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# Optimization of external beam radiation therapy

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### 1 Motivation

Teletherapy is a cancer treatment that uses ionizing radiation to extinguish tumor cells. These ionizing particles are delivered via a linear accelerator, an instrument that rotates around the patient distributing radiation at every feasible angle. The treatment's goal is to use the smallest dose required to eliminate the tumour while sparing healthy organs. To accomplish this, the linear accelerator incorporates a tool called Multileaf Collimator (*MLC*), a set of moving blades that assumes the format of the radiation field to match the borders of the target tumor. In 2003, Allen Holder presented a linear programming model for the dosage delivery problem [2], which calculates the *MLC*'s optimal arrangement for each treatment angle. However, the implemented data to test the model was a single handmade image for each plan, expected to be interpreted as an X-Ray. This project aims to validate Holder's model with CT scans of real patients using the dataset *TROTS*[1] and introduce solution analysis tools used by medical physicists.

## 2 Optimization problem

TROTS works with a discretization in voxels of the tomography's three-dimensional reconstruction and conveniently builds the pencil-beam matrix for the model. Let  $a_{ij}$  be the dose attenuation coefficient of the i-th voxel with the j-th beamlet, as shown in figure 1. The decision variable  $x_i$ , called pencil-beam, is a weight that relates with the amount of time the associated beamlet is opened allowing radiation to pass through, and the total dosage received by the i-th voxel of the structure is given by the linear relationship  $d_i = \sum_j a_{ij} x_j$ . Besides, the rows of A can be reordered, generating submatrices that correspond to tumor tissue (PTV, Planning TargetVolume), critical tissue (**PRV**, Planning Risk Volume), and healthy (good) tissue, respectively:  $A_T$ ,  $A_C$ , and  $A_G$ . Furthermore, the dose prescription vectors are designated by:  $TUB \in \mathbb{R}^{m_t}$ (Tumor Upper Bound),  $TLB \in \mathbb{R}^{m_t}$  (Tumor Lower Bound),  $CUB \in \mathbb{R}^{m_c}$  (Critical tissue Upper Bound) and  $GUB \in \mathbb{R}^{m_g}$  (Good tissue Upper Bound). From the objective function, w is a scalar; t, c, and g are called *elastic* variables. Associated with them,  $l, u_c, u_q, L, U_c$ , and  $U_G$  are different ways of measuring elasticity, of which Holder proposed two distinct approaches: the absolute analysis and the average analysis. In the absolute analysis,  $l = L = e_{m_t}$ ,  $u_c = U_c = e_{m_c}$ , and  $u_G = U_G = e_{m_g}$ , where e is the all-one vectors, and the subscript represents the dimension of the vector or matrix. Likewise, in the average analysis,  $l = \frac{1}{m_t} e_{m_t}$ ,  $u_c = \frac{1}{m_c} e_{m_c}$ ,  $u_g = \frac{1}{m_g} e_{m_g}$ ,  $L = I_{m_t \times m_t}, U_C = I_{m_c \times m_c}$  and  $U_G = I_{m_g \times m_g}$ .

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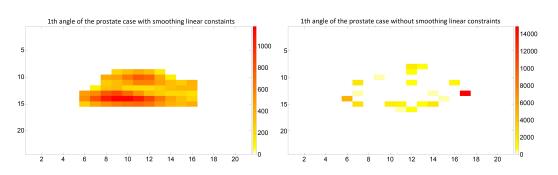
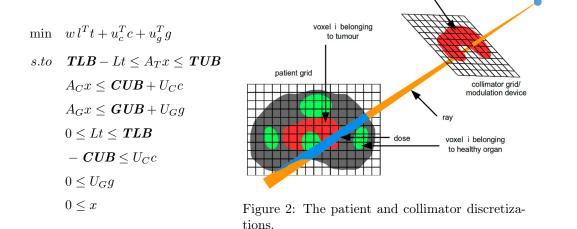


Figure 1: Comparison between two ideal fluences using a  $20 \times 20$  MLC.

beamlet j in line with tumour

beam source



## 3 Conclusions

Computational tests showed that the current bigger data slows down convergence significantly, and that some treatment plans are not attainable. Furthermore, the tests revealed new model limitations: insufficiency in the model's interpretation of the results, treatment angles unaccounted for, and unfeasible solutions for the MLC. These problems were addressed by using proper analysis routines and implementing new linear constraints that smoothen the resultant MLC's shape. The effect of these new constraints  $SLB \leq A_S x \leq SUB$ , where  $A_S$  is the smoothing linear matrice, when choosing the lower bound SLB and upper bound SUB correctly can be seen in the figure 1. With these major problems fixed, and given the great advantage that this model takes by using interior points methods showed in [2], the authors' endeavor to create a specific path-following interior points algorithm for the modified model.

#### References

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