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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-desired distribution of dose within a patient to an acceptable distribution for 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 contribution of each of many sample rays from different gantry positions and locations within the beam, and (2) iterating the relative contributions of the sample rays with physician-desired dose contours and constraints to find an acceptable weight for each ray. This information (1) shows immediately whether a physician-specified treatment can be implemented in the clinic, (2) reduces the chance 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 radiotherapist (physician) choses a treatment dose for the tumor and specifies the maximum allowable doses for the critical organs. At this point, a dosimetrist must choose the beam directions and beam weights to accomplish the goals of the radiotherapist. He will try to achieve (1) a uniform dose distribution across the tumor, (2) a minimum dose to the critical organs and other non-diseased tissues, and (3) a minimum of complexity in the technical setup.

Most often the experience and judgment of the dosimetrist quickly leads to an efficacious setup. Moreover, for a single transverse section, the dosimetry calculation usually 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, which do 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 modes, local boosts, etc. These cases can be time consuming and worrisome. 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? How does one know when one is close to an optimal plan in these complex cases?

Further, there is presently a general trend to three-dimensional treatment planning using several (4 to 20) CT sections. However, 3-D treatment planning is much more difficult because (1) the dosimetrist must visualize the 3-D geometry to chose the beam orientations, (2) the computation 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-calculation by trial and error, efforts have been made to have a computer determine the optimal treatment plan once tumor and critical-organ contours and dose limits have been specified by the physician[1-6]. The computer would then specify the setup parameters (gantry angles, beam size and shape, wedges, blocks, etc.) and the beam weights for the ideal treatment plan. Thus far these attempts at optimal treatment planning have been confined to the 2-D (single transverse section) case and even so have not been particularly efficacious. The reason for their lack of success is that when one includes all the setup parameters, the computer must explore and compare every possible setup in a multidimensional parameter space if the dosimetrist is to be truly omitted from the planning procedure. The calculation rapidly becomes expensive. For example, if 72 possible gantry angles (every 5 deg) are examined for 10 different beam widths and 10 different blocks or wedge orientations, we have to calculate the dose distribution for 72 x 10 x 10 = 7200 beams (for say 5500 sample points per beam). If each beam

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

A local optimization[7] in which the dosimetrist chooses a zero-order setup by judgment and the computer searches around that chosen setup, is an alternative to exhaustive global searching. However, this procedure still takes considerable time if wedges, blocks, and beam widths are varied, and cannot easily be extended to 3-D treatment planning where even zero-order judgment can be difficult.

Most often the problem in 3-D treatment planning and in difficult 2-D tumor-organ geometries is to find any feasible solution which satisfies the physician's criteria, or indeed whether any feasible solution is even possible. In this paper we describe a computer efficient method which seeks feasible (rather than optimal) solutions and which has possibilities for extension to 3-D treatment planning. In our feasibility approach, we attempt to satisfy the physician's treatment specifications by weighting rays through the patient. Any set of ray weights that achieves a dose distribution in the patient consistent with the physician's criteria is accepted as a valid solution. If the space of feasible solutions is large, any solution in that space is acceptable; it is usually easy to tighten constraints if many solutions are possible.

In our approach, we separate dosimetry planning into two parts.

In the first part, we determine a dose distribution composed of a contribution from every possible ray (of an adequate set of sample rays) through the patient. No blocks, wedges, or beam widths are considered. The weights of each of the (sample) rays are iterated (from initial beam weight of zero) until a treatment plan as consistent as possible with the specifications of the physician is achieved. If the physician specifications can not be completely met, we obtain an indication of how closely we can approach them.

The first part of our dosimetry calculation thus returns a map of feasible ray weights for all possible rays through the patient. Rays that never pass through the tumor target will always have zero weight. Rays that pass through critical organs will have less weight than those that do not. A tumor surrounded by critical organs will have a feasible solution (if one exists) corresponding essentially to equal beam weights for all directions (e.g. rotation therapy in 2-D).

If a therapy machine could be constructed that could turn on and off individual rays at each gantry position, then the mathematical solution would also be a practical treatment plan. Without such a sophisticated therapy machine, however, we must shape each beam (gantry position) with various devices to achieve a practical solution (treatment plan) for the machine available. The second part of dosimetry planning will thus fit wedges, blocks, and beam width to implement in the clinic (as closely as possible) the mathematical solution for the feasible 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. The first part is more important, since if we merely display the weights of every ray through a patient in ray space (defined below), the dosimetrist can in fact choose a near optimal clinical setup with relatively little effort.

At this preliminary stage of our research, we are concentrating on the primary or first collision component of the dose distribution, neglecting the scatter contribution. This assumption decreases the calculation times for any treatment plan. After the "feasible" plan is obtained, a calculation incorporating the scatter dose should be performed and adjustments made. We are also confining 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 u of the source and the angle A from the central ray (Fig. 1). Instead of the angle A, we can use the distance w between the gantry axis (x=y=0) and the intersection of the ray with a plane perpendicular to the central ray at distance d from the source, so that

$$w = d \tan A \qquad (1)$$

where d is the SAD (source-to-axis distance). We call the u,w plane the ray space. Any point (u,w) in the ray space corresponds to one and only one ray. Although rays (u,0) and $(u+\pi,0)$ 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 u is $[0,2\pi]$ and the domain of w is [-W,W] where W = max w = maximum beam width.

If a point in the patient at location (r,s) is also on the ray (u,w) then by the law of sines

$$r / \sin A = d / \sin(A+u-s) \qquad (2)$$

From Eqs. (1) and (2)

$$w = r \sin(u-s)/[1 - (r/d) \cos(u-s)] \qquad (3)$$

Thus as long as r/d is small, a fixed point (r,s) of the patient (and fixed SAD = d) will essentially trace out a sine wave in u,w ray space. Expanding in r/d, we find

$$w/r = \sin(u-s) + (r/2d)\sin[2(u-s)] + \ldots \qquad (4)$$

For $r/d < 0.1$, 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 s.

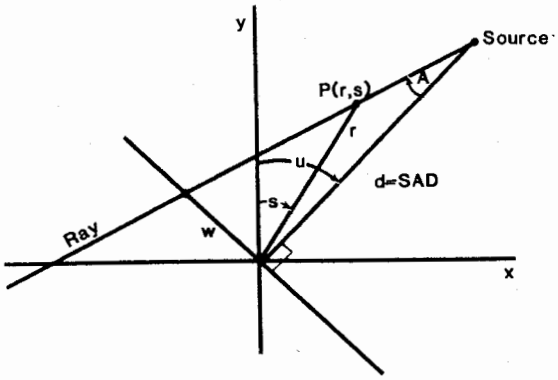

Fig. 1 Patient Space

In ray space, a small tumor region of the patient will map into a bundle of adjacent sine waves. Similarly, critical organ regions will map into sine wave bundles. If we have a ray space map 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. What our algorithm does is provide contours in the u,w ray space for the beam weights that satisfy the treatment specified by the physician. (See Fig. 2).

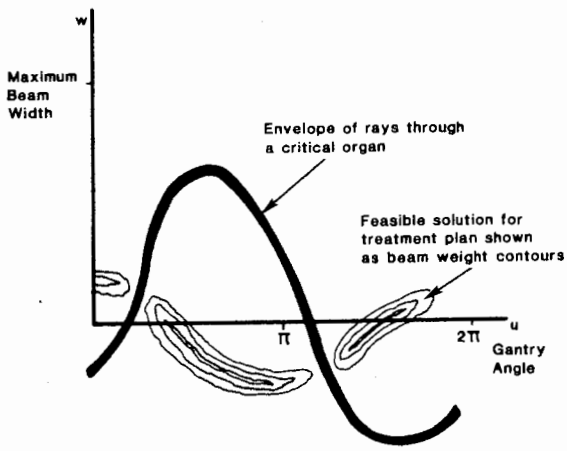

Fig. 2 Ray Space

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) $D_p(u)$ is calculated at pixel p for a beam source at gantry angle u. (The quantity $D_p(u)$ is obtained with the zero-field-size tissue-phantom-ratio for the depth of pixel p, multiplied by the appropriate inverse-square-law correction.) The value of $D_p(u)$ is then apportioned among the sample rays from u encompassing the pixel (Fig. 3) by

$$a_{ip} = \frac{1/L_{ip}}{\sum_k 1/L_{kp}} D_p(u) \qquad (5)$$

where a_{ip} is the contribution of sample ray i in u,w to the relative dose at pixel p, and L_{ip} is the perpendicular distance from the centroid of pixel p to ray i. If by chance the pixel centroid lies exactly on ray i, then $a_{ip} = 1$ and $a_{jp} = 0$ 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).

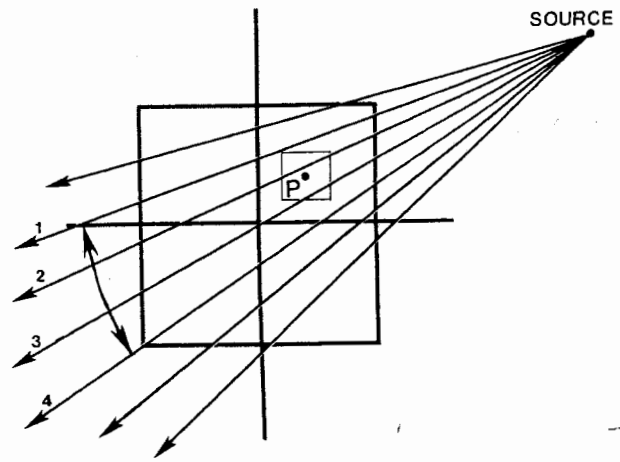

Fig. 3 Relative dose through pixel p is apportioned among rays labelled 1 to 4 to obtain quantities a_{ip}.

After the a_{ip} have been calculated for all the values of u, and the rays in u,w have been numbered consecutively, the physician constraint for a pixel p can be written

$$\sum_i a_{ip} x_i \leq b_p \qquad (6)$$

where b_p is the maximum dose allowed for pixel p, and x_i 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 a_{ip} and b_p are negative numbers (otherwise the "less than" symbol must be changed to a "greater than" symbol).

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

$$x_i^{k+1} = x_i^k + c_k a_{ip} \qquad (7)$$

improves the value x_i at each step k until a feasible solution for all the x_i is achieved (if one exists) which satisfies Eq. (6). The mathematics of the particular iteration algorithm we use to choose the c_k will be discussed in another publication[8].

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 x,y transverse section of the patient. Typically 1/3 cm pixels (with say a 91 x 61 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 72 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,w 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 w along the beam width.

Step 5: For each pixel, apportion the dose caused by a unit beam at gantry angle u among those sample rays w passing through or straddling the pixel. 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,w).

Step 6: We now find the weight (essentially the time of exposure or number of monitor units) for each (sample) ray so that the final dose distribution to the patient will satisfy the physican's specifications. As an initial guess, assume that the weights of all the possible rays through the patient are zero. Apply an iteration procedure to find weights for each ray through the patient that are more consistent with the physician's constraints. 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 dosimetrist should be able to look at the contours plotted in the u,w 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 possiblities 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 research into generating "feasible" solutions (treatment plans) in which all rays through a patient are given a weight so that the physician constraints are satisfied (whether or not optimally).

Our initial efforts have been limited to a single slice of a patient and a planar ray space. Extension of our work to 3-D patient geometry requires a 4-D ray space u,z,v,w where u is the gantry angle of the beam, z is the location of the beam along the patient axis, and v,w locates the ray in the beam window (the plane perpendicular to the central ray at the SAD). All rays through 3-D space except those along the patient axis can be mapped to points in the 4-D ray space u,z,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 computations by considering only the rays that pass through the tumor region.

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