

From Toxicity Testing in the 21st Century to New Approach Methodologies (NAMs) and Next Generation Risk Assessment (NGRA): Making Safety Decisions Without Harming Animals

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Safety & Environmental Assurance Centre,
Unilever

08/05/2024



Unilever

Paul L. Carmichael

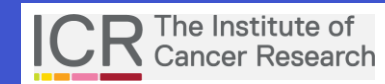
- First degree in Biochemistry (Toxicology)



- PhD in Biochemistry from King's College



- Postdoctoral Scientist in carcinogenesis and genotoxicity



- Senior Lecturer Faculty of Medicine at Imperial College



- Toxicology Senior Science Leader, SEAC, Unilever



- Academic links at Brown, Peking & Wageningen Universities



Web Resource

- SEAC's Website for what we are discussing today:

www.TT21C.org

Ensuring Safe Ingredients for Foods, Drinks, Homecare and Cosmetic Products

Risk Based Approach:

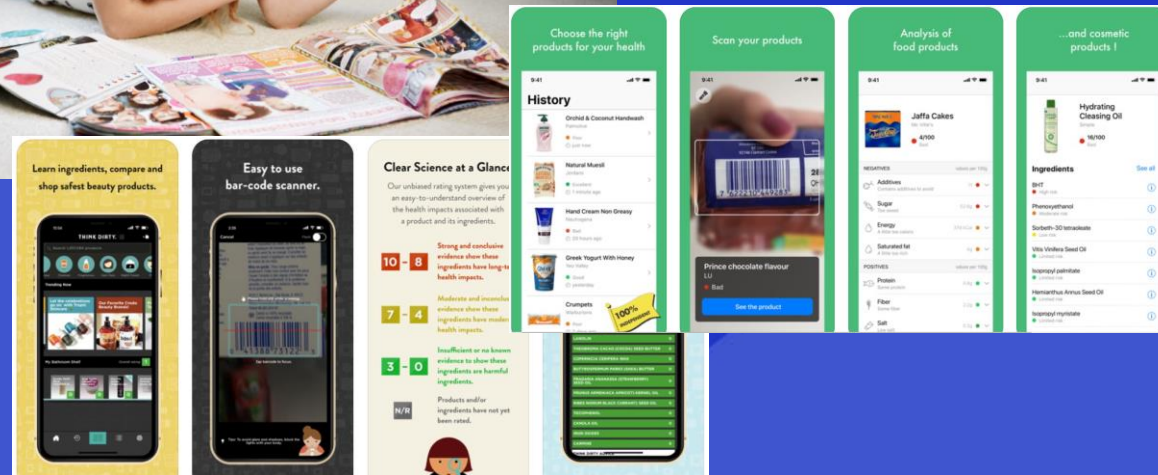
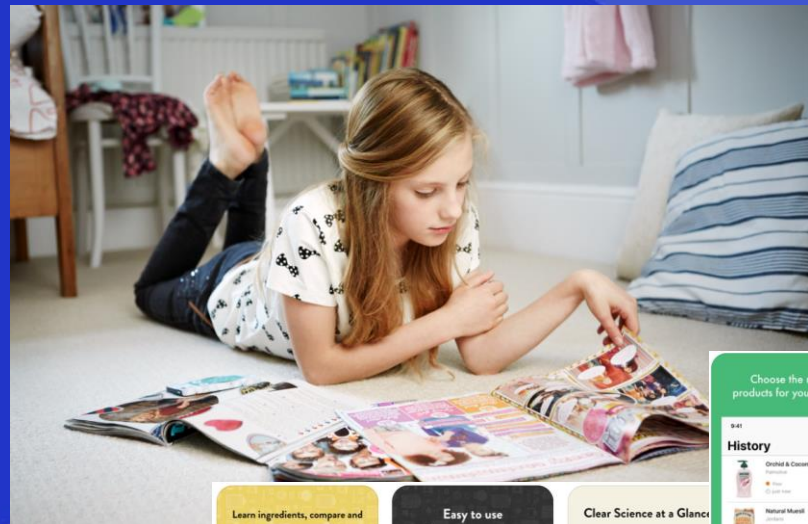
Considers both the hazard and the exposure to evaluate the risk

Can we safely use % of ingredient in product?

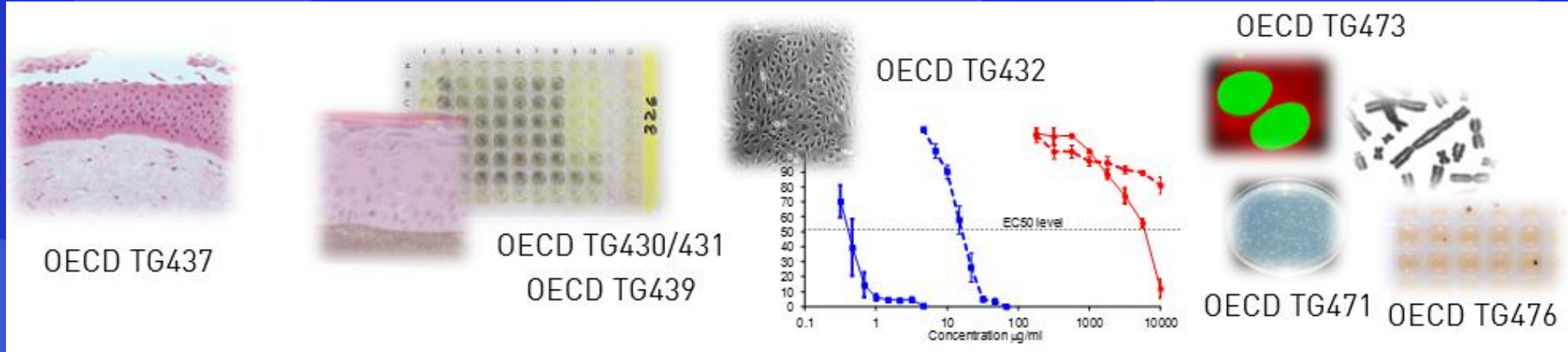
For **consumers; workers;**
the **environment**



All Consumers Want Safe Products But Majority Want Them *Not Tested On Animals* + Transparency

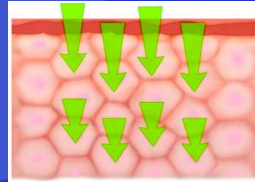


Use of Existing OECD *In Vitro* Approaches

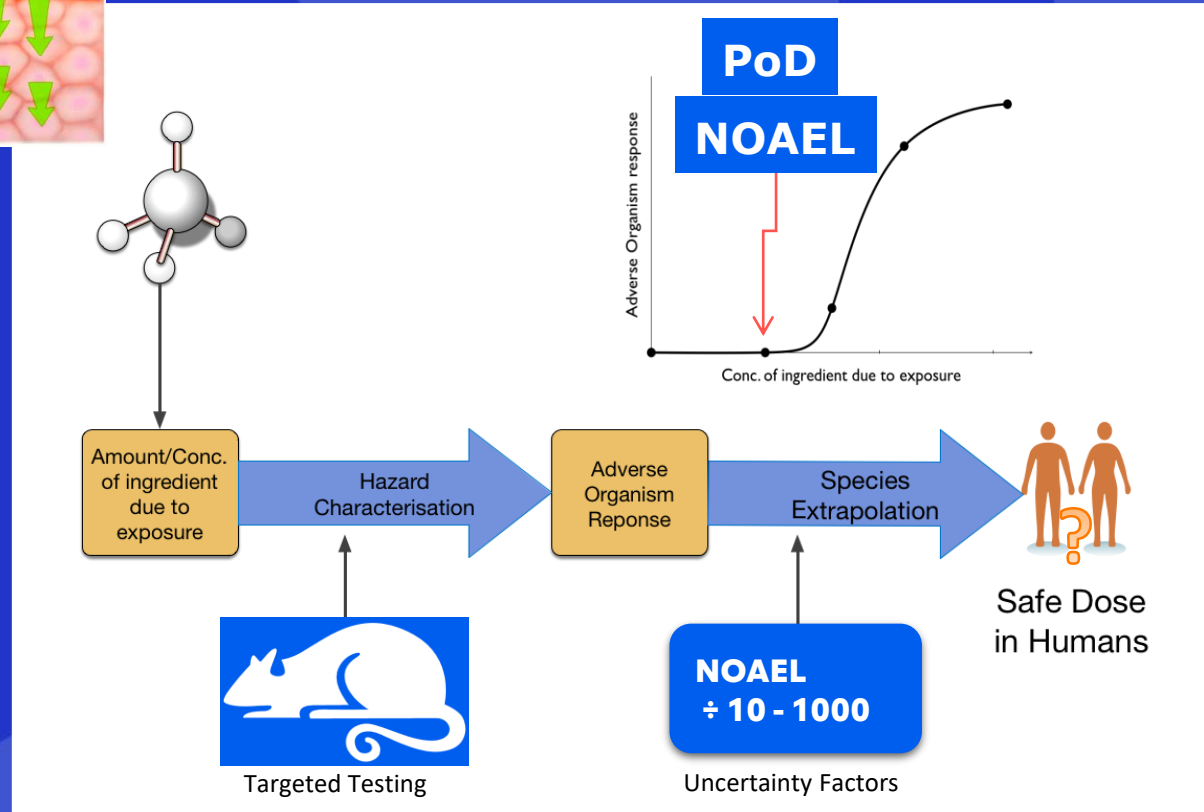


Skin and eye irritation; skin sensitization; phototoxicity; mutagenicity

But What About Systemic Toxicity?



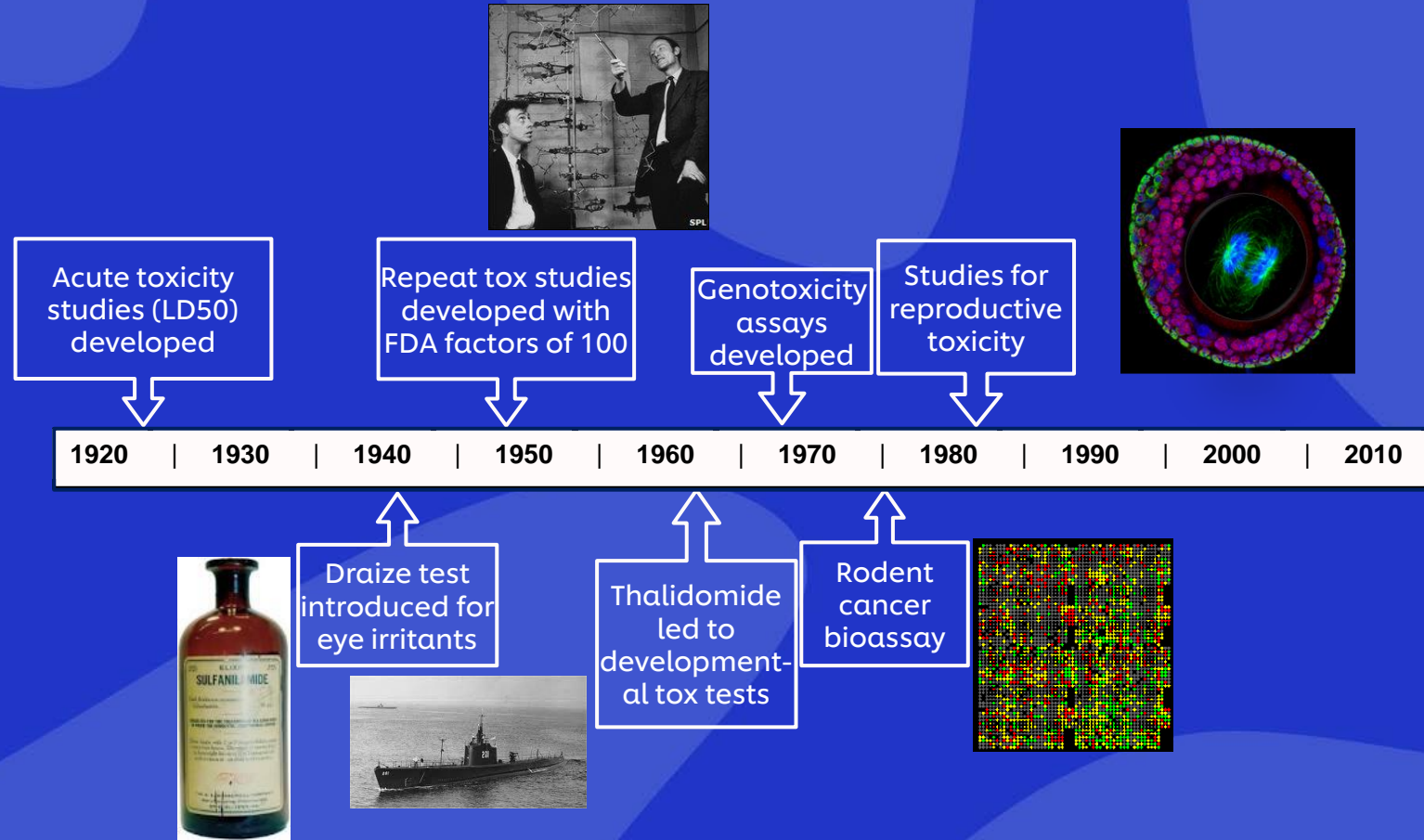
Is it safe?



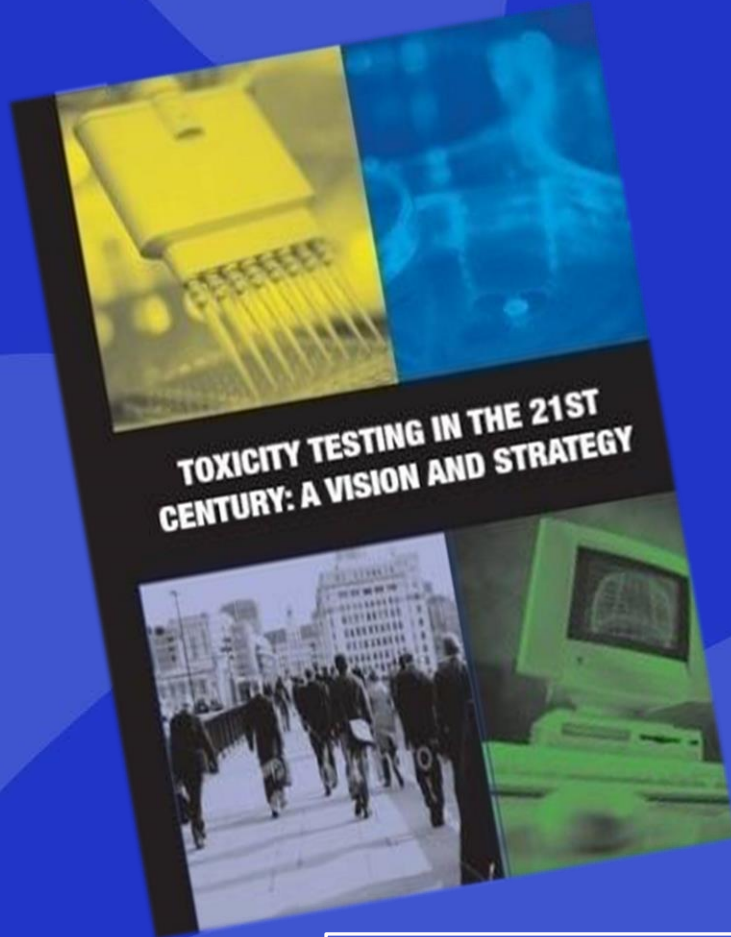
e.g. 90 Day Repeat Dose Study

It has served us well enough

Mechanistic? Human-based?



2007 Toxicity Testing in the 21st Century (TT21C)

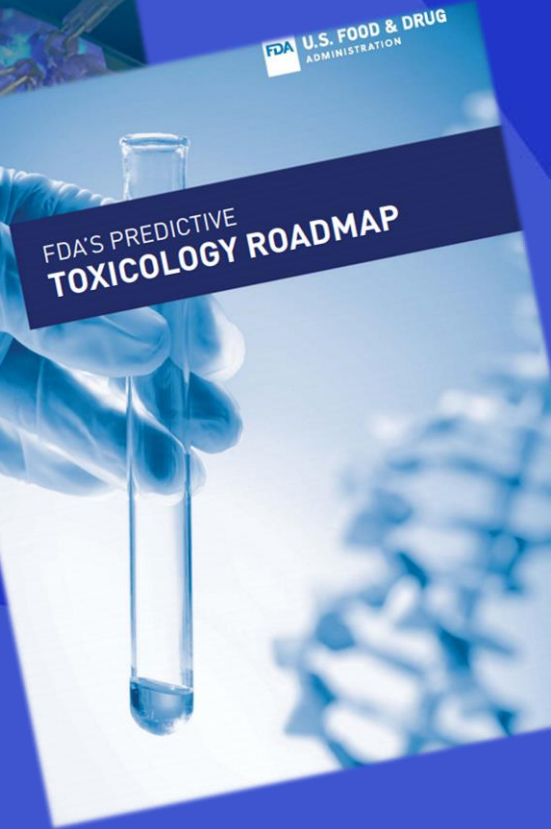
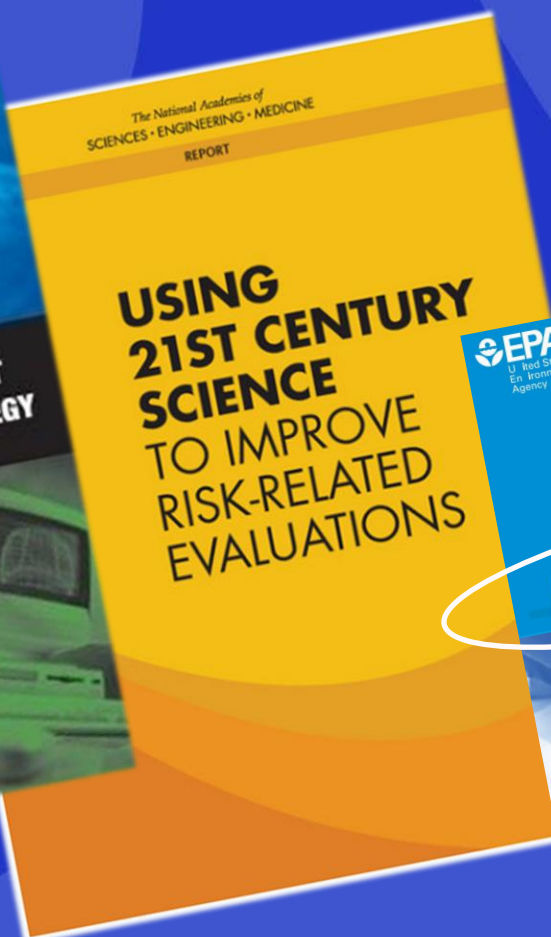
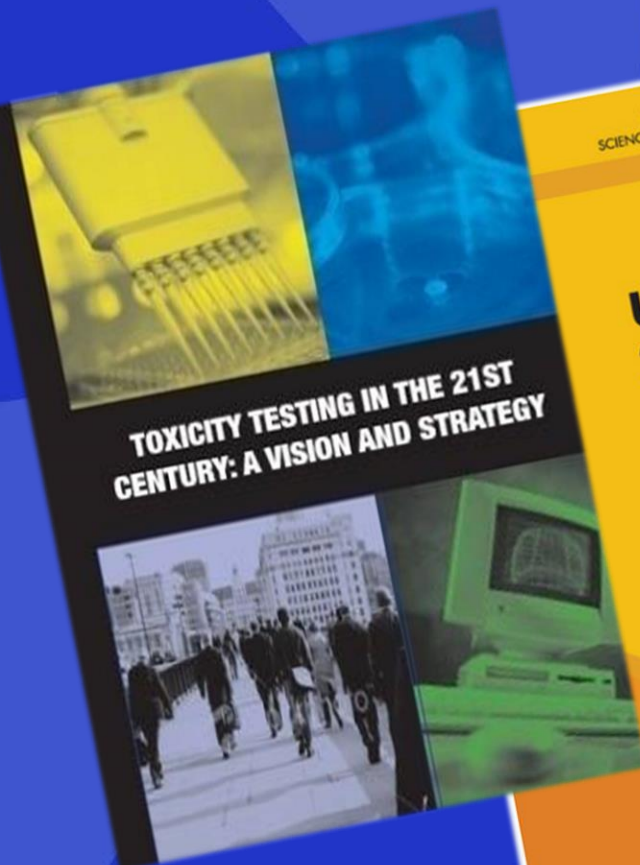


“Advances in toxicogenomics, bioinformatics, systems biology, and computational toxicology could transform toxicity testing from a system based on whole-animal testing to one founded primarily on in vitro methods that evaluate changes in biologic processes using cells, cell lines, or cellular components, preferably of human origin.”

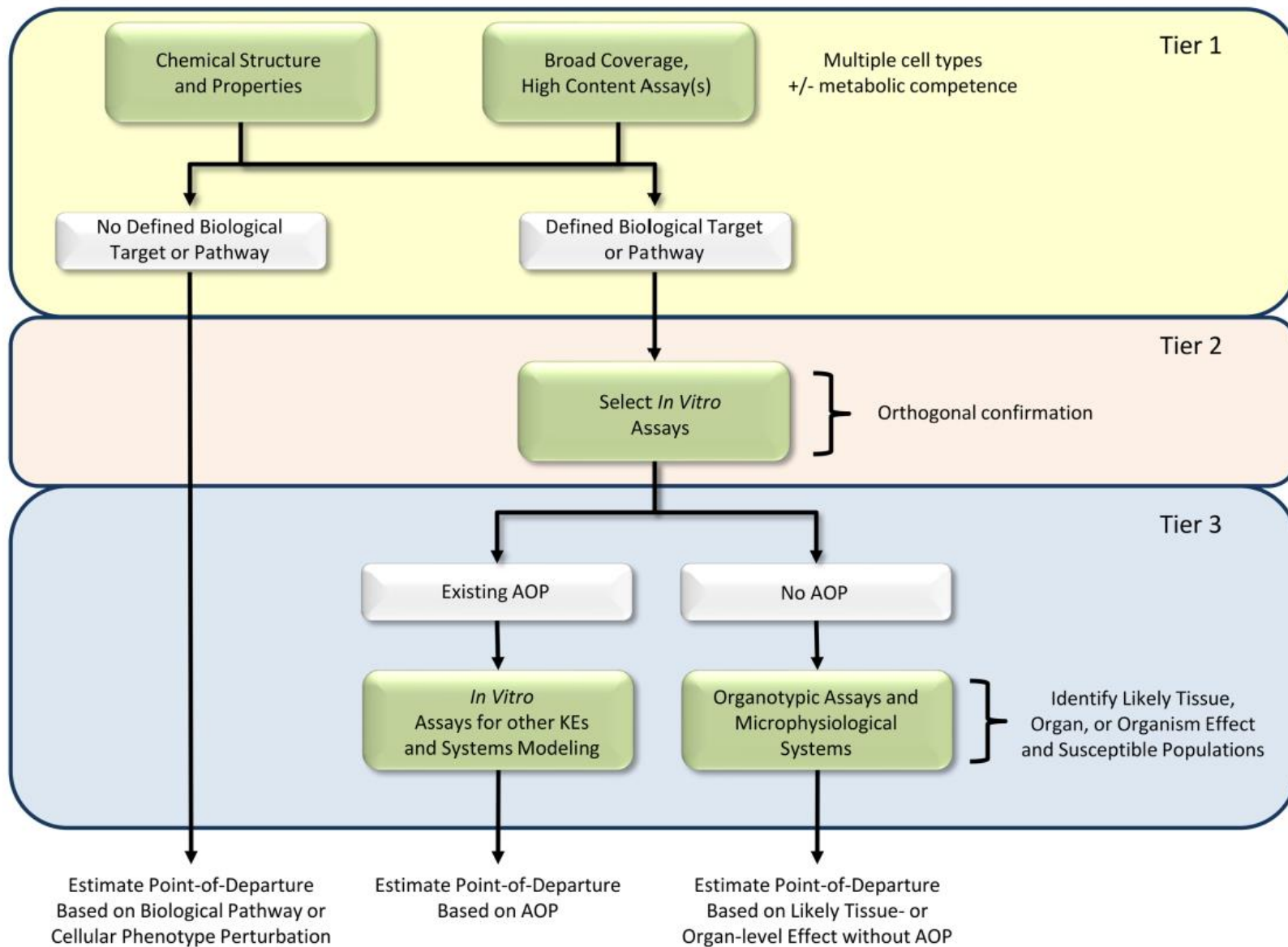


Perturbation of ‘toxicity pathways’ and stress responses

TT21C + NGRA



THE EPA BLUEPRINT



FORUM

The Next Generation Blueprint of Computational Toxicology at the U.S. Environmental Protection Agency

Russell S. Thomas,^{*,1} Tina Bahadori,[†] Timothy J. Buckley,[‡] John Cowden,^{*} Chad Deisenroth,^{*} Kathie L. Dionisio,[‡] Jeffrey B. Frithsen,[§] Christopher M.



Principles of NGRA from ICCR



4 Main overriding principles:

- » The overall goal is a human safety risk assessment
- » The assessment is exposure led
- » The assessment is hypothesis driven
- » The assessment is designed to prevent harm

3 Principles describe how a NGRA should be conducted:

- » Following an appropriate appraisal of existing information
- » Using a tiered and iterative approach
- » Using robust and relevant methods and strategies

2 Principles for documenting NGRA:

- » Sources of uncertainty should be characterized and documented
- » The logic of the approach should be transparently and documented

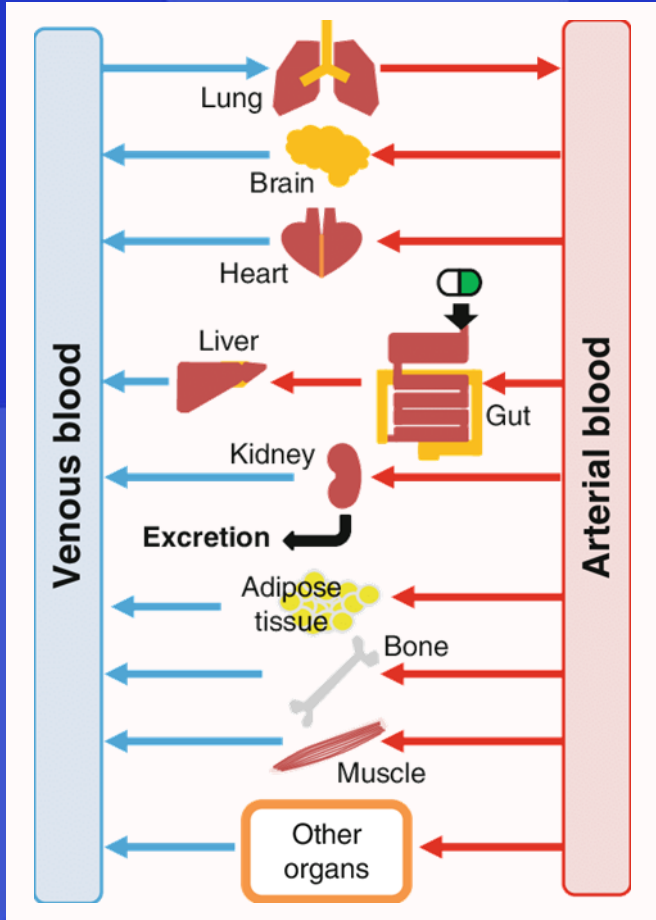
Applied dose



| Product types | Face cream | Shampoo | Body Lotion |
|--|-------------|----------------|-------------|
| Amount of product used per day (g/day) using 90th percentile | 1.54 | 10.46 | 7.82 |
| Frequency of use | 2 times/day | 1 time/day | 2 time/day |
| Amount of product in contact with skin per occasion (mg) | 770 | 10460 | 3910 |
| Ingredient inclusion level | 0.1% | 0.1% | 0.1% |
| Skin surface area (cm ²) | 565 | 1440 | 15670 |
| Leave on or rinse off | leave on | rinse off | leave on |
| Exposure duration per occasion | 12 hours | 24 hours | 12 hours |
| For rinse off product, retention factor of finished product on skin ^b | n.a. | 0.01 | n.a. |
| Amount of ingredient in contact with skin per occasion (mg) | 0.77 | 0.105 | 3.91 |
| Local dermal exposure per occasion (µg/cm ²) | 1.36 | 0.073 | 0.25 |
| Systemic exposure per day (mg/kg) | 0.02 | 0.00154 | 0.12 |

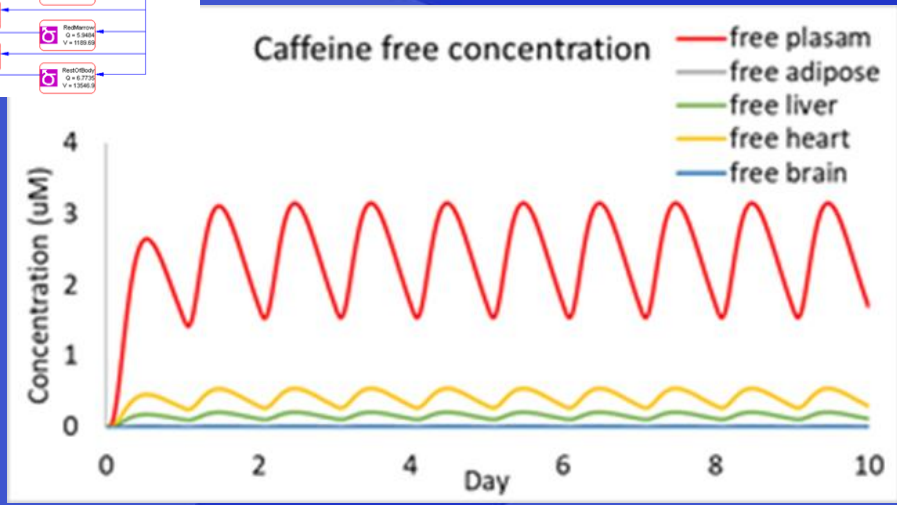
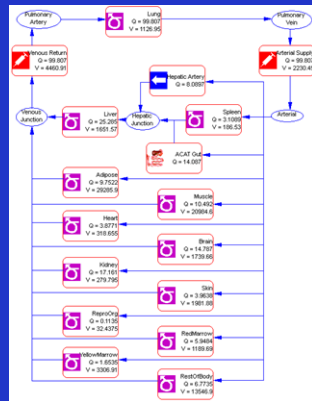
- Exposures to face cream and body lotion above threshold of toxicological concern (TTC) depending on Cramer classification
- Shampoo exposure would be below all non genotoxic TTC
- Only face cream and body lotion risk assessment progress to NGRA

PBK (Physiologically Based Kinetic) Modelling



substrate
S9/Microsomes
cofactor

Model Input:
Physiological parameters
Partition coefficients
Kinetic constants (in vitro)



Uptake from GI tract

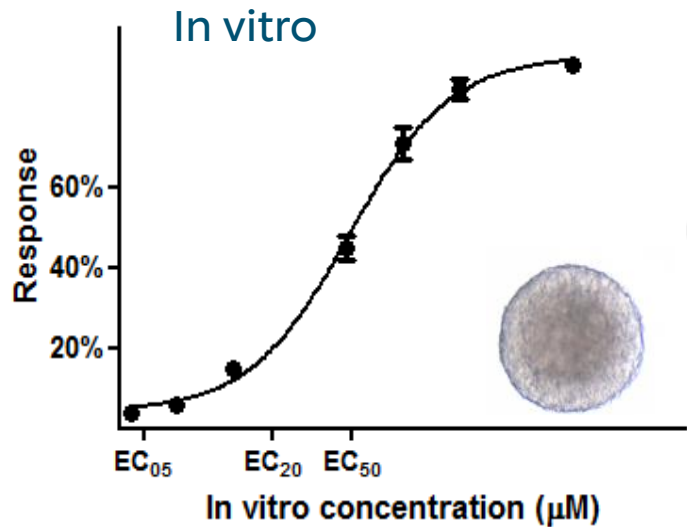
Transport from arterial to venous blood

Metabolism

$$dA/dt = + K_A * A_{GI} + QL * (CA - CV) - V_{max} * CL / (K_m + CL)$$

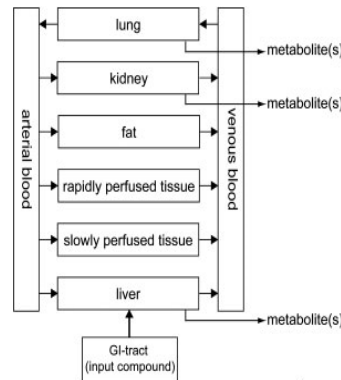
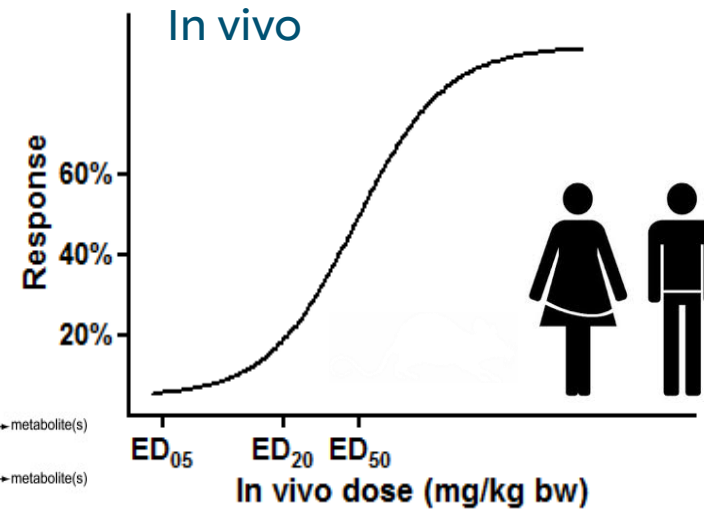
- Predicting systemic exposure
- Enabling us to select and test relevant doses
- Increased role for clinical work to confirm systemic exposure levels

One Interpretation of TT21C: Quantitative *in vitro* to *in vivo* extrapolation



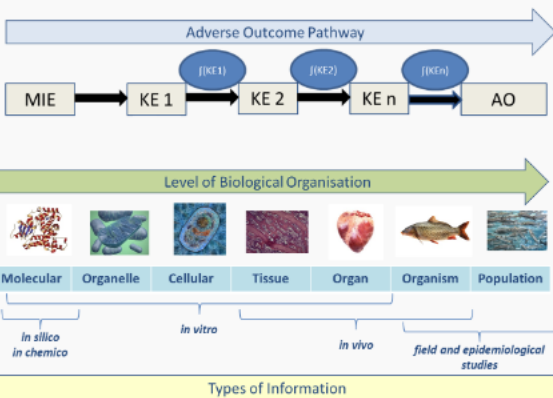
PBK
reverse
dosimetry

➔



points of departure (PoD)
for risk assessment

IATA based on the AOP concept



Another Interpretation: Tox21/ToxCast ~700 HTS Biological Pathways Assays



<https://www.epa.gov/chemical-research/toxicity-forecasting>

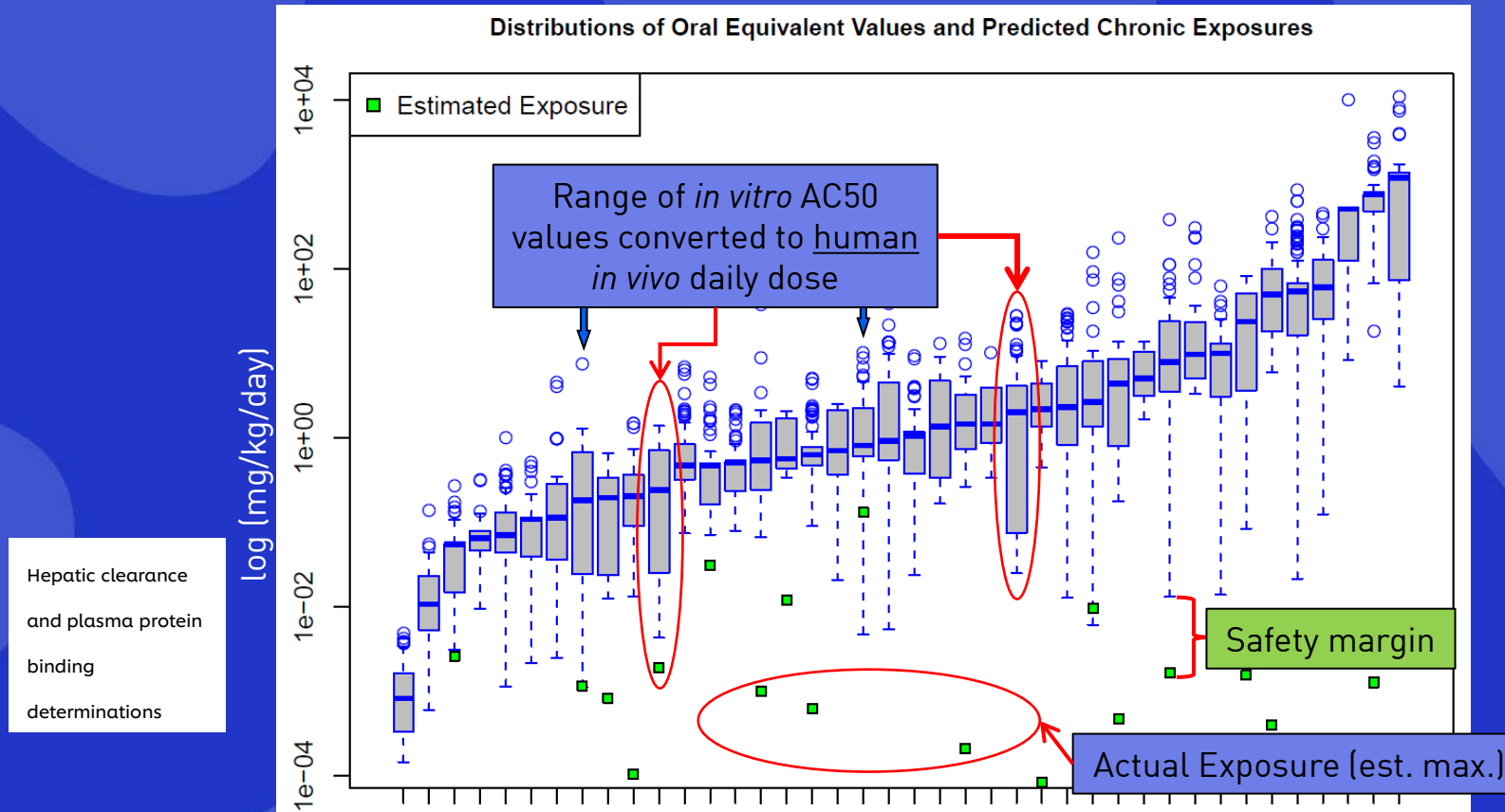
National Institute of Environmental Health Sciences (NIEHS) / National Toxicology Program (NTP)

National Center for Advancing Translational Sciences (NCATS)

U.S. Food and Drug Administration (FDA)

National Center for Computational Toxicology (EPA)

In Vitro Bioactivity vs Bioavailability

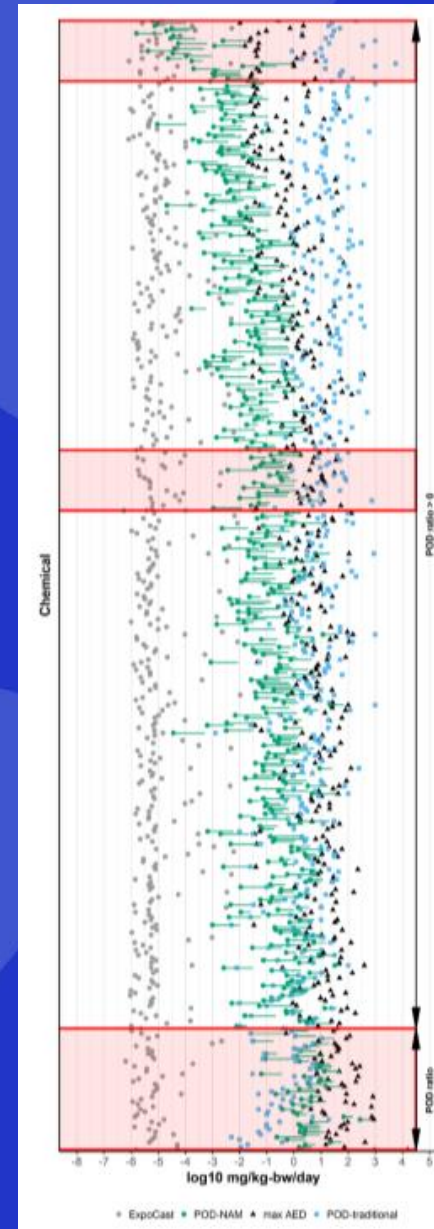
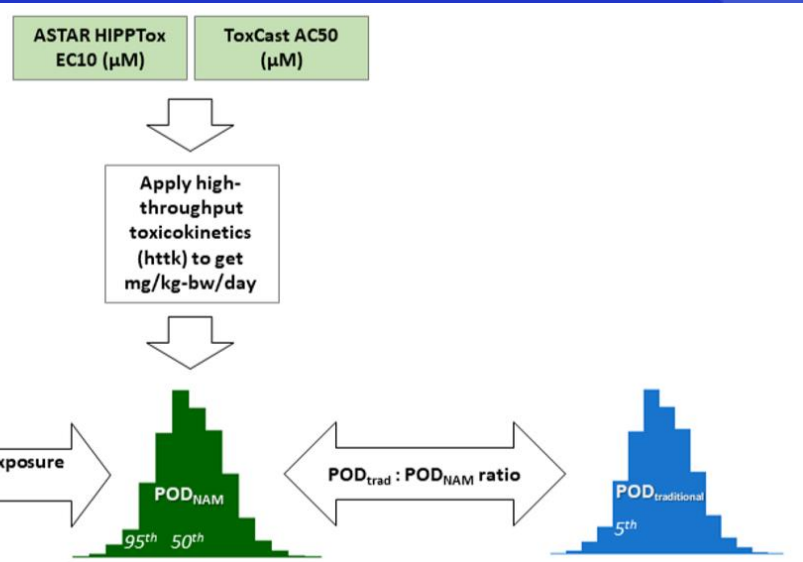


“Protection not Prediction”

EPA, NTP, HC, A*STAR, ECHA, EFSA, JRC, RIVM...



APCRA
ACCELERATING THE PACE OF
CHEMICAL RISK ASSESSMENT

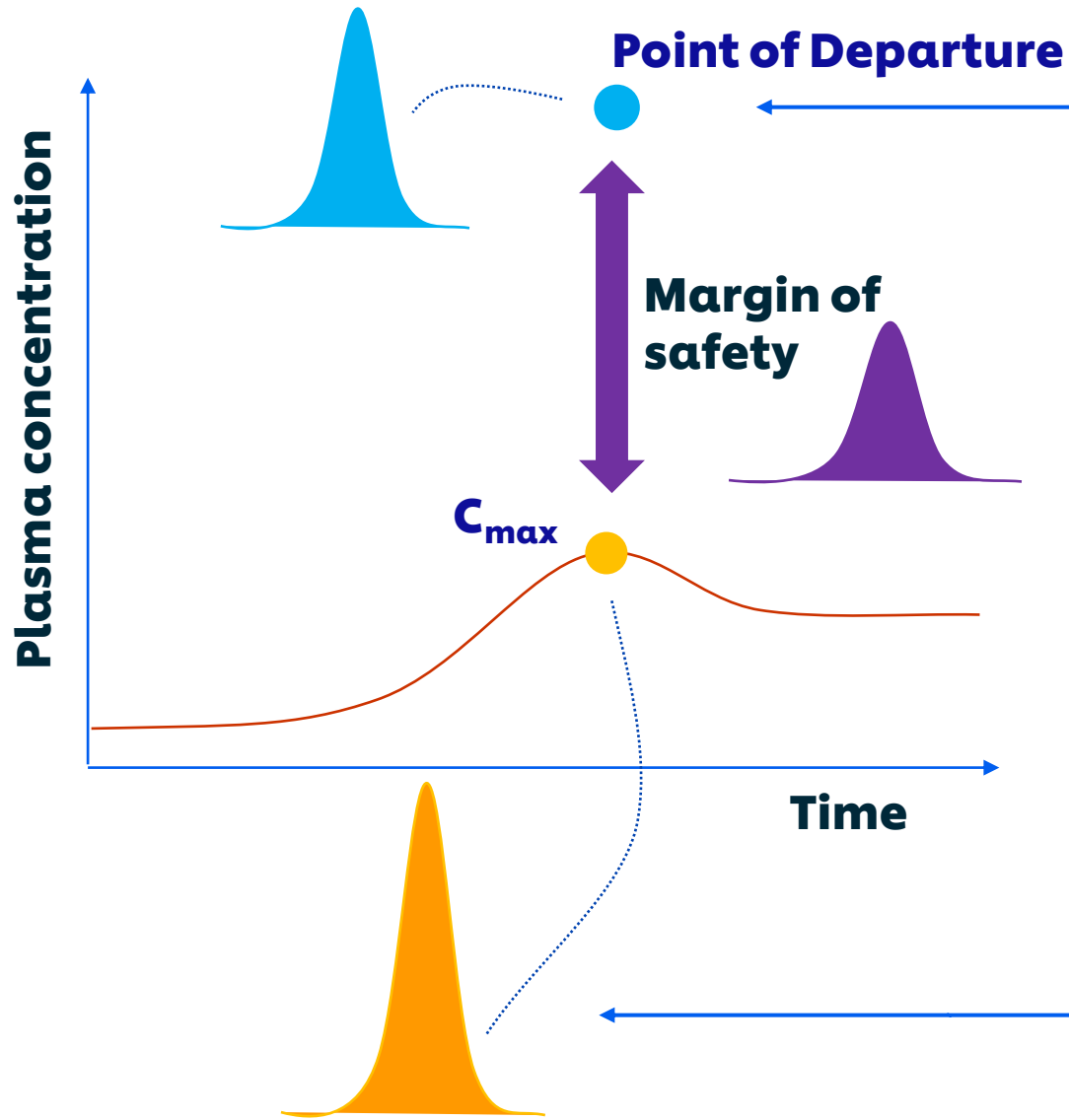


414/448 chemicals =
*92% of the time this
naïve approach appears
conservative*

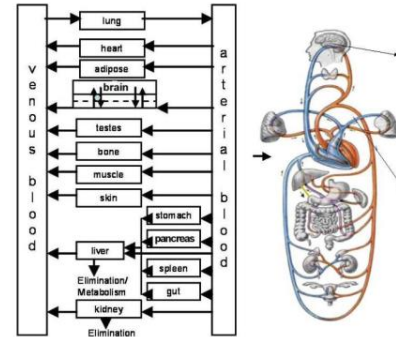


Katie Paul-Friedman *et al.* 2019 *Tox Sciences*, October Issue

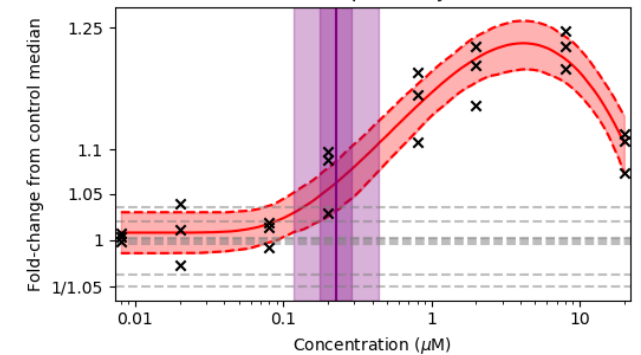
The Margin of Safety Approach



**Exposure models
(PBK, free/total
concentration)**



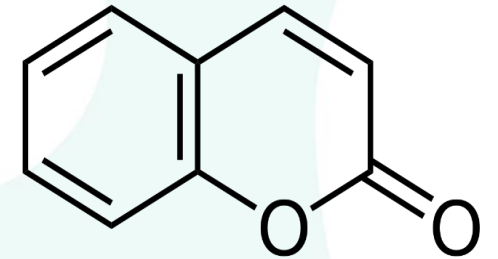
**NAM* Point of departure
derived from *in vitro*
concentration-response**



*NAM = New Approach Methodology

A case study approach – human health safety assessment required for...

0.1% COUMARIN IN FACE CREAM FOR EU MARKET (NEW FRAGRANCE)



Assumed that:

- Coumarin was 100% pure
- No *in vivo* data was available such as animal data, history of safe use (HoSU) or clinical data or use of animal data in read across

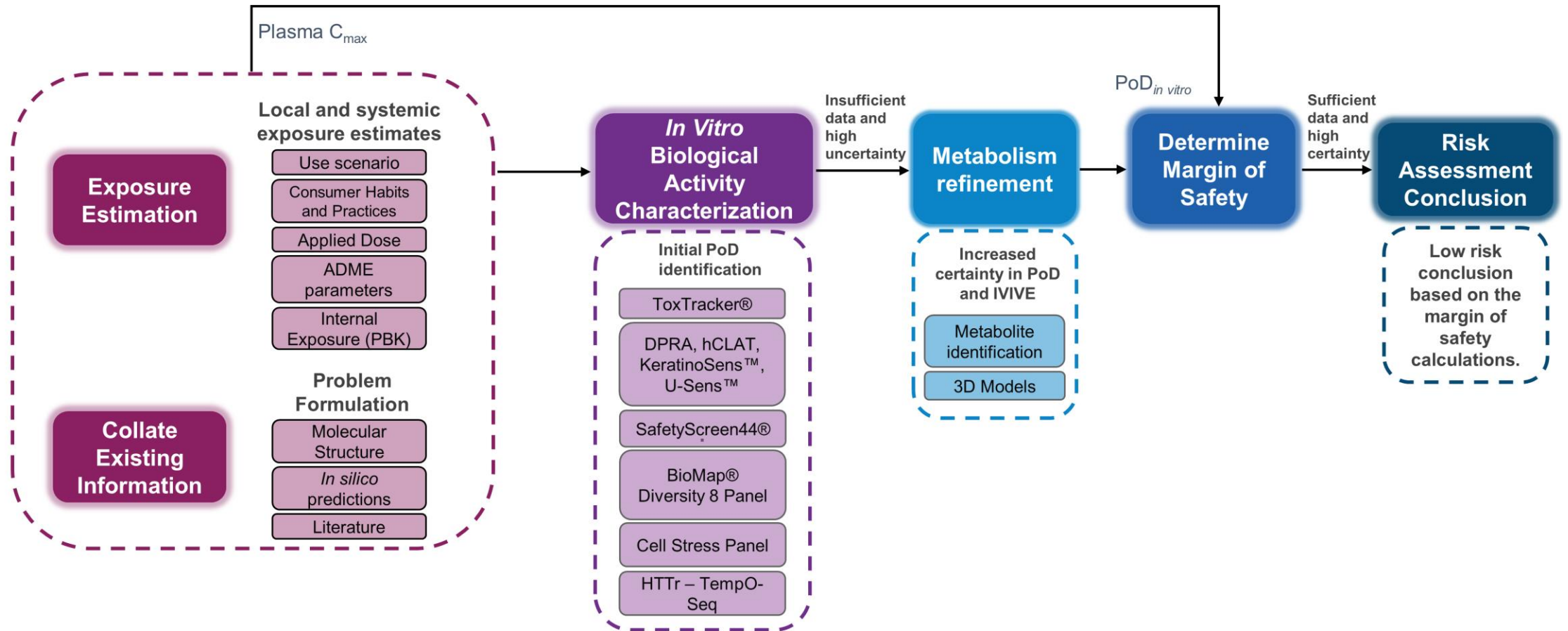


A Next-Generation Risk Assessment Case Study for Coumarin in Cosmetic Products

Maria T. Baltazar,¹ Sophie Cable, Paul L. Carmichael, Richard Cubberley, Tom Cull, Mona Delagrange, Matthew P. Dent, Sarah Hatherell, Jade Houghton, Predrag Kukic, Hequn Li, Mi-Young Lee, Sophie Malcomber, Alistair M. Middleton, Thomas E. Moxon, Alexis V. Nathanail, Beate Nicol, Ruth Pendlington, Georgia Reynolds, Joe Reynolds, Andrew White, and Carl Westmoreland

Baltazar *et al.*, (2020) *Tox Sci* Volume 176, Issue 1, 236–252

Next-Generation Risk Assessment case study workflow for 0.1% coumarin in face cream

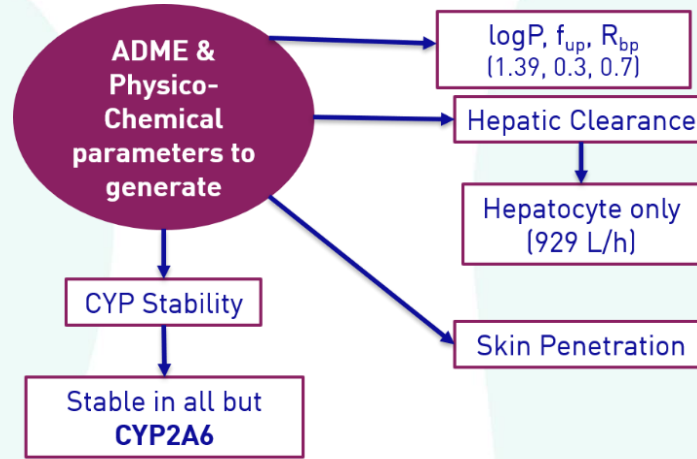


NAMs used to estimate internal concentration

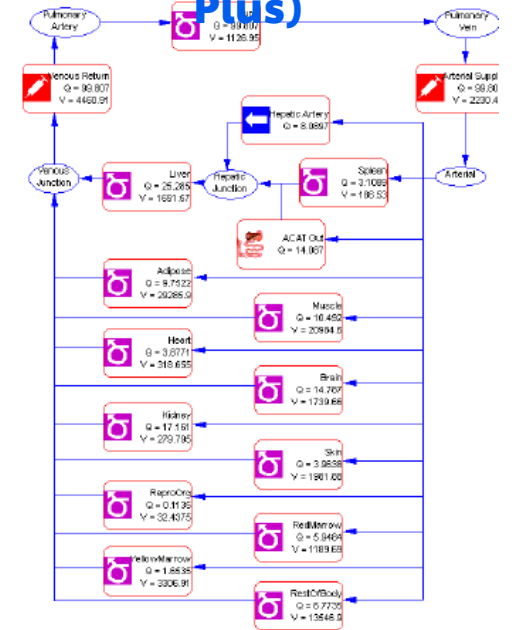
Exposure Estimation

Local and systemic exposure estimates

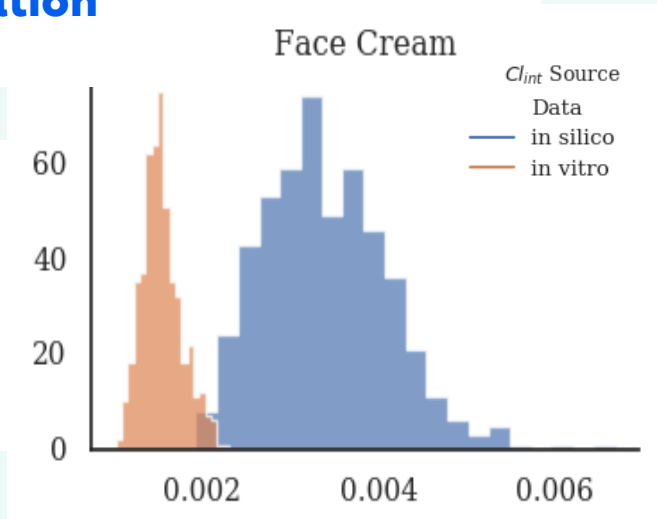
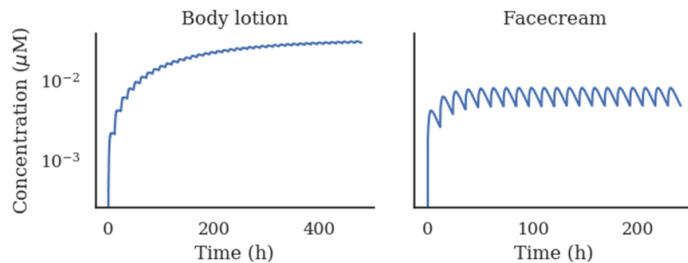
- Use scenario
- Consumer Habits and Practices
- Applied Dose
- ADME parameters
- Internal Exposure (PBK)



GastroPlus® (Simulations Plus)



Simulated plasma concentration of coumarin after dermal exposure:



Moxon *et al.*, (2020). Application of physiologically based kinetic (PBK) modelling in the next generation risk assessment of dermally applied consumer products. Toxicology in Vitro Volume 63

NAMs used to predict biological activity based on chemical structure

Collate Existing Information

Problem Formulation

- Molecular Structure
- In silico predictions**
- Literature

ToxTree

The screenshot shows the ToxTree interface with a chemical structure of a cyclic amide and a list of rules. The 'Look Hazard' section is highlighted in red, showing rules like 'Q11 Has a heterocyclic ring with complex substituents, Yes'.

Derek nex

The screenshot shows the Derek nex interface with a chemical structure and a table of hazard predictions. The table has columns for ID, Endpoint, Species, and Action. One entry is highlighted in red: '113005 Chromosome damage in vivo in rodent mesothelial cells'.

OECD

QSAR TOOLBOX

The screenshot shows the OECD QSAR Toolbox interface, which is a complex web-based tool for QSAR analysis.

In silico models to predict Molecular initiating events (MIEs)

Meteor nex

OXFORD

SOT Society of Toxicology
www.toxsci.oxfordjournals.org

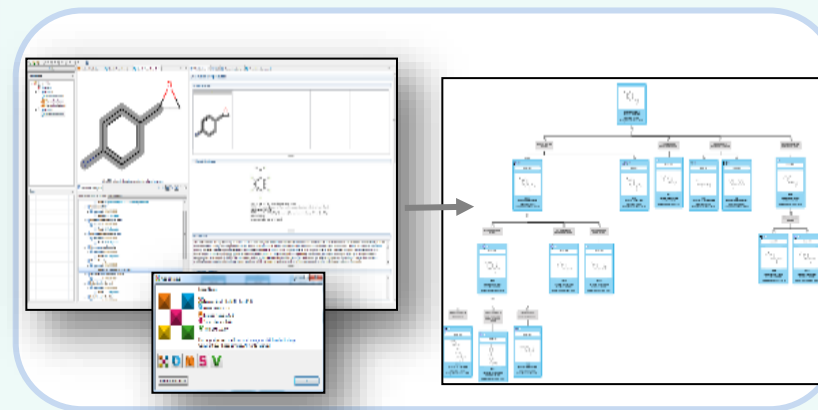
ToxSci 20 Years

TOXICOLOGICAL SCIENCES, 165(1), 2018, 213–223

doi: 10.1093/toxsci/kfy144
Advance Access Publication Date: July 18, 2018
Research Article

Using 2D Structural Alerts to Define Chemical Categories for Molecular Initiating Events

Timothy E. H. Allen,* Jonathan M. Goodman,*¹ Steve Gutsell,[†] and Paul J. Russell[†]



NAMs used to characterize the biological activity of coumarin

In Vitro Biological Activity Characterization

Initial PoD identification

ToxTracker®

SafetyScreen44®

BioMap®
Diversity 8 Panel

Cell Stress Panel

HTTr – TempO-Seq

To investigate possible interactions between coumarin and the 83 key targets involved in drug attrition

PERSPECTIVES

A GUIDE TO DRUG DISCOVERY — OPINION

Reducing safety-related drug attrition: the use of *in vitro* pharmacological profiling

Joanne Bowes, Andrew J. Brown, Jacques Hamon, Wolfgang Jarolimek, Arun Sridhar, Gareth Waldron and Steven Whitebread

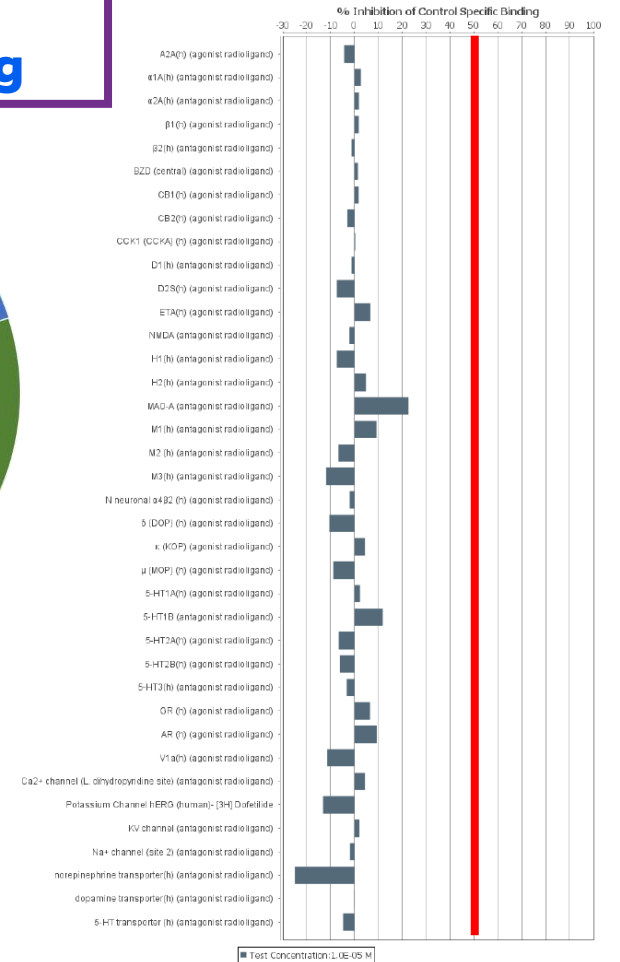
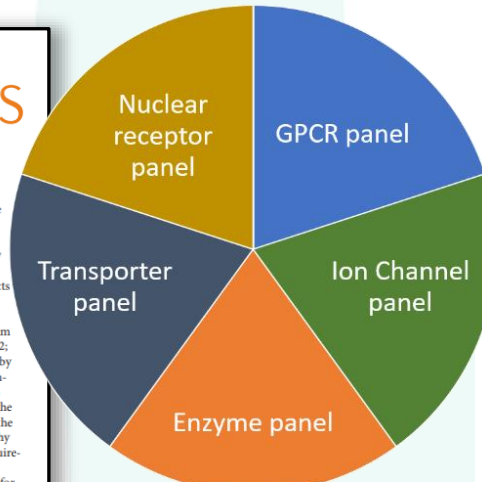
Abstract | *In vitro* pharmacological profiling is increasingly being used earlier in the drug discovery process to identify undesirable off-target activity profiles that could hinder or halt the development of candidate drugs or even lead to market withdrawal if discovered after a drug is approved. Here, for the first time, the rationale, strategies and methodologies for *in vitro* pharmacological profiling at four major pharmaceutical companies (AstraZeneca, GlaxoSmithKline, Novartis and Pfizer) are presented and illustrated with examples of their impact on the drug discovery process. We hope that this will enable other companies and academic institutions to benefit from this knowledge and consider joining us in our collaborative knowledge sharing.

Decreasing the high attrition rate in the drug discovery and development process is a primary goal of the pharmaceutical industry. One of the main challenges in achieving this goal is striking an appropriate balance between drug efficacy and potential adverse effects¹ as early as possible in order to reduce safety-related attrition, particularly in the more expensive late stages of clinical development. Gaining a better understanding of the safety profile of drug candidates early in the process is also crucial for reducing the likelihood of safety issues limiting the use of approved drugs, or even leading to their market withdrawal, bearing in mind the growing societal and regulatory emphasis

target (or targets), whereas secondary effects are due to interactions with targets other than the primary target (or targets) (that is, off-target interactions). Off-target interactions are often the cause of ADRs in animal models or clinical studies, and so careful characterization and identification of secondary pharmacology profiles of drug candidates early in the drug discovery process might help to reduce the incidence of type A ADRs.

In vitro pharmacological profiling involves the screening of compounds against a broad range of targets (receptors, ion channels, enzymes and transporters) that are distinct from the intended

safety testing of drug candidates and are designed to prevent serious ADRs from occurring in clinical studies.
The only *in vitro* pharmacology assay that is absolutely required by regulatory authorities is one that measures the effects of new chemical entities on the ionic current of native (I_h) or heterologously expressed human voltage-gated potassium channel subfamily H member 2 (KCNH2; also known as hERG)². The mechanism by which blockade of hERG can elicit potentially fatal cardiac arrhythmias (torsades de pointes) following a prolongation of the QT interval is well characterized³, and the seriousness of this ADR is one reason why this assay is a mandatory regulatory requirement. Receptor binding studies are also recommended as the first-tier approach for the assessment of the dependence potential of novel chemical entities⁴.
However, current regulatory guidance does not describe which targets should constitute an *in vitro* pharmacological profiling panel and does not indicate the stage of the discovery process at which *in vitro* pharmacological profiling should occur. Nevertheless, the general trend for most pharmaceutical companies is to perform this testing early in drug discovery to reduce attrition and to facilitate better prediction of ADRs in the later stages of drug discovery and development.
Here, for the first time, four major pharmaceutical companies (AstraZeneca, GlaxoSmithKline, Novartis and Pfizer) share their knowledge and experiences of the innovative application of existing screening technologies to detect off-target interactions of compounds. The objective of this article is to describe the rationale and main advantages for the use of *in vitro* pharmacological profiling, to discuss best practices and to



NAMs used to characterize the biological activity of coumarin



In Vitro Biological Activity Characterization

Initial PoD identification

ToxTracker®

SafetyScreen44®

BioMap®
Diversity 8 Panel

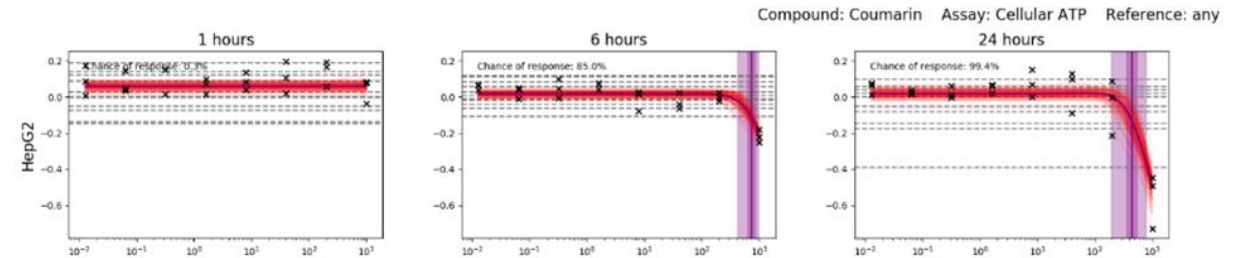
Cell Stress Panel

HTTr – TempO-Seq

**36 Biomarkers;
3 Timepoints;
8 Concentrations;
~10 Stress Pathways**

- Mitochondrial Toxicity
- Oxidative Damage
- DNA damage
- Inflammation
- ER stress
- Metal stress
- Heat Shock
- Hypoxia
- Cell Health

Dose-response analysis and in vitro PoD derivation



| Biomarkers | Cell type | Stress pathway | PoD (µM) | Effect | Concentration dependency score (CDS) |
|-------------------------------|-----------|------------------------|----------------|--------|--------------------------------------|
| ATP (6h) | HepG2 | cell health | 794 (363-977) | down | 0.98 |
| ATP (24h) | HepG2 | cell health | 617 (282-891) | down | 1 |
| Phospholipidosis (24h) | HepG2 | cell health | 759 (437-977) | down | 0.93 |
| GSH (24h) | HepG2 | oxidative stress | 851 (301-1000) | up | 0.92 |
| IL-8 (24h) | HepG2 | inflammation | 912 (575-1000) | down | 0.61 |
| OCR (1h) | HepG2 | mitochondrial toxicity | 62 (2.6-776) | | 0.6 |
| OCR (6h) | NHEK | mitochondrial toxicity | 468 (214-794) | down | 1 |
| OCR (24h) | NHEK | mitochondrial toxicity | 309 (138-1000) | | 0.52 |
| Reserve capacity (1h) | NHEK | mitochondrial toxicity | 44 (23-96) | | 1 |
| Reserve capacity (6h) | NHEK | mitochondrial toxicity | 759 (302-1000) | down | 0.9 |
| Reserve capacity (24h) | NHEK | mitochondrial toxicity | 794 (295-1000) | | 0.55 |



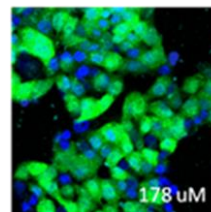
TOXICOLOGICAL SCIENCES, 2020, 1-23

doi: 10.1093/toxsci/ktaa054
Advance Access Publication Date: May 6, 2020
Research article

FEATURED

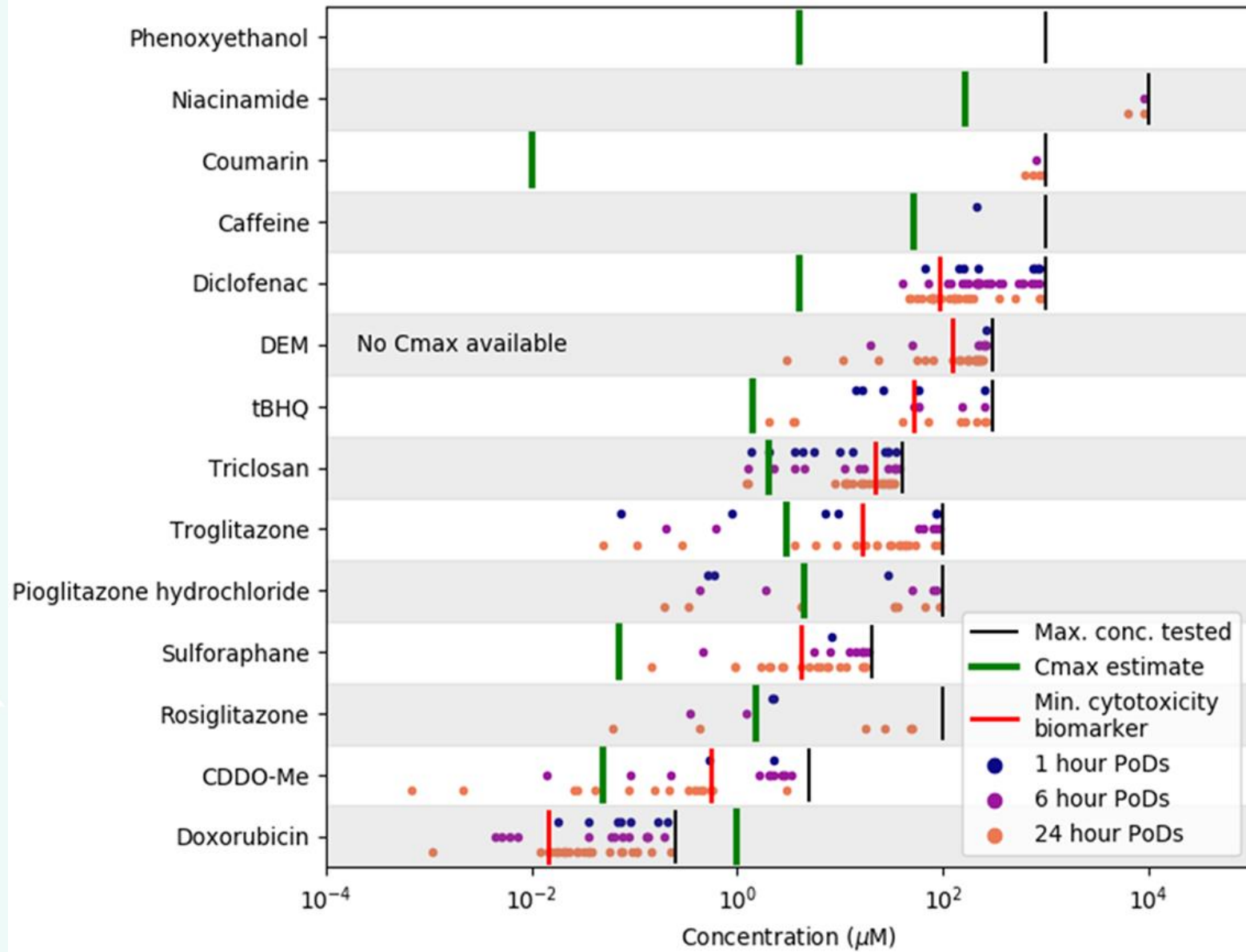
Identifying and Characterizing Stress Pathways of Concern for Consumer Safety in Next-Generation Risk Assessment

Sarah Hatherell,* Maria T. Baltazar,* Joe Reynolds,* Paul L. Carmichael,* Matthew Dent,* Hequn Li,* Stephanie Ryder,† Andrew White,* Paul Walker † and Alistair M. Middleton*¹



¹Unilever Safety and Environmental Assurance Centre, Colworth Science Park, Sharnbrook, Bedfordshire





NAMs for in vitro bioactivity: HTTr (Tempo-Seq)



High-Throughput Transcriptomics Gene Expression Profiling (HTTr)

1. Defining a safe operating exposure for systemic toxicity using a **NOTEL** (No Transcriptional Effect Level)
2. Defining compound similarity grouping (Read Across)

NOTEL is the derived concentration of a compound that does not elicit a meaningful change in gene expression (i.e. the threshold of the concentration that elicits minimal mechanistic activity)

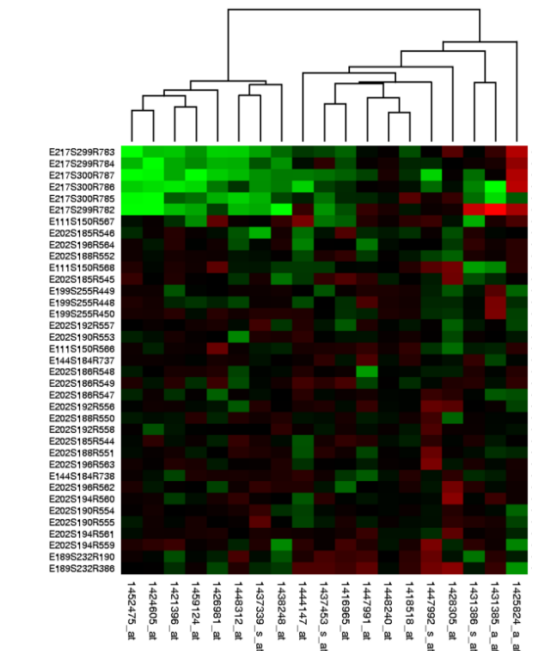
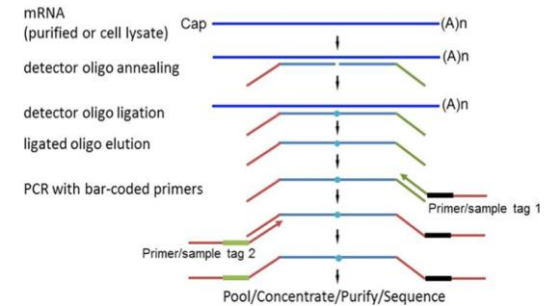
Cell lines (chosen to express a range of relevant receptors)

MCF-7 – human breast adenocarcinoma cell line

HepG2 – human liver carcinoma

HepaRG – terminally differentiated hepatic cells that retain many characteristics of primary human hepatocytes + as spheroids

N-HEK – primary normal human epidermal keratinocytes



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SafetyScreen44®

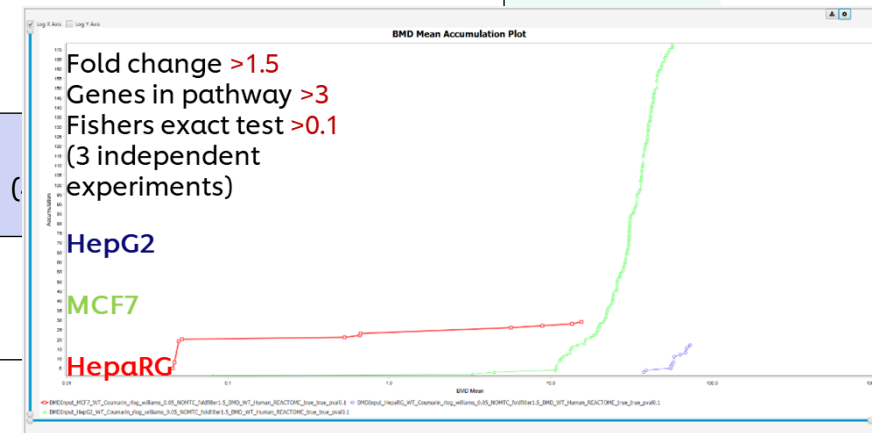
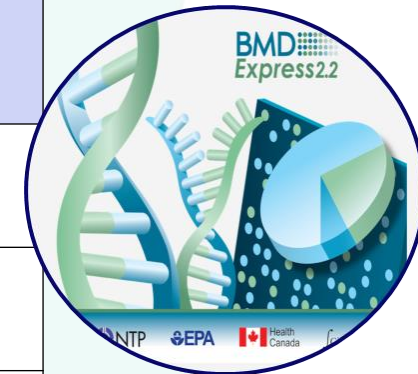
BioMap®
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HTTr – TempO-Sea

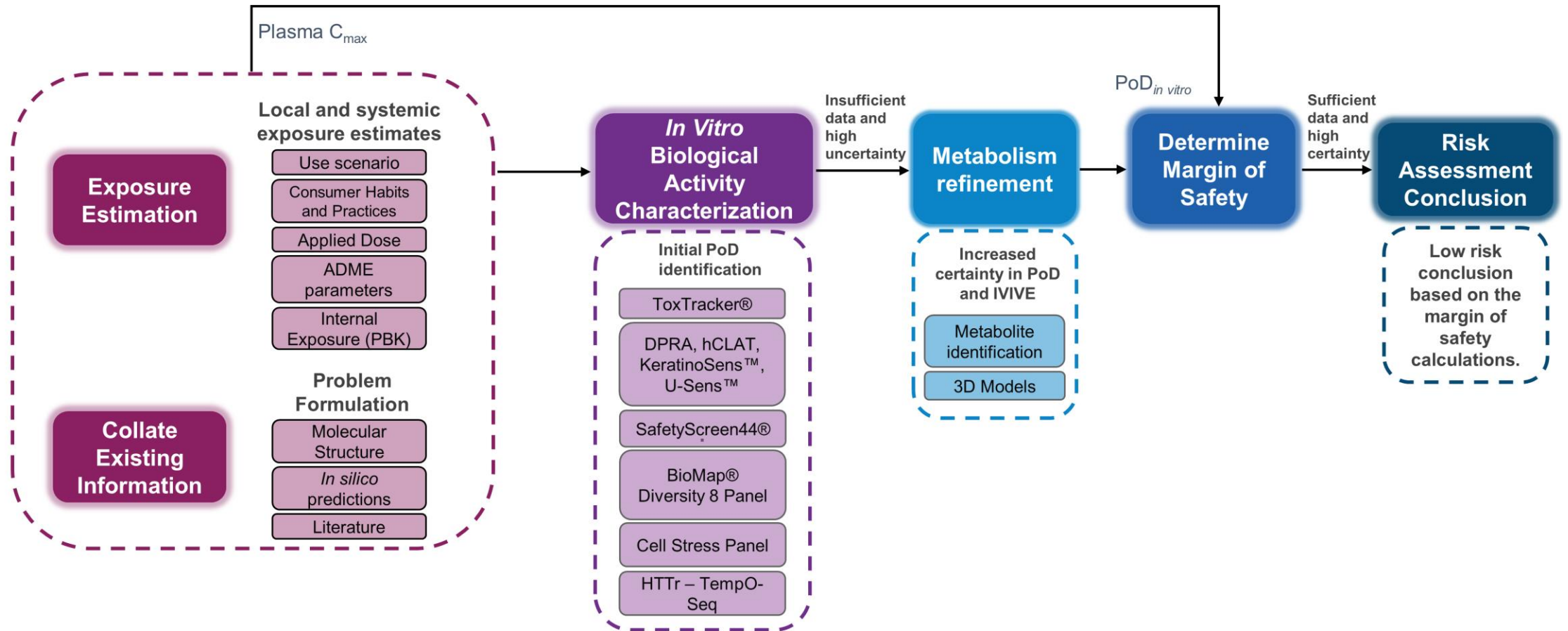
Transcriptomics can be applied as a broad nontargeted biological screen – PoD determination using BMDexpress

| Cell model | HepG2 | MCF7 | HepaRG 2D |
|---|----------------|--------------|---------------|
| Pathway level tests PoD_T (μM) | (308 pathways) | (0 pathways) | (17 pathways) |
| 20 pathways with the lowest p value | | | |
| Reactome | 70 | NA | 58* |
| 20 pathways with the lowest BMD | | | |
| Reactome | 44 | NA | 58* |
| BMD of Reactome pathway with lowest BMD that meets significance threshold criteria | 31 | | |
| Gene level tests PoD_T (μM) | (1570 genes) | | |
| Mean BMD of 20 genes with largest fold change | 6 | | |
| Mean BMD of genes between 25th and 75th percentile | 17 | | |

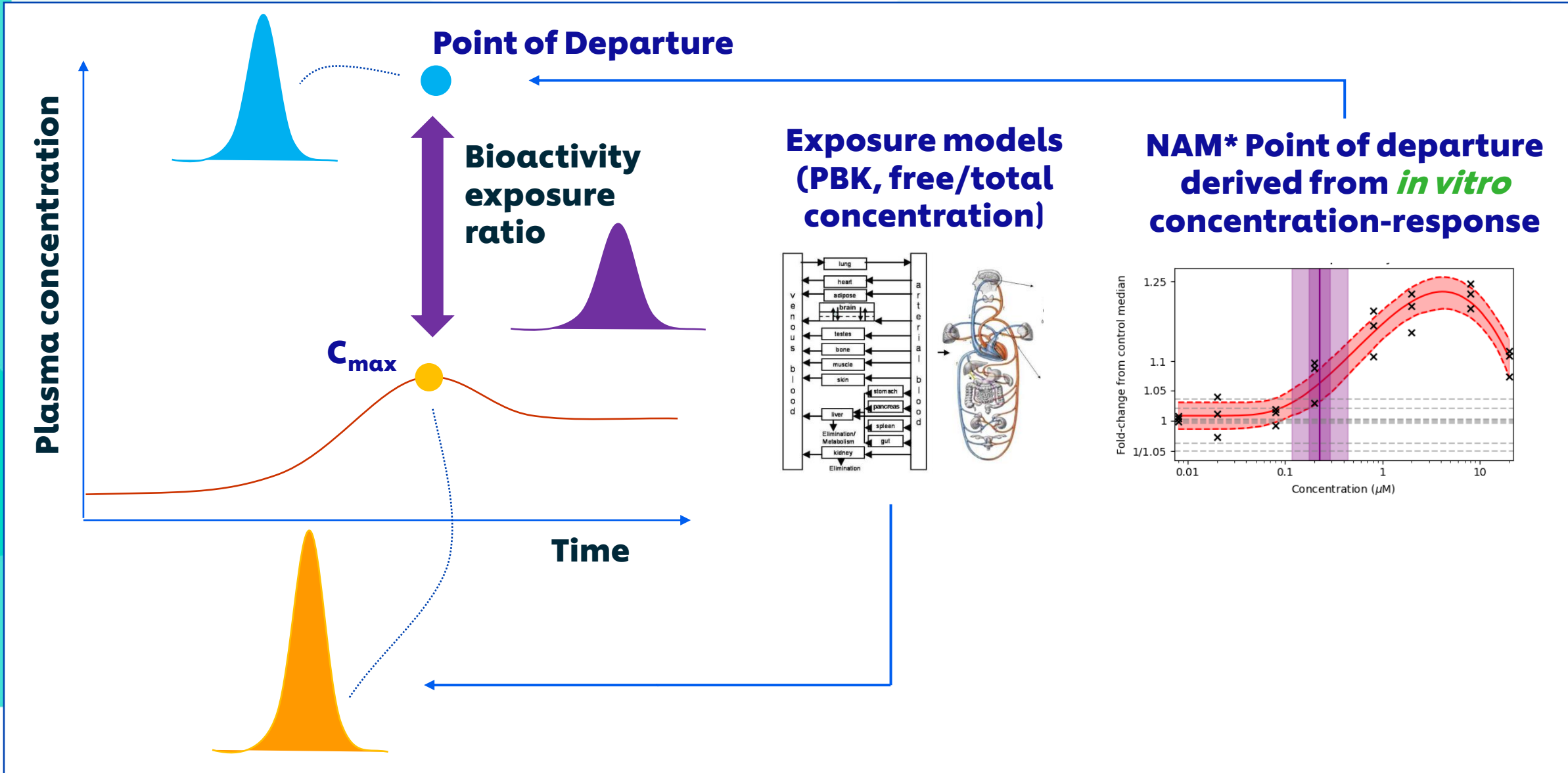


Farmahin, R., Williams, A., Kuo, B. et al. Recommended approaches in the application of toxicogenomics to derive points of departure for chemical risk assessment. *Arch Toxicol* **91**, 2045–2065 (2017). <https://doi.org/10.1007/s00204-016-1886-5>

Next-Generation Risk Assessment case study workflow for 0.1% coumarin in face cream

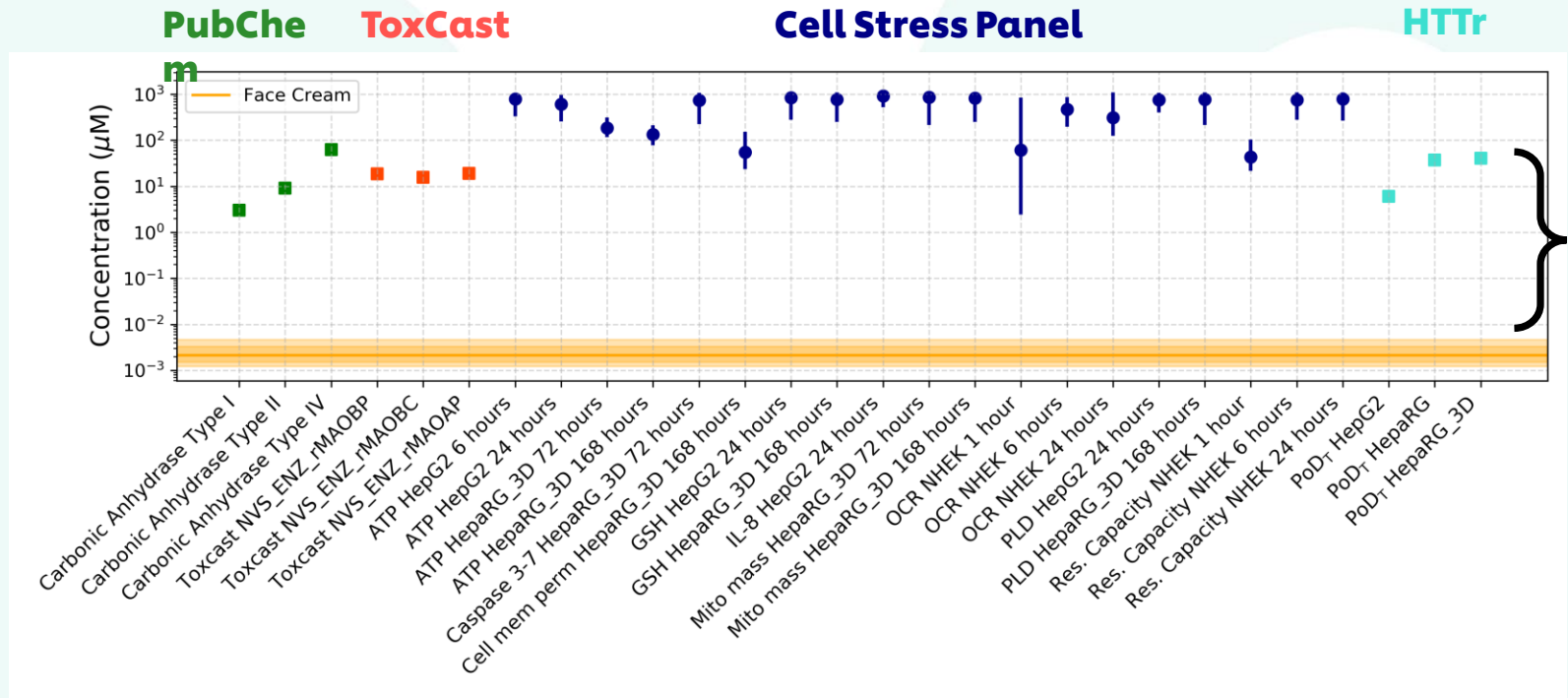


The Margin of Safety Approach



Determination of MoS using NAMs and risk assessment conclusion

Determine Margin of Safety



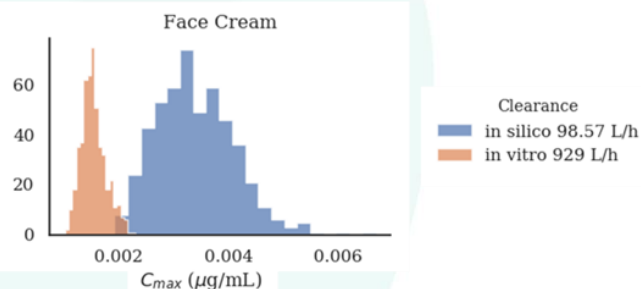
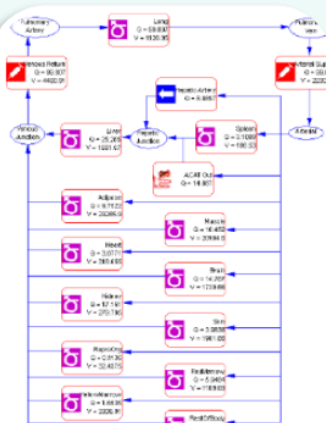
Margin of safety

The 5th percentile of the MoS distribution ranged between 706 and 96738

- In this case study:
- Weight of evidence suggested that the inclusion of 0.1% coumarin in face cream is safe for the consumer

The Key Elements in our NGRA Approach

PBK Modelling



Toxicology in Vitro (2020), 63, 104746

In vitro pharmacological profiling

PERSPECTIVES

A GUIDE TO DRUG DISCOVERY — OPINION

Reducing safety-related drug attrition: the use of *in vitro* pharmacological profiling

Joanne Breen, Andrew J. Brown, Jacques Homan, Wolfgang Juronick, Arun Sridhar, Gareth Waldron and Steven Whitbread

Abstract In vitro pharmacological profiling is increasingly being used earlier in the drug discovery process to identify undesirable off-target activity profiles that could hinder or halt the development of candidate drugs or even lead to market withdrawal if discovered after a drug is approved. Here, for the first time, the rationale, strategies and methodologies for *in vitro* pharmacological profiling at four major pharmaceutical companies (AstraZeneca, GlaxoSmithKline, Novartis and Pfizer) are presented and illustrated with examples of their impact on the drug discovery process. We hope that this will enable other companies and academic institutions to benefit from this knowledge and consider joining us in our collaborative knowledge sharing.

Decreasing the high attrition rate in the drug discovery and development process is a primary goal of the pharmaceutical industry. One of the main challenges in achieving this goal is striking an appropriate balance between drug efficacy and potential adverse effects as early as possible in order to reduce safety-related attrition, particularly in the more expensive late stages of clinical development. Gaining a better understanding of the safety profile of drug candidates early in the process is also crucial for reducing the likelihood of safety issues limiting the use of approved drugs, or even leading to their market withdrawal, having to incur the massive financial and regulatory costs.

target (or targets), whereas secondary effects are due to interactions with targets other than the primary target (or targets) that is off-target interactions. Off-target interactions are often the cause of ADRs in animal models or clinical studies, and careful characterization and identification of secondary pharmacology profiles of drug candidates early in the drug discovery process might help reduce the incidence of type A ADRs.

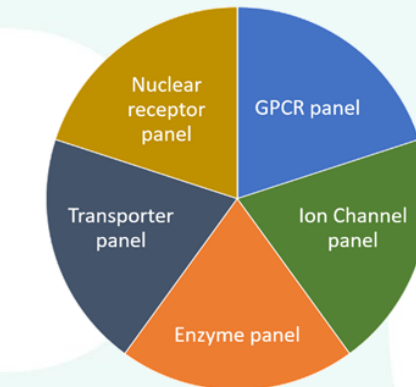
In vitro pharmacological profiling involves the screening of compounds against a broad range of targets (receptors, enzymes, transporters, etc.) that are chosen from the scientific

safety testing of drug candidates and are designed to prevent serious ADRs from occurring in clinical studies.

The *in vitro* pharmacology assay that is absolutely required by regulatory authorities is one that measures the effects of new chemical entities on the ion currents of native I_{Ca} in heterologously expressed human voltage-gated potassium channel subfamily 11 member 2 (hKCNJ2), also known as hERG2. The mechanism by which blockade of hERG2 can affect potentially fatal cardiac arrhythmias (torsades de pointes) following a prolongation of the QT interval is well characterized^{1,2}, and the assessment of this ADR is one reason why this assay is a mandatory regulatory requirement. Receptor binding studies are also recommended as the first tier approach for the assessment of the dependence potential of novel chemical entities³.

However, current regulatory guidance does not describe which targets should constitute an *in vitro* pharmacological profiling panel and does not indicate at what stage of the discovery process at which *in vitro* pharmacological profiling should occur. Nevertheless, the general trend for most pharmaceutical companies is to perform this testing early in drug discovery to reduce attrition and to facilitate better prediction of ADRs in the later stages of drug discovery and development.

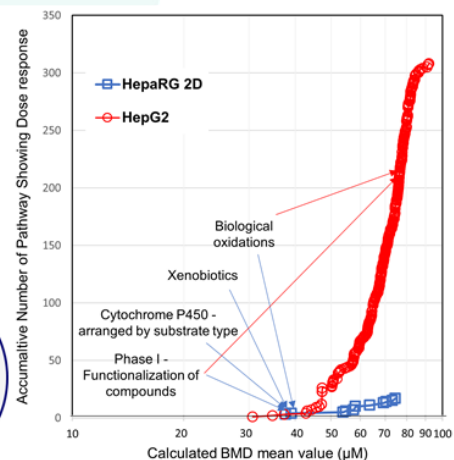
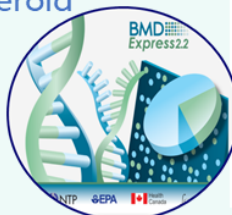
Here, for the first time, four major pharmaceutical companies (AstraZeneca, GlaxoSmithKline, Novartis and Pfizer) share their knowledge and experience of the innovative application of existing screening technologies to detect off-target interactions of compounds. The objective of this article is to describe the rationale and main strategies for the use of an *in vitro* pharmacological profiling panel to reduce safety-related attrition, to discuss best practices and to



Transcriptomics

- Use of full human gene panel ~ 21k
- 24 hrs exposure
- 7 concentrations
- 3 cell lines HepG2/ HepaRG/ MCF7
- 3D HepaRG spheroid

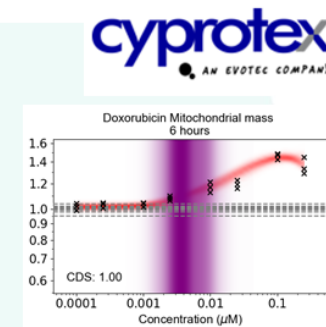
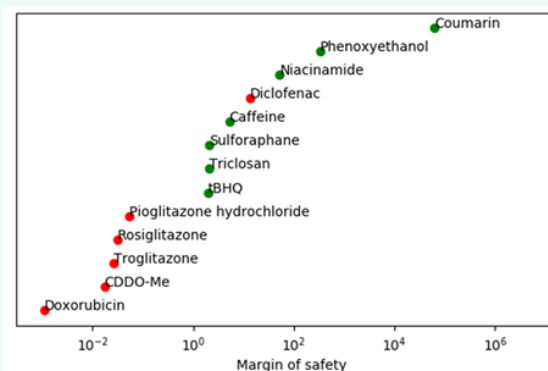
BMDexpress 2



Cellular Stress Pathways

13 chemicals, 36 Biomarkers; 3 Timepoints; 8 Concentrations; ~10 Stress Pathways

- Exposure scenario adopted for chemical is 'low risk'** (from consumer goods perspective)
- Nicotinamide [food, cosmetics]
 - Caffeine [beverages, cosmetics]
 - Phenoxyethanol [cosmetics]
 - Sulfonaphane [food]
 - tBHQ [antioxidant]
 - Triclosan [antimicrobial]
- Exposure scenario adopted for chemical is 'high risk'** (from consumer goods perspective)
- CDDO-Me [drug]
 - DEM [industrial chemical]
 - Doxorubicin [drug]
 - Diclofenac [drug]
 - Troglitazone [drug]
 - Pioglitazone [drug]
 - Rosiglitazone [drug]

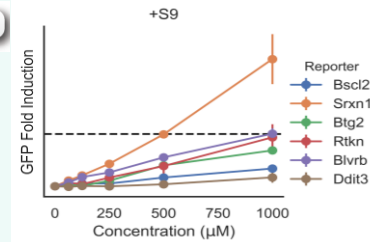
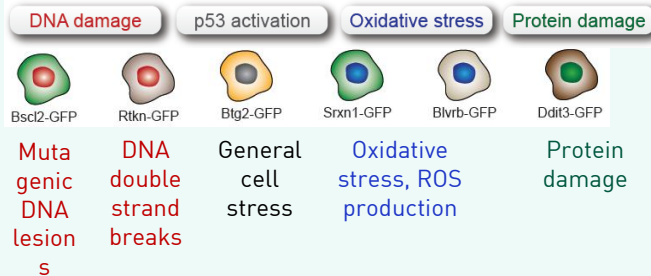


Toxicol Sci (2020), 176, 11-33

NGRA is hypothesis-driven – examples of bespoke assays used in the coumarin case study

Genotoxicity assessment: ToxTracker®

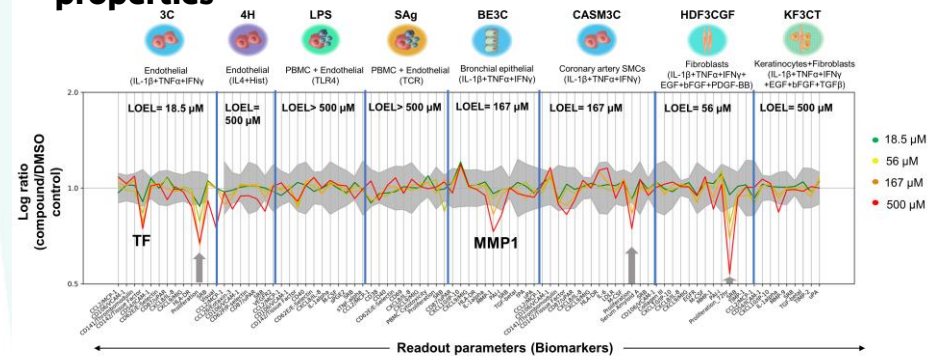
- Coumarin and its metabolites triggered genotoxicity alerts



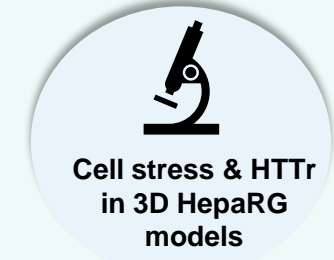
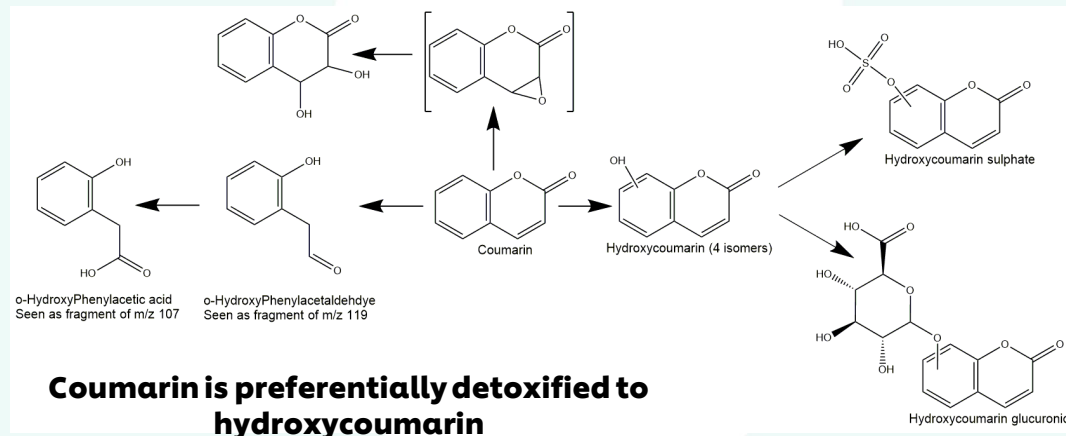
6 GFP reporter mouse embryonic stem (mES) cells

Immunomodulatory screening assay: BioMap® Diversity 8 Panel

- Coumarin predicted to have anti-inflammatory properties

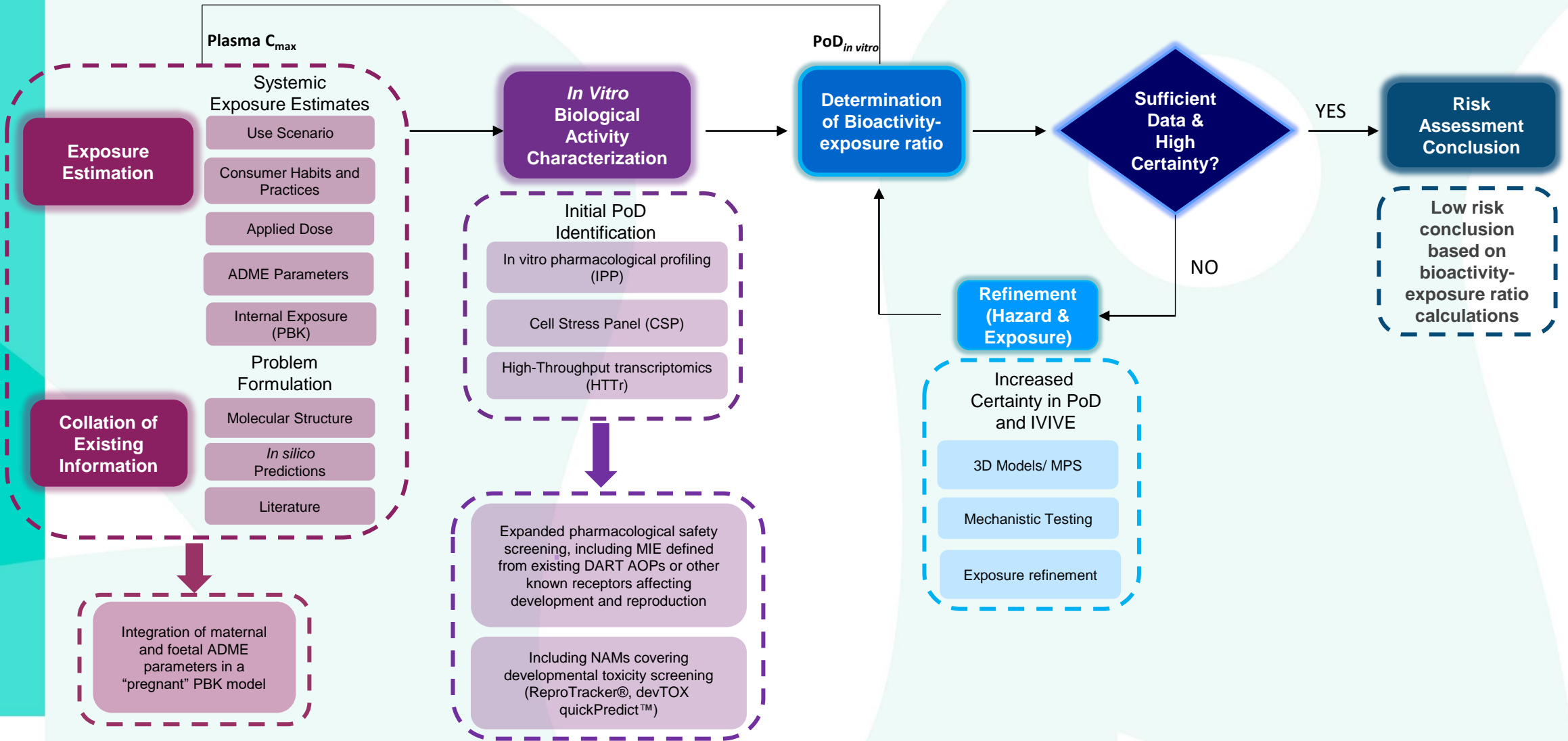


Metabolite identification & PoD refinement



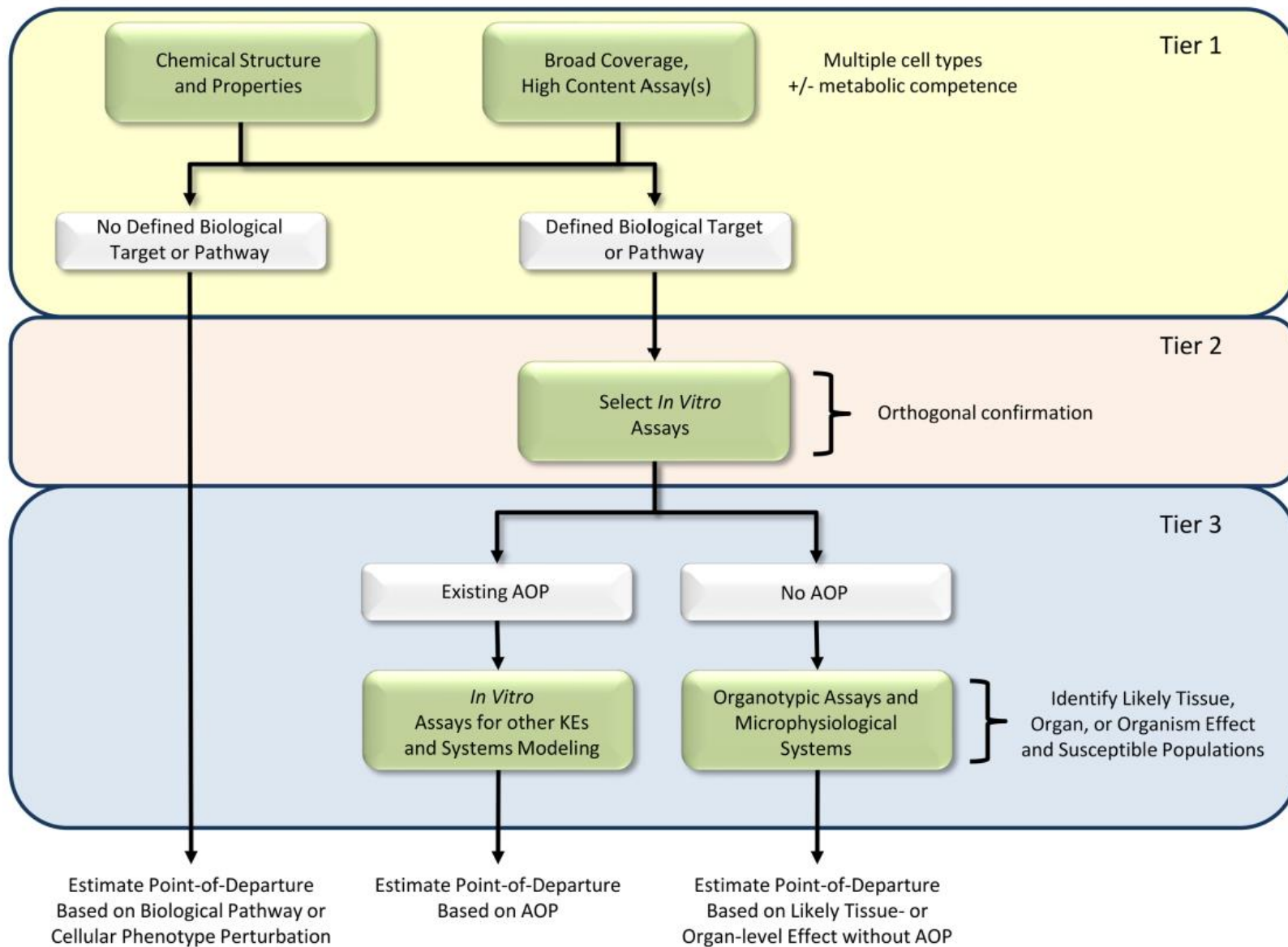
- Low bioactivity also found in a metabolic competent cell model (HepaRG 3D)
- PoDs range: 41-871 µM – similar range as in from 2D cells

Integrating DART Safety Assessment into Existing NGRA Framework



An NGRA framework with additional NAMs relevant for DART endpoints

The EPA Blueprint



FORUM

The Next Generation Blueprint of Computational Toxicology at the U.S. Environmental Protection Agency

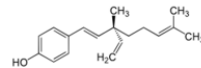
Russell S. Thomas,^{*,1} Tina Bahadori,[†] Timothy J. Buckley,[‡] John Cowden,^{*} Chad Deisenroth,^{*} Kathie L. Dionisio,[‡] Jeffrey B. Frithsen,[§] Christopher M.



Dent *et al.*, (2018) Toxicological Sciences

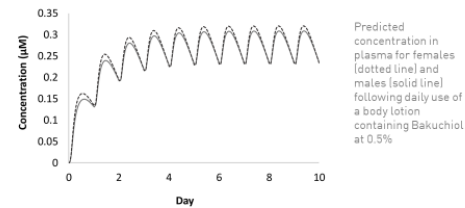
Androgen Receptor Antagonism

- Problem formulation: Can Bakuchiol be safely used at 0.5% in a body lotion or a shampoo?
 - Calculate exposure –above TTC for both exposure scenarios
 - Perform literature search – no ‘definitive’ toxicology data but indications of hormonal activity
 - In-silico screen – suggestive of AR interaction



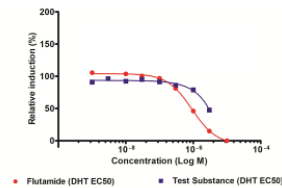
Physiologically-Based Kinetic Modelling

- Low-tier assessment based on predicted/scaled values



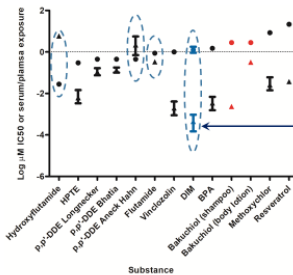
Bakuchiol Dose Response Data

- Dose-response data generated in a human-relevant system
- (AR-CALUX® assay)



Comparing Exposure and Effect Concentrations

Triangles show plasma or serum levels, circles show IC₅₀ values for bakuchiol and several anti-androgens



50 g

What is an appropriate 'Margin of Exposure'?



Using Dietary Comparator Ratios to Benchmark Risk

- Calculation of Exposure:Activity Ratios (After Becker *et al.* 2015 *Regul. Toxicol. Pharmacol.* 71(3), 398–408):

$$EAR \text{ (unitless)} = \frac{\text{Exposure (plasma exposure in } \mu\text{M)}}{\text{Activity (IC}_{50} \mu\text{M)}}$$

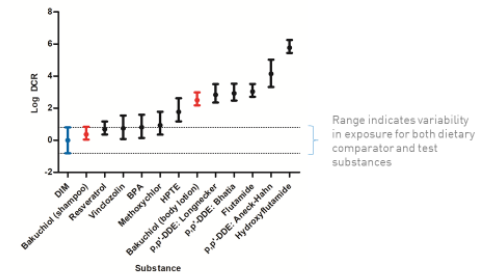
$$DCR = \frac{EAR \text{ (test substance)}}{EAR \text{ (dietary comparator)}}$$

If DCR<1 the activity of the test substance exposure would be lower than the activity of the dietary comparator exposure which has a history of safe use



40

Dietary Comparator Ratios



Range indicates variability in exposure for both dietary comparator and test substances

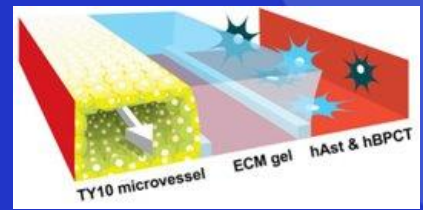


Microphysiological Systems (MPS)

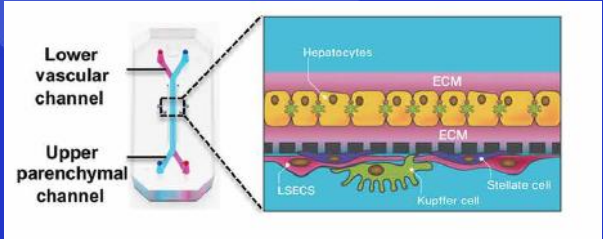
TissUse



Mimetas



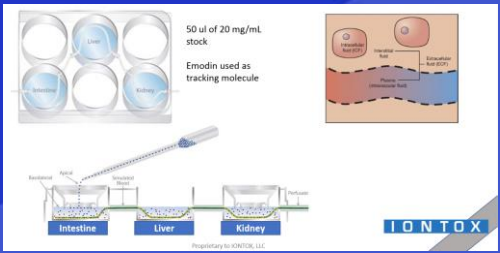
Emulate



CNBio



IonTox



Conclusions

Changing global environment for toxicology

- Consumers are demanding change; calls for non-animal, next generation risk assessments
- NGRA is a framework of non-standard, bespoke data-generation, driven by the risk assessment questions
- Enabling a transition from using data from tests in live animals to one founded on understanding the effects of chemicals in humans using computational approaches and *in vitro* methods that evaluate changes in biologic processes using human cells
- Constructed from *in silico* modelling approaches and *in vitro* solutions
- Need to ensure quality/robustness of the non-standard (non-TG) work and to characterise uncertainty to allow informed decision-making (BENCHMARKING)
- Shortcomings will be addressed by current and future research
- More research, creativity and examples needed to land this successfully with regulators

The NEW Gold Standard

Was:

- Rodents
- Pathology
- High-dose apical endpoints
- No adverse effect level
- Uncertainty factors

Is Now:

- Broad-based NAMs
- Implementing new NAMs
- Exposure led (PBK)
- **Bioactivity not pathology**
- **Protection not prediction**
- **Underpinned by
Computational modelling**

News Releases from Headquarters > Research and Development (ORD)

CONTACT US

EPA and Unilever Announce Major Research Collaboration to Advance Non-animal Approaches for Chemical Risk Assessment

August 19, 2021

Contact Information

EPA Press Office (press@epa.gov)

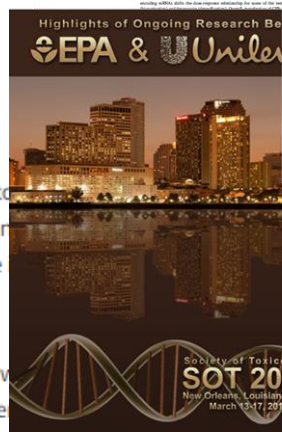
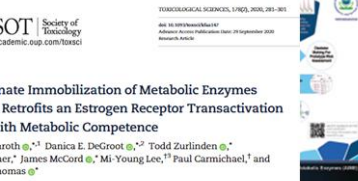
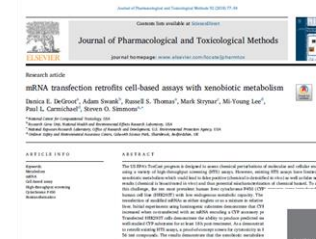
WASHINGTON – Today, the U.S. Environmental Protection Agency (EPA) and Unilever announced a collaborative agreement to better ways to assess chemical risks associated with consumer products. This agreement builds on prior cooperation between Unilever regarding New Approach Methods (NAMs), which are a promising alternative to conventional toxicity testing that are to reduce reliance on the use of animals.

EPA and Unilever have been jointly evaluating and using NAMs since 2015. This collaboration is helping EPA implement its New Methods Work Plan and is the foundation for new efforts to demonstrate that these novel approaches can help decision makers protect consumers, workers and the environment.

“EPA is a pioneer in developing and applying NAMs to identify and quantify risks to human health, while reducing the use of animal chemical toxicity testing,” said **H. Christopher Frey, Deputy Assistant Administrator for Science Policy in EPA’s Office of Research and Development**. “We are excited to continue the collaboration with Unilever, which enhances the robustness of our mutual efforts to demonstrate the use of NAMs.”

The new collaborative effort aims to establish a framework for the Next Generation of Risk Assessments based on NAMs. Such assessments are intended to quantify health risks to humans with sufficient scientific rigor to replace conventional animal-based methods and to support EPA’s mission to protect human health and the environment.

This collaboration will bring together **more than \$2 million** in both monetary and in-kind contributions, including scientific expertise and equipment, to develop a comprehensive NAMs dataset for a minimum of 40 chemicals. The chemicals will be selected and grouped such



The Alginate Immobilization of Metabolic Enzymes Platform Retrofits an Estrogen Receptor Transactivation Assay With Metabolic Competence
Chad Deisenroth^{1,*}, Danica E. DeGroot^{2,*}, Todd Zur Linden^{3,*}, Andrew Eicher⁴, James McCord^{5,*}, Mi-Young Lee^{1,3}, Paul Carmichael¹, and Russell S. Thomas⁶

¹Center for Computational Toxicology and Exposure, Office of Research and Development, U.S. Environmental Protection Agency, Research Triangle Park, North Carolina 27711 and ²Safety and Environmental Assurance Center, Unilever, Colworth Science Park, Bedford, Sharnbrook MK43 9QJ, UK



Press Release 19 August 2021

Thank you!

Supporting papers:
Toxicological Sciences 'Highly Cited Collection'
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<https://youtu.be/5Z2S8MnKp7g>

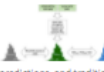
COLLECTION Highly Cited Articles

Toxicological Sciences publishes a broad spectrum of impactful research in the field of toxicology. Explore a selection of highly cited articles, published during the past 10 years, that are making an impact in the research community and celebrate the increase to 4.849 of *Toxicological Sciences* latest impact factor. All articles are freely available for you to download, read, and enjoy until 31st of December 2021.

Utility of *In Vitro* Bioactivity as a Lower Bound Estimate of *In Vivo* Adverse Effect Levels and in Risk-Based Prioritization

Katie Paul Friedman et al.


Toxicological Sciences, Volume 173, Issue 1, January 2020, Pages 202–225, <https://doi.org/10.1093/toxsci/kfz201>

 Use of high-throughput, *in vitro* bioactivity data in setting a point-of-departure (POD) has the potential to accelerate the pace of human health safety evaluation by informing screening-level assessments. The primary objective of this work was to compare PODs based on high-throughput predictions of bioactivity, exposure predictions, and traditional hazard information...

Novel Therapeutic Approaches Against Acetaminophen-induced Liver Injury and Acute Liver Failure

Hartmut Jaeschke et al.


Toxicological Sciences, Volume 174, Issue 2, April 2020, Pages 159–167, <https://doi.org/10.1093/toxsci/kfaa002>

 Liver injury and acute liver failure caused by acetaminophen (APAP, N-acetyl-p-aminophenol, paracetamol) overdose is a significant clinical problem in most western countries. The only clinically approved antidote is N-acetylcysteine (NAC), which promotes the recovery of hepatic GSH. If administered during the metabolism phase, GSH scavenges the reactive metabolite...

A Next-Generation Risk Assessment Case Study for Coumarin in Cosmetic Products

Maria T Baltazar et al.


Toxicological Sciences, Volume 176, Issue 1, July 2020, Pages 236–252, <https://doi.org/10.1093/toxsci/kfaa048>

 Next-Generation Risk Assessment is defined as an exposure-led, hypothesis-driven risk assessment approach that integrates new approach methodologies (NAMs) to assure safety without the use of animal testing. These principles were applied to a hypothetical safety assessment of 0.1% coumarin in face cream and body lotion. For the purpose of evaluating the use of NAMs...

The Impact of Environmental Chemicals on the Gut Microbiome

Karen Chiu et al.


Toxicological Sciences, Volume 176, Issue 2, August 2020, Pages 253–284, <https://doi.org/10.1093/toxsci/kfaa065>

 Since the surge of microbiome research in the last decade, many studies have provided insight into the causes and consequences of changes in the gut microbiota. Among the multiple factors involved in regulating the microbiome, exogenous factors such as diet and environmental chemicals have been shown to alter the gut microbiome significantly. Although diet substantially contributes...

The Next Generation Blueprint of Computational Toxicology at the U.S. Environmental Protection Agency

Russell S Thomas et al.

Toxicological Sciences, Volume 169, Issue 2, June 2019, Pages 317–332, <https://doi.org/10.1093/toxsci/kfz058>

 The U.S. Environmental Protection Agency (EPA) is faced with the challenge of efficiently and credibly evaluating chemical safety often with limited or no available toxicity data. The expanding number of chemicals found in commerce and the environment, coupled with time and resource requirements for traditional toxicity testing and exposure characterization, continue to underscore the need for...



Decision making in Next Generation Risk Assessment (NGRA)

Using Computational Models to Make Sense of Complex Data

08/05/2024



Unilever

Learning objectives

- Understanding of how models are used to make predictions or analyse data in toxicology, and how they can be useful.
- Awareness of different modelling approaches currently used in risk assessment (e.g., Bayesian inference, physiologically based kinetic models etc), illustrated with examples taken from case studies.
- Understand how to get started using computational approaches to analyse data (including open access tools and other resources).

About me

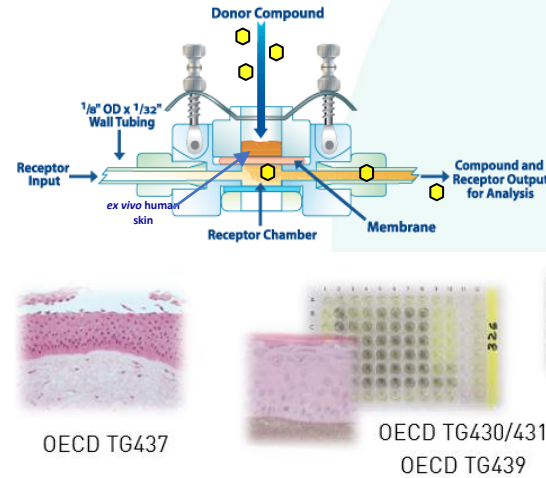
- Degree in Mathematics from the University of Edinburgh
- PhD in Applied Mathematics from the University of Nottingham
- Postdocs in Germany at the University of Freiburg and the University of Heidelberg
- Joined Unilever in 2014, hired as a mathematical modeller
- Science leader in Computational Toxicology



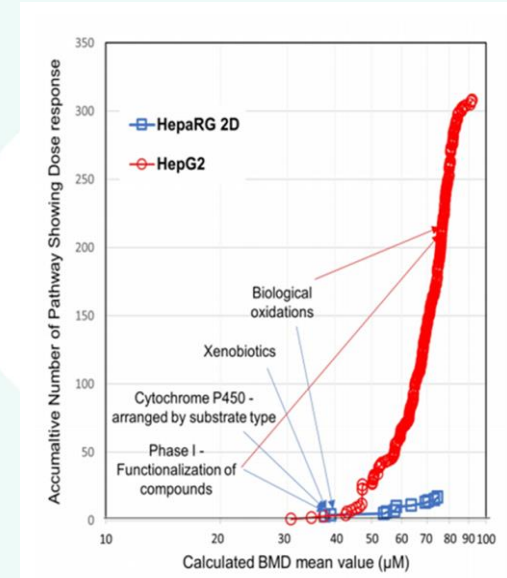
Next Generation Risk Assessment is highly interdisciplinary



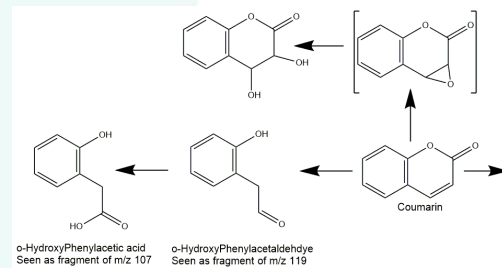
Risk assessment



Biology



Bioinformatics



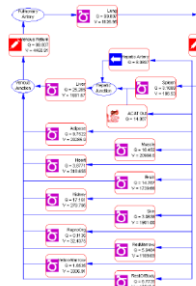
Chemistry

$$y_t = \underbrace{\begin{bmatrix} w_{g,1}^{(1)} & \dots & w_{g,1}^{(m)} \\ \vdots & & \vdots \\ w_{g,n_y}^{(1)} & \dots & w_{g,n_y}^{(m)} \end{bmatrix}}_C \underbrace{\begin{bmatrix} \phi_g^{(1)}(x_t, u_t) \\ \vdots \\ \phi_g^{(m)}(x_t, u_t) \end{bmatrix}}_{\bar{\varphi}_g(x_t, u_t)} + e_t.$$

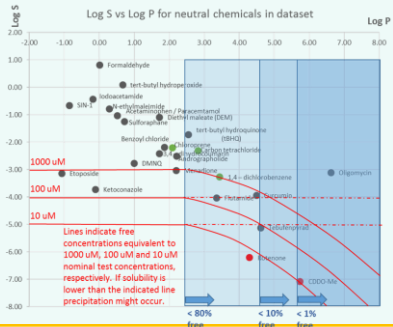
Mathematical and statistical modelling

Back to the toolbox

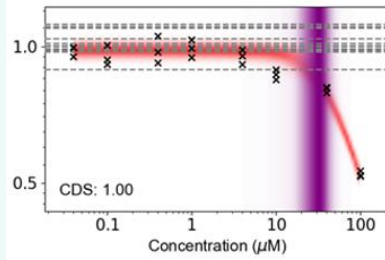
PBK models



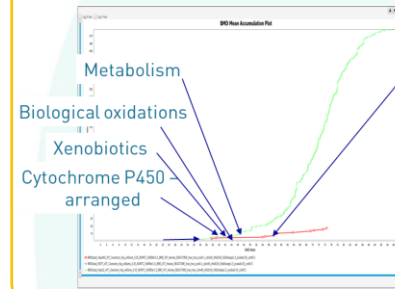
Free concentration



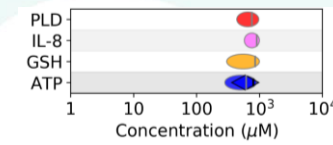
Conc. Resp. models



HTTr



CSP

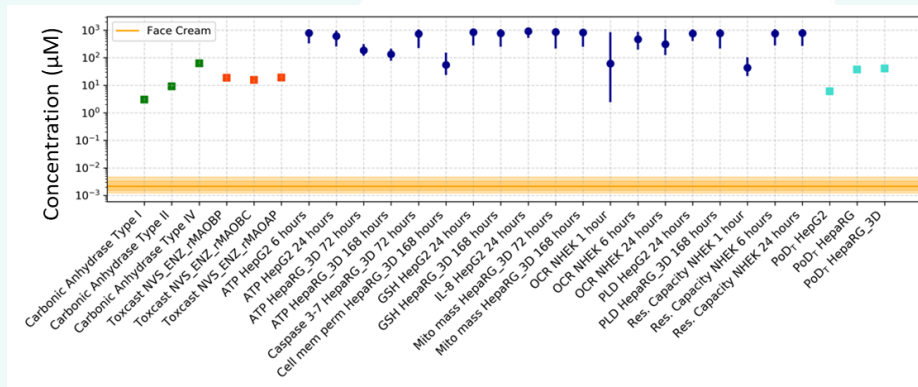


IPP

| Target | IC50 (uM) | IC20 (uM) | IC80 (uM) | IC90 (uM) |
|--------|-----------|-----------|-----------|-----------|
| PLD | 1000 | 100 | 10 | 1 |
| IL-8 | 1000 | 100 | 10 | 1 |
| GSH | 1000 | 100 | 10 | 1 |
| ATP | 1000 | 100 | 10 | 1 |

• All binding and enzymatic assay results were negative at 10 uM, including COX-1 and COX-2
 • Highest inhibition (22%) was for MAO-A

Bioactivity exposure ratio



Inform safety decision

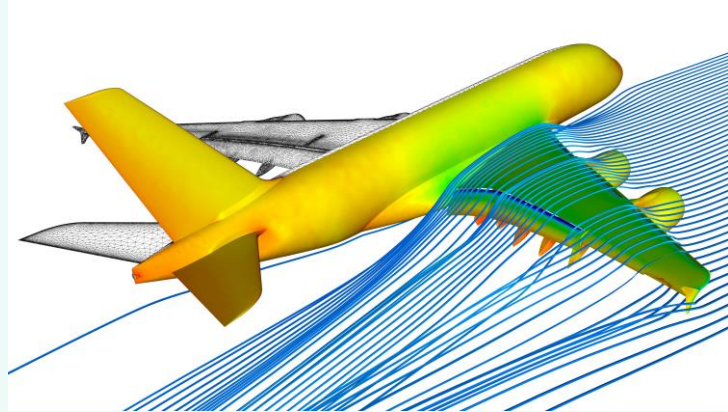
HTTr: High-throughput transcriptomics

CSP: Cell Stress Panel

IPP: In vitro pharmacological profiling

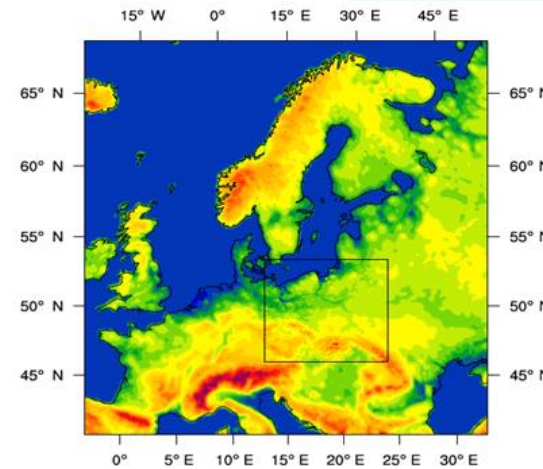
Computational models and their impact on everyday life

Air transport



dlr.de

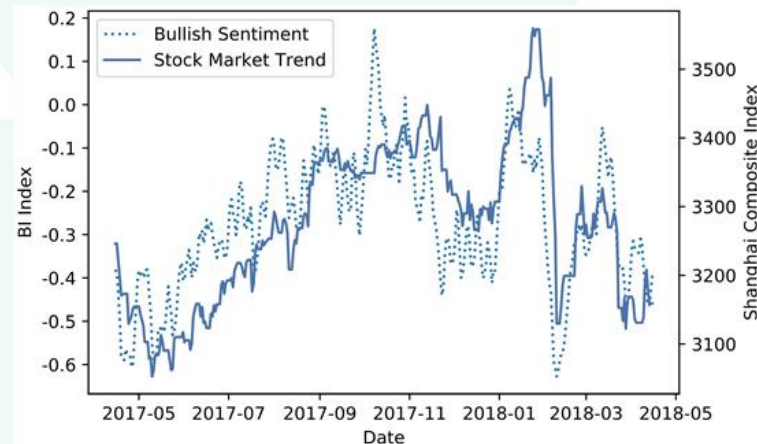
Weather forecast



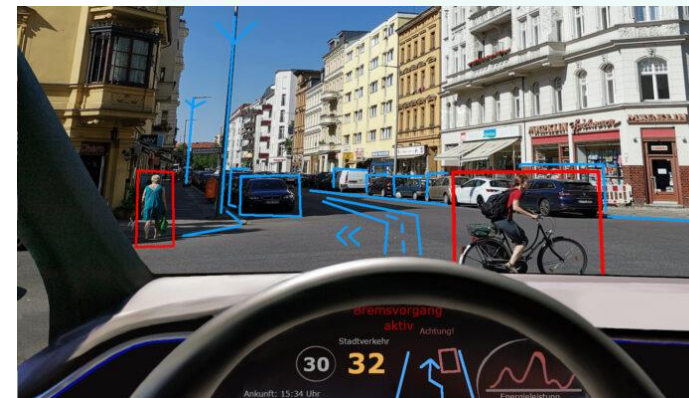
Satnav



Stock market

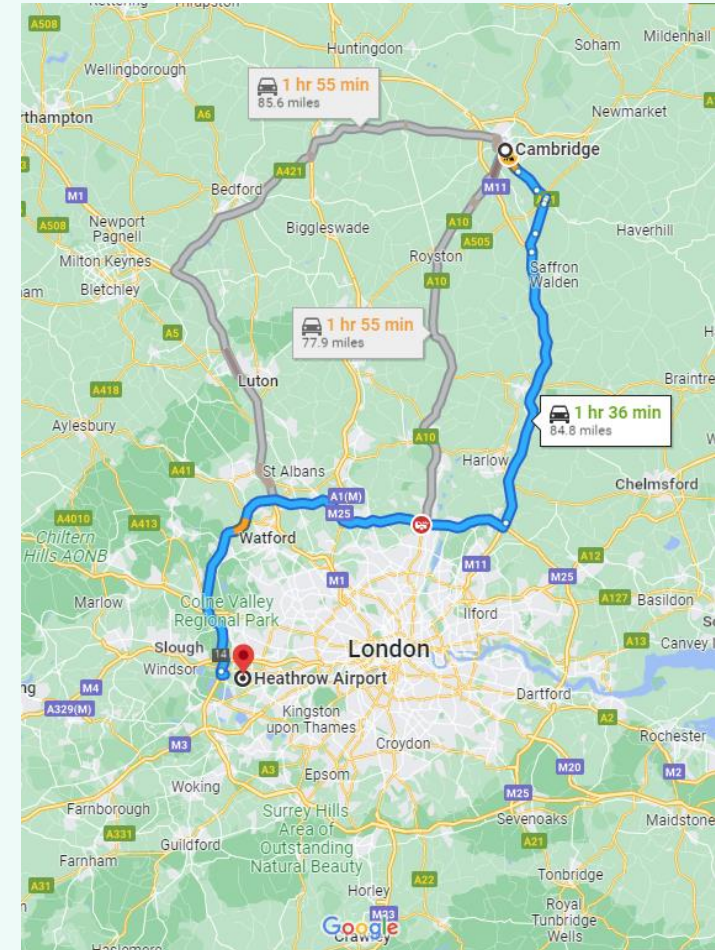
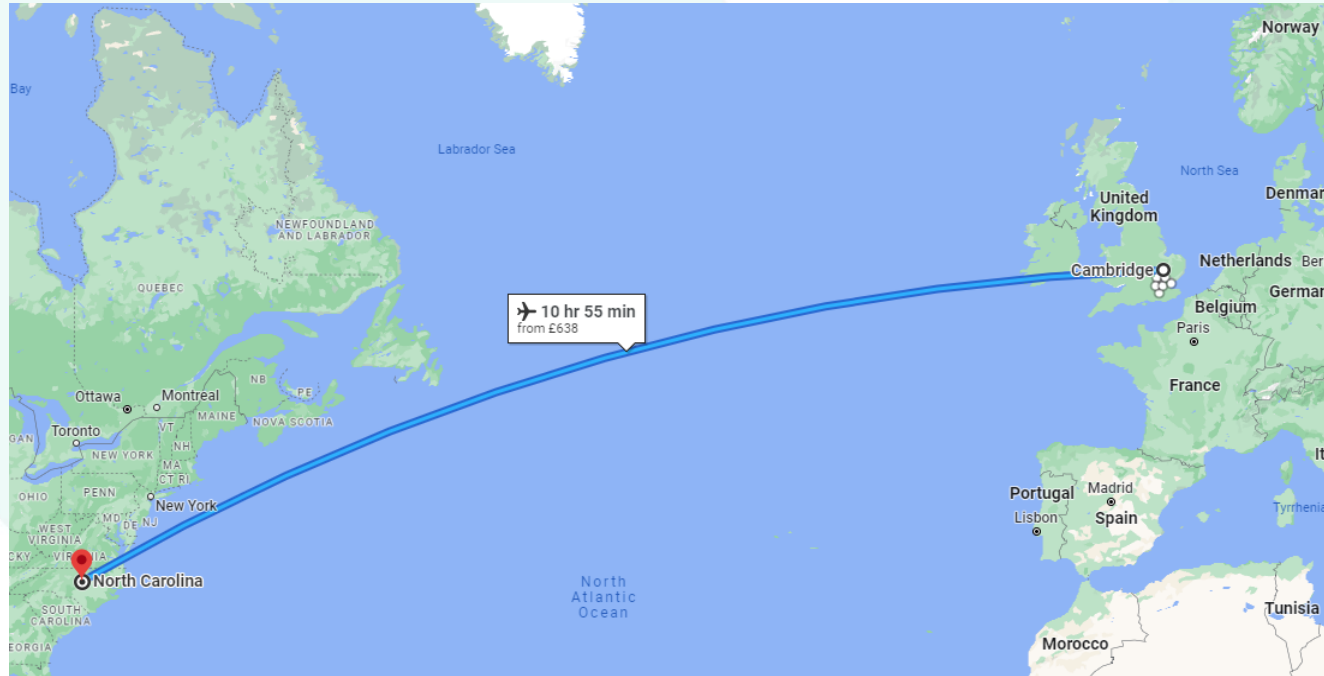


Self driving cars



digitalgyan.org

A simple example: my journey from the UK to the US



- How long will the journey take?
- How early should I leave?
- How much fuel will I need?



Imagine a time before Google Maps...



[This Photo](#) by Unknown Author is licensed under [CC BY-SA](#)

What you want to know:

- Time it takes to get from home to the airport
- How early do you have to leave

What information you have:

- Distance from Cambridge to London
- Travel by car

Construct a (very) simple model:

- Model:

$$Time = Distance/Speed$$

- 'Data':

$$Distance = 55 \text{ miles}$$

- Assume:

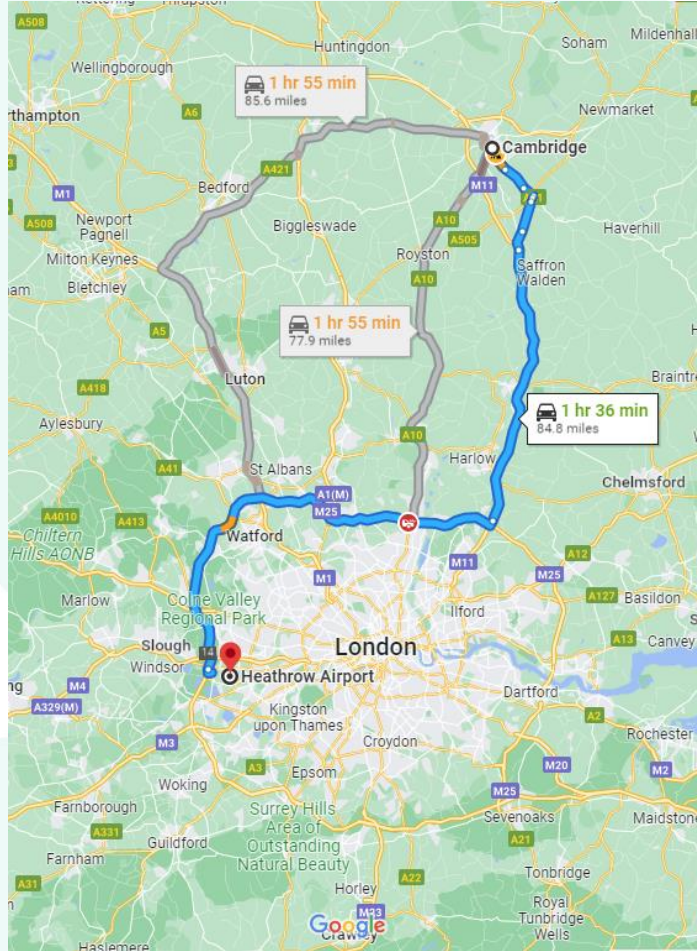
$$Speed = 60 \text{ miles per hour}$$



Using the model make a decision

- You need to arrive to the airport by 12noon to catch your flight
- Based on your assumptions, your model prediction it will take 55 minutes
- Should you 'trust' the model and leave at 11.05?

Using models to make decisions



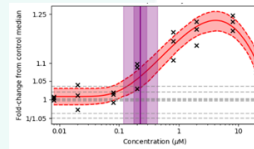
- Sitting behind Google maps is a far more complex and sophisticated set of models
- Informed by huge, complex datasets
- Provides estimation of journey time(s) based on route and time of day
- Even though it is more accurate, Google Maps can still go wrong!
- As a decision maker, both our model and Google Maps are potentially useful, but require judgement in terms of how you interpret their predictions.

Using these approaches together to make safety decisions

Hazard identification and characterisation of ingredients



Point of departure derived from concentration-response data

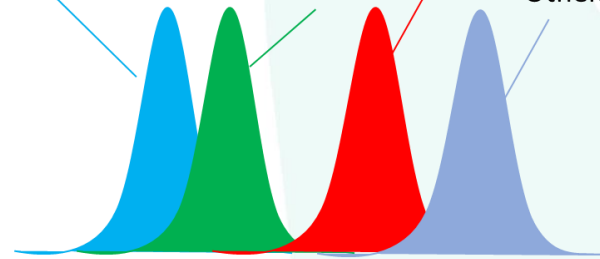


Cellular stress assays

Transcriptomics

Receptor binding

Others



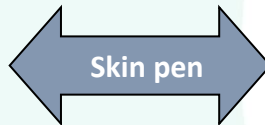
Risk Assessment

Calculation of Bioactivity Exposure Ratio (BER)

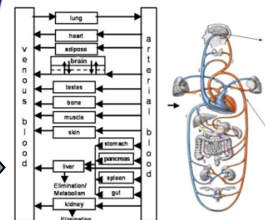


The BER/MoE is defined as the ratio of the PoD and the relevant exposure estimate

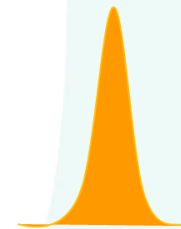
Consumer Exposure characterisation



Exposure models (PBK, free/total concentration)

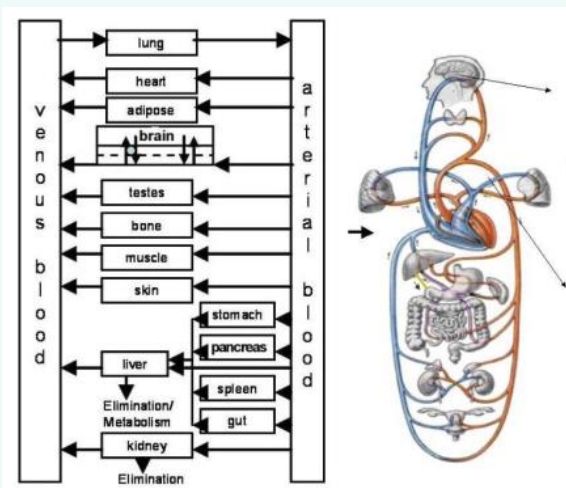


Exposure estimation: Plasma C_{max}

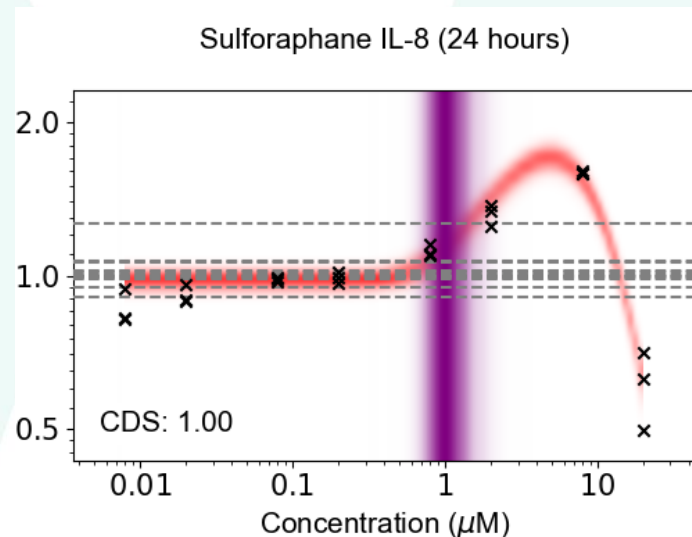


Different types of computational approaches used in NGRA

Physiologically-based kinetic (PBK) modelling



Dose response modelling



In silico tools

Chemical identifier: O=C(C)N[C@@H](C(=O)O)C[C@H](O)C1

Available structure attributes:
 Cramer rules: High (Class III)
 SMILES: O=C(C)N[C@@H](C(=O)O)C[C@H](O)C1
 cdlComment: Created from SMILES
 toxTree.site.cramer.Cram... | N, J1, J3, J1, G4, J7, J1, L...

Structure diagram:
O=C(C)N[C@@H](C(=O)O)C[C@H](O)C1

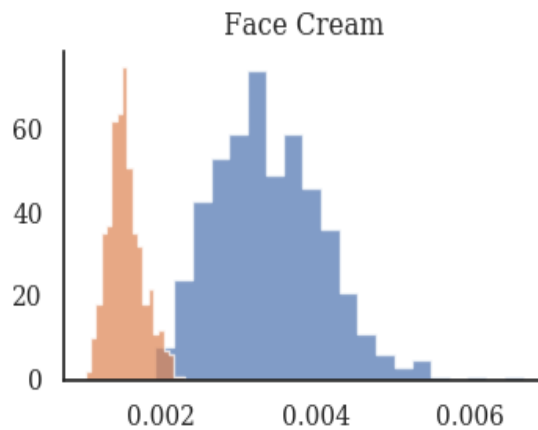
Completed.

Toxic Hazard by Cramer rules:
 Low (Class I)
 Intermediate (Class II)
 High (Class III)

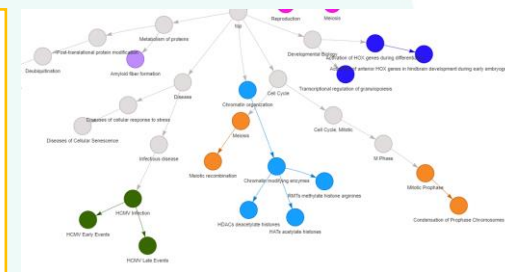
Verbose evaluation:
 Q1: Is a heterocyclic ring with complex substituents. Yes
 Q3: Has sufficient number of sulfonate or sulfamate groups. No Class: High (Class III)
 O=C(C)N[C@@H](C(=O)O)C[C@H](O)C1

ToxTree

Statistical models of uncertainty and variability

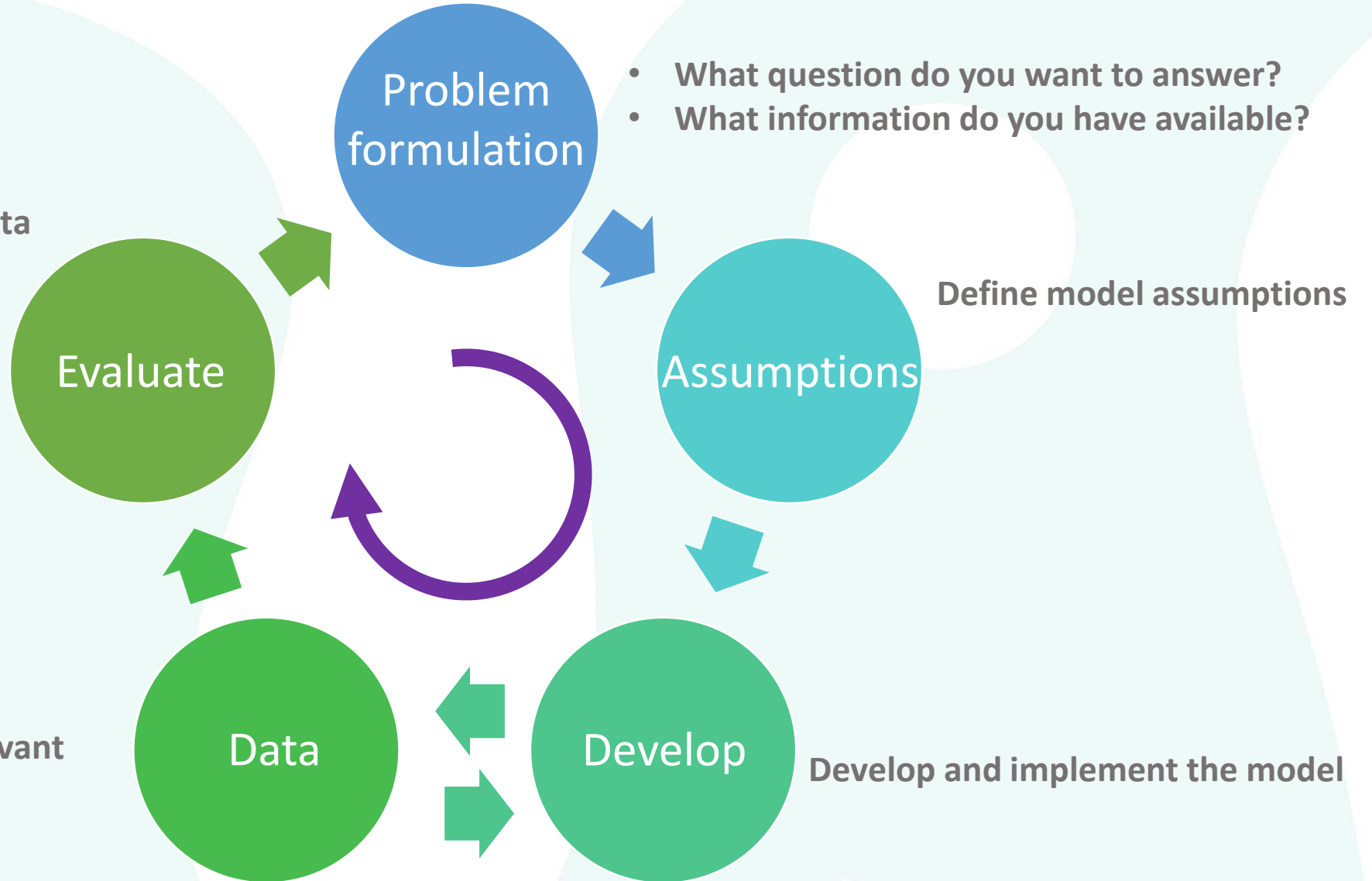


Bioinformatics tools for analysing omics data



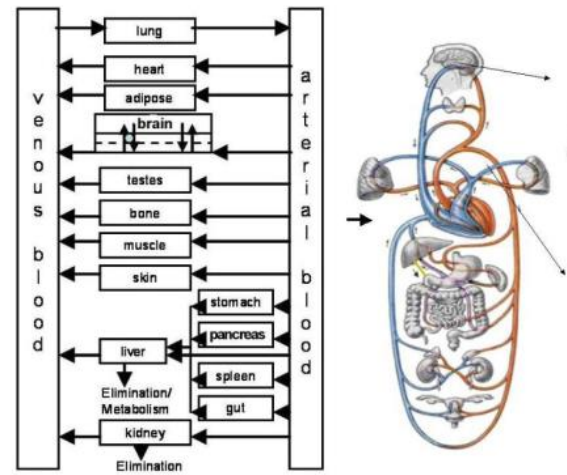
Principles of model development and the wet-dry cycle

How does the model perform?
Does it describe the data well?



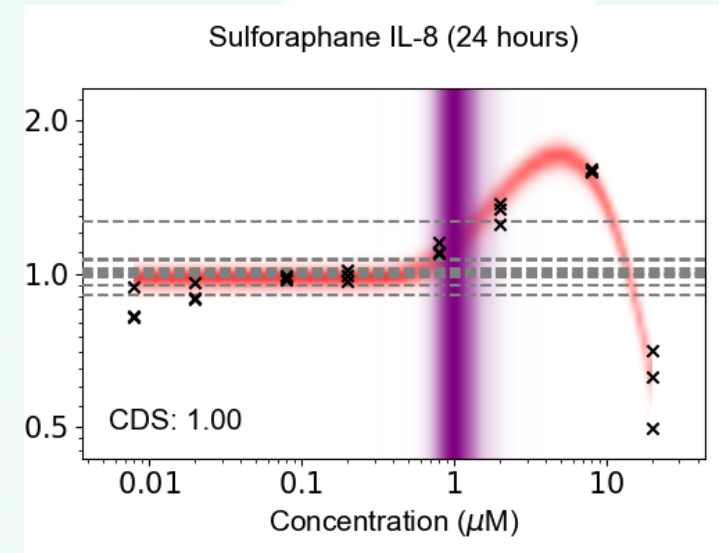
Two examples of computational models used NGRA

Physiologically-based kinetic (PBK) modelling



Example of **bottom-up** modelling approach

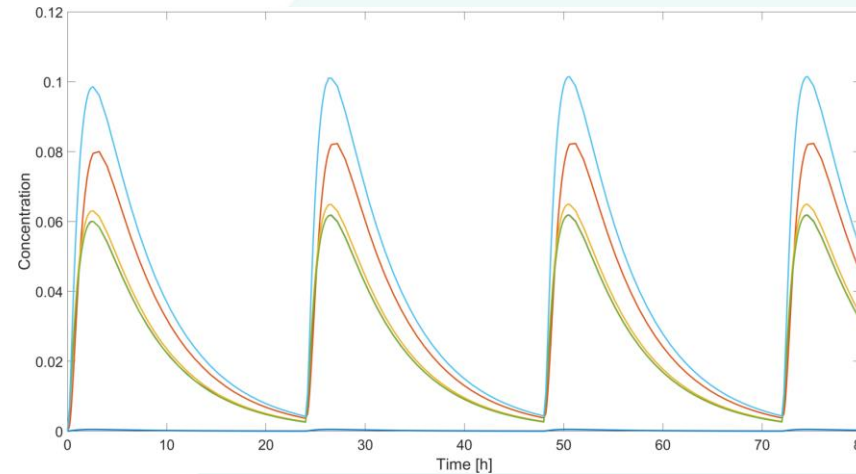
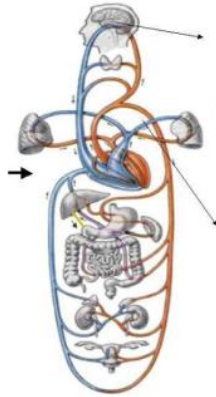
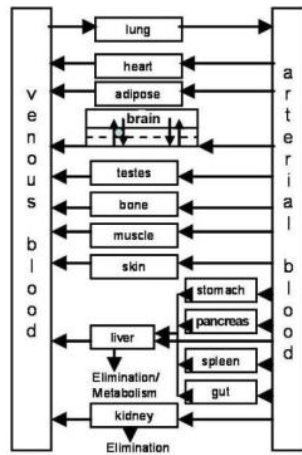
Dose response modelling



Example of **top-down** modelling approach

Physiologically based (Pharmacokinetic) models

Physiologically-based (pharmaco) kinetic models

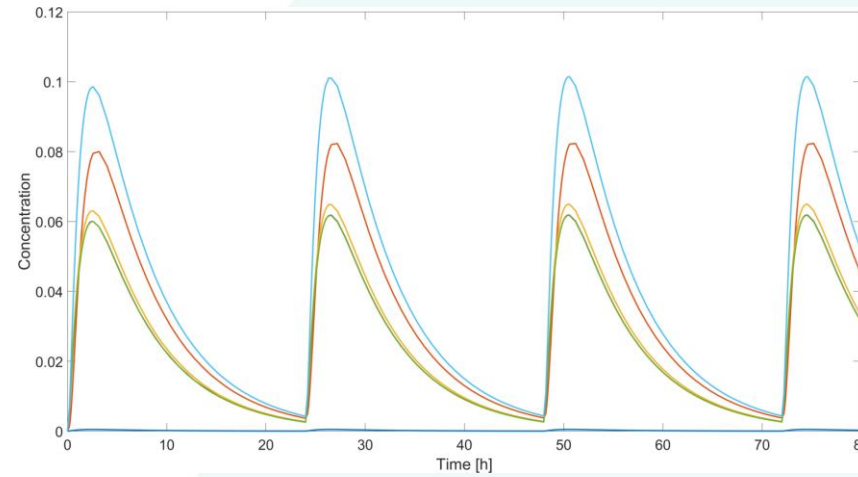
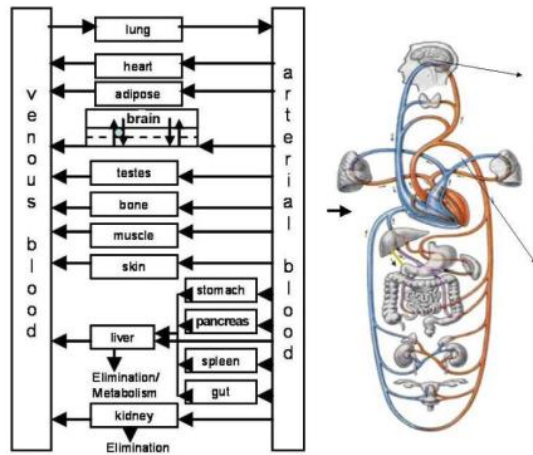


Problem: Quantify amount (e.g., concentration) of substance across different organs/regions of the body over **time** and for different **exposure routes**

Assumptions:

- Different regions of the body (e.g. organs) are divided into separate compartments
- Connection between compartments reflects physiology
- Movement of substances between compartments are governed by biophysical processes such as diffusion, perfusion, active transport etc

Physiologically-based (pharmaco)kinetic models



Develop

- Example equations:

Rate of change of the amount (e.g. nanograms) of chemical in liver

$$V_{Liver} \frac{dC_{Liver}}{dt} = Q_{Liver} \left(C_V - \frac{C_{Liver}}{P_{Liver}} \right) - \frac{V_{max} C_{Liver}}{K_m + C_{Liver}}$$

Total blood flow rate into liver (mL/h)

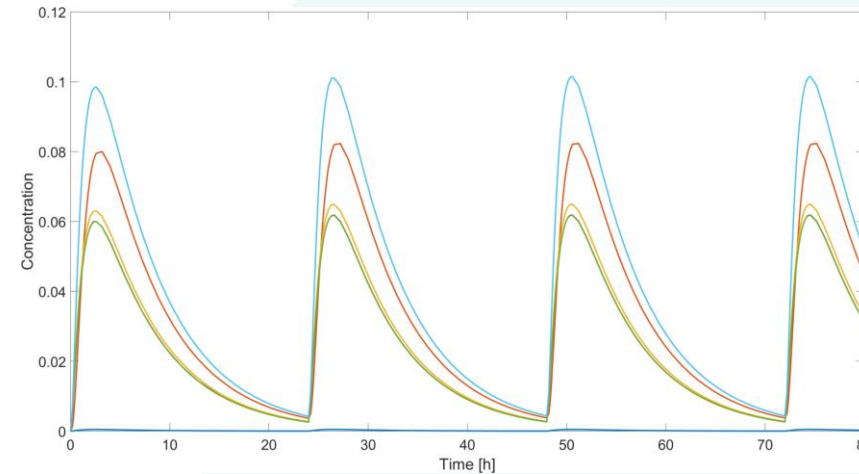
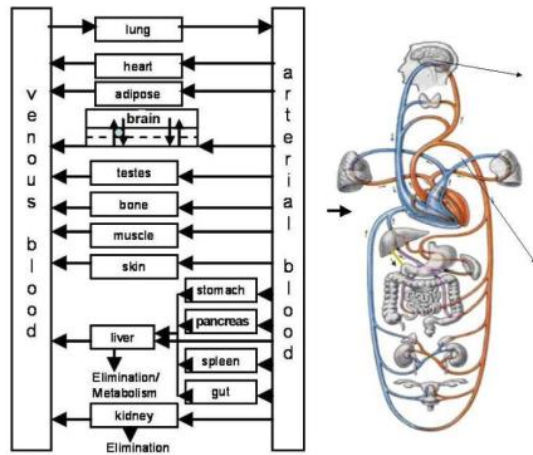
Concentration in liver (ng/mL)

Metabolism

Concentration in blood (ng/mL)

Liver: blood partition coefficient

Case study: Physiologically-based (pharmaco)kinetic models



Data:

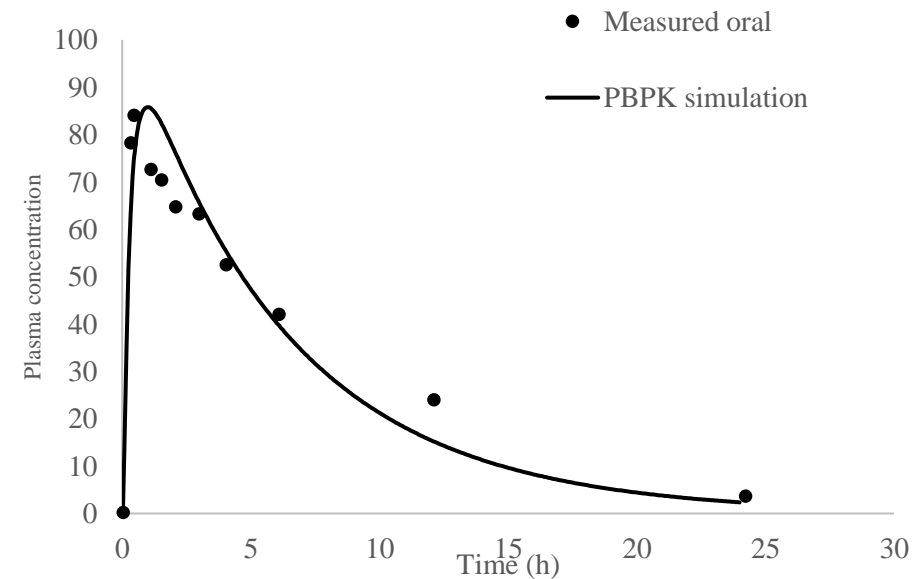
- Information sources on model parameters:
 - *In silico* predictions
 - *In vitro* data (e.g. clearance rate)
 - Historical data (e.g. on physiological parameters such as weight/height distributions).
- Human PK data on measured concentration over time in plasma, urine etc

Case study: Physiologically-based (pharmaco)kinetic models

Evaluate

- Compare model predictions against measured PK data
- Example:
 - Niacinamide used as face cream
 - Model parameters informed using *in silico* or *in vitro* data

| Parameter | Value | Reference |
|---|---|--|
| LogP | -0.37 | (Martin 1996) |
| pKa | 13.39 (strongest acidic); 3.63 (strongest basic) | ChemAxon |
| Solubility | 500000 mg/L (at 25 °C) | MERCK INDEX (1996) |
| Fraction unbound in plasma | 0.82 | Predicted (ADMET predictor) |
| human blood-to-plasma partition ratio | 1.7 | Predicted (ADMET predictor) |
| V _{max} (CYP2E1) | 60.14 pmol/mg min (In vitro human liver microsomes) | (Real, Hong, and Pissios 2013) |
| K _m | 2.98 mM | (Real, Hong, and Pissios 2013) |
| Cl _{renal} | 6.098 L/h | Predicted (GastroPlus) as glomerular filtration rate (GFR) x fraction unbound in protein (Fup) |
| Intestinal absorption: effective permeability (P _{eff} cm/s) | 5×10 ⁻⁴ cm/s | Fitted from oral human pharmacokinetic study (Bussink et al. 2002) |

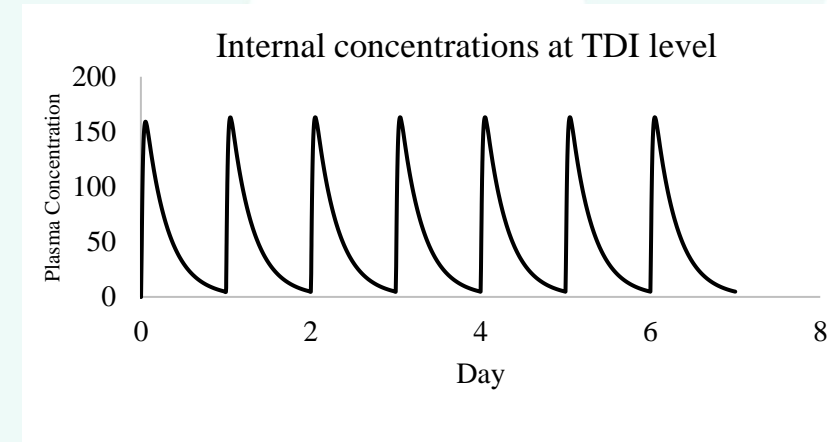
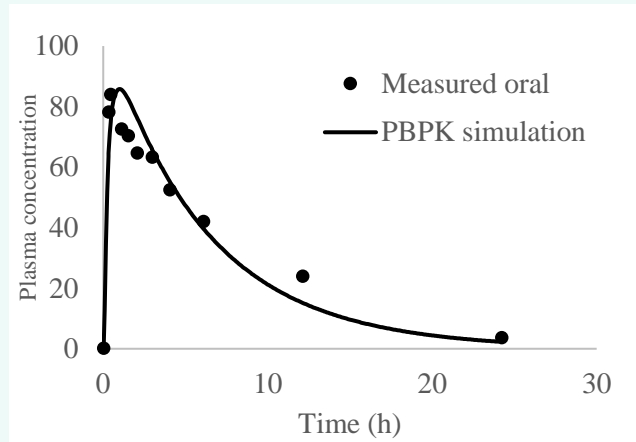


Bussink, et al 2002 *Radiotherapy and Oncology*

Hatherell, et al 2020 *Toxicological Sciences*

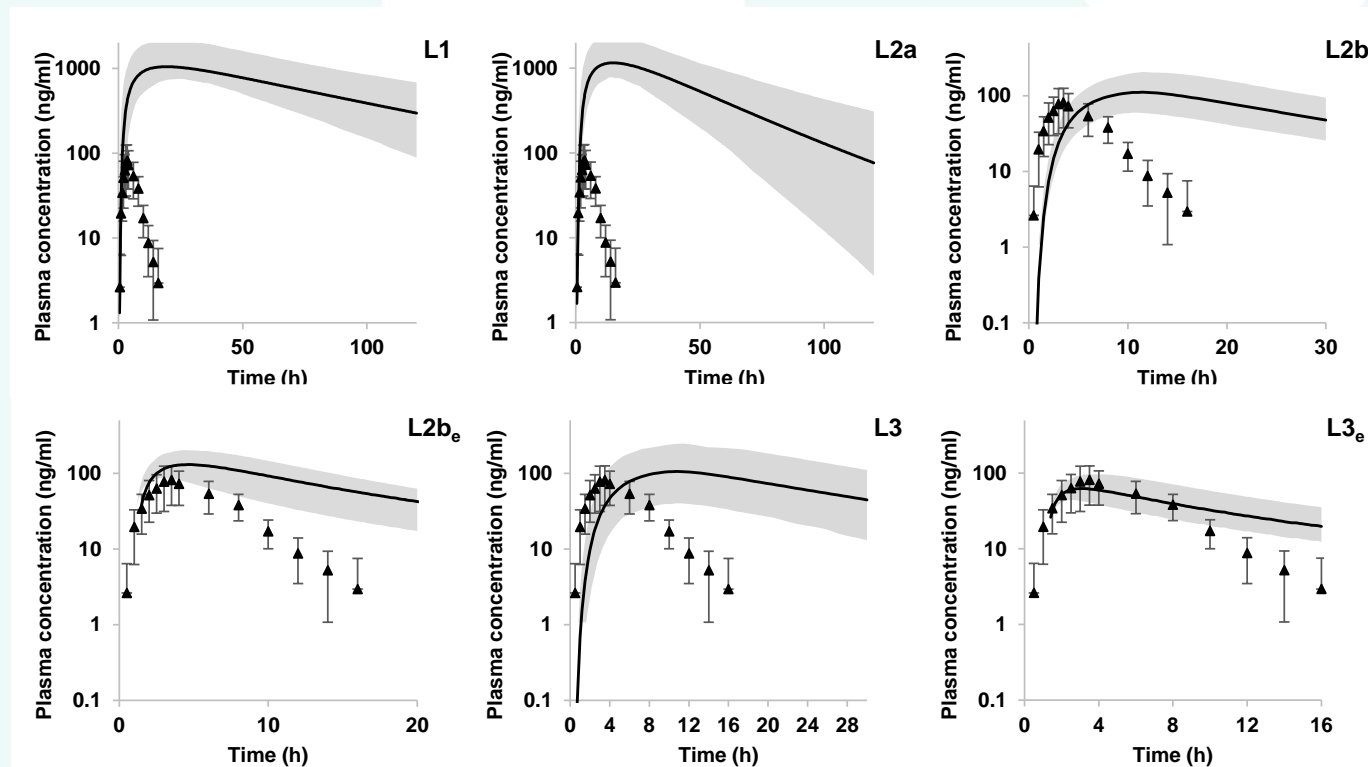
Case study: Physiologically-based (pharmaco)kinetic models

- Can use the model to then make predictions for other dosing regimes



Different parameterisation levels on model accuracy

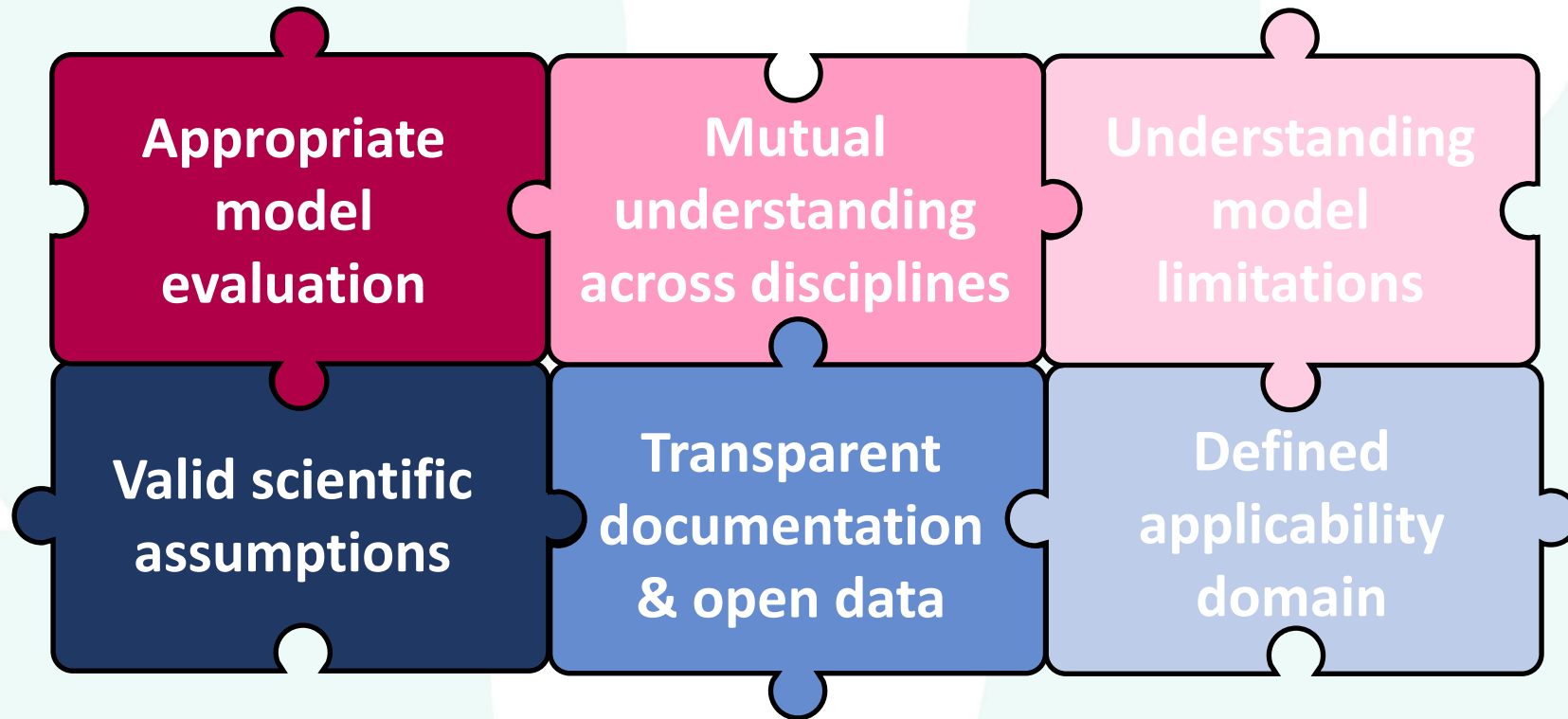
- Models will almost always be informed using imperfect data.
- Given the models are used for decision making, it is important to quantify **uncertainty** in how wrong the models can be



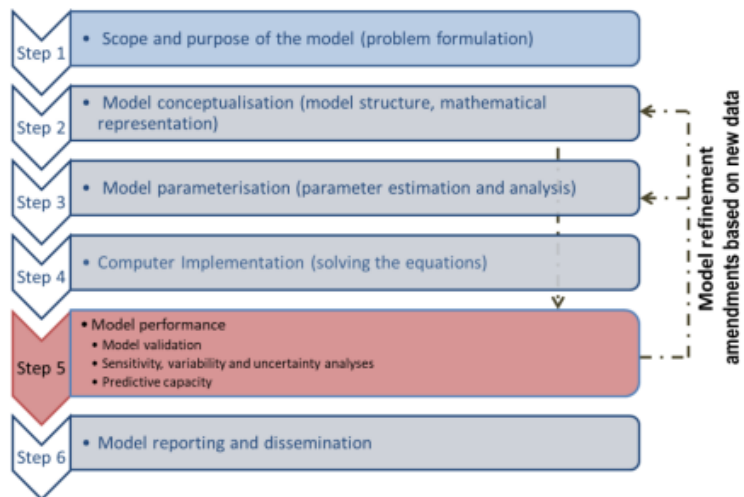
Li et al, (2022) PBK modelling of topical application and characterisation of the uncertainty of C_{max} estimate: A case study approach, Toxicology and Applied Pharmacology, Volume 442

Challenges in the acceptance of using computational approaches in NGRA

What do you think?



OECD guidance on best practice for PBK model development



| | LEVEL OF CONFIDENCE | | |
|--|---|---|---|
| | NONE | | HIGH |
| Biological basis | The model parameters, structure or assumptions are consistent with neither the biology nor the current state of knowledge regarding the kinetics of the chemical. | The biological basis of some model parameters, structural elements or assumptions is questionable. | The model parameters and structure have reasonable biological basis and are consistent with available kinetic data in several experiments using a single set of input parameters. |
| Model simulations of data | Model is unable to reproduce the shape (i.e. bumps, valleys) of the kinetic time course curves, neither for the chemical of interest nor for a suitable analogue. | Model reproduces the shape of part but not all of the kinetic time course curves, either for the chemical of interest or suitable analogue. | Model reproduces consistently all kinetic data, including the shape of time course profiles for chemical of interest. |
| Uncertainty in input parameters and model output; Sensitivity of model output to input parameters | No uncertainty and sensitivity analyses were performed | Local Sensitivity Analysis supports the robustness of the model. | Global Sensitivity Analysis supports the robustness of the model. |

Guidance document on the characterisation, validation and reporting of Physiologically Based Kinetic (PBK) models for regulatory purposes



Series on Testing and Assessment
No. 331

IPCS
INTERNATIONAL PROGRAMME ON CHEMICAL SAFETY

WHO ILO

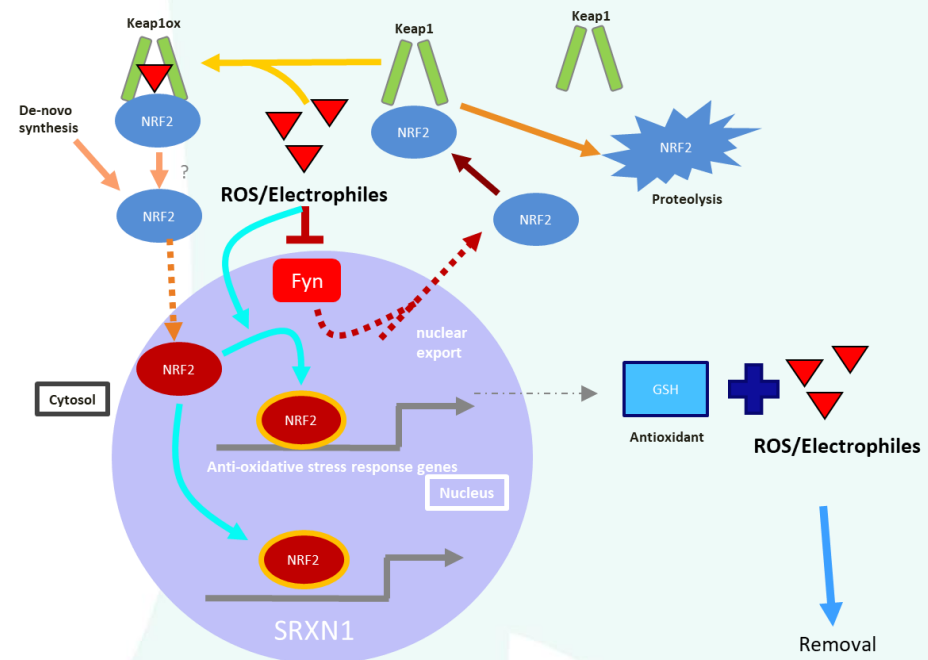
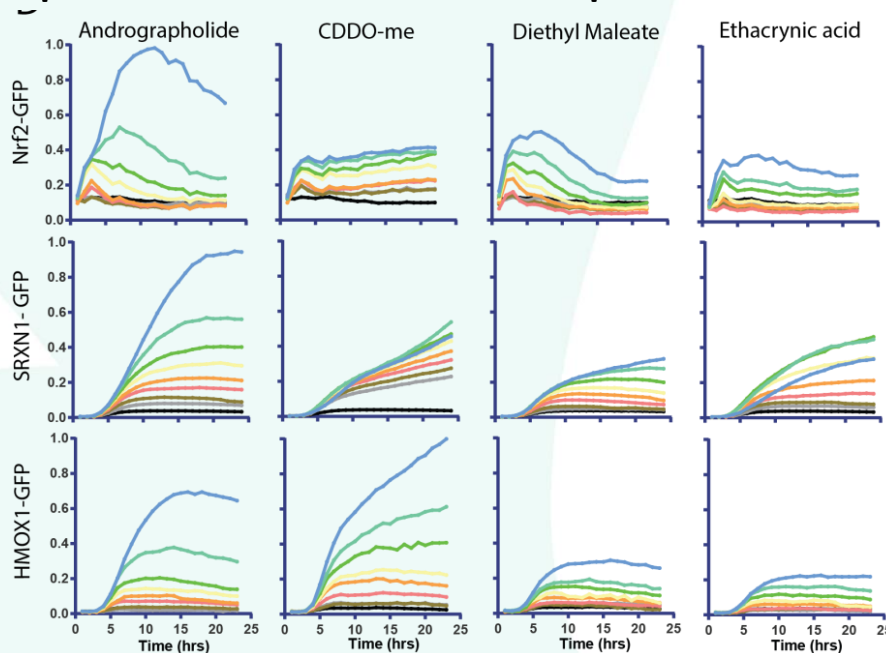
IPCS Harmonization Project

Characterization and Application of Physiologically Based Pharmacokinetic Models in Risk Assessment

- <https://www.who.int/publications/i/item/9789241500906>
- <https://www.oecd.org/chemicalsafety/risk-assessment/guidance-document-on-the-characterisation-validation-and-reporting-of-physiologically-based-kinetic-models-for-regulatory-purposes.pdf>

Going beyond PB(P)K models

- The basic principles to bottom up modelling can be used in lots of other areas relevant to toxicology and risk assessment
- For example, for developing models of gene expression network or signalling pathways.
- The key challenge with these is there is limited data to decide on parameter or even equations.



Bas ter Braak et al, Mapping the dynamics of Nrf2 antioxidant and NFκB inflammatory responses by soft electrophilic chemicals in human liver cells defines the transition from adaptive to adverse responses (submitted)

Top down vs bottom modelling

Bottom up

Model behaviour is an emergent property of the 'rules' chosen for the model

Observed phenomena vs model



E.g., change in concentration between liver and plasma dictated by perfusion

Define 'rules' of how different variables interact



E.g., concentration of X in the plasma, liver etc

Define individual model variables

Top down

Visualise the data, what are the key variables? How are do they appear to be related?

Observed phenomena



Define key variables and (statistical) relationships

Develop model based on observations



Does the model provide a good description of the data?

Evaluate the model

Dose response models

The cell stress panel

Intended to cover off non-specific modes of action that lead to cell stress or mitochondrial toxicity

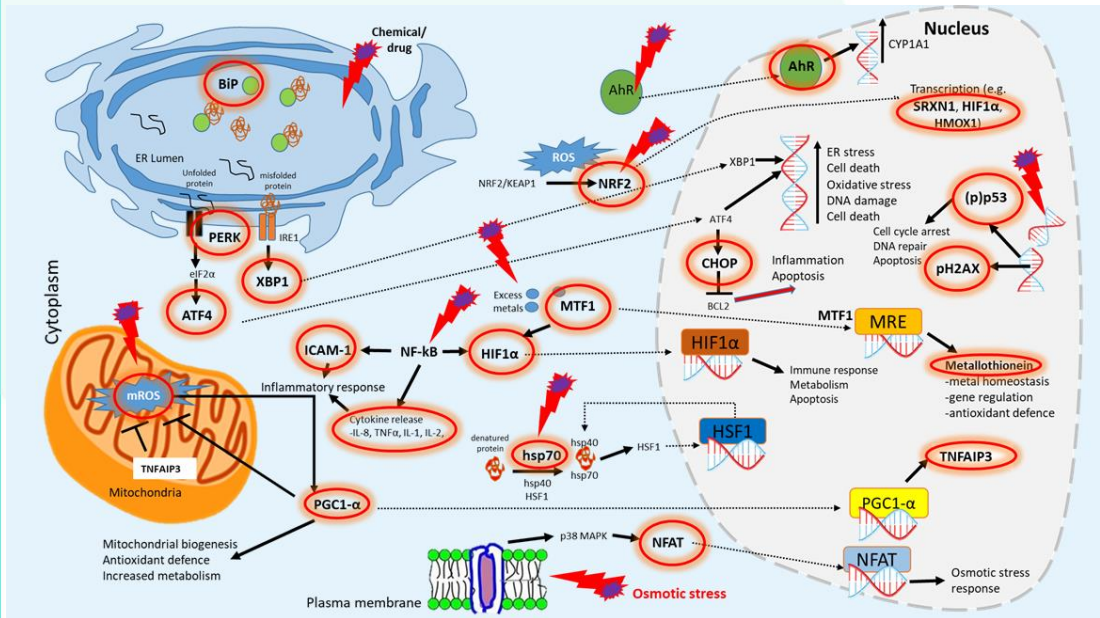


Image kindly provided by Paul Walker (Cyprotex)

OXFORD
SOT | Society of Toxicology
academic.oup.com/toxsci

TOXICOLOGICAL SCIENCES, 2020, 1-23

doi: 10.1093/toxsci/kfaa054
Advance Access Publication Date: May 6, 2020
Research article

Identifying and Characterizing Stress Pathways of Concern for Consumer Safety in Next-Generation Risk Assessment

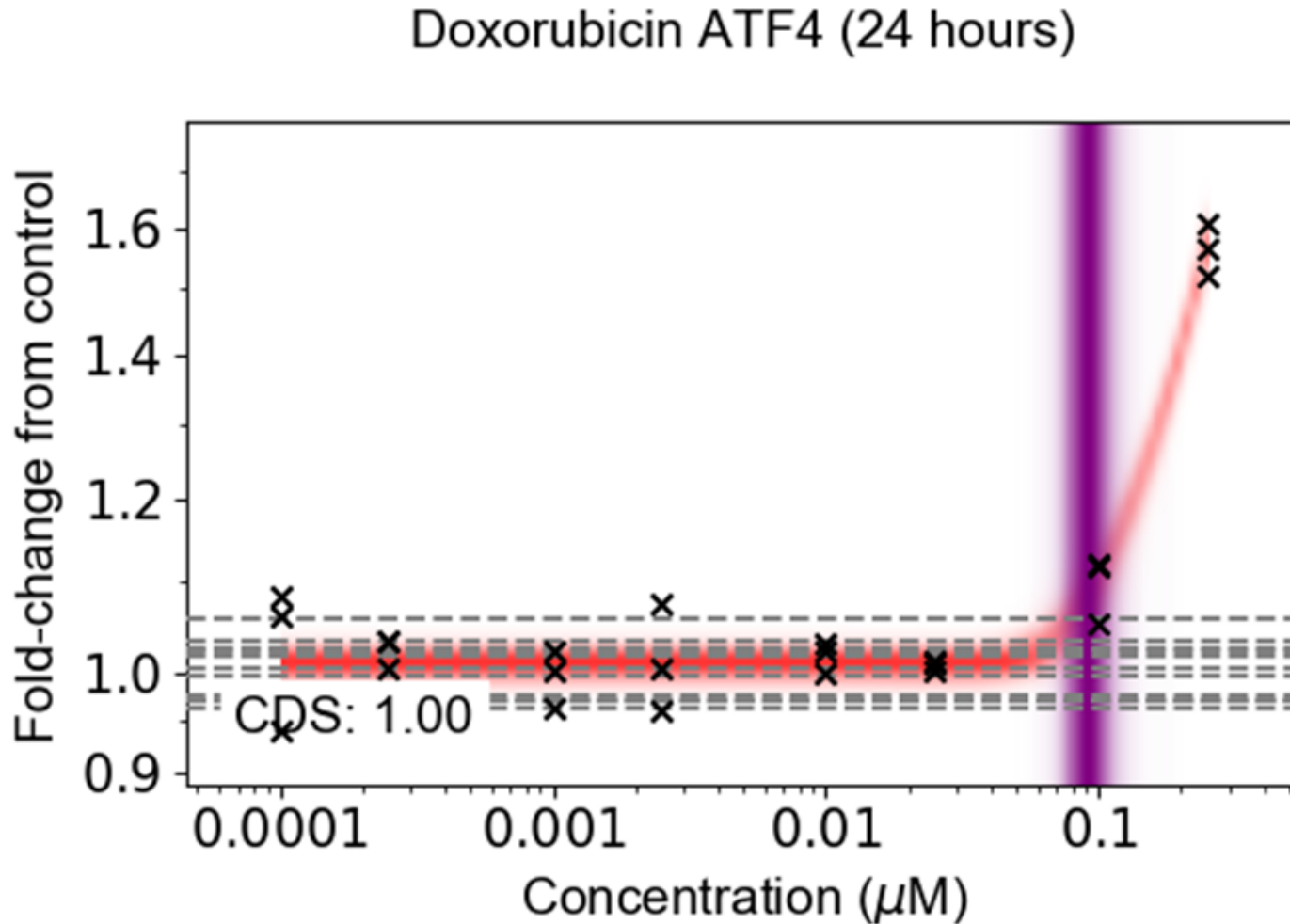
Sarah Hatherell,* Maria T. Baltazar,* Joe Reynolds,* Paul L. Carmichael,* Matthew Dent,* Hequn Li,* Stephanie Ryder,[†] Andrew White,* Paul Walker ,[†] and Alistair M. Middleton*¹

*Unilever Safety and Environmental Assurance Centre. Colworth Science Park. Sharnbrook. Bedfordshire

36 biomarkers identified that were representative of key stress pathways, mitochondrial toxicity and cell health.

Cell stress biomarkers predominantly measured using high content imaging. Includes Extracellular Flux assay to measure mitochondrial function.

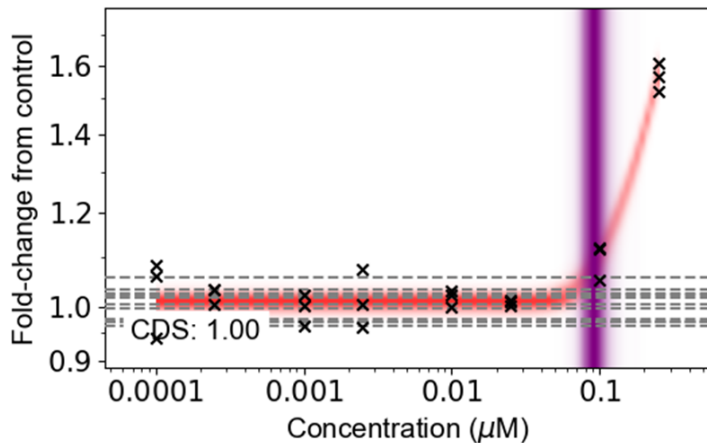
Dose response analysis and estimating PODs



Dose response analysis and estimating PODs

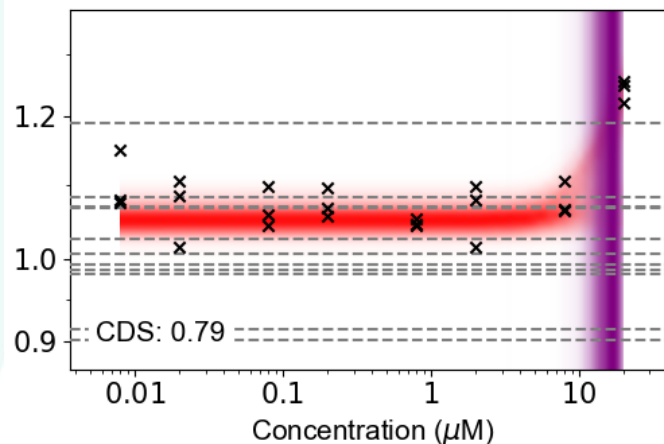
Clear effect

Doxorubicin ATF4 (24 hours)



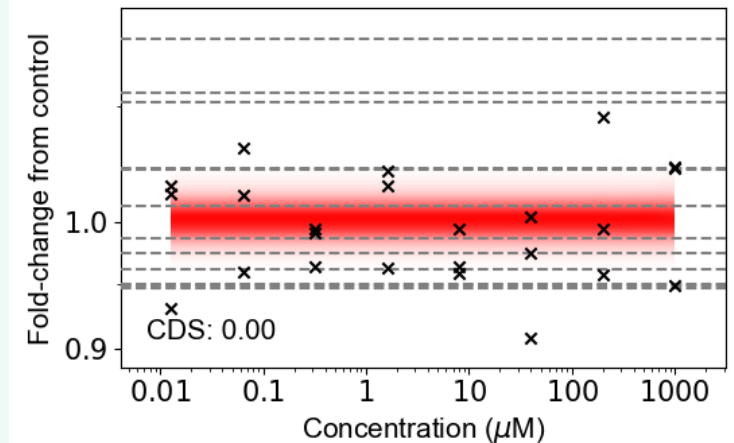
Is there an effect here?

Sulforaphane DNA struct (24 hours)



No effect

Caffeine ROS (24 hours)



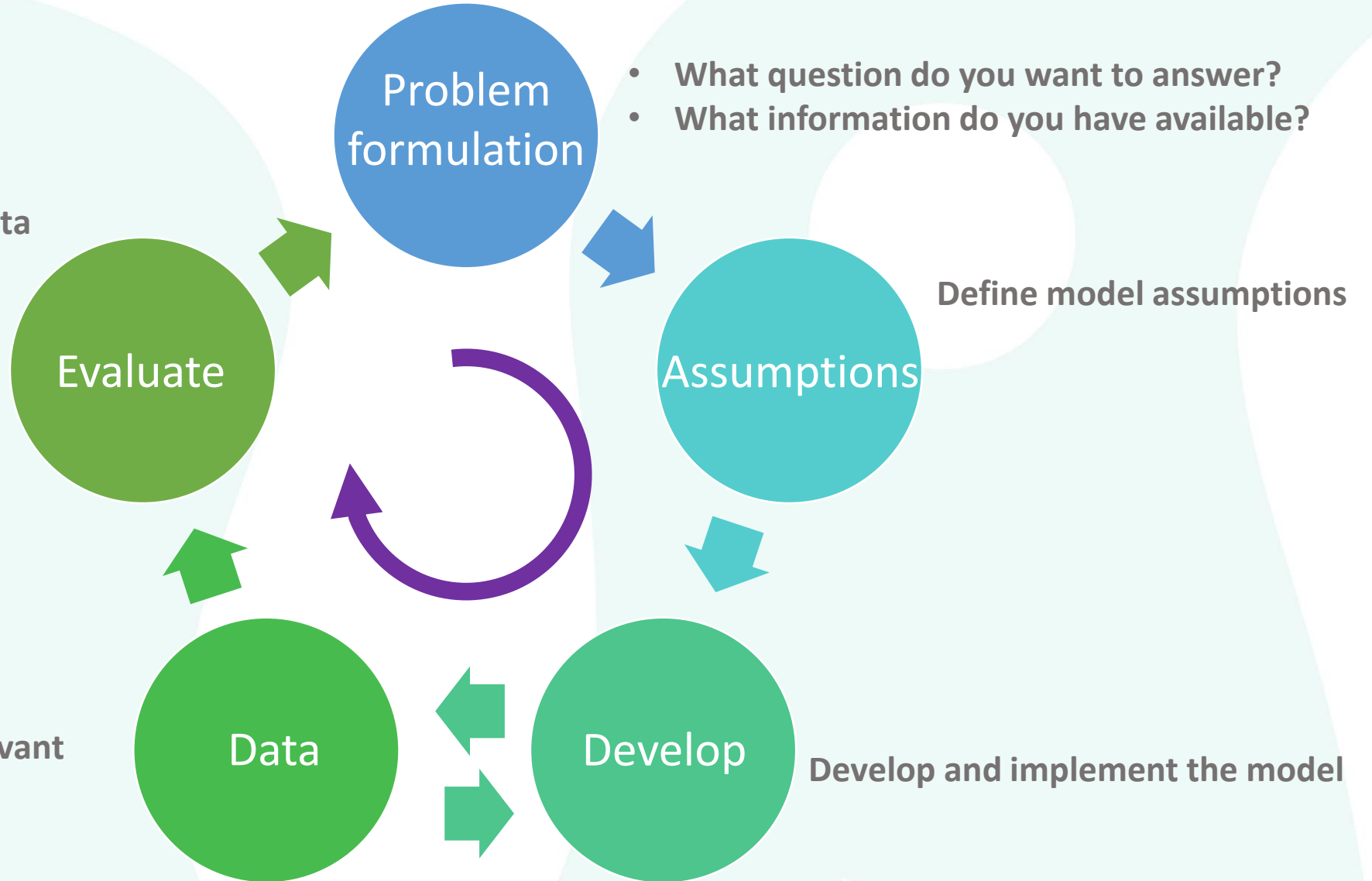
- Broadly, there are two approaches to doing this – **parametric** and **non-parametric**
- We will focus on the **parametric** approach

Principles of model development and the wet-dry cycle

How does the model perform?
Does it describe the data well?

- What question do you want to answer?
- What information do you have available?

Define model assumptions

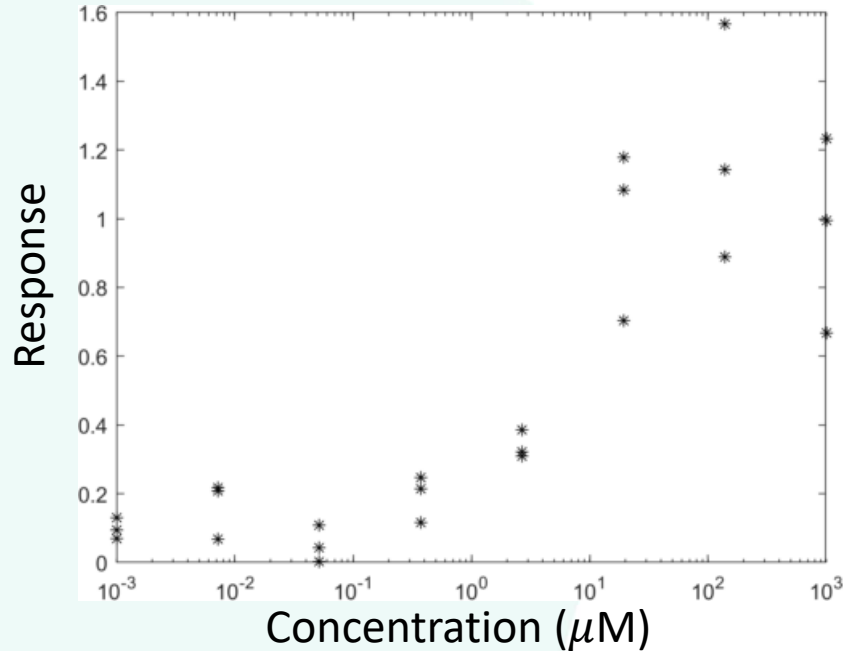


Generate/curate relevant data

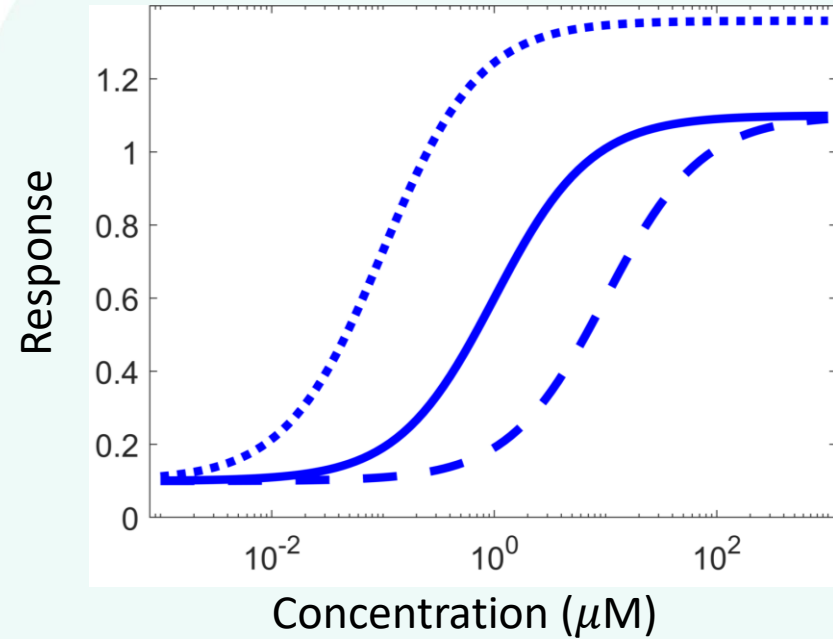
Develop and implement the model

Developing a dose response model

Example dose response data

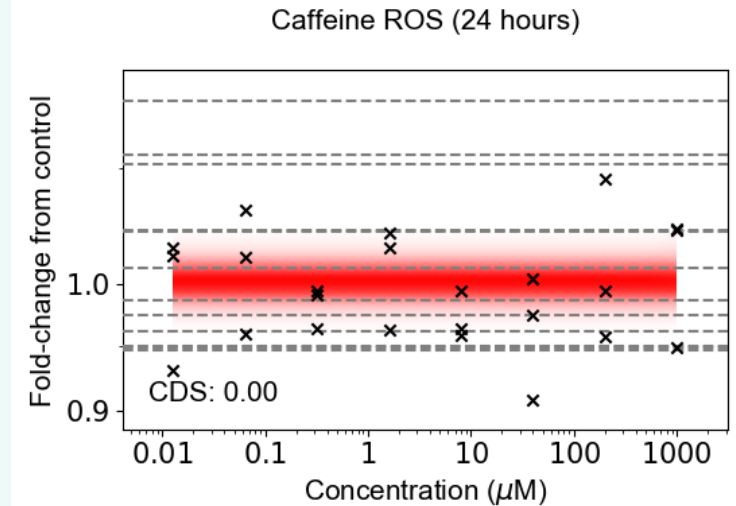
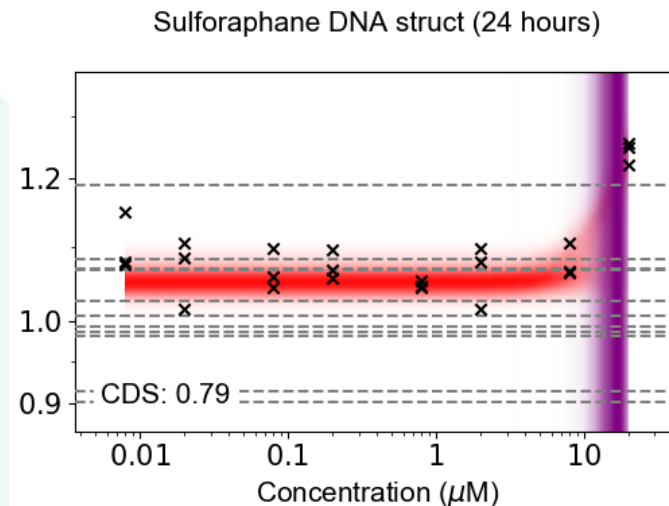
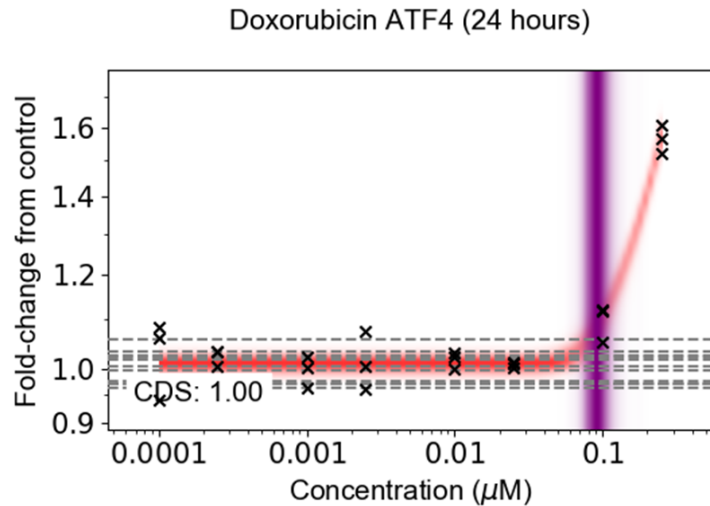


Hill function



- **Problem:** We want to know:
 - Does the chemical have an effect on our biomarker
 - At what concentration does this occur?
 - We want to quantify the uncertainty in these.
- **Assumption:** There is an increase in our biomarker, which can be captured using a Hill function.

Bayesian statistics – what and why



- We want to quantify uncertainty in whether a certain event occurs, e.g.
 - Whether there is a concentration-dependent effect.
 - Whether you will reach the airport in 2 hours.
- One way to do this is through Bayesian statistics – our current approach to NGRA uses it a lot!
- Here, ‘the probability’ is a number that reflects the **plausibility** of some event occurring based on some data.

Bayesian statistics – what and why

Bayesian probability:

- Probability reflects the **plausibility** or **belief** in some event being true.
- Provides framework for updating plausibility based on available data.
- For example, can talk about the **probability of a hypothesis being true**, or a parameter taking on a certain value.
- Key terms: credible interval, priors, posterior

Frequentist probability

- What people are normally taught in school
- Basis for **p-values** and **hypothesis testing**
- Probability reflects the relative frequency at which an event occurs in many over many repeated trials.
- Only really relevant when dealing with **well-defined random experiments**
- Can't use it to talk about the probability of a 'parameter taking a certain value' or a 'hypothesis being true'.



Thomas Bayes, 1701-1761

Bayesian statistics – what and why

Bayesian interpretation of probability

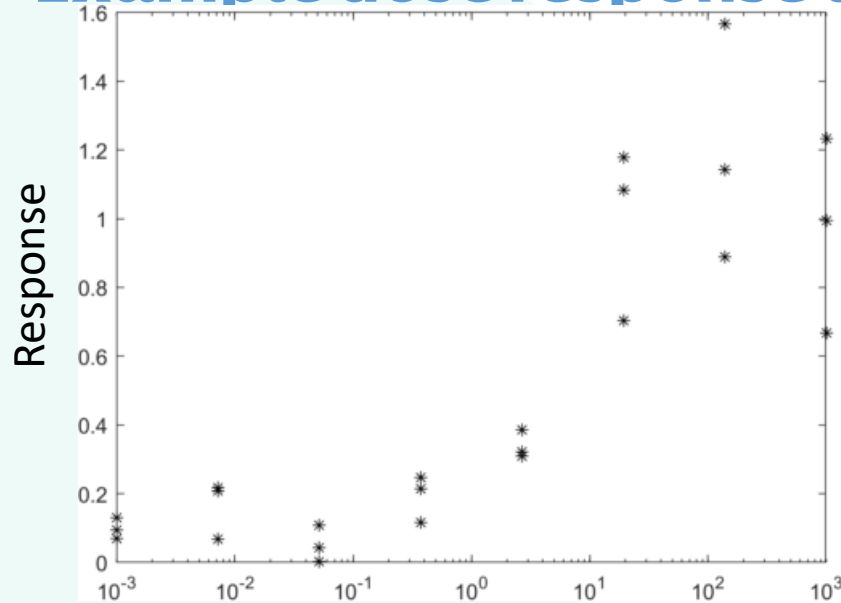
- Probability quantifies the plausibility of some event.
- **Bayes' theorem:**

The diagram illustrates Bayes' theorem with three blue boxes: 'Posterior' on the left, 'Likelihood' in the middle, and 'Prior' on the right. An arrow points from 'Posterior' to the left side of the equation. An arrow points from 'Likelihood' to the numerator of the fraction. Another arrow points from 'Prior' to the numerator of the fraction. The equation is:
$$P(X|D) = \frac{P(D|X)P(X)}{P(D)}$$

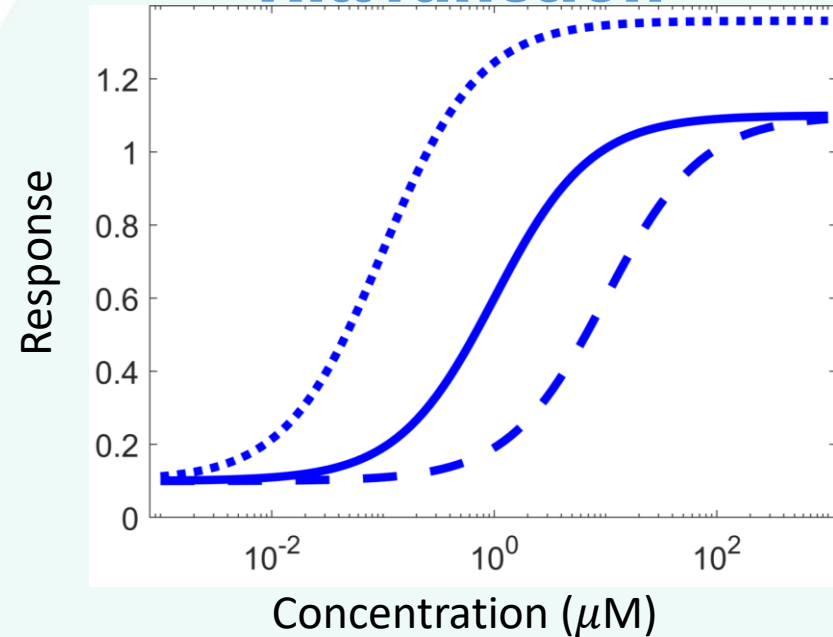
- Here, D is the data and X is random variable
- E.g., $X - V_{\max}$ parameter, D – experimental observations
- The key things are the likelihood, the prior and the posterior:
 - **Posterior:** probability that V_{\max} takes a certain value
 - **Likelihood:** probability of the data, given V_{\max}
 - **Prior:** probability reflecting initial assumptions V_{\max}

Back to the dose response example

Example dose response data



Hill function

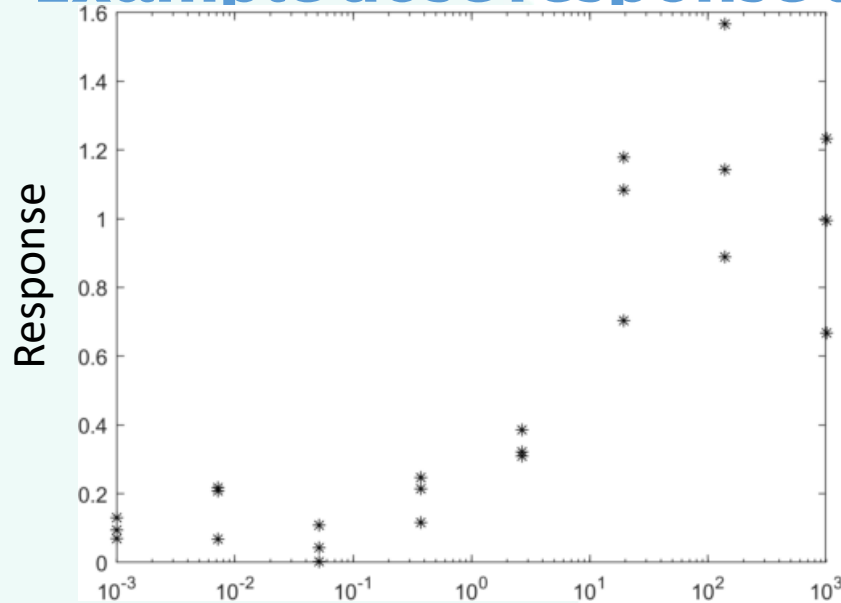


Develop

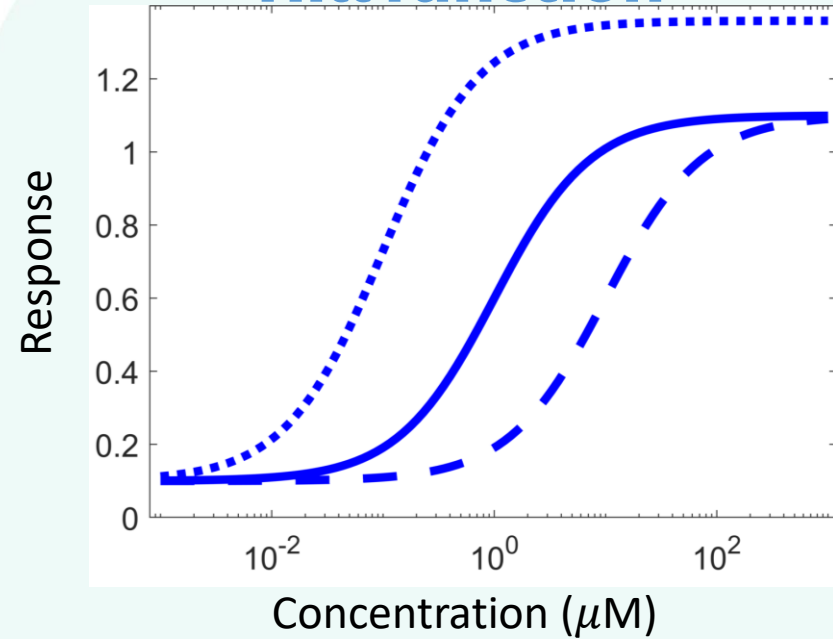
- Main building blocks of the model:
 - Measured data = Mean Response + Observational Noise
 - $y = f(x|C, \theta, V_{max}) + \eta$
- y and x are the observations and concentrations respectively.
- Assume η is normally distributed with standard deviation σ

Using Bayesian models to quantify uncertainty

Example dose response data



Hill function



Develop

- Hill equation:

$$f(x|C, \theta, V_{max}) = V_{max} \frac{x}{x + \theta} + C$$

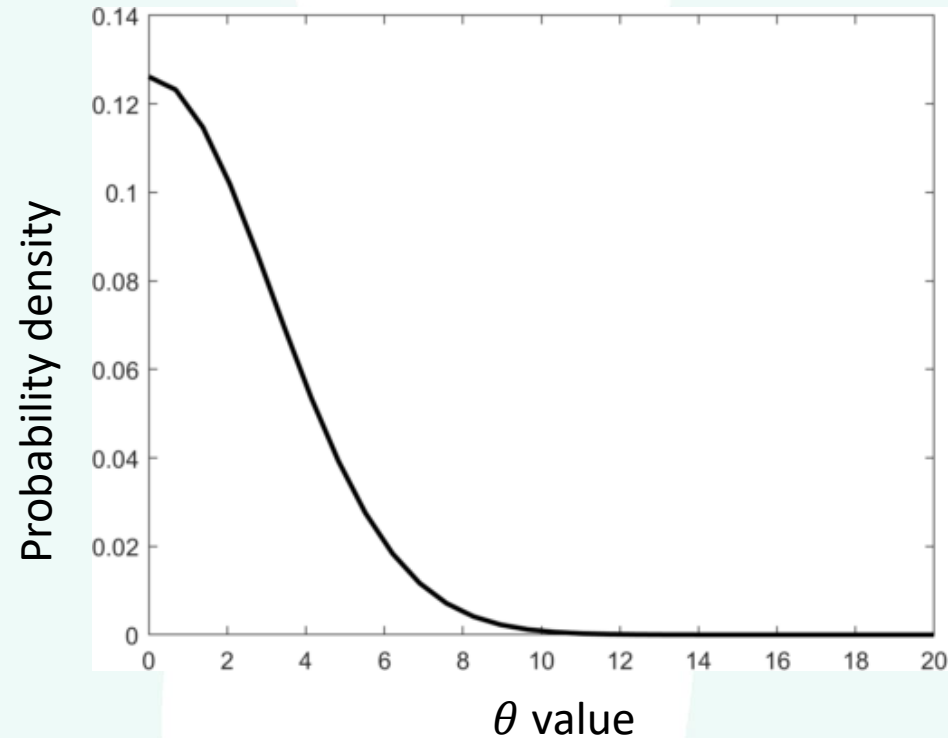
- (full Hill equation has exponent on x and θ to obtain sharper curves)

Example of a prior

Develop

- Have parameters θ , C , V_{max} and σ – need to be learned from the data

Prior for θ (threshold value)

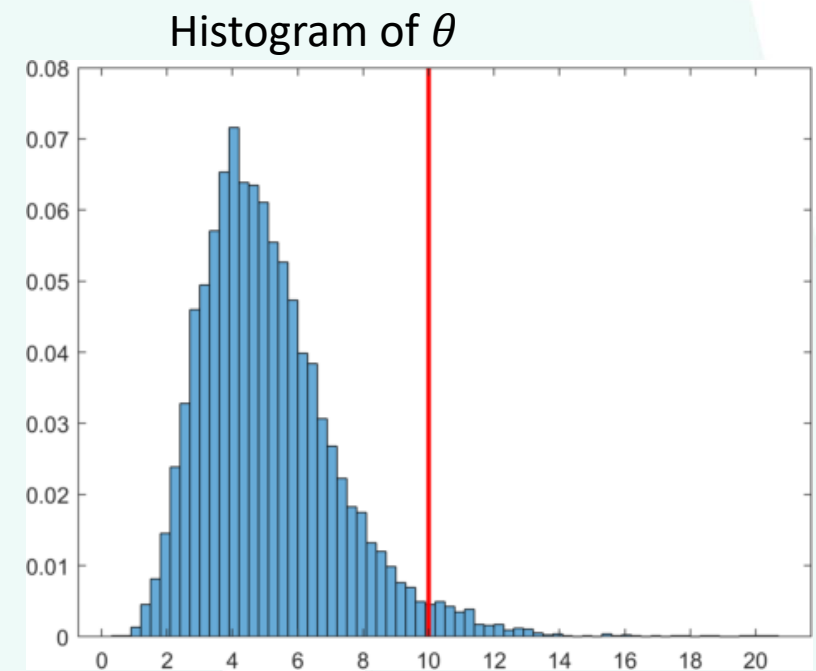
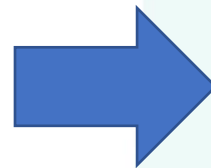
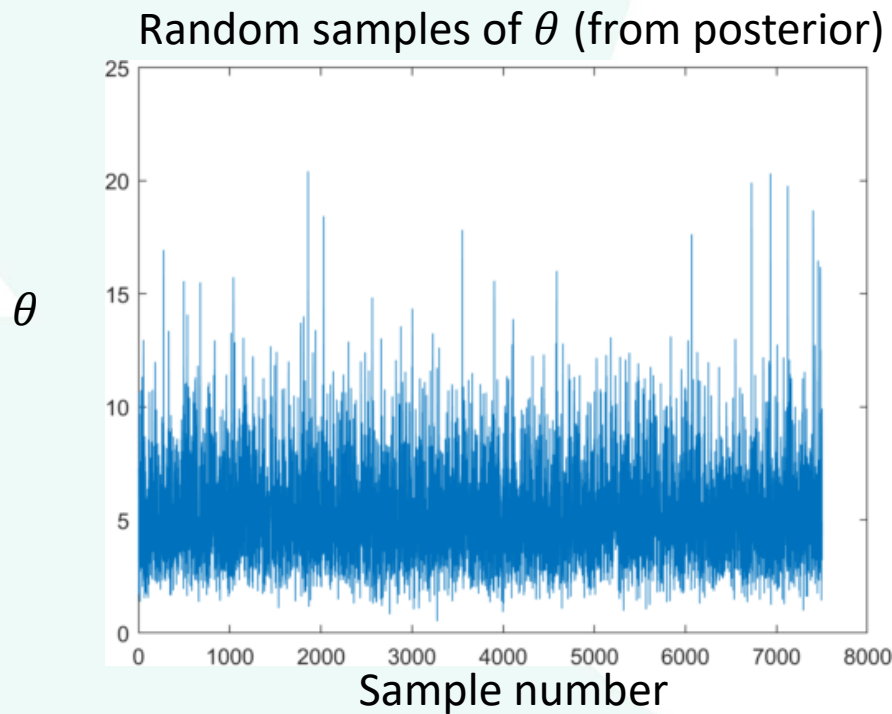


Data

- Typically you only have the measured values that you are fitting to, but you could incorporate prior knowledge (e.g. biologically plausible values) into the prior.

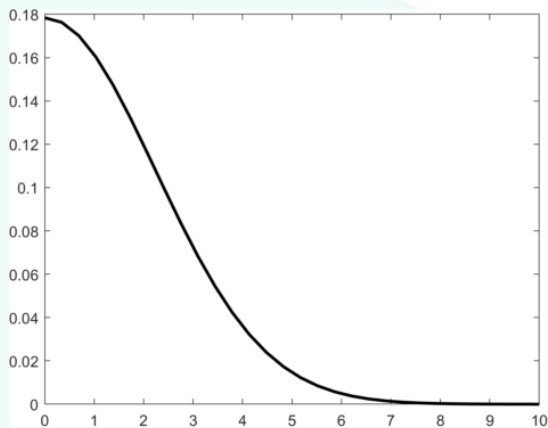
Learning parameters from the data

- One things that's important to know about Bayesian statistics is that for most problems, it is impossible to get an exact solution to the posterior.
- Resort to using methods like **Markov Chain Monte Carlo (MCMC)** to take random samples from the distribution.

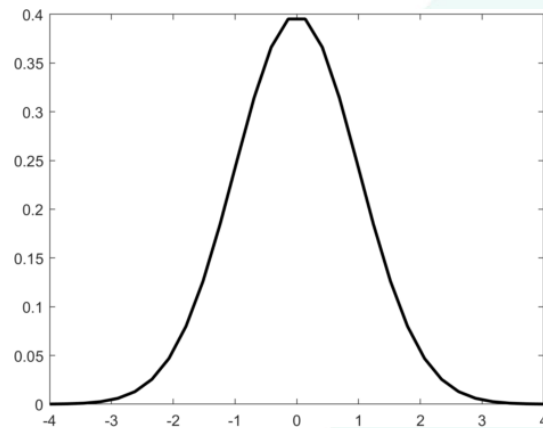


Learning parameters from the data

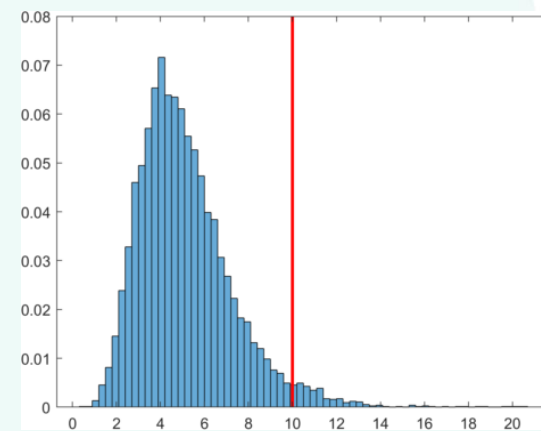
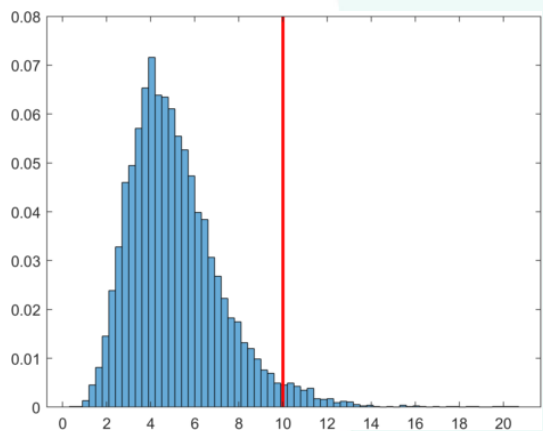
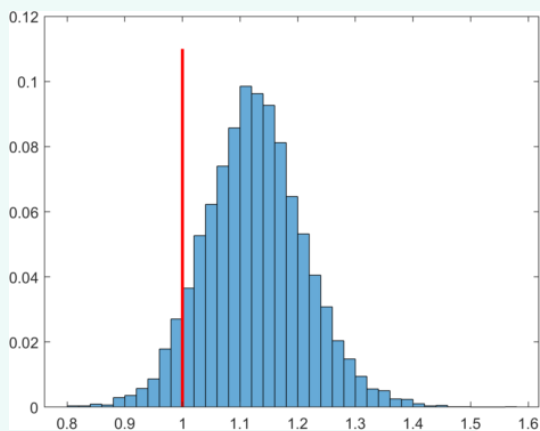
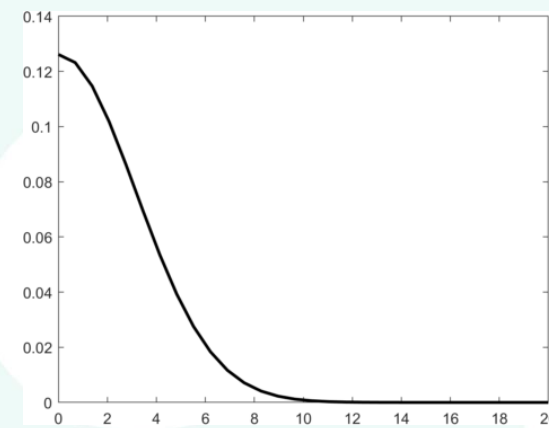
Vmax



C

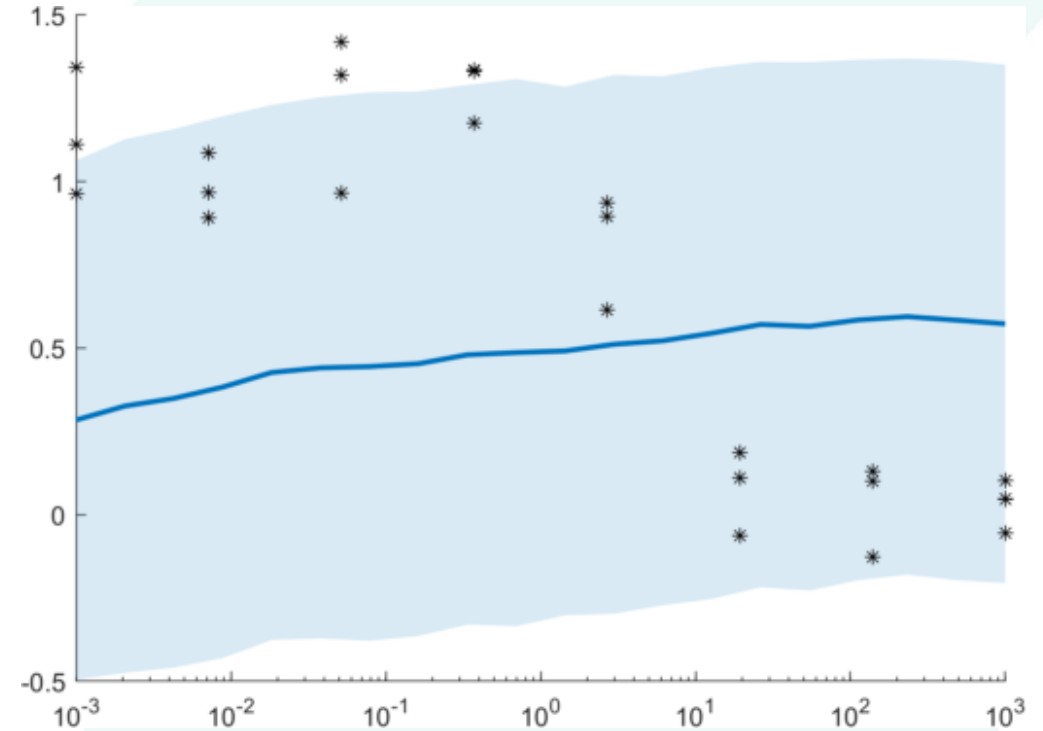
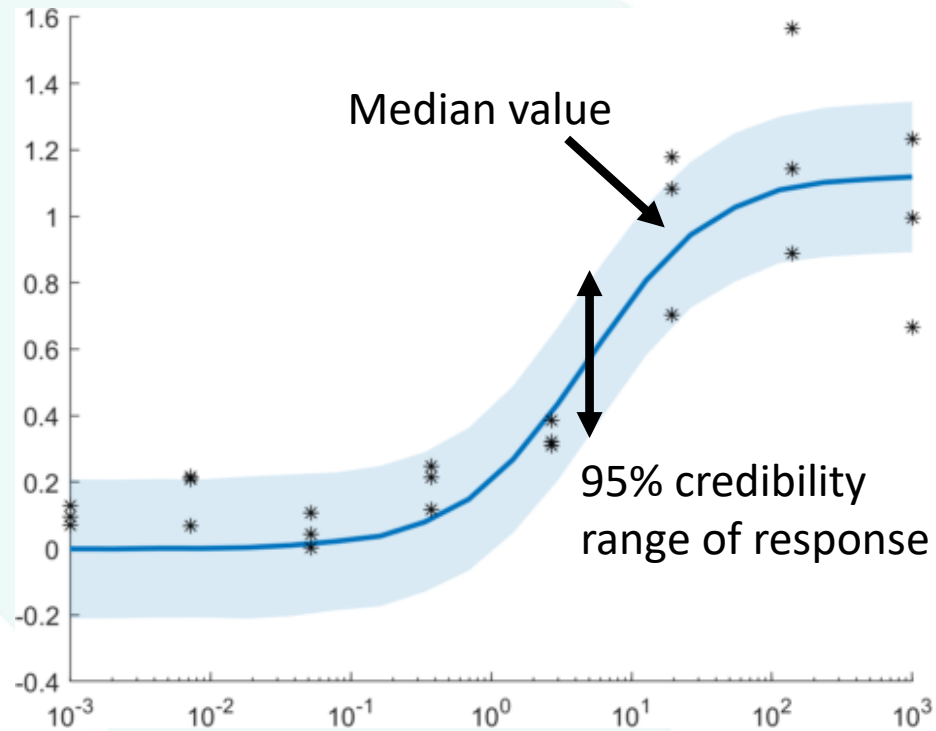


C



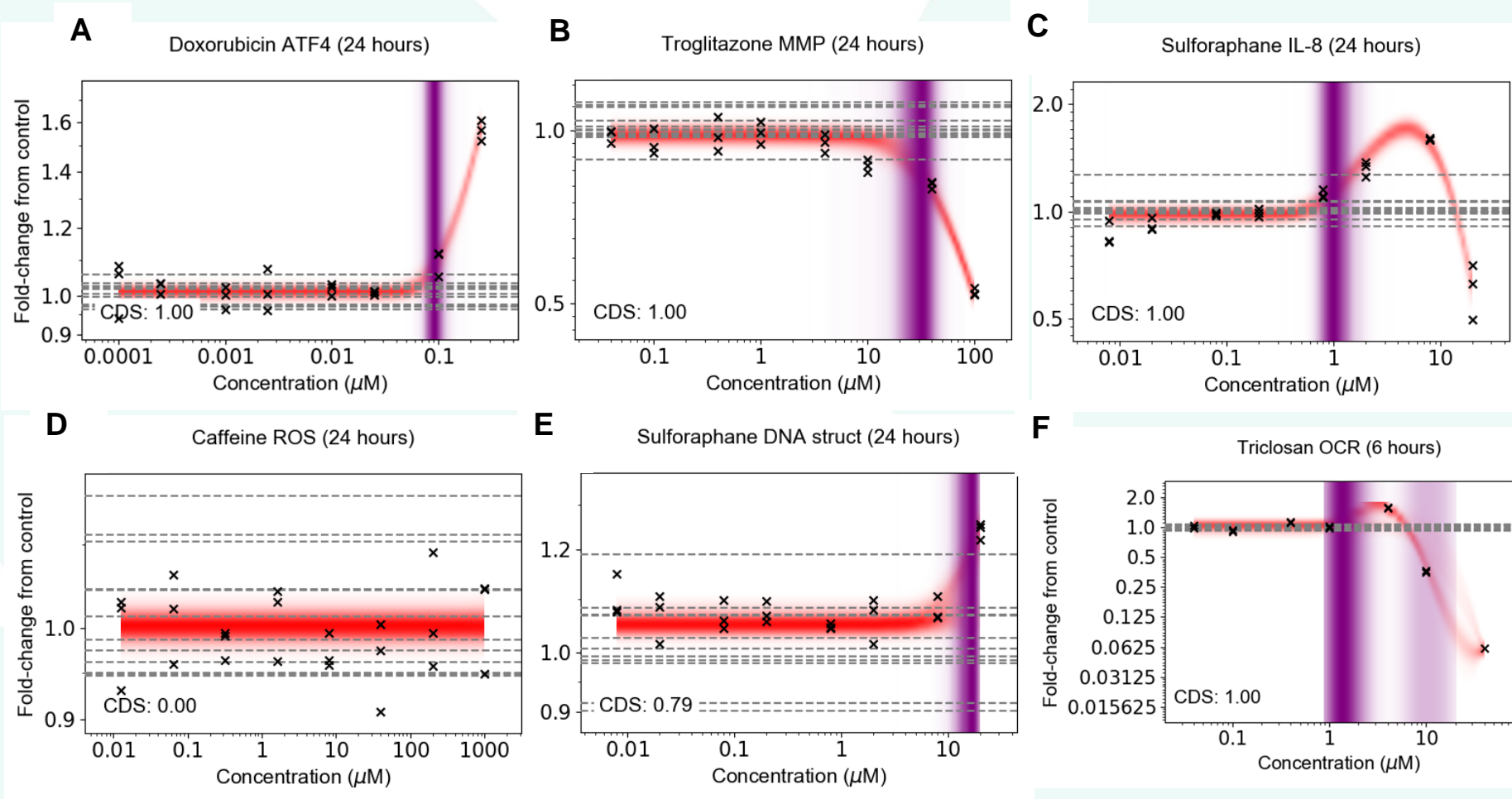
CORRECT LATER ON

Evaluating the dose response model



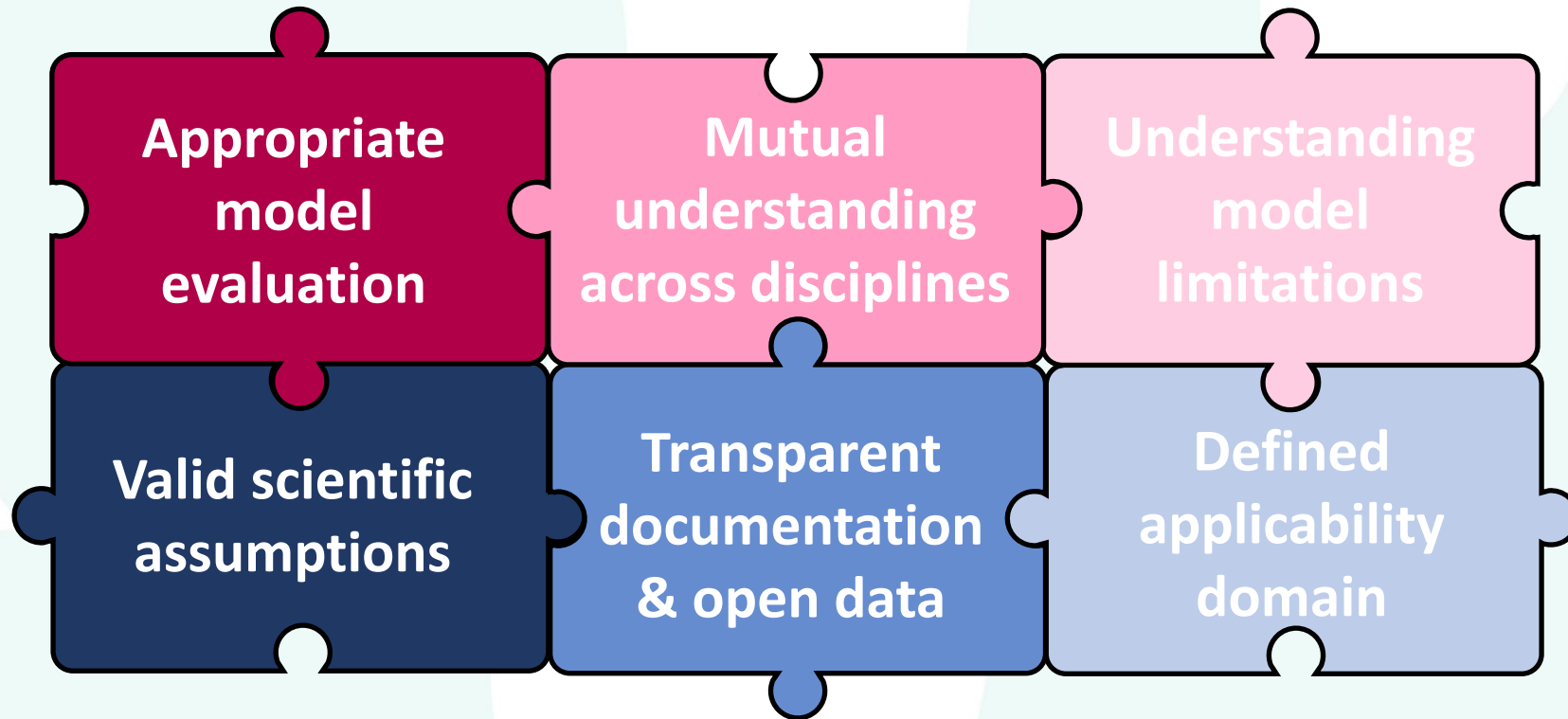
- Bayesian models can be evaluated by comparing the predictive distributions to the training data
- When using parametric models is to fit data to multiple models and decide which one is best
- Sometimes you can miss effects, not because there is no effect, but because the model does a poor job of describing the data

Back to the cell stress panel



Challenges in the acceptance of using computational approaches in NGRA

What do you think?



Top down vs bottom modelling

Bottom up

Model behaviour is an emergent property of the 'rules' chosen for the model

Observed phenomena vs model



E.g., change in concentration between liver and plasma dictated by perfusion

Define 'rules' of how different variables interact



E.g., concentration of X in the plasma, liver etc

Define individual model variables

Top down

Visualise the data, what are the key variables? How are do they appear to be related?

Observed phenomena



Define key variables and (statistical) relationships

Develop model based on observations



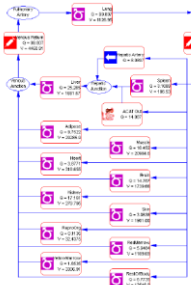
Does the model provide a good description of the data?

Evaluate the model

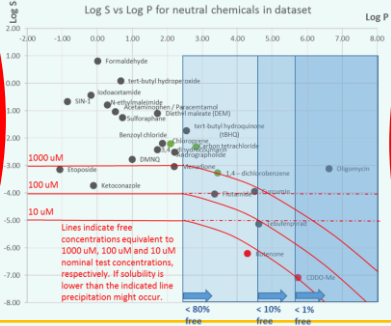
Evaluating a toolbox of NAMs

Back to the toolbox

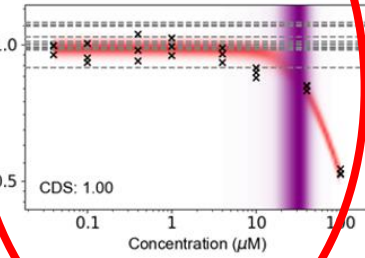
PBK models



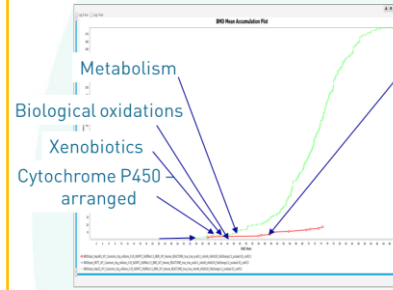
Free concentration



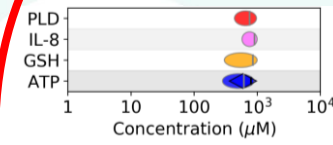
Conc. Resp. models



HTTr



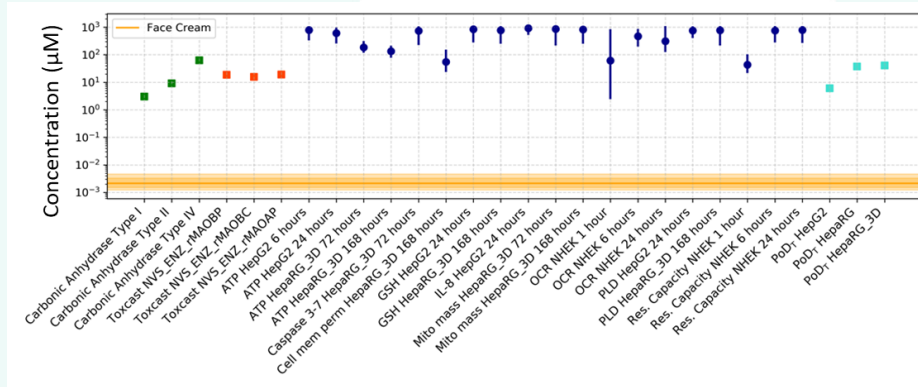
CSP



IPP

- All binding and enzymatic assay results were negative at 10 μ M, including COX-1 and COX-2
- Highest inhibition (22%) was for MAO-A

Bioactivity exposure ratio



Inform safety decision

HTTr: High-throughput transcriptomics

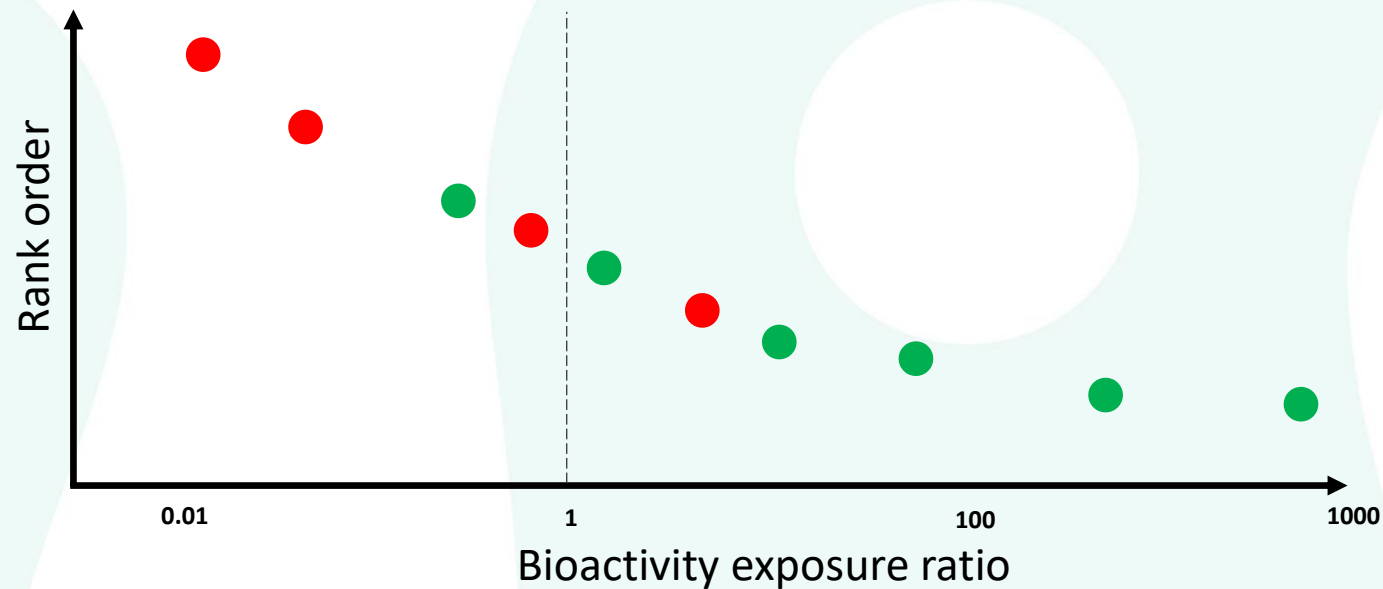
CSP: Cell Stress Panel

IPP: In vitro pharmacological profiling

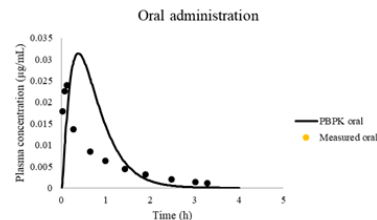
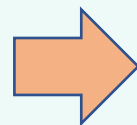
An evaluation strategy for the toolbox

Chemical exposures scenarios

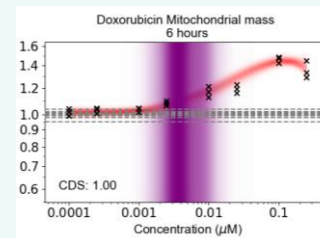
- 'Low' risk (from consumer goods perspective) – e.g. foods, cosmetics
- 'High' risk (from consumer goods perspective) – e.g. drugs



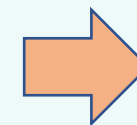
Define typical use-case scenarios benchmark chemical-exposures; Mixture of High and low risk



PBK models of systemic exposure

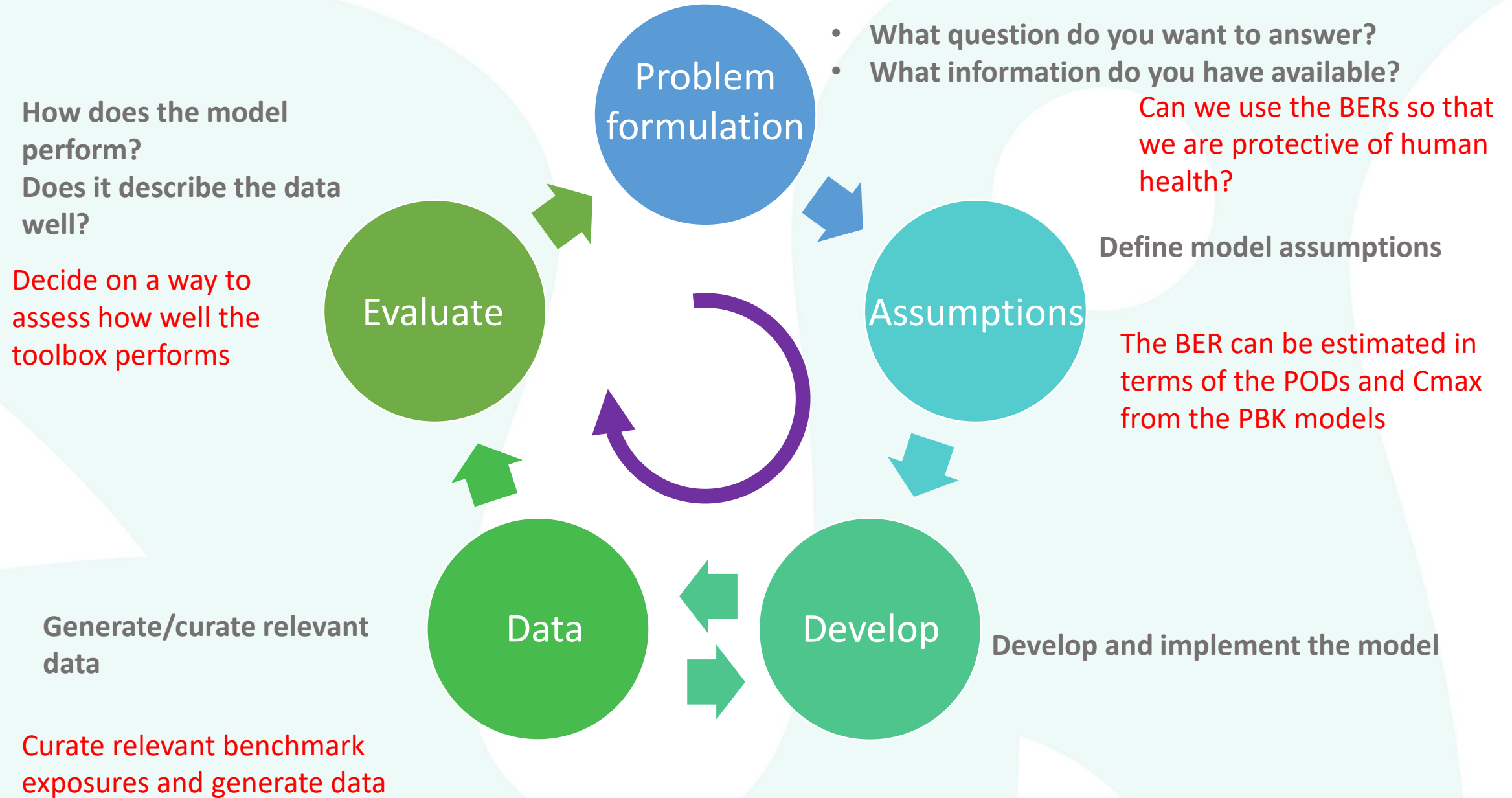


In-vitro cell assays, estimate PoDs



Calculate the bioactivity exposure ratio

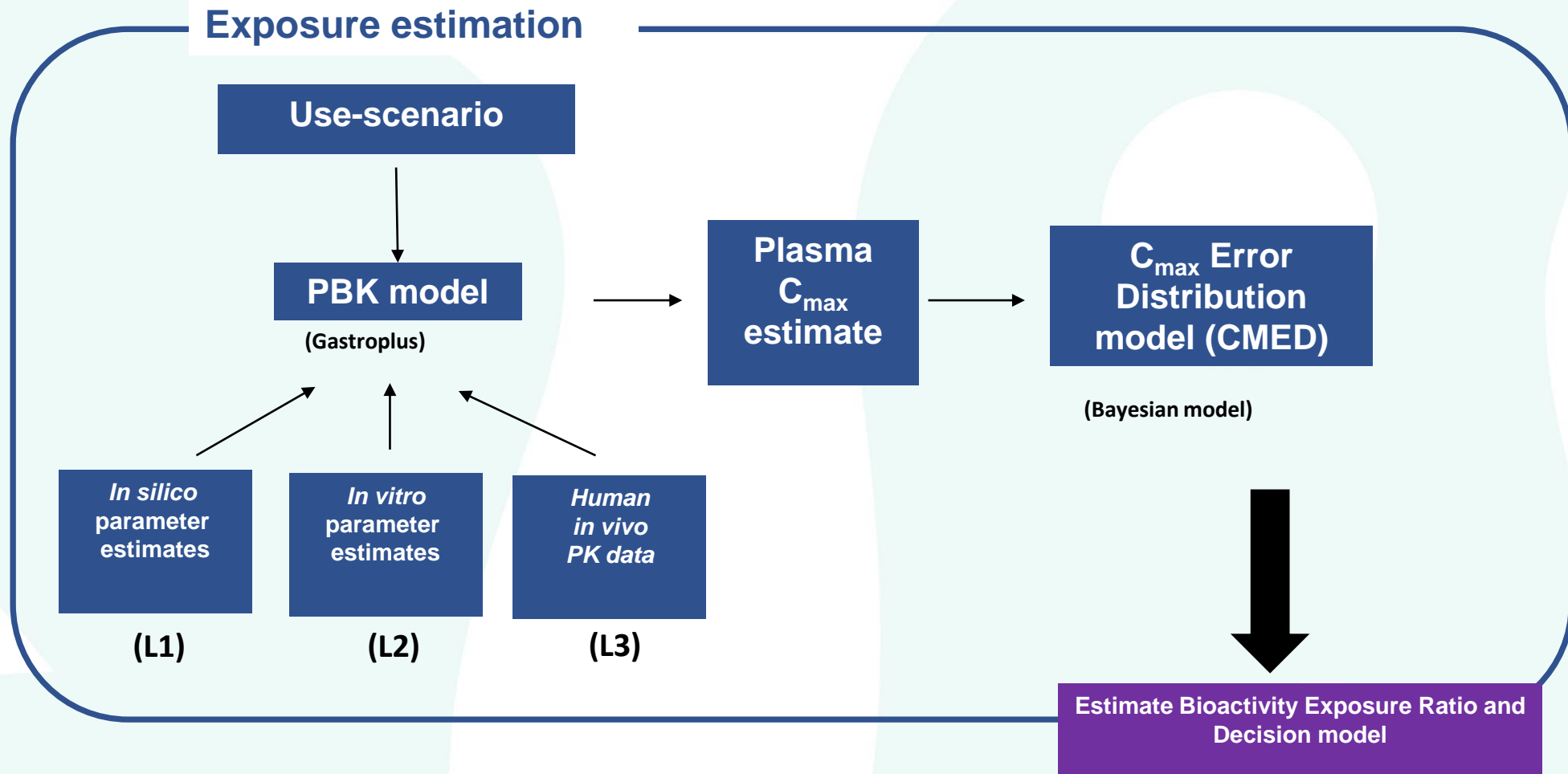
Thinking about it in terms of model development



Identifying suitable benchmarks for the evaluation

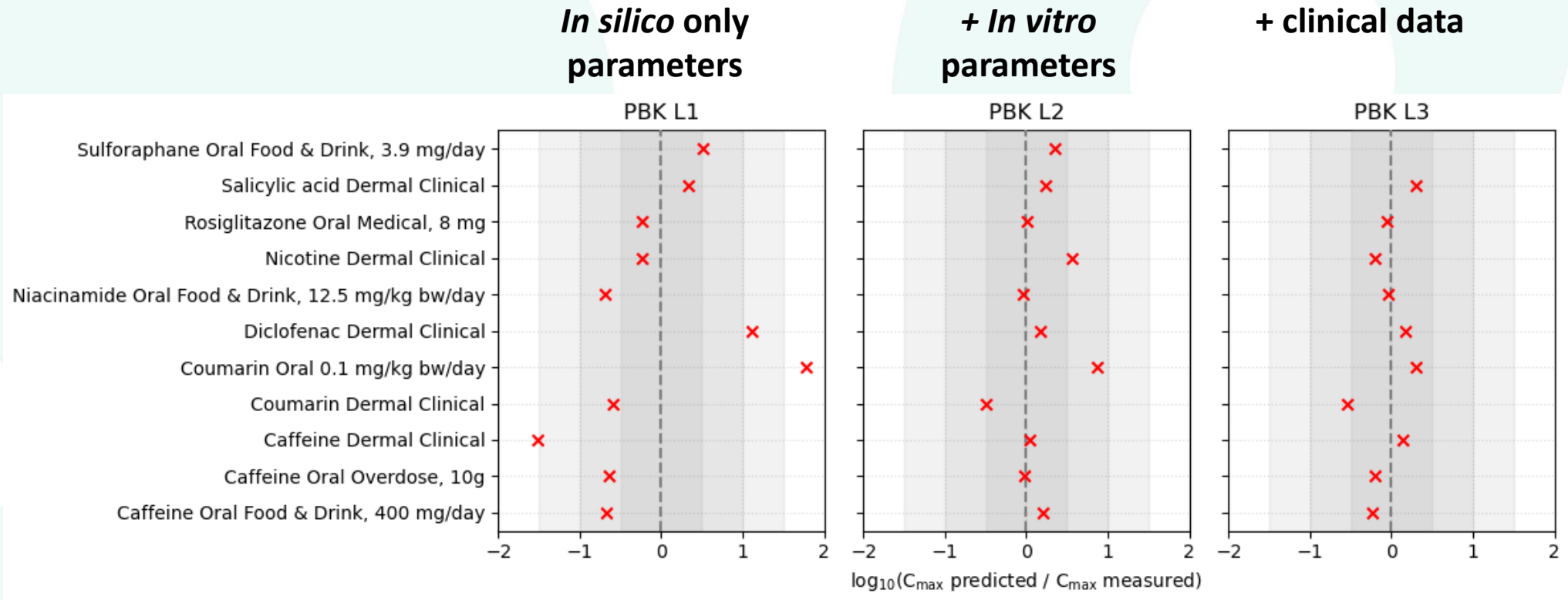
| Chemical | Exposure scenario | Risk classification |
|----------------------------|--|---------------------|
| Oxybenzone | 2 scenarios: 0.5%; 2% sunscreen | Low risk |
| Caffeine | 2 scenarios: 0.2% shampoo & coffee oral consumption 50 mg | Low risk |
| Caffeine | 10g – fatal case reports | High risk |
| Coumarin | 3 scenarios: 4 mg/d oral consumption; 1.6% body lotion (dermal); TDI 0.1 mg/kg oral | Low risk |
| Coumarin | 400 mg/kg clinical trial ~ 14 months | High risk |
| Hexylresorcinol | 3 scenarios: Food residues (3.3 ug/kg); 0.4% face cream; throat lozenge 2.4 mg | Low risk |
| BHT | Body lotion 0.5% | Low risk |
| Sulforaphane | 2 scenarios: Tablet 60 mg/day; food 4.1-9.2 mg/day | Low risk |
| Niacinamide | 4 scenarios: oral 12.5-22 mg/kg; dermal 3% body lotion and 0.1 % hair condition | Low risk |
| Thalidomide | 3 scenarios: oral tablet 50 mg, 100 mg, 400 mg | High risk |
| Doxorubicin | 75 mg/m ² IV bolus 10 min; 21 days cycles; 8 cycles | High risk |
| Rosiglitazone | 8 mg oral tablet | High risk |
| Valproic Acid (VPA) | 2 scenarios: oral tablet 1000 mg & > 60 mg/kg | High risk |
| Paraquat | Accidental ingestion 35 mg/kg | High risk |

Using PBK models to predict C_{max}



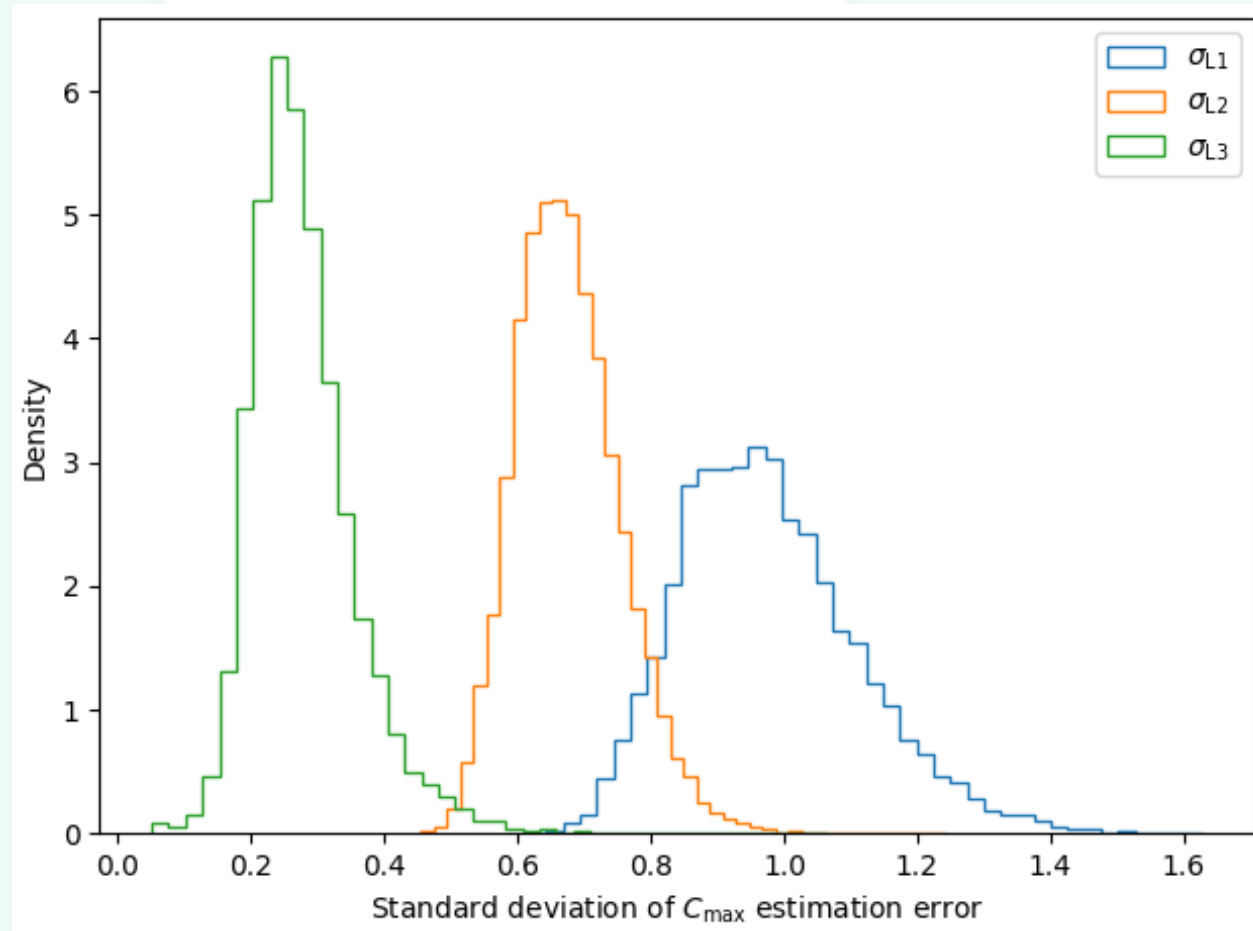
- Used a (**bottom-up**) PBK model to predict C_{max} under different parameterisations
- Used a (**top down**) Bayesian statistical model to quantify the potential error in the est

Quantifying the error in the C_{max} estimates

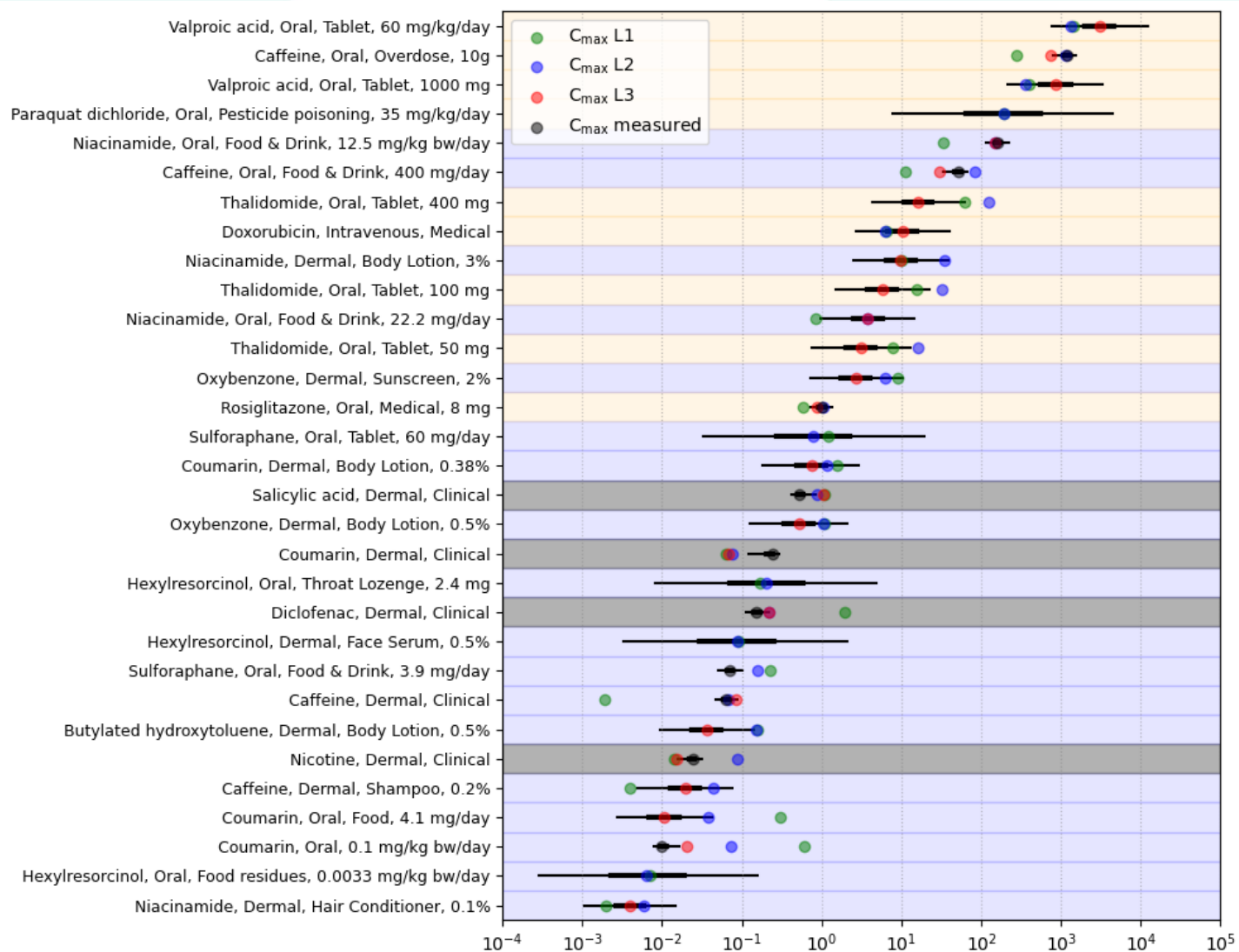


- The PBK prediction error decreases as we go through the different parameterisation levels
- This is an empirical observation

Using a Bayesian model to learn the prediction error

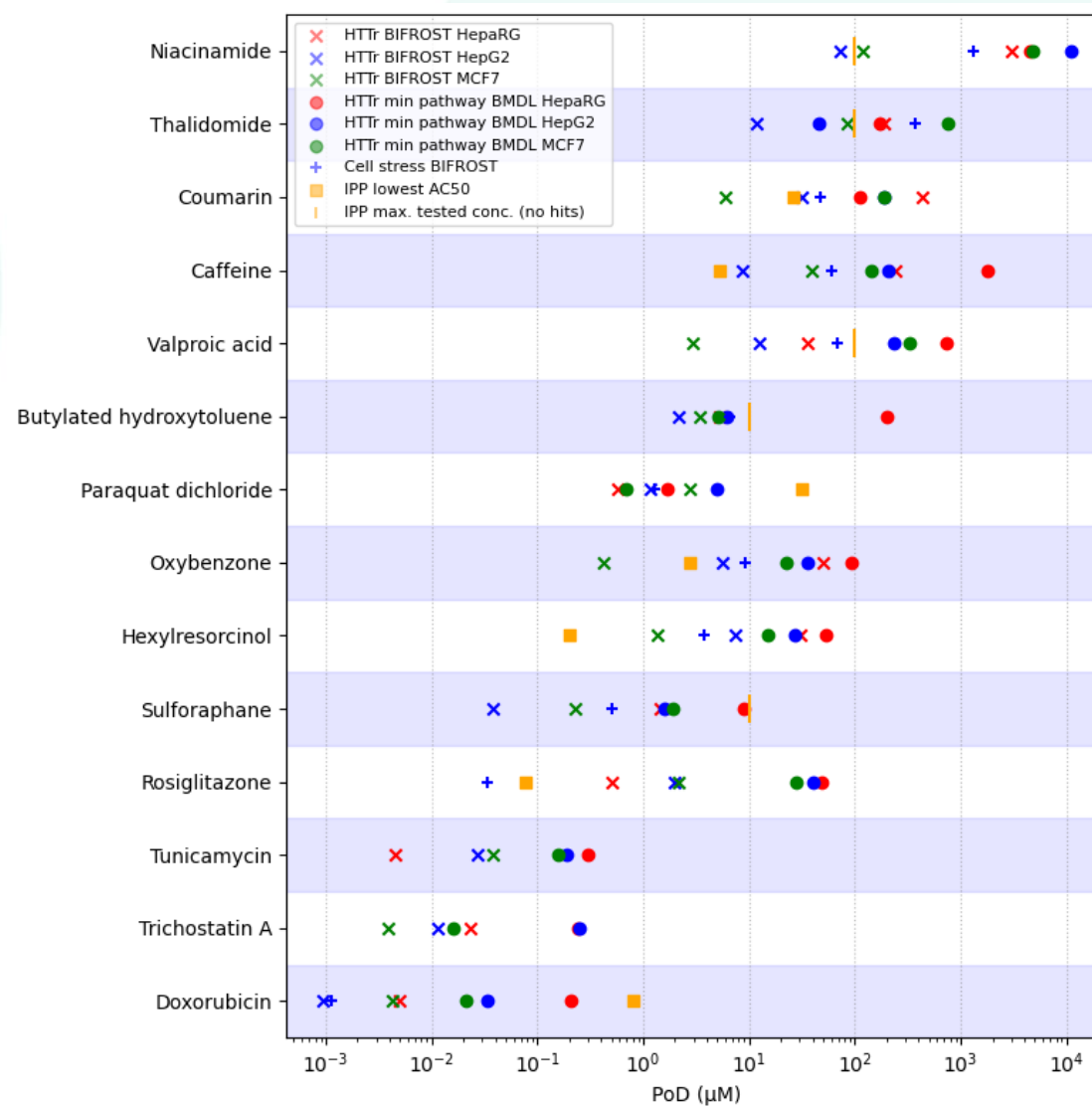


Using PBK models to predict Cmax

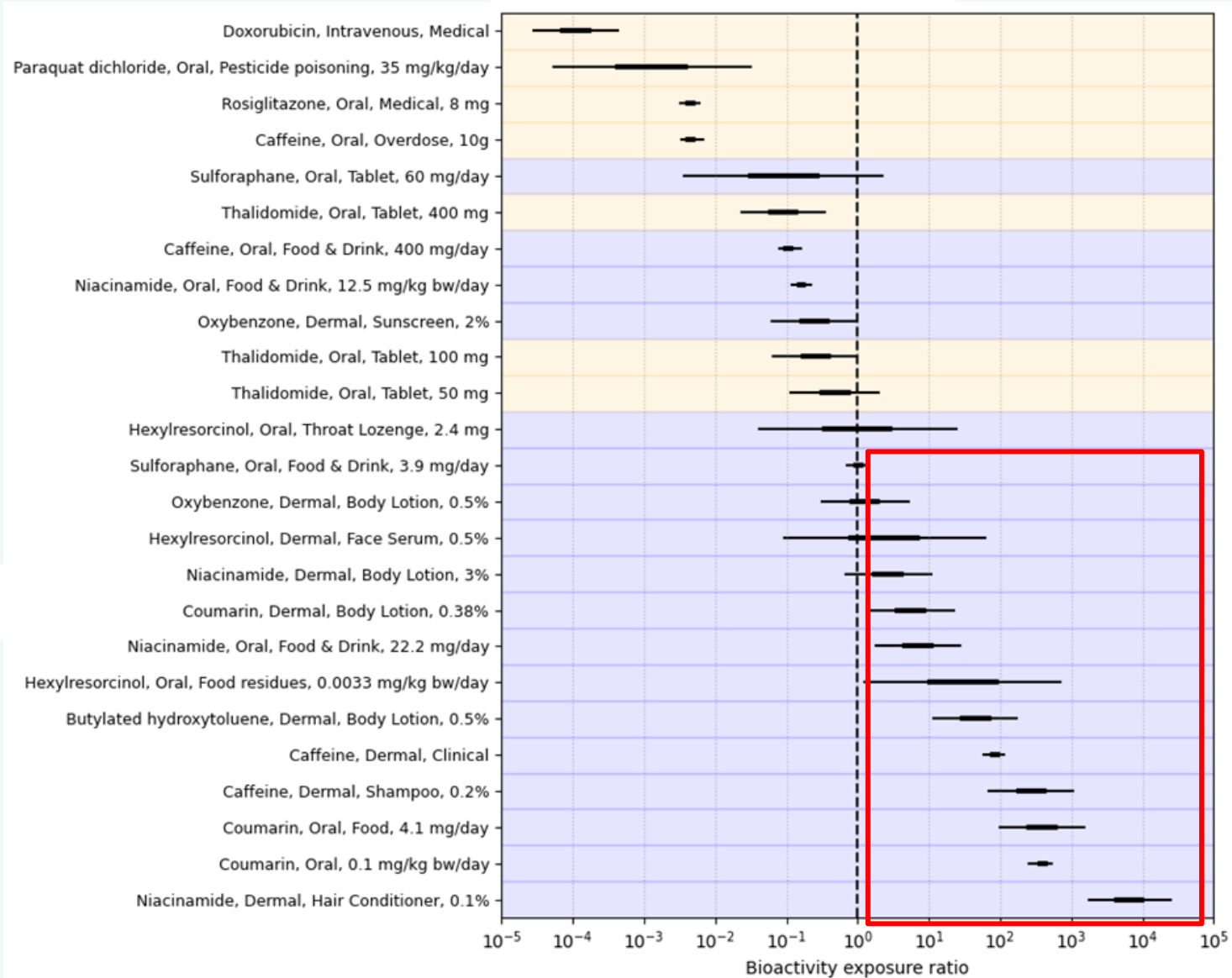


PODS from the bioactivity platforms

Dose response plots



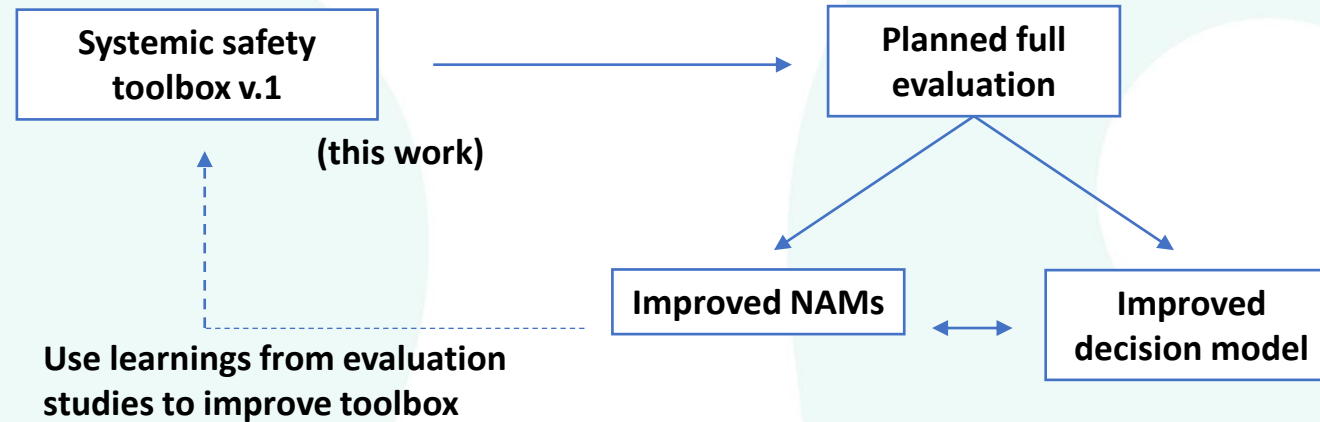
Initial results indicate the toolbox is protective



- Blue: low risk chemical-exposure scenario
- Yellow: high risk chemical-exposure scenario

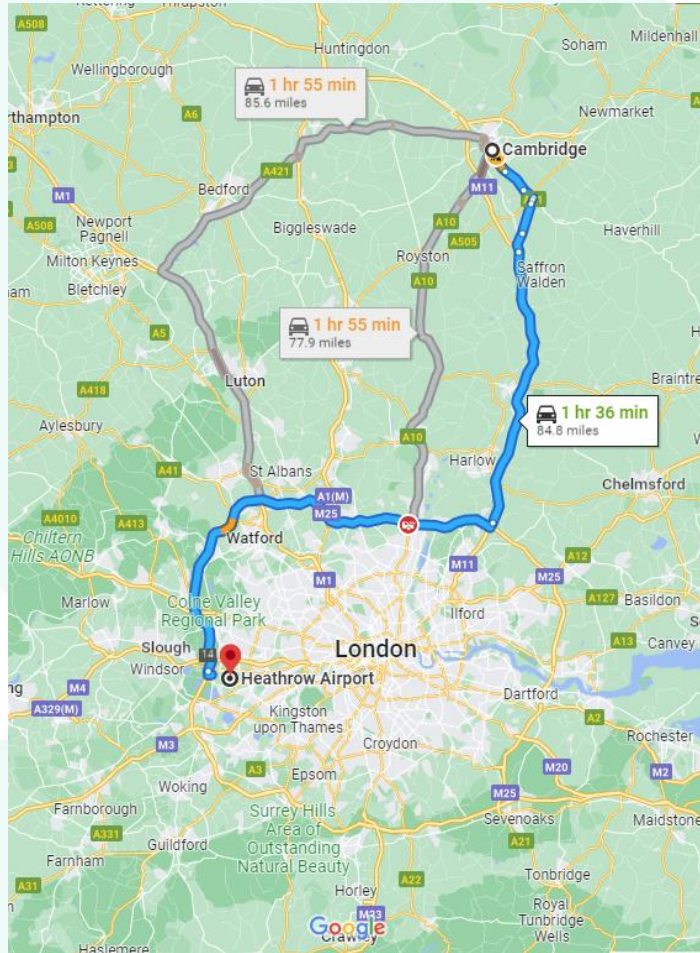
- Protectiveness: 100%
- Utility: 62%

Next step for the toolbox – the full evaluation

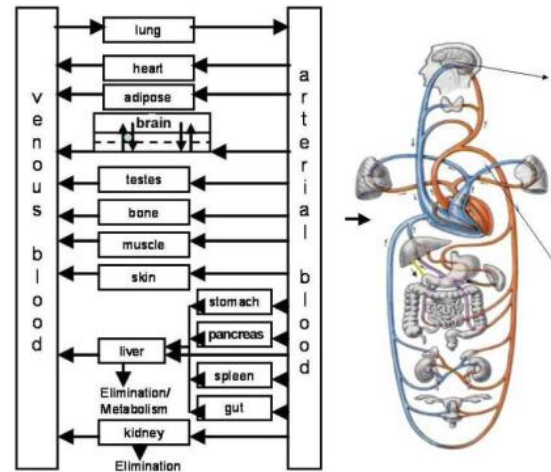
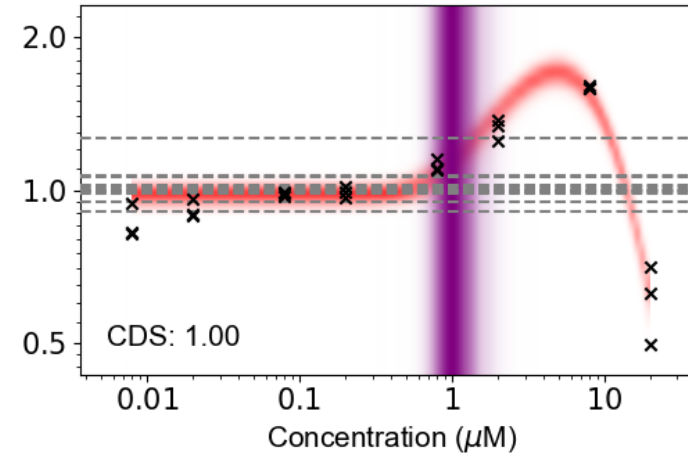


- Planning to extend evaluation to ~40 chemicals with ~60 associated **high risk** and **low risk** exposure scenarios.
- Also in collaboration with US-EPA, expanding range of NAMs
- Adopt **iterative approach** to evaluating and then identifying potential improvements to the toolbox.
- Use of concepts from used model evaluation and development should help build confidence in the approach.

Thinking about the future...



Sulfuraphane IL-8 (24 hours)



A screenshot of the ToxTree software interface. The window title is 'ToxTree (Estimation of Toxic Hazard - A Decision Tree Approach) v2.6.6'. The chemical structure shown is CC(=O)N1C[C@@H](C(=O)O)C[C@H](O)C1. The interface displays available structure attributes, Cramer rules, and a list of toxic hazard classes. The 'High (Class III)' class is highlighted in red.

ToxTree


Gastroplus

Getting started with computational approaches...

Learning to code vs using existing tools

Programming

Graphical user interfaces

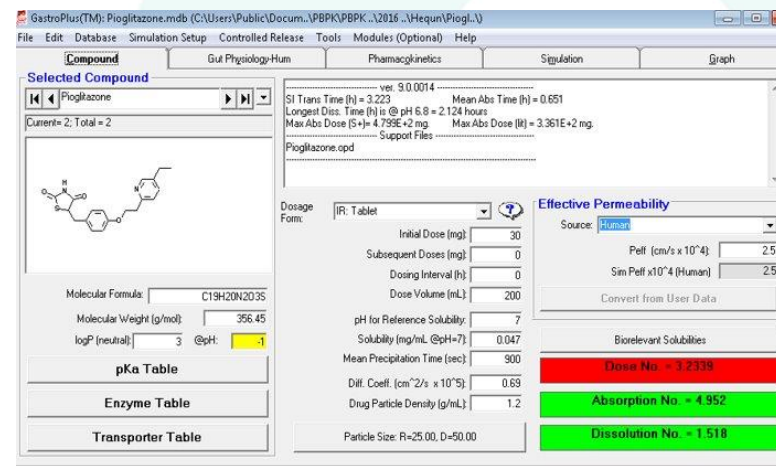


R
The Language of Technical Computing

python™

```
1 # Source on Save
2 # setwd("C:/Users/aj1stair/middleton/one-drive - unilever/work/computer code/sample_plots_for_slides/")
3 # Sys.setenv(PATH = paste(Sys.getenv("PATH"), "C:/Rbuildtools/3.5/bin/",
4 # Sys.setenv(R1NMF = "C:/Rbuildtools/3.5/mfng_32/bin", RBP = ":"))
5 # Sys.setenv(LOCAL_CPPFLAGS = "-march=core17 -use-icc17")
6 #
7 # phgbuid:has_buid_tools(debug = TRUE)
8 # options(buildtools.check = NULL)
9 # options(mc.cores = parallel::detectCores())
10
11
12 library(codetools)
13 library(devtools)
14 library(reshape)
15 library(rstan)
16 library(R.matlab)
17
18
19 F_true <- function(x) {
20
21   f=10*(x+10^5)+1
22   return(F)
23 }
24
25 randn <-function(N,M){
26
27   mymat=matrix(rnorm(N*M,mean=0,sd=1), N, M)
28   return(mymat)
29 }
30
31 x_data=10^seq(-3, 3, length.out = 8)
32 x_data_predict=10^seq(-3, 3, length.out = 20)
33 y_data=10^(log10(F_true(x_data))+.1*randn(length(x_data),3))+.1*randn(length(x_data),3)
34 Nreps=3
35 ndoses=length(x_data)
36 ndoses_predict=length(x_data_predict)
37 mydata = list(ndoses=as.integer(ndoses),Nreps=as.integer(Nreps),ndoses_predict=as.integer(ndoses_predict), xdata=x_data,ydata=y_data,xdata_predict=x_data_predict
38 source("mystarmodel.R")
39 starmodelfirst <- starmodel(model_code = starmodeltext, verbose = TRUE)
40 stan_output <- sampling(starmodelfirst,data=mydata, iter=5000, chains=3, cores=3)
41
42
43 extract_parameters=extract(stan_output)
44 writeMat("stanresults_badfit.mat",extract_parameters=extract_parameters,data_tr=fn=mydata)
45
```

PBK software



GastroPlus(TM): Pioglitazone.mdb (C:\Users\Public\Docum...PBPK\PBPK_12016_1\Hequn\Piogli...)

Selected Compound: Pioglitazone

SI Trans Time (h) = 3.223 Mean Abs Time (h) = 0.651
Longest Dis. Time (h) @ pH 6.8 = 2124 hours
Max Abs Dose (S+) = 4.799E+2 mg Max Abs Dose (h) = 3.361E+2 mg

Compound: Pioglitazone.epd Support Files

Molecular Formula: C19H20N2O3S
Molecular Weight (g/mol): 356.45
logP (neutral): 3 @pH: -1

Effective Permeability: Source: Human
Peff (cm²/s x 10⁻⁴): 2.5
Sim Peff x10⁻⁴ (Human): 2.5

Chow No. = 1.2338
Absorption No. = 4.952
Dissolution No. = 1.518



Dose response software



tcpl 2.0
Data Processing
National Center for Computational Toxicology, US EPA

https://cran.r-project.org/web/packages/tcpl/vignettes/Data_processing.html



<https://benchmarkdose.com/>

References

Baltazar *et al.*, (2020) A Next-Generation Risk Assessment Case Study for Coumarin in Cosmetic Products *Toxicol Sci* 176(1): 236-252 <https://doi.org/10.1093/toxsci/kfaa048>

Bowes *et al.*, (2012) Reducing safety-related drug attrition: the use of in vitro pharmacological profiling *Nat Rev Drug Discov* 11(12):909-22 <https://doi.org/10.1038/nrd3845>

Dent *et al.*, (2018) Principles underpinning the use of new methodologies in the risk assessment of cosmetic ingredients *Comp Tox* 7: 20-26 <https://doi.org/10.1016/j.comtox.2018.06.001>

Hatherell *et al.*, (2020) Identifying and Characterizing Stress Pathways of Concern for Consumer Safety in Next-Generation Risk Assessment *Toxicol Sci* 176(1): 11-33 <https://doi.org/10.1093/toxsci/kfaa054>

Moxon *et al.*, (2020) Application of physiologically based kinetic (PBK) modelling in the next generation risk assessment of dermally applied consumer products *TIV* 63:104746 <https://doi.org/10.1016/j.tiv.2019.104746>

Paul-Friedman *et al.*, (2019) Utility of In Vitro Bioactivity as a Lower Bound Estimate of In Vivo Adverse Effect Levels and in Risk-Based Prioritization *Toxicol Sci* 173(1):202-225 <https://doi.org/10.1093/toxsci/kfz201>

Rotroff *et al.*, (2010) Incorporating Human Dosimetry and Exposure into High-Throughput In Vitro Toxicity Screening *Toxicol Sci* 117(2): 348-358 <https://doi.org/10.1093/toxsci/kfq220>

Rajagopal *et al.*, (2022). Beyond AOPs: A Mechanistic Evaluation of NAMs in DART Testing. *Frontiers in toxicology*, 4. <https://doi.org/10.3389%2Fftox.2022.838466>

Li *et al.*, (2022) PBK modelling of topical application and characterisation of the uncertainty of C_{max} estimate: A case study approach, *Toxicology and Applied Pharmacology*, Vol 442(1) <https://doi.org/10.1016/j.taap.2022.115992>