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The effect of dose calculation accuracy on inverse treatment planning

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Abstract
The effect of dose calculation accuracy during inverse treatment planning for intensity modulated radiotherapy (IMRT) was studied in this work. Three dose calculation methods were compared: Monte Carlo, superposition and pencil beam. These algorithms were used to calculate beamlets, which were subsequently used by a simulated annealing algorithm to determine beamlet weights which comprised the optimal solution to the objective function. Three different cases (lung, prostate and head and neck) were investigated and several different objective functions were tested for their effect on inverse treatment planning. It is shown that the use of inaccurate dose calculation introduces two errors in a treatment plan, a systematic error and a convergence error. The systematic error is present because of the inaccuracy of the dose calculation algorithm. The convergence error appears because the optimal intensity distribution for inaccurate beamlets differs from the optimal solution for the accurate beamlets. While the systematic error for superposition was found to be $\sim 1\%$ of $D_{\text{max}}$ in the tumour and slightly larger outside, the error for the pencil beam method is typically $\sim 5\%$ of $D_{\text{max}}$ and is rather insensitive to the given objectives. On the other hand, the convergence error was found to be very sensitive to the objective function, is only slightly correlated to the systematic error and should be determined for each case individually. Our results suggest that because of the large systematic and convergence errors, inverse treatment planning systems based on pencil beam algorithms alone should be upgraded either to superposition or Monte Carlo based dose calculations.

(Some figures in this article are in colour only in the electronic version)
1. Introduction

Accurate calculation of dose distributions for radiation therapy has long been a goal of medical physicists. The more advanced current dose calculation algorithms, such as the superposition/convolution method (Boyer and Mok 1985, Mackie et al 1985, Mohan et al 1986, Ahnesjö et al 1987), can accurately compute dose in most instances. However, the accuracy of currently available dose computation models for planning of radiation treatments is limited by the physics assumptions used by the models (Woo and Cunningham 1990, Metcalfe et al 1993, Keall and Hoban 1995, 1996, Yu et al 1995, Mohan 1997) and in extreme cases, even these advanced methods can result in dose errors of several per cent. Discrepancies compared to true dose distributions may be clinically significant for some cases.

Monte Carlo based dose calculations can compute dose with an accuracy that surpasses that of all of the conventional algorithms (Mohan 1997). Monte Carlo dose calculation accuracy is theoretically limited only by (i) the daily change in patient anatomy (due to patient positioning, motion, or physiological changes), (ii) the uncertainty with which patient materials can be estimated, accuracy/completeness of the source model (including the accelerator head modelling), (iii) the accuracy of the measured data used to commission the Monte Carlo dose calculation algorithm and (iv) the accuracy of the cross sections used.


Most commercial inverse treatment planning systems for intensity modulated radiation therapy (IMRT) such as Corvus (NOMOS Corporation, Sewickley, PA), Helios (Varian Medical Systems Inc, Palo Alto, CA), Plato (Nucletron Corporation, Columbia, MD), Helax-TMS (MDS Nordion, Ontario, Canada) rely on fast but approximate dose calculation algorithms such as the finite-sized pencil beam method. The systematic errors in the PB dose calculation algorithms affect not only the calculated dose distribution, but also a convergence error appears due to the optimization process. It is hypothesized that the magnitude of this convergence error will depend on both the systematic errors inherent in the dose calculation and the objective function used during the optimization process. The convergence error, which occurs because of the use of inaccurate dose calculation, is similar to the noise convergence error analysed previously (Jeraj and Keall 2000), which appears when Monte Carlo dose calculations (burdened with the statistical error) are used in inverse treatment planning.

The main aim of this paper is thus to investigate the effect of the dose calculation accuracy on inverse treatment planning and characterize both systematic and convergence errors for several different treatment scenarios.
2. Systematic and convergence errors

Let us denote a solution of inverse treatment planning (intensity distribution) with \( w_X \). This is a vector consisting of the weight (or importance or intensity) of each beamlet (or bixel). A beamlet is the dose distribution resulting from one beam element. Index \( X \) indicates that a particular solution of the inverse treatment planning is dependent on the \( X \) dose calculation method used to obtain beamlet \( B^X \). \( w_X \) is calculated by minimizing a given objective function, OF,

\[
\min_{w \in P} \text{OF}(B^X)
\]

where \( P \) represents the space of possible solutions.

The dose distribution vector is a product of the weight distribution and beamlet dose distributions. The dose distribution for \( X \) beamlets based on \( X \) dose calculation, \( d^X \), is obtained by summing up the beamlets according to the calculated solution of inverse treatment planning, so that it can be written

\[
d^X = w_X B^X.
\]

In the absence of dose calculation error, \( w_X \) and \( d^X \) would correspond to the true optimal solution to the inverse treatment planning problem. However, in the presence of dose calculation error, \( w_X \) and \( d^X \) may differ from the true optimal solution. Although attainment of error-free dose distributions is not possible, use of the most accurate dose calculation algorithm allows the best estimation of the optimal solution. The closest approximation to an error free model are Monte Carlo (MC) dose calculations, thus, this was used for the reference dose calculation. In order to evaluate the accuracy of a given dose calculation algorithm it is worth recalculating the obtained plan with the Monte Carlo beamlets and the dose distribution obtained in this way is

\[
d^{MC} = w_X B^{MC}.
\]

Because of the physics approximations in the beam model and dose calculation of individual beamlets, a systematic error in the inverse treatment plan is always present. The systematic error of an inverse treatment plan is the difference between dose distributions computed with the original (dose algorithm \( X \)) and an error-free dose calculation algorithm (presumed to be MC). Hence the systematic error of the plan can be determined by subtracting these two distributions

\[
\Delta_X^{\text{sys}} = d^X - d^{MC} = w_X (B^X - B^{MC}).
\]

The beamlets calculated with the \( X \) calculation method can be written as the sum of an accurate beamlet \( B^{MC} \) and some added systematic error \( S^X \)

\[
B^X = B^{MC} + S^X.
\]

Thus equation (4) can be simply written as

\[
\Delta_X^{\text{sys}} = w_X S^X.
\]

4 In reality there is no error-free Monte Carlo dose calculation. In any Monte Carlo treatment planning system there are errors due to inaccuracy of the physical models employed (which are very small for standard Monte Carlo codes), source model used (simplification of the source model together with the accelerator geometry uncertainties), commissioning errors etc. However, it is reasonable to expect that these errors are smaller or equal than in any conventional treatment planning system based on non-Monte Carlo dose calculation (e.g. convolution/ superposition, pencil beam). In addition, one should be aware that Monte Carlo calculations will always be burdened with some statistical error. However, Jeraj and Keall (2000) have shown that if the statistical uncertainty is small enough, the solutions can be considered to be the same as those which would be obtained with the calculations without the statistical error.
In general, $\Delta X_{\text{syst}}$ is case dependent because it depends on a particular solution of the inverse treatment plan $w_X$. The systematic error will also vary with each beamlet due to the different anatomy being traversed by each beamlet. However, unless $w_X$ varies substantially, $\Delta X_{\text{syst}}$ is approximately constant and corresponds to the weighted average error of the beams from different directions.

An additional error, called the convergence error appears as a direct consequence of the systematic error. This is due to the inverse treatment planning algorithm converging to the ‘optimal’ solution for the inaccurate beamlets, which is different from the optimal solution for the accurately calculated beamlets. In order to estimate the convergence error of a plan, one needs to know the difference between the optimized dose distribution ($d^{MC}_X$) and the optimized dose distribution if an accurate dose distribution was used during the optimization ($d^{MC}_{MC}$):

$$\Delta X_{\text{conv}} = d^{MC}_X - d^{MC}_{MC} = (w_X - w_{MC})B^{MC}.$$  (7)

Because the solution of the inverse problem is obtained through optimization, it is not possible to predict the magnitude of the convergence error in general. However, as long as the systematic error is small, the shape of the solution space (defined with the objective function) is only slightly perturbed. Therefore, one might expect that convergence error correlates to the systematic error. On the other hand, a large systematic error may significantly change the shape of the solution space, and hence it may be expected that for large systematic errors correlation between the convergence and systematic error is lost.

3. Material and methods

Three calculation methods were used for this work: Monte Carlo, superposition and pencil beam. The Monte Carlo beamlet calculations were performed using EGS4 (Nelson et al 1985) with usercodes BEAM (Rogers et al 1995) and DOSXYZ (Ma et al 1995) and the MCV interface (Siebers et al 2000) to the Pinnacle™ (ADAC Laboratories, Milpitas, CA) treatment planning system. For the plans considered in the study the combined statistical uncertainty at $D_{\text{max}}$ was less than 0.1%. Therefore, the effect of the statistical uncertainty on the results (Jeraj and Keall 2000) can be neglected. The superposition calculations were performed using Pinnacle’s collapsed cone convolution algorithm. The pencil beam calculations were adapted from Mohan and Chui (1987) and include density corrections, essentially based on the ratio of tissue air ratios (RTAR) method. They were also interfaced to the Pinnacle treatment planning system. There was no inter-normalization of the three dose calculation algorithms. However, implicit normalization of dose values at 10 cm in a water phantom was done during commissioning. The comparisons performed in this study used an extended two-dimensional geometry, where the third dimension was assumed to be invariant. This geometry was constructed by taking a single patient CT slice, and copying this slice to superior and inferior positions. This assumption does not affect the general conclusions of this work; however, the errors obtained here are slightly underestimated because of more favourable conditions (not lost electronic equilibrium in the third dimension) for the cases where considerable geometrical variations exist in all three directions.

All beamlet calculations were of size $1 \times 5$ cm$^2$ at the isocentre and using 6 MV Varian 2100 Clinac beam model. To investigate any difference between the dose calculation algorithms in water, calculations for all the three calculation methods were performed for the central axis beamlets at 100 cm SSD in water only and water/lung/water phantom. The water/lung/water phantom had a slab of lung material ($\rho = 0.25$ g cm$^{-3}$) inserted between 4 and 12 cm. Dose calculation voxel sizes in both phantoms were $0.5 \times 0.5 \times 1.0$ cm$^3$. 
For the patient geometry calculations, three treatment sites were chosen, lung, prostate and head and neck. The dose calculation voxel size for the patient geometry was $0.5 \times 0.5 \times 1.0 \text{ cm}^3$. For all the three dose calculation algorithms, $1 \times 5 \text{ cm}^2$ beamlets were calculated for each element of seven equispaced fields, with the isocentre within the tumour volume.

For the purpose of this study the MCI–Monte Carlo based inverse treatment planning algorithm (Jeraj and Keall 1999) was adapted to allow non-Monte Carlo beamlet calculations. MCI uses fast simulated annealing (Szu and Hartley 1987) for the optimization.

Several different dose-based objection functions were used in this work. One objective function is in the square form, with quadratic penalties for all tissues (henceforth referred to as quadratic (tumour)):

$$\text{OF} = \sum_T \frac{C_T}{N_T} \sum_{i \in T} (d_i - D_T)^2$$

where $C_T$ is the weight of a tissue type $T$ and $d_i$ is the dose in a voxel $i$ of type $T$. $D_T$ is the desired dose in a tissue type $T$ (required mean dose in tumour and 0 for other tissue types) and $N_T$ is the number of voxels of type $T$. In the exponential/quadratic form, $T$ represents tumour tissue and $T'$ all other tissues. Throughout this paper the normal and critical structures are penalized using square penalties. The tissue weighting factors $C_T$ were generally equal to 1, except when the critical tissue was to be spared, then $C_T$ was set to 10. Cases with different objective functions were examined because the ‘optimal dose distribution’ depends on the chosen objective function and convergence is sensitive to the shape of the objective function in the vicinity of the global minimum. In addition to the above so-called soft constraints, hard constraints were also imposed (in a form of an extremely high penalty in the objective function), where the dose in the organ was limited to remain within the prescribed dose levels. The dose in the tumour was required to be within the ICRU limits of 95–107% (ICRU 1993) and in the case of sparing, the upper dose limit was set for different critical structures (spinal cord in head and neck tumour, lung and spinal cord in lung tumour and rectum in prostate tumour).

For all the three dose calculation methods, the optimal beam weights $w_{MC}$, $w_S$ and $w_{PB}$ were determined (subscripts MC, S and PB refer to Monte Carlo, superposition and pencil beam, respectively) yielding dose distributions $d_{MC}$, $d_S$ and $d_{PB}$. These dose distributions were then also recalculated by taking the superposition and pencil beam optimized beam weights yielding $d_{MC}^S$ and $d_{PB}^P$. The above optimization process was repeated for the different objective functions. All the comparisons and evaluations of the systematic and convergence errors were done with the assumption that Monte Carlo dose calculation is the most accurate and therefore both other methods, superposition and pencil beam, were compared against it. As already mentioned the systematic error of Monte Carlo dose calculation was neglected in this study.

In order to differentiate between the convergence error due to the dose calculation algorithm used, and the convergence error of the optimizer (for example, if the optimizer found a local minimum using one algorithm and a global minimum using another dose calculation algorithm), convergence close to the global minimum is necessary. Running optimization from different starting weight vectors and comparing the final converged solutions tested this
convergence. Several possibilities were tested: initial weight vectors being 0, 1 and a random array. In addition, the optimization using beamlets calculated with a given dose calculation method was started from the solution obtained with another dose calculation method (e.g. a previously optimized plan with superposition/convolution beamlets was reoptimized for Monte Carlo beamlets). The standard deviation of the observed differences gives a measure of the convergence error of the optimization routine employed in MCI. A more thorough investigation of the optimization convergence can be found in Wu et al (2001). In addition, for some cases the temperature parameter of the simulated annealing algorithm (which defines the rate of accepting unfavourable solutions) was set to zero through the whole optimization process. In this case the simulated annealing algorithm becomes equivalent to the steepest descent method. No differences in the results were observed, except of a different convergence error of the optimizer.

4. Results

4.1. Depth dose distributions

Depth dose curves and dose profile curves for beamlets in a water phantom as calculated by Monte Carlo, superposition and pencil beam methods are shown in figure 1. These depth dose curves agree well (maximum deviation is 2%) in a water phantom for narrow beams (similarly for broad beams as well). Even though very different dose calculation methods were used, ranging from the simple pencil beam calculations to the complex Monte Carlo simulations, there is almost no difference in depth dose curves. Also the integral dose was approximately equal for all the three different dose calculation algorithms. There were some small variation of the integral dose observed for real beamlets (of the order of few %), but not as a systematic error. Figure 1 shows that the pencil beam dose calculation method has a narrower penumbra for the small field than the Monte Carlo or superposition methods. This profile difference is because the pencil beam method tries to match profiles for broad beams with electronic equilibrium on central axis, whereas the model-based Monte Carlo and superposition methods do not use this assumption.

The similarity of the three dose calculation methods seen in a water phantom disappears when the narrow beam dose distributions are compared in a water/lung/water phantom. Very notable differences can be observed in both depth dose curves and lateral profiles as shown in figure 2.

While both Monte Carlo and superposition correctly predict the decrease and lateral spread of the dose in the low density lung tissue because of the increased range of electrons, pencil beam calculations only account for the decreased photon attenuation. Note also a few per cent error behind the low density region due to the differences in accounting for photon scattering. These results are consistent with those of Arnfield et al (2000) who intercompared Monte Carlo, superposition and Batho methods.

4.2. Systematic error

The effect of the systematic error was examined for inverse treatment plans for three different sites: head and neck, lung and prostate. Graphical results will be given for the lung example, but the summary of the results will be given for all three cases and different objectives.

In figure 3 central slice isodose distributions of the lung tumour plans optimized with each of the three dose calculation methods optimized using the exponential (tumour) objective function are given. For the superposition and pencil beam based optimizations, the dose
Figure 1. 6 MV 100 cm SSD depth dose curves (top) and profiles at 10 cm depth (bottom) in water for narrow $1 \times 5$ cm$^2$ fields as calculated by Monte Carlo, superposition (collapsed cone convolution) and pencil beam dose calculation. While depth dose curves agree well, the pencil beam dose profile shows an underdose in the penumbra region.

The initial plans ($d_{MC}^{MC}$, $d_{S}^{S}$ and $d_{PB}^{PB}$) look very similar, as do the dose area histograms in figure 4. However when the dose is evaluated with an accurate calculation algorithm (MC), discrepancies are apparent. While the dose differences are not very significant for superposition, the pencil beam plan overestimates the actual dose delivered to the tumour (delivery based on the pencil beam weights would result in an underdosing of the tumour), highlighting the danger of using inaccurate dose calculation methods. Actual dose coverage of the tumour for the pencil beam plan is very poor, resulting into about 8% average underdose distributions using the optimized intensities but MC dose calculations ($d_{S}^{MC}$ and $d_{PB}^{MC}$) are given to allow observation of the systematic error.
in the tumour, which can also be seen from dose area histograms given in figures 4, 6 and table 1.

The differences between the original and recalculated dose distributions for both superposition and pencil beam plans are shown in figure 5. The histograms of the differences indicating the systematic error of the plans are given in figure 6.

The results show significant systematic errors for pencil beam calculations. This is not surprising, as the limitations of pencil beams in heterogeneous media are well known (Woo and Cunningham 1990, Metcalfe et al 1993, Keall and Hoban 1995). Since most of the commercial inverse treatment planning systems still rely on pencil beam based dose
Figure 3. Optimal (left) and recalculated (right) dose distributions for the lung tumour case: Monte Carlo \(d_{MC}^{MC}\) (upper left), superposition \(d_{S}^{S}\) (middle left), recalculated superposition \(d_{S}^{MC}\) (middle right), pencil beam \(d_{PB}^{PB}\) (lower left) and recalculated pencil beam \(d_{PB}^{MC}\) (lower right). The following isodose curves are shown: 20% (blue), 50% (green), 70% (yellow), 90% (orange) and 95% (red). The objective function used for the optimization in these cases was exponential (tumour) with sparing of the left lung.

calculations, care should be exercised to avoid the possibility of large discrepancies between the calculated and actual or achieved dose distributions. Similar errors for IMRT plans have been reported by Wang et al (1998) and Ma et al (2000) when recalculating pencil beam treatment plans (conventional and IMRT) with Monte Carlo dose calculations, but differ from those of Laub et al (2001) probably because the beam directions in their work were chosen such that the computationally problematic lung region was largely avoided.

4.3. Convergence error

The convergence error was examined for the head and neck, lung and prostate cases using the various objective functions. Graphical results will be given for the lung case only, but the summary of the results for all sites will be given for all the three cases.
Figure 4. Dose area histograms for the central slice of the lung tumour case for original dose distributions $d_{MC}$, $d_S$ and $d_{PB}$ (top) and recalculated dose distributions $d_{MC}$, $d_{MC}^S$ and $d_{MC}^PB$ (bottom). Dose area histograms of $d_{X}^{MC}$, $d_{X}^{S}$ and $d_{X}^{PB}$ are plotted with solid, dashed and dotted lines, respectively. Note significant underdose for recalculated pencil beam based optimization.

In figure 7 the convergence error is presented for both superposition and pencil beam calculation. The convergence error, which is due to the difference in the optimized intensity distributions for different types of dose calculations used in the comparison, is presented in terms of the dose distribution differences. This highlights the effect of the convergence error on the final plan. Histograms of the dose differences are shown in figure 8. In the histograms the mean difference was set to zero because the mean difference of the convergence error just compensates the mean difference of the systematic error to satisfy the required dose in the tumour. Only the relative spread (not the normalization) is important for quantification of the convergence error. Note that this is only one way of quantification of the convergence error and other measures could be used to test effectiveness of the optimization convergence.
Figure 5. Differences in dose distributions for the lung tumour case indicating the systematic error of the plan: superposition optimized—recalculated with Monte Carlo beamlets $(\Delta_{\text{sys}} = d_S - d_{\text{MC}}: \text{left})$ and pencil beam optimized—recalculated with Monte Carlo beamlets $(\Delta_{\text{sys}} = d_{\text{PB}} - d_{\text{MC}}: \text{right})$. Absolute differences in units of $D_{\text{max}}$ are given at right.

Table 1. Systematic and convergence errors for superposition and pencil beam dose calculations. The mean difference and standard deviations are given for the systematic error and the range of standard deviations for the convergence error. The ranges in the convergence error indicate the differences observed between different objective functions. (a) Errors for the lung tumour and left lung, (b) errors for the prostate tumour and rectum and (c) errors for the head and neck tumour and spinal cord.

(a) Superposition Pencil beam

<table>
<thead>
<tr>
<th>Error (%$D_{\text{max}}$)</th>
<th>Tumour</th>
<th>Lung</th>
<th>Tumour</th>
<th>Lung</th>
</tr>
</thead>
<tbody>
<tr>
<td>Systematic</td>
<td>$-0.1 \pm 2$</td>
<td>$-1 \pm 1$</td>
<td>$+8 \pm 3$</td>
<td>$+6 \pm 5$</td>
</tr>
<tr>
<td>Convergence</td>
<td>2–5</td>
<td>1–4</td>
<td>3–6</td>
<td>6–7</td>
</tr>
</tbody>
</table>

(b) Superposition Pencil beam

<table>
<thead>
<tr>
<th>Tumour</th>
<th>Rectum</th>
<th>Tumour</th>
<th>Rectum</th>
</tr>
</thead>
<tbody>
<tr>
<td>Systematic</td>
<td>$-0.3 \pm 2$</td>
<td>$-1 \pm 1$</td>
<td>$+5 \pm 1$</td>
</tr>
<tr>
<td>Convergence</td>
<td>2–5</td>
<td>2–7</td>
<td>3–6</td>
</tr>
</tbody>
</table>

(c) Superposition Pencil beam

<table>
<thead>
<tr>
<th>Tumour</th>
<th>Spinal cord</th>
<th>Tumour</th>
<th>Spinal cord</th>
</tr>
</thead>
<tbody>
<tr>
<td>Systematic</td>
<td>$-1 \pm 2$</td>
<td>$-3 \pm 1$</td>
<td>$-3 \pm 2$</td>
</tr>
<tr>
<td>Convergence</td>
<td>3–6</td>
<td>1–3</td>
<td>3–4</td>
</tr>
</tbody>
</table>
As can be seen from the results, convergence errors are larger for the pencil beam dose calculation, as one could expect, based on the larger systematic errors. However, as it will be presented later, the convergence error is only approximately proportional to the systematic error of the used dose calculation method, because it strongly depends on the objective function as well.

Based on the optimizer convergence tests the optimizer convergence error was estimated to be below 0.5% for tumour and about 1–2% for regions outside, which is much smaller
Does accuracy in inverse treatment planning 403

Figure 7. Differences in dose distributions for the lung tumour case indicating the convergence error of the plan: superposition plan—Monte Carlo plan \( \Delta_{\text{conv}}^{\text{S\_MC}} = d_{\text{S\_MC}} - d_{\text{MC}} \) \((\text{left})\) and pencil beam—Monte Carlo plan \( \Delta_{\text{conv}}^{\text{PB\_MC}} = d_{\text{MC\_PB}} - d_{\text{MC}} \) \((\text{right})\). Absolute differences in units of \( D_{\text{max}} \) are given at right.

than the observed convergence error for different types of beamlets used (compare to table 1). The values agree with the convergence error as determined in Jeraj and Keall (2000). Using a larger number of simulated annealing iterations (typically \( 10^6 \) iterations were used) would even further reduce this convergence error.

4.4. Errors for different sites

A summary of the results for all three examined tumour sites (head and neck, lung and prostate) for different types of objective functions is given in table 1. The results presented are the differences in the mean values and standard deviations for the plots of the differences as shown in figures 6 and 8. Even though three different sites were examined together with different objectives used in the optimization, the following numbers should be used only as an illustration and rough estimate of the errors one might expect. In order to draw general conclusions and provide reliable numbers a broad multicase study should be performed, not just a few specific cases considered, as in all the studies so far.

For the cases studied, the systematic error was found to be rather small for superposition dose calculation (\( \sim 1\% \) of \( D_{\text{max}} \), however, it was significant for pencil beam dose calculation (\( \sim 5\% \) of \( D_{\text{max}} \)) for the cases examined. Large systematic errors could be anticipated from the phantom studies shown previously. Even though one could argue that with appropriate normalization one could reduce large differences in the mean dose delivered, large standard deviations would remain a problem. The case dependence and the magnitude of the systematic errors suggest a warning for the treatment planning systems that rely on pencil beam dose calculations for inverse (or conventional) treatment planning. On the other hand, small differences between superposition and Monte Carlo based inverse treatment planning results
Figure 8. Histogram of the differences in dose distributions for the lung tumour case indicating the systematic error of the plan: superposition plan—Monte Carlo plan \((\Delta_{\text{conv}}^S = d_{\text{MC}}^S - d_{\text{MC}}^\text{top})\) and pencil beam—Monte Carlo plan \((\Delta_{\text{conv}}^{PB} = d_{\text{MC}}^{PB} - d_{\text{MC}}^\text{bottom})\). Only tumour and left lung histograms are shown. Absolute differences in units of \(D_{\text{max}}\) are given.

raise a question how much the Monte Carlo dose calculation is indeed needed for inverse (or conventional) treatment planning. It is also interesting to note that the systematic error is insensitive to the given objectives because of the global similarity of the plans.

Examination of the convergence errors shows that the error is approximately proportional to the systematic error of the dose calculation used. Therefore, the convergence error for superposition is generally smaller than it is for pencil beam dose calculations. However, use of different objective functions imposes a large spread in the convergence and the correlation to the systematic error is therefore rather low. Because of the uncertainty in the definition of the optimality (in terms of a given objective function), the clinical importance of the convergence
Does accuracy in inverse treatment planning error is questionable. However, from a mathematical point of view, once the objectives are defined all deviations from the global minimum solution represent an error.

5. Conclusions

The use of inaccurate dose calculation in iterative inverse treatment planning for IMRT introduces two errors in the plan. One is the systematic error, which is similar to the systematic error in the conventional treatment planning. The second is the convergence error that appears because the optimization converges to the solution optimal for the inaccurate dose calculation beamlets, which is different from the solution for the accurate dose calculation. The convergence error is similar to the noise convergence error, which appears when Monte Carlo dose calculation is used in inverse treatment planning (Jeraj and Keall 2000).

A study of three cases (head and neck, lung and prostate) with the use of several different objective functions was performed to characterize both errors. While the systematic error was found to be small for superposition (1%), it was much larger for pencil beam dose calculation (up to 8%), even though dose calculations in water were accurate to within 1%.

The convergence error is dependent on the systematic error of the dose calculation method, however, it is also very strongly dependent on the specified objectives. It was found to be smaller for superposition than the pencil beam method for the objectives studied. Because of the current uncertainty in the definitions of the optimality and the objective function, the clinical significance of the convergence error is questionable. The clinical significance of the convergence error could be reduced if the final dose calculation is performed with an accurate dose calculation. In the case that the final plan, based upon an accurate dose calculation, is judged to be still acceptable, the existence of a better plan (i.e. removal of the convergence error) is of little consequence. If, however, compromises still exist in the final plan, the existence of the convergence error could be clinically important.

As both the systematic and convergence errors were significant for the pencil beam calculations, the results suggest that vendors and users who currently use pencil beam based dose calculations for IMRT should upgrade to either superposition or Monte Carlo based dose calculation, at least for the final dose calculation to eliminate the systematic error. The same reason (lack of accuracy) that has been driving treatment planning system vendors and users to improve their dose calculation algorithms for conventional forward treatment planning, should be considered in IMRT to include better dose calculation in inverse treatment planning as well.

Comparison between importance of dose calculation accuracy and statistical uncertainty for inverse treatment planning (Jeraj and Keall 2000) shows that the systematic and convergence errors for superposition type of dose calculation are approximately equal to 2% statistical error of a Monte Carlo dose calculation. Therefore, to gain anything with the use of Monte Carlo dose calculation in inverse treatment planning, precision of the dose calculation should be below 2% for the final dose distribution, which is in agreement with Keall et al (2000) for Monte Carlo precision in conventional treatment planning. However, since there is also some systematic error in the definition of the linear accelerator geometry and/or source model used for characterizing the phase space of particles used in Monte Carlo simulations, which are typically of the order of 1–2%, superposition dose calculation in inverse treatment planning might be sufficient for the current accuracy of dosimetry protocols and geometry modelling in Monte Carlo simulations. On the other hand, the difference in speed between superposition and fast Monte Carlo dose computations is getting smaller and smaller; therefore, one might still prefer employing Monte Carlo dose calculation to avoid potential problems with the accuracy (especially in difficult cases like head and neck, metal
implants, etc), which might be even more severe when the actual beam delivery is taken into account.

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