Stochastic Expansion of Radionuclide Inhalation Dosimetry for Radiation Countermeasures Application

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Releases from nuclear or radiological security events may result in significant internal radiation contamination through inhalation of particulate contaminants, given the prolonged suspension of particles in the air post-event. Consequently, the assessment of internal radiation dose exposure relies heavily on mathematical frameworks, particularly biokinetic models, which aim to determine the biodistribution of radionuclides over time post-exposure. For radionuclides inhaled into the body, specialized models have been developed, known as the human respiratory tract model (HRTM). These models have undergone refinement, incorporating deterministic quantities outlined by the International Commission on Radiological Protection (ICRP) in Publication 66 and subsequently updated in Publication 130. The HRTM encompasses various components, including particle deposition in airways, radioactive decay, systemic biokinetic modeling, and dose estimate. While the ICRP utilizes reference models to establish biokinetic and dosimetric quantities for the computation of dose coefficients, the complexity of inhaled radionuclide metabolism necessitates the utilization of expanded stochastic models. These models must capture a broader range of population-specific variabilities to facilitate accurate dose estimation and reconstruction. Furthermore, uncertainty and sensitivity analyses are indispensable, particularly in consequence management scenarios in which early-phase decisions regarding site-boundary dose estimates and administration of medical countermeasures must be made, incorporating case-specific conditions and individual characteristics.

The aim of this study was to assess the variability in deterministic biokinetic/dosimetry models in representing the stochastic nature of radionuclide metabolism in a non-reference population exposed to realistic source terms. To achieve this, a physiologically-enhanced biokinetic and dose coefficient model based on ICRP Publication 130 HRTM and associated systemic biokinetics was developed. Uncertain parameters in the human respiratory tract were studied, and stochastic analysis was conducted using Latin Hypercube Sampling. The most important parameters were determined with the Random Forest machine learning algorithm coupled with SHapley Additive exPlanations (SHAP). The uncertainty and variability in deterministic ^{131}I biokinetic and dosimetry models will be discussed as an inhalation case study.