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Monte Carlo for variability simulation and uncertainty

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Office of Research and Development
Center for Computational Toxicology and Exposure

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Overview

- Uncertainty vs. Variability in HTTK model parameters
- Characterizing key uncertainty in chemical-specific TK parameters
  - Fraction unbound in plasma protein (Fup)
  - Intrinsic hepatic clearance rate (Clint)
- Characterizing variability: HTTK-Pop for human TK variability
- Relative contributions of uncertainty and variability to TK model predictions
- Simulating sensitive subpopulations

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Uncertainty vs. variability in HTTK model parameters

Review: HTTK model parameters

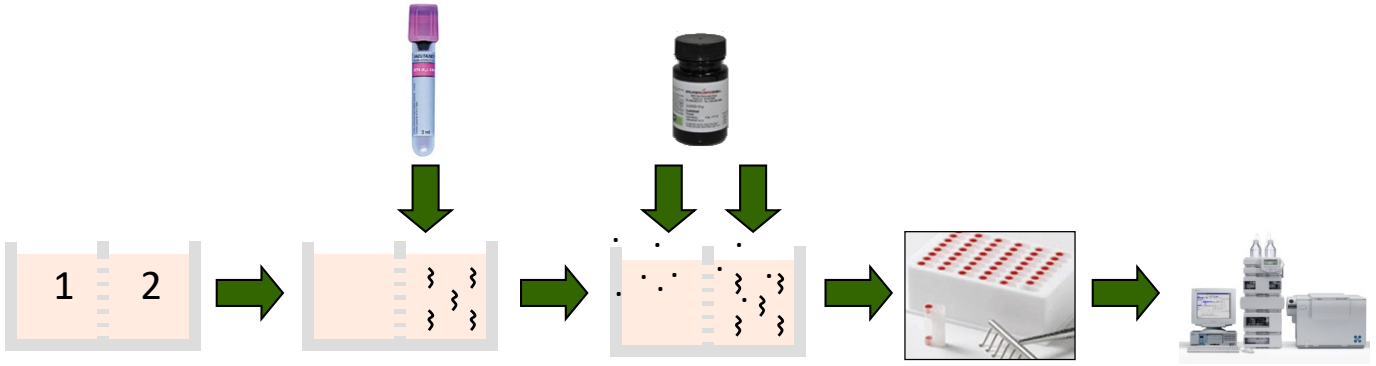
Chemical-specific parameters	
Intrinsic hepatic clearance rate (CLint)	Measured in HT *in vitro* assays (Rotroff *et al.* 2010; Wetmore *et al.* 2012, 2014, 2015; Wambaugh *et al.* 2019) or predicted *in silico* (Sipes *et al.* 2017)
Fraction unbound to plasma protein (Fup)	
Tissue:blood partition coefficients (for compartmental models)	Predict from phys-chem properties and tissue properties (Pearce et al., 2017)
Physiological parameters	
Tissue masses (including body weight)	Gathered from data available in the published literature [Wambaugh et al. 2015; Pearce et al. 2017a]
Tissue blood flows	
Glomerular filtration rate (passive renal clearance)	
Hepatocellularity	

Chemical-specific parameters measured *in vitro* carry measurement uncertainty

Chemical-specific parameters	
Intrinsic hepatic clearance rate (CLint)	Measured in HT *in vitro* assays (Rotroff *et al.* 2010; Wetmore *et al.* 2012, 2014, 2015; Wambaugh *et al.* 2019)
Fraction unbound to plasma protein (Fup)	

CLint: Cryo-preserved hepatocyte suspension
Shibata *et al.* (2002)

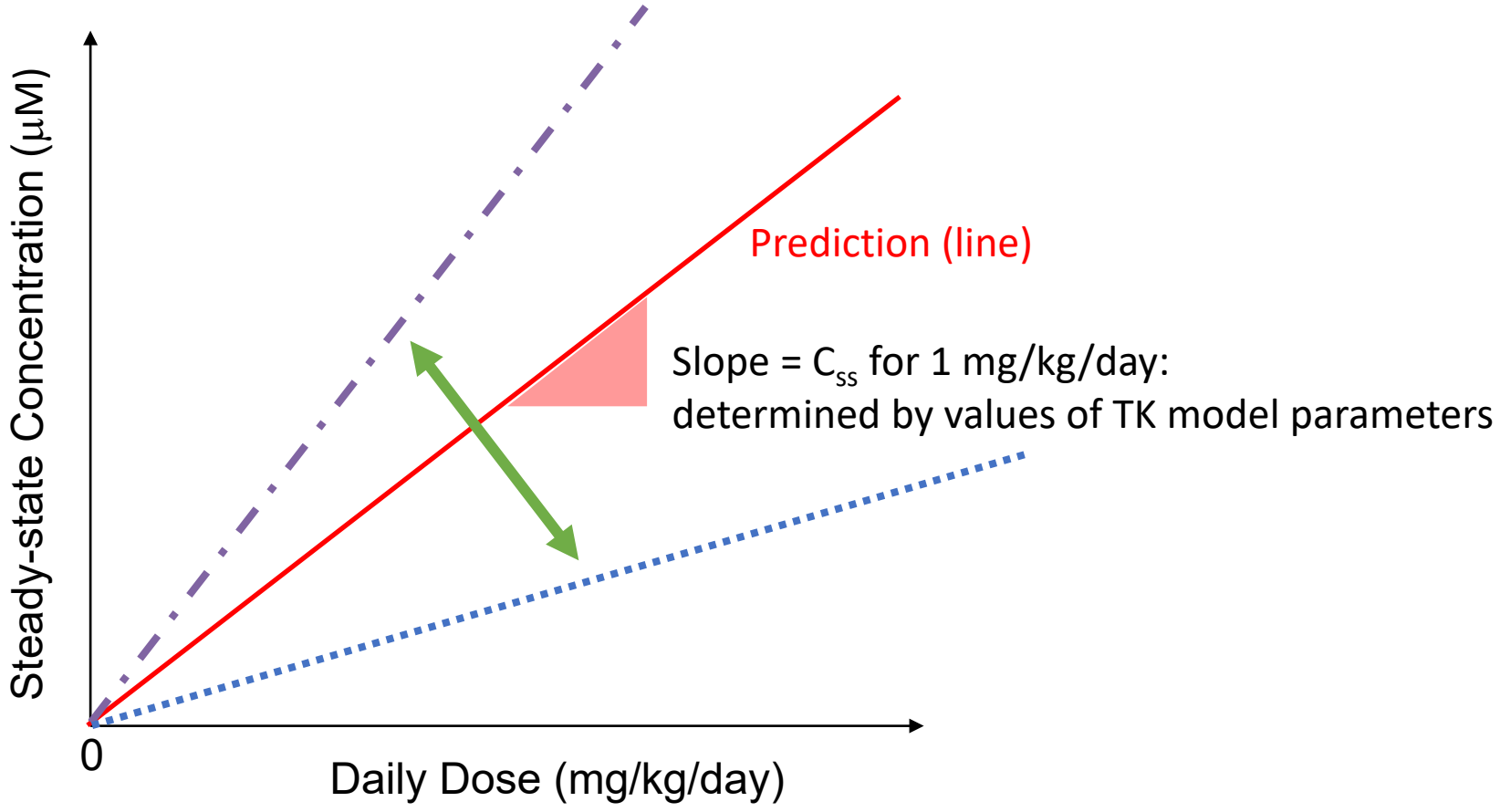
Fup: Rapid Equilibrium Dialysis (RED)
Waters *et al.* (2008)



Parameters represent biology — so they have population variability

Chemical-specific parameters	
Intrinsic hepatic clearance rate (CLint)	Represent chemical-body interactions — vary with individual genetics, environmental factors, age, etc.
Fraction unbound to plasma protein (Fup)	
Tissue:blood partition coefficients (for compartmental models)	
Physiological parameters	
Tissue masses (including body weight)	Represent physiology — vary with individual genetics, environmental factors, age, etc.
Tissue blood flows	
Glomerular filtration rate (passive renal clearance)	
Hepatocellularity	

HTTK model parameters determine the slope relating Css to daily dose – need to propagate both uncertainty & variability



Wambaugh et al. (2019)

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Approach to uncertainty & variability: Monte Carlo

- Characterize uncertainty in chemical-specific parameters Fup and Clint in terms of probability distributions
- Characterize population variability in physiological parameters in terms of (correlated) probability distributions
- Draw samples from distributions: “simulated population”
- Evaluate HTTK model for each “simulated individual” in the “simulated population”
- Describe resulting distribution of HTTK model predictions

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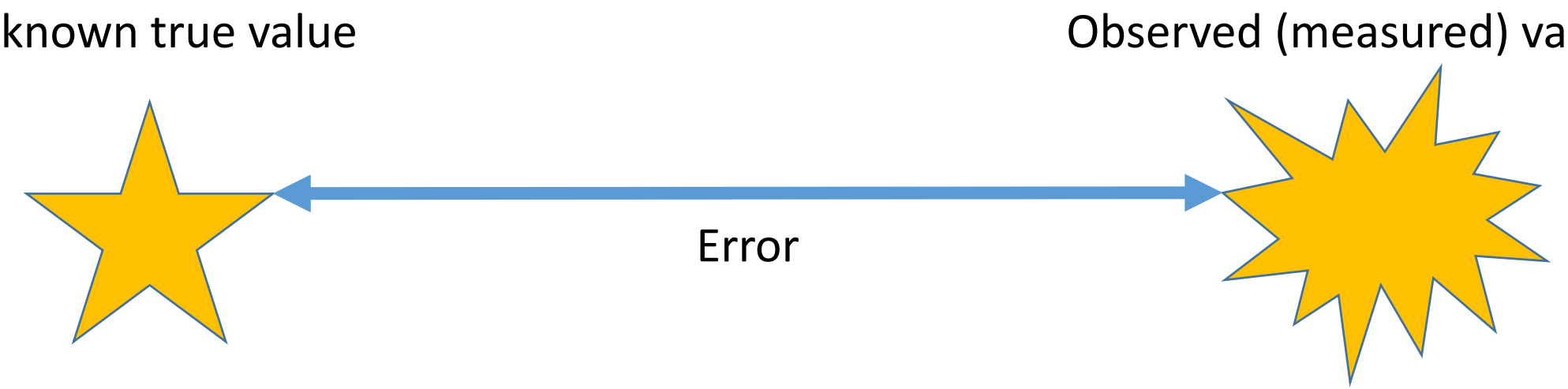
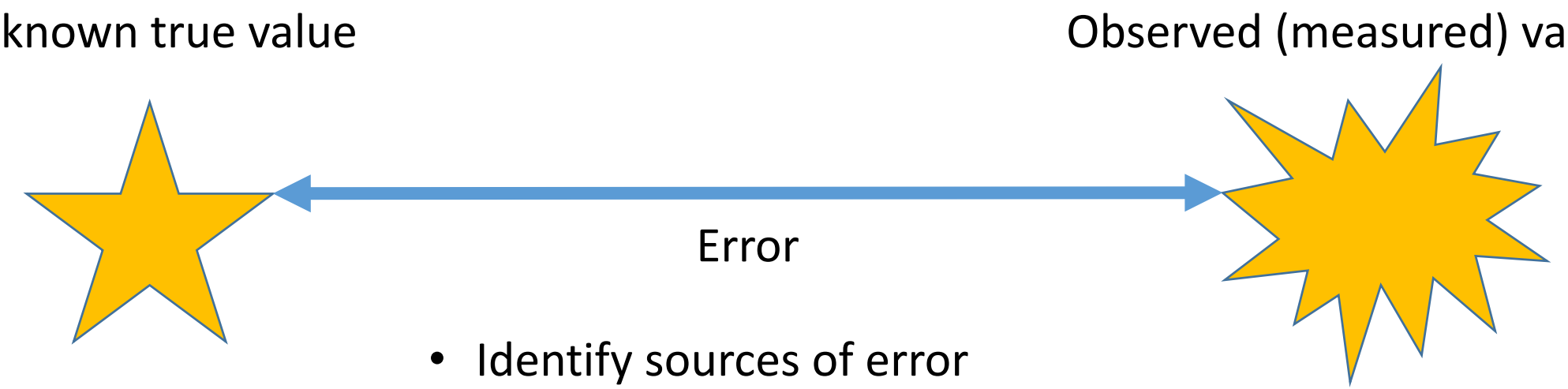
Characterizing key uncertainty in chemical-specific TK parameters

General approach to uncertainty quantification



General approach to uncertainty quantification

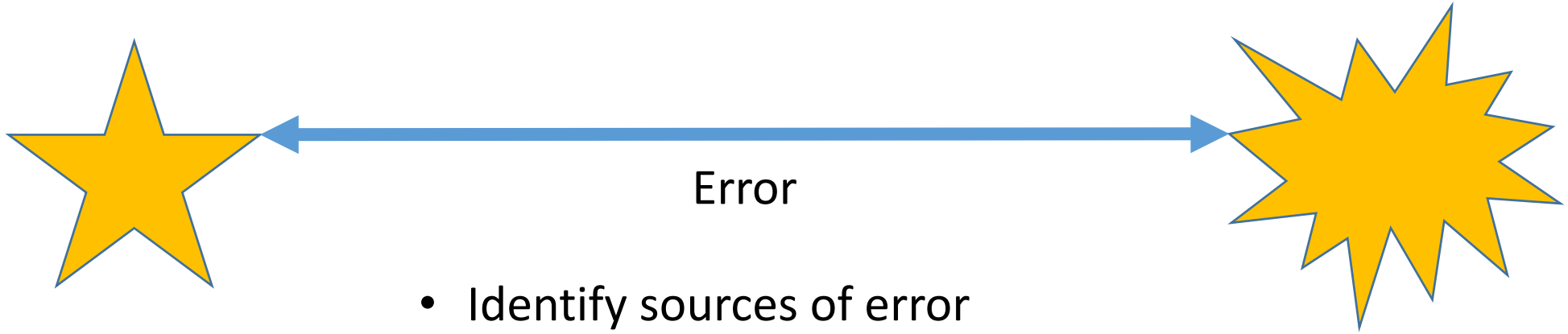


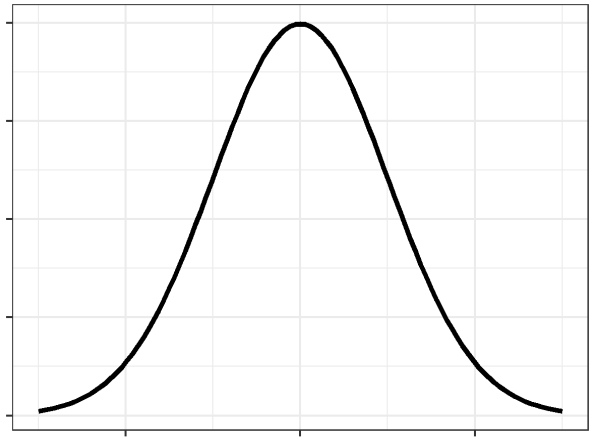
- Identify sources of error
- Develop mathematical model of error

General approach to uncertainty quantification

Unknown true value

Observed (measured) value





- Identify sources of error
- Develop mathematical model of error

Bayesian inference:
Find a *distribution* of possible true values compatible with the observed values, under this error model

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Uncertainty in Fup

Fup: How to measure *in vitro* using Rapid Equlibrium Dialysis (RED)

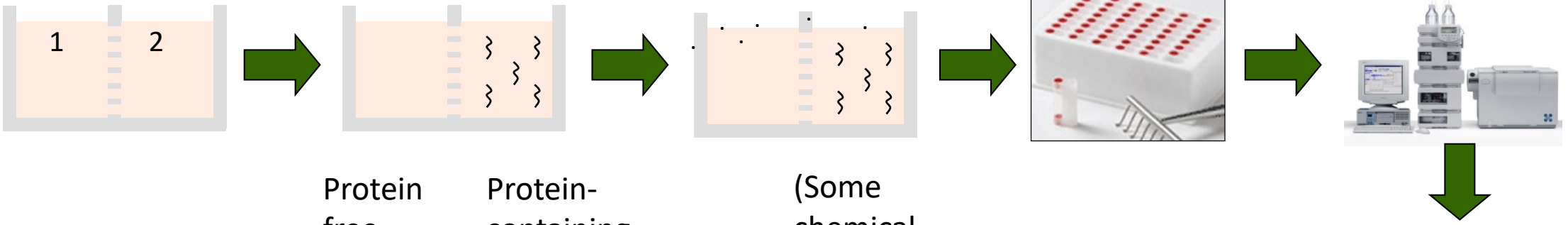
Semi-permeable membrane (chemical can pass, but not protein)

Add plasma to one side

Add chemical

Let equilibrate (until unbound conc. equal on both sides)

Use mass spectrometry to measure chemical conc. from each side



Protein free side

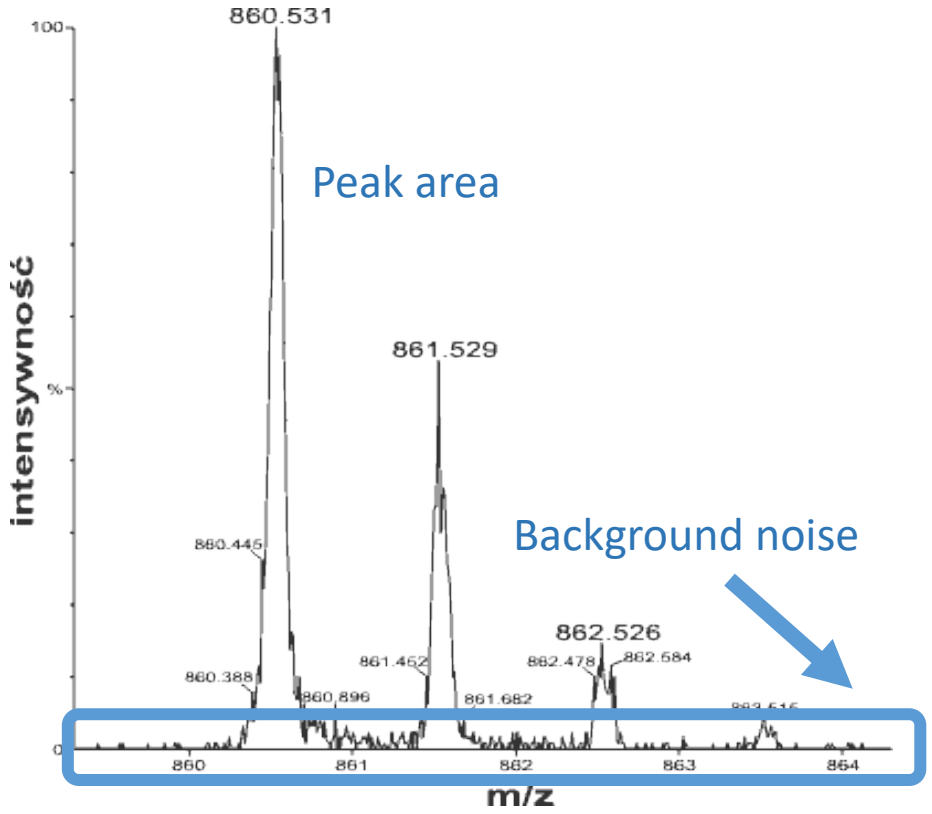
Protein-containing side

(Some chemical will bind to protein)

$$F_{up} = \frac{\text{Protein−free conc.}}{\text{Protein−containing conc.}}$$

Waters et al. (2008); Rotroff et al. (2010); Wambaugh et al. (2019)

Sources of measurement uncertainty: Mass spectrometry



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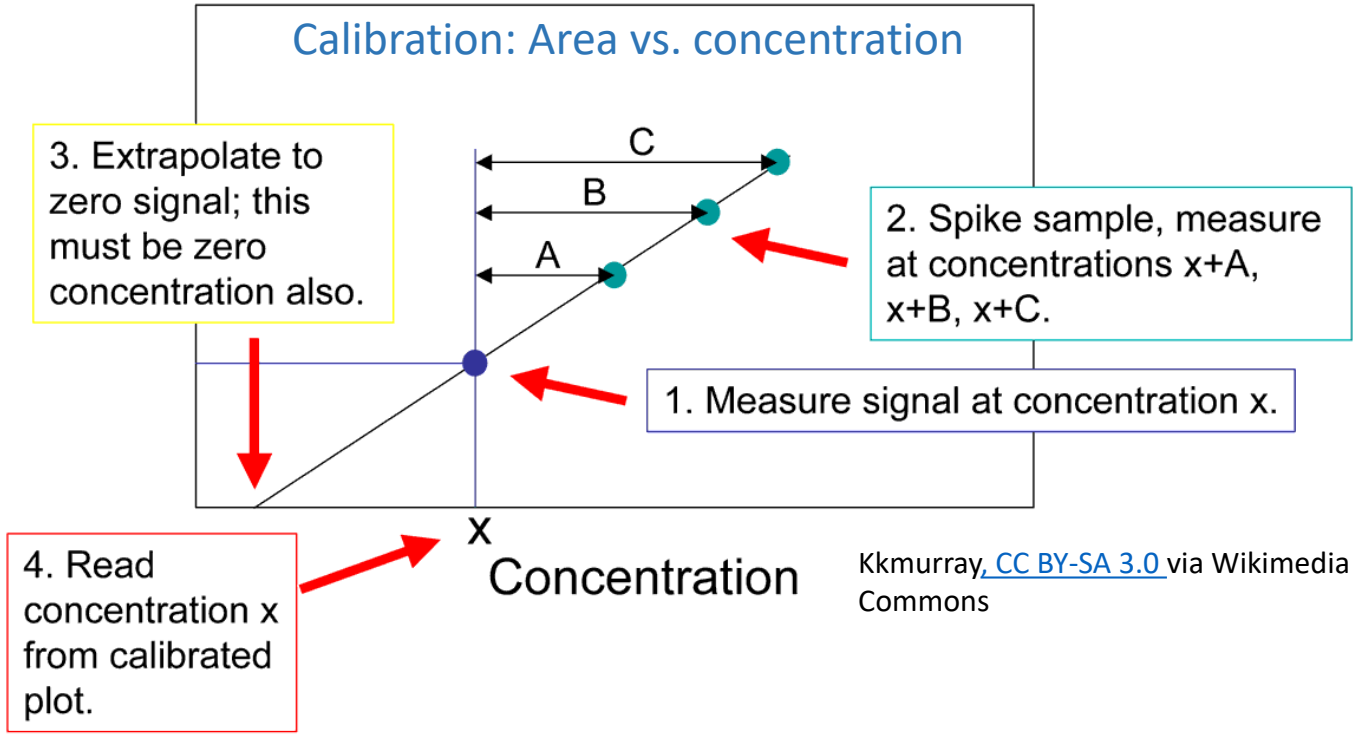
- Instrument noise
- Limit of quantification (LOQ)
- Instrument calibration

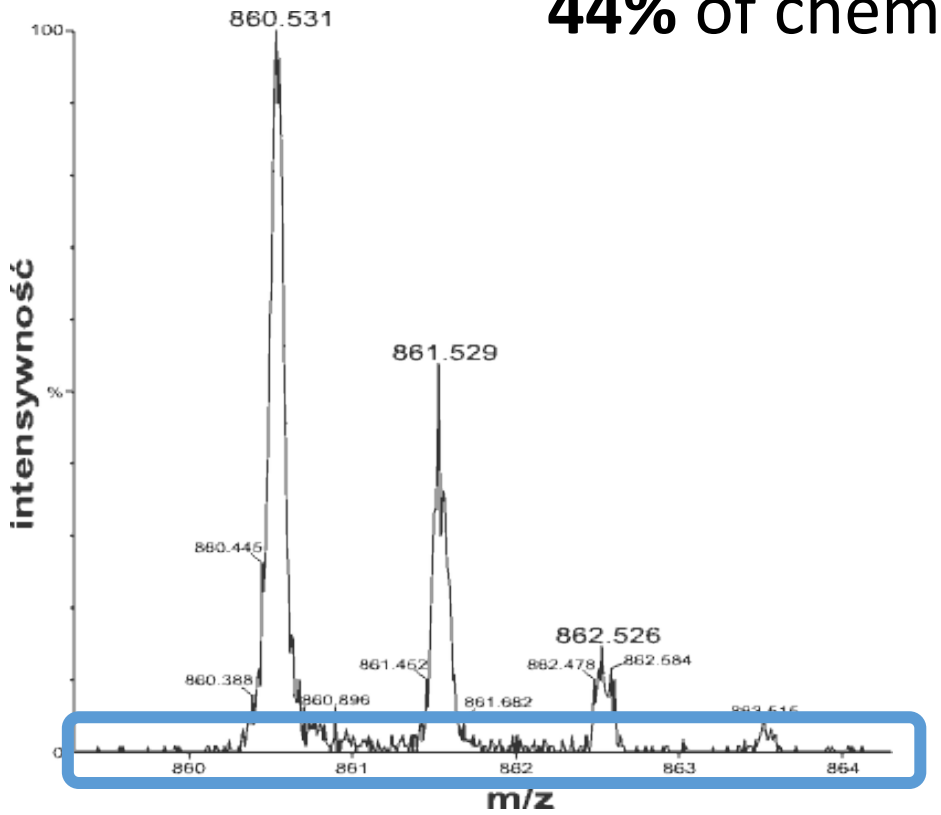


Kkmurray, CC BY-SA 3.0 via Wikimedia Commons

Wambaugh et al. (2019)

LOQ is a problem in the RED assay for highly-bound chemicals

44% of chemicals in Wambaugh et al. (2019)



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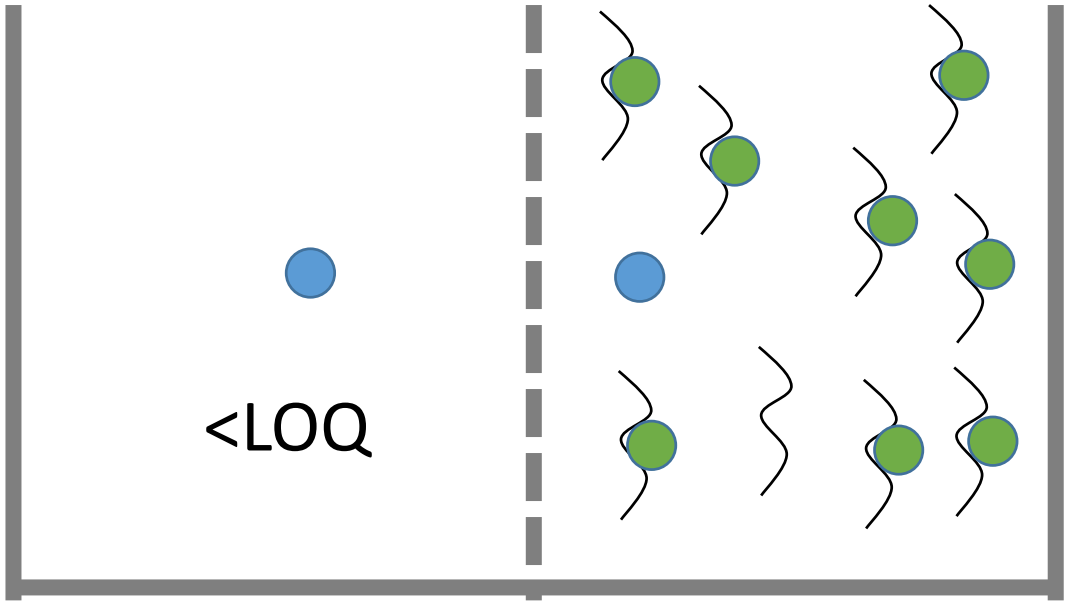
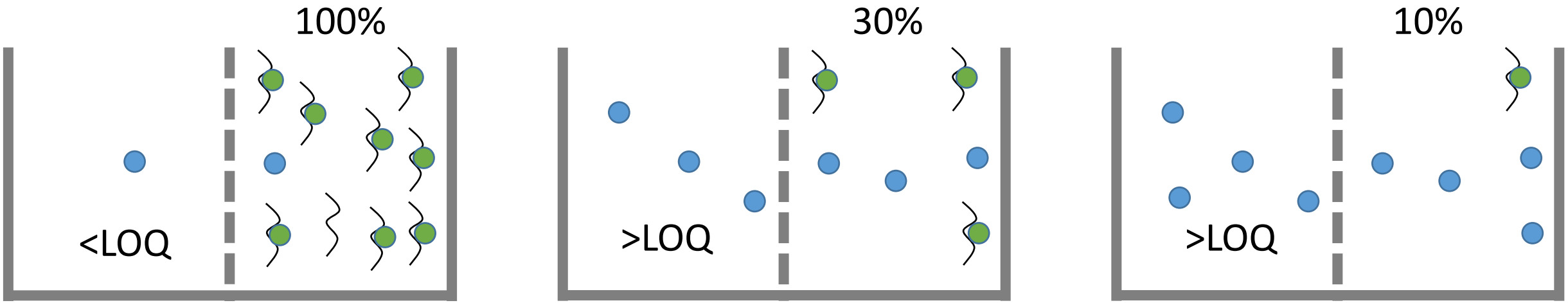


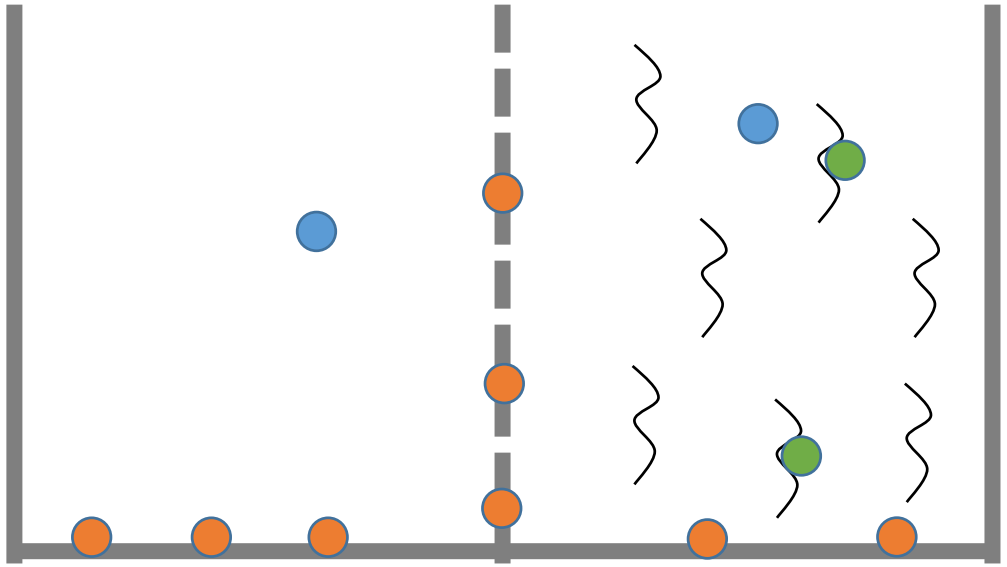
Approach to <LOQ problem:
Repeat RED assay with varying amounts of protein



Estimate dissociation constant K_d
(strength of binding affinity between chemical and protein)

Wambaugh et al. (2019)

Additional source of uncertainty:
Non-specific chemical binding to membrane or walls

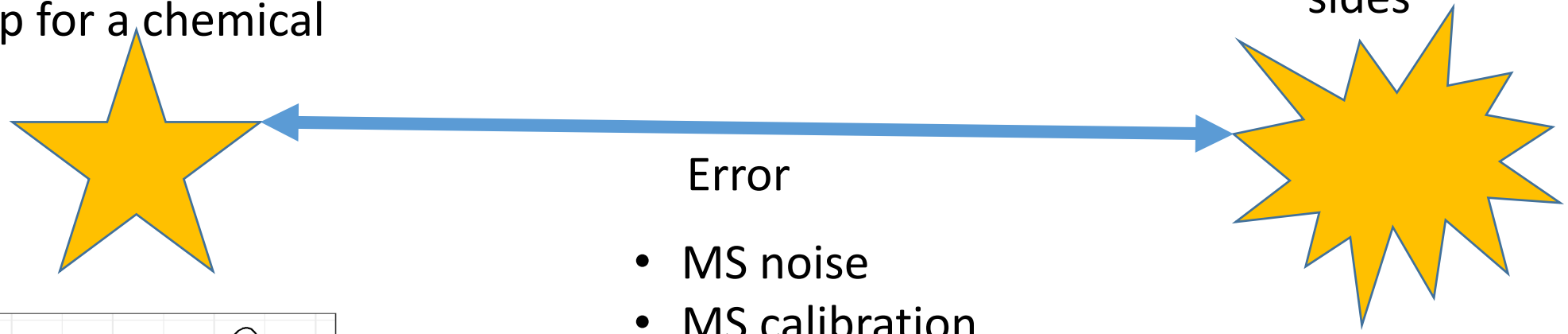


Wambaugh et al. (2019)

Bayesian inference model for Fup uncertainty

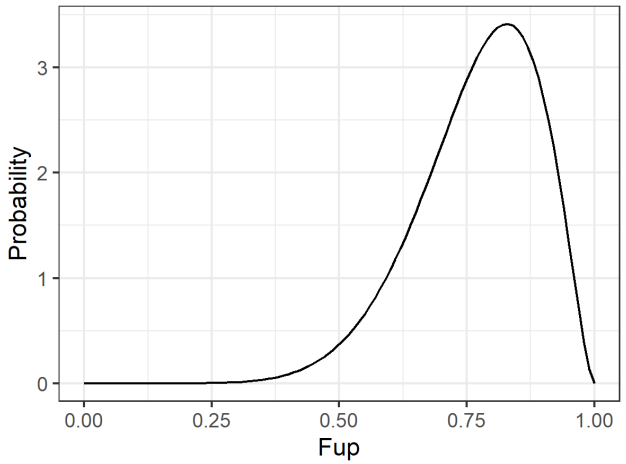
Unknown true value:
Fup for a chemical

Observed (measured) value:
MS peak areas for protein-free and protein-containing sides



Error

- MS noise
- MS calibration
- LOQ
- Non-specific binding



Wambaugh et al. (2019)

Result: *Distribution* of Fup values for a chemical

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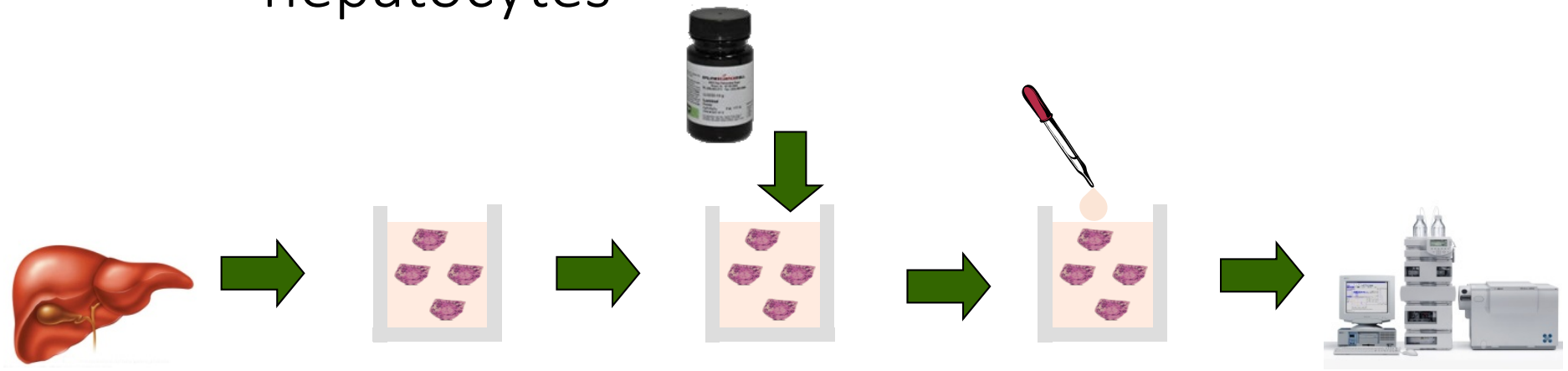
Uncertainty in CLint

CLint: How to measure *in vitro* using pooled human hepatocytes

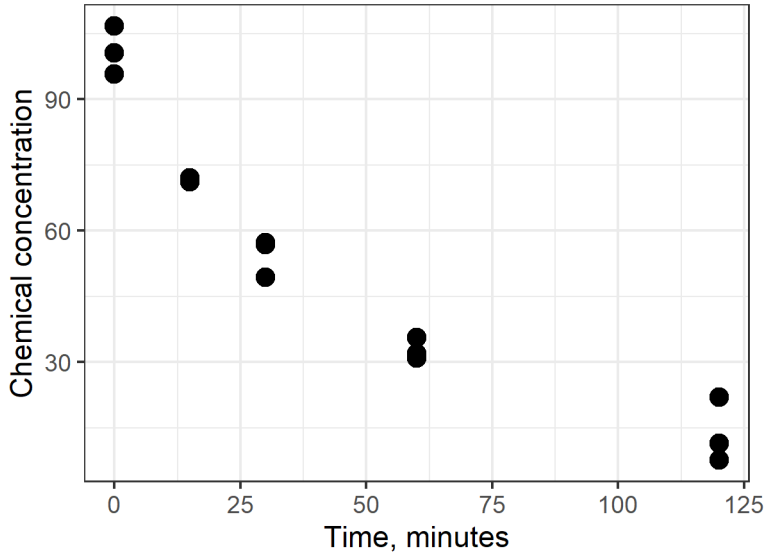


Culture donated human hepatocytes from 10 adult volunteers

Add known amount of chemical

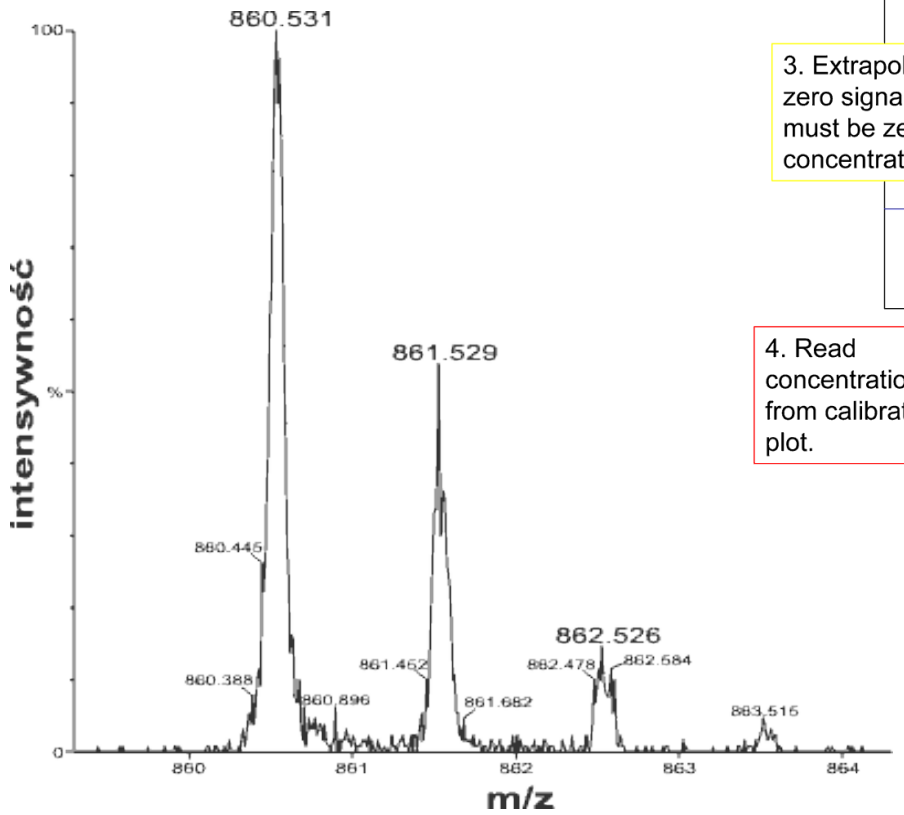
Measure chemical concentration remaining at 0, 15, 30, 60, and 120 minutes

CLint can be estimated from fitting a decaying exponential



Rotroff et al. (2010); Wetmore et al. (2012, 2015); Wambaugh et al. (2019)

Mass spec uncertainties also apply to CLint



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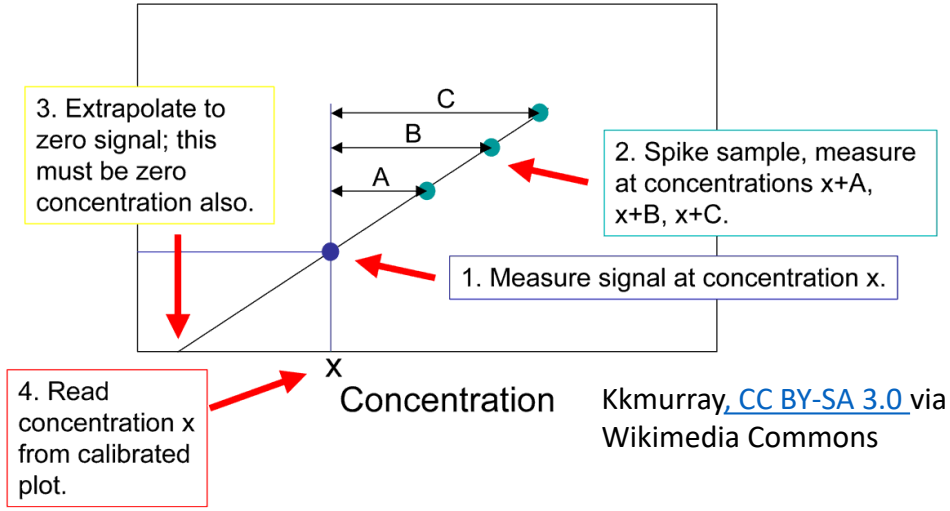
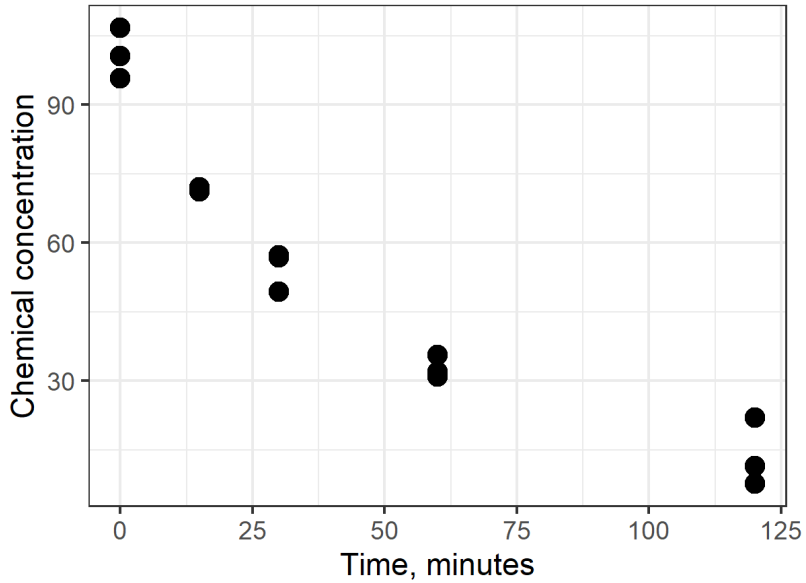


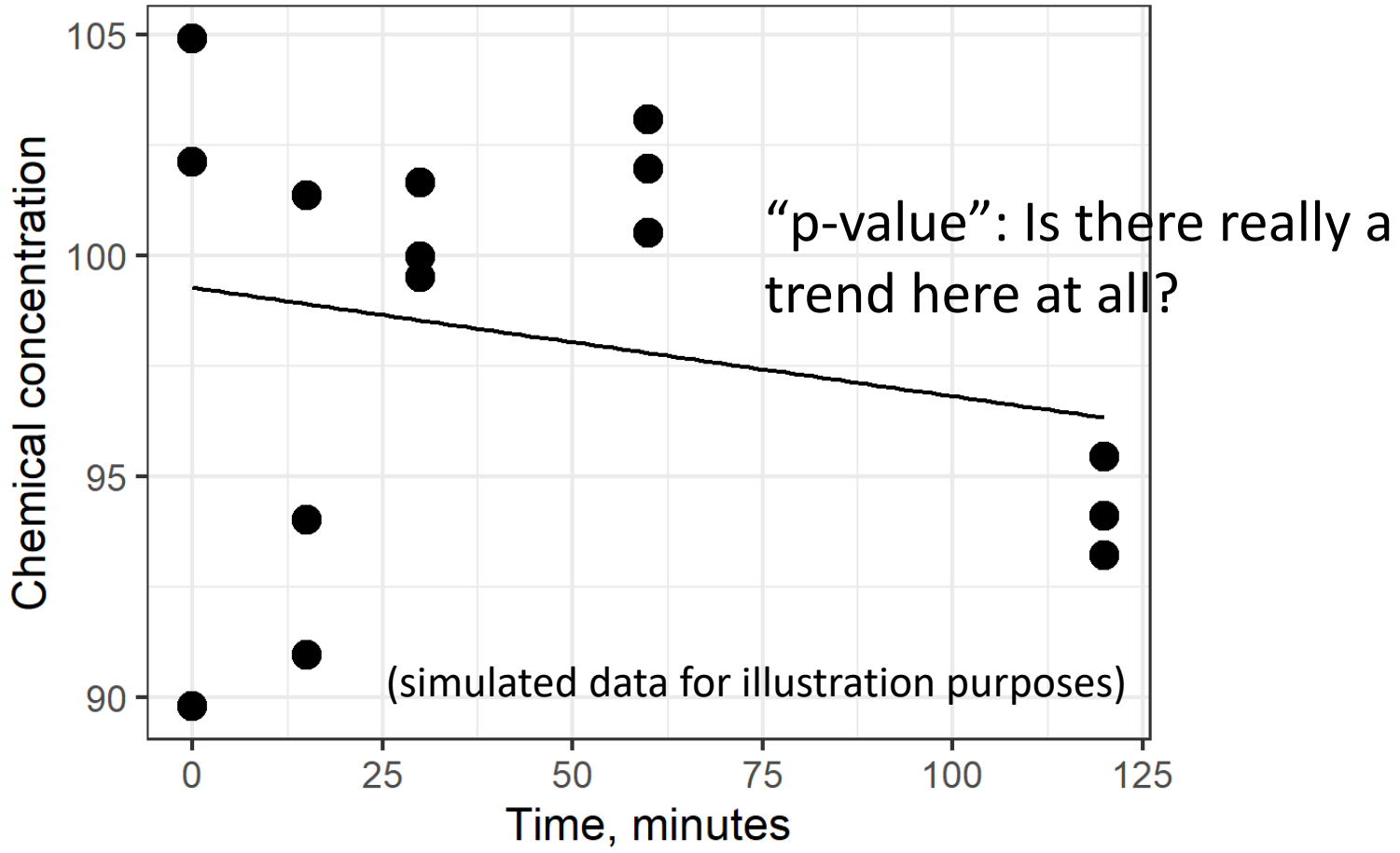
Kkmurray, CC BY-SA 3.0 via Wikimedia Commons

- Uncertainty in peak area
- LOQ
- Calibration curve



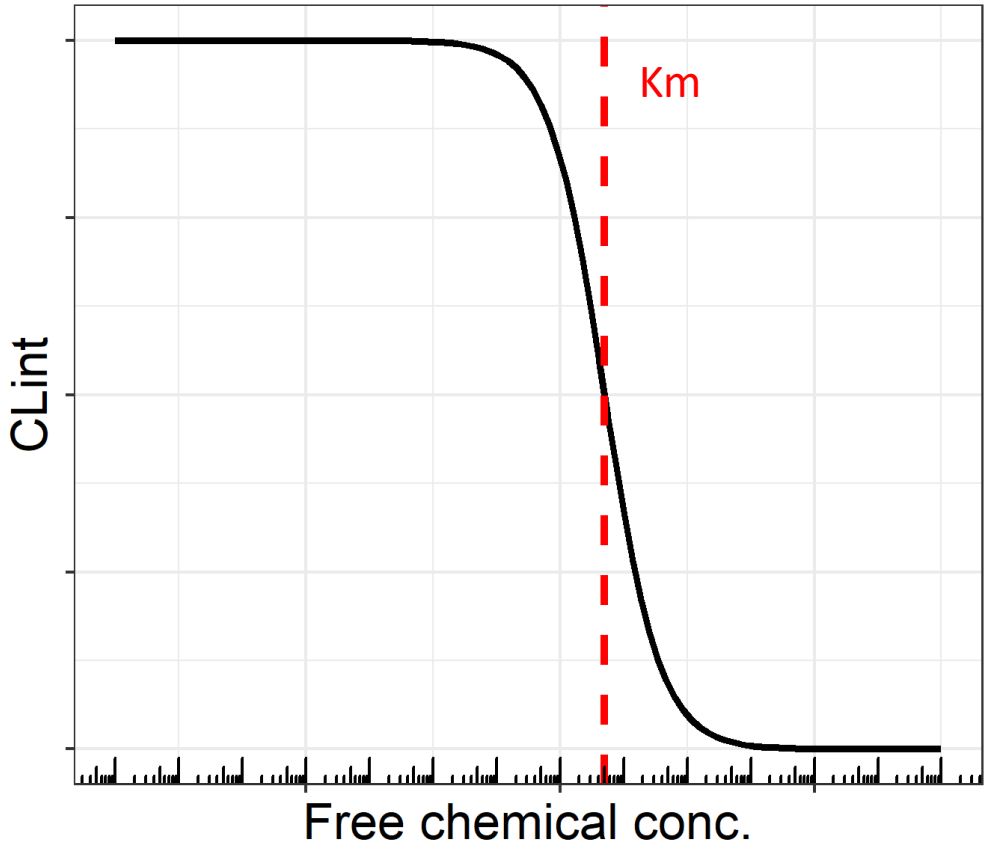
Wambaugh et al. (2019)

Additional uncertainty source: Is chemical really metabolized at all?

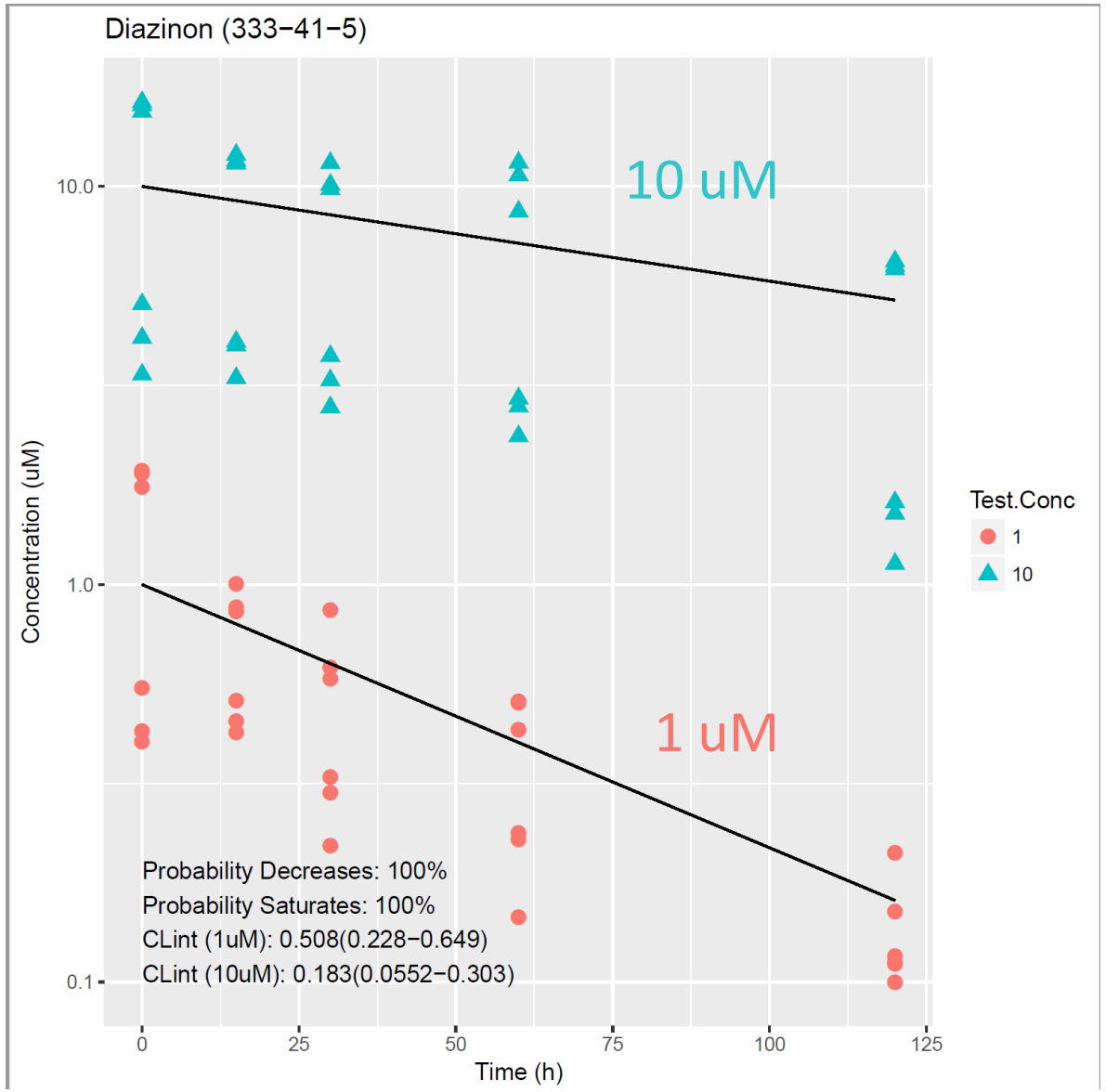


Wambaugh et al. (2019)

Additional uncertainty source: Saturable metabolism



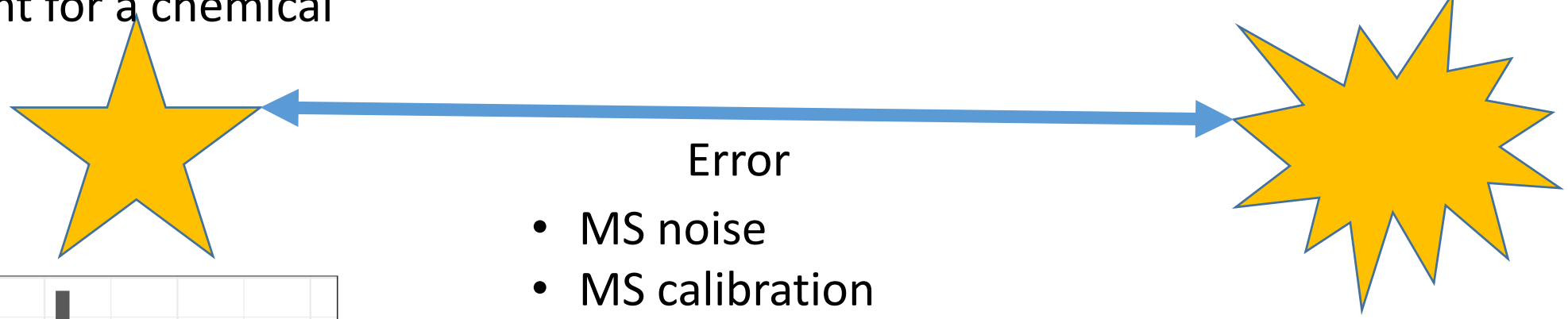
Wambaugh et al. (2019)



Bayesian inference model for Clint uncertainty

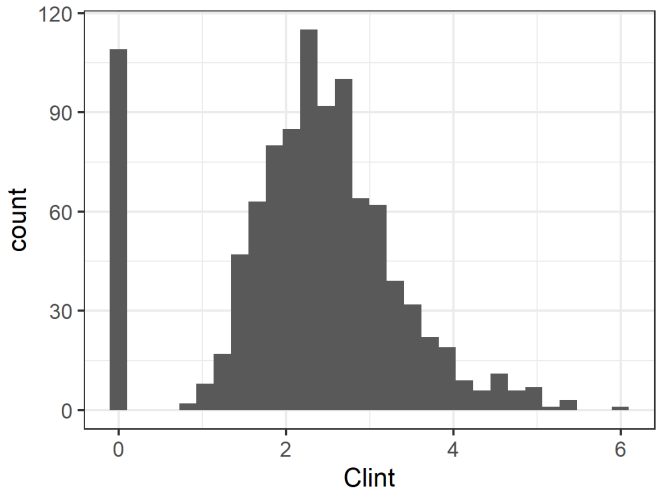
Observed (measured) value:
MS peak areas at 5 time points

Unknown true value:
Clint for a chemical



Error

- MS noise
- MS calibration
- LOQ
- Probability of no metabolism
- Probability of saturation



Wambaugh et al. (2019)

Result: *Distribution* of Clint values for a chemical

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Characterizing variability: HTTK-Pop for human TK variability

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HTTK physiological parameters

Physiological parameters
Tissue masses (including body weight)
Tissue blood flows
Glomerular filtration rate (passive renal clearance)
Hepatocellularity

Data source for population physiology: CDC NHANES

CDC NHANES = Centers for Disease Control National Health and Nutrition Examination Survey

Large, representative, ongoing survey of US population: demographics, body measures, medical examination data….

NHANES does measure:

Sex
Age
Height
Weight
Serum creatinine

NHANES does not measure:

Tissue masses
Tissue blood flows
GFR (kidney function)
Hepatocellularity

Ring et al. (2017)

Correlated Monte Carlo approach to simulating population variability in physiology: HTTK-Pop

Sample NHANES measured quantities for actual NHANES individuals (capturing covariance):

- Sex
- Age
- Height
- Weight
- Serum creatinine

Regression equations from literature (McNally *et al.*, 2014) (+ residual marginal variability)

Predict physiological TK quantities (as used by generic TK model) for each individual:

- Tissue masses
- Tissue blood flows
- GFR (kidney function)
- Hepatocellularity

(Similar approach used in SimCYP [Jamei et al. 2009], GastroPlus, PopGen [McNally et al. 2014], P3M [Price et al. 2003], physB [Bosgra et al. 2012], etc.)

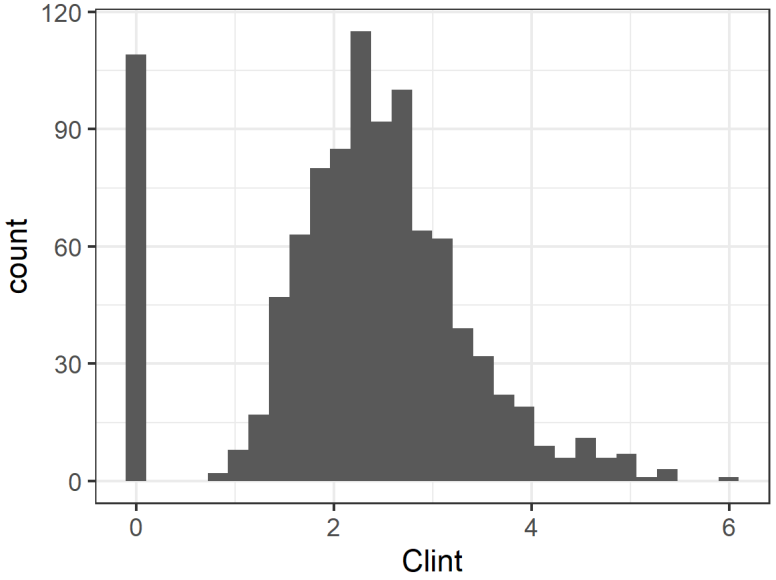
Ring *et al*. (2017)

Chemical-specific parameters have both uncertainty and variability

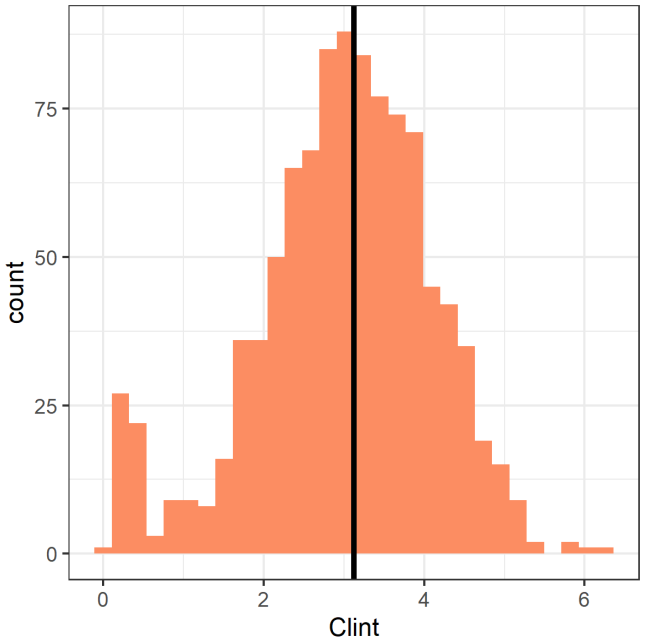
Chemical-specific parameters	
Intrinsic hepatic clearance rate (CLint)	Carry uncertainty from *in vitro* measurements **Also** have population variability: represent chemical-body interactions — vary with individual genetics, environmental factors, age, etc.
Fraction unbound to plasma protein (Fup)	

Chemical-specific TK parameters: Two-stage Monte Carlo approach to modeling both *measurement uncertainty* and *population variability*

Step 1: Draw 1 sample from uncertainty distribution and treat as "population average" value

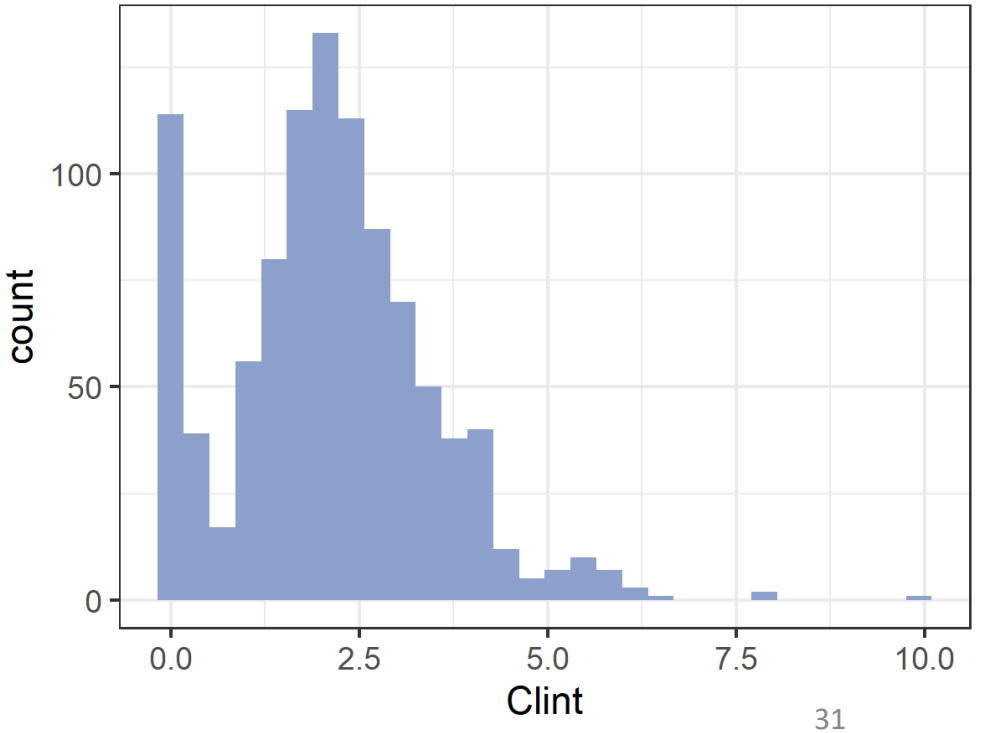


Step 2: Assume population variability (30% CV) around the sampled "population average" value from Step 1, and draw 1 sample



For CLint: Add 5% "poor metabolizers" (10% of original pop. average)

Repeat Steps 1 and 2 for each simulated individual to get sampled values that include both uncertainty & variability



Wambaugh et al. (2019)

Putting it all together: A table of HTTK model parameters for each "simulated individual" in a "simulated population"

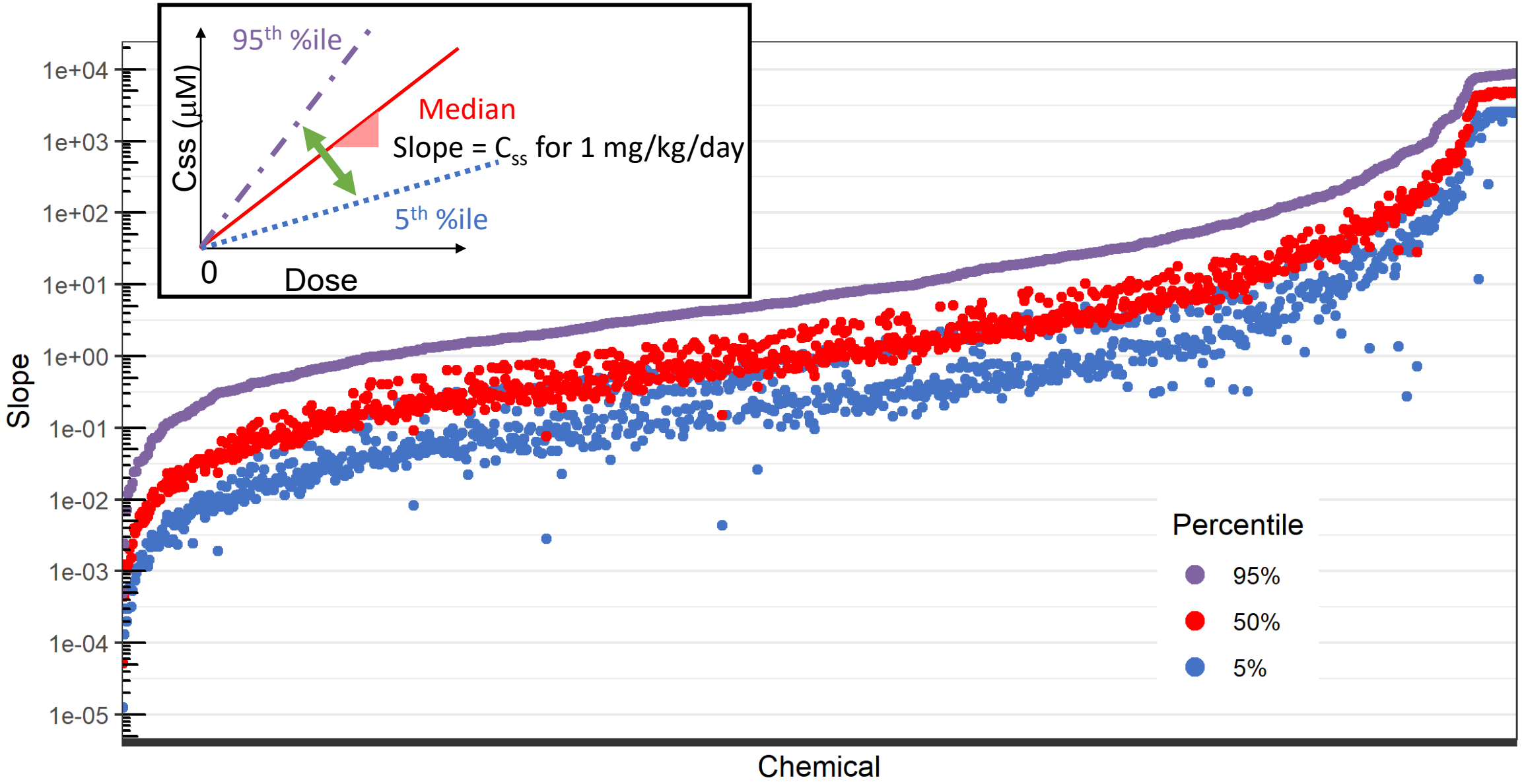
SEQN	Demographics		Body measures		Tissue volumes	Blood flows	GFR	Hepatocellularity	Fup	Clint
	Sex	Age	Ht	Wt						
67184	M	42	171	955	[…]	[…]	[…]	[…]	[…]	[…]
52034	M	0	73	9	[…]	[…]	[…]	[…]	[…]	[…]
64847	F	11	154	47	[…]	[…]	[…]	[…]	[…]	[…]
51787	F	22	166	87	[…]	[…]	[…]	[…]	[…]	[…]
49889	M	9	147	50	[…]	[…]	[…]	[…]	[…]	[…]
64606	F	59	169	115	[…]	[…]	[…]	[…]	[…]	[…]
45549	F	50	165	80	[…]	[…]	[…]	[…]	[…]	[…]
[…]	[…]	[…]	[…]	[…]	[…]	[…]	[…]	[…]	[…]	[…]

httk R package automates this Monte Carlo sampling & model evaluation process

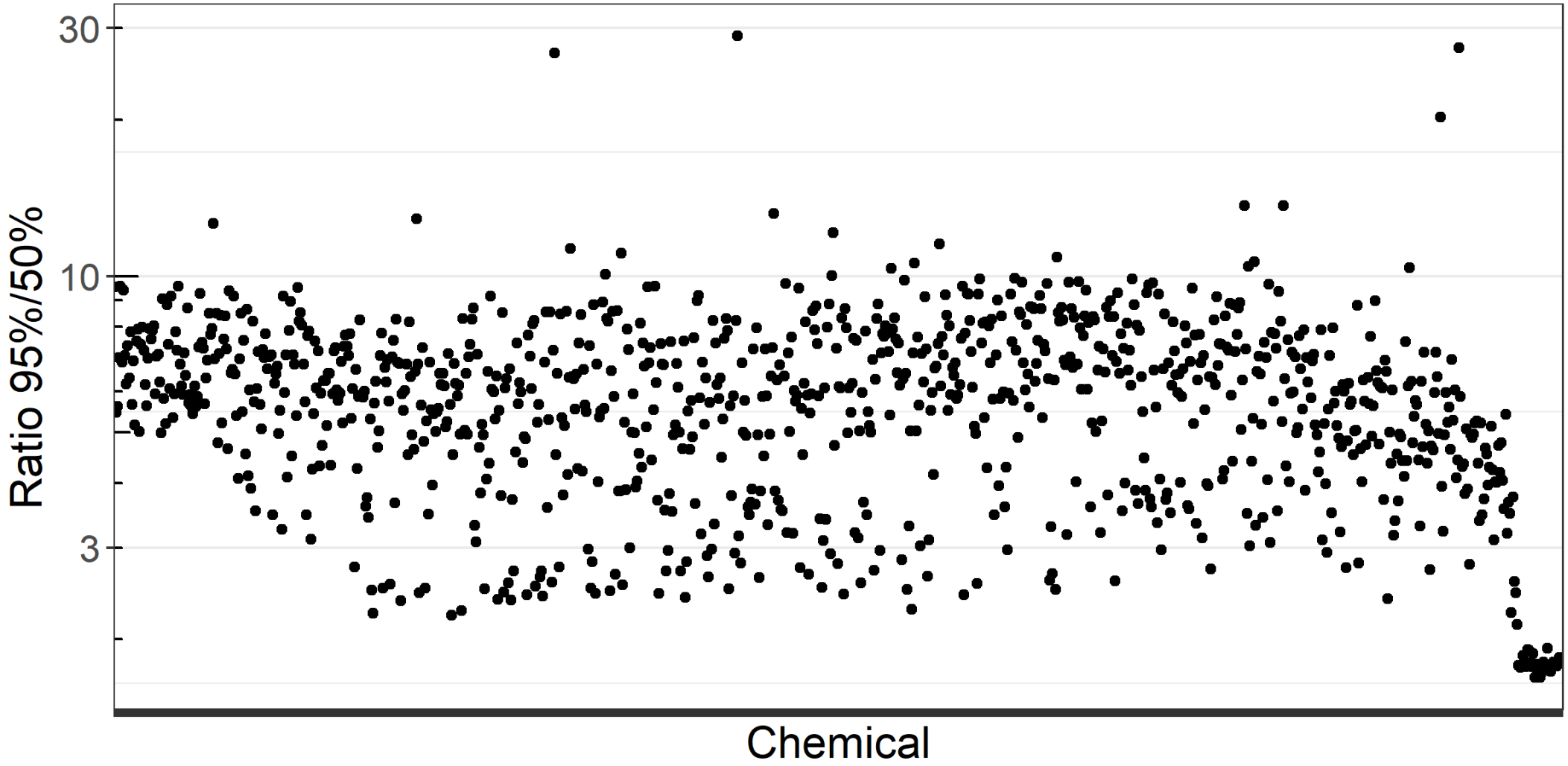
```
> library(httk)
> set.seed(42)
> #Css for 1 mg/kg/day = slope
 calc_mc_css(chem.name="benzo(a)pyrene",
             which.quantile = c(0.95, 0.5, 0.05))

Human plasma concentration returned in mg/L units
for 0.95 0.5 0.05 quantile.
   95%    50%     5%
68.510 13.070  3.742
```

Result: Percentiles of predicted Css vs. dose slope



Another way to visualize: ratio of 95th percentile to median (roughly, how wide is the Css slope distribution?)



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Relative contributions of variability & uncertainty

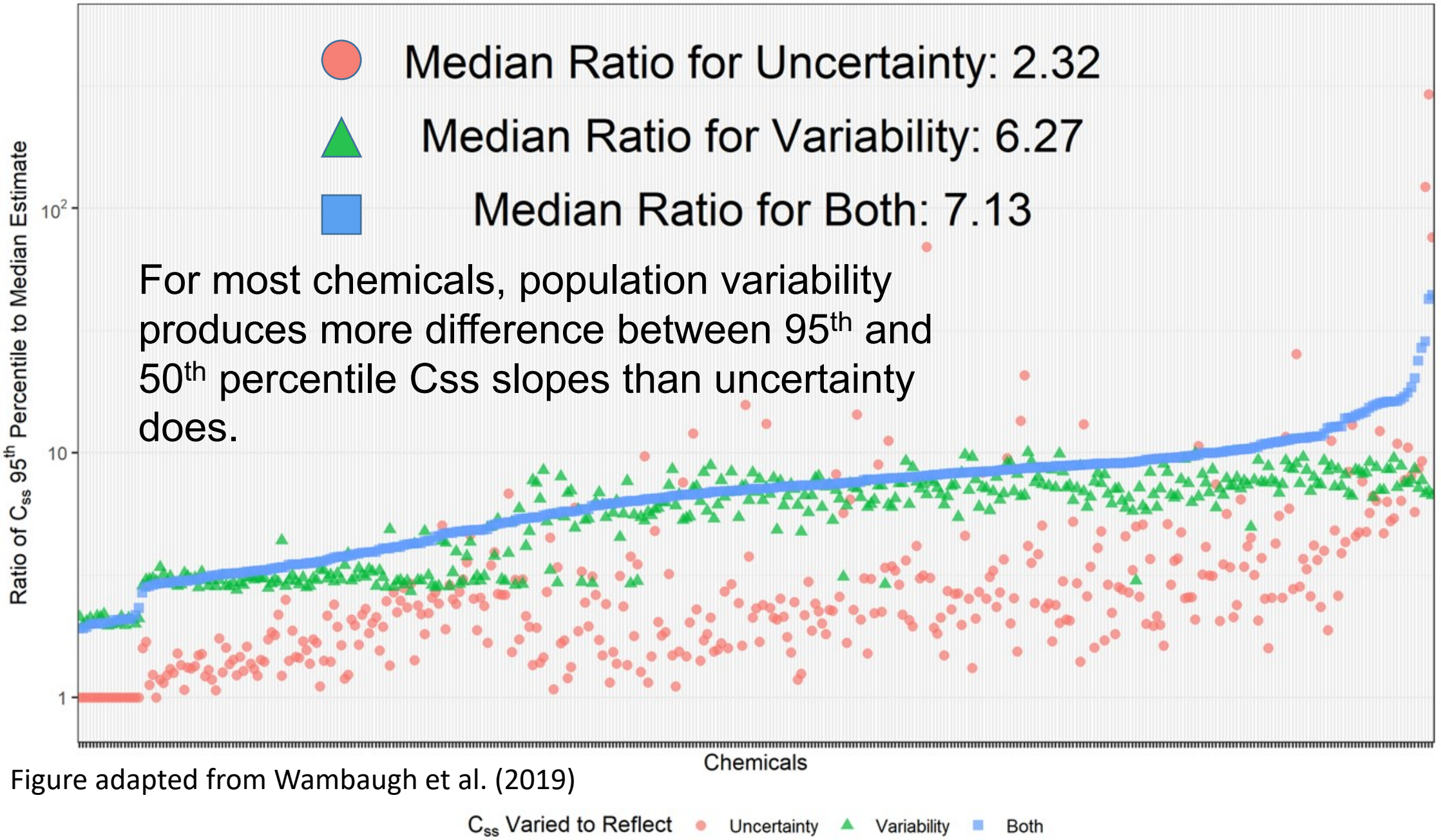

Figure adapted from Wambaugh et al. (2019)

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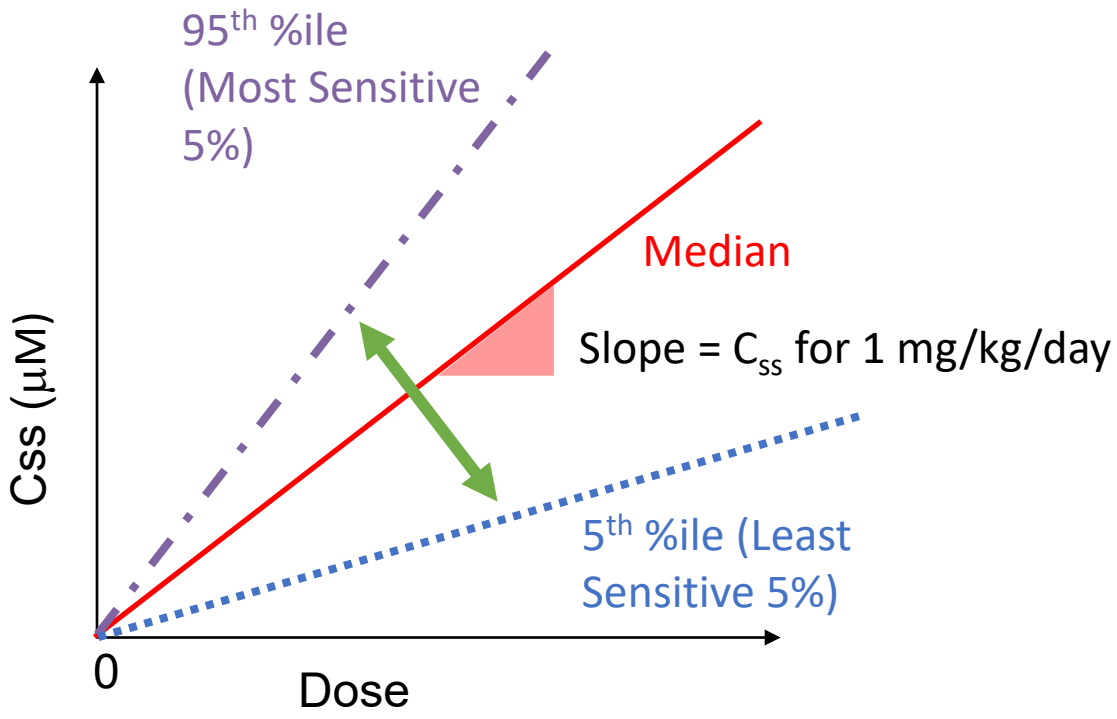
Simulating sensitive subpopulations

Identifying potentially sensitive sub-populations



Who is in the most sensitive portion of the population?

What does this slope distribution look like for kids, for example?

Or people over 65?

To answer this question: Need to model TK variability for specified sub-populations

Ring et al. (2017)

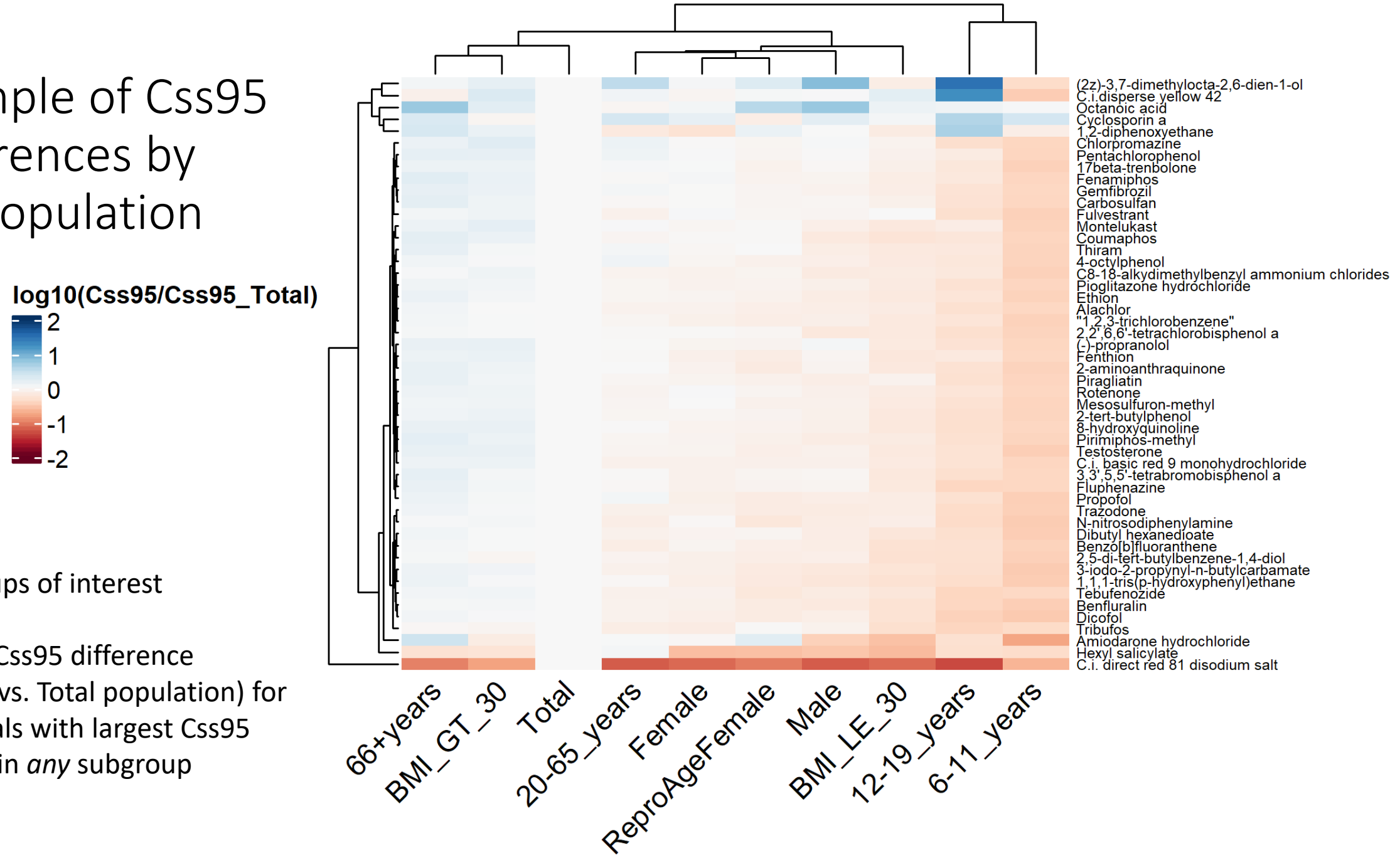
HTTK-Pop can generate simulated subpopulations with user-specified demographics

Use `httkpop.generate.args` argument to `calc_mc_css()` function: Takes a named list of arguments

Name of list element	User can specify…	Example		Default if not specified
`agelim_years`	Age limits in years	`c(6,11)`	Ages 6-11 years	All NHANES (0-79 years)
`agelim_months`	Age limits in months	`c(0,36)`	Ages 0-36 months	All NHANES (0-79 years)
`gendernum`	# of males and females	`list(Male = 1000, Female = 0)`	1000 males, 0 females	Randomly selected from NHANES
`weight_category`	BMI category	`c('Overweight', 'Obese')`	BMI > 25 (overweight & obese)	c('Underweight', 'Normal', 'Overweight', 'Obese')

HTTK-Pop generates physiology based on NHANES respondents in the specified demographic groups

Example of Css95 differences by subpopulation



10 subgroups of interest

Heatmap: Css95 difference (subgroup vs. Total population) for 50 chemicals with largest Css95 difference in *any* subgroup

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Conclusions

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Conclusions

- Uncertainty vs. Variability in TK model parameters
  - Measurement uncertainty: Chemical-specific parameters measured *in vitro*
  - Population variability: Physiological & chemical-specific parameters
- Characterizing key uncertainty in chemical-specific TK parameters
  - Fraction unbound in plasma protein (Fup)
  - Intrinsic hepatic clearance rate (Clint)
- Characterizing variability: HTTK-Pop for human TK variability
  - Correlated Monte Carlo approach based on CDC NHANES data
- Relative contributions of uncertainty and variability to TK model predictions
  - For most chemicals, population variability has larger effect
- Simulating sensitive subpopulations
  - HTTK-Pop can simulate populations with user-specified demographics

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Thank you!

Questions?

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References

1. Rotroff DM, Wetmore BA, Dix DJ, et al. Incorporating human dosimetry and exposure into high-throughput in vitro toxicity screening. Toxicological Sciences. 2010;117(2):348-358
2. Wetmore BA, Wambaugh JF, Allen B, et al. Incorporating High-Throughput Exposure Predictions With Dosimetry-Adjusted In Vitro Bioactivity to Inform Chemical Toxicity Testing. Toxicological Sciences. 2015 Nov;148(1):121-36
3. Wambaugh JF, Wetmore BA, Pearce R, Strope C, Goldsmith R, Sluka JP, et al. Toxicokinetic Triage for Environmental Chemicals. Toxicol Sci. 2015;147(1):55-67.
4. Ring CL, Pearce RG, Setzer RW, et al. Identifying populations sensitive to environmental chemicals by simulating toxicokinetic variability. Environment International. 2017 2017/09/01/;106:105-118.
5. Shibata Y, Takahashi H, Chiba M, Ishii Y. Prediction of hepatic clearance and availability by cryopreserved human hepatocytes: an application of serum incubation method. Drug Metab Dispos. 2002;30(8):892-6.
6. Waters NJ, Jones R, Williams G, Sohal B. Validation of a rapid equilibrium dialysis approach for the measurement of plasma protein binding. J Pharm Sci. 2008;97(10):4586-95.
7. Wetmore BA, Wambaugh JF, Ferguson SS, et al. Integration of dosimetry, exposure, and high-throughput screening data in chemical toxicity assessment. Toxicological Sciences. 2012 Jan;125(1):157-74.
8. Wetmore BA. Quantitative in vitro-to-in vivo extrapolation in a high-throughput environment. Toxicology. 2015;332:94-101.

9. Wambaugh JF, Wetmore BA, Ring CL, Nicolas CI, Pearce RG, Honda GS, et al. Assessing Toxicokinetic Uncertainty and Variability in Risk Prioritization. Toxicol Sci. 2019;172(2):235-51.
10. Sipes NS, Wambaugh JF, Pearce R, et al. An Intuitive Approach for Predicting Potential Human Health Risk with the Tox21 10k Library. Environmental Science & Technology. 2017 2017/09/19;51(18):10786-10796.
11. Pearce RG, Setzer RW, Davis JL, Wambaugh JF. Evaluation and calibration of high-throughput predictions of chemical distribution to tissues. J Pharmacokinet Pharmacodyn. 2017b;44(6):549-65.
12. Jamei M, Marciniak S, Feng K, et al. The Simcyp® population-based ADME simulator. Expert Opinion on Drug Metabolism & Toxicology. 2009;5(2):211-223.
13. McNally K, Cotton R, Hogg A, Loizou G. PopGen: A virtual human population generator. Toxicology. 2014;315:70-85.
14. Price PS, Conolly RB, Chaisson CF, Gross EA, Young JS, Mathis ET, et al. Modeling Interindividual Variation in Physiological Factors Used in PBPK Models of Humans. Critical Reviews in Toxicology. 2003;33(5):469-503.
15. Bosgra S, van Eijkeren J, Bos P, Zeilmaker M, Slob W. An improved model to predict physiologically based model parameters and their inter-individual variability from anthropometry. Crit Rev Toxicol. 2012;42(9):751-67.
16. Wetmore BA, Allen B, Clewell HJ, 3rd, et al. Incorporating population variability and susceptible subpopulations into dosimetry for high-throughput toxicity testing. Toxicological Sciences. 2014 Nov;142(1):210-24.