A fluence-convolution method to calculate radiation therapy dose distributions that incorporate random set-up error

This article has been downloaded from IOPscience. Please scroll down to see the full text article.


(http://iopscience.iop.org/0031-9155/47/19/302)

View the table of contents for this issue, or go to the journal homepage for more

Download details:
IP Address: 129.78.32.23
The article was downloaded on 10/05/2012 at 14:51

Please note that terms and conditions apply.
A fluence-convolution method to calculate radiation therapy dose distributions that incorporate random set-up error

W A Beckham¹,², P J Keall³ and J V Siebers³

¹ Department of Physics and Astronomy, University of Victoria, Victoria, BC, Canada
² Department of Medical Physics, BC Cancer Agency, Vancouver Island Centre, Victoria, BC, Canada
³ Department of Radiation Oncology, Virginia Commonwealth University, Richmond, VA, USA

E-mail: WBeckham@bccancer.bc.ca

Received 28 May 2002
Published 18 September 2002
Online at stacks.iop.org/PMB/47/3465

Abstract
The International Commission on Radiation Units and Measurements Report 62 (ICRU 1999) introduced the concept of expanding the clinical target volume (CTV) to form the planning target volume by a two-step process. The first step is adding a clinically definable internal margin, which produces an internal target volume that accounts for the size, shape and position of the CTV in relation to anatomical reference points. The second is the use of a set-up margin (SM) that incorporates the uncertainties of patient beam positioning, i.e. systematic and random set-up errors. We propose to replace the random set-up error component of the SM by explicitly incorporating the random set-up error into the dose-calculation model by convolving the incident photon beam fluence with a Gaussian set-up error kernel. This fluence-convolution method was implemented into a Monte Carlo (MC) based treatment-planning system. Also implemented for comparison purposes was a dose-matrix-convolution algorithm similar to that described by Leong (1987 Phys. Med. Biol. 32 327–34). Fluence and dose-matrix-convolution agree in homogeneous media. However, for the heterogeneous phantom calculations, discrepancies of up to 5% in the dose profiles were observed with a 0.4 cm set-up error value. Fluence-convolution mimics reality more closely, as dose perturbations at interfaces are correctly predicted (Wang et al 1999 Med. Phys. 26 2626–34, Sauer 1995 Med. Phys. 22 1685–90). Fluence-convolution effectively decouples the treatment beams from the patient, and more closely resembles the reality of particle fluence distributions for many individual beam-patient set-ups. However, dose-matrix-convolution reduces the random statistical noise in MC calculations. Fluence-convolution can easily be applied to convolution/superposition based dose-calculation algorithms.
1. Introduction

In 1999, the International Commission on Radiation Units and Measurements (ICRU) released its report on prescribing, recording and reporting photon beam therapy (ICRU 1999). In this report, a two-step process of expanding the clinical target volume (CTV) to form the planning target volume (PTV) was introduced. The initial step involves determining an internal target volume (ITV) by adding an internal margin (IM) to the CTV to account for the size, shape and position of that CTV in relation to anatomical reference points. The subsequent step surrounds the ITV with a set-up margin (SM) that explicitly incorporates beam-positioning uncertainties, namely systematic and random set-up errors.

Determination of the extent of the IM is a clinical process in which the radiation oncologist uses information on tumour extent (both macroscopic and microscopic) as well as estimates of the nature of organ motion, which is likely to occur during the delivery of a fractionated course of external beam radiation therapy, to estimate the required IM. The IM is not the focus of this paper.

SM definition, on the other hand, is physically definable and is attributable to two factors. The first factor is systematic set-up error caused by geometric errors in the imaging, treatment planning and treatment phases of patient management. The result of a systematic error is that the delivery of treatment consistently ‘misses’ the target volume. A method to reduce systematic error has been described in the literature (Bel et al 1993). The second factor influencing the SM is unavoidable random set-up uncertainty, which is caused by slight variations in patient position from day to day during the course of fractionated radiation therapy. This aspect is the focus of this paper.

Random set-up uncertainty results in three-dimensional (3D) dose distributions that are not consistent with static dose distributions produced by treatment-planning systems. The current approach relies on idealized alignment of treatment beams to a pre-treatment ‘snapshot’ of the patient (i.e. CT scans). This fact was recognised early by Leong (1987) and developed by others (Bel et al 1996, Keall et al 1999, Lujan et al 1999a, 1999b, Zavgorodni 2000), who found that the treatment planning dose distributions could incorporate the random set-up uncertainty by geometrically ‘smearing’ the static dose distribution (assuming a large number of dose fractions). Such an approach should be indicative of the dose distribution delivered during a multi-fraction treatment. The accuracy of this dose-matrix-convolution method in the homogeneous phantom case was found acceptable in a previous study (McCarter and Beckham 2000), but it was speculated in that paper that there would be some discrepancies in accuracy in the case of radiation transport through heterogeneous tissues. For such a case, it was suggested that the incident beam fluence should be decoupled from the calculation of dose spreading in tissue.

Furthermore, since the set-up error is caused by ‘uncertainties in patient positioning and alignment of the therapeutic beams’ (ICRU 1999), it seems intuitive to include this as an uncertainty between the beam and the patient, as suggested elsewhere (Keall et al 1999), rather than including it by expanding the ITV, as suggested in ICRU report 62 (1999). The idea, therefore, is to remove the step of adding a SM to the ITV. One would then calculate a blurred dose distribution and adjust field sizes to provide adequate coverage of the ITV, with e.g. a 95% isodose surface.

The aims of this study were to (a) describe and implement a fluence-convolution method that explicitly includes the set-up error between the beam and the patient, and (b) compare the results of this method with a dose-matrix-convolution method in a homogeneous and heterogeneous geometry.
2. Materials and methods

2.1. Dose-calculation model

All dose calculations were performed using Medical College of Virginia’s (MCV) implementation (Siebers et al 2000) of the EGS4 Monte Carlo (MC) code (Nelson et al 1985) with user-codes BEAM (Rogers et al 1995) and DOSXYZ (Ma et al 1995) interfaced to the Pinnacle3 (ADAC Laboratories, Milpitas CA 95035) treatment-planning system. The MC method was used, because of its capability to produce accurate dose results, particularly at tissue interfaces (Wang et al 1999, Sauer 1995). Coordinates of particles exiting the treatment head (BEAM) simulation are written to a file (termed the phase space file). This phase space file is read by the patient dose-calculation code (DOSXYZ). As explained below, for MC simulations, the positional coordinates of the particles can be modified to model repositioning uncertainty, prior to the calculation of resultant dose in tissue.

2.2. The dose-matrix-convolution method

The dose-matrix-convolution method introduced by Leong (1987) to account for random set-up error can be represented by the following equation. The treatment-planning system dose matrix, $D$, (which assumes a perfect set-up of the beam, and a stable and static patient matching pre-treatment CT images throughout a course of treatment), is convolved with the two-dimensional (2D) Gaussian random set-up error kernel $S$ to obtain $D_d(r)$, the dose at point $r$ that includes set-up error

$$D_d(r) = S \otimes D = \int S(r - r') D(r') \, dr'.$$  \hspace{1cm} (1)

In the case of a discrete dose grid, the integral becomes a summation and can be evaluated numerically.

2.3. The fluence-convolution method

Our method involves convolving the photon beam fluence for each treatment beam, $\Phi$, with a 2D Gaussian random set-up error kernel, $S$, to obtain $\Phi_f(r)$, the fluence at point $r$ that includes set-up error

$$\Phi_f(r) = S \otimes \Phi = \int S(r - r') \Phi(r') \, dr'.$$  \hspace{1cm} (2)

In practice, $S$ would normally be quantified from antero-posterior and lateral projections, so, for arbitrarily angled beams, moments of $S$ perpendicular to the beam central axis would be used. Thus, $S$ would vary with gantry angle. For MC-based dose algorithms, the fluence is re-mapped particle by particle by sampling $S$ in $x$ and $y$ (perpendicular to the beam axis), and by independently shifting each of the particle’s $x$ and $y$ position coordinates in the phase space file. The direction coordinates of the particles were not changed, but these could be included in the future to account for beam-patient rotational errors in set-up. The method assumes a multi-fraction treatment delivery, as the ensemble of particles in one fraction, for example, is correlated (ignoring intra-fraction motion), so in this single fraction case this type of resampling would be invalid. Note that the set-up uncertainty in the beam ($z$) direction was not included in the calculations presented here due to the nature of the BEAM (Rogers et al 1995) phase space file data being stored at a given plane. In principle, accounting for variations in the beam direction is possible. However, variations in the beam direction
Profile Depth = 5.0 cm

Profile Depth = 11.5 cm

Figure 1. The phantom used for the dose calculations in this study. There are two $3 \times 3 \times 3$ cm$^3$ heterogeneities placed at 10 cm depth; the dark one has a relative electron density of 0.3 g cm$^{-3}$ representing lung and the light one 1.8 g cm$^{-3}$ representing bone. The remainder of the phantom has unit density. The position of the dose profiles for figure 2 (5 cm depth) and figure 3 (11.5 cm depth) are shown.

(SSD changes) tend to average out and will therefore have very little effect on the dose distribution (McCarter and Beckham, 2000), unlike those in the $x$ and $y$ directions.

2.4. Comparison of the two techniques

A $30 \times 30 \times 30$ cm$^3$ heterogeneous phantom was devised to allow comparison of the two techniques. This phantom is shown in figure 1. There are two $3 \times 3 \times 3$ cm$^3$ heterogeneities placed at 10 cm depth, the dark one has a relative electron density of 0.3 g cm$^{-3}$ representing lung and the light one 1.8 g cm$^{-3}$ representing bone. The remainder of the phantom has unit density. Also shown in figure 1 are the lines along which dose profile data were taken. Dose profiles at 5.0 cm depth in the phantom (i.e. at a depth not affected by the heterogeneities), using both convolution methods, were compared as a benchmark where the results should be identical. Gaussian set-up values of $\sigma = 0.4$ cm and 1.0 cm for $S$ were used in the assessment. The comparison of the two methods was repeated for profiles at 11.5 cm depth, where the heterogeneous phantom effects should be maximized. All dose calculations were performed using a voxel size of $0.2 \times 0.5 \times 1.0$ cm$^3$ in the $x$, $y$ and $z$ directions, respectively. The MC calculations ran until the uncertainty in the maximum dose voxel was less than 2%. A 6 MV photon beam (100 cm SSD and field size of $12 \times 12$ cm$^2$) was used in all cases. The source corresponding phase space file consisted of $10^7$ particles and approximately $10^8$ particles from that phase space file were transported into the $30 \times 30 \times 30$ cm$^3$ phantom. Other EGS4 parameters used were ECUT & AE 700 keV with PCUT & AP 10 keV.
Fluence-convolution accounting for random set-up in radiotherapy planning

Figure 2. Dose profiles at 5.0 cm depth in the phantom shown in figure 1 for fluence-convolution and dose-matrix-convolution methods for set-up error values of (a) \( \sigma = 0.4 \) cm, and (b) \( \sigma = 1.0 \) cm.

The statistical uncertainty assessment (~2%) derived from these calculations was evaluated such that correlated events (such as recycling particles from the original phase space) were included within each sample. Thus, the uncertainty assessment included any ‘inherent’ or ‘residual’ noise from the phase space file, as well as the uncertainty arising from the statistical uncertainties of all MC calculations. In our calculations, we would expect the residual phase space noise to be very low, as the particles were recycled only ten times each, and thus the likelihood of correlated interactions in any given voxel in a 3D geometry is small.

A mathematical explanation of the difference between fluence-convolution and dose-matrix-convolution is given in the appendix.

3. Results and discussion

3.1. Calculations in homogenous media

Figure 2 shows the results of the dose profile comparison for \( \sigma = 0.4 \) and 1.0 cm set-up error values. These profiles were taken at 5.0 cm depth in a homogeneous part of the phantom shown in figure 1. It is clear that in the homogeneous case, the two methods agree to within the statistical noise of the calculation. Note that for the dose-matrix-convolution method, the effect of the statistical noise (inherent in all MC calculations) has been averaged. The dose-matrix-convolution, being a weighted sum of many voxels, blurs and spatially averages the noise (like a low-pass filter).

3.2. Calculations in heterogeneous media

Figure 3 shows the differences between the two convolution methods in the presence of inhomogeneities. These profiles were taken at 11.5 cm depth in a heterogeneous part of the phantom shown in figure 1 for \( \sigma = 0.4 \) and 1.0 cm set-up error values. In regions where the density is constant, dose-matrix-convolution profiles are similar to the fluence-convolution profiles. However, near the lung and bone boundaries, the averaging process of dose-matrix-convolution underpredicts the dose perturbation. For the cases studied, the magnitude of these
Figure 3. Dose profiles at 11.5 cm depth in the phantom shown in figure 1 for fluence-convolution and dose-matrix-convolution methods for set-up error values of (a) $\sigma = 0.4$ cm and (b) $\sigma = 1.0$ cm.

Differences increases as the set-up error increases. The maximum dose difference between the fluence-convolution method and the dose-matrix-convolution results is approximately 5% for both cases shown. Intuitively, the larger the set-up error, the larger will be the difference between the curves.

It is clear that the fluence-convolution method more closely simulates reality than dose-matrix-convolution, preserving the disequilibrium effects at density change interfaces that are blurred by dose-matrix-convolution.

3.3. Application of fluence-convolution in practical radiation oncology

Use of the fluence-convolution method requires accurate definition of the ITV and knowledge of the random set-up error associated with the particular treatment. The random set-up error, in particular, will likely vary from institution to institution and possibly even from therapist to therapist within a given institution.


Random set-up error for specific sites has been reported as variable from institution to institution, as noted in the review by Booth (Booth and Zavgorodni 1999). However, within a given institution, by applying quantitative portal imaging to established radiation therapy treatment set-up methods, 3D values of the set-up errors can be established.

Fluence-convolution is particularly applicable to breast radiotherapy and other cases where the CTV extends close to the patient surface. A normal CTV-to-PTV expansion leaves part of the PTV outside the skin (or immediately adjacent to it), and most planning systems will assign zero dose outside of the body contour. This would cause problems with the dose-matrix-convolution method in that the dose blurring of zero values into the patient near the air interface would produce an artefact. Accounting for random set-up error using fluence-convolution (and perhaps also accounting for organ motion to first order) could alleviate this problem.
4. Conclusion

A method that accounts for random set-up error between the treatment beam and the patient during fractionated radiotherapy by adding uncertainty between the beam and the patient has been described. This so-called fluence-convolution method treats the set-up error differently than the method suggested by the ICRU (1999), which recommends the expansion of the ITV. Fluence-convolution would be implemented by covering the ITV by, for example, the 95% isodose surface with a blurred dose distribution, in contrast to covering the PTV by 95% with a static dose distribution.

The idea, therefore, is to remove the step of adding an SM to the ITV. One would then calculate a blurred dose distribution and adjust field sizes to provide adequate coverage of the ITV, with e.g. a 95% isodose surface.

The fluence-convolution method has been implemented within an MC-based dose-calculation algorithm. Also implemented for comparison purposes was a dose-matrix-convolution algorithm similar to that described by Leong (1987). Fluence and dose-matrix-convolution agree in homogeneous media as expected. However, for the heterogeneous phantom calculations, discrepancies of up to 5% in the dose profiles were observed with a 0.4 cm set-up error value. Fluence-convolution mimics reality more closely, as dose perturbations at interfaces are correctly predicted. However for the MC-based algorithm, dose-matrix-convolution reduces the random statistical noise in the calculations. Fluence-convolution could easily be applied to convolution/superposition based dose-calculation algorithms.

Acknowledgments

The authors thank Devon Murphy for carefully reviewing and improving this manuscript. PJK and JVS acknowledge the financial support of NIH Grant CA 74158.

Appendix. The mathematical difference between using fluence-convolution and dose-matrix-convolution methods to account for set-up error

Superposition dose-calculation theory (Mackie et al 1985, Boyer and Mok 1986, Mohan et al 1986, Ahnesjö et al 1987) has been used in this appendix to mathematically explain the difference between fluence-convolution and dose-matrix-convolution in accounting for set-up error.

A1. Homogeneous media

In homogeneous media, the kernel used in superposition calculations is invariant, and the superposition reduces to a convolution. Thus, for the fluence-convolution method, the dose, $D_f$, is a convolution of the set-up error, $S$, with the TERMA (Ahnesjö et al 1987), $T$, followed by a convolution with the energy deposition kernel, $K$,

$$D_f = (S \otimes T) \otimes K.$$  (3)

For the dose-matrix-convolution method, the dose, $D_d$, is a convolution of the TERMA with the kernel followed by a convolution with set-up error

$$D_d = S \otimes (T \otimes K).$$  (4)

As the convolution function is distributive, for homogeneous media $D_f = D_d$ (as observed in figure 2).
A2. Heterogeneous media

In heterogeneous media, the kernel, $K$, becomes $K(\rho_{ave}^{r-r'}, r - r')$, where $r$ is the dose deposition point, $r'$ is the photon interaction site and $\rho_{ave}^{r-r'}$ is the average density between $r$ and $r'$. Thus, the fluence-convolution method can be written as

$$D_f(r) = \int_{r'} S(r' - r'') T(r'') \, dr'' \, K(\rho_{ave}^{r-r'}, r - r') \, dr'. \quad (5)$$

The dose-matrix-convolution method becomes

$$D_d(r) = \int_{r'} S(r - r'') \left( \int_{r'} T(r') K(\rho_{ave}^{r-r'}, r'' - r') \, dr' \right) \, dr''. \quad (6)$$

The difference between these two equations is that in fluence-convolution, the kernel is integrated with the TERMA before accounting for the set-up error, whereas in dose-matrix-convolution, the kernel is integrated with the TERMA before accounting for the set-up error. Therefore, for heterogeneous media $D_f \neq D_d$ (as observed in figure 3).

References

Ahnesjö A, Andreo P and Brahme A 1987 Calculation and application of point spread functions for treatment planning with high energy photon beams Acta Oncol. 26 49–56


Zelefsky M J et al 1999 Quantification and predictors of prostate position variability in 50 patients evaluated with multiple CT scans during conformal radiotherapy *Radiother. Oncol.* **50** 225–34