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ON THE FULLY DISCRETIZED MODEL FOR THE INVERSE PROBLEM OF RADIATION THERAPY TREATMENT PLANNING

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ABSTRACT

Radiation therapy concerns the delivery of a proper dose of radiation to a tumor volume without causing irreparable damage to healthy tissue and critical organs. Radiation therapy treatment planning (RTTP) involves a forward problem and an inverse problem. The first refers to calculating the dose distribution delivered by a specified radiation beam configuration to a measured patient cross section. The inverse problem refers to calculating and determining a radiation beam configuration that will provide a specified dose distribution. Since there exists no analytic closed-form mathematical formulation of the forward operator, the inverse problem actually calls for computerized inversion of data. This is achieved here by construction of a fully discretized model leading to a system of linear inequalities. These inequalities are solved either by (1) a row-action method or (2) a block-Cimmino algorithm which allows the assignment of weights within each block of inequalities. Consequences and limitations of this new approach are discussed.

1. INTRODUCTION

Radiation therapy treatment planning (RTTP) refers to the process of specifying sufficient parameters to achieve the goal of delivering a total radiation dose such that it adequately controls the tumor while sparing normal tissues and organs. These parameters include precisely defining the position of the tumor and other salient anatomic structures, dose limits for the tumor and critical organs, and radiation machine characteristics. Conceptually, there are two separate problems. An inverse problem where the necessary beam configuration is determined to deliver a specified dose to a particular region and a forward problem of calculating the dose distribution delivered to a radiation field by a specific beam configuration. Many clinical, physical, mathematical, radiation beam computer simulation and radiobiological considerations play a role in this process.

Our aim here is to construct a mathematical model that will enable a computational solution to the inverse problem involved in the treatment planning. The novelty of our approach is that it aims at a computational inversion of data for which mathematical inversion formulae cannot be satisfactorily derived. Our initial simulations show that this method is capable of producing a clinically acceptable treatment plan in an automated manner [1-3]. The scope of this manuscript does not allow a full exposition of every detail; such information and pertinent references are available [1-4]. Here our discussion is restricted to the two-dimensional (2D) case, i.e. the patient's cross-section is assumed planar and all radiation sources lie within its plane. An important feature of our model and method, however, is its immediate conceptual extension to three-dimensions (3D). The complexity of parameters in 3D RTTP is markedly increased over that in 2D RTTP. Whereas in 2D RTTP a ray is specified by only two dimensions (gantry angle of the source and angle relative to the central ray), in 3D RTTP a ray requires four dimensions (the gantry angle and patient transverse section for source location, and two dimensions to locate the ray in the beam window). Nevertheless, the same model, which leads to a system of linear inequalities, carries over exactly into 3D; only the geometry involved in deriving the inequalities must be modified. A systematic, rapid, accurate, flexible, and feasible simulation process has obvious advantages against a tedious trial and error method. By easing and improving the application of RTTP, the potential rewards of more precise 3D radiotherapy can be evaluated.

2. THE FORWARD AND INVERSE PROBLEMS

The empirical knowledge of the effects of interaction between radiation and biological matter can be symbolically represented by

$$D(r,\theta) = \Delta[\rho(u,w)](r,\theta). \qquad (1)$$

The dose distribution function $D(r,\theta)$ represents the dose absorbed at a point within a patient's

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cross-section, whose polar coordinates are (r,θ) and $\rho(u,w)$ is the radiation intensity distribution. The latter function represents the radiation field generated by fan-beam sources located at points of a circle (the gantry circle) surrounding the cross-section that has to be irradiated. In writing (1), we implicitly assume the existence of an operator Δ called the dose operator, which for any given patient's cross-section maps any given radiation intensity distribution $\rho(u,w)$ onto a uniquely determined dose distribution $D(r,\theta)$.

The forward problem of calculating $D(r,\theta)$ for any given $\rho(u,w)$ cannot be described by a closed-form mathematical expression. However, good experience and partial formulas acquired over the years yield today some widely used software packages which enable a computational solution of the forward problem. Such computations are commonly referred to as dosimetry.

We are interested in solving the inverse problem of (1), i.e., to find a radiation intensity distribution $\rho(u,w)$ that, when applied to a given cross-section, will deliver a prescribed dose distribution $D(r,\theta)$. The dose operator Δ cannot be represented mathematically in a closed-form formula without making many harsh assumptions which idealize the description of the situation to an extent that it becomes unrealistic. Therefore we develop a model and a method that solve the inverse problem computationally. This is well termed as computational inversion of the data.

3. THE FEASIBILITY APPROACH AND FULL DISCRETIZATION

Our process for solving computationally the inverse problem can be broken into two main phases which are described schematically in Figures 2 and 3. Two principal decisions lead to this method. The first decision is to aim at a feasible solution rather than aim at rigorous inversion at all. By this we mean that the physician treatment prescriptions are assumed to be given in the form of upper and lower bounds $\overline{D}(r,\theta)$ and $\underline{D}(r,\theta)$, respectively, for the required and permitted doses everywhere within the patient's cross-section. This leads to the problem of finding a radiation intensity distribution $\rho(u,w)$ which will satisfy

$$\underline{D}(r,\theta) \leq \Delta[\rho(u,w)](r,\theta) \leq \overline{D}(r,\theta), \qquad (2)$$

for all (r,θ) in the patient's cross-section.

The second decision is to fully discretize the model before hand. The patient's cross-section is discretized into a finite fine grid of points given by $\{(r_j,\theta_j)\}, j=1,2,\ldots,J$. This is a standard procedure which is commonly used. But, in addition, we also discretize the parameter space of the radiation beam sources via $\{(u_i,w_i)\}, i=1,2,\ldots,I$. This process of full discretization leads to the following system of linear interval inequalities.

$$\underline{D}_j \leq \sum_{i=1}^{I} x_i d_{ij} \leq \overline{D}_j, \quad j=1,2,\ldots,J,$$
$$x_i \geq 0, \quad i=1,2,\ldots,I. \qquad (3)$$

Here $\underline{D}_j = \underline{D}(r_j,\theta_j)$, $\overline{D}_j = \overline{D}(r_j,\theta_j)$ are given by the physician. The unknowns $\{x_i\}$, $i=1,2,\ldots,I$, are the ray weights of the individual rays into which the fan-beam sources of radiation have been discretized, and d_{ij} is the dose deposited at the point (r_j,θ_j) due to a unit intensity of radiation along the i-th ray. The fully discretized model is described in Figure 1 where the grid points in the cross-section are represented by square pixels numbered consecutively from 1 to J. T represents a target for which a dose is prescribed. Organs B_1, B_2, and B_3, are 'critical', with upper limits imposed on permitted dose. C is the complimentary part of the cross-section, the normal tissue background, which also has a bound to the dose it can tolerate. The ray weights, indexed with pairs of indices in Figure 1, are to be identified with the x_i's in the text.

4. ITERATIVE ALGORITHMS

In [1] we applied to the system (3) the relaxation method of Agmon, Motzkin, and Schoenberg (AMS). This is a row-action method in the terminology of [5], where details and references may be found. At present [4], we use another iterative algorithm which performs projections simultaneously onto the halfspaces determined by the system (3). This is our newly developed block-Cimmino algorithm [4] which is a block version of the Cimmino's algorithm for linear inequalities discussed in [6-7]. This algorithm allows us to lump inequalities related to all pixels of the same organ into blocks and process them simultaneously. Within each block we may assign weights to inequalities, thereby biasing the resulting solution towards additional information given by the physician regarding the relative importance of various regions within each organ. Another advantage of Cimmino's algorithm over the AMS-algorithm is that it produces a convergent sequence of iterates even if the system (3) is inconsistent, i.e., has no solution.

When the iterative algorithm is applied to the system (3), the computations are stopped after a finite number of iterations. The current iterate $x^k = (x_i^k)_{i=1}^I$, which is an I-dimensional vector, is taken as an approximate solution to the system (3). This is called the basic solution and its components are the individual ray weights x_i, $i=1,2,\ldots,I$.

5. DERIVATION OF A BASIC SOLUTION AND A CLINICAL TREATMENT PLAN

We conclude by briefly discussing several further details as depicted in Figures 2 and 3. All blocks in these diagrams are numbered consecutively for easy reference. Block 3 represents and assumes the availability of a state-of-the-art computer program for forward calculation. Given discretization data for pixels, beams, and rays (block 1), and data about the patient's cross-section and the treatment machine parameters (block 2), it calculates the numbers $\{D_{sj}\}$, $s=1,2,\ldots,S$; $j=1,2,\ldots,J$. Each D_{sj} is the dose absorbed at location j of the cross-section (i.e., (r_j,θ_j)) due to a unit intensity of radiation from source s on the gantry circle. The apportionment scheme of block 4 distributes these values among individual rays. The resulting d_{ij}'s are the coefficients of the system (3) which needs also the physician requirements from block 5. An iterative algorithm in block 7 produces then an approximate basic solution of ray weights.

If a treatment machine existed which could deliver pencil thin single rays of controlled intensity, then the basic solution could have been implemented clinically. Since this is not the case, we use this solution as input to the process described in Figure 3 which first employs a beam reduction scheme which extracts from the basic individual ray solution a clinically acceptable treatment plan. After reducing the number of beams, we correct the plan to incorporate the effect of scattered radiation. Initially the calculations in the system of Figure 2 were for primary dose only. More details are included in [4].

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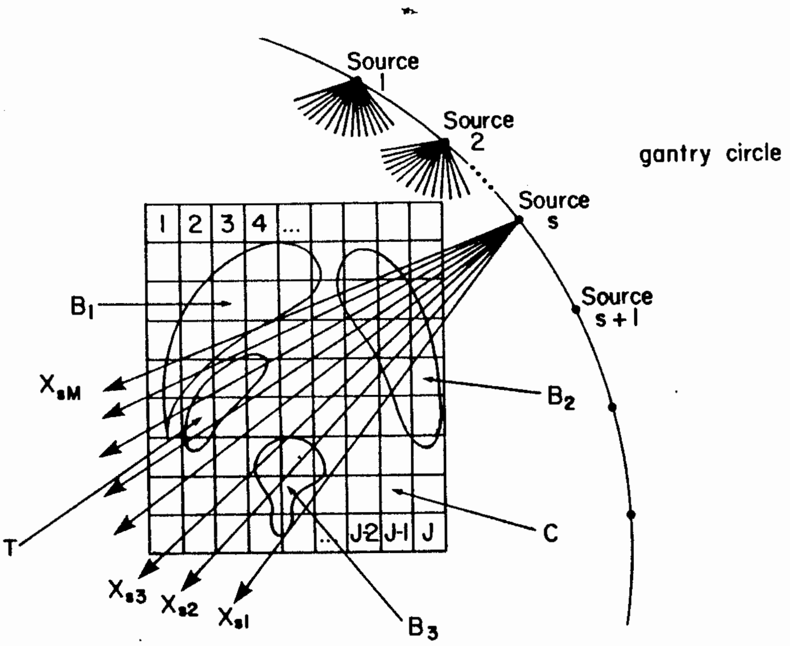

Figure 1. The fully discretized model for radiation therapy treatment planning.

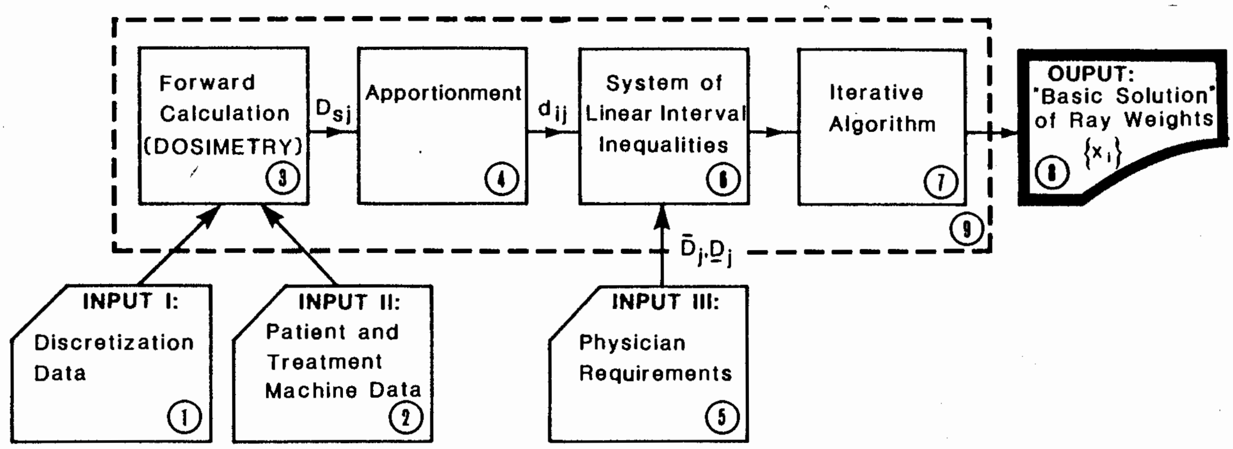

Figure 2. Derivation of the basic solution of ray weights from physician requirements, patient and machine data, and discretization.

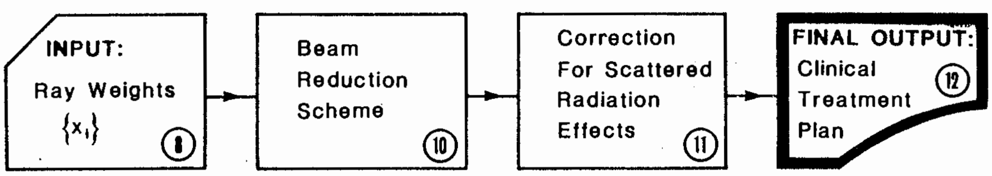

Figure 3. Derivation of the clinical treatment plan from a basic solution of ray weights.