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A beamlet-free algorithm for efficient optimization of proton therapy plans based on Monte Carlo simulations

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INTRODUCTION

Accurate Monte Carlo dose calculation and comprehensive optimization of the treatment plan robustness are recommended for proton therapy treatment planning. However, **such treatment optimization is generally costly in terms of computation time and memory usage** due to the necessity to compute a large number of beamlets (3D dose distribution for each spot). These limitations often lead to a trade off with the plan quality and restrict some applications.

AIM

In this study, we designed **a beamlet-free algorithm** for the optimization of proton therapy plans that relies on Monte Carlo dose calculation. Because this method does not involve any beamlet information, it has the potential to greatly **reduce memory usage and computation time**.

BACKGROUND: Beamlet-based optimization

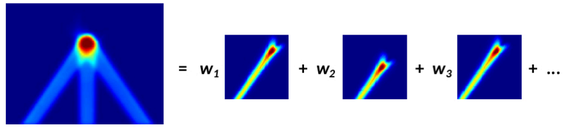
The optimization of proton PBS plans using conventional beamlet-based methods typically comprises three steps:

Spot selection:
The plan structure is established by calculating the energy layers required to cover the entire target thickness. For each layer, spots are placed according to a grid pattern.

Beamlet calculation:
The contribution of each spot is determined by pre-computing their individual 3D dose distribution.

This process can be very impractical due to the long computation time of Monte Carlo simulations and the number of spots that increases with the number of uncertainty scenarios considered for the robust optimization.

Spot weight optimization:
The total dose distribution is then obtained by calculating the weighted sum of all beamlets. These weights (w_i) are iteratively optimized until the resulting total dose distribution meets clinical objectives.

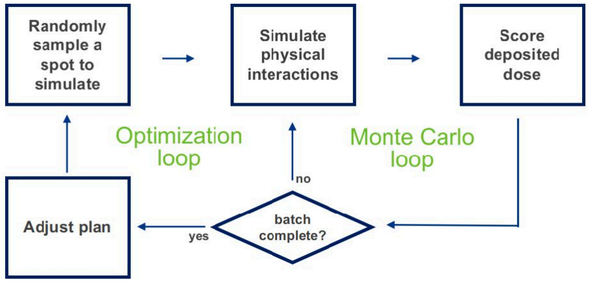


METHOD: New beamlet-free optimization

We propose a novel optimization method that does not require the beamlet information. Our beamlet-free algorithm optimizes proton PBS treatment plans with a **single Monte Carlo simulation**.

The algorithm evaluates if particles contribute either positively or negatively to the objective function during their simulation and adjusts spot weights accordingly. Thereby, the objective function is evaluated many times (once every few particles), but only considering the traversed voxels.

This micro-optimization approach is similar to the stochastic gradient descent used in machine learning, where only a small part of the dataset if evaluated at each iteration.

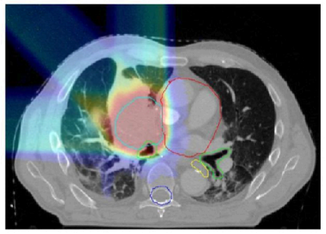


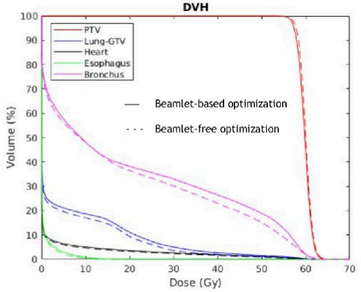
RESULTS

The beamlet-free algorithm was implemented in the open-source Monte Carlo code MCsquare [1,2]. The beamlet-based optimization was performed by the open-source optimizer MIROpt [3] and used MCsquare for beamlet calculation.

Both methods were compared for the optimization of a **lung tumor proton therapy treatment** (PTV volume of 195 cm^3). The treatment plan is composed of 3 beams and 9064 spots. Dosimetric results were evaluated on the respective final dose distributions, calculated with MCsquare (34 million simulated particles leading to a statistical noise of less than 2%).

Both methods achieved **similar target coverage and organ sparing**. However, the **beamlet-free algorithm offered better performances** by significantly reducing the computation time (reduced by 59%) and RAM memory requirements (reduced by 91%).





	Beamlet-based optimization	Beamlet-free optimization
Dosimetric results:		
Target D95	57,4 Gy	57,8 Gy
Lung Dmean	5,2 Gy	4,6 Gy
Heart Dmean	1,9 Gy	1,7 Gy
Esophagus Dmean	0,5 Gy	0,4 Gy
Bronchus Dmean	20,2 Gy	18,8 Gy
Computation time:		
Pre-processing	7 min	7 min
Beamlet computation	48 min	*NA*
Optimization	25 min	27 min
Final dose calculation	2 min	*NA*
Total	82 min	34 min
Memory requirements:		
Storage drive	10 GB	2 GB
RAM	22 GB	2 GB

CONCLUSIONS

Conventional proton PBS plan optimization requires the calculation of beamlets, leading to long computation time and huge memory requirements. Our novel **beamlet-free optimization algorithm significantly reduces the computation time and memory usage**.

The improved efficiency opens the path towards more complex applications, such as the integration of more comprehensive robustness scenarios, the optimization of additional parameters (LET, delivery time, ...), online adaptive proton therapy, and the optimization of more complex delivery modalities (Arc-PT, flash therapy, ...)

Moreover, the method is **not limited to proton therapy** and could be applied to any Monte Carlo dose calculation.

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