

## Comparison between different dose calculation algorithms available in TRiP98 and between the beam model of HIT and GSI

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Last year the dose profiles behind thick bone-like targets and interfaces between bone-like material and water in the entrance channel were studied [1]. The experiment was performed at the 'Heidenger Ion-Beam Therapy Center' (HIT) and the experimental results were compared with different simulations of the Treatment Planning System (TPS), TRiP98 [3]. The aim of the experiment was to validate TRiP98 for cases with thick inhomogeneous material in the beam entrance channel.

### TRiP98 dose calculation algorithms

TRiP98 was developed at GSI for the radiotherapy pilot project and is constantly updated and used as a research prototype. The program performs physical and biological dose calculations and optimizations, amongst other tasks. The aim of the optimization process is to deliver the prescribed dose as homogeneously as possible in the tumor volume and, simultaneously, to reduce the dose in the healthy tissue and especially in the Organs At Risk (OAR).

The calculation of the physical dose distribution can be performed by three different implemented algorithms, which can be used for treatment planning. The classical one (CL) uses a fast interpolation technique between the 4 beam raster points neighbouring a CT voxel [2]. It offers very fast overview calculations but is less precise at the edges of the dose distribution. A more advanced algorithm is all-points (AP). In contrast to the CL algorithm all points in the neighborhood are considered and the actual Gaussian shape of each beam spot is considered. AP is more precise than the CL algorithm, but also more time consuming. The latest and most precise one is multiple scattering (MS) [4]. For the MS algorithm the dose calculation is identical with the AP one, but the beam broadening with increasing depth is taken into account by adding a second Gaussian with a FWHM reflecting multiple coulomb scattering and nuclear angular distributions. AP and MS can be enhanced by accounting for the divergence of the beam as it exits the beam pipe (APDB and MSDB).

### Results

The treatment plans for the experiment at HIT were optimized with the APDB algorithm, since base data for the more advanced MSDB algorithm was not available at this time. Hence small deviation between the measured data and the treatment planning were found. Recalculations with MSDB was performed with a HIT-specific pencil beam data base as soon as it became available [5]. Differ-

ences between the calculations with MSDB and APDB for the HIT-specific base data are shown in figure 1.

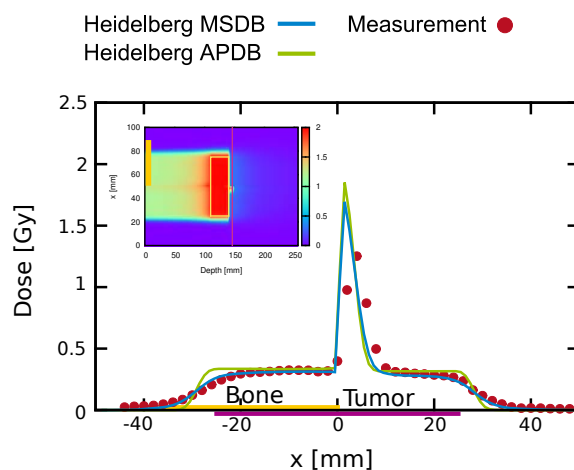


Figure 1: Comparison between the two different algorithms apdb and msdb of the HIT beam model and the measured data.

Therefore a precise recalculation of data measured at HIT is now possible with TRiP98.

In addition it is shown in [6], that the differences in the beam models of GSI and HIT are negligible and play no important role for recalculations.

### References

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