

From sources to biomarkers:
A hierarchical Bayesian approach for
human exposure modeling

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Abstract

The long-term objective of this research project is to characterize multi-pollutant (arsenic, lead, cadmium, and chromium) human exposures by linking sources to biomarkers using a multi-scale (individual level, county level) hierarchical Bayesian model (HBM) that describes how multi-media pathways contribute to direct routes of exposure. Our approach is to use a statistical model that has explicit stages for pollutant sources, global and local environmental levels, personal exposures, and biomarkers. By analyzing these stages simultaneously, we provide an analysis of exposure pathways from the sources of toxic substances in the environment to biomarker levels observed in individuals. The complexity of our approach, in terms of levels of hierar-

chy, variety of (misaligned) data sources, and computational requirements, illustrates what is now possible using hierarchical Bayesian models. Our HBM draws on individual-specific measurements from the National Human Exposure Assessment Survey (NHEXAS) Phase I, supplemented by arsenic concentration measurements in topsoil and stream sediments. We focus on arsenic and its air, soil, water, and food pathways of exposure for individuals in the U.S. Environmental Protection Agency's Region 5 - Illinois, Indiana, Michigan, Minnesota, Ohio, and Wisconsin. After fitting the HBM, we report on the relative importance of the different pathways of arsenic exposure. In addition, we provide a discussion of generalizations to more complicated pathways, other regions, and a multivariate model.