

Improving Uncertainty Estimates of Plutonium Activity Concentration in Human Skeleton from Individual Bone Sample Analyses

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At the United States Transuranium and Uranium Registries (USTUR), 87% of deceased Registrants are partial-body tissue donors with two to six bones commonly collected at autopsy. The most collected bone samples are rib, sternum, vertebral body, patella, clavicle, and femur middle shaft. The most frequent 2-bone combinations are rib/sternum (157) and rib/ vertebral body (155). These bone samples are relatively easier to collect postmortem and, therefore, they are non-random convenience samples not representative of the entire skeleton. To estimate plutonium activity concentration in the skeleton (C_{skel}) from measured concentrations in individual bone samples (C_{bone}), the USTUR has developed a latent bone modelling (LBM) approach based on principal component regression (PCR) using C_{skel} values for 13 non-osteoporotic whole-body tissue donors, as well as C_{bone} data for 90 samples from each donor. LBM was implemented by using Python into a simple graphical user interface, EasySkelLBM, which calculates C_{skel} and associated uncertainty from two or more bone sample measurements. Although LBM has been shown to provide a better estimate of C_{skel} compared to the average of C_{bone} values, the associated uncertainty is based on convenience sample only and does not represent the true uncertainty in the C_{skel} estimate. This study developed a method to improve uncertainty estimates of C_{skel} based on all possible C_{bone} combinations of representative bones. To select representative bones, a loading plot of principal component analysis (PCA) was used to identify clusters or highly correlated bones, and 13 bones were selected from the original 90 bones. The PCR was then applied to 13 cases and 13 selected bones. For a given number of bones, PCR models were fit for all possible bone combinations. There are 78, 286, 715, 1,287, and 1,716 combinations for 2, 3, 4, 5 and 6 bones, respectively. The standard deviation of the residuals (SD_{res}) of all combinations for each of the 13 cases was used to determine the uncertainties associated with the estimated C_{skel} . Linear regression was used to derive a relationship between SD_{res} and C_{skel} for a given number of bone samples. The results showed that the most collected bone samples were clustered on the PCA loading plot, and, therefore, underestimated uncertainties. In general, the higher uncertainties were associated with a lower C_{skel} and a smaller number of analyzed bones. The coefficient of variation ($SD_{\text{res}}/C_{\text{skel}}$) was stable at $C_{\text{skel}} \geq 10 \text{ Bq kg}^{-1}$. †Presented by S.Y. Tolmachev.

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