FAST OPTIMAL BEAM DETERMINATION FOR CONFORMATION RADIOTHERAPY TREATMENT PLANNING

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ABSTRACT

Conformation radiotherapy, which involves intensity modulation of photon treatment beams, offers considerable advantages compared to conventional radiotherapy, since it has the potential for accurately matching the prescribed and delivered dose distributions, hence enabling the effective treatment of complex tumour scenarios. Associated (inverse) treatment planning methods address a constrained linear optimisation problem involving the determination of intensity modulation functions from the prescribed target dose, optimisation criteria and imposed constraints. Many of the reported inverse planning techniques require a considerable number of iterations for algorithm convergence, making them unattractive for clinical use. This paper reports the significant improvement in convergence time possible using a dynamic relaxation technique applied to a Bayesian optimisation process. Performance of the algorithm is illustrated using a complex concave tumour scenario.

1 INTRODUCTION

Conformation radiotherapy, also known as conformal radiotherapy, involves tailoring a tumourcidal dose envelope to a target volume, whilst minimising the radiation dose to normal tissues and organs [1]. This may be achieved theoretically, by altering the applied radiation beam profiles, mathematically termed intensity modulation functions (IMFs), and may be practically realised using multileaf collimators or dynamic wedging [1].

Conformation radiotherapy treatment planning (RTP), also known as inverse planning, involves the determination of IMFs from the prescribed target dose distribution, given the optimisation criteria and imposed constraints. A variety of inverse planning techniques have been reported in the literature [2-8]. However, due to the number of iterations required for convergence, many of them involve a considerable computation overhead, an important issue in practical algorithm implementation for clinical use. This overhead may be reduced using ASICs, parallel architectures and/or reconfigurable platforms [9,10]. However, these tend to be very expensive for relatively low volume applications, and so tackling the source of the problem, by reducing the number of iterations, offers a much better approach.

In this paper, a dynamic relaxation technique is reported for a Bayesian optimisation process [5,7], which demonstrates a significant improvement in convergence time.

2 DOSE COMPUTATION

The computation of dose distribution in RTP is based on the principle of superposition; the resultant dose at a point is equal to the algebraic summation of independent doses delivered by a number of radiation beams at different orientations.

Including both primary and scatter dose contributions, the resultant dose distribution $D(j)$ within a target region, due to I radiation beams, each with M pencil beams $B_i(m)$ $\{m=1,2,...,M\}$, is given by [5-7],

$$D(j) = \sum_{i=1}^{I} \sum_{m=1}^{M} a_i(m, j) B_i(m); \quad j = 1,2,\ldots, J \tag{1}$$

where $D(j)$ $\{j=1,2,...,J\}$ is known as the dose distribution, B_i is the i-th radiation beam distribution, and $a_i(m, j)$ represents the dose contribution of pencil beam $B_i(m)$ to a dose computation point j.

Equation (1) may be rewritten in matrix form as follows,

$$\mathbf{D} = \mathbf{AB} \tag{2}$$

Equation (2), which is linear, enables the dose vector **D** to be determined from the absorption matrix **A**, and the radiation beam vector **B**.

Determination of $a_i(m, j)$ depends on many factors, such as target tissue characteristics, radiation beam energy etc [1]. However, since scattered radiation attenuates quickly, and is second or third-order in comparison to the primary dose, it is usually neglected in most simplified dose computation models [1]. These models generally use an exponential attenuation form for $a_i(m, j)$ given by,

$$a_i(m, j) = \exp\left[-\mu_0 d_{im}(j)\right] \tag{3}$$

where μ_0 is 0.04/cm for 6MV radiation, and $d_{im}(j)$ is the distance of pencil beam $B_i(m)$ from the entry point of the patient's body to the dose computation point. This is also the simplified model used in the work reported here.

The inverse planning problem requires determination of the beam vector **B** in terms of the dose vector **D** and the absorption matrix **A**. Direct inversion is not possible since **A** is very large, non-Toeplitz, rectangular and extremely sparse (typically only 1-2% non-zero elements). The optimisation technique reported here involves a minimum norm optimisation criterion [5,7], although a maximum entropy method has also been implemented successfully [5-7].

3 DYNAMIC RELAXATION ALGORITHM

Optimisation based on a minimum norm criterion requires the determination of IMFs from a limited number of radiation beams $B_i(m)$ $\{i=1,2,...,I;\ m=1,2,...,M\}$, such that the norm of the total beam energy is minimised [5,7].

This may be written as a constrained optimisation problem as follows,

$$Min\|B\| = \left(\sum_{i=1}^{I} \sum_{m=1}^{M} B_i^2(m) \right)^{1/2} \tag{4}$$

subject to,

(i) the computed dose distribution **D** matching the prescribed dose distribution $\mathbf{D}_0$,

$$\mathbf{AB} = \mathbf{D}_0 \tag{5}$$

(ii) non-negativity of beams,

$$B_i(m) \geq 0; \quad i = 1,2,\ldots,I; \quad m = 1,2,\ldots,M \tag{6}$$

(iii) critical areas receiving dose D_{crit} lower than a specified tolerable low dose D_{low},

$$D_{crit} < D_{low} \tag{7}$$

The physical reasoning behind the minimum norm criterion is that the unavoidable leakage of radiation to healthy tissues and critical areas during tumour treatment should be minimised.

The minimum norm solution of eq.(2), subject to eqs.(4)-(7), has been reported in [5,7], where an iterative procedure with fixed relaxation was used. However, although fixed relaxation gives a reasonable performance, it involves many iterations for convergence, and is unable to cope with frequently changing and complex conditions e.g. different geometrical shapes encountered with tumour/critical regions. Dynamic relaxation offers this ability and achieves much faster convergence.

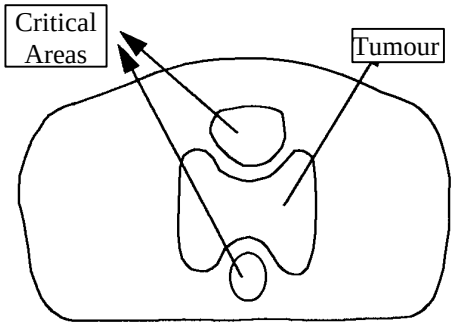

Figure 1 Outline of tumour and critical areas within analysis section.

A dynamic relaxation technique involving the following extended algorithm was therefore investigated,

$$B_i^{(k+1)}[m_i(j)] = B_i^{(k)}[m_i(j)] + r^{(k)} \frac{a_i[m_i(j), j]}{\sum_{j'} a_i[m_i(j'), j']} [D_0(j) - D^{(k)}(j)] \tag{8}$$

$$B_i^{(k)}(m) = \max[B_i^{(k)}(m), 0]; \quad i = 1,2,\ldots,I; \quad m = 1,2,\ldots,M \tag{9}$$

$$\mathbf{D}^{(k)} = \mathbf{A}\mathbf{B}^{(k)} \tag{10}$$

$$D_{crit}^{(k)} = \min[D_{crit}^{(k)}, D_{low}] \tag{11}$$

$$r^{(k+1)} = r^{(k)}(1 + \Delta_k) \quad < 2.0 \tag{12}$$

where $m_i(j)$ represents the pencil beam which passes through dose point j. The parameter $r^{(k)}$ is a relaxation parameter confined to the interval $0<r<2.0$, and in eq.(12),

$$\Delta_k = \Delta; \quad 0 \leq R^{(k)} - R^{(k-1)} < \Delta R \quad = 0; \quad otherwise \tag{13}$$

in which Δ is the specified percentage increase of the relaxation parameter, $R^{(k)}$ represents a percentage measurement of high dose volume within the target, and ΔR is a specified expected percentage increase of $R^{(k)}$ in each iteration step.

To initiate the iterative process, filtered projections of the prescribed dose were chosen as the initial IMF values [5,7]. Termination of the process occurs at the *k*-th iteration where eqs.(5-7) are satisfied and where the mismatch of the computed and prescribed high dose volumes is within a specified tolerable rate. This was chosen as 2% for the results reported here.

4 RESULTS AND DISCUSSION

The proposed algorithm was applied to a two-dimensional RTP scenario, involving a CT scan, and which concerned the treatment of a concave tumour, when two critical regions were present within the concavity, as depicted in Figure 1. Eleven external beams, equally distributed between $[0, 2\pi]$, were employed. The dose distribution specifications were as follows;

Tumour interior	95-100%
Tumour edge	95%
Critical areas	< 60%

Initially, $r^{(0)} = 0.6$ and $\Delta R = 1\%$. Δ was set to 0%, 1%, 3%, 5% and 10%.

Figure 2 shows $R^{(k)}$, the percentage value of high dose volume within the target, as a function of Δ, after 100, 76, 36, 26 and 20 iterations, with termination values of 97.44%, 98.03%, 98.10%, 98.25% and 98.39%, respectively. The variation of $r^{(k)}$ during the iterations is shown in Figure 3.

Figure 4 shows the 11 optimal beam profiles after 20 iterations $(\Delta = 10\%)$ and the corresponding dose distribution. The two critical areas are well outside the 60% isodose region. The dose value $(mean \pm std)$ within the tumour volume is $102.12 \pm 2.6\%$, which is very acceptable, clinically.

5 CONCLUSIONS

A dynamic relaxation algorithm has been developed to reduce the computation overheads normally associated with minimum norm conformation RTP. Application to a difficult two-dimensional concave tumour scenario, has demonstrated a significant performance improvement.

REFERENCES

[1] Webb, S., 1993: The Physics of Three-Dimensional Radiation Therapy: Conformation Radiotherapy, Radiosurgery and Treatment Planning, *IOP Publishing Ltd*, Bristol and Philadelphia.

[2] Special Issue on Conformation Radiotherapy Optimisation (1995*), Int. J. of Imaging Systems and Technology* **6**.

[3] Vance, R., W.A. Sandham and T.S. Durrani (1994), Optimisation of beam profiles in conformal therapy using genetic algorithms, *Phys. Med. Biol.* **39a**, 518.

[4] Scarth, S., W.A. Sandham and R. Wilkinson (1994), Conformation radiotherapy optimisation using distributed simulated annealing, *Proc. 7th Int. Conf. of the Eur. Assoc. Sig. Proc.*, 13-16 Sep 1994, Edinburgh, Scotland, 904-07.

[5] Yuan, Y., 1993: New Extensions for Tomographic Imaging and Conformation Radiotherapy Treatment Planning, *Ph.D. Thesis*, University of Strathclyde, Glasgow, Scotland.

[6] Sandham, W.A., Y. Yuan and T.S. Durrani (1995), Conformal therapy using maximum entropy optimisation (invited paper), *Int. J. of Imaging Systems and Technology* **6**, 80-90.

[7] Yuan, Y., W.A. Sandham, T.S. Durrani, J.A. Mills and C. Deehan (1994), Application of Bayesian and maximum entropy optimisation to conformation radiotherapy treatment planning, *Int. J. Applied Sig. Proc.* **1(1)**, 20-34.

[8] Yuan, Y., W.A. Sandham and T.S. Durrani (1994), Towards beam-based optimisation for conformation RTP, *Proc. 11th Int. Conf. on the use of Computers in Rad. Therapy*, 20-24 Mar 1994, Manchester, UK, 250-51.

[9] Sandham, W.A., R. Vance, Y. Yuan, C. Deehan and J. Mills (1993), Transputer implementation of a 3-D radiotherapy treatment planning algorithm. In *Transputer Applications and Systems '93*, IOS Press, **vol 2**, 1298-1310.

[10] Villasenor, J. and W.H. Mangione-Smith (1997), Configurable computing, *Scientific American* **276(6)**, 66-71.

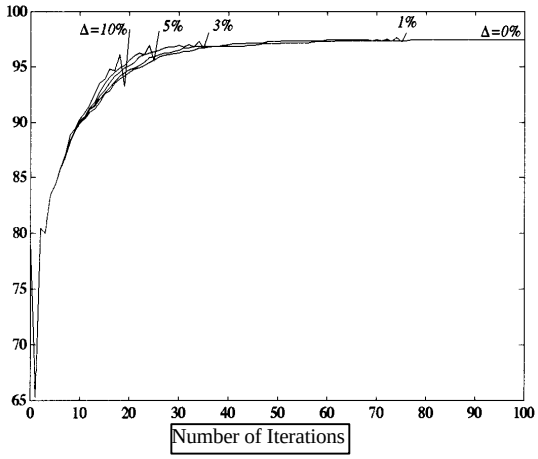

Figure 2 Percentage of high dose volume within tumour.

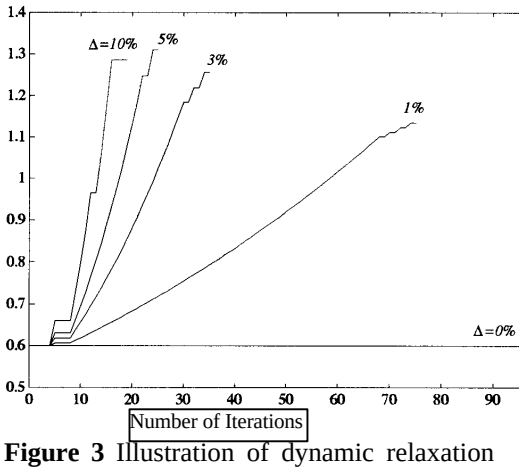

Figure 3 Illustration of dynamic relaxation during optimisation.

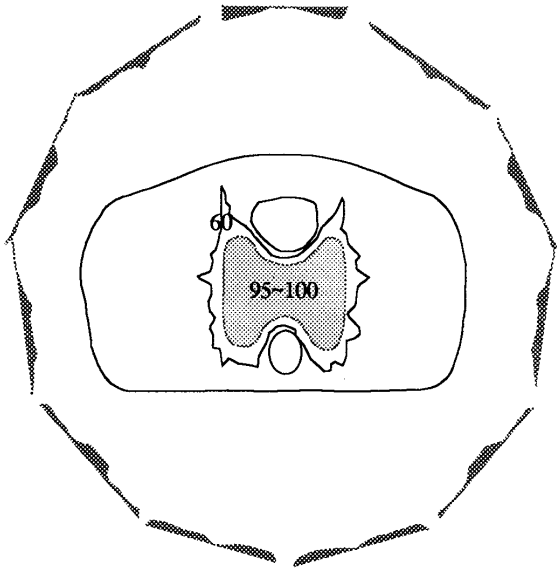

Figure 4 IMFs for 11 optimal treatment beams.