

Mapping a Path to Disease: Quantifying the risk of exposure to environmental chemical mixtures via a common molecular target using a geospatial modeling approach

Kristin Eccles, Agnes Karmaus, Nicole Kleinstreuer, Fred Parham, Cynthia Rider, John Wambaugh, Kyle Messier

National Institute of Environmental Health Sciences
Division of Translational Toxicology

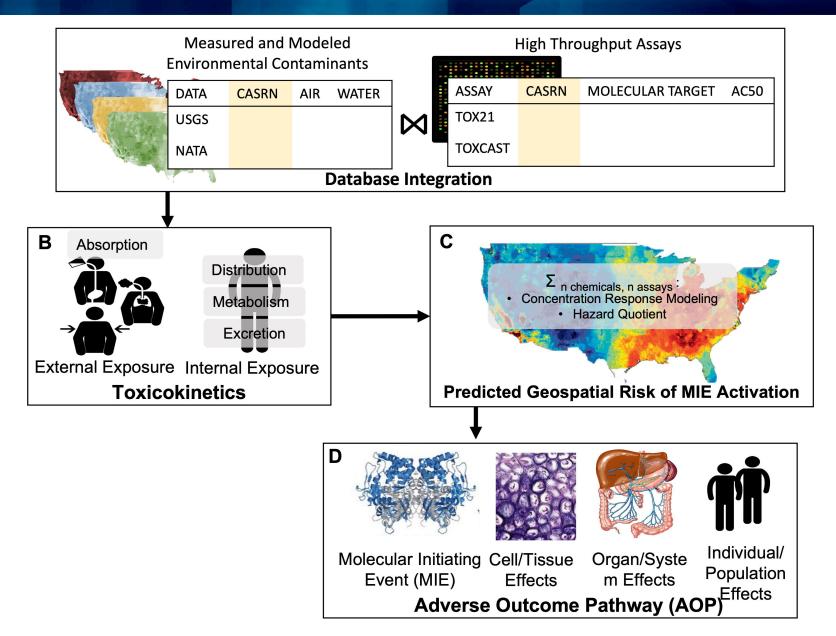
kristin.eccles@nih.gov



Introduction

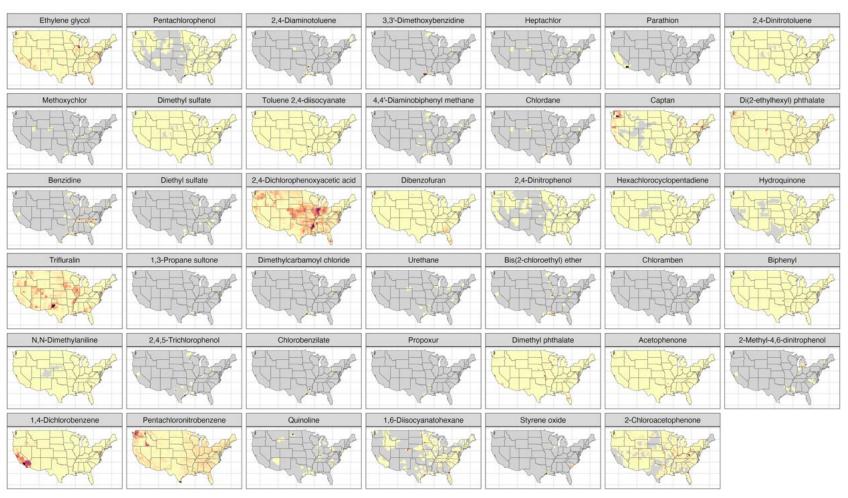
- Real-world chemical exposures are complex mixtures heterogeneously distributed across space.
 - Traditional risk assessments use a chemical-by-chemical approach and apical disease endpoints.
- New methods for toxicity testing, such as high throughput screening (HTS) assays, can quantify chemical hazards
- HTS data inform on molecular level changes that act on a biological pathway
 - Multiple exposures can be integrated based on chemicals that act on the same pathway.





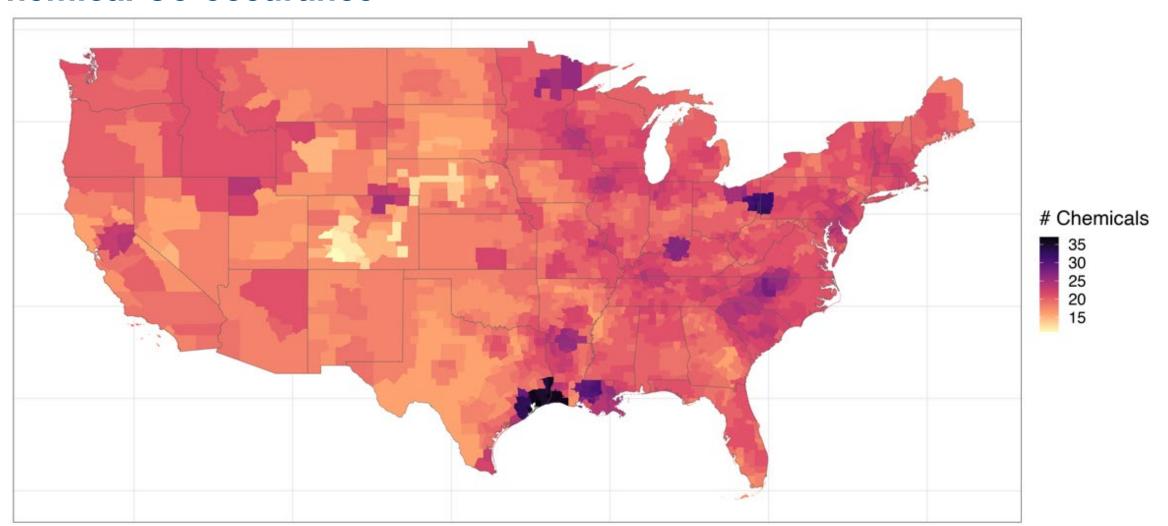
Chemical Data: National Air Toxics Assessment (NATA)

- Chemical transport model
 - Emissions
 - Chemistry
 - Meteorology
- Average annual chemical concentration in 2014 by census tract
- n chemicals in NATA = 188
- n chemical activate CYP1A1_Up = 41

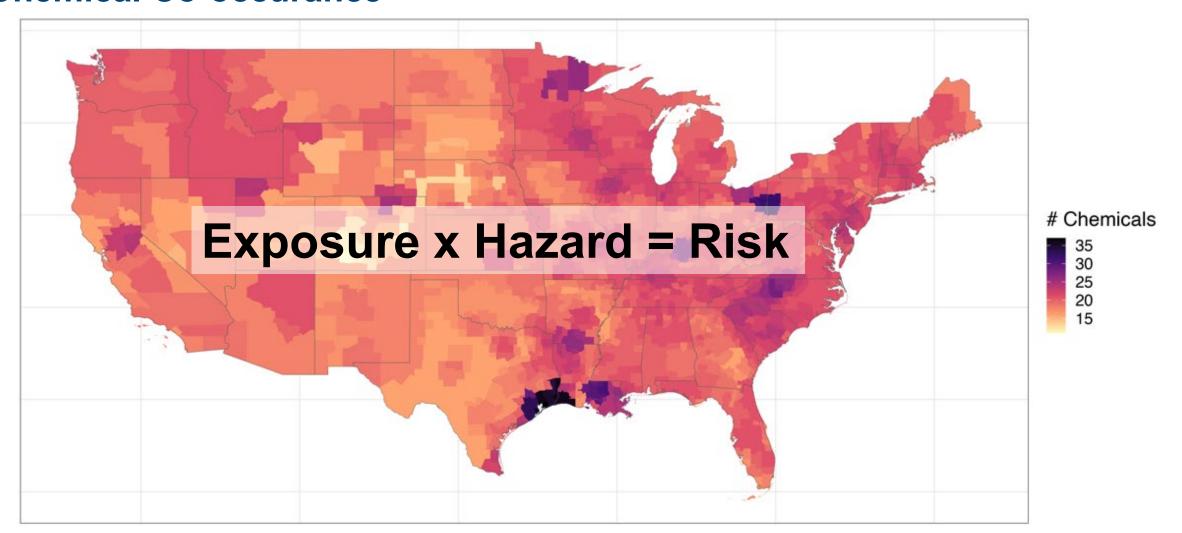




Chemical Co-occurance



Chemical Co-occurance



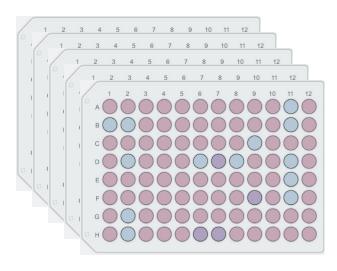


Hazard Data: Curated TOX21 High Throughput Assay Data

 Hazard Data: Exposure response parameters from the EPA developed pipeline (n assays=1457, n chemicals=9298)

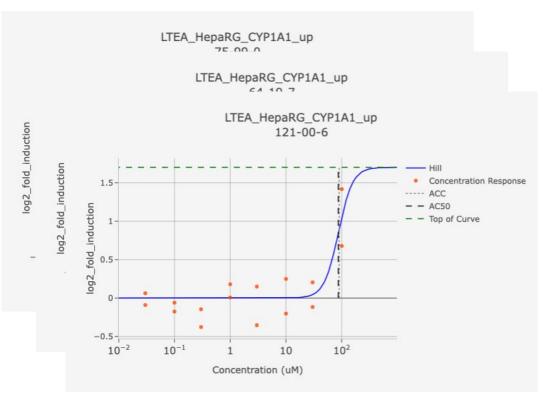
EPA data is then curated with additional QA/QC by the NIEHS/NTP Integrated Chemical

Environment



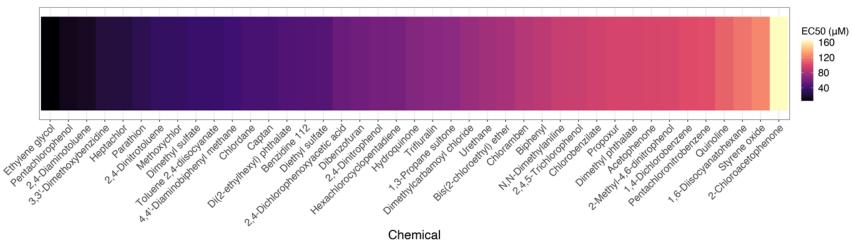
R: tcpl pipeline



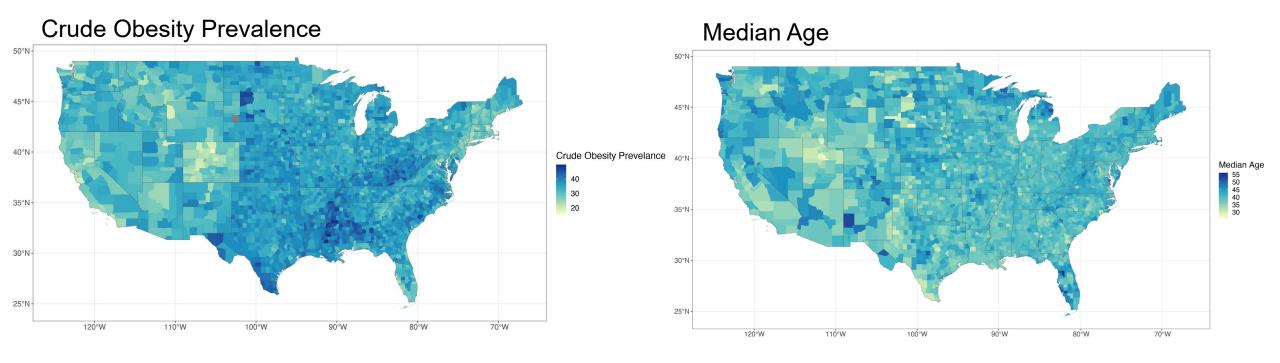


Hazard Data: High Throughput Assay

- Increase transcription factor expression of CYP1A1 (LTEA_HepaRG_CYP1A1_up)
- The gene encodes for one of the cytochrome P450 superfamily of enzymes
 - Responsible for Phase I metabolism → can results in carcinogenic intermediates
 - Also necessary for metabolic functions (e.g., steroidogenesis)
- Expression is induced by exposure to some polycyclic aromatic hydrocarbons
 - E.g., cigarette smoke



Population Data by County

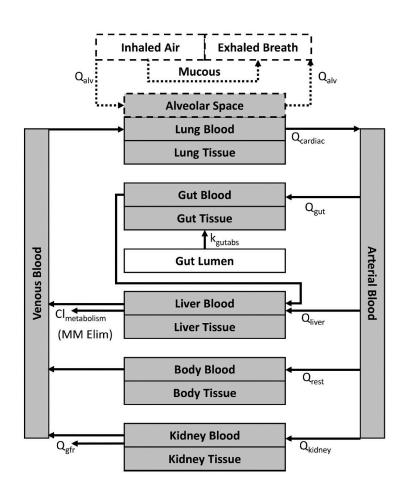


Key for estimating spatial variation of:

- Internal exposure via rate of inhalation
- Steady State Plasma (Blood) Concentration via hepatic clearance

External concentration → Internal dose → Steady state plasma concentration

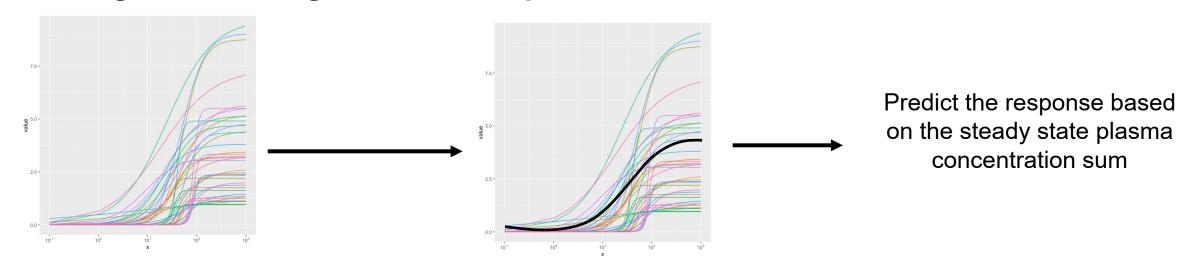
- 1. Inhalation rate by county
 - Affected by age and obesity status
- 2. Physiologically based toxicokinetic (PBTK) modeling links inhaled dose to a plasma concentration
 - httk: 3 compartment model (lung, liver, blood)
 - ADME controlled by: Chemical parameters and Hepatic Clearance
 - Affected by age and obesity status
 - E.g., Younger age = higher metabolic clearance = Lower steady state plasma concentration





Steady state plasma concentration -> Combined risk of molecular perturbation

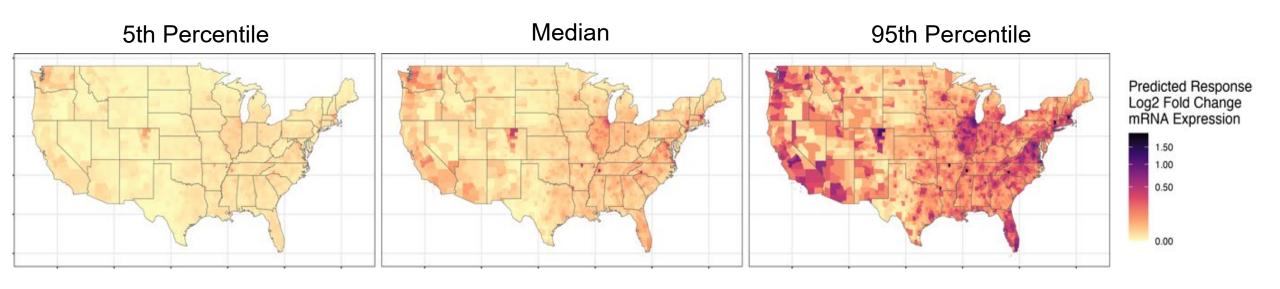
1. Generalized Concentration Addition/ Response Addition: Predicting the Log2 Fold Change in mRNA Expression



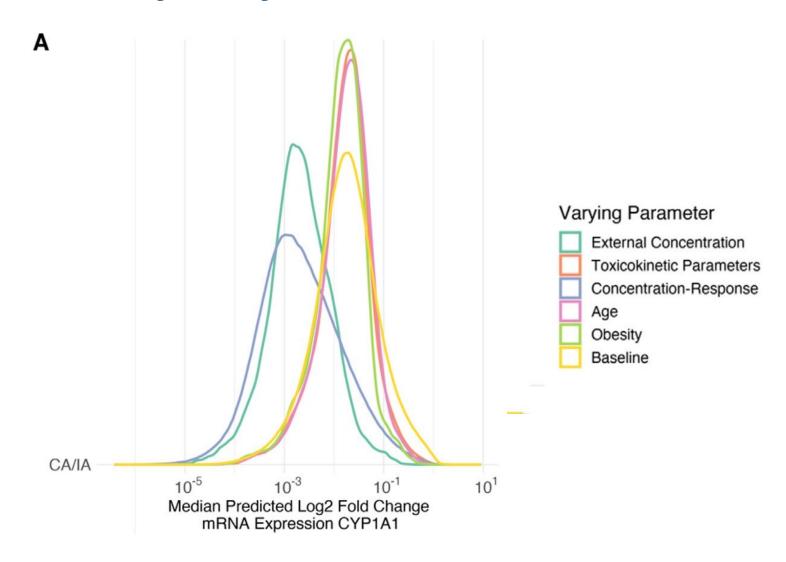
2. Hazard Index

$$HI = \Sigma_{n} \frac{Steady\ State\ Plasma\ Concentration}{Concentration\ at\ 10\%\ Activity\ (AC10)}$$

Mapped Risk of Molecular Perturbation



Monte Carlo Uncertainty Analysis





Conclusions

- This method integrates multiple geospatial chemical exposures with chemical potency, for chemicals that act on the same molecular target
- Can be expanded to other chemical, assays, geographic extents
- Ongoing work: use this workflow to link molecular level perturbations with adverse cardiovascular outcome data
- Build a weight of evidence linking environmental exposures to health outcomes

Molecular Adverse **Key Events Initiating Event** Outcome Receptor/ligand Gene activation Altered tissue Disease interaction development Protein production Impaired development Altered tissue DNA binding Altered signaling · Impaired reproduction function Protein oxidation Cell-cell interactions

Thank you

Questions

kristin.eccles@nih.gov

kristineccles