

Validation of Geant4 fragmentation models in ^4He ion therapy

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Background: The use of ^4He ions for radiotherapy has had growing interest in recent years due to its favourable characteristics for certain treatments.

Monte Carlo codes continue being more common in medical physics applications, such as independent verification of treatment planning or radiation field studies, knowledge of how well certain Monte Carlo codes or models reproduce experimental measurements grows increasingly important. This study presents validation of the Geant4 toolkit for its use in ^4He ion radiotherapy.

Material and Methods: Three different published experimental data sets of fragment measurements were used to compare against Geant4, version 11. The experimental studies included Arico et al. [1], Marafini et al. [2] and Rovituso et al. [3]. Quantities compared were the fragment build-up curves, beam attenuation, angular and energy distributions of fragments. Fragments were simulated using three alternative models available in Geant4, the binary intranuclear cascade (BIC), the quantum molecular dynamics (QMD) and the Liege intranuclear cascade (INCL).

Preliminary results: Comparing experimental and simulated angular distributions against one another showed all models to significantly under-produce fragments in the forward direction, with the difference being amplified for thicker targets. The INCL model reproduced experimental fragment distributions of protons the best, with an agreement of 42% for angles between 0-30 degrees of the beam's direction. When considering more lateral directed angles, above ~10 degrees INCL differed within 17% of experiment. With BIC and QMD performing similar to one another, having an agreement within ~60% of experiment. Protons are especially important in helium ion therapy, since they are the most abundantly produced fragment and have the largest range and lateral scattering, making them especially relevant for dose to healthy tissue. For energy distributions, INCL gave the worst agreement for protons, while QMD gave the best.

[1] Arico et al. *Phys Med Bio*, 62, 2017, 8003-8024

[2] Marafini et al. *Phys Med Bio*, 62, 2017, 1291-1309

[3] Rovituso et al. *Phys Med Bio*, 62, 2017, 1310-1326