Comparison of TORT and MCNP Dose Calculations for BNCT Treatment Planning*

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Introduction

Clinical trials to determine the efficacy of Boron Neutron Capture Therapy (BNCT) have been initiated in the U.S. at the Beth Israel-Deaconess Medical Center, Harvard Medical School (BIDMC) and the Massachusetts Institute of Technology (MIT) for the treatment of melanomas and glioblastomas and at Brookhaven National Laboratory (BNL) for the treatment of glioblastomas. An essential and time-consuming part of the preparation for treatments is the prediction of dose distributions in the patient so that appropriate beam orientations and exposure times can be decided. Medical physicists at BNL use the BNCT_RTPE treatment planning software[1] developed by the Idaho National Engineering Laboratory (INEL), while the BIDMC/MIT team uses their internally developed NCTPLAN software.[2] Both of these programs use Monte Carlo methods to simulate the transport of neutrons and gamma rays from the external beam into the patient's anatomy and to calculate the resulting dose components. In the case of BNCT_RTPE, dose calculations are accomplished using the INEL-developed rtt_MC Monte Carlo module, which is specially tailored for BNCT applications. At BIIDMC/MIT, dose calculations are performed using the standard MCNP4A code[3] developed by Los Alamos National Laboratory. In both cases, the dose calculations are computationally intense and reductions in the running times would greatly expedite the treatment planning process.

The purpose of the present study was to assess the relative computational merit of using a deterministic code to calculate dose distributions for BNCT applications. In our study, the TORT discrete ordinates code[4] developed by Oak Ridge National Laboratory was used to replace the MCNP4A code in the dose analysis for a BIDMC/MIT human subject. The viability of TORT for this application was demonstrated by INEL in earlier dosimetry studies using a dog head phantom.[5] However, the surface-based anatomical model produced by the image analysis portion of INEL's BNCT_RTPE code is not directly compatible with the orthogonal mesh requirements of TORT, hence TORT can not be easily incorporated into their treatment planning system. In contrast, the NCTPLAN program generates a voxel model of the subject's anatomy, which is ideally suited for solution using deterministic methods such as TORT. In a voxel-type model, the orthogonal geometry can be represented exactly and the fine spatial distribution of the dose is calculated directly.

Analysis Model and Parameters

The computational model used for this study represented the lower leg of a peripheral melanoma study subject treated by BNCT at BIDMC/MIT and is shown in Fig. 1. The model is based on computed tomography (CT) images in the region of a melanoma and was generated by the image processing portion of NCTPLAN.[2] The MCNP model contained 11,025 voxel cells, while the TORT model was expanded to 15,782 mesh cells to fully enclose the leg segment and the disk source. Fig. 1 also shows the bounding box for the TORT model and the disk source at the exit of the MITR-II epithermal beam collimator. The segmentation portion of NCTPLAN reduced the high-resolution CT data into 1 cm^3 voxels and reduced the number of possible material compositions to 15 different combinations of tumor, muscle, bone, and air. These compositions correspond to the different shades of gray in the model shown in Fig. 1.

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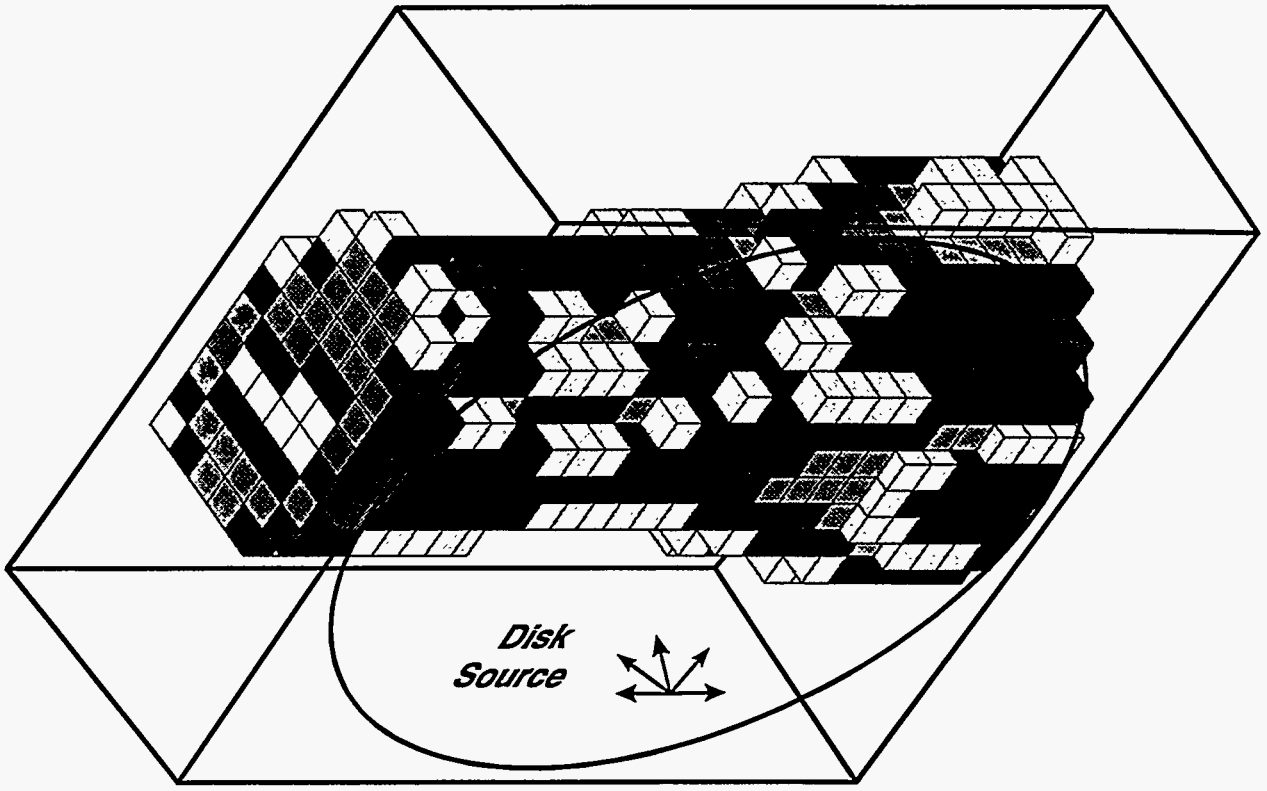

Fig. 1. Voxel model of leg segment produced by NCTPLAN.

Several parameters for both the MCNP and the TORT codes were varied in the study, including different nuclear data libraries and options, number of MCNP histories, and TORT input parameter such as mesh size, order of Legendre expansion of the anisotropic scattering, and the weighting parameter (theta) for the finite-difference model. For each of the cases, the MCNP and TORT results were compared for each of 2247 preselected cells for boron kerma and muscle kerma responses, including kermas due to thermal neutrons, fast neutrons, and gamma rays. Conclusions were made based on the frequency distributions of MCNP-to-TORT ratios for the 2247 cells and by observing the number of cells for which the TORT results were within 1, 2, or 3 fsd (fractional standard deviation) of the mean MCNP values.

Analysis Results

In terms of the MCNP variations, it was found that no significant difference was observed between using nuclear data from Version V or Version VI of the Evaluated Nuclear Data File (ENDF). On the other hand, a substantial improvement was observed (compared to the reference TORT case) when the $S(\alpha,\beta)$ thermal scattering kernels were included in MCNP. A relatively significant change was observed when the number of particle histories was increased from 3 million to 10 million. Comparisons of the results from these two calculations are shown in Fig. 2 for the $^{10}B(n,\alpha)$ dose and for total muscle dose.

In terms of the TORT variations, only slight differences (less than 7% max. change) were observed between using "off the shelf" multigroup cross sections, specifically cross sections from the BUGLE-93 library,[6] and cross sections which were specially weighted for this application. Also, reducing the mesh size to 0.5 cm resulted in relatively modest changes (less than 15% max. change) in the converged fluxes. Increasing the order of Legendre expansion of the cross sections from P_3 to P_5 yielded no significant changes. The parameter which impacted the TORT results the most was the value of theta, a weighting factor internal to the flux solution model. Figure 3 shows the effect of changing the value of theta from

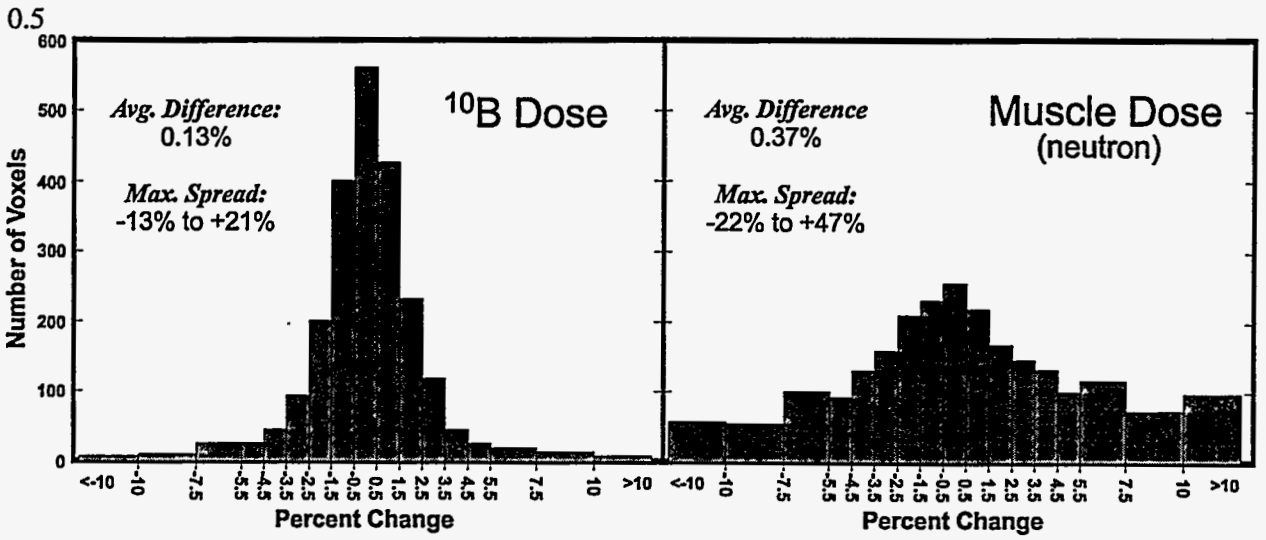

Fig. 2. Change in MCNP results when going from 3 million to 10 million particle histories.

to 0.9 (theta must be in the range of 0 to 1). While the higher energy responses showed only modest impact, the thermal responses showed a significant bias due to different theta values.

The reference MCNP and TORT cases were selected to be those which yielded a +/-5% agreement between the two methods for >95% of the comparison cells. For MCNP, this corresponded to using ENDF/B-VI nuclear data with the S(α,β) data and 10 million particle histories. The corresponding TORT calculation used flux-weighted 47-neutron/20-photon group cross sections with P_3 Legendre expansion, an S_{12} angular quadrature, 1 cm mesh size, and a value of 0.9 for theta. These specifications yielded the desired agreement for all dose responses, including the boron-10 dose and the muscle dose due to thermal neutrons, fast neutrons, and gamma rays as shown if Fig. 4.

With respect to computational time, the reference MCNP calculation required 2790 min. on an IBM RISC/6000, Model 560 workstation. In contrast, the reference TORT calculation required 188 min., nearly a factor of 15 times faster than MCNP. Increasing the Legendre order to P_5 increased TORT's running time only 17% to 220 min. Running times for MCNP were roughly proportional to the number of particle histories.

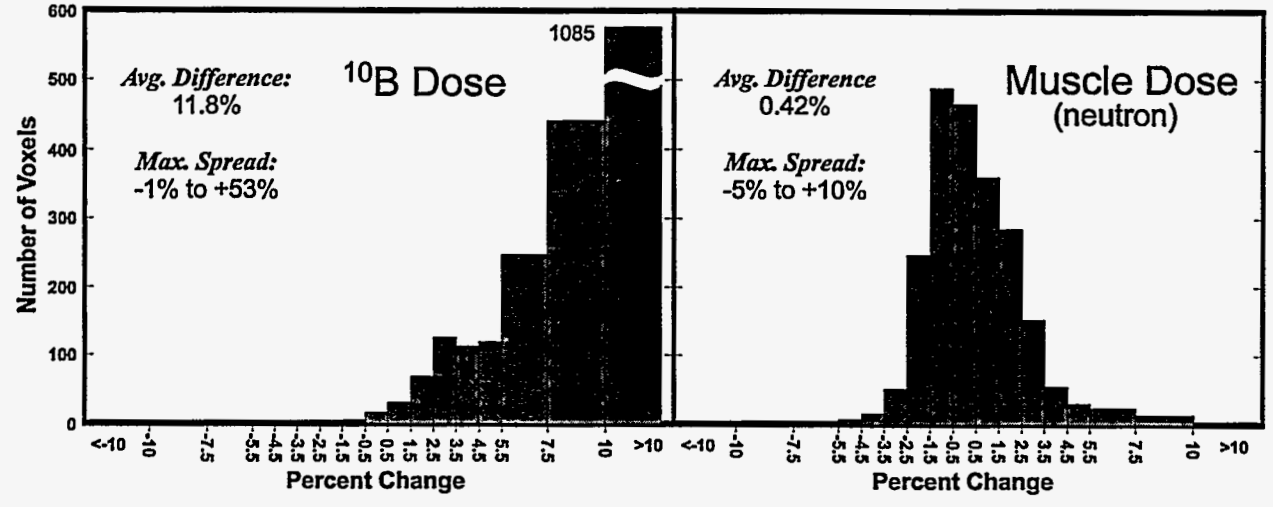

Fig. 3. Change in TORT results when going from a theta value of 0.5 to 0.9.

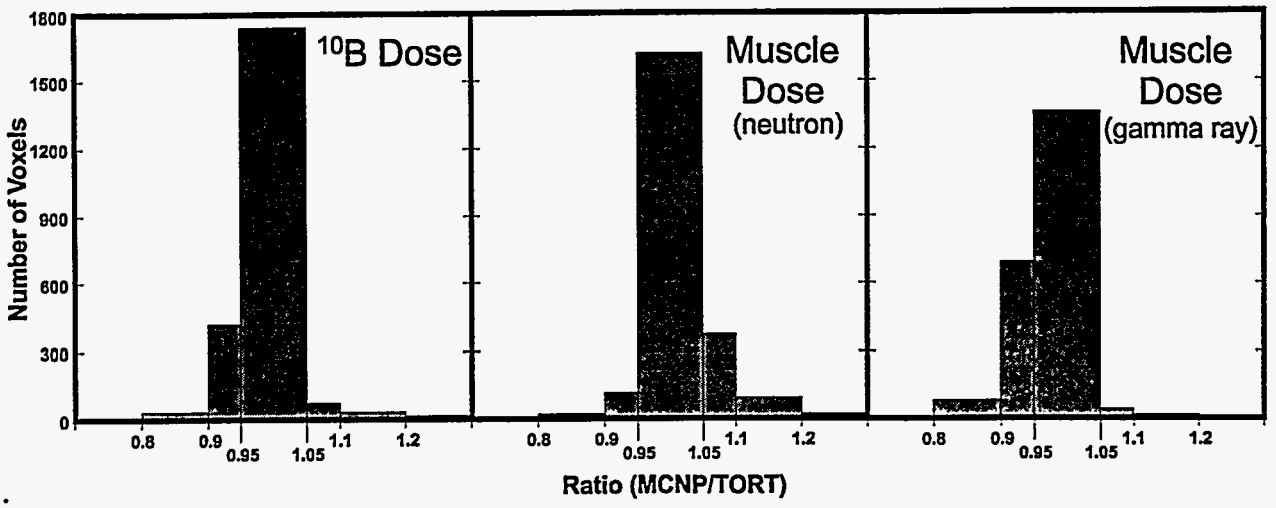

Fig. 4. Comparison of MCNP and TORT results for reference cases.

Conclusions

It is expected that with additional refinement and tailoring of the codes to this specific application, the performance of both MCNP and TORT can be improved further. It is clear from this study, however, that deterministic codes such as TORT offer the best and most natural choice for application to BNCT treatment planning for voxel-based anatomical models. For these cases, the voxel geometry can be modeled exactly and the deterministic method provides a direct solution of the dose components at every mesh cell. With proper selection of the numerical quadratures and flux model options, the deterministic method can yield fast and highly accurate solutions.

Acknowledgments

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