Development report

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> Is the CBCT read properly?

> Is the VF probing done at the appropriate position?

> How to fix the MHD/MHA output?

> Warping the endpoint and entrance point should not be done in parallel. When going further from the tramp center, a bigger angle should be applied!

1 Algorithm

This is the implemented algorithm:

1. Read patient data

2. Assign a WEPL range to each spot using lut

3. Raytrace each spot to get endpoint coordinates

   (a) Lose energy and WEPL voxel-by-voxel
   (b) Stop if outside of CT, no WEPL or no energy

4. Probe vector field at the endpoint positions

5. Apply VF at endpoints

6. Apply VF at starting points, neglecting the depth dimension with respect to the treatment plane (not individual spots)

7. Raytrace each spot in the CBCT to get endpoint coordinates

8. Compare with warped endpoint calculated at step 5 (along the same line, only depth difference)

9. Assign energy shift for the depth difference: how to translate to energy?

The adaptation is then:

- XY inside the treatment plane as given by the VF for each spot

- Energy as given by the range difference at last step

This effectively removes the layer organization in positions and energies.

2   Ray Tracing

1. A single ray is initialized per spot.

2. The ray losses energy following the CSDA.

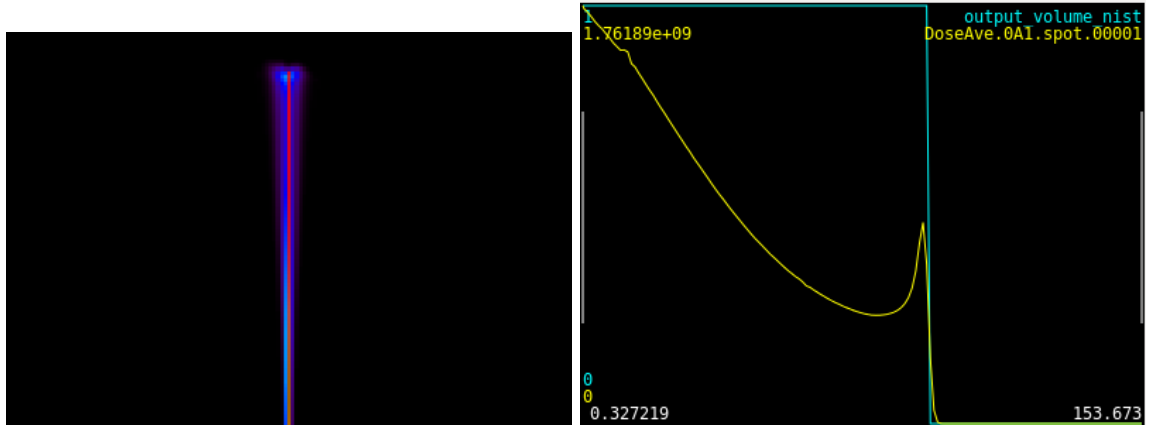3. When the ray has zero energy the endpoint is scored.

Figure 1: Beam with no σ and ϵ in a patient (P15) and ray traced trajectory.

3   Vector field probing