

## GPU-BASED FAST-MONTE CARLO TOOL FOR PROTON THERAPY

Taynná V. R. Almeida<sup>1,2</sup>; R. Cassetta<sup>2</sup>; G. Magro<sup>3</sup>; M. Ciocca<sup>3</sup>; M. Riboldi<sup>2</sup>; G. Baroni<sup>2,3</sup>; V. Denyak<sup>1</sup>; V. Patera<sup>4</sup>; A. Schiavi<sup>4</sup>

<sup>1</sup>Faculdades Pequeno Príncipe, Curitiba, Brazil.

<sup>2</sup>Politecnico di Milano, Milan, Italy,

<sup>3</sup>Centro Nazionale di Adroterapia Oncologica, Pavia, Italy,

<sup>4</sup>La Sapienza, Roma, Italy

**Introduction:** In the current clinical practice, analytical treatment planning systems (TPS) are used for the plan optimization due to their short calculation time. However, to achieve fast dose calculations, several approximations should be made in analytical algorithms, which might compromise the accuracy and increase the discrepancy between the calculated and the actual dose distributions. Higher precision would be obtained by using Monte Carlo (MC) tools, nevertheless, the extensive computational times make them unattractive for clinical implementation. Graphical processing units (GPUs) are a frequently used option to achieve fast calculations. In this study, an under development *fast*-Monte Carlo tool called FRED will be analyzed for proton therapy simulations.

**Methods:** The current application of FRED is to double-check the dose distribution through treatment plan recalculation. To reduce computational time without losing accuracy, the physics interactions considered were those with the most significant contribution to the proton therapy treatment. They are: stopping power and energy straggling for the energy deposition, multiple coulomb and nuclear scattering for the beam lateral aperture and nuclear interactions for secondary fragments production. Treatment plans recalculations with FRED have been performed following the same procedures currently applied at *Centro Nazionale di Adroterapia Oncologica* (CNAO - Italy). CNAO patient's DICOM files were selected from a glioblastoma multiforme (GBM) case. Inside FRED, a python code is used to read DICOMs and create the necessary input files for the simulations. FRED relies on CUDA (Computed Unified Device Architecture), a GPU programming environment developed by NVIDIA. Due to its high accuracy, FLUKA was used as the reference *full*-Monte Carlo tool. To verify the systematic agreement between the full three-dimensional (3D) dose distribution produced by FLUKA and FRED, the gamma-index method was employed. Time performances were compared.

**Results and Discussion:** Differences in physical doses are shown in Figure 1. The gamma-index between FLUKA (reference map) and FRED (evaluated map) had a pass-rate of 99% on the whole calculation volume for 2% of dose difference (DD) and 2 mm of distance to agreement (DTA).

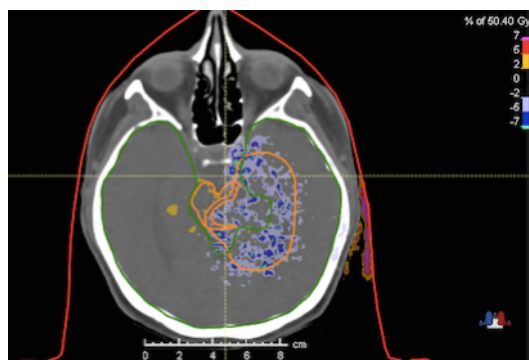


Figure 1. Dose difference between FLUKA and FRED simulations, where FRED shows higher dose than FLUKA into a PTV region, in orange. The red line represents the skin surface.

Previous study on a water phantom demonstrated that the rate of passing voxels test decreased when it was selected only voxels with dose greater than 1.5 Gy each, that means the PTV. Furthermore, it was expected some limitations particularly emerging from deep ranges such as energies greater than 230 MeV. That occurs due to the model of nuclear inelastic interaction implemented, which for long ranges is not sufficiently accurate and has to be improved. It may explain a higher PTV dose in FRED with 85% pass-rate. The study also showed that with 4 NVIDIA GPUs, FRED took 0.05  $\mu$ s per primary. On the other hand, with CPU architecture, FLUKA took 1340  $\mu$ s per primary.

**Conclusions:** Gamma-index passing-rate results were very promising. FRED tool showed considerable dose calculation accuracy for proton therapy. In terms of time, since running on GPU, FRED is up to twenty-six times faster than the *full*-Monte Carlo code of reference.