

Protection Agency

ABSTRACT

- Biomonitoring data provides insight into the chemicals, and their concentrations, commonly present in humans, but it is also important to know which chemicals in the environment contribute to the observed metabolites for the sake of estimating exposure and risk.
- Here we used Bayesian methodology to infer ranges of exposure for parent chemicals consistent with biomarkers identified in urine samples from the U.S population by the National Health and Nutrition Examination Survey (NHANES).
- Metabolites were linked to their parent chemicals using information from the NHANES reports and text mining of PubMed abstracts for metabolite names and synonyms.
- We calculated chemical exposure and risk estimates for various population groups.
- We investigated exposure to children between the ages of 0 and 5, a population group that was debuted in the 2015-2016 NHANES cohort (measurement data for 50 metabolites).

METHODS

This work is an update to the method presented in Wambaugh et al 2014. Briefly, metabolite urine concentration measurements from NHANES (CDC 2016) are used in a Bayesian inference model to estimate mean parent chemical exposures across various population groups. NHANES data from 2011-2016 were added and the code has been converted into an R package that will be made public. Results were generated using data available from the most recent cohort to obtain the current exposure estimates. The functions calc tkstats() and calc mc css() from the HTTK package (Pearce et al 2017) were used to obtain bioactivity: exposure (BER) ratios.

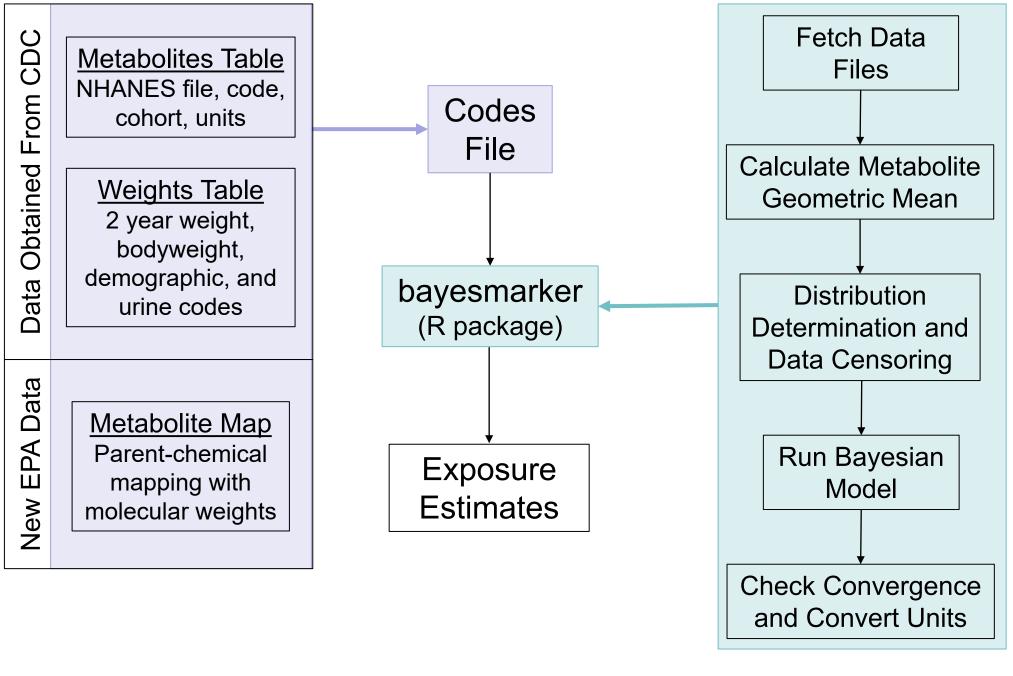
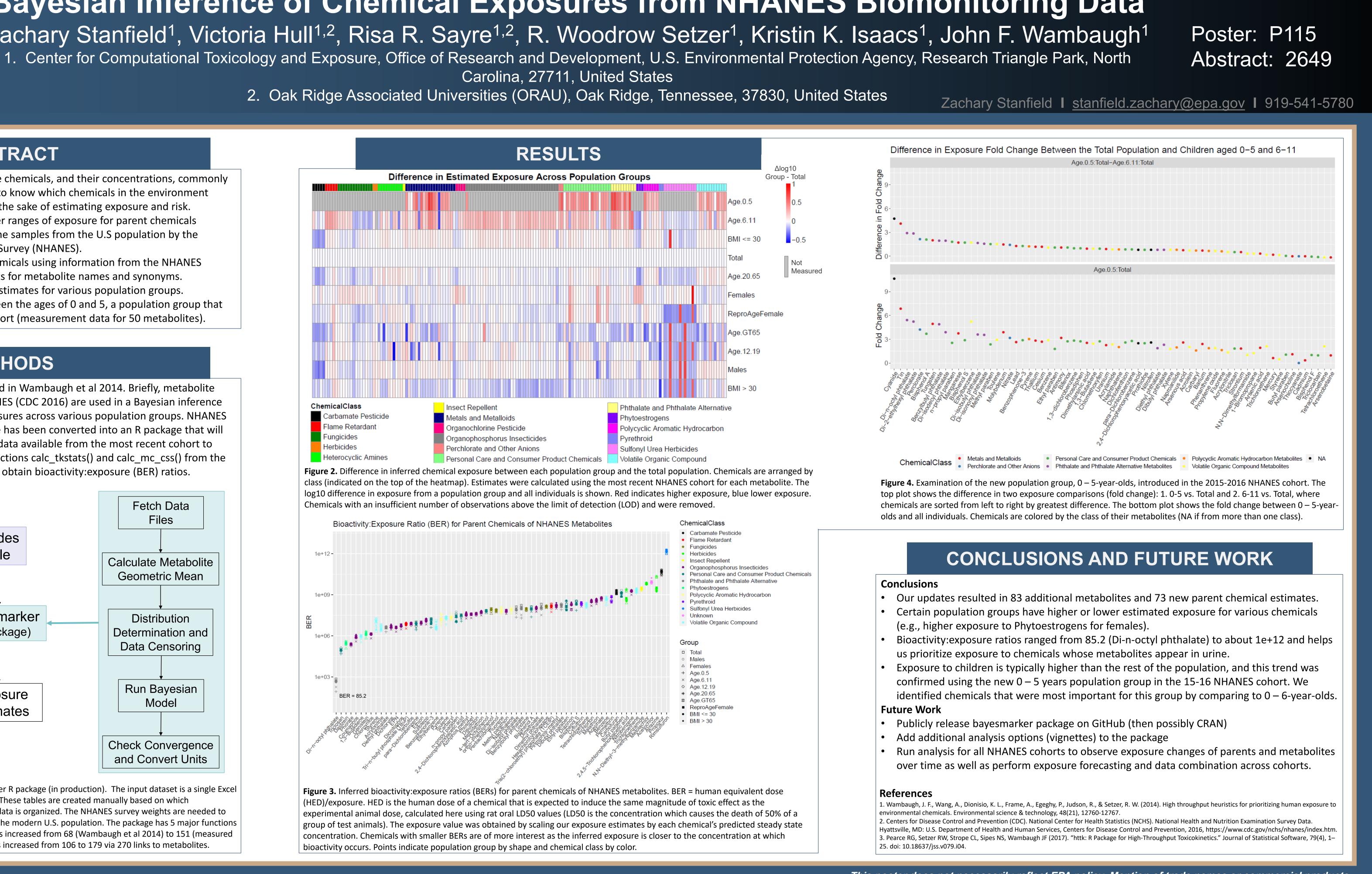


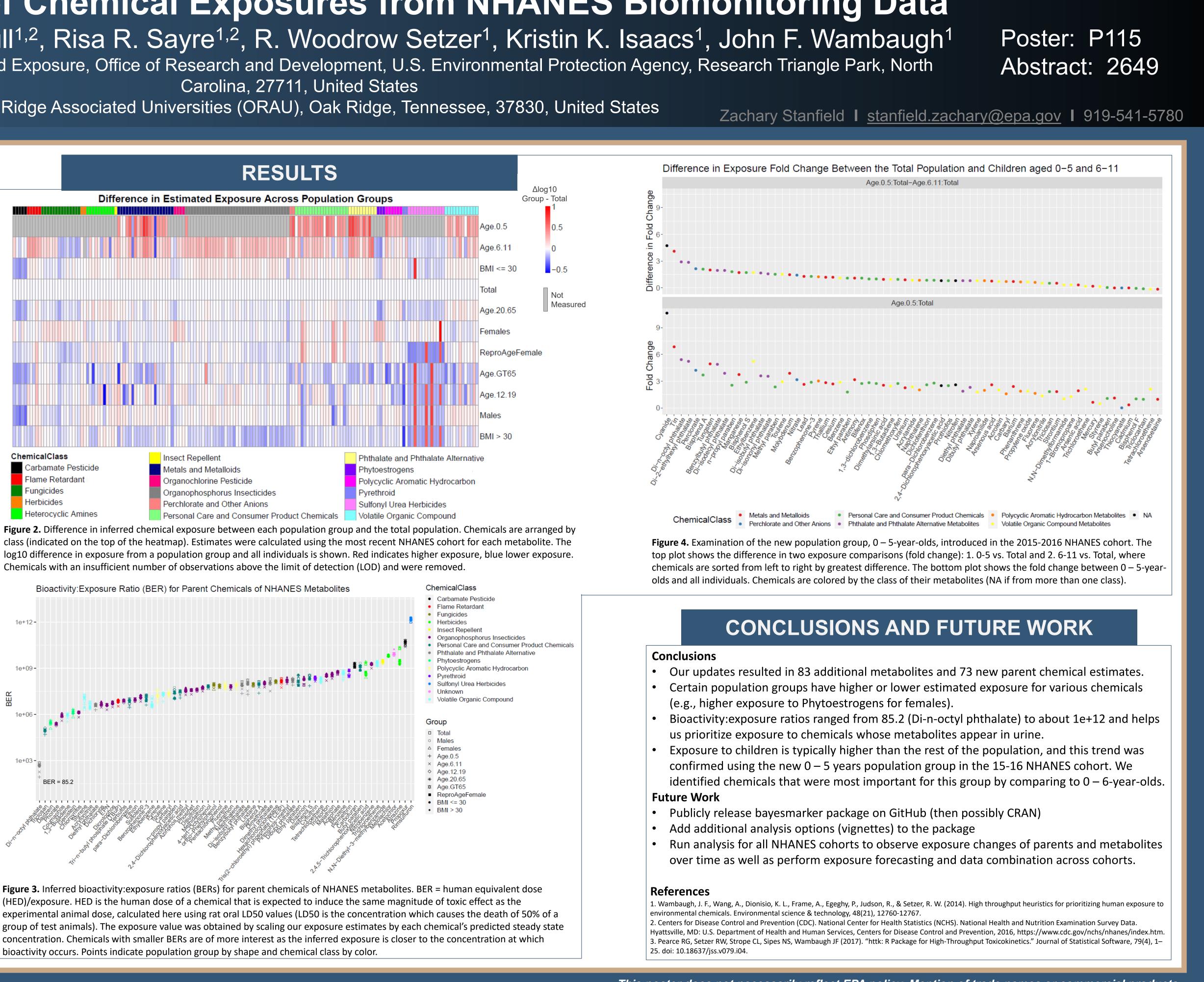
Figure 1. Depiction of general workflow for the bayesmarker R package (in production). The input dataset is a single Excel file that has 3 sheets (tables; described in the purple box). These tables are created manually based on which metabolites/cohorts are of interest and how the NHANES data is organized. The NHANES survey weights are needed to translate from their oversampling procedure to represent the modern U.S. population. The package has 5 major functions (descriptions in green box). The number of metabolites was increased from 68 (Wambaugh et al 2014) to 151 (measured in at least one cohort) and the number of parent chemicals increased from 106 to 179 via 270 links to metabolites.

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