

Characterizing Exposure Trends from NHANES Urinary Biomonitoring Data Zachary Stanfield¹, Victoria Hull^{1,2}, Risa R. Sayre^{1,2}, R. Woodrow Setzer¹, Kristin K. Isaacs¹, John F. Wambaugh¹ 1. Center for Computational Toxicology and Exposure, Office of Research and Development, U.S. Environmental Protection Agency, Research Triangle Park, North

ABSTRACT

- Knowing which environmental chemicals contribute to metabolites observed in humans is necessary for meaningful estimates of exposure and risk from biomonitoring data. It is also important to understand how these exposures might be changing over time.
- We employed a recently developed approach (a publicly available R package called "bayesmarker") using Bayesian methodology to infer ranges of exposure to parent compounds consistent with urinary biomarker levels reported in the National Health and Nutrition and Examination Survey (NHANES), which is representative of the U.S. population.
- Metabolites were linked to their parent chemicals using information from the NHANES reports and text mining of PubMed abstracts for metabolite names and synonyms.
- Chemical exposures were inferred for each NHANES cohort individually to identify temporal exposure trends for 179 unique parent chemicals of 151 NHANES metabolites.
- Exposure differences in population groups were also examined for unique patterns.

METHODS

The R package "bayesmarker" (github.com/USEPA/CompTox-HumanExposure-bayesmarker) is made up of 5 functions that are called in succession. The needed input is a single Excel file that has 3 tables, which are created manually based on the metabolites/cohorts of interest and organization of the NHANES data. Exposures are inferred by running the full modeling pipeline on each NHANES cohort individually from 1999-2016 to observe temporal changes in exposure. The output are exposure distributions via Markov chains for 10 different population groups based on age, gender, and body mass index. The package also allows for combining data from multiple cohorts to improve statistical power and reduce the uncertainty in exposure inferences. This was demonstrated by comparing changes in exposure using all data from 2000-2010 with data from 2011-2016.

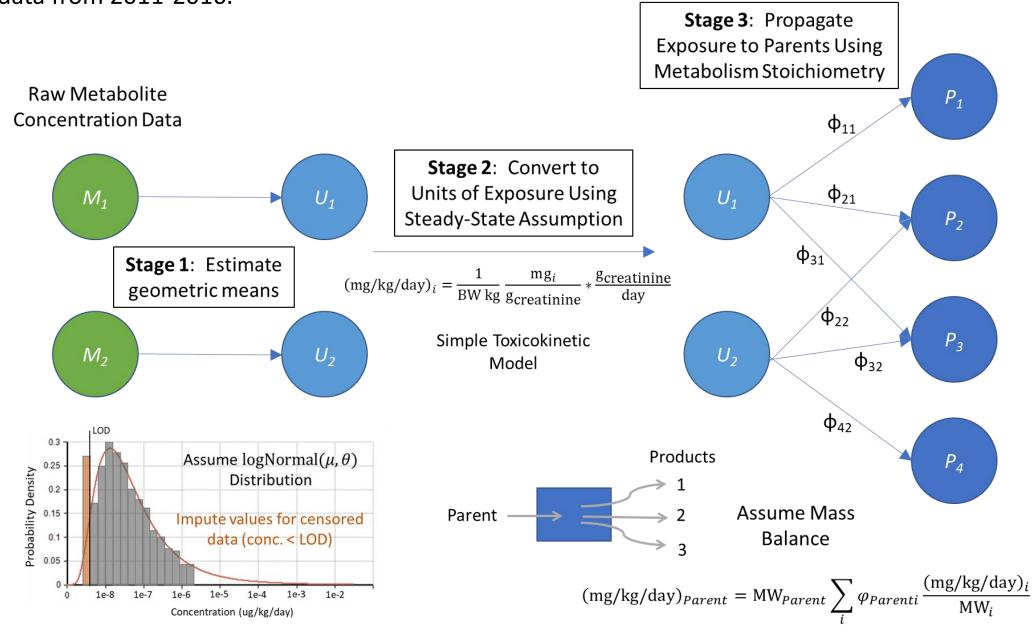
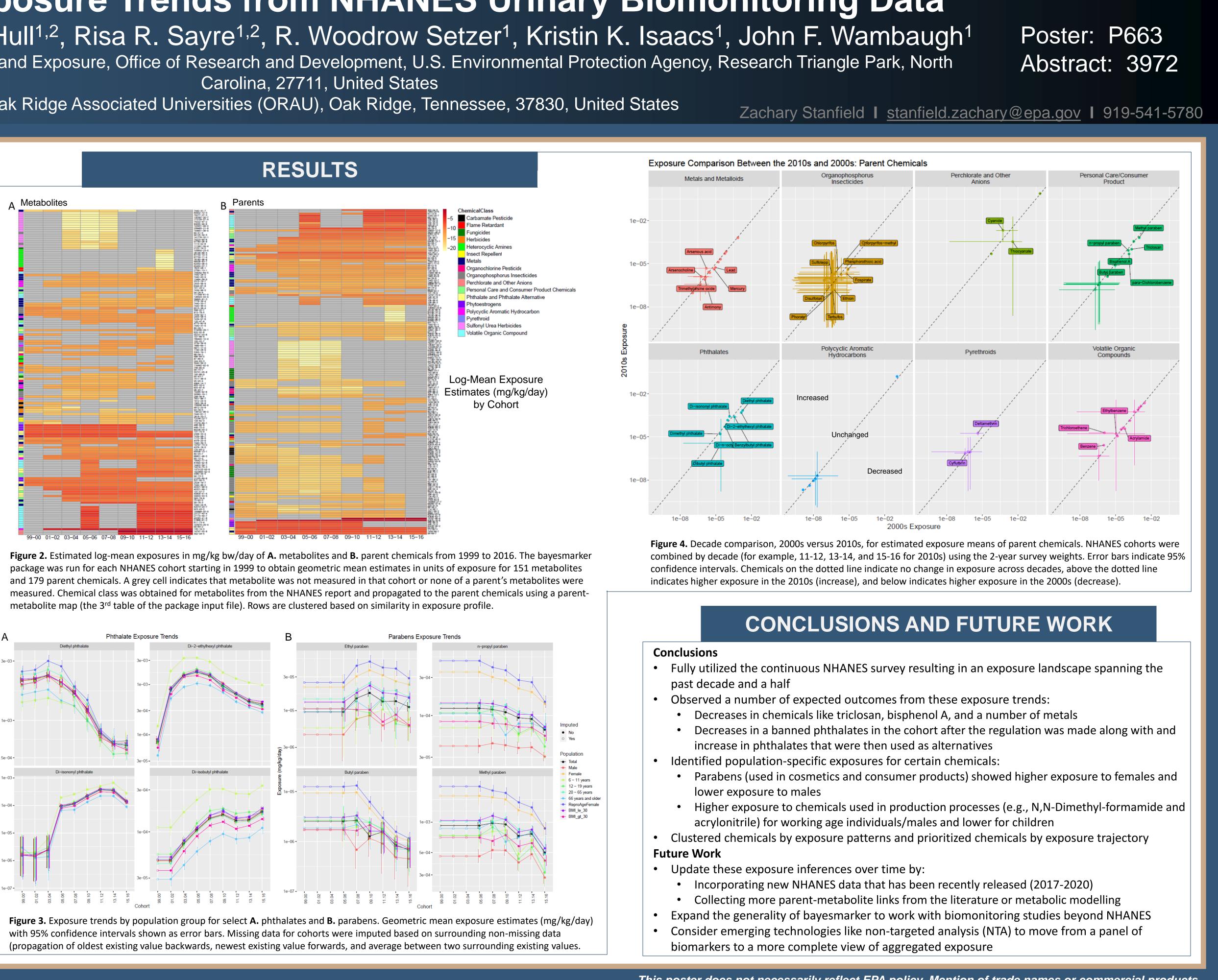
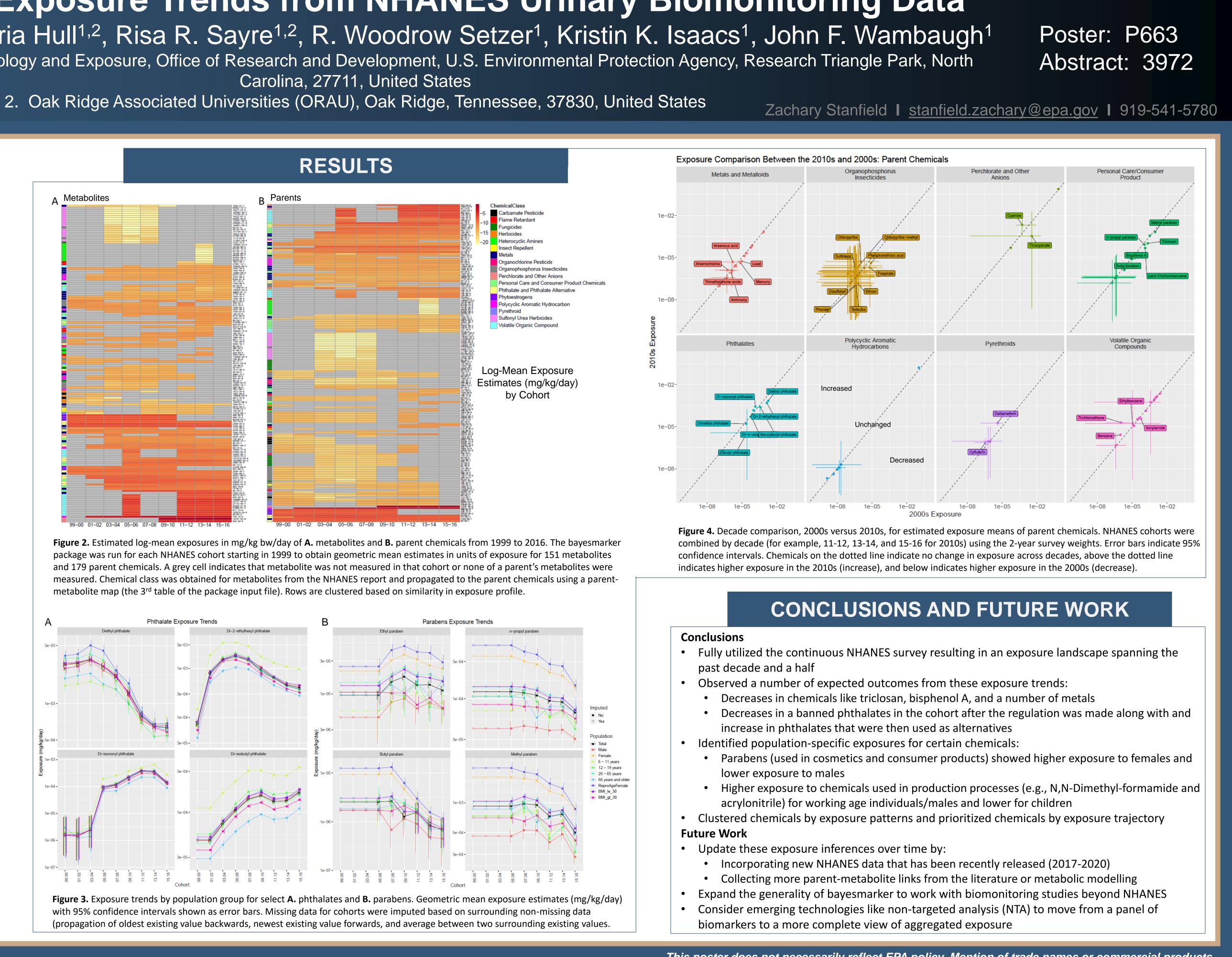


Figure 1. Depiction of the modeling pipeline used by bayesmarker. The statistical model has three stages: 1. Calculate distribution statistics (mean, standard deviation, etc.) for the population urine concentration measurements, 2. Convert to units of exposure via a simple toxicokinetic model assuming steady-state with creatinine correction, and 3. Propagate exposures from metabolites to parent chemicals using known metabolic links while assuming mass balance.

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