A Stochastic Model of Space Radiation Transport as a Tool in the Development of Time-Dependent Risk Assessment

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A new computer model, the GCR Event-based Risk Model code (GERMcode), was developed to describe biophysical events from high-energy protons and heavy ions that have been studied at the NASA Space Radiation Laboratory (NSRL) [1] for the purpose of simulating space radiation biological effects. In the GERMcode, the biophysical description of the passage of heavy ions in tissue and shielding materials is made with a stochastic approach that includes both ion track structure and nuclear interactions. The GERMcode accounts for the major nuclear interaction processes of importance for describing heavy ion beams, including nuclear fragmentation, elastic scattering, and knockout-cascade processes by using the quantum multiple scattering fragmentation (QMSFRG) model [2]. The QMSFRG model has been shown to be in excellent agreement with available experimental data for nuclear fragmentation cross sections [3].

For the mono-energetic beams specified by the charge (Z) and mass (A) and kinetic energy (E), the GERMcode evaluates the ions' physical properties of linear-energy transfer (LET), range (R), and nuclear absorption in a shielding material. In addition, a set of biophysical properties are evaluated, such as the Poisson distribution of particles or delta-ray hits for a specified dose (D) in the cellular area, radial dose on tissue, and the frequency distribution of energy deposition in a DNA volume. Basic radiobiological responses such as cell survival curves, mutation, chromosomal aberrations, and representative mouse tumor induction curves are also described [4,5]. The GERMcode also calculates the radiation transport along the NSRL beam line at a fixed number of user specified depths, at multiple positions along the Bragg curve of the particle in a selected shielding material, or at several organ depths of a biological sample for the primary ion and its secondary particles. The effects of nuclear fragmentation of the beam at those depths are evaluated for the depth-dose response, cumulative charge distribution, multiplicity of light ions, and downgraded energy of ions from heavy ion events. The basic radiobiological response models are evaluated for the mixed particle field at various depths.

Given the cellular track model parameters by the scientists participating in NSRL experiments, the GERMcode provides the data needed for the interpretation of their experiments, including the ability to model the beam line, the shielding of samples and sample holders, and the estimates of basic physical and biological outputs of the designed experiments. Follow-on versions will be updated for the neutron elastic scattering, neutron forward-backward scattering, and multiple-layer shielding materials. A new approach of risk assessment should be based on time-dependent biological events due to the signaling times for activation and relaxation of biological processes in the cell and tissue. Thus, the trakcking of the time of events will be added for GCR simulation. Also, pions, electrons, and gamma-rays will be added, as well as the modification of energy conservation for high multiplicity events in nuclear reactions, due to the directional effects for some low-energy processes. By utilizing ProE/Fishbowl ray-tracing analysis [6], the GERMcode will be the bi-directional randiation transport code as a main tool to develop new time-dependent biological response models.

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