

## Fast 4D dose calculation with TRiP4D\*

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### Introduction

Treatment planning for scanned ion beams includes time intense calculation tasks (e.g. plan optimization and dose calculation) that take in the order of hours to complete. As reported in various publications treatment planning for moving tumors with a scanned ion beam has to account for the target motion via special 4D treatment techniques [1]. These techniques rely on a time resolved CT scan (4DCT) and an image registration map between all phases of this 4DCT. The additional dimension (time) elongates the calculation time for a 4D dose distribution. Rescanning, a motion mitigation technique that scans the target multiple times applying only a fraction of the total dose per scan, elongates the dose calculation proportional to the number of scans. This caused one single dose calculation of a rescanned treatment plan of a small cardiac volume to run longer than 45 hours. As these calculations are time critical for a planned experimental validation study which is planned for 2014, we worked on accelerating the 4D dose calculation of TRiP4D[2, 3] to be able to complete the treatment planning in a reasonable time frame.

### Materials and Methods

The aim of reducing the dose calculation time from hours to minutes needed substantial improvement only possible with a combination of code optimization, reducing the overall workload and parallel execution.

The dose calculation routine of TRiP4D was profiled using the AIX profiler gprof. The profiler revealed the calculation of the water equivalent path length (WEPL) as the most time consuming function in a physical dose calculation as the WEPL of each voxel entering this calculation has to be calculated. We were able to reduce the number of interpolation steps carried out by this routine and thereby reduced the time spent for calculating the WEPL.

Additionally we restricted the dose calculation to a subset of voxels (see figure 1) and we added a new functionality to TRiP4D which determines the dose calculation window using the maximum lateral dimension of all fields. The treatment setup for treating atrial fibrillation will feature two lateral opposing fields so the dose calculation window in these cases has an optimal size (see figure 1). Finally the dose calculations have been carried out with an IBM Blade-Server PS701 (8 Cores, 4 hyper threads each) using the full amount of 32 parallel threads [4].

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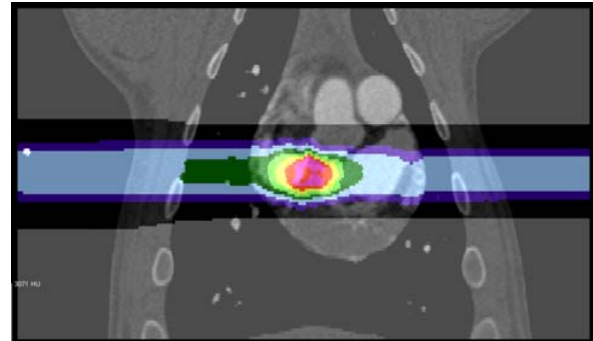


Figure 1: Coronal dose-cut from a treatment simulation for upcoming experiments. The dose is only calculated in the non shaded area around the two beam ports.

### Results/Conclusion

The improvements reduced the time for 4D (rescanning) dose calculation to below 30 min (see table 1). Besides permitting the dose calculations for the planned experiments, fast 4D dose calculation also allows robustness studies with large parameter spaces in the future.

Table 1: Dose calculation time for all improvements made

<i>TRiP4D</i> <sub>version</sub>	time of dose command
original	> 45h
+ changed WEPL routine	29h
+ dose window only	5.5h
+ 32 threads	< 0.5h

### References

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