Monte Carlo Validation of Internal Dosimetry Algorithms

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For routine bioassay, an internal dosimetry algorithm operates on sets of bioassay measurements and possible followup measurements to determine a scenario of intakes and committed doses that may have occurred for different workers. The algorithm must address the following questions:

- What bioassay measurement level is indicative of a new intake (decision level)?
- How is the decision level affected by prior intake(s) that may have occurred? If previous intake(s) have occurred, the measured excretion must exceed the amount resulting from the previous intakes in order to imply a new intake. Uncertainties of the extrapolated excretion from earlier intakes are important in determining the new decision level.

The performance of an algorithm may be judged by the rate of false positives and false negatives. For definiteness, we define a false negative as a case where no intake is calculated, but the true dose exceeds a nominal Classical MDA. The “loss function” is a weighted sum of the number of false positives and false negatives, with the weighting factors being the costs associated with each. We hope to stimulate a discussion of what these relative costs might be. A measure of the quality of an internal dosimetry algorithm is the average loss rate. For example, assuming equal weighting of false positives and false negatives, the loss rate would be the number of incorrect decisions (``wrong calls’’--false positive or false negative) per 1000 cases.

In order to calculate average loss rates, we have developed a Monte Carlo internal dosimetry algorithm validation tool. This calculational tool generates simulated bioassay data for a worker population. The program assumes a probability per unit time that intakes occur, a distribution of the intake amount (log normal), and a discrete distribution of type of intake (solubility class) and particle size. With this program, we generate data sets (typically of 1000 cases) of simulated bioassay data, where for each of the cases we have full knowledge of the true intake(s) and dose. We then analyze the simulated bioassay data with the internal dosimetry algorithm we wish to test and calculate the losses.

Our goal is to compare algorithms, including Bayesian and classical. As our first step in this process we shall present results on the performance of a Bayesian algorithm (available from www.lanl.gov/bayesian) with various choices of parameter values.