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Molecular Imaging at Cellular Level: Theoretical treatment using Geant4 code

Abstract:

Introduction: Molecular imaging is a model of visualization the cellular function and follow-up the molecular process in living organisms. Positron Emission Tomography (PET) is one of these imaging modalities. The essential objective in molecular imaging modalities is to gain images with optimized quality and exhaustive data of object to provide a detailed report about the measurement of radioactive tracers distribution in vivo. Spatial resolution is one of the factors that limit the realization of this goal. Whenever, the overlapping measurement between two objects as accurately as possible an excellent image resolution will be obtained. This study will focus on how closely micro tracks can be resolved in an image formed by the nuclear emulsion film traversed with a positron; this will be presented in a theoretical treatment using Geant4 code.

Simulation study: This study provides a model for determining the resolution of positron-Nuclear Emulsion image. This model based on Monte Carlo Simulation- Geant4 code (1), Object –Oriented data analysis framework (2), Reconstruction algorithm (Iterative Correction) (3), FEDRA library (4) and Allen et al method (5). We propose an innovative technique rely on the nuclear emulsion film detector for positron radiography. Human cells are labeled with the positron emitting radiotracer to be loaded to the nuclear emulsion film detector. Positron tracks are detected and the positions of positrons passing through the patient's body are measured to produce more sophisticated image with high precision reconstruction. Three mandatory classes will be implemented: G4VUserDetectorConstruction to design the nuclear emulsion sheets, G4VUserPhysicsList to implement the positron source and all the expected physical processes from the interaction of the concerned particle with a matter and G4VUserPrimaryGenerationAction to design the positron particle travelling along the z axis with energy selected 1 MeV positioned at the center of two detectors in a Cartesian coordinate system with an isotropic momentum direction.

Results and conclusion: This model provides a resolution limit $\sim 10 \mu\text{m}$ for the distance of closest approach squared. This result allows a quantitatively exploring the prospects for the use of positron imaging techniques at the cellular metabolic scale using Emulsions. This model develops a trace reconstruction and vertex search algorithm which allows controlling the randomness of the positron's path by accessing the annihilation vertex. This would provide a visual representation similar to that obtained with PET, but at the cellular level.

References:

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