolution/superposition have been compared with PHITS 3.02[6] Monte Carlo simulation code in virtual homogeneous phantom with various irradiation beam field sizes.

3. Results and Discussion

PHITS result uncertainty was less than 3% at a depth of 2 cm. The discrepancies or relative error, measured at a depth of maximum dose, were within 5% and got smaller as the beam field size increases. The comparison results of the time taken for dose calculation between convolution/superposition and PHITS are shown in Table 1.

The metric to measure the discrepancy between C/S and PHITS was the relative error $Err_{rel} = |\frac{D_{C/S}-D_{PHITS}}{D_{PHITS}}|$. For the boron dose, the relative error range was from a minimum of 2% to a maximum of 6%. For nitrogen dose case, is was from a minimum of 4% to a maximum of 9%. The hydrogen dose had a higher difference which is around 25%. The high discrepancy in the hydrogen dose can be explained as due to the difference between ENDF and JENDL nuclear library; as the MCNP6 code results less fast neutrons compared to the PHITS code in human brain.

Table 1. *Dose calculation time comparison between C/S neutron dose calculator and PHITS Monte Carlo code for 30×30 mm^2 mono-directional neutron beam in a virtual homogeneous phantom*

	CPU(Intel)		Calculation time	Uncertainty at a depth of 2cm
	Cores	Processor base frequency		
CS	1	2.80 GHz	56 sec	-
PHITS	4	2.80 GHz	48 h	3~5%
	48	2.67 GHz	4 h	

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