Fast Monte Carlo simulation on a voxelized human phantom deformed to a patient

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Purpose: A method for performing fast simulations of absorbed dose using a patient's computerized tomography (CT) scan without explicitly relying on a calibration curve is presented.

Methods: The method is based on geometrical deformations performed on a standard voxelized human phantom. This involves spatially transforming the human phantom to align it with the patient CT image. Since the chemical composition and density of each voxel are given in the phantom data, a calibration curve is not used in the proposed method. For this study, the Monte Carlo (MC) code PENELOPE has been used as the simulation of reference. The results obtained with PENELOPE simulations are compared to those obtained with PENFAST and with the collapsed cone convolution algorithm implemented in a commercial treatment planning system.

Results: The comparisons of the absorbed doses calculated with the different algorithms on two patient CTs and the corresponding deformed phantoms show a maximum distance to agreement of 2 mm, and in general, the obtained absorbed dose distributions are compatible within the reached statistical uncertainty. The validity of the deformation method for a broad range of patients is shown using MC simulations in random density phantoms. A PENFAST simulation of a 6 MV photon beam impinging on a patient CT reaches 2% statistical uncertainty in the absorbed dose, in a 0.1 cm³ voxel along the central axis, in 10 min running on a single core of a 2.8 GHz CPU.

Conclusions: The proposed method of the absorbed dose calculation in a deformed voxelized phantom allows for dosimetric studies in the geometry of a patient CT scan. This is due to the fact that the chemical composition and material density of the phantom are known. Furthermore, simulation using the phantom geometry can provide dosimetric information for each organ. The method can be used for quality assurance procedures. In relation to PENFAST, it is shown that a purely condensed-history algorithm (class I) can be used for absorbed dose estimation in patient CTs. © 2009 American Association of Physicists in Medicine. [DOI: 10.1118/1.3245877]

Key words: Monte Carlo, PENELOPE, collapsed cone convolution, phantom image registration

I. INTRODUCTION

The Monte Carlo (MC) method is increasingly used in the clinical context for radiotherapy applications.^{1,2} A common source of type B uncertainties (those of nonstatistical origin) in MC simulations of the absorbed dose in patient computerized tomography (CT) scans is the conversion from Hounsfield units (HU) to medium composition and mass density data. The CT scan of the patient must be introduced into the MC simulation in order to estimate the absorbed dose in each voxel. However, general-purpose radiation transport MC codes cannot deal with HU, the units in which CT scans are expressed. The chemical composition and the material density are the required data from each voxel for a MC simulation. Therefore, a conversion process from HU to pairs of values that indicate the mass density and medium composition is required prior to the simulation itself. For this conversion, the calibration curve of the CT scanner is normally

used. However, external information must be entered into the conversion process since two quantities (density and medium) are inferred out of a single quantity (HU) for each voxel. Several approaches have been devised for such conversion,³ but all of them depend on the calibration phantom used. Calibration phantoms are made of tissue equivalent materials and the calibration curve obtained with them would not be the same if biological tissues were employed.⁴

In this article, a method that does not explicitly rely on a calibration curve for performing MC estimations of the absorbed dose in a patient CT scan is proposed. It is based on simulations run on a voxelized human phantom⁵ that has been deformed to match a given patient CT image. In that way, the chemical composition and density of each voxel depend on the definition of the phantom. Moreover, this phantom does not have the problem of the anthropomorphic ones, which do not align the patient's geometry.^{6,7} This

method allows for dosimetric studies of the absorbed dose in a geometry that registers the morphological characteristics of the patient. Also, if it is required to know the absorbed dose in an organ not included in the CT scan of a patient that has been already treated, it is possible to deform the original anthropomorphic phantom using the patient's CT scan and other anatomical information on the patient (weight, height, and perimeter at different heights) in order to obtain an approximate CT scan of the patient that includes the organ of interest not originally scanned. With this CT, an approximate calculation of the absorbed dose in the organ of interest at the time of treatment can be done, and it can be evaluated if the applied treatment could have been the origin of a second cancer.

Both the original patient CT scans and the deformed phantoms have been used for calculating the absorbed dose in two patients (pelvic and thoracic regions) from a 6 MV photon beam. The dose calculation codes used for this task were PENELOPE,⁸ PENFAST (Ref. 9) (a fast MC algorithm), and the collapsed cone convolution (CCC) algorithm implemented in the commercial treatment planning system (TPS) ADAC Pinnacle.¹⁰ The latter was applied only to the pelvic region and was used to test the method in a clinical setting carried out at the Oncology Center Grupo IMO.

The MC programs applied to the different CT geometries under consideration are briefly described in Sec. II. Section III describes the CT geometries studied and the processing carried out for modifying the geometrical characteristics of the voxelized human phantom. Comparisons of the results obtained with each simulation are given in Sec. IV. Conclusions are drawn in Sec. V.

II. MC CODES USED FOR THE SIMULATION OF THE LINAC AND THE ESTIMATION OF THE ABSORBED DOSE IN CT GEOMETRIES

In order to estimate the absorbed dose in a CT geometry using a MC algorithm, the clinical linear accelerator (linac) that will be used during the treatment must be modeled. For this study, a 6 MV beam of a Varian Clinac 2100 C/D has been used. The simulation of the linac head has been done using the PENELOPE code with the main program PENMAIN. The geometry of the linac and the configuration files for PENMAIN have been generated with AUTOLINAC (Automatic linac Constructor).¹¹ AUTOLINAC is a FORTRAN program that generates geometry and configuration files of linacs to be simulated with PENELOPE. The code does not require the user to know the geometrical details and the most adequate variance-reduction techniques for a particular simulation. A library of preprogramed parts of linacs with movable accessories, such as multileaf collimators, electron applicators, and wedges, is coded inside AUTOLINAC together with a set of adaptive variance-reduction techniques.

Several lateral and depth dose profiles were experimentally measured with the linac under consideration. These profiles were used to tune in the energy of the primary electron source. A monoenergetic point primary electron source has been used in the simulation of the linac. Compatible results

below the 2% (2σ level) statistical uncertainty have been obtained between the simulated profiles and the experimental ones.

The simulations related to the CT geometries under consideration have used a $20 \times 5 \text{ cm}^2$ field size. With a PENELOPE simulation, a phase-space file (PSF) produced by 4×10^6 primary showers was created at 65.4 cm from the target, containing 13×10^6 particles. In producing this PSF, rotational splitting with a splitting factor of 15 was applied.¹¹ Rotational splitting is a variance-reduction technique in all aspects equivalent to azimuthal particle redistribution,¹² except for the sampling of the azimuthal angle, which is constant. Also, interaction forcing [as it is coded in PENELOPE (Ref. 8)] was applied in the simulation of the target and primary collimator. The tallied PSF produced an absorbed dose map in a water phantom that showed 2% statistical uncertainty (2σ level) in the directly irradiated area at 5 cm depth. With subsequent simulations, the PSF has been transported into different CT geometries using two different MC FORTRAN programs, namely, PENELOPE (linked to PENCT) and PENFAST.

On the one hand, PENCT is a main program that does conventional MC calculation of dose distributions in CT structures using the general-purpose code PENELOPE. PENELOPE implements accurate physical interaction models (limited only by the required generality) and a robust tracking algorithm for electrons and positrons.^{13,14} PENCT takes advantage of the geometrical simplicity of the CT structure and allows the use of variance-reduction methods (particle splitting and interaction forcing) without altering the physics and tracking algorithms of PENELOPE. Since PENCT is just a main program of PENELOPE, it allows for all the materials present in the PENELOPE database and new materials can be created provided either the chemical composition or the stoichiometric formula is known.

On the other hand, PENFAST (Ref. 9) simulates coupled transport of photons, electrons, and positrons in voxelized geometries. This algorithm is based on the same physical interaction models used in the general-purpose code PENELOPE, but it implements a different transport mechanics for electrons and positrons. PENFAST differs from other fast MC algorithms in the sense that it consistently uses complete-grouping condensed, also known as class I in the terminology of Berger, simulation¹⁵ for electron and positron transport. In class I simulation, the collective effect of all interactions undergone by a transported electron along a given path length is simulated, in an approximate manner, with a single computational step. The use of class I simulation for absorbed dose estimation in radiotherapy has been hindered by the inability of multiple-scattering theories to accurately account for energy straggling effects. PENFAST avoids this problem by using multiple-scattering distributions generated with PENELOPE. This procedure frees this class I algorithm from one of the major limitations of conventional multiple scattering theories. Another important limitation of class I algorithms is that the multiple-scattering distributions correspond to fixed path lengths in an unlimited medium; therefore, they are not applicable when the trans-

FIG. 1. Lateral profiles of the absorbed dose along the central x axis at a depth of 10 cm using a monochromatic photon 1 MeV point source. PENELOPE simulation in soft tissue phantom shown with squares. PENFAST simulation in water phantom shown with diamonds. Uncertainty bars (3σ) are not shown since they are smaller than symbol size.

ported electron (positron) gets closer than the fixed path length to an interface. To circumvent this problem, approximate scaling rules are used in PENFAST. They modify the residual path length and the effective stopping power according to the local material composition and density. PENFAST uses a simplified photon transport model adapted to CT geometries, which introduces an artificial interaction mechanism, the delta scattering,¹⁶ with a mean free path that changes from voxel to voxel so to obtain a constant total mean free path across the whole CT. PENFAST uses the same total photon cross sections as PENELOPE but employs simplified differential cross sections for Compton scattering and pair production. This is discussed in more detail in Ref. 9. PENFAST has in its database energy loss and angular distributions for water, air, compact bone [ICRU (Ref. 17)], lung [ICRP (Ref. 18)], lead (for collimating inserts), and titanium (for prostheses). Additionally, it gives the possibility of generating new materials for the database. The gain in efficiency and simulation speed with respect to PENELOPE is about a factor of 5 for both electron and photon beams.

In order to test the accuracy of the PENFAST simulation of water respect to simulating soft tissue with PENELOPE, two simulations of a monochromatic point source of 1 MeV photons impinging on the surface of a $20 \times 20 \times 20 \text{ cm}^3$ voxelized homogeneous phantom (voxel size of $0.2 \times 0.2 \times 0.2 \text{ cm}^3$) were run. In one case, the simulation was run using PENELOPE and the phantom was filled with soft tissue to reproduce the conditions of the radiation transport inside the body of the patient. In the other case, the code used was PENFAST and the phantom was filled with water, reproducing the conditions of the simulation inside the soft tissue regions of the patient with the approximations assumed by PENFAST. Both phantoms were homogeneous with a density of 1 g/cm^3 . Figure 1 shows the lateral profiles of the absorbed dose along the central x axis at a depth of 10 cm for both simulations. In order to appreciate the tail of the penumbra, the absorbed doses have been plotted in loga-

rithmic scale. Both profiles coincide even five orders of magnitude below the maximum dose.

III. DESCRIPTION OF THE VOXELIZED GEOMETRY FILES FOR PENELOPE AND PENFAST SIMULATIONS

Two CT scans centered on the pelvic and thoracic regions of male patients have been used for this study. The original images have dimensions equal to $47.974 \times 47.974 \times 30.800$ and $47.974 \times 47.974 \times 25.200 \text{ cm}^3$; they are formed by $512 \times 512 \times 44$ and $512 \times 512 \times 36$ voxels, respectively, for the pelvic and thoracic CT scans, yielding a voxel size equal to $0.0937 \times 0.0937 \times 0.700 \text{ cm}^3$. MC simulations have been performed on reduced $128 \times 128 \times 44$ and $128 \times 128 \times 36$ grids, although one simulation was run for benchmarking purposes on the $512 \times 512 \times 44$ grid of the pelvis. For the reduced grids, voxels have been grouped in the original CT scans by means of downsampling each slice from 512×512 to 128×128 voxels. This was done by picking 1 HU out of every 2^2 pixels from the original 512×512 CT data, yielding a piecewise-constant interpolant based on the nearest neighbor.

A cubic spline interpolation has been applied to the calibration data of the CT scanners that were used for obtaining the images of the considered patients. The obtained calibration curves were used for assigning a mass density and a medium composition to each HU present in the original CT scans of the patients. Throughout this article the medium composition and the mass density of each voxel will be referred to as “medium-density pairs.”

Since PENELOPE and PENFAST have different material databases, the conversion from HU to medium composition depends on the code to be used. The mass density assignment is the same for both codes. The simulations on the patient CT done with PENELOPE use the following materials: Water, skin (ICRP), adipose tissue (ICRP), soft tissue (ICRP), striated muscle (ICRU), testes (ICRP), air, brain (ICRP) (used for medulla in bones), compact bone (ICRU), and lung (ICRP).^{17,18} On the other hand, simulations on the patient CT run with PENFAST use only water, compact bone, air, and lung. Constrained to the region of the patient scanned, any medium which is neither bone, air, nor lung, is considered to be water in PENFAST. The density map of the patient is the same, independent of the MC code used for the simulation.

The voxelized male adult phantom used in this study has been the one prepared by Kramer *et al.* called MAX.⁵ The original MAX phantom contains $158 \times 74 \times 487$ voxels representing the whole body, each one with size equal to $0.36 \times 0.36 \times 0.36 \text{ cm}^3$. The portions of the original MAX phantom corresponding to the pelvic and thoracic regions have been geometrically aligned to the two patient geometries considered. This deformation process is driven by the constrained optical flow formulation for image registration¹⁹ combined with a spatially adaptive model. In addition to the intensity constraint, our method introduces spatial constraints based on Gaussian probability distribution functions of the

FIG. 2. CT scan images and deformation process of the MAX phantom. The left column corresponds to the pelvic case, while the right column corresponds to the thoracic case. [(a) and (b)] Central slices of the patient CT images at 512×512 grid size. [(c) and (d)] Original MAX-phantom images at 158×74 grid size, which correspond to the same slice than the patient CTs (a) and (b). [(e) and (f)] Processed images (dMAX phantoms), 128×128 , obtained after the geometrical deformation was applied to the MAX phantom in the pelvic and thoracic regions.

elements in the deformation field. This constraint makes the method suitable to deform the MAX-phantom toward the patient CT, while preserving the topology of the image data and dealing with large deformations. The deformation method is independent of the anatomical site. However, the accuracy and the computational cost are dependent on the shape similarities between the MAX phantom and the patient CT. In this article, the registered MAX phantoms or deformed phantoms are referred to as “dMAX phantoms.”

In order to study the effect on the absorbed dose not including an anatomical structure, the femur heads of the pelvic case were not included in the corresponding dMAX phantom. In contrast, the dMAX phantom corresponding to the thoracic case was fully registered. To study the influence of the accuracy of the registration of the MAX phantom on the patient CT image, the registration process was prematurely halted before the full number of iterations was completed. The deformed MAX phantom obtained in this case was termed the “ill-deformed dMAX phantom.”

CT images of dMAX phantoms have been produced at resolutions of $512 \times 512 \times 44$ and $128 \times 128 \times 44$ in order to approach the pelvic patient CT region and at resolutions of $512 \times 512 \times 36$ and $128 \times 128 \times 36$ in order to approach the thoracic patient CT region. Figure 2 shows the results of the registration process in which the original MAX phantom was deformed to the two considered patient CT geometries. The geometrical deformations were applied to the whole consid-

TABLE I. Materials present in the geometry of each combination of code and CTs tested. The lung material is used only in the thoracic case study.

	Patient CTs	dMAX phantoms
PENELOPE	Air	Air
	Skin	Skin
	Soft tissue	Soft tissue
	Bone	Bone
	Muscle	Muscle
	Water	Water
	Lung	Lung
	Testes	
	Brain	
PENFAST	Adipose	
	Water	Water
	Bone	Bone
	Air	Air
	Lung	Lung

ered volumes, that is, the 44 and 36 slices, consisting of 158×74 voxels each, for the pelvic and thoracic cases, respectively. In the pelvic case, only a predefined set of organs of interest was registered, namely, the bladder, the hip bones, the rectum, and the body contour. In the thoracic case, all anatomical structures were registered.

The materials used for the PENELOPE simulations of dMAX phantoms were water, skin (ICRP), soft tissue (ICRP), compact bone (ICRU), striated muscle (ICRU), air, and lung (ICRP, only for the thoracic case).^{17,18} For the simulations with PENFAST, the materials used were the same for dMAX phantoms as for the patient CTs (water, bone, air, and lung). Table I summarizes the materials used for each combination of code and CT geometry. Lung has only been used in the simulations related to the thoracic region since the pelvic CTs did not include any lung tissue.

Figure 3 shows the material maps at the central slice used for PENELOPE and PENFAST simulations. Each tone corresponds to a different material. On the first column the material maps of the pelvic case are shown, whereas the second column corresponds to the thoracic case. Figure 4 shows the density maps on the central slice for both patients (pelvic and thoracic). PENELOPE and PENFAST codes use the same density maps.

Even though in this article we only compare the absorbed dose obtained in two patient CT images to the ones obtained on the corresponding dMAX phantoms, the generality of the deformation method presented can be inferred from the following. For a given linac beam, the absorbed dose in a tissue depends on three variables: (i) The materials the beam encounters along its path, (ii) the length of the path that the beam travels along each material, and (iii) the mass density of the different voxels crossed. The material whose presence is more relevant in the MC simulation is bone, and both the patient CT image and the dMAX phantom have bone defined in the same zones (with the exception of the femur heads for the pelvic case that will be discussed later). The distances traveled by the beam inside the different materials on both,

FIG. 3. Comparison among material maps used. Only the central slices are shown. The left column corresponds to the pelvic case, while the right column corresponds to the thoracic case. [(a) and (b)] Patient CT images for PENELOPE simulations at 512×512 resolution, [(c) and (d)] patient's CT images for PENELOPE simulations at 128×128 resolution, [(e) and (f)] dMAX-phantom CT images for PENELOPE simulations at 128×128 resolution, and [(g) and (h)] dMAX-phantom CT images for PENFAST simulations at 128×128 resolution.

the patient's CTs and the dMAX phantoms, are the same in all cases since the deformations on the dMAX phantoms have been done in such a way that the volume of the registered organs and the body contours correspond to the ones of the corresponding patient's CTs. However, the density of the patient CT images differs at each voxel from the one of the corresponding dMAX phantom since the patient presents the normal density fluctuations from voxel to voxel, while the MAX phantom, and hence the dMAX phantoms, have a homogeneous density for each considered material, namely, the nominal density of each ICRU and ICRP tissue employed.^{17,18} Therefore, a study on the effect of using different densities for patient's CT scans and the dMAX phantoms is required.

Figures 5(a) and 5(b) show maps of the relative density difference, in logarithmic scale, between the two patient's CT scans and the corresponding dMAX phantoms for the

FIG. 4. Density maps used in both PENELOPE and PENFAST algorithms at 128×128 resolution. Mass densities are expressed in g/cm^3 and are shown in grayscale. (a) Patient's CT image of the pelvic region. (b) Patient's CT image of the thoracic region.

isocenter slices. It can be seen that the larger differences are obtained from the bones, the bladder (filled with water for the MC simulation), and the lung, which are smaller than 12%. For the adipose tissue, the percentage relative difference is smaller than 7%, whereas for the soft tissue and muscle, this value reduces to less than 3%. There are a few voxels located on the skin of both patient CTs in which the relative density differences between the patient CT and the dMAX phantom is a thousand times larger. These voxels correspond to the body contour. The fact that the density of air is about thousand times smaller than that of the skin and soft tissue explains this effect on some of the contour voxels. For the rest of slices, the results are the same. Figure 5(c) shows the relative difference between the thoracic patient CT and the ill-deformed dMAX phantom at the isocenter slice. The homogeneous tone areas around the heart correspond to

FIG. 5. Relative density differences, in logarithmic scale, for the isocenter slices shown in different tone scale for each voxel. (a) Differences between the patient CT and the dMAX phantom in the pelvic region. (b) Differences between the patient CT and the dMAX phantom in the thoracic region. (c) Differences between the patient CT and the ill-deformed dMAX phantom in the thoracic region. (d) Differences between dMAX phantom and ill-deformed dMAX phantom in the thoracic region. Light colored voxels in (d) correspond to a percentage relative difference of 13%, while black voxels indicate that the density in both phantoms is the same. All densities are calculated on the low resolution, 128×128 , CT images.

regions in which the registering process was incomplete due to the premature stop of the algorithm. Figure 5(d) shows the relative density difference between the dMAX phantom and the ill-deformed dMAX phantom for the thoracic case. Since both phantoms are based on the MAX phantom, which exhibits homogeneous densities in its anatomical structures, only two tones appear on the plot. The light region corresponds to regions where the full deformation was not captured because the registration process was prematurely halted.

The last step for statistically validating the proposed method is to evaluate the effect that variations in the mass density have on the absorbed dose. From calculations on the available density data of different tissues,^{20–23} it can be inferred that the density variation among patients is about 7% for water, 5% for bone, and 3% for muscle and soft tissue. These variations are within the maximum relative differences found between the patient CT images and the dMAX phantoms mentioned above. It is reasonable to assume that density variations in a given tissue among human beings follow a normal distribution, with mean equal to the nominal density quoted by ICRU and ICRP tables, and standard deviation equal to a half of the relative maximum difference observed in our case study (standard deviations of water, bone, and adipose tissue equal to 0.04, 0.03, and 0.02 g/cm³, respectively). With this assumption, two phantoms were prepared for each material under consideration, one having all voxels with the tissue at the nominal density, and the other one with densities chosen at random following the normal distribution just described. PENELOPE simulations were run on all phantoms using the 20×5 cm² PSF and the absorbed dose at each voxel was obtained. Relative differences in the absorbed dose between the homogeneous and the normally distributed phantoms were within 1% for each material. In Fig. 6 the isodose distributions for the bone, water, and adipose tissue phantoms are shown. Thin isodose lines correspond to simulations run on the homogeneous phantoms, while thick lines correspond to phantoms with densities following a random normal distribution. The materials chosen for the plot are the ones that presented a larger density variability between the patient CTs and the dMAX phantoms. These conclusions are not strongly dependent on the width of the normal distribution used for constructing the phantom. Pilot simulations were run using standard deviations that doubled the ones quoted, yielding the same conclusions.

IV. RESULTS OF ABSORBED DOSES OBTAINED WITH PENELOPE, PENFAST AND PINNACLE'S CCC

IV.A. Simulation efficiency of the MC codes

For measuring the effectiveness of the anatomical deformation method and the MC algorithms studied herein, the common definition of the efficiency ϵ at a voxel of reference placed 5 cm deep into the patient/dMAX-phantom body along the central axis (CAX) (Ref. 24) will be used. This definition is given by (see, for example, the PENELOPE manual⁸)

FIG. 6. Relative isodose lines (80%, 60%, 40%, and 20%) obtained with PENELOPE simulations using the 20×5 cm² PSF on 40×40×40 cm³ phantoms made of bone, water, and adipose tissue. Thin lines correspond to simulations run on homogeneous phantoms (densities of 1.85, 1, and 0.92 g/cm³ for bone, water, and adipose tissue, respectively), while thick lines correspond to phantoms with a random normal distribution of densities. In total, the figure shows isodose lines obtained from six phantoms (three different materials at two different density maps for each material).

$$\epsilon = \left(\frac{\bar{E}}{\sigma_E} \right)^2 \frac{1}{T}, \quad (1)$$

where T is the CPU time of the simulation, $\bar{E}$ is the average energy deposited to that voxel, and σ_E is the standard deviation of $\bar{E}$. Additionally, the intrinsic efficiency of the simulation, that is, the efficiency independent of the number of histories and the CPU speed, is defined as

$$\epsilon_N = \epsilon \frac{T}{N}, \quad (2)$$

where N is the number of simulated histories. It can be argued that the intrinsic efficiency is related to the amount of information delivered to the voxel of reference by particle history.

Finally, the speed s of a simulation is defined as

$$s = \frac{N}{T}. \quad (3)$$

All MC simulations in this article have been run on an iMac desktop computer with a 2.8 GHz Intel Core 2 Duo CPU (running in a single core). The codes have been compiled by the Intel Fortran Compiler 10.1 for Mac OS X, using the -fast option.

Table II shows benchmark results for the MC simulations performed on the low and high resolution CT images of the pelvic case. It can be seen that PENFAST is from five to six times more efficient than PENELOPE irrespective of the CT

TABLE II. Comparison of benchmark results obtained for MC simulations of the pelvic case considered with the low and high resolution grids. The efficiency, intrinsic efficiency, and statistical uncertainty are calculated in the reference voxel located 5 cm deep into the body of the patient and dMAX-phantom CTs along CAX. The associated percentage statistical uncertainty in the dose is given to 1σ level.

	$128 \times 128 \times 44$				$512 \times 512 \times 44$	
	PENFAST		PENELOPE		PENFAST	
	Patient	dMAX phantom	Patient	dMAX phantom	Patient	dMAX phantom
Time (min)	18.5	17.1	101.4	85.8	23.9	20.8
s ($s^{-1} \times 10^3$)	3.48	3.95	0.64	0.75	2.70	3.10
ϵ (s^{-1})	3.41	3.39	0.67	0.79	0.49	0.50
ϵ_N (10^{-3})	0.98	0.86	1.05	1.05	0.18	0.16
D (eV/g primary e^-)	0.89	0.88	0.89	0.88	0.91	0.85
Uncertainty (%)	1.63	1.70	1.57	1.57	3.78	4.02

geometry used. It must be said that the PENELOPE simulations were run with simulation parameters that attained about the maximum possible speed while keeping approximately the same accuracy. The PENELOPE transport parameters determine the average angular deflection between two consecutive hard elastic collisions (C_1), the maximum fractional energy loss between two hard elastic collisions (C_2), and the cutoff energy for hard inelastic interactions and hard bremsstrahlung emission (W_{cc} and W_{cr} , respectively).⁸ The transport parameters chosen for the PENELOPE simulations were $C_1=C_2=0.1$ and $W_{cc}=200$ keV and $W_{cr}=50$ keV. The absorption energies in all materials were set to 200 keV for electrons and positrons and 50 keV for photons. For reaching the higher efficiency of the fast MC code, PENFAST performs repetitive interaction forcing combined with delta interactions throughout the CT, thus producing particles with a smaller amount of information. The slightly smaller intrinsic efficiencies of the PENFAST simulations with respect to the PENELOPE ones are an indication of the much higher interaction forcing performed in the PENFAST simulation. The same voxel of reference (located 5 cm deep into the body of the patient along CAX) was set on all MC simulations. The absolute dose in this voxel is presented in Table II together with the relative percentage uncertainty at this voxel. All the absorbed doses obtained are compatible within the statistical uncertainty, irrespective of the code or CT used. It is worth noting that the fast MC algorithm yields statistical uncertainties smaller than 1.7% (1σ) in a voxel size equal to $0.3748 \times 0.3748 \times 0.700$ cm³ in less than 20 min using a single core of a CPU. On the other hand, PENELOPE yields the same statistical uncertainty in about 1.5 h, a time which is within quality assurance requirements. Even though the number of voxel-boundary crossings of particles increases by an order of magnitude in the high resolution CT images with respect to the low resolution ones, the PENFAST simulation speed is only reduced in 25%. Since all MC simulations use the same PSF as energy source, the variance of the simulations performed on the high resolution CT images is obviously larger. Similar simulation times are obtained for the thoracic case.

IV.B. Comparison of dose distributions

Two metrics have been used to quantitatively compare the dose distributions obtained with the MC codes and the CCC algorithm, namely, the gamma test (Γ) and the Hausdorff distance. The gamma test based on the method of Bakai *et al.*,²⁵ which is analogous to the one proposed by Low *et al.*,²⁶ was used to compare the whole 3D absorbed dose distributions. The Γ test was applied with 1% acceptance level on absorbed dose maps of the pelvic and thoracic CTs. In each gamma test the absorbed doses of the reference CT were compared up to the tenth nearest neighbor in the tested CT. The quality index $\gamma(\mathbf{r}_{a,b})$ of the Γ tests determines the pass-fail criteria when comparing the dose distribution b against a reference distribution a . If $\gamma(\mathbf{r}_{a,b}) \leq 1$, the calculation passes, otherwise it fails. $\mathbf{r}_b$ is the dose position in the CT being tested respect to the dose found in the CT of reference.

The Hausdorff distance is defined on the space of non-empty closed bounded subsets of a metric space.²⁷ It measures how far two subsets of this metric space are from each other. Let isodoses of the patient, $\mathcal{I}_{pa}$, and dMAX-phantom CT, $\mathcal{I}_{dm}$, be two nonempty subsets, the Hausdorff distance, $d_H(\mathcal{I}_{pa}, \mathcal{I}_{dm})$, is defined by

$$d_H(\mathcal{I}_{pa}, \mathcal{I}_{dm}) = \max\left\{\sup_{x \in \mathcal{I}_{pa}} \inf_{y \in \mathcal{I}_{dm}} d(x, y), \sup_{y \in \mathcal{I}_{dm}} \inf_{x \in \mathcal{I}_{pa}} d(x, y)\right\}, \quad (4)$$

where sup is the supremum, inf is the infimum, and $d(x, y)$ is the Euclidean distance between the isodose values x and y , $x \in \mathcal{I}_{pa}$ and $y \in \mathcal{I}_{dm}$.

IV.B.1. Results obtained on the pelvic case

In order to test the viability of the method in clinical routine, the pelvic dMAX phantom was adapted to the dicom format to be read by ADAC Pinnacle and simulated with the CCC algorithm included within this TPS.

The comparison between the relative dose obtained on the pelvic patient CTs and the corresponding dMAX phantoms using Pinnacle's CCC algorithm yields a maximum $\gamma_{\max}^{\text{CCC}}(\mathbf{r}_{pa, dm}) = 0.56$ (the following abbreviations have been

FIG. 7. Γ Histograms for the patient CTs and the corresponding dMAX phantoms of the pelvic region. (a) Simulations with CCC on patient CT and dMAX phantom. (b) Simulations with CCC and PENELOPE on dMAX phantom. (c) Simulations with PENELOPE and PENFAST on the patient CT. (d) Simulations with PENELOPE and PENFAST on the dMAX phantom. (e) Simulations with PENELOPE on patient CT and dMAX phantom. (f) Simulations with PENFAST on patient CT and dMAX phantom.

used in these expressions: CCC=Pinnacle's CCC, pe=PENELOPE, pf=PENFAST, pa=patient CT, dM=dMAX phantom). Regarding the MC simulations, the absolute doses obtained on the patient and dMAX-phantom CTs have been compared obtaining $\gamma_{\max}^{\text{pe}}(\mathbf{r}_{\text{pa,dM}})=0.45$ and $\gamma_{\max}^{\text{pf}}(\mathbf{r}_{\text{pa,dM}})=0.24$. In general, the quality indices obtained are much smaller than the maximum values just quoted, and 100% of the voxels passed all the Γ tests carried out on the pelvic case. The behavior of the quality indices obtained with the Γ tests performed are in agreement with the conclusions inferred from the comparison of the root mean squared differences discussed below. The two MC codes have been compared through the Γ test using the patient CT image,

obtaining $\gamma_{\max}^{\text{pa}}(\mathbf{r}_{\text{pe,pf}})=0.19$, which is the smallest maximum value found in the Γ tests. This result shows that both codes produce essentially the same results, and the small differences arise from the differences in the material composition between the PENELOPE and the PENFAST patient CTs. Figure 7 shows the histogram distribution of each Γ test considered for the pelvic case.

The Hausdorff distance was applied on the isodose lines in the coronal and axial directions along the CAX. The results for the 95%, 90%, 80%, 70%, 50%, and 35% relative isodose lines obtained on the 128×128 pelvic CTs are shown in Table III for all simulation algorithms and Table IV

TABLE III. Hausdorff distance of the dose distribution to the pelvic patient CT and the corresponding dMAX phantom for all simulation algorithms considered, PENFAST, PENELOPE, and CCC. Study applied to the low resolution, $128 \times 128 \times 44$, CTs. Statistical uncertainties are given at 2σ level and distances are expressed in centimeters.

Isodoses (%)	$\Delta\{\text{Pat}, \text{dMAX}\}$		
	PENFAST	PENELOPE	CCC
95	0.89 ± 0.05	0.79 ± 0.01	0.67 ± 0.02
90	0.75 ± 0.08	0.88 ± 0.08	0.28 ± 0.05
80	0.73 ± 0.10	0.85 ± 0.18	0.45 ± 0.21
70	0.83 ± 0.28	0.81 ± 0.28	0.35 ± 0.31
50	0.88 ± 0.29	0.89 ± 0.28	0.78 ± 0.35
35	0.91 ± 0.31	0.92 ± 0.31	0.58 ± 0.37

for MC based comparison, where $\Delta\{\text{Pat}, \text{dMAX}\}$ refers to the variation obtained between the patient CT and the dMAX phantom and ΔMC refers to the variation obtained between PENELOPE and PENFAST simulations for both the patient CT and the dMAX phantom. The Hausdorff distance calculated for the CCC simulation gives account of the differences between the patient and the dMAX-phantom CTs in the region where each isodose curve is plotted. The Hausdorff distance applied to the MC simulations gives not only a measure of the differences between both CTs but also the statistical uncertainty associated with the stochastic nature of MC methods. For this reason, all distances associated with the CCC are smaller than their MC counterparts. It can be seen that the larger differences in the pelvic case between the patient CT and the corresponding dMAX phantom are located in the region around the 50% and at the 95% isodose (near the bone areas). These areas are the ones that, in fact, show the largest differences between the patient and the dMAX-phantom CTs. Some areas were not included in the deformation process, as mentioned before, so the patient CT has a larger bone volume than the corresponding dMAX phantom. The same analysis cannot be performed on the Hausdorff distances obtained from MC simulations, since statistical uncertainties mask the differences between both CTs.

TABLE IV. Hausdorff distance of the dose distribution to the pelvic patient CT and the corresponding dMAX phantom for the MC (PENFAST and PENELOPE) based simulation algorithms considered. Study applied to the low resolution, $128 \times 128 \times 44$, CTs. Statistical uncertainties are given at 2σ level and distances are expressed in centimeters.

Isodoses (%)	ΔMC	
	Patient CT	dMAX phantom
95	0.74 ± 0.06	0.84 ± 0.06
90	0.64 ± 0.08	0.81 ± 0.08
80	0.69 ± 0.19	0.82 ± 0.19
70	0.65 ± 0.28	0.75 ± 0.28
50	0.87 ± 0.28	0.89 ± 0.29
35	0.89 ± 0.30	0.91 ± 0.31

Fig. 8. Isodoses (95%, 90%, 80%, 70%, 50%, and 35%) on the isocenter slice of the pelvic patient CT image computed on the patient CT and dMAX phantom with $128 \times 128 \times 44$ voxels. Thick lines correspond to results obtained with PENFAST, whereas thin lines correspond to results obtained with PENELOPE: (a) MC simulations on patient CT and (b) MC simulations on dMAX phantom.

The absolute absorbed doses for the whole CT volumes obtained with the MC simulations were also compared taking the root mean squared difference of the absolute dose voxel per voxel between pairs of simulations and using all voxels conforming each CT. Each of the results obtained is compared to the maximum dose of the first simulation of each pair comparison. The root mean squared difference between the PENFAST and the PENELOPE simulation on the low resolution patient CT image (pelvis) amounts to 1.3% of the maximum absolute dose in the 3D voxelized structure calculated with PENFAST. The comparisons done on the dMAX phantoms and the patient CTs yield 2.6% and 2.2% when PENELOPE and PENFAST are used, respectively, for the pelvic case. The larger percentage difference between the pelvic dMAX-phantom and the patient CTs when simulated with PENELOPE in comparison with PENFAST arises from the larger number of materials present in the PENELOPE patient CT image than in the PENFAST one. In all cases the observed differences are within acceptable clinical uncertainties.

The qualitative validations of the pelvic case are shown in Figs. 8–10. These figures show the relative isodose lines obtained with the different simulation algorithms in the isocenter slice of the patient CT and dMAX phantom. In all these plots, the relative isodose lines correspond to 95%, 90%, 80%, 70%, 50%, and 35% of the maximum dose of each case studied. The isodose lines have been superimposed on the isocenter slice of the patient CT image to illustrate the qualitative validations. The data used for plotting all MC isodose lines have been taken directly from the simulations without applying any kind of smoothing or averaging algorithm.

In Fig. 9 a comparison between the isodoses obtained on the pelvic patient CT and the corresponding dMAX phantom is done using all simulation codes: (a) PENFAST, (b) PENELOPE, and (c) CCC. In terms of the absorbed dose, simulations on the patient CT and dMAX-phantom images are equivalent. The differences observed in the 35% and 50% isodose lines are due to the number of organs used in the deformation process. A higher number of preselected organs including, for example, the femur would improve the results in the regions where organs were not deformed. Notice that the differences in the absorbed dose between the two CTs

FIG. 9. Isodoses (95%, 90%, 80%, 70%, 50%, and 35%) on the isocenter slice of the pelvic patient CT image computed on the patient CT and dMAX phantom with $128 \times 128 \times 44$ voxels in all cases except (d), where $512 \times 512 \times 44$ voxels were used. Thick lines correspond to patient CTs, whereas thin lines correspond to dMAX phantoms: (a) Simulations with PENELOPE (low-res), (b) simulations with PENELOPE, (c) simulations with CCC, and (d) simulations with PENFAST (high-res).

appear after the beam crosses the femur heads. This effect can also be noticed from the Hausdorff distance. Zankl *et al.*²⁸ also observed a similar dependence on the absorbed dose due to differences in anatomical structures when comparing several human voxelized phantoms.

The isodose lines shown in Fig. 9(d) (512×512 grid) are compatible with the ones plotted in Fig. 9(a) (128×128 grid), but with a larger statistical uncertainty because of the larger number of voxels. Both figures correspond to simulations performed with PENFAST on the patient CTs and the corresponding dMAX phantoms.

Figure 10 shows comparisons of the results obtained on the pelvic case using the MC algorithms and the CCC algorithm. Figure 10(a) shows the isodose lines obtained with PENELOPE and the CCC algorithm on the patient CT. Figure 10(b) shows the isodose lines obtained with PENFAST and the CCC algorithm on the pelvic dMAX phantom. Small differ-

FIG. 10. Isodoses (95%, 90%, 80%, 70%, 50%, and 35%) on the isocenter slice of the pelvic patient CT image computed on the patient CT and dMAX phantom with $128 \times 128 \times 44$ voxels. Thick lines correspond to simulations run with (a) PENELOPE and (b) PENFAST, whereas thin lines correspond to calculations done with the CCC algorithm. (a) Simulations on the patient CT. (b) Simulations on the corresponding dMAX phantom.

FIG. 11. Isodoses (95%, 90%, 80%, 70%, 50%, and 35%) on the isocenter slice of the thoracic patient CT image computed on the patient CT and dMAX phantom with $128 \times 128 \times 36$ voxels. (a) PENELOPE simulation on patient CT (thick line) and dMAX phantom (thin line). (b) PENFAST simulation on patient CT (thick line) and dMAX phantom (thin line). (c) PENFAST (thick line) and PENELOPE (thin line) simulations on patient CT. (d) PENFAST (thick line) and PENELOPE (thin line) simulations on the corresponding dMAX phantom.

ences in the absorbed dose calculated with MC methods and the CCC algorithm appear behind the bone areas. Back-scattering on the bone regions of the CT is slightly underestimated by the CCC algorithm since this code assumes that the medium where radiation transport occurs is water.

The build-up region, where the beam enters the body of the patient, presents discrepancies between the MC and the CCC algorithms for the pelvic case. Pinnacle's CCC algorithm produces results in the build-up regions that are in reasonable agreement with MC simulated and experimental data,²⁹ hence, the differences do not arise from the radiation transport algorithm itself, but from geometrical restrictions on the body contour imposed by Pinnacle's CCC algorithm since isodose lines are forced to be closed inside the body contour.

FIG. 12. (a) Isodoses (95%, 90%, 80%, 70%, 50%, and 35%) on the isocenter slice of the thoracic patient CT image estimated with PENELOPE simulations using the ill-deformed dMAX phantom (thick lines) and the dMAX phantom (thin lines). (b) Isodoses (95%, 80%, 70%, 50%, 35%, and 15%) on the isocenter slice of the thoracic patient CT image estimated with PENFAST simulations using a three beams configuration on the patient CT (thick lines) and the corresponding dMAX phantom (thin lines).

FIG. 13. Γ Histograms for patient CT, dMAX phantom, and ill-deformed dMAX phantom of the thoracic region: (a) Simulations with PENELOPE on patient CT and dMAX phantom. (b) Simulations with PENFAST on patient CT and dMAX phantom. (c) Simulations with PENELOPE and PENFAST on the patient CT. (d) Simulations with PENELOPE and PENFAST on the dMAX phantom. (e) Simulations with PENELOPE on dMAX phantom and ill-deformed dMAX phantom. (f) Simulations with PENFAST using the three beam configurations on the patient CT and the dMAX phantom.

IV.B.2. Results obtained on the thoracic case

Figure 11 shows the isodose lines obtained in the isocenter slice of the patient CT and dMAX phantom for the thoracic case. Also, like in the pelvic case, the $20 \times 5 \text{ cm}^2$ PSF was used. The PENELOPE and the PENFAST codes produce compatible results when they are used to estimate the absorbed dose distribution on the thoracic patient CT [Fig. 11(c)]. The same happens when these two codes are used to calculate the absorbed dose distribution on the thoracic dMAX phantom [Fig. 11(d)]. Figure 11(a) shows the isodose

lines obtained with PENELOPE simulations run using the thoracic patient CT and the corresponding dMAX phantom. A maximum distance to agreement of 2 mm is observed inside the body contour. The same maximum distance to agreement is observed when the dose distributions of the patient CT and the dMAX phantom are estimated with PENFAST [Fig. 11(b)]. These discrepancies on the absorbed dose arise from the different lung densities present in the thoracic patient CT and the corresponding dMAX phantom. Although using the dMAX phantom introduces these discrepancies in the ab-

TABLE V. Hausdorff distance of the dose distributions applied to the thoracic case. $\Delta\{\text{Pat}, \text{dMAX}\}$ refers to the comparison between patient CT and the corresponding dMAX phantom. ΔMC refers to the comparison between the MC codes PENFAST and PENELOPE. Studies applied to the low resolution, $128 \times 128 \times 36$, CT images. Statistical uncertainties are given at 2σ level and distances in centimeters.

Isodoses (%)	Pat ΔMC	PENFAST $\Delta\{\text{Pat}, \text{dMAX}\}$	dMAX ΔMC	PENELOPE $\Delta\{\text{Pat}, \text{dMAX}\}$
95	0.71 ± 0.06	0.72 ± 0.02	0.41 ± 0.09	0.89 ± 0.08
90	0.36 ± 0.07	0.63 ± 0.07	0.40 ± 0.09	0.63 ± 0.08
80	0.80 ± 0.07	0.85 ± 0.08	0.33 ± 0.09	0.87 ± 0.08
70	0.60 ± 0.08	0.93 ± 0.07	0.48 ± 0.09	0.95 ± 0.09
50	0.91 ± 0.10	0.99 ± 0.08	0.64 ± 0.09	0.94 ± 0.09
35	1.10 ± 0.13	1.26 ± 0.11	0.84 ± 0.13	1.07 ± 0.12

sorbed dose, it must be taken into account that the dose distribution obtained on the patient CT presents larger uncertainties respect to the actual radiotherapy treatment since the lung tissue has large density variations during the radiotherapy treatment due to the breathing cycle of the patient.

Figure 12(a) shows the isodose lines obtained from PENELOPE simulations on the thoracic dMAX phantom and the ill-deformed dMAX phantom. There are noticeable discrepancies between the two calculations, in particular, around the heart where the ill-deformed dMAX phantom did not converge. The maximum distance to agreement between isodoses lines is 7 mm.

Finally, the applicability of the method has been tested using several fields. For doing so, the PSF was rotated 90° around CAX and was later used in three positions: The original position perpendicular to CAX, 60° to the left side of the patient, and 60° to the right of the patient (following the arc defined by the gantry movement). At each position, one-third of the particles contained in the PSF was transported into the CT geometry using PENFAST. As it is expected, using several angles of incidence for the PSF reduces the differences between the absorbed dose distributions estimated using the patient CT or the corresponding dMAX phantom. All isodose lines above 35% relative uncertainty estimated with both CTs are compatible within the uncertainty, and only the 15% isodose line shows a discrepancy of 2 mm, depending on the CT geometry used.

Figure 13 shows the Γ tests applied to the thoracic case. The values obtained are $\gamma_{\text{max}}^{\text{pe}}(\mathbf{r}_{\text{pa}, \text{dM}}) = 0.17$, $\gamma_{\text{max}}^{\text{pf}}(\mathbf{r}_{\text{pa}, \text{dM}}) = 0.43$, $\gamma_{\text{max}}^{\text{pa}}(\mathbf{r}_{\text{pe}, \text{pf}}) = 0.28$, $\gamma_{\text{max}}^{\text{dM}}(\mathbf{r}_{\text{pe}, \text{pf}}) = 0.35$, and $\gamma_{\text{max}}^{\text{pe}}(\mathbf{r}_{\text{dM}, \text{ill-dM}}) = 1.8$. All simulations passed the Γ test with 100% of the voxels conforming the CTs except for the ill-deformed phantom, where most of the voxels showed a gamma index larger than 1. In that figure it is also noticed that the overall minimum gamma indices are obtained with the three beam treatment configurations.

Tables V and VI show the Hausdorff distance comparison of the thoracic study. The isodose lines estimated with PENFAST on the patient CT and the corresponding dMAX phantom shown a maximum distance of 1.26 cm at 35%. The agreement improves when the CTs are irradiated using three beams. As it is expected, the agreement on the cases that

TABLE VI. Hausdorff distance of the dose distributions applied to the thoracic case. $\Delta\{\text{Pat}, \text{dMAX}\}$ refers to the comparison between patient CT and the corresponding dMAX phantom. “ill-dMAX” refers to the ill-deformed dMAX phantom. Studies applied to the low resolution, $128 \times 128 \times 36$, CT images. Statistical uncertainties are given at 2σ level and distances are expressed in centimeters.

Isodoses (%)	PENELOPE $\Delta\{\text{Pat}, \text{ill-dMAX}\}$	PENFAST (3 beams) $\Delta\{\text{Pat}, \text{dMAX}\}$	PENELOPE $\Delta\{\text{dMAX}, \text{ill-dMAX}\}$
95	9.56 ± 0.08	0.95 ± 0.10	5.55 ± 0.07
90	9.48 ± 0.10	0.65 ± 0.08	4.67 ± 0.08
80	9.41 ± 0.09	0.73 ± 0.09	4.67 ± 0.08
70	9.36 ± 0.09	0.75 ± 0.09	4.59 ± 0.09
50	9.31 ± 0.10	0.80 ± 0.09	4.67 ± 0.09
35	8.81 ± 0.14	0.83 ± 0.12	6.00 ± 0.13

involve the ill-deformed dMAX phantom is poor.

Finally, the root mean square difference between PENFAST and PENELOPE simulations on the thoracic patient CTs amounts to 2.1% of the absolute absorbed dose. The root mean square difference of the absolute absorbed dose obtained on the thoracic patient CT and the corresponding dMAX phantom is 2.9% when both simulations are run either with PENELOPE or PENFAST.

V. CONCLUSIONS

A method for performing MC simulations of the absorbed dose in patients without explicitly depending on a calibration curve for converting HU into medium composition and mass density data has been tested. The method is based on the geometrical deformation of a standard voxelized human phantom to align a given patient CT image. The deformed phantom and the patient CT yield, in general, compatible absorbed dose distributions, within 2% (1σ) statistical uncertainty. When discrepancies appear, the distance to agreement is smaller than 2 mm. Furthermore, MC simulation on the deformed phantom is about 15%–20% more efficient than the simulation on the actual patient’s CT. The accuracy of the simulation results obtained on the deformed phantom depends on the number of anatomical structures defined in the deformation process and the fact that the phantom must be fully deformed in order to obtain reliable results. The method is general enough to allow the deformation of the voxelized phantom to register any patient CT image.

The deformed phantom method can also be used with a commercial TPS, and therefore the validity of the deformation method applied to an anthropomorphic phantom for dose calculation is not limited to MC simulations. MC results obtained with the different CT geometries and tested codes have been compared against the results obtained with the commercial TPS ADAC Pinnacle using the CCC algorithm, yielding all algorithms compatible results within the statistical uncertainty.

This article presents the first results obtained in patient CT structures with the fast MC algorithm PENFAST. PENFAST simulations are from five to six times faster than PENELOPE. A statistical uncertainty in the absorbed dose of 2% (1σ) at

5 cm depth into the body of the patient can be reached in 10 min using a 6 MV photon beam PSF and a voxel size slightly smaller than 0.1 cm^3 .

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