Parallelization of plan-optimization for TRiP98 *

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Introduction

In clinical practice treatment protocols of inter-fractional moving tumours like the prostate carcinoma foresee only one optimization of a treatment plan. The margins are therefore enlarged to compensate the expected daily variation [1]. Organs adjacent to the prostate (e.g. bladder, rectum) however will in part be enclosed in the high dose regions when increasing the margins. Their tolerance dose limits the maximum therapeutic target dose. Variations of geometrical changes could also be considered via adaptive treatment methods that modify a treatment plan on a daily bases. This approach guarantees the best compromise between target coverage and sparing healthy tissue.

We aim on speeding up the complete therapy planning procedure for particles (e.g. daily CT-scan, contouring, plan-optimization and plan-verification) to a point where treatment delivery can directly follow a daily CT-scan and the patient can be kept in the immobilisation device. Amongst other requirements this demands fast optimization of treatment plans. In this scope the optimization part of the treatment planning code for particles TRiP98 [2;3] has been modified to run on a multi-core environment.

Material and Methods

The dose calculation of TRiP98 has already been modified to support multi threaded calculations [4]. All calculations carried out for dose verification are independent so that parallelizing this sector worked very well. Plan optimization starts with setting up a large dose correlation matrix (DCM) which contains a list of beam positions per target voxel that contribute to its total dose. During optimization the complete DCM has to be accessible and be kept in memory. The iterative optimization process can therefore not be calculated in parallel. However the dose calculation which is needed prior to each iteration has no such dependency and can be spread over multiple cores.

In the current implementation setting up the DCM and inter step dose calculation has been parallelized according to the scheme shown in figure 1.

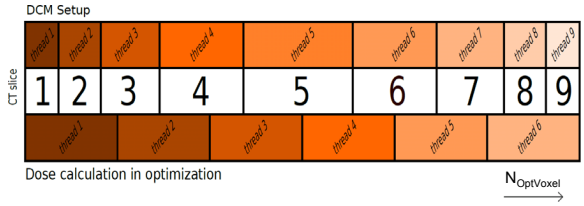

Figure 1: Illustration of OptVoxel distribution along the different threads.

Results / Current status

The speed up factor for parallel DCM set up increases with the DCM's size (figure 2). For small DCMs (e.g. single field (SF)) the time needed to create a thread restricts the total calculation speed. Also the performance of the parallel optimization depends on the DCM size. Multi field (MF) calculations therefore benefit more from utilising multiple cores.

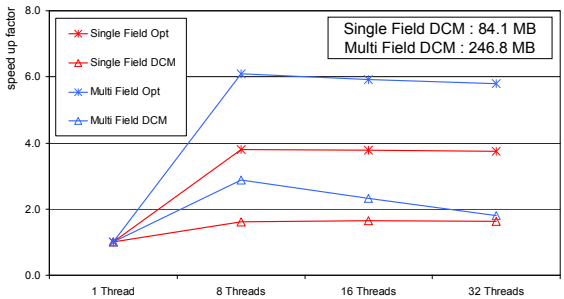

Figure 2: Performance of the parallelized code

The calculations have been carried out with an IBM Blade-Server PS701 (8 Cores, 4 Hyper-threads each). Due to the underlying architecture the algorithms show their peak performance when calculating on 8 threads.

The example calculation shown in figure 2 represents an optimization of the biological effective dose for a prostate cancer case using a grid spacing of 2mm and a planning CT with 256x256 voxels per slice. On the target with 4853 voxels (~55.5cm^3) 200 optimization steps were carried out. Calculations with one thread took 1290 sec and 1780 sec for SF and MF respectively. These times could be reduced to 340 sec for SF and 290 sec for MF.

References

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