Dosimetry Optimization

Abstract

Biological tissues are sensible to radiations in a non-linear manner [Liu03], and slight variations in dose can have significant biological effects. Organs have differing sensibilities to radiation, which increases further the difficulty in formulating the goals to achieve when designing a radiation dose. Some organs can tolerate high cumulative doses if the radiation is well distributed. In contrast, others may withstand high doses at localized points ("hot spots") but cannot handle large doses overall. To address these differences, clinicians impose dose-volume histogram constraints in addition to the prescribed dose. Although the ideal objective is to minimize or eliminate radiation exposure to organs, achieving 0 Gy is impossible. The necessity of finding compromises drives the need for advanced optimization techniques to generate fluence maps that best satisfy the medical constraints. Therefore, various techniques can be used to calculate fluence maps (i.e., performing the critical fluence map optimization step). In this chapter, we explore some fluence map optimization techniques.

Contents

1 Discretization

The optimization process starts with transforming the continuous nature of both the radiation field and the human body into discrete elements. This transformation enables computation with modern computers.

1.1 Fluence Map Discretization: Bixels

Fluence maps are broken down into discrete elements called "bixels" (**be**am **el**ements). Bixels represent small and independent beams of radiation.

The width of each bixel is constrained by the width of the multi-leaf collimator leaves. Modern multi-leaf collimator systems typically have a leaf width of 0.5 cm.

The height of a bixel can be selected arbitrarily, as the leaf can move continuously. Nevertheless, square bixels (akin to image pixels) are commonly used and will be employed throughout this manuscript.

Bixels whose beams do not affect the planning target volume are typically excluded from calculations to improve computational efficiency. Activating these bixels could only degrade dose quality by increasing the dose to organs at risk without benefiting the dose distribution within the planning target volume.

1.2 Human Body Discretization: Voxels

The human body of the patient is also divided into discrete elements, as it is a three dimensional object, the lements are "voxels" (**vo**lume **el**ements). Each voxel represents a small portion of tissue within the patient's body, and will determine the granularity of the dose computed.

The maximum resolution of the voxel grid is defined by the planning image, which is typically a CT scan. To reduce computational demands, it is common practice to resample the planning image. In this manuscript, where new techniques are explored, we have opted to resample the voxel grid to a resolution of 5 mm, ensuring a balance between computational efficiency and accuracy.

Additionally, to further optimize the computational process, only voxels corresponding to the planning target volume (PTV) and organs at risk (OARs) are retained for calculations. This selective approach reduces unnecessary computation.

1.3 Dose-Influence Matrix

The Dose-Influence Matrix (or DI-Matrix) links the discretized fluence map (the bixels values) and the discretized dose distribution within the patient (the dose on each voxel). This matrix defines how the radiation from each individual bixel influences the dose delivered to every voxel in the patient's body.

We start by converting the 2D fluence map, composed of individual bixel values, into a column vector b. Similarly we represent dose distribution in the 3D space of the patient as a vector d, where each entry corresponds to the dose in a specific voxel. The DI-Matrix L governs the relationship between these vectors b and d via the matrix-vector multiplication $d = Lb$. This mathematical operation computes the total dose at each voxel by summing the contributions from all active bixels (here, we assume that the effect of bixels is linear).

The DI-Matrix is constructed by simulating the radiation delivered by each individual bixel. For each bixel, the jaws of the multi-leaf collimator are virtually opened to allow only that specific beamlet through. A radiation

transport model is employed to calculate the dose deposited in each voxel, taking into account the beam's spread and attenuation as it travels through the body. The resulting 3D dose deposition is used to fill one column of the matrix L, corresponding to that bixel's influence on all voxels. Repeating this process for each bixel generates the entire DI-Matrix.

The accuracy of the dose calculation dependents on the precision of the DI-Matrix. Simple models like pencil beam approximations, which assume a linear trajectory with minimal scattering, are considered as too coarse. In contrast, more advanced simulations, such as Monte Carlo methods, provide a detailed and accurate dose calculation, although at a higher computational cost. In this manuscript, we employ a collapsed cone convolution techniques, which balances between efficiency and accuracy.

2 Naive Method

3 Constraints and Importance Factors

3.1 Dose Volume Histograms

3.2 Constraints Formulation

3.3 Optimization Problem

Ideal

Practical

4 Dose Mimicking

5 Optimization Algorithm Review for Dosimetry

5.1 Introduction

5.2 Methods

5.3 Data

5.4 Objective function

5.5 Open-source Optimizers

(Stochastic) Gradient Descent

Conjugate Gradient

Newton

SLSQP

RMSprop

BFGS-based

Pure BFGS

L-BFGS

Adam-based

Pure Adam

RAdam

NAdam

AdamDelta

Adamax

Rprop

Other optimizers variations

5.6 Results

Newton's method

Best Algorithms

LBFGS vs BFGS

5.7 Discussion

References

[Liu03] Shu-Zheng Liu. Nonlinear dose-response relationship in the immune system following exposure to ionizing radiation: Mechanisms and implications. *Nonlinearity in Biology, Toxicology, Medicine*, 1(1):15401420390844483, 2003. PMID: 19330113.