Moving to personalized Nuclear Medicine: An in silico perspective

Over the last few years, the introduction of computer science in the field of medical physics is rapidly evolving, in the trend of personalized medicine. Monte Carlo (MC) simulations are increasingly being used for dosimetry purposes either in diagnostic (PET-SPECT-CT) or in therapeutic applications, serving as the gold standard for dosimetry assessment in Nuclear Medicine. GATE is an open-source toolkit based on the Geant4 code, extensively validated for Emission/Transmission Tomography and Radiotherapy.

The evolution of imaging and RT techniques has raised the development of high resolution computational models, that serve as mimicking the interior, and exterior anatomical features of the human or the animal body. Computational phantoms have been integrated with MC techniques, to simulate radiation transport inside the human body, for modeling as more realistically as possible the clinical acquisitions, determining the ionizing interactions within the body.

Modern medicine evolves toward the personalization of clinical protocols as the quantification of absorbed dose per organ/tissue of interest, is of great importance taking into account patient's anatomical and physical variability. Absorbed dose in pediatrics is highly debated, as children are more radiosensitive than adults (definition of the S-values calculation). Project ERROR (<u>https://error.upatras.gr/</u>) aims to the creation of a pediatric dosimetry platform, which will offer to the clinician the possibility to predict the absorbed dose per organ during diagnosis and therapy.

Recently, new techniques have been raised through MC, such as radiobiology, theragnostics, nanoparticle interactions, etc. Thus, MC simulations are extended to model the interactions in multi-scale level, from cellular/nucleus to organ/tissue (whole-body) aiming to predict the biological damage during irradiation (physical, chemical, and physico-chemical). In all applications, we should aim to the personalization of the protocols, based on a multidisciplinarity perspective, validating steps-by-step our models and considering the limitations of such techniques (e.g. execution time).

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