FEASIBILITY SOLUTIONS IN RADIATION THERAPY TREATMENT PLANNING

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ABSTRACT

Radiation therapy treatment planning can be described as a two-step process which involves (1) the mapping from a physician-specified distribution of dose within a patient area to an acceptable distribution of the weights of the possible rays through the patient and (2) the clinical implementation of that mapping. At present, both steps of RTP are done by specialists on the basis of experience, judgment, and trial and error. In this paper we describe a computer technique which determines step (1) of treatment planning. We obtain the weights for all possible rays through a patient by (1) determining the relative dose contributions of each of many sample rays from different gantry positions and locations within the beam, and (2) iteratively determining the relative contributions of the sample rays with physician-desired dose contours and constraints to find an acceptable weight for every ray. This information (1) shows immediately whether a physician-specified treatment can be implemented in the clinic, (2) reduces the change of missing optimal beam positions, and (3) makes it easier to choose the positions and beam shapes of a clinically-implementable treatment plan.

INTRODUCTION

In conventional radiation therapy planning (RTP) with photon beams, the tumor and critical organs are outlined on a transverse section. The radiologist (physician) chooses a treatment dose for the tumor and specifies the maximum allowable dose to any critical organ. At this point, a dosimetrist must choose the beam directions and beam weights to accomplish the goals of the radiotherapy. In RTP, we wish to achieve (1) a uniform dose distribution across the tumor, (2) a minimum dose to critical organs, (3) a minimum dose to the normal tissues, and (3) a minimum dose to the normal tissues.

Most often the experience and judgment of the dosimetrist quickly leads to an efficient setup. Moreover, for a single transverse section, the dosimetry calculation typically takes only a few minutes, so that the calculation can be repeated for slightly different setups (trial and error) to achieve confidence that a near-optimal setup has been achieved.

There are a number of cases, however, where it present a challenge, such as tumors near the spinal or optic nerves, near a kidney, etc. The dosimetrist must then consider a large number of possible setups involving wedges, blocks, fixed and/or rotation nodes, local boosters, etc. These cases can be time consuming and unwarranted. How can one tell if there exists any feasible treatment plan which satisfies the physician's specifications? Should one accept a plan after so many tries if there is a possibility of a significantly better plan? Now does one know when one is close to an optimal plan in these complex cases?

Further, there is presently a general trend towards three-dimensional treatment planning using several (4 to 20) CT sections. However, 3D treatment planning is much more difficult because (1) the dosimetrist must visualize the 3D geometry to choose the beam orientations, (2) the computerization takes longer, thereby making trial and error more expensive, and (3) there will be many more variables in planning, thus less confidence that a calculated treatment plan is near optimal.

To avoid both the need to rely on the experience and judgment of the dosimetrist and the need of repeated re-calculations by trial and error, efforts have been made to have a computer determine the optimal treatment plan once the tumor and critical organ contours and dose limits have been specified by the physician. The computer would then specify the setup parameters (gantry angles, beam axis, etc.) and the beam weights for the ideal treatment plan. Thus for these attempts at optimal treatment planning have been confined to the 2D (single transverse section) area and even so have not been particularly efficacious. The reason for this lack of success is that when one includes all the dose parameters, the computer must explore and compare every possible setup in a multidimensional parameter space.

Besides, if the dosimetrist is to be truly omitted from the planning procedure, the calculation rapidly becomes expensive. For example, if 32 possible gantry angles (every 5 deg) are examined for 30 different beam weights and 10 different blockers or wedge orientations, we have to calculate the dose distribution for 72 x 10 x 10 x 7200 beams (say 5500 sample points per beam).

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tions 10 sec to calculate, we would need 20 hours for a 2-D calculation. Coarsest stepping is always possible, but with the risk that the optimal solution will "fall through the cracks" thus obviating any gain.

A local optimization in which the dosimetrists choose a zero-order setup by judgment and the computer checks on it. This is an alternative to exhaustive global searching. However, this procedure still takes considerable time if wedges, blocks, and beam width to implement in the clinic (as closely as possible) the mathematical solution for the dose distribution of ray weights (achieved in the first part).

In this paper, we describe only the first part of the automated dosimetry problem, namely the calculation of the distribution of ray weights. For the "feasible" plan is obtained, a calculation incorporating the scatter dose should be performed and adjustments made. We are still compiling the calculation at present to a single transverse section of a patient. The extension of our algorithm to 3-D, which is our ultimate objective, adds complexity but no fundamental difficulties. Presently we are in the process of testing our software for the single section case.

RAY SPACE OF A SINGLE TRANSVERSE SECTION

A ray through a point P is specified by the gantry angle \( \alpha \) of the source and the angle \( \theta \) from the central ray (Fig. 1). Instead of the angles \( \alpha \) and \( \theta \), we can use the distance \( w \) between the gantry axis \( \{l(x,y)\} \) and the intersection of the ray with the plane perpendicular to the central ray at distance \( d \) from the source, so that

\[
w = d \tan \alpha
\]

where \( d \) is the SAD (source-to-axis distance). We can then represent the plane \( \{x, y, z\} \) in the ray space corresponding to one and only one ray. Although rays \( (u, v) \) and \( (u, v, w) \) are coincident in space, they are physically distinct since they are opposite in direction. In ray space, separate points may distinguish spatially coincident rays of opposite direction. The domain of \( w \) is \([0, \pi]\) and the domain of \( \phi \) is \([-\pi, \pi]\) where \( W = w \) is the maximum beam width.

If a point \( P \) is at location \((u,s)\), it also lies on the ray within the law of sines,

\[
r / \sin \alpha = c / \sin(a - s)
\]

From Eqs. (1) and (2)

\[
w + r \sin(a - s) / (1 - (r/s) \cos(w))
\]

Thus as long as \( r/s \) is small, a fixed point \( r/s \) or the patient (and fixed SAD \( + d \)) will essentially trace out a slice in \( w, \phi \) ray space. Expanding in \( r/s \), we find

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\[ w = \sin(\omega \cdot r) \cdot \sin[2(\omega \cdot s)] \ldots \] (4)

For \( r \leq 0.1 \), the higher harmonic distortion of the sine wave is less than 5%. The amplitude of the sine wave is the distance \( r \) of the point from the gantry axis, and the phase is the angle \( \omega \).

**Fig. 1 Patient Space**

In ray space, a small tumor region of the patient will map into a bundle of adjacent sine waves. Similarly, critical or organ regions will map into sine wave bundles. If we have a ray space mapping of the tumor and critical organs, we can plan a treatment by trying to pick rays (points in the \( u,w \) plane) which lie in the tumor sine-wave bundle but not in the sine-wave bundles of the critical organs. Our algorithm does this within the \( u,w \) ray space for the beam weights that satisfy the treatment plan set by the physician. (See Fig. 2).

**Fig. 2 Ray Space**

**DOSE APPORTIONMENT**

A relative dose distribution in the patient due to unit relative beam strength from gantry angle \( u \) can be apportioned among a chosen set of sample rays. Only the rays that pass through the pixel or immediately straddle the pixel are used for apportionment. The relative dose (i.e., the dose per unit time or dose per monitor unit) \( D_u(p) \) is calculated at pixel \( p \) for a beam source at gantry angle \( u \). (The quantity \( D_u(p) \) is obtained with the zero-field-size tissue-patient-ratio for the depth of pixel \( p \), multiplied by the appropriate inverse-square-law correction.) The value of \( D_u(p) \) is then apportioned among the sample rays from \( u \) encompassing the pixel (Fig. 3) by

\[
s_{up} = \frac{1/\lambda_{up}}{k} \frac{1/\lambda_{wp}}{D_u(p)}
\] (5)

where \( s_{up} \) is the contribution of sample ray \( i \) in \( u,w \) to the relative dose at pixel \( p \), and \( \lambda_{up} \) is the perpendicular distance from the centroid of pixel \( p \) to ray \( i \). It by chance the pixel centroid lies exactly on ray \( i \), then \( s_{up} = 1 \) and \( s_{wp} = 0 \) for rays \( i \) and \( j \) from source \( u \) and \( j \neq i \).

The summation over \( k \) is taken over all the rays from \( u \) through the pixel \( p \) together with the two rays from \( u \) straddling the pixel on either side (Fig. 3).

**Fig. 3 Relative dose through pixel \( p \) is apportioned among rays labelled \( i \) to \( k \) to obtain quantities \( s_{up} \).**
After the $X_{ip}$ have been calculated for all the values of $i$, and the rays in $u,v$ have been numbered consecutively, the physician constraint for a pixel $p$ can be written

$$X_{ip} \leq X_p$$

(6)

where $X_p$ is the maximum dose allowed for pixel $p$, and $X_{ip}$ is the unknown weight (or time or monitor units) for ray $i$. If $p$ is a pixel in the tumor region, then the constraints for the treatment can also be written in the form of Eq. (6) if $X_{ip}$ and $X_p$ are negative numbers (otherwise the 'less than' symbol must be changed to a 'greater than' symbol).

To solve for the unknown values $X_p$, we initially choose $X_p = 0$ for every ray $i$. The iteration procedure

$$X_{ip} = X_{ip} + c_i X_p$$

(7)

improves the value $X_p$ at each step $k$ until a feasible solution for all the $X_p$ is achieved (if one exists) that satisfies Eq. (6). The mathematics of the particular iteration algorithm we use to choose the $c_i$ will be discussed in another publication.

FEASIBILITY ALGORITHM

We can now outline the calculation for the feasibility program.

Step 1: Read in the machine parameters and TPR tables for zero-field size. Read in the contours for the patient, for the internal organs, and for the tumor region. Read in the physician-desired constraints on the dose distribution.

Step 2: Choose a sampling array for the $u,v$ transverse section of the patient. Typically 1/3 cm pixels (with a ray 51 x 51 grid can be used).

For each pixel, determine whether the pixel lies within the tumor region, a critical organ, or otherwise, and assign the value of the physician chosen constraint to the pixel.

Step 3: Calculate separately the dose distribution resulting from a beam of unit strength at each of the (72) sample values of gantry angle $u$. Store the dose distribution due to each gantry angle (beam position) in a separate file. Use no blocks, wedges, or filters to modify the given beam profile. Since scatter radiation is omitted, this calculation for $T_2$ separate dose distributions (one for each gantry angle) takes only a few seconds longer than the calculation for a single dose distribution.

Step 4: Choose a sampling array for the $u,v$ ray space to sample all possible rays through the patient. Typically there are 72 values of the gantry angle $u$ (every 5 deg around the gantry) and say 72 values of $v$ along the beam width.

Step 5: For each pixel, proportion the dose caused by a unit beam at gantry angle $u$ among those sample rays $w$ passing through or straddling the $p,w$. Repeat for all gantry angles $u$. The data used are the dose distributions calculated in step 3. We thus calculate the constants $a_{ip}$ corresponding to the relative dose contribution by ray $i$ to pixel $p$ where $p$ ranges over the pixels in $x,y$ and $i$ ranges over the sample rays in $u,v$.

Step 6: We now find the weight (essentially the time or exposure or number of monitor units) for each (sample) ray so that the final dose distribution to the patient will satisfy the physician's specifications. Rays that never enter the tumor region remain always at zero weight. If a feasible solution exists for the physician-specified constraints, the final set of beam weights for all possible rays through the patient should provide such a mathematically-feasible treatment plan. Otherwise, a treatment plan as close to feasible as possible is given together with a warning to the user. The particular feasible solution finally derived depends on the choice of the initial starting weights for the rays and the choice of iteration algorithm.

At this stage, a dosimeter should be able to look at the contours plotted in the $u,v$ plane for the beam weights and choose a clinically-practical subset for a first guess at a difficult treatment plan.

DISCUSSION

Because of the plethora of possibilities for beam positioning in 3-D treatment planning and because of the enormous amount of computer time needed for automated global optimization programs, we have begun to search for humanly-acceptable (mathematically-feasible) solutions (treatment plans) in which all rays through a patient are given a weight so that the physician's specifications are satisfied (whether or not optimally).

Our initial efforts have been limited to a single slice of $95 \times 95$ patient and $11 \times 11$ ray plane. Extension of our work to 3-D patient geometry requires a $95 \times 95 \times 95$ ray space $u,v,w$, where $u,v$ is the gantry angle of the beam, $z$ is the location of the beam along the patient axis, and $u,v,w$ locates the ray in the beam plane (the plane perpendicular to the central ray at the SSD). A ray passes through 3-D space except those along the patient axis can be mapped to points in the 2-D ray space $u,v,w$.

The primary advantage of feasible solutions over optimal solutions is the much smaller search range (no blocks, wedges, beam widths, and beam lengths as separate parameters), thus less computer time. We also save computation by considering only the rays that pass through the tumor region.

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REFERENCES


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