

AbstractID: 8726 Title: Investigation of Dose Interpolation Errors with a 4D Monte Carlo Method

Purpose: Tracking dose deformations from a source to target geometry typically interpolates source voxel doses to estimate target geometry doses. This study investigates errors inherent to the interpolation method.

Method and Materials: A hypothetical 24x24x24 voxels deforming water phantom is created such that its deformation involves voxel splitting and coalescence. The phantom is irradiated by a 6MV beam. Dose at its original status is calculated by EGSnrc/DOSXYZnrc and mapped to the deformed status by the dose interpolation approach. Deformed dose is also directly computed using analytical functions.

A 4D MC method is implemented as a modification of EGSnrc/DOSXYZnrc. It separates the particle transport and energy scoring grids. Particle transport occurs in the source image, while particle energy deposition events are tracked at the target image. Dose is computed as energy deposited per unit mass in the target voxel. The 4D MC is used calculate the dose on the deforming phantom irradiated by a beam parallel and perpendicular to the phantom's deformation, respectively. The deformation resultant voxel coalescence or splitting occurs along the beam direction as well as at the beam edge. Their results are compared with the dose calculated by the interpolation method.

Results: The doses calculated by the 4D MC code have less than 0.45% errors from analytical estimates on the deforming water phantom. The interpolation method has a deviation of 2.7% in its depth profile with a beam parallel to tissue deformation and a maximum of 23.5% at the edge of the 6MV beam.

Conclusion: The dose interpolation method ignores the different energy contributions made by each source voxel to the deformed voxel in the case of voxel coalescence, as occurs as lungs deform from inhale to exhale. This may result in a large discrepancy in the deformed dose, especially at beam edges.