

FLUKA Monte Carlo calculations for hadrontherapy application

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Abstract

Monte Carlo (MC) codes are increasingly spreading in the hadrontherapy community due to their detailed description of radiation transport and interaction with matter. The suitability of a MC code for application to hadrontherapy demands accurate and reliable physical models for the description of the transport and the interaction of all components of the expected radiation field (ions, hadrons, electrons, positrons and photons). This contribution will address the specific case of the general-purpose particle and interaction code FLUKA. In this work, an application of FLUKA will be presented, i.e. establishing CT (computed tomography)-based calculations of physical and RBE (relative biological effectiveness)-weighted dose distributions in scanned carbon ion beam therapy.

1 Introduction

A major advantage for the application of carbon ion beams in tumour therapy is their so called “inverse” depth-dose profile with a pronounced maximum at the end of range (Bragg peak), in conjunction with their increased relative biological effectiveness (RBE) in the tumour volume in comparison to the lower effectiveness in the surrounding health tissue [1]. Besides these advantages due to electromagnetic interaction, carbon ion beams experience nuclear reactions which cause a significant alteration of the radiation field. This shows mainly through a loss of primary beam particles and a build-up of secondary lower-charge fragments [2]. In particular, the lower-charge fragments, having longer ranges than the primary beam, give rise to the characteristic dose tail beyond the Bragg peak. Moreover, the light fragments scatter more than the heavier primaries thus broadening the irradiation field in the patient. Furthermore, the biological effectiveness of the fragments is different from that of the primary carbon ions [3] and it has to be included in the biological effect calculations. At the GSI Helmholtzzentrum für Schwerionenforschung Darmstadt, Germany, the analytical treatment planning system (TPS) TRiP98 (TReatment planning for Particles, 1998) [4,5] has been clinically used in connection with the GSI pilot project for carbon ion beam therapy [6]. TRiP98 is coded for being applied to the GSI 3D active beam delivery, which combines intensity-controlled lateral deflection based on the raster scan system [7] with discrete selection of accelerator beam parameters (energy, focus, intensity). The physical beam model of TRiP98 relies on an external database which takes into account the energy loss, the energy loss straggling and the projectile fragmentation [8,4]. For RBE-weighted dose calculations, TRiP98 is based on the Local Effect Model (LEM) [3,9,10] which is used to reproduce the dependency of the RBE on the type of the irradiated tissue, on the biological endpoint and on the ion beam characteristics. For biological inverse planning, an optimization process is implemented in TRiP98 in order to provide a uniform RBE-weighted dose distribution in the target volume according to the planning prescription. The result of the optimization is an output file containing the beam phase space information for each treatment field: pencil beam energy, lateral width and position (x,y) at the isocenter as well as fluence distribution.

In this work, we describe a novel methodology for establishing CT (Computed Tomography)-based calculations of physical dose and RBE-weighted dose distributions in carbon ion beam therapy using the FUKA MC code [11,12]. We performed CT-based forward re-calculations of absorbed and RBE-weighted dose for a clivus chordoma patient treated at GSI. The patient case has been planned with TRiP98. MC CT-based calculations required the proper handling of the patient CT images and of the TRiP98 WEPL (water-equivalent path length) – HU (Hounsfield unit) calibration curve (as described in section 2.1) as well as the coupling of FLUKA to the LEM model for the evaluation of RBE-weighted dose distributions [2] (as outlined in section 2.2). Among the simulated beam ports of the total treatment fraction, section 3 shows a representative comparison of the MC dose/RBE-weighted dose results (dose to tissue) with the corresponding TRiP98 quantities (dose to water).

2 Material and Methods

2.1 Handling of patient CT with related information

In view of re-calculating patient plans, we have used the approach proposed in Schneider *et al* [13] and already applied in Paganetti *et al* [14] and Parodi *et al* [15] in proton therapy to convert the CT data, expressed in HUs, into mass density and chemical composition. The patient CT data are processed before the starting of the simulation and converted into an appropriate file format to be input into FLUKA. According to the logic of FLUKA, all voxels with the same HU value are identified as a spatial region. In order to reduce the number of materials to be used in FLUKA the segmentation of the CT in several HU intervals proposed by Schneider *et al* [13] and extended by Parodi *et al* [14] have been applied. The materials defined in FLUKA are characterized via the mentioned segmentation and the ‘nominal’ density, i.e. the density at the HU corresponding to the center of the HU intervals. Nuclear and electromagnetic processes depend, in first approximation, on the mass density and on the stopping power ratio, varying with the HU values within each material

characterized only by the ‘nominal’ density in the MC. To account for this, CT number dependent scaling factors for electromagnetic and nuclear interactions are introduced to adjust the stopping power values and mass density, respectively [15].

TPSs are essentially based on the assumption of water targets and the main idea to account for longitudinal density variations is to apply the concept of WEPL when an ion traverses a CT voxel. High density voxels correspond to water-equivalent path lengths larger than that for water, low density voxels to shorter water-equivalent path lengths. In this way the trajectory of an ion is transformed from the CT system into a water-equivalent system in the beam-eye-view. TRiP98 adopts an experimentally established WEPL curve based on the measurements of residual ranges behind tissue-equivalent phantom materials as well as bovine and human bony tissue in comparison to ranges in water [16,17]. This calibration curve has to be matched by the MC calculations for assuring a correct estimation of the experimental carbon ion range as a function of HUs.

Starting from the electron density and mean ionization energy for the nominal materials corresponding to the segmentation implemented in FLUKA, the carbon ion stopping power relative to water (ρ_s) has been calculated using the approximation proposed in Schneider *et al* [18] for proton therapy application, neglecting the shell and density corrections of the Bethe-Bloch formula (which are only minor for the energy range and materials of therapeutic relevance [19,20]):

$$\rho_s = \rho_e \frac{\log\left[\frac{2m_e c^2 \beta^2}{I_m(1-\beta^2)}\right] - \beta^2}{\log\left[\frac{2m_e c^2 \beta^2}{I_{water}(1-\beta^2)}\right] - \beta^2} , \tag{1}$$

where ρ_e is the relative electron density, βc is the carbon ion velocity, m_e is the electron mass and I_m is the mean ionization energy of the target atoms. The carbon ion stopping power relative to water ρ_s represents a good approximation of the WEPL. Hence, in order to match the same experimental WEPL calibration as used in TRiP98 for determining the Bragg peak position in dependence of the HU value, the electromagnetic scaling factors (f_{EM}) for FLUKA have been calculated as:

$$f_{EM} = \frac{WEPL}{\rho_s} . \tag{2}$$

For validating the introduced approach and the related f_{EM} calculations, we simulated the irradiation of phantoms, corresponding to different CT numbers, with several mono-energetic carbon ion pencil beams. The obtained Bragg peak positions were compared with the TRiP98 results. In figure 1 a satisfactorily comparison between TRiP98 (solid line) and FLUKA (dashed line) results using the calculated scaling factors is shown for 270 MeV/u carbon ion pristine Bragg peaks simulated in phantoms corresponding to different HU values. Both TRiP98 and FLUKA results are normalized using the same number of primary carbon ions. It should be noticed that adjusting the FLUKA stopping power calculations for reproducing the same semi-empirical HU-WEPL calibration curve used by the TPS does not mean to benchmark the MC dose calculation engine against the TRiP98 predictions, but only to ensure their consistency in terms of calculated Bragg-peak positions.

2.2 Calculation of absorbed dose and RBE-weighted dose

In our simulations, we calculate dose correcting the ‘nominal’ material density to the ‘real’ value by means of the same factors used to rescale nuclear processes [15] and for RBE-weighted dose simulations [2]. RBE-weighted dose distributions are calculated using the same RBE tables as in TRiP98 by applying, prior to the start of the simulation, the *low dose approximation approach*

described in [10].

The RBE database consists of α_D and β_D , i.e. the coefficients of the linear and quadratic terms of cell survival after ion irradiation, for the components of the mixed radiation field as a function of the particle energy, particle type and cell line. In the simulation, whenever energy is deposited by a certain radiation type, the following two quantities, in addition to the dose D , are stored: $\alpha_D \cdot D$ and $\sqrt{\beta_D} \cdot D$. Then applying the methods described in [2] one can derive RBE-weighted dose results. Dose and RBE-weighted dose results of TRiP98 are saved with the same spatial resolution of the CT image of the treated patient; the FLUKA grid for scoring dose/RBE-weighted dose has been thus chosen according to the planning CT.

3 Results

Figures 2 and 3 show representative comparisons between FLUKA and TRiP98 calculations of 2D distributions (Fig. 2) and profiles (Fig. 3) of absorbed and RBE-weighted dose for a clivus chordoma patient treated at GSI. The FLUKA particle transport was performed on a CT scan of 106 slices with 256×256 transaxial pixels each. The pixel dimension is about 1.21 mm and the distance between two consecutive slices is 3 mm. The cranial carbon ion treatment field enters the patient from the right side of the Fig. 2 (sagittal views). The depth-profiles are sampled along the lines shown in the upper-left panels of Fig. 2.

4 Discussion

An important aspect in view of re-calculations of clinical treatment plans is the implementation of CT-dependent stopping power correction factors in order to force the MC to follow the same CT-range calibration curve as the TPS. Our implementation has been validated by calculating Bragg peaks in phantoms of different CT numbers with carbon ion beams at 270 MeV/u. The differences between the Bragg peak positions calculated by FLUKA on the basis of the introduced stopping power correction factors and by TRiP98, as shown in Fig. 1, are less than 1 mm (the histogram bin width is 0.5 mm). The discrepancies in the absolute value are due to the different weighting of the energy deposition calculating *dose to water* in the TRiP98 and *dose to tissue* in FLUKA and to the different description of electromagnetic/nuclear processes in FLUKA and in TRiP98. In fact, as described in the section 2.2, TRiP98 considers the CT phantoms as equivalent to water by stretching the ion path using the WEPL table (*dose to water*), while in our calculations we divide the energy deposition (already normalized per unit volume) by the real density of tissue corresponding to the CT number (*dose to tissue*). The differences in the fragmentation tails are mainly influenced by the different composition of the mixed radiation field due to differences in nucleus-nucleus reactions modeling [2] and in target definition: water in TRiP98 and various materials in FLUKA.

In Figs. 2 and 3 we presented dose/RBE dose calculations for a treatment field delivered to a clivus chordoma patient at GSI. In general, the shapes of the MC calculated distributions agree with the TRiP98 ones. Exceptions occur in the cases more sensitive to the limitations of the analytical dose calculations similarly to the findings in proton therapy simulations [14,15]. These especially include regions of large density variation. In fact TPSs are typically less accurate than the MC computational engines in the transport of the radiation in the presence of large tissue heterogeneities. This is due to the intrinsic limitations of the water-equivalent stretching in depth, i.e. they account for the specific tissue composition only by corresponding adjustment of the penetration depth. In contrast, MC codes accurately model electromagnetic and nuclear processes keeping into account the specific tissue elemental composition obtained from a stoichiometric calibration of the CT scan. A clear example is given by Fig. 3 which shows a dose/RBE-weighted dose profile sampled along the line depicted in upper-left panel of Fig. 2. In the plateau region the FLUKA and the analytical results agree

satisfactorily while in the high dose region they differ where the CT values are considerably different from 0, i.e., when the mass density is substantially different from that of water, such as in bony structures. Finally differences have been found in the tail of dose distributions. The low dose tail is due to energy deposition by the fragments, mainly H and He, produced in nuclear fragmentation. As already pointed out in Mairani *et al* [2] the different handling of nuclear reactions in the analytical code and in the MC code can explain the differences in the tails. Using the interface to LEM outlined in section 2.3 it has been possible to calculate RBE-weighted dose distributions as shown in the bottom-left panels of Fig. 2 and in the right panels of Fig. 3. In the high dose/RBE-weighted dose region of the profiles depicted in Fig. 3, the dose/RBE-weighted dose by primary carbon ions only contributes as 81 % and 89% to the total absorbed/RBE-weighted dose respectively. The enhancement in the biological dose is due to the higher values of RBE of carbon ions compared to fragments at these depths.

5 Conclusion

Among the manifold applications of the FLUKA MC code for hadrontherapy, in this work we have presented a first contribution towards the goal of making a MC validation tool of analytical carbon ion beam treatment planning. In particular, it has been described a methodology for establishing CT-based calculations of absorbed/RBE-weighted dose. Reasonably good agreement has been observed with the calculations of the TRiP98 TPS for a clinical case treated at GSI. Differences between MC and TPS were mainly observed in those situations more sensitive to the well known limitations of pencil beam calculations, such as the handling of nuclear interactions as well as the beam transport in large tissue heterogeneities.

Acknowledgments

We would like to thank Michael Krämer for the usage of TRiP98.

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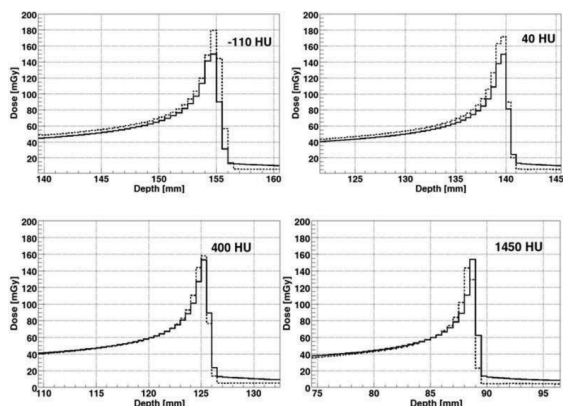


Figure 1 Comparison between TRiP98 (solid line) and FLUKA (dashed line) results for 270 MeV/u carbon ion pristine Bragg peaks calculated in phantoms corresponding to the indicated HU value. Both TRiP98 and FLUKA results are normalized using the same number of primary carbon ions

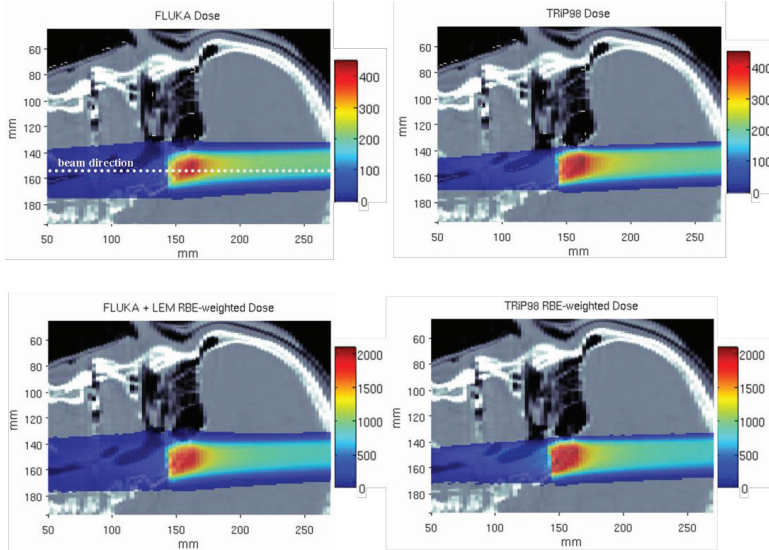


Figure 2 2D MC calculated dose (top-left panel) and RBE-weighted dose (bottom-left panel) distributions (color wash) in comparison to the planned treatment (top-right panel: dose; bottom-right panel: RBE-weighted dose) and overlaid to the gray-scale planning CT for a clivus chordoma patient treated at GSI with carbon ion beams. The carbon ion beam enters the patient from the right side of the figure. The color-bars display dose/RBE-weighted dose values in mGy/mGyE. The dotted line in the top-left panel depicts the position where the profiles shown in figure 3 are sampled.

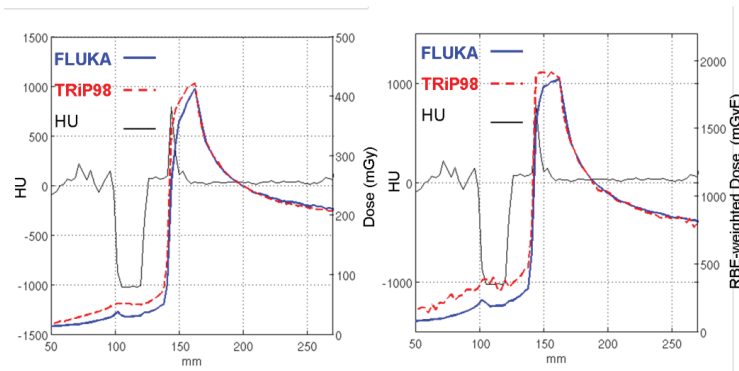


Figure 3 Comparison between MC (thick solid line) and TRIP98 (thick dashed line) calculated absorbed depth-dose (left panel) and RBE-weighted dose (right panel). The depth-dose profiles are sampled along the line depicted in upper-left panel of figure 2. The thin solid line represents the HU profile.