Automated dose verification software for proton therapy plans using Geant4/TOPAS

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Abstract

Due to the PB algorithm's limited accuracy, a higher accuracy dose verification tool is a legal requirement for proton therapy. Therefore, we developed an automated treatment plan dose verification framework based on the Monte-Carlo (MC) algorithm. The MC beam model was derived from commissioning data. CT and treatment plan from TPS were input and fed into our automated. The developed tool was validated and compared with the PB algorithm of Pinnacle3 TPS for 85 prostate patients. The difference between the PB dose and the MC dose of our automated tool was evaluated using gamma analysis (3 mm/3%, and 2mm/2% criteria) and mean absolute errors. Although the result shows good agreement and the passing rate was about 96.7%, the difference of all the indices was found to increase as the degree of tissue heterogeneity increased. The MC dose has a higher MAE in CTV, and femoral head compared to the PB dose. The automated software can facilitate patient plan verification in institutions and be useful for other clinical applications.

Introduction

Due to its Bragg peak characteristic, proton radiotherapy has increased clinical use in the last decade. It has more homogeneous, conformal, and normal sparing than conventional radiotherapy. The actual dose distribution may differ from the planned dose because of the existence of uncertainties such as dose calculation uncertainties, anatomy changes, and so on[1]. Therefore, providing accurate dose calculation tools is essential for treatment planning and plan quality assurance.

Due to its high computation speed, the pencil beam (PB) analytic algorithm is widely used in commercial treatment planning systems (TPS). It uses the water-equivalent thickness longitudinally and assumes that the material on the central axis is laterally homogeneous[2]. Particularly in inhomogeneous tissues, the approximation of multiple Coulomb and nuclear reactions in the PB algorithm leads to dose discrepancy and range uncertainties[3]. The Monte-Carlo methods, regarded as the gold standard for dose calculation in radiotherapy, simulate physics interactions by many random sampling cross-sectional interactions[4]. Thus, developing the MC dose recalculation tool for post-planning dose verification is necessary for hospitals.

This study aims to build an automated MC dose re-calculation framework for proton therapy treatment plans. Additionally, we compared it with the PB algorithm in prostate cancers. The dose discrepancy was evaluated using the gamma analysis method (3mm/3% and 2mm/2%). The mean error between the MC dose and PB dose also was calculated to evaluate the dose discrepancy.

Method and Material

An automated MC re-calculation framework was developed for dose checking of treatment plans. Figure 1 shows the workflow of the proposed tool. The Geant4-based TOPAS toolkit was used in our study[5]. The default physics list contains G4EMStandardPhysics_option4, HadronPhysics-QGSP_BIC_HIP, G4DecayPhysics, G4IonBinaryCascade Physics, G4HadronElasticPhyscisHP, and G4Stopping Physics. The IMPT plans were optimized in the Pinnacle3 TPS, v15.0 (Philips Healthcare, Fitchburg, WI, USA) and calculated by the PB algorithm. The DICOM data (CT, RS, and RN) were exported from TPS and then fed into our tool. After the simulation, the dose calculated by the MC tool was compared with that of the PB algorithm.

2.1 Beam modeling

The beam data library (BDL), which contains beam parameters for various energies, is implemented in TOPAS as a look-up table. These parameters must be tuned to align the Monte-Carlo simulation with experimental measurement. The BDL includes three sections: energy spread, phase space, and the number of protons per MU.
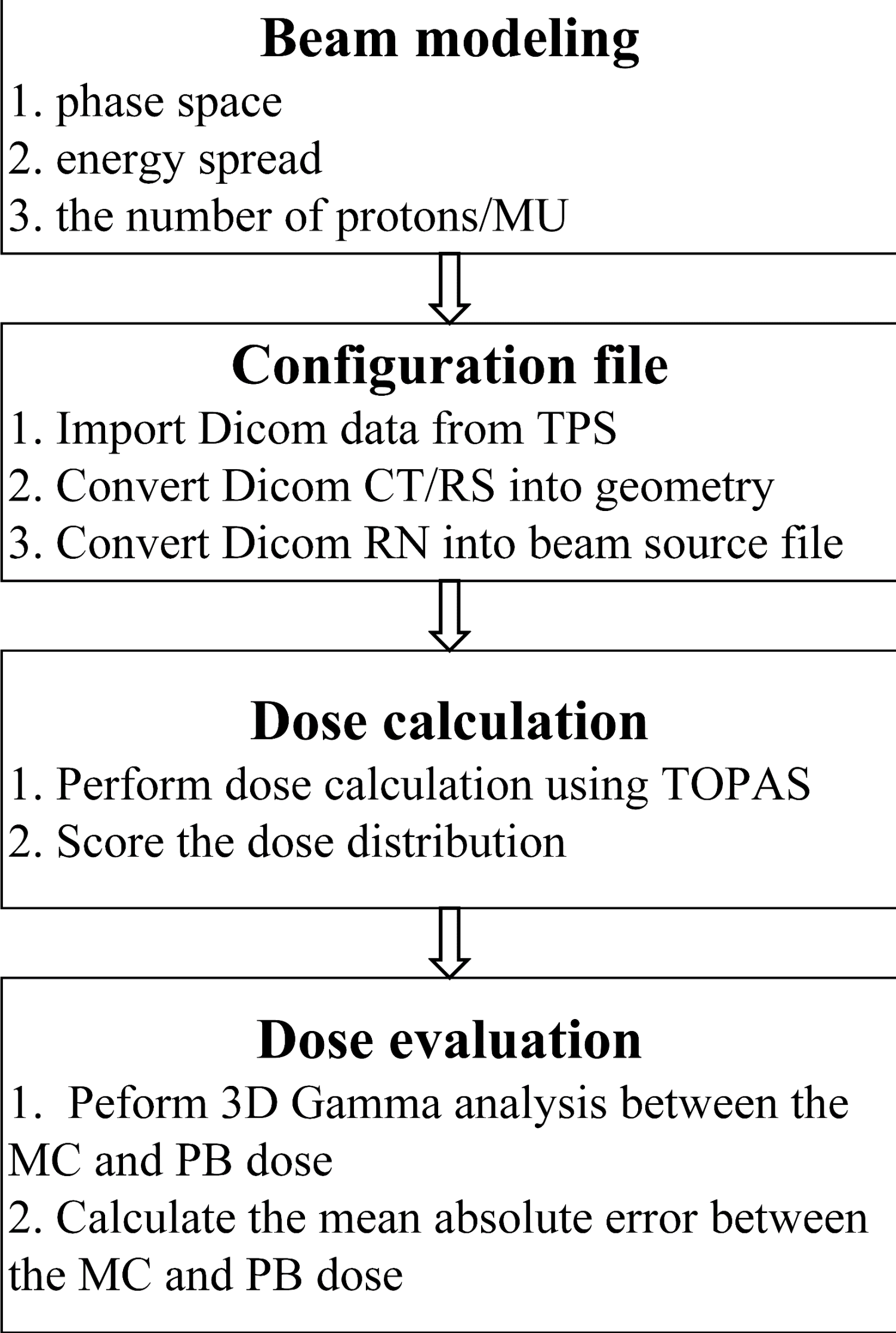
Beam modeling
1. phase space
2. energy spread
3. the number of protons/MU

Configuration file
1. Import Dicom data from TPS
2. Convert Dicom CT/RS into geometry
3. Convert Dicom RN into beam source file

Dose calculation
1. Perform dose calculation using TOPAS
2. Score the dose distribution

Dose evaluation
1. Peform 3D Gamma analysis between the MC and PB dose
2. Calculate the mean absolute error between the MC and PB dose

Figure 1: The workflow of our automated Monte-Carlo dose calculation tool.

2.2 Patient data

In our study, 85 cases of prostate cancer were used. An institutional review board-approved protocol for retrospective data collecting included all patients. The beam angle was set at 90° and 270°, and all of the patient's plans were optimized using the multi-field optimization technique. The planning target volume (PTV), clinical target volume (CTV), bladder, rectum, left femoral head, and the right femoral head was contoured by radiation oncologists.

2.3 Dose evaluation

The 3D dose distribution calculated by the MC algorithm was compared to that of the PB algorithm. The difference was assessed using the mean absolute error between the PB dose and the MC dose. The 3D gamma index analysis (using 3%/3 mm and 2%/2mm criteria) was also used to evaluate the difference.

Result

Figure 2 shows the PB dose and MC dose distribution as well as their difference map, and DVH plots. While their DVH and dose distribution were comparable, there was a dose discrepancy in the high dose-gradient region. Additionally, the CTV, Bladder, and femoral head of the DVH in the Monte-Carlo method changed significantly from those in the PB algorithm.

The MAE between the MC dose and the PB dose was calculated and presented in Table 1. The MC dose had a higher MAE in CTV, and femoral head compared to the rectum and bladder. This also demonstrated that the PB dose has more calculation uncertainties in the complex tissue. Table 2 shows the gamma analysis result between the MC dose and the PB dose. Among the 85 prostate patients, the average gamma passing rate (2mm/2% criteria) was about 96.7%.

Table 1: The mean absolute error relative to the maximum dose value between the MC dose and PB dose in CTV and OARs .

	CTV	Bladder	Rectum	Left femoral head	Right femoral head
MAE	3.74% ±1.21%	1.01% ±0.66%	0.84% ±0.36%	1.38% ±0.26%	1.31% ±0.32%

Table 2: The gamma passing rate (3mm/3% and 2mm/2%) between the MC dose and PB dose, shown as mean ± standard deviation.

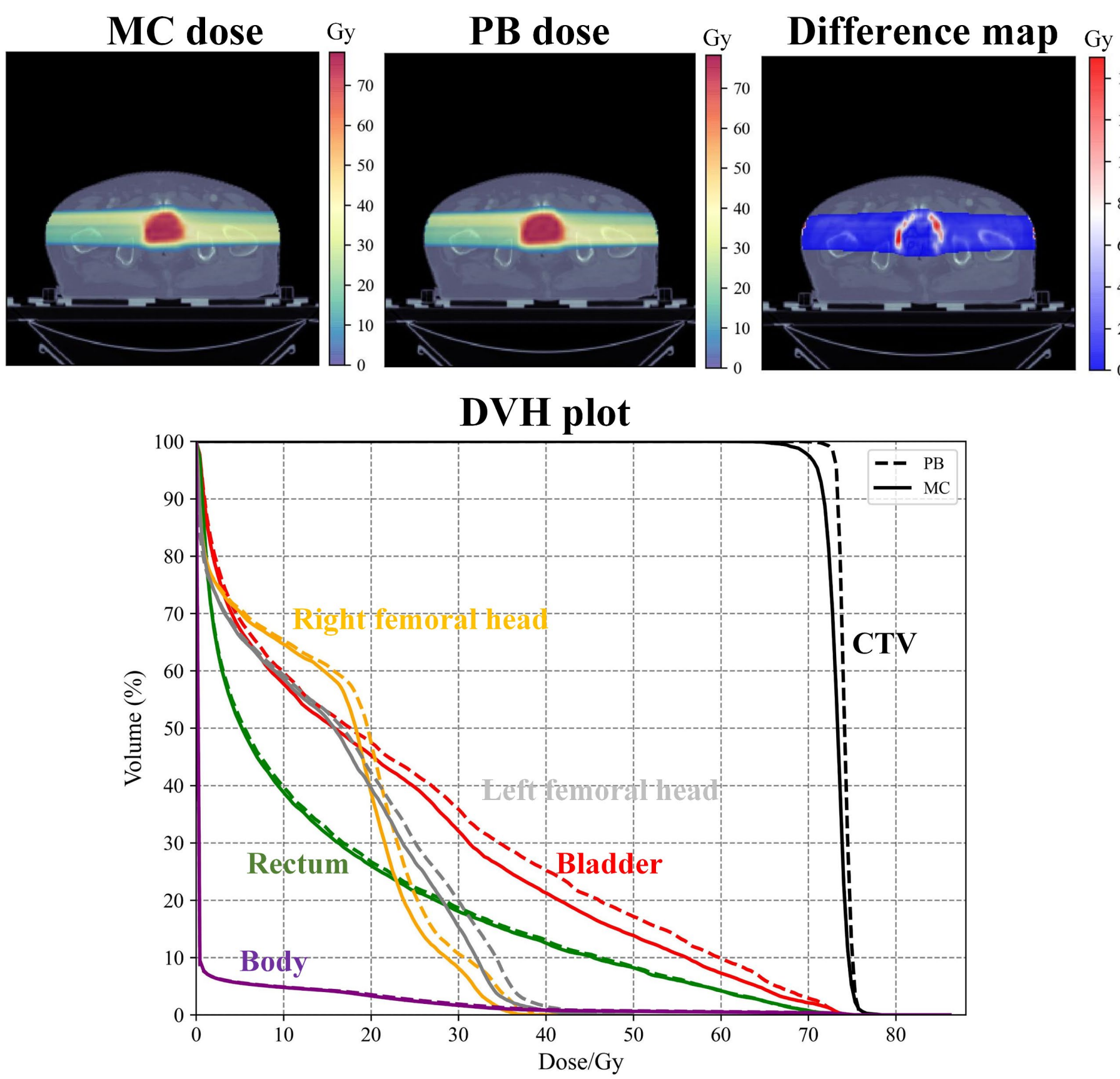|	Left femoral head	Right femoral head
Gamma passing rate	98.88%±0.92%	96.76%±1.95%

Figure 2: The dose result of the PB algorithm and MC algorithm, the dose difference map, and the DVH plot.

Discussion and Conclusion

In our study, the MC-based dose re-calculation tool was developed for dose checking in clinical. We compared the MC dose with the PB dose, showing a relatively significant difference in high-dose-gradient regions. Without an in-depth understanding of command line deployment, and function dependencies, clinical users can employ this tool and integrate it into commercial TPS. Excerpt for the physics dose, this tool also can calculate the dose-to-water, linear energy transfer, and dose deposited by another particle radiotherapy.

However, the huge calculation time is a significant problem for employing the tools in treatment plan optimization. It takes about 10 hours (compared to minutes for the analytical calculation within the TPS) to calculate a patient plan dose. Recent MC simulation studies have focused on improving MC calculation speed by simplifying the physics process and deploying parallel computing.

In summary, we developed an automated MC dose re-calculation tool. It is a crucial tool for the dose verification and quality control of treatment plans. Additionally, the automated tool can easily be implemented in other institutions and be useful for other clinical applications.

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