Inferring Population Exposure from Biomonitoring Data on Urinary Concentrations

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Biomonitoring studies such as the National Health and Nutrition Examination Survey (NHANES) are valuable to exposure assessment both as sources of data to evaluate exposure models and as training sets to develop heuristics for rapid-exposure-assessment tools. However, linking individual measurements of urine concentrations of a metabolite back to an individual's exposure rate is generally difficult, because: urine concentrations need to be converted to excretion rates; parent chemical exposures are inferred from multiple, sometimes overlapping metabolites measured in urine; and the same observation may be due to a less-recent, large exposure or a more-recent, smaller exposure. While individual measures are problematic, we demonstrate approaches to solutions for the above problems for population distributions of exposure. We calibrate models for gender-, ethnicity-, age-, and bodyweight-dependent predictors of creatinine production rate for the US population, based on the 2009-2010 NHANES sample. We use Bayesian methods to infer parental exposure given measurements on metabolites, allowing for the fact that multiple parents may result in the same metabolite. Results of simulations with stochastic exposure scenarios demonstrated that simple models assuming steady-state exposure give approximately the correct population median, but that the population variance of exposure depends on the exposure variance, the frequency of exposure events, and aspects of pharmacokinetics, and is thus is more problematic. However, the population variance can be bounded, and even uncertain knowledge of pharmacokinetic properties can help improve exposure estimates. *This abstract does not necessarily reflect EPA policy.*