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Impact of parameter distribution assumptions on distributional estimates of human equivalent doses Celia Schacht

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Outline

- Background and motivation Schacht et al. 2024*
- Methods
 - Generating human equivalent doses (HEDs)/ Parameter distributions and Monte Carlo methods for Physiologically Based Pharmacokinetic (PBPK) models
 - Testing HED distributions & percentiles
 - Establishing influential parameters
- Results
- Takeaway points



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Evaluating the impact of anatomical and physiological variability on human equivalent doses using PBPK models

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Introduction/Background

Human Equivalent Dose/Concentration (HED/HEC): Human concentration (inhalation, ppm) or dose (oral, mg/kg) of a substance expected to induce the same magnitude of toxic effect for a human as that observed for lab animals exposed to a known concentration or dose

- Fixed (average) parameter values \rightarrow point-estimate HEDs: ignores variability.
- Probabilistic framework proposals assume that some risk distributions are lognormally distributed (NRC, WHO IPCS-International Program on Chemical Safety).
 - Parameter distributions are also commonly described as lognormal or normal (justification for shape not supported by data, Crump et al. 2010).
- We generated HEDs using various sets of assumptions about input parameter distributions to then characterize HED distributions using two PBPK models: DCM (U.S. EPA IRIS Report, 2011) and chloroform (CF) (Sasso et al., 2013).
- How are HED distributions affected by different assumptions about underlying PBPK model parameter distributions?
 - Do model parameter distribution shapes and/or bounds significantly affect the shapes of HEDs?
 - When data are limited, how can we identify the parameters most influential to the HEDs?

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Methods: Chemicals & Dosing Patterns for Humans



Chloroform Model

Methods: HED Calculation & Monte Carlo Methods



Compare HED distributions 1. How close are the medians? How close are the extreme percentiles? 2. Are they lognormal?



1. Compare the HED distribution percentiles across each parameter distribution type.

- ► Find pairwise % difference.
 - Find maximum difference of pairwise % difference (MPPD).
- 2. Test HED distributions for lognormality.
 - How much do they deviate from lognormality?
 - ► Royston's V': Turns the Shapiro-Francia test statistic W → departure index V'.
 - ► $V' \leq \approx 2 \rightarrow \text{data is lognormal.}$

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Methods: Finding the most Influential Parameters

- Sensitivity analysis: methods to determine how the uncertainty in the output of a mathematical model can be attributed to different sources of uncertainty in its inputs/parameters (Sensitivity analysis and PBPK: Evans, 2001; Hsieh, 2018; McNally, 2011).
 - Local One-at-a-time (OAT) methods that perturb parameters around nominal values.
 - Simple to implement and inexpensive but can be misleading if there are non-negligible interactions among multiple parms or nonlinear processes.
 - Global calculates the contribution of a parameter over the entire parameter space.
 - Examples: Morris Screening, Sobol' Indices.
 - Variance-based methods find the percentage to output variance contributed by:
 - Each parameter alone

Results: MPPD values – How did HEDs Differ?

MPPD: The maximum pairwise percent difference across parameter distributions at each HED percentile.

For example:

Oral chloroform HEDs/70 y.o. females HEDs:

- 50th percentile generated by 5 different parameter distribution types only differed by 3.8%, at most.
- 1st percentile: 13.1% max difference.



Results: Departure from lognormality



- DCM HEDs deviated more from lognormality $(V' \gg 2)$.
- HEDs derived from inhaled doses conformed more to lognormality than oral doses.
- Deviations from lognormality are due to extreme percentiles/long tails.
- Long tails result from extreme values for influential parameters...



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Results: ... Which Influential Parameters?

- Global sensitivity analysis reveals the most influential parameters* for the output: amount oral DCM metabolized in the liver.
 - ▶ Total effects: % contribution to the output variation.
- Skewed/Low HEDs can result from individuals simulated with:
 - Very low liver volume.
 - Very high cardiac output.
- Skewed/high HEDs (tails) can result from:
 - Low cardiac output.
 - Low metabolism rate.
- Notice that PB (blood:air PC) and non-listed parameters have very little effect on HED distributions (in this case!).

*Influential parameters: parameters for which more accurate representations of parameter uncertainty and variability may be important.



Parameters that account for $\sim 100\%$ of Total Effects: Fractional tissue volumes (liver, fat, slowlyperfused), maximum metabolic rate & affinity, cardiac output

Parameter key			
BW	Body mass		
Fractional tissue volumes			
VFC		Fa	t
VLC		Liver	
VKCTXC		Kidney cortex	
VKMEDC		Kidney Medulla	
VRC/VSC		Rapidly/Slowly-perfused	
Flow rates			
QLC		Liver flow rate	
QKCTXC		Cortex flow rate	
QCC		Cardiac output	
QPC/	QPC/VPR Respiration		
Chemical-specific			
VMAXC, KM, VMRATIO		,	Metabolic parameters
PB			Blood:air PC

- Influence of parameters depends on the dose metric being tested, route of exposure, & chemical/compound group.
 - Kidney parameters influence kidney dose metrics, etc.
 - Respiration rate influences inhalation cases.
 - Some parameters may be more influential in relation to metabolically active compounds (such as VOCs) than other chemical classes.
 - Dose is also a factor (linear vs nonlinear effects).



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Note: Schacht et al. (2024) only considered 2 PBPK models/2 dose metrics/2 routes of exposure – influential/important parameters may differ for other models/dose metrics/routes of exposure!

Discussion/Conclusion – Takeaway Messages

- The distribution types* (i.e. truncated normal & lognormal, untruncated lognormal, and uniform) used to represent uncertainty/variability in human parameter values:
 - ▶ Have little impact on the **central tendencies** of the HED distributions.
 - **Do impact extreme percentiles** of HED distributions.

*parameter distributions have the same mean and variance.

- Tails in HEDs are more responsive to changes in extreme quantiles of input parameters.
 - Thus, it is important to get accurate estimates of these parameter distribution's highest and lowest values (i.e., most sensitive populations).
 - Consider the accuracy of the distribution, not just its "family".

- Lognormality of HED distributions is scenario-dependent.
 - ▶ Chloroform/amount metabolized in kidney & inhalation routes $\rightarrow \approx$ LN.
 - ▶ DCM/amount metabolized in liver & oral routes \rightarrow deviations.

Not all parameters are created equal

- Predictions of dose metrics/HEDs (central estimates or extreme percentiles) can be greatly improved by having precise knowledge about certain input parameter distribution shapes & variances (but not all).
 - Some input parameters will have little/no effect on predictions of central estimates/extreme percentiles.
- Schacht et al. (2024) discussed the input parameters or situations for which it is important to allocate time and resources to collect data to develop more accurate representations of parameter uncertainty and variability.
- Some parameters exert more influence on certain outputs than others.
 - When parameter data is limited, sensitivity analysis may be used to identify the parameters for which accurate estimates are most important.

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Thank you!

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