

Physiological based pharmacokinetics models: Application to liver function

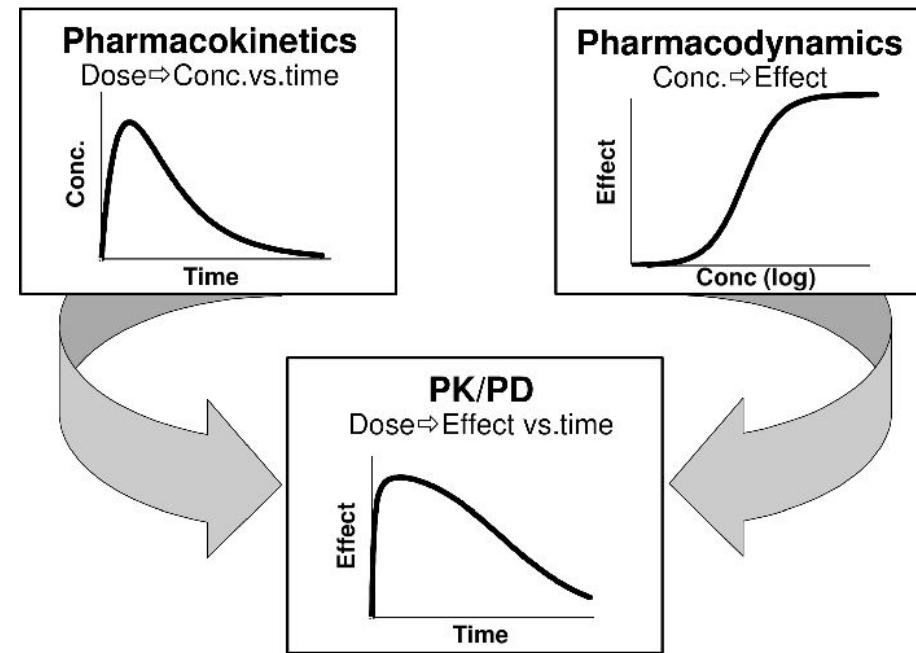
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livermetabolism.com

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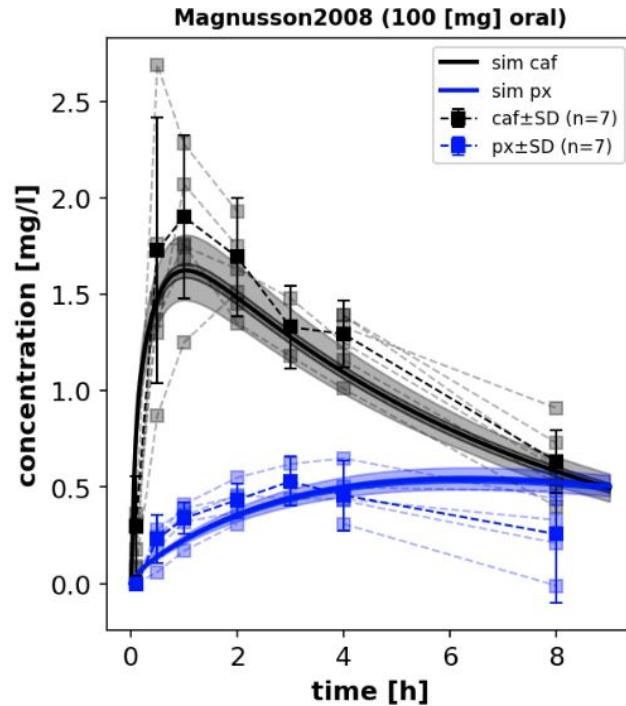
Pharmacokinetics & pharmacodynamics

- **Pharmacokinetics** is what the body does to the drug, i.e., how the drug is absorbed, distributed, metabolized & excreted (**drug disposition**)
- **Pharmacodynamics** is what the drug does to the body (**therapeutic effects**)





100 mg oral caffeine



Pharmacokinetic parameters

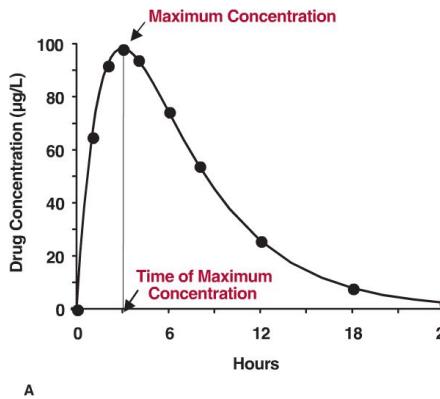


FIGURE 2-1. Drug concentration-time curve following a single oral dose showing the maximum systemic exposure (C_{max}) and the time of its occurrence (t_{max}). The concentration could represent drug in whole blood, plasma, or serum.

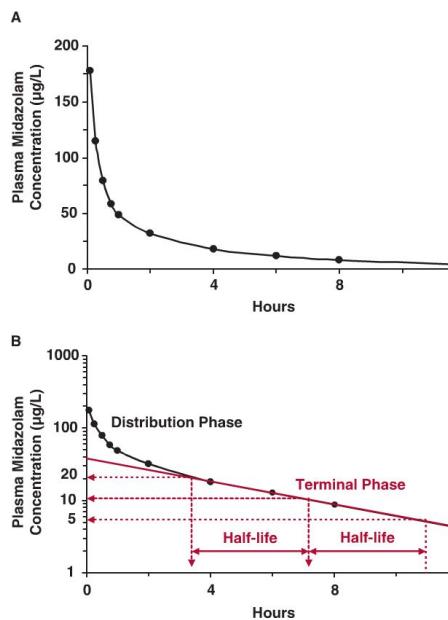


FIGURE 3-4. A. Plasma concentration of midazolam with time in an individual after an 8.35-mg i.v. bolus dose of midazolam hydrochloride (7.5 mg of the base) in a healthy adult. B. The data in A are redisplayed as a semilogarithmic plot. Note the short distribution phase. (From: Penttiläinen PJ, Väistö L, Himberg JJ, Crevoisier C. Pharmacokinetics of midazolam following i.v. and oral administration in patients with chronic liver disease and in healthy subjects. *J Clin Pharmacol* 1989;29: 272–277.)

- **C_{max}** : Maximal concentration
- **T_{max}** : time of maximal concentration
- **AUC** : area under the curve
- **k_{el}** : elimination rate fitting linear part of terminal phase (log)
- **$t_{1/2}$** : half-life ($= \ln 2/k_{el}$) time for concentration to fall to half
- **Vd** : volume of distribution ($= CL/k$), dilution space
- **CL**: clearance ($= \text{Dose}/\text{AUC}$, $= \text{Dose}/C(0)_{\text{extrapolated}}$)

Compartment models

- Pharmacokinetics can be modeled via simple compartment models
- Main processes (**ADME**)
 - **Absorption**
 - **Distribution**
 - **Metabolization**
 - **Elimination**

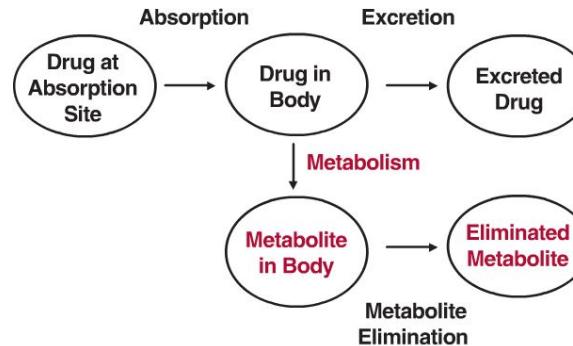


FIGURE 2-5. A drug is simultaneously absorbed into the body and eliminated from it, by excretion and metabolism. The processes of absorption, excretion, and metabolism are indicated with arrows and the compartments with ovals. The compartments represent different locations and different chemical species (color = metabolite). Metabolite elimination may occur by further metabolism or excretion.

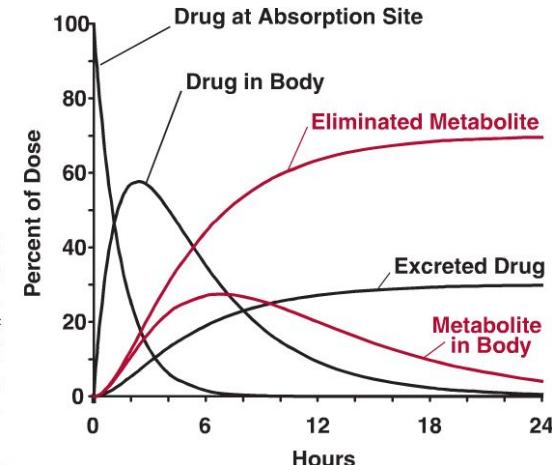
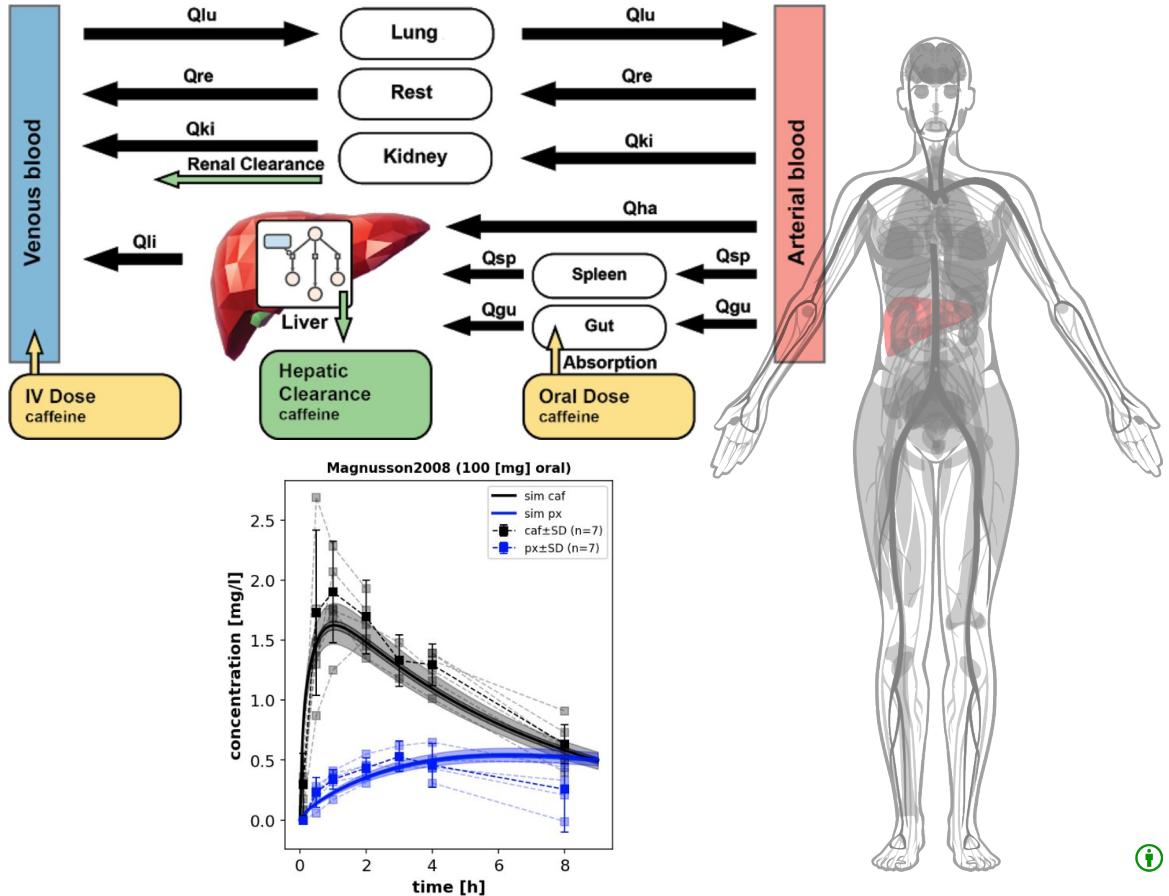


FIGURE 2-6. Time course of drug and metabolite in each of the compartments shown in Fig. 2-5. The amount in each compartment is expressed as a percentage of the dose administered. In this example, all the dose is absorbed. At any time, the sum of the molar amounts in the five compartments equals the dose.

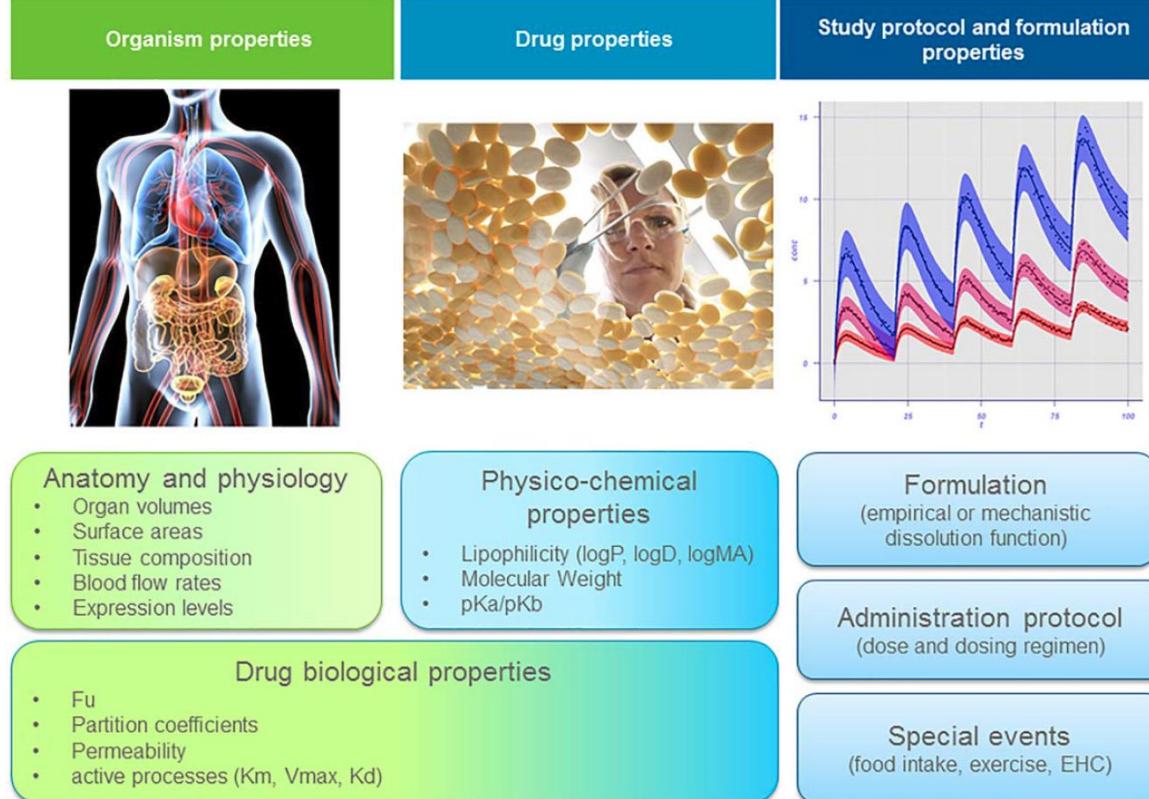
Physiological-based pharmacokinetics models (PBPK)



- **Human physiology *in silico***
Combines information on the drug with knowledge on the physiology and biology at organism level
- **Time dependent concentrations** of substances/drugs in organs, blood & urine
- **High pharmacological relevance** since it enables the estimation of drug exposure not only in plasma but also at the site of action

PBPK Models

Building blocks of a PBPK model



Compartments

- organs

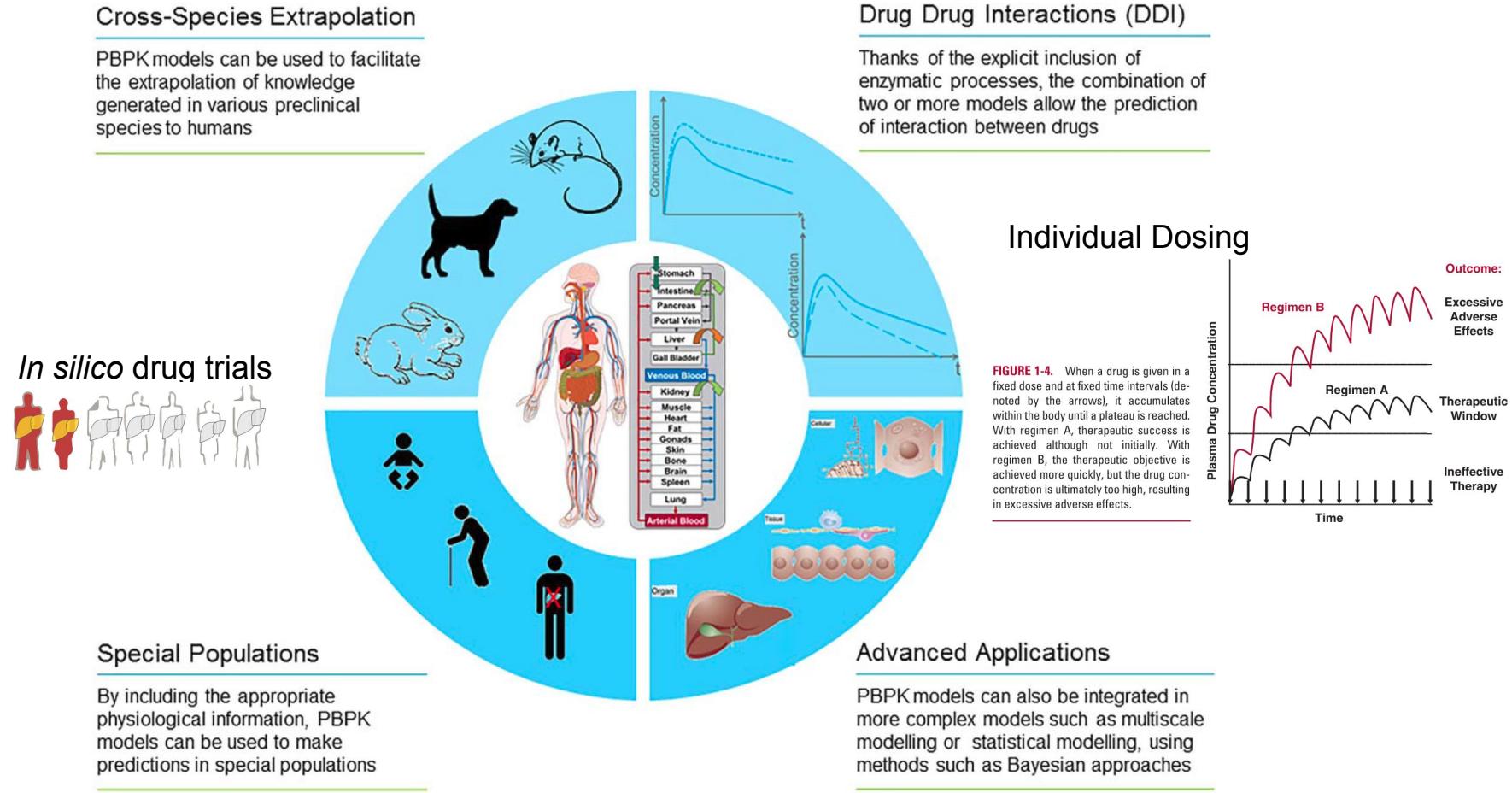
State variables:

- drug & metabolite amounts

Ordinary Differential equations (ODE) & rules

- Blood flows, Transport

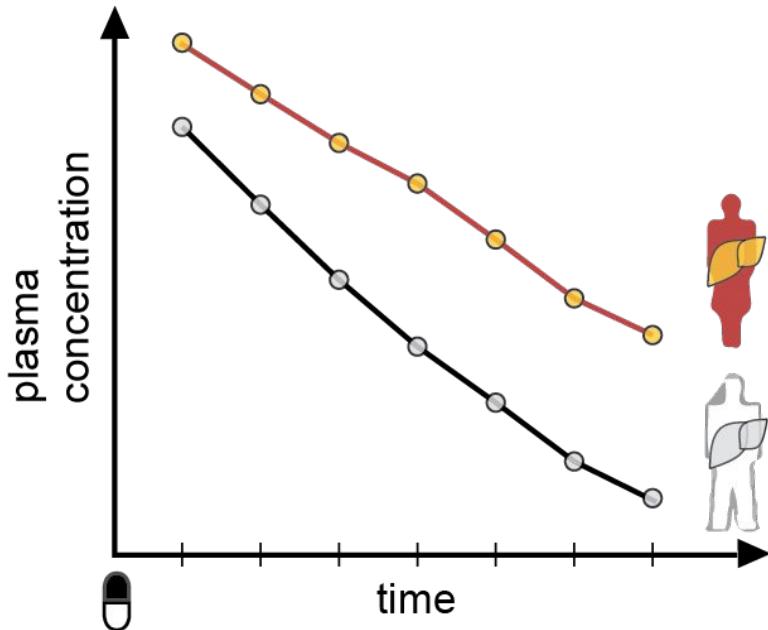
PBPK Applications



Liver function

- Diagnostics
- Monitoring disease progression & interventions
- Functional capacity
(transplantation & resection)





Dynamical liver function tests

Liver specific clearance of test substance

- Rate of (dis-)appearance as proxy for liver function (**pharmacokinetics**)
- Caffeine, LiMAX, galactose (GEC)

Challenges

- Dose dependency
- Large interindividual variability

Large inter-individual variability

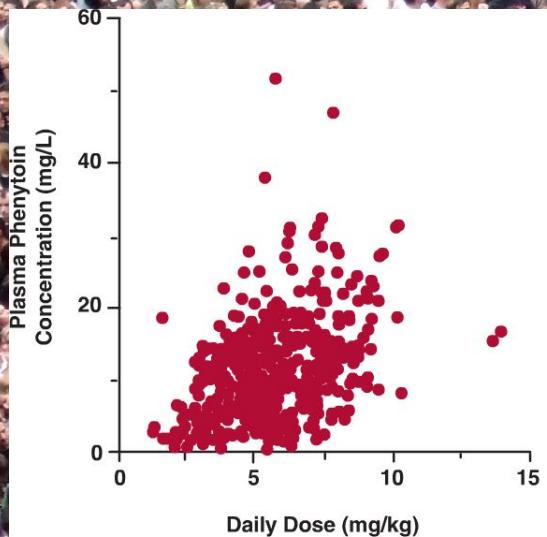


FIGURE 1-7. Although the average plasma concentration of phenytoin on chronic dosing tends to increase with the dosing rate, there is large variation in the individual values. (From: Lund, L. Effects of phenytoin in patients with epilepsy in relation to its concentration in plasma. In Davies DS, Prichard BNC, eds. Biological Effects of Drugs in Relation to Their Plasma Concentration. London and Basingstoke: Macmillan, 1973:227–238.)

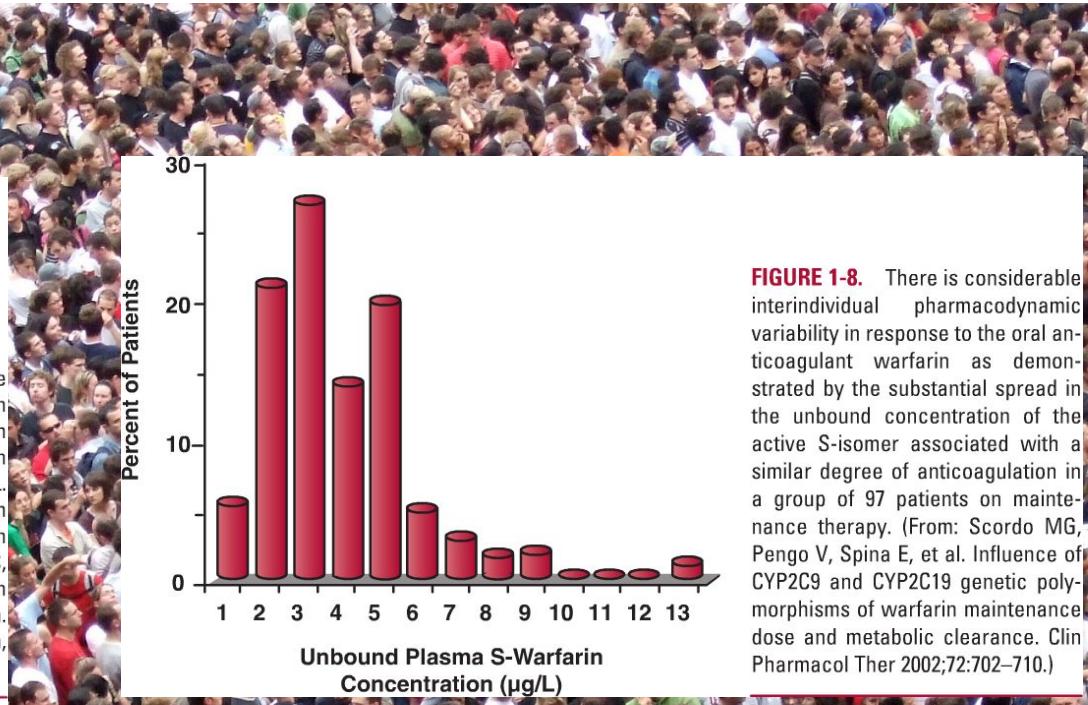


FIGURE 1-8. There is considerable interindividual pharmacodynamic variability in response to the oral anticoagulant warfarin as demonstrated by the substantial spread in the unbound concentration of the active S-isomer associated with a similar degree of anticoagulation in a group of 97 patients on maintenance therapy. (From: Scordo MG, Pengo V, Spina E, et al. Influence of CYP2C9 and CYP2C19 genetic polymorphisms of warfarin maintenance dose and metabolic clearance. Clin Pharmacol Ther 2002;72:702–710.)

Variability in Liver Enzymes

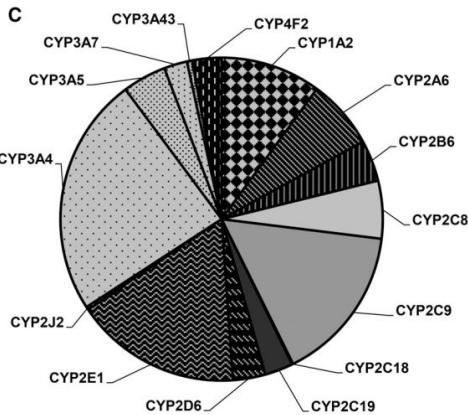


Fig. 1. Bar graph (A and B) and pie chart (C) of weighted mean abundances of cytochrome P450 enzymes in livers from adult Caucasians. Error bars represent weighted standard deviation values. n , the number of livers.

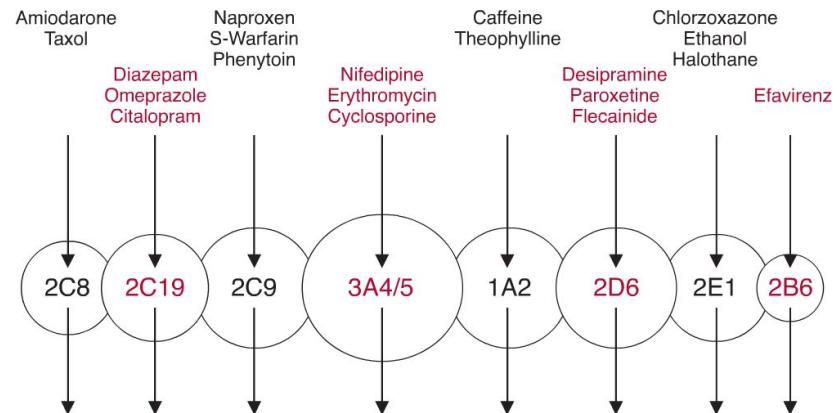
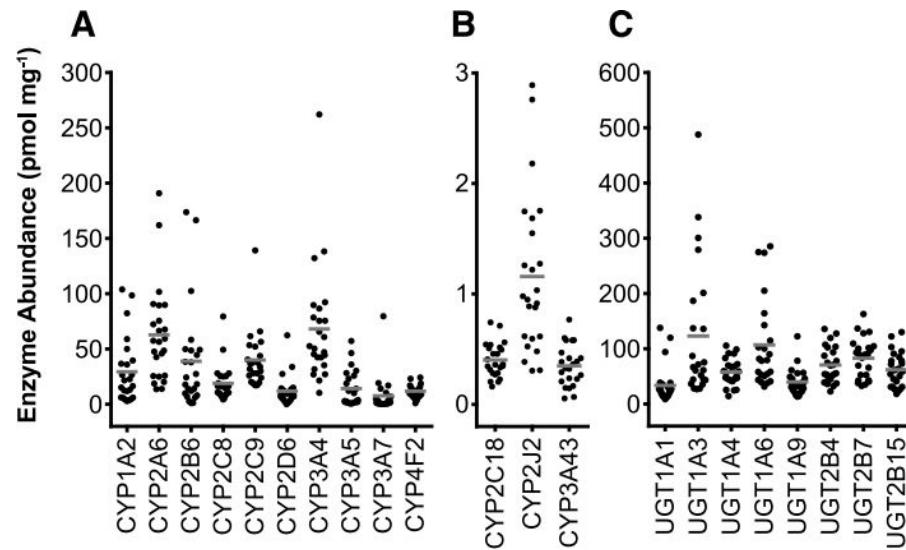


FIGURE 5-3. Graphic representation of the different forms of human cytochrome-P450 enzyme (circles) with different but often overlapping substrate specificities. The arrows indicate the single metabolic pathways. Representative substrates are listed above each enzyme.

Fig. 2. A scatter plot of the measured abundance values of P450 (A and B) and UGT (C) enzymes. The number of samples is 24 for each enzyme except CYP2C9, CYP3A5, CYP3A7, CYP3A43, UGT1A3, UGT1A4, and UGT1A6 ($n = 23$). Lines indicate population means of the sets of data.

Pharmacogenomics

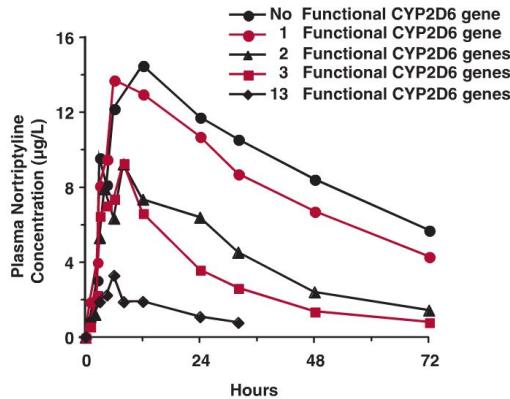


FIGURE 13-2. Strong genetic influence in the pharmacokinetics of nortriptyline is clearly demonstrated by the high correlation between the plasma concentration–time profile and the number of functional CYP2D6 genes possessed by an individual; the larger the number of functional genes, the higher is the clearance and the lower is the exposure profile following a single 25-mg dose of nortriptyline. (From: Dalén P, Dahl ML, Bernal Ruiz ML, et al. 10-Hydroxylation of nortriptyline in white persons with 0, 1, 2, 3, and 13 functional CYP2D6 genes. *Clin Pharmacol Ther* 1998;63:444–452.)

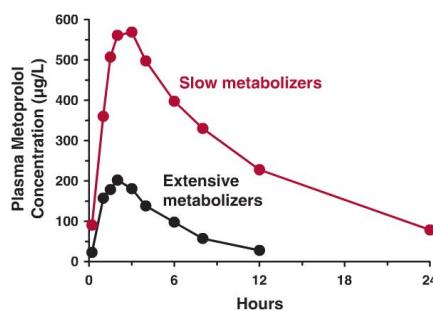


FIGURE 13-3. Plasma metoprolol concentrations after a single oral dose of 200-mg metoprolol tartrate were much higher in poor (colored line) than in extensive (black line) CYP2D6 metabolizers. Because metoprolol is a drug of high hepatic clearance, the difference between poor and extensive metabolizers is expressed in the large difference in oral bioavailability, because of differences in first-pass hepatic loss. (From: Leonard MS, Silas JH, Freestone S, et al. Oxidative phenotype—a major determinant of metoprolol metabolism and response. Reprinted by permission of *New Eng J Med* 1982;307:1558–1560.)

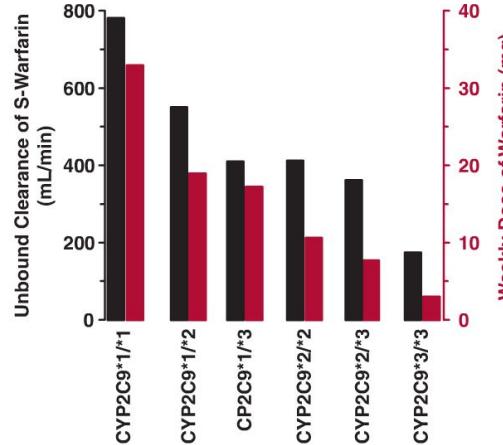
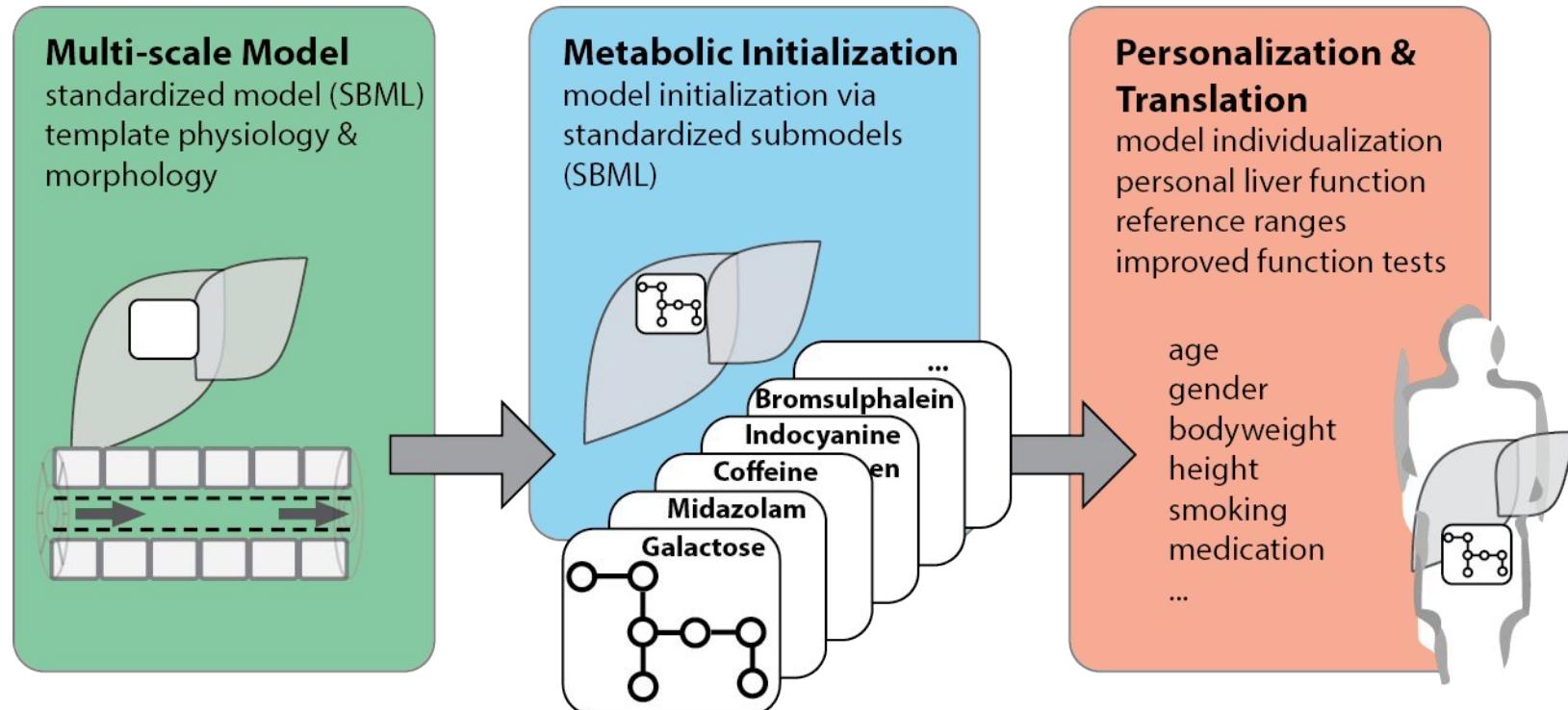
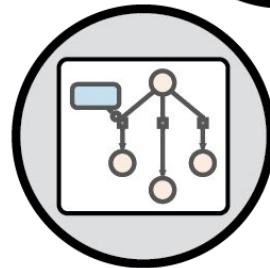
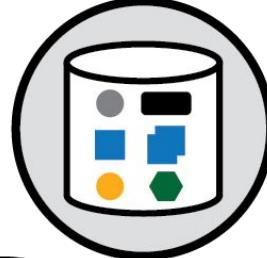


FIGURE 13-4. Genetics plays a significant role in the maintenance dose requirement of warfarin used in the treatment of various cardiovascular diseases. Shown are the unbound clearance of S-warfarin (black) in groups of patients with different CYP2C9 genotypes, all titrated and stabilized to a narrow target INR (International Normalization Ratio) range, a measure of anticoagulation, of between 2 and 3, and the mean weekly maintenance dose (obtained by summing the daily dose over 1 week, in color). Warfarin is administered as the racemate, with most of the therapeutic effect associated with the more active S-isomer, which is primarily eliminated by CYP2C9-catalyzed metabolism. Homozygous patients with two wild-type alleles (denoted by CYP2C9*1/*1) have the highest S-warfarin clearance and require the highest maintenance dose, and those with two of the most deficient alleles (CYP2C9*3/*3) have the lowest clearance and need the smallest maintenance dose. Heterozygous patients have intermediate clearance. However, as noted in Fig. 12-4 (Chapter 12, *Variability*), in addition to pharmacokinetic variability, there is also considerable interindividual variability in pharmacodynamics of this compound. (From: Scordo MG, Pengo V, Spina E, et al. Influence of CYP2C9 and CYP2C19 genetic polymorphisms of warfarin maintenance dose and metabolic clearance. *Clin Pharmacol Ther* 2002;72:702–710.)

Modeling dynamical liver function tests

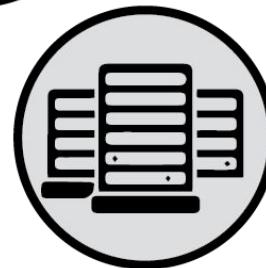


Standardized
Data Software for
modeling

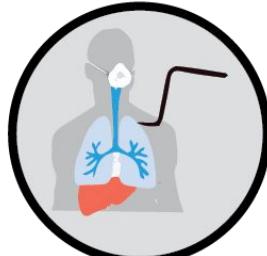


Reproducible
models

LIVER
FUNCTION

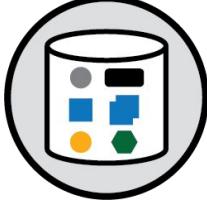


Compute
Infrastructure

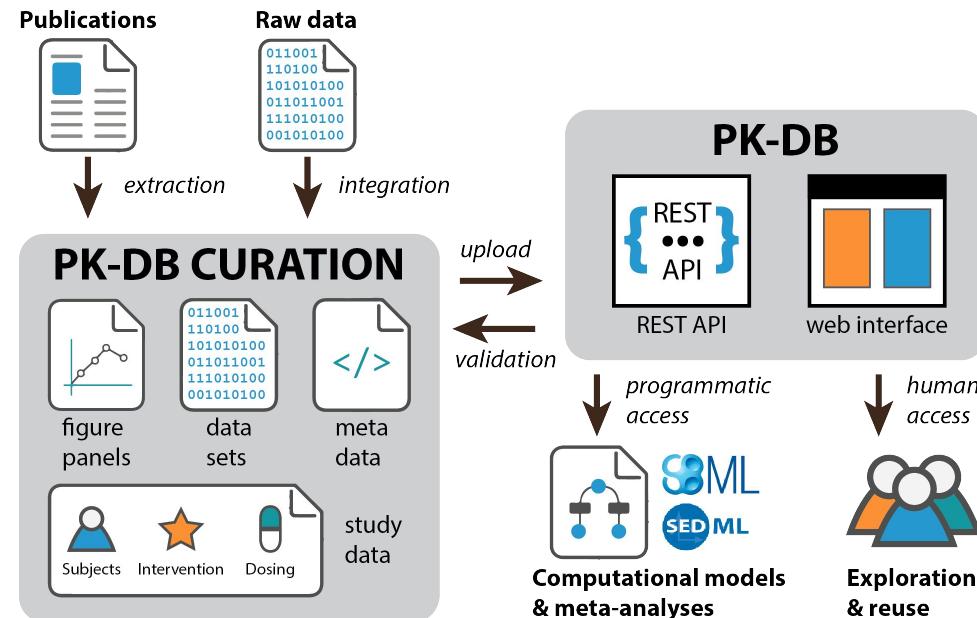


Applications

Standardized
Data



Pharmacokinetics database (PK-DB)

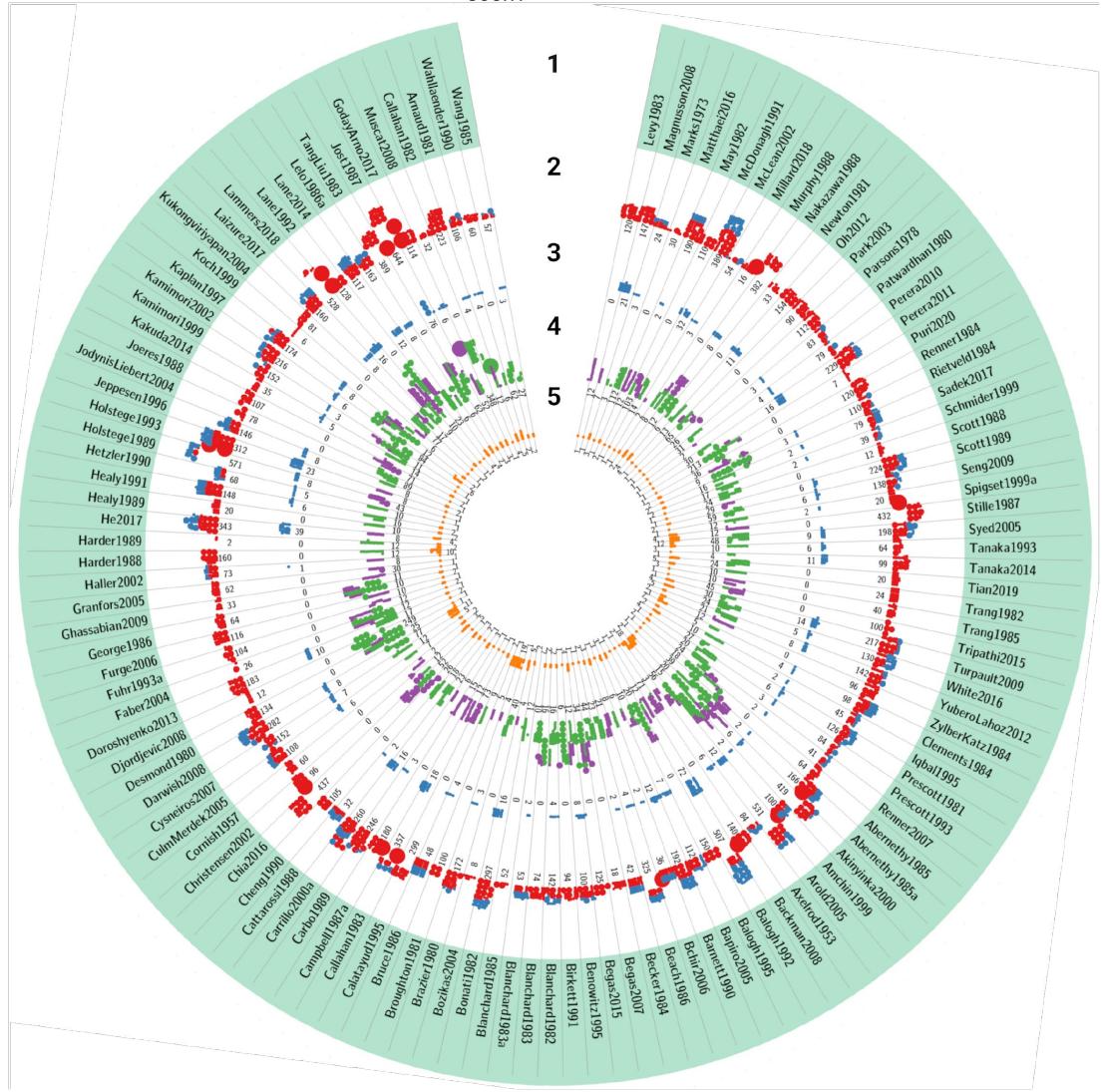


Grzegorzewski J, Brandhorst J, Green K, Eleftheriadou D, Duport Y, Barthorsch F, Köller A, Ke DYJ, De Angelis S, König M.

PK-DB: pharmacokinetics database for individualized and stratified computational modeling.

Nucleic Acids Res. 2021 Jan 8;49(D1):D1358-D1364. doi: [10.1093/nar/gkaa990](https://doi.org/10.1093/nar/gkaa990).
PMID: 33151297; PMCID: PMC7779054.

<https://pk-db.com>

1 STUDY**2** OUTPUT COUNT**3** TIMECOURSE COUNT**4** SUBJECT COUNT**5** INTERVENTION COUNT

549

Studies

1614

Groups

7613

Individuals

1599

Interventions

77844

Outputs

3653

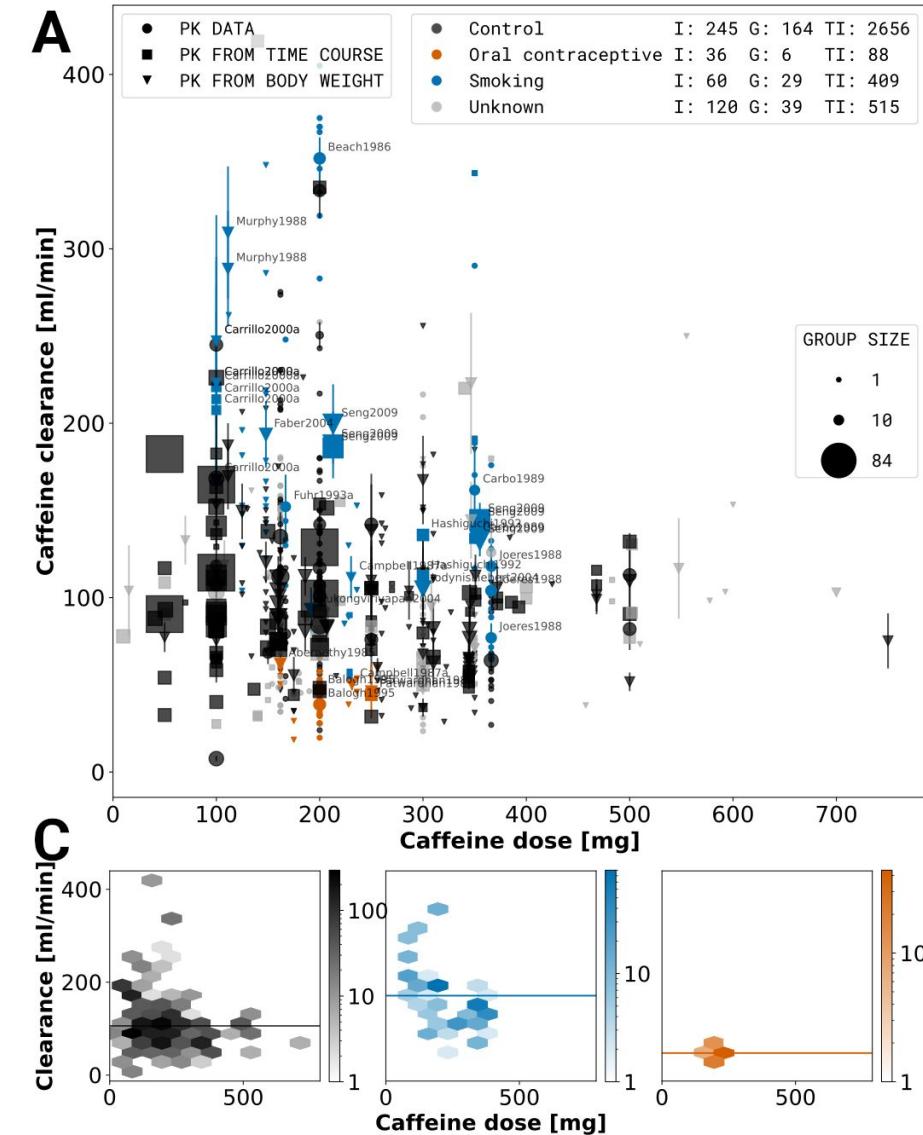
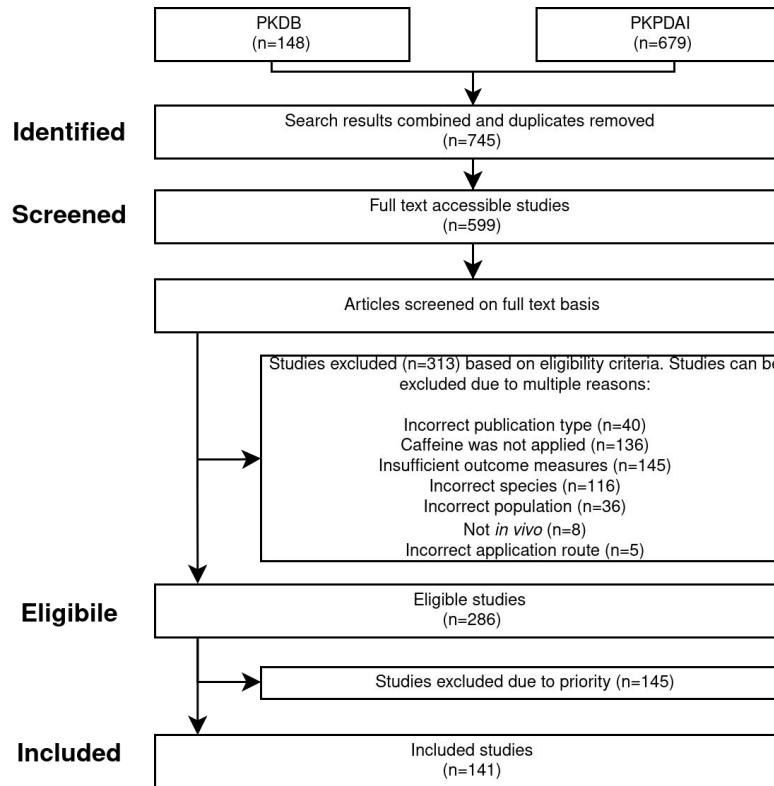
Timecourses

81

Scatters

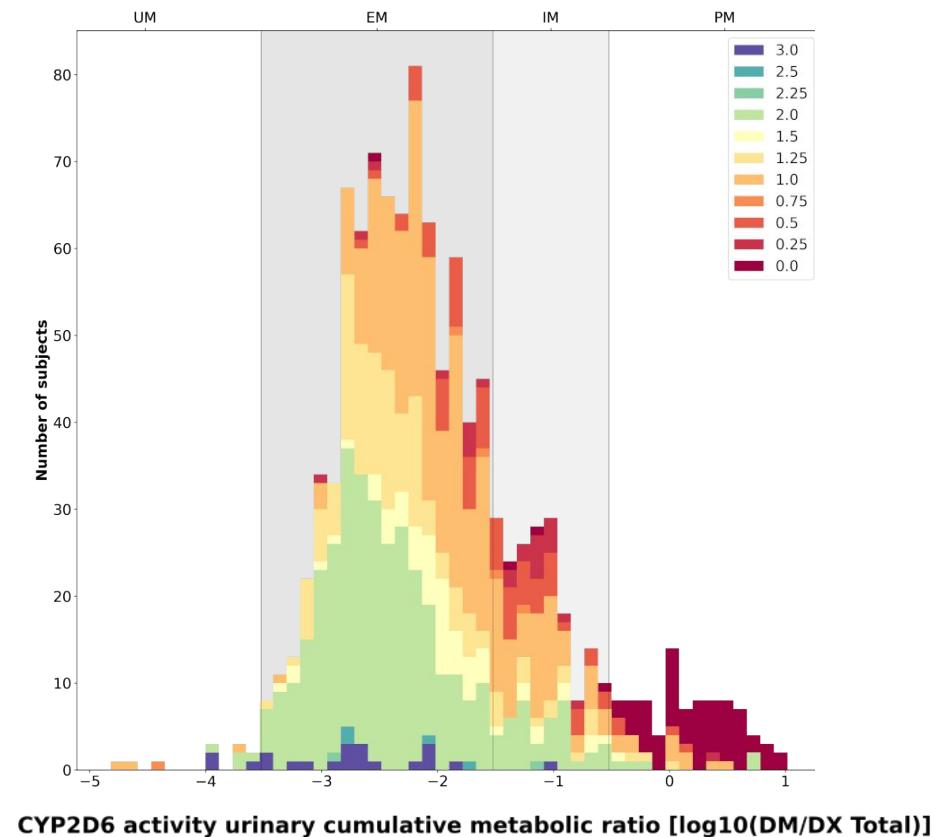
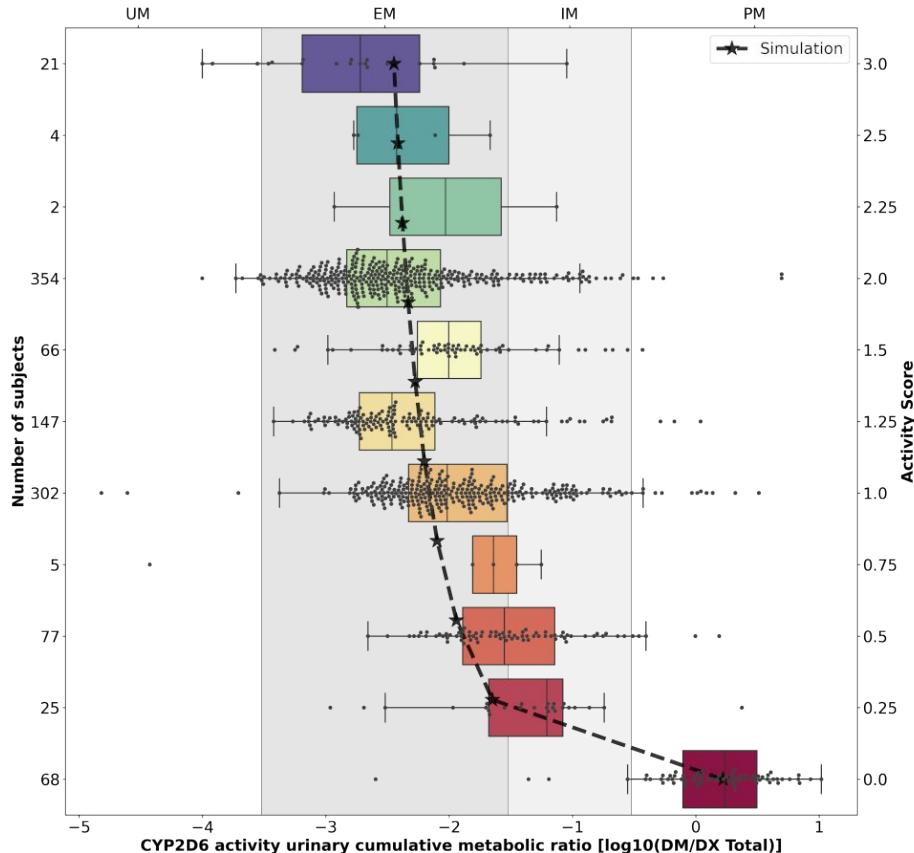
Lifestyle factors (caffeine)

- **Stratification into subgroups**
depending on smoking and/or oral contraceptive use

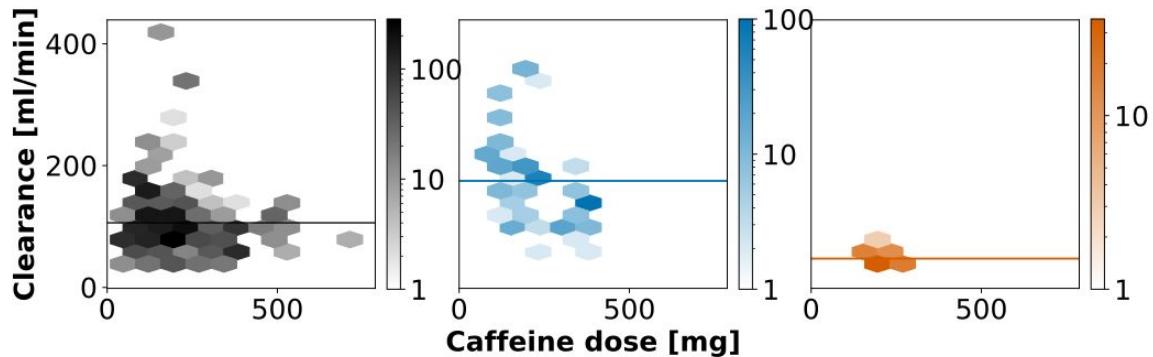
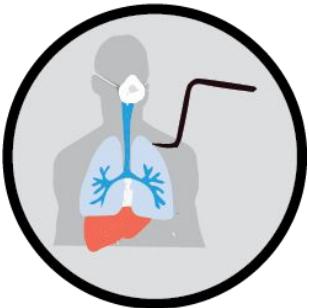


Genetic variants (CYP2D6)

- **Stratification into subgroups** depending on genetic variants & copy numbers (dextromethorphan)



Applications



Caffeine

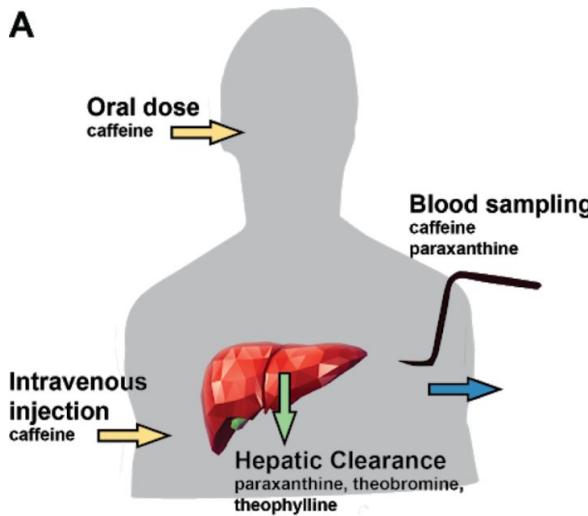
Stratified/personalized predictions by accounting for lifestyle & medication

Cooperation Partners

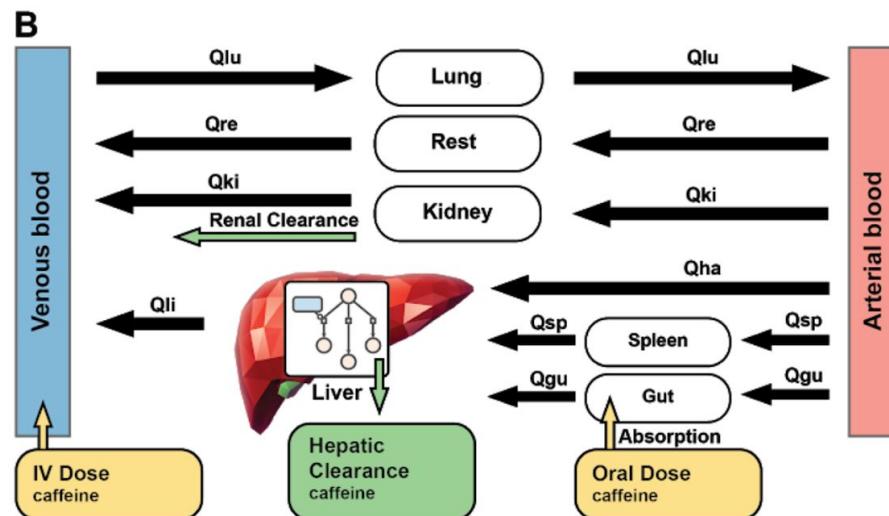
- Clinical partners; Dr. Hofmann & Prof. Schwab

Physiologically based caffeine model

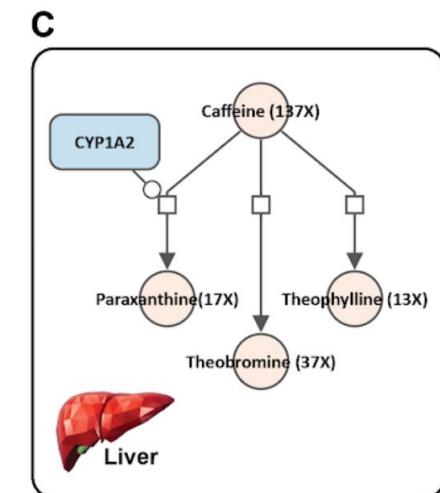
A



B



C

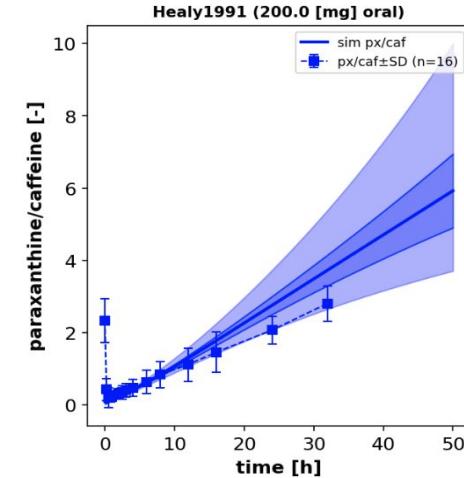
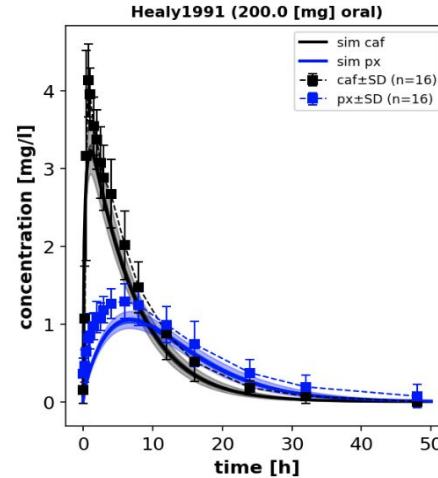
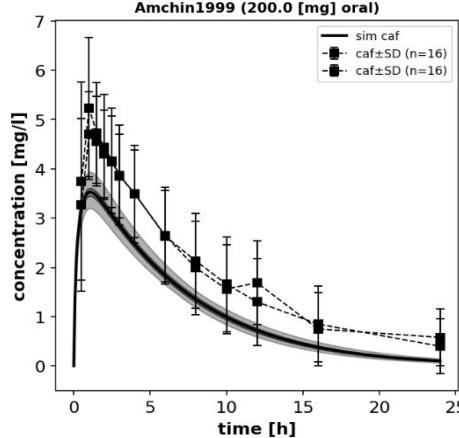
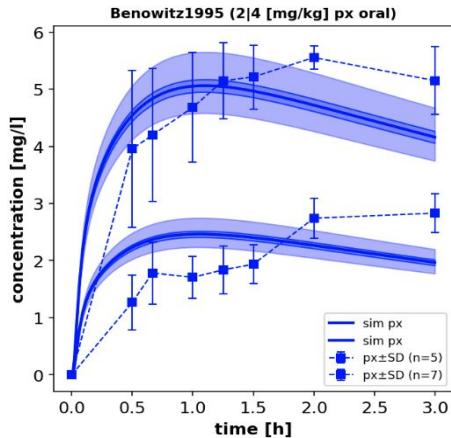
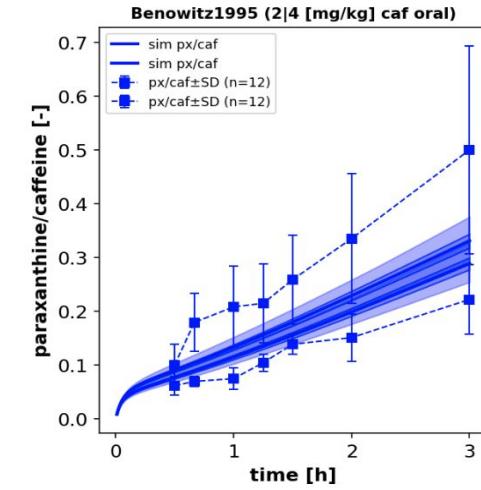
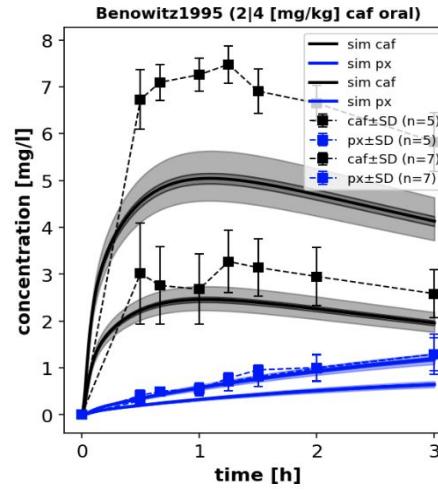
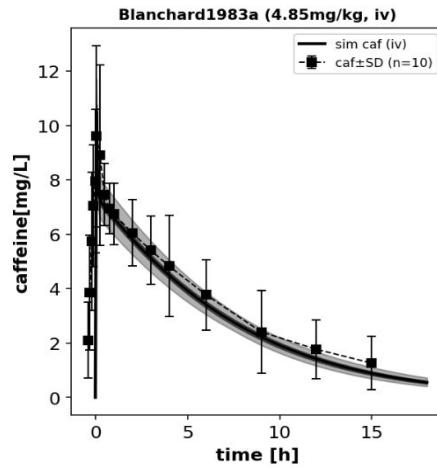
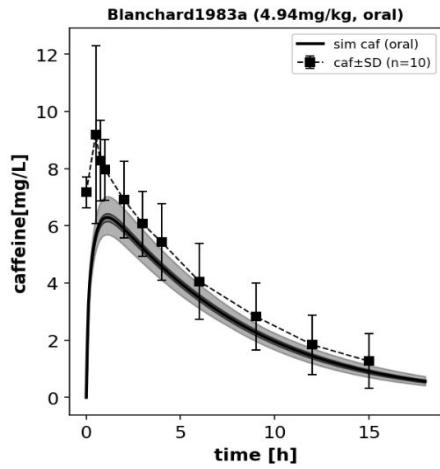


- Caffeine metabolized by **CYP1A2** to paraxanthine,
- Classical liver function test
 - Time course of caffeine
 - Caffeine/paraxanthine ratio

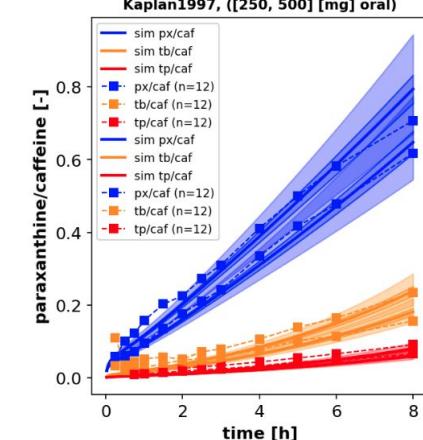
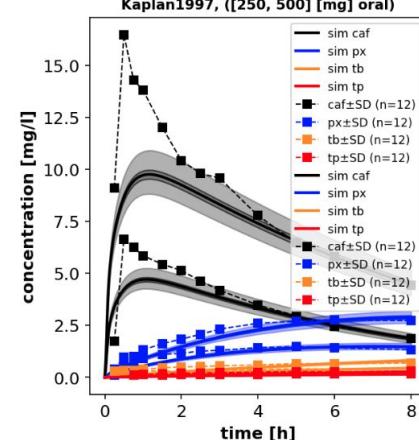
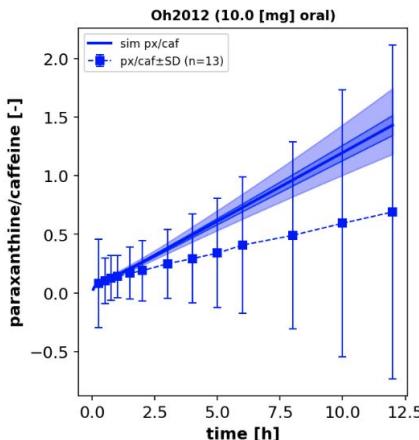
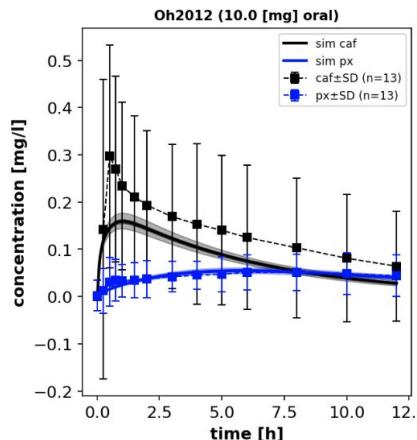
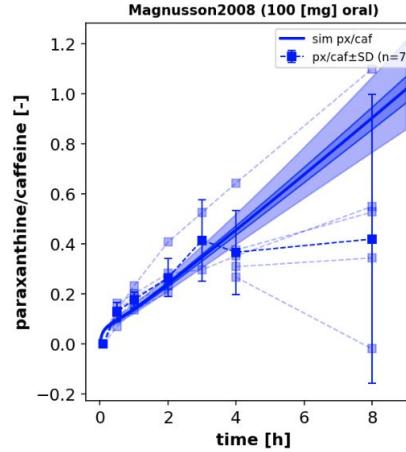
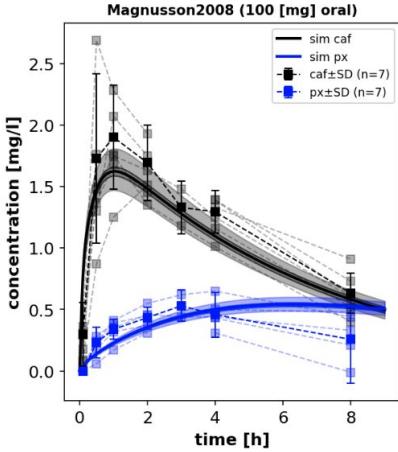
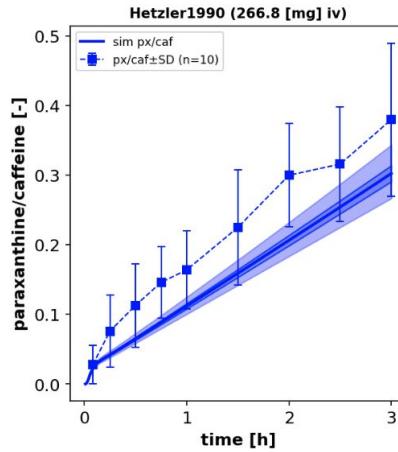
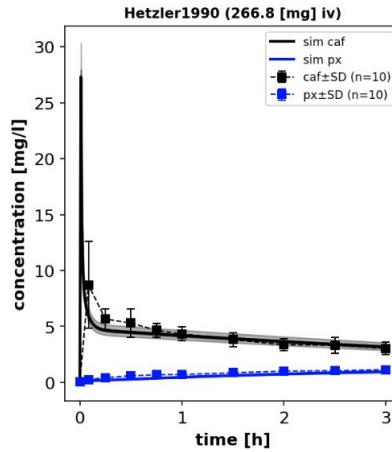
Challenges

- Large inter-subject variability
 - Effects of lifestyle on expression (induction smoking)
 - Effects of medication (oral contraceptives)
- Dose dependency

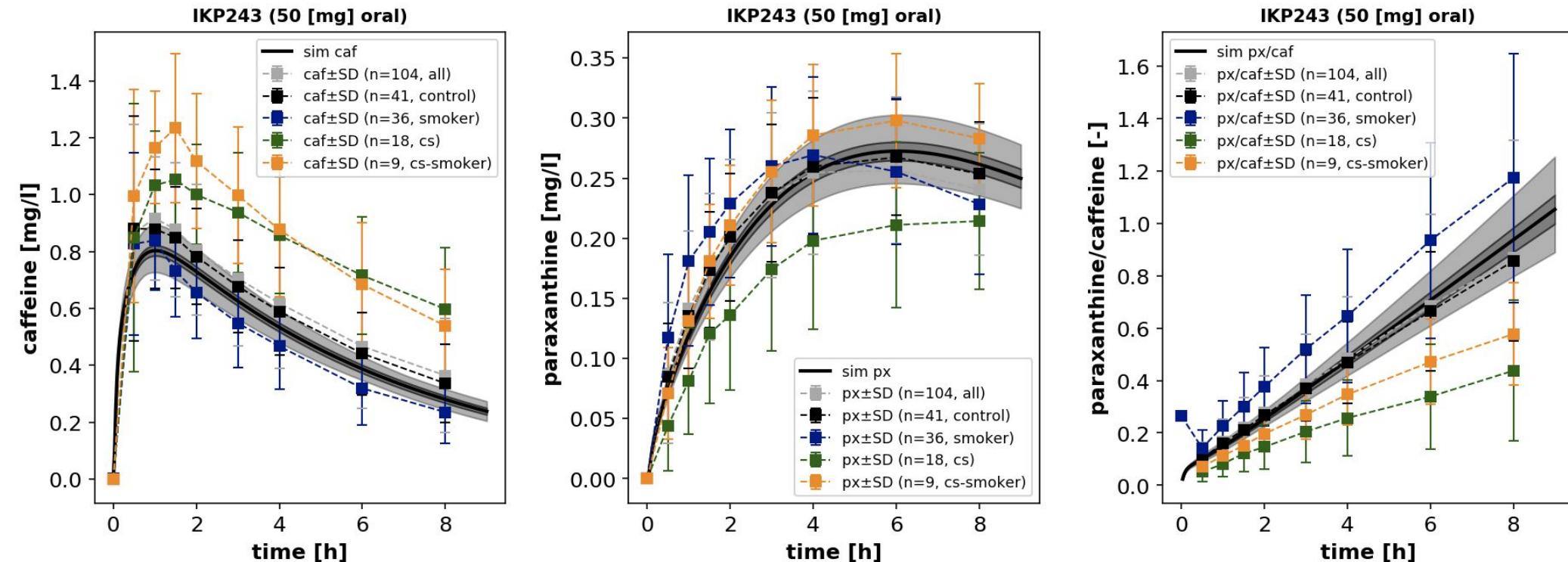
Model performance (training)



Model performance II (training)

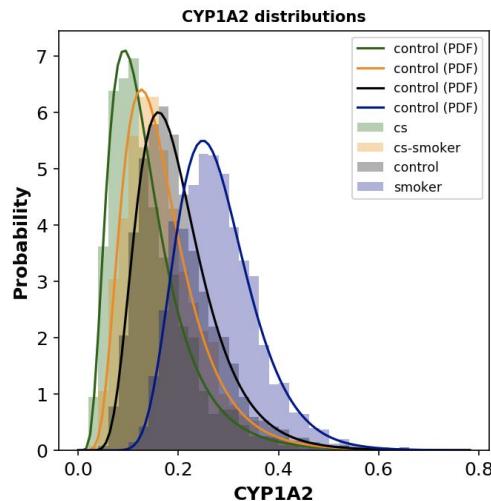


Stratification by smoking & contraceptives

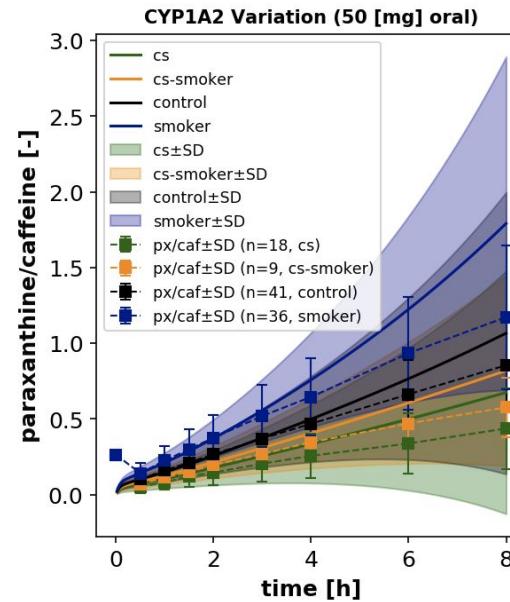
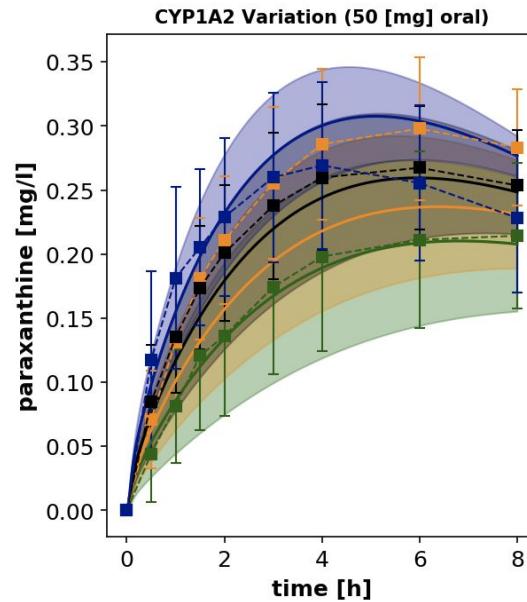
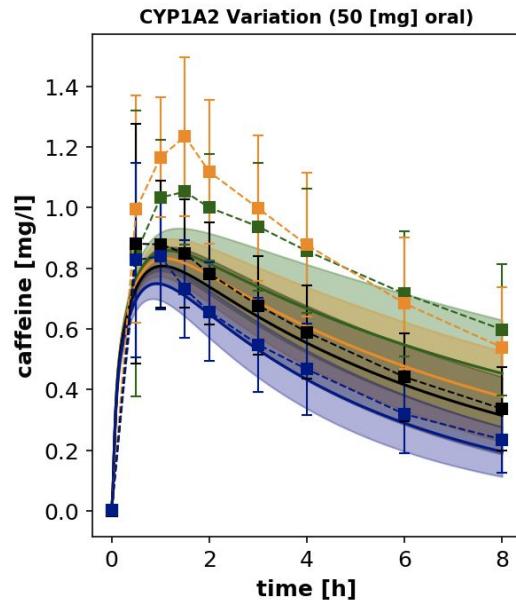


contraceptives (cs)
contraceptives-smoker (cs-smoker)
control
smoker

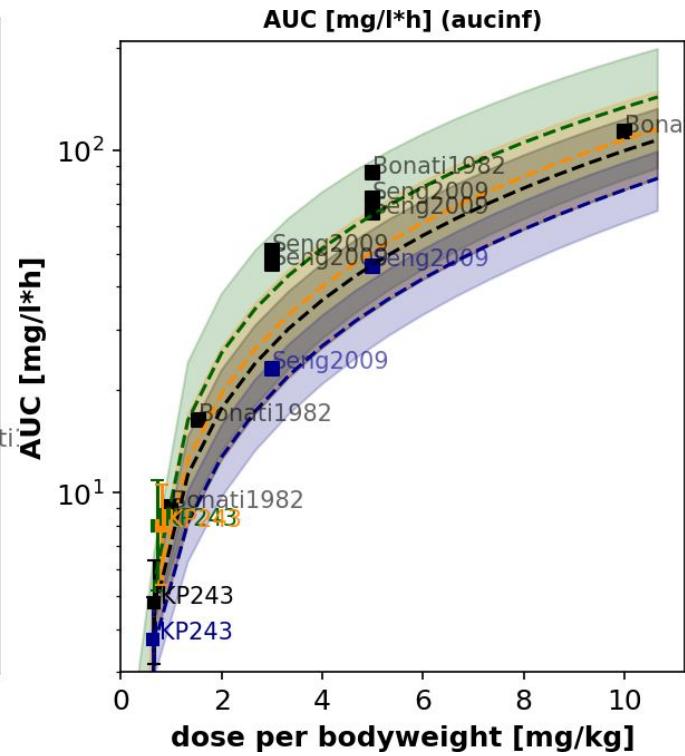
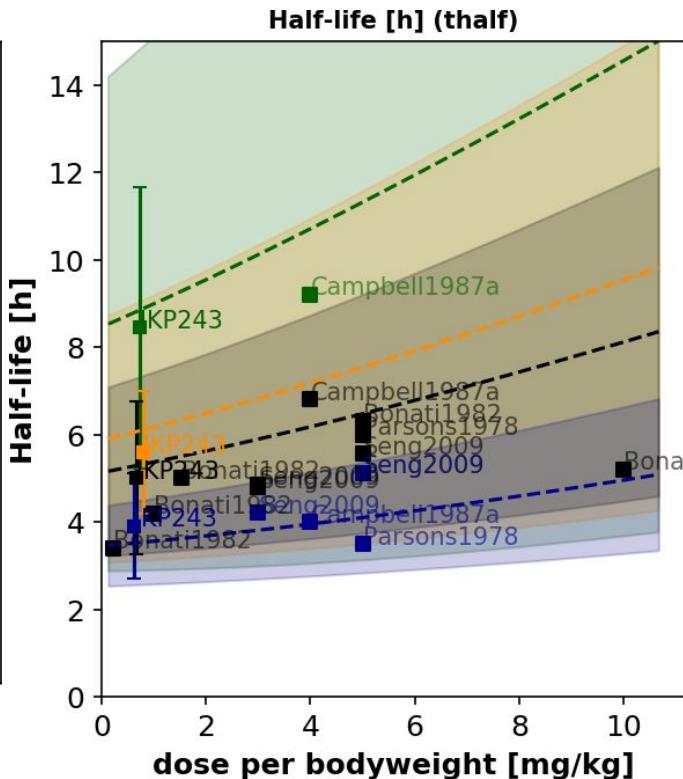
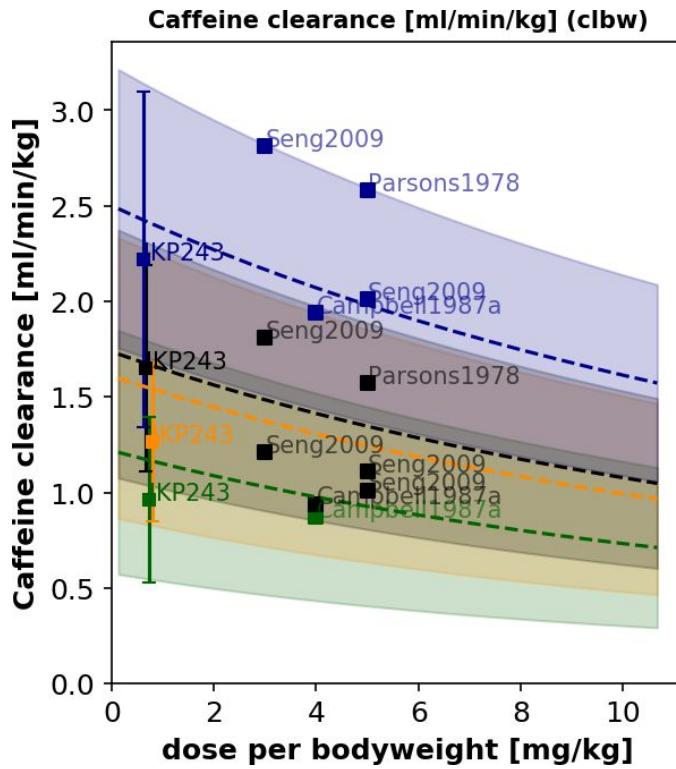
CYP1A2 distributions



contraceptives (cs)
contraceptives-smoker (cs-smoker)
control
smoker

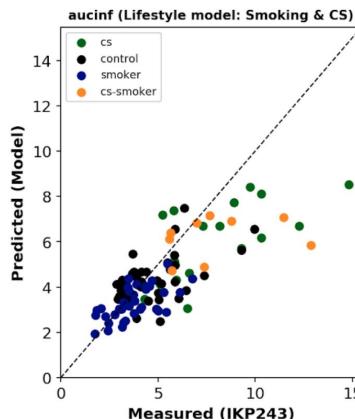
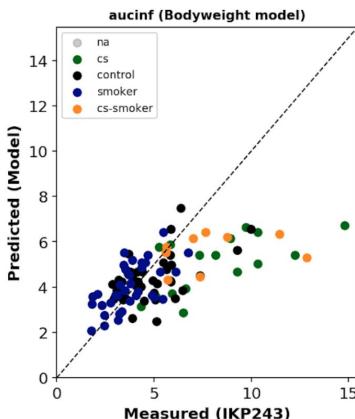
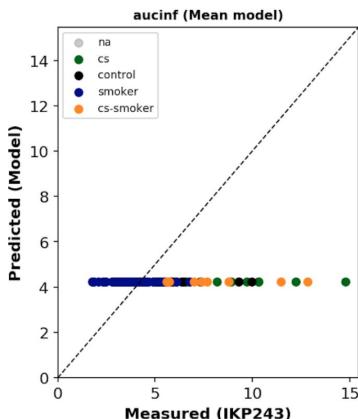
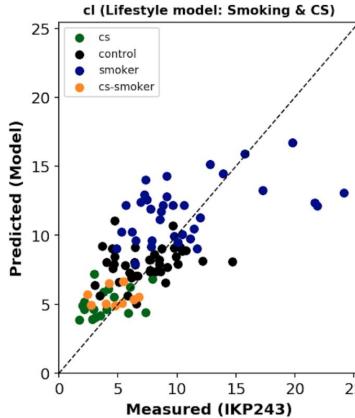
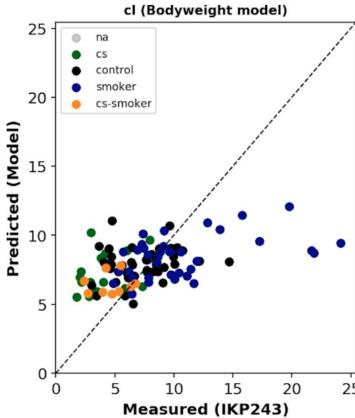
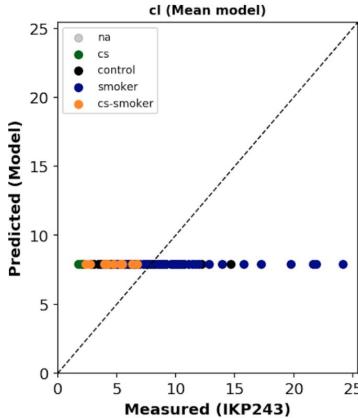


Stratified dose-dependent pharmacokinetics (validation)



Individualized predictions

Clearance



mean

anthropometric

lifestyle



contraceptives (cs)

contraceptives-smoker (cs-smoker)

control

smoker

- Improved predictions of pharmacokinetic parameters by account for individual lifestyle factors (smoking)

- Results directly transfer to all drugs metabolized via CYP1A2

CYP1A2 & caffeine pharmacokinetics

- CYP1A2 expression altered by many lifestyle factors
- Strong effect: **Smoking**
- Altered function test results

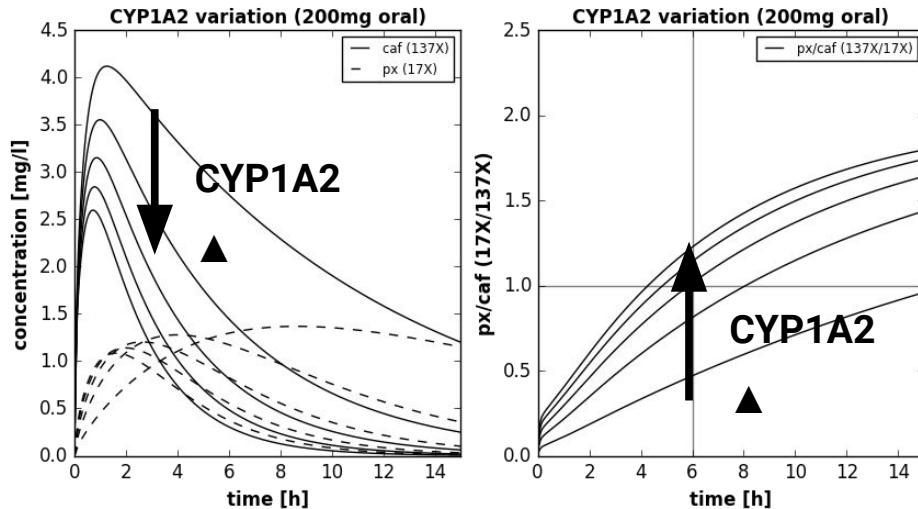


Table 4. Parameter estimates of covariates obtained for logarithmic clearance values using the paraxanthine/caffeine ratio method (equation 1)

Covariate	Symbol used in equation 5	Estimate	95% Confidence interval		Mean resulting change of clearance (factor)
			Lower bound	Upper bound	
—	Intercept	0.264	-0.015	0.542	—
Coffee intake (litre day ⁻¹)	Slope _{coffee}	0.368	0.287	0.449	1.445
Body mass index (kg m ⁻²)	Slope _{BMI}	-0.010	-0.018	-0.002	0.990
Cigarettes/day					
Non-smokers	$V_{smoking\ habit\ index}$	0	—	—	Reference
1–5		0.195	0.065	0.324	1.215
6–10		0.383	0.253	0.509	1.467
11–20		0.504	0.386	0.621	1.655
>20		0.543	0.430	0.655	1.721
Oral contraceptives					
No	$V_{oral\ contraceptive\ index}$	0	—	—	Reference
Yes		-0.332	-0.236	-0.428	0.717
Country					
Germany	$V_{country\ of\ residence\ index}$	0	—	—	Reference
Bulgaria		-0.209	-0.356	-0.061	0.811
Slovakia		-0.303	-0.450	-0.156	0.739
Sex					
Male	$V_{sex\ index}$	0	—	—	Reference
Female		-0.111	-0.178	-0.044	0.895

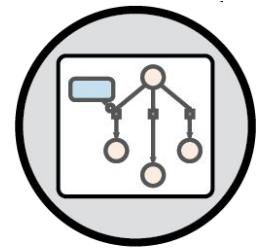
CYP1A2 induction ▲

- Clearance ▲
- kel ▲
- T_{1/2} ▼
- T_{max} ▼
- px(17X)/caf(137X) ▲

Software for
modeling



Modelling Tools, Software, Workflows & Standardization



Reproducible
models

Version control

GitHub is a code hosting platform for version control and collaboration. It lets you and others work together on projects from anywhere.

Version control

- Diffs & Branches

Collaborative editing

- Pull requests

Continuous integration

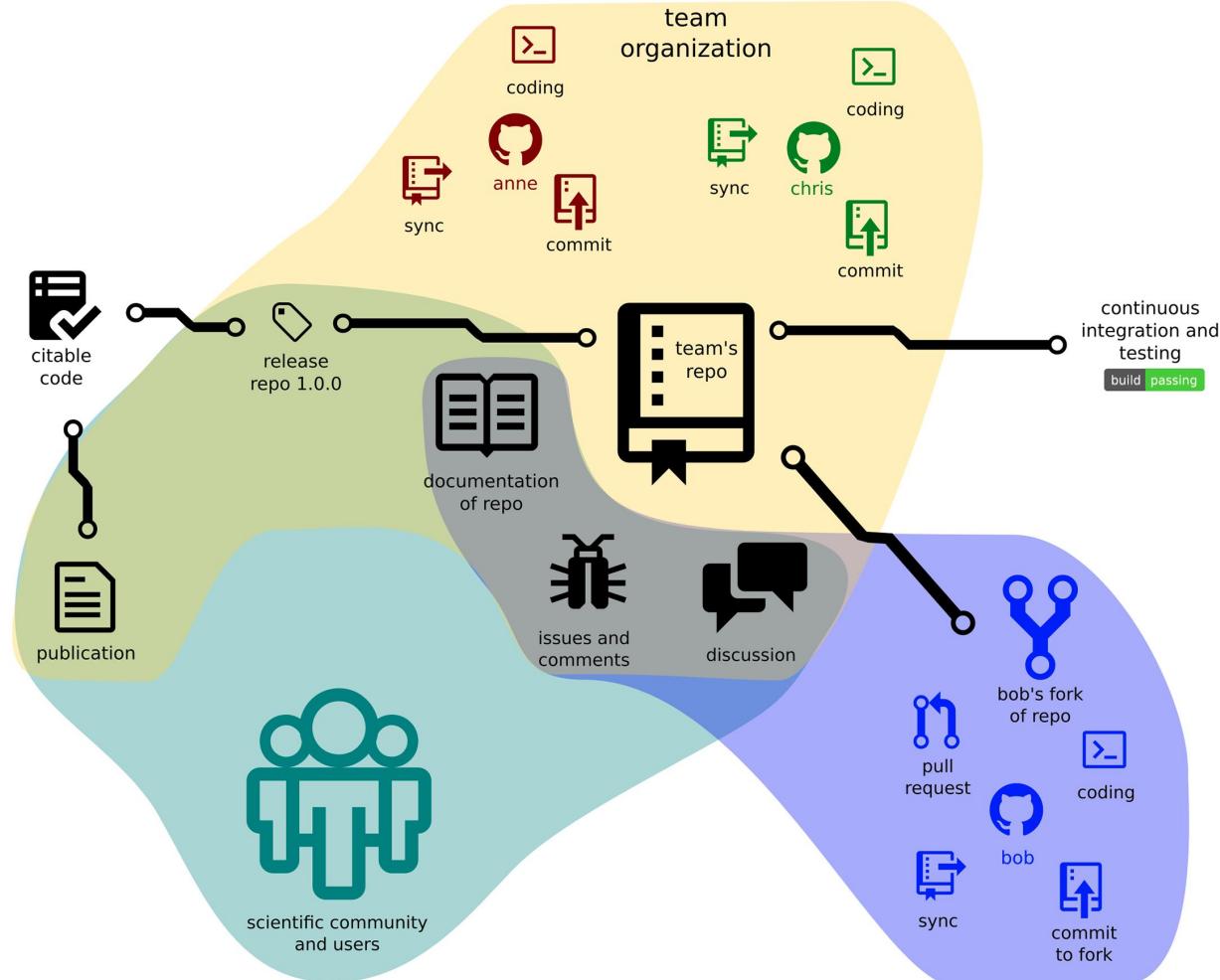
- unit tests

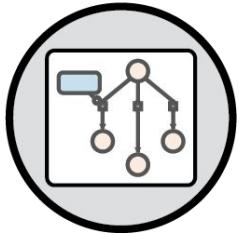
- Commit hooks

Releases & snapshots (citable code)

Issue tracker

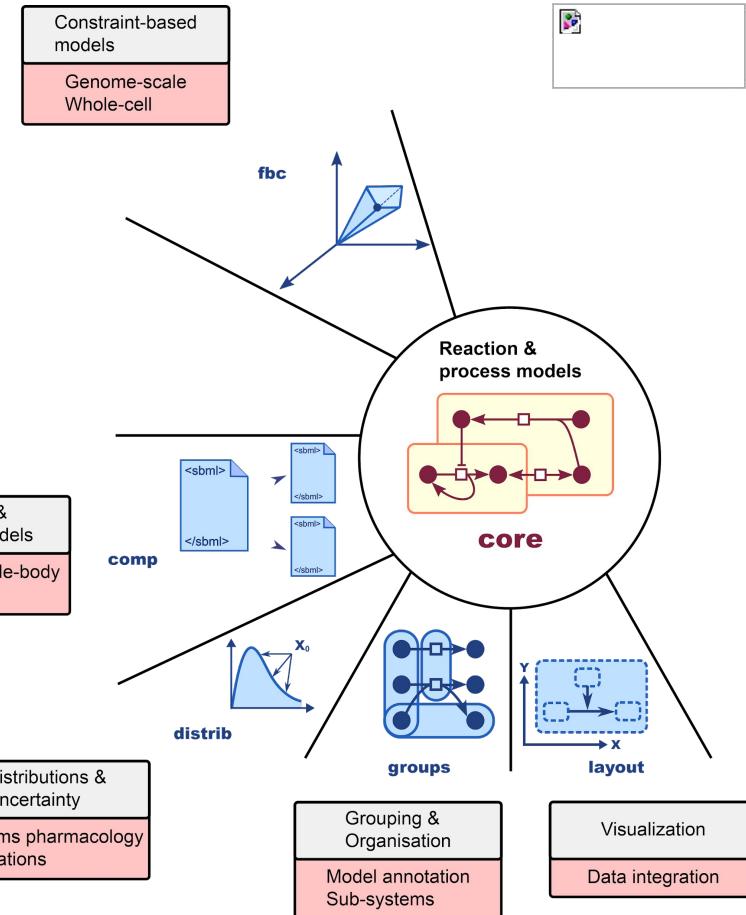
Work anywhere & offline





Standardization

- Reproducible & exchangeable model encoding (**SBML**)
- Annotations to modelling, biological and medical ontologies (**SBML core**)
- Hierarchical models/multi-scale models (**SBML comp**)
- Automatic unit validation
- Distributions in models & uncertainty in data and parameters (**SBML distrib**)
- Mass- & charge balance (**SBML fbc**)
- **Use wide range of tools** (visualization, parameter fitting, simulation, ...)



The Systems Biology Markup Language (SBML): Language Specification for Level 3 Version 2 Core

M. Hucka, F. Bergmann, C. Chaouiya, A. Dräger, S. Hoops, S. Keating, **M. König**, N Le Novère, C. Myers, B. Olivier, S. Sahle, J. Schaff, R. Sheriff, L. Smith, D. Waltemath, D. Wilkinson, F. Zhang, **J Integr Bioinform**. 2019 [accepted]

Simulation experiment description markup language (SED-ML) level 1 version 3 (L1V3).
Bergmann FT., Cooper J, **König M**, Ion Moraru I., Nickerson D., Le Novère N., Olivier BG., Sahle S., Smith L., and Waltemath D, **J Integr Bioinform** 2018, 3

Harmonizing semantic annotations for computational models in biology
Neal, **König**, Nickerson, Misirli, Kalbasi, Dräger, ..., Waltemath
Brief Bioinform. 2018 Nov 21. doi: 10.1093/bib/bby087

```
// -- Begin Antimony block converted from MAPKcascade.xml
// Created by libAntimony v2.9.3
model1 *MAPKcascade()
...
// Reactions:
J0: MKKK => MKKK_P; J0_V1*MKKK/((1 + (MAPK_PP/J0_Ki)^J0_n)*(J0_K1 + MKKK));
J1: MKKK_P => MKKK; J1_V2*MKKK_P/(J1_KK2 + MKKK_P);
J2: MKK => MKK_P; J2_K3*MKKK_P*MKK/(J2_KK3 + MKK);
J3: MKK_P => MKK_PP; J3_k4*MKKK_P*MKK_P/(J3_KK4 + MKK_P);
J4: MKK_PP => MKK_P; J4_V5*MKKK_PP/(J4_KK5 + MKK_PP);
J5: MKK_P => MKK; J5_V6*MKKK_P/(J5_KK6 + MKK_P);
J6: MAPK => MAPK_P; J6_K7*MKKK_PP+MAPK/(J6_KK7 + MAPK);
J7: MAPK_P => MAPK_PP; J7_K8*MKKK_PP+MAPK_P/(J7_KK8 + MAPK_P);
J8: MAPK_PP => MAPK_P; J8_V9*MAPK_PP/(J8_KK9 + MAPK_PP);
J9: MAPK_P => MAPK; J9_V10*MAPK_P/(J9_KK10 + MAPK_P);
...
end
// -- End Antimony block

// -- Begin PhraSEDML block converted from main.xml
// Created by libphrasedml v1.0.7
// Models
model1 = model "MAPKcascade"

// Simulations
sim1 = simulate uniform(0, 4000, 1000)

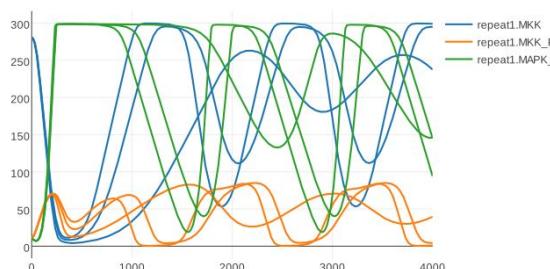
// Tasks
task1 = run sim1 on model1

// Repeated Tasks
repeat1 = repeat task1 for model1.J1_KK2 in [1, 10, 40], reset=true

// Outputs
plot "Sampled Simulation" repeat1.time vs repeat1.MKK, repeat1.MKKK_P, repeat1.MAPK_PP
// -- End PhraSEDML block
```



Sampled Simulation



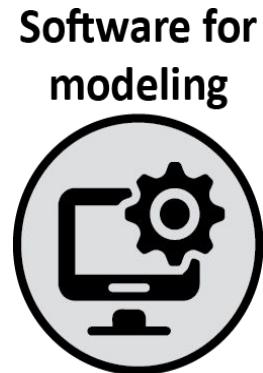
Simulation & Analysis

- **roadrunner:** high performance SBML simulator
 - Compile to machine code, cluster-ready
- **tellurium:** python based modeling environment for SBML models

libRoadRunner: a high performance SBML simulation and analysis library.
 Somogyi, Bouteiller, Glazier, **König**, Medley, Swat, Sauro.
Bioinformatics. 2015

Tellurium Notebooks - An Environment for Dynamical Model Development, Reproducibility, and Reuse
 Medley K, Choi K, **König M**; Smith L, Gu S, Joseph Hellerstein, Sealfon S., Sauro HM.
PLoS, Comp. Bio. 2018

Tellurium: An Extensible Python-based Modeling Environment for Systems and Synthetic Biology
 K Choi, JK Medley, **M König**, K Stocking, L Smith, S Gua, HM Sauro
Biosystems. 2018 Jul 24. pii: S0303-2647(18)30125-4.



Visualization

Session: /home/mkoenig/git/cy3sbml/src/main/resources/sessions/Koenig_demo_10.cys

File Edit View Select Layout Apps Tools Help

Control Panel Network Nodes Edges

Koenig_demo_10

Main: Koenig_demo_10 36(0) 69(0)

Koenig_demo_10 13(0) 14(0)

Main: Koenig_demo_10 36(0) 69(0)

Main: Koenig_demo_10 13(0) 14(0)

Enter search term...

Koenig_demo_10 Main: Koenig_demo_10

Results Panel cy3sbml Model : Koenig_demo_10 (Koenig_demo_10) L3V1 Koenig Demo Metabolism Description This is a demonstration model in SBML format. The content of this model has been carefully created in a manual research effort. This file has been produced by Matthias Koenig. Terms of use Copyright © 2016 Matthias Koenig. Redistribution and use of any part of this model, with or without modification, are permitted provided that the following conditions are met: 1. Redistributions of this SBML file must retain the above copyright notice, this list of conditions and the following disclaimer. 2. Redistributions in a different form must reproduce the above copyright notice, this list of conditions and the following disclaimer in the documentation and/or other materials provided with the distribution. This model is distributed in the hope that it will be useful, but WITHOUT ANY WARRANTY; without even the implied warranty of MERCHANTABILITY or FITNESS FOR A PARTICULAR PURPOSE.

Cell

A bA (A import) v3 (C → A) v1 (A → B) v2 (A → C) v4 (C → B) B bB (B export) C bC (C export)

Diagram showing a metabolic network with three compartments: A, B, and C. Compartment A contains metabolites v1, v2, v3, v4, and v5. Compartment B contains metabolite v6. Compartment C contains metabolites v7, v8, v9, and v10. Reactions include v1 (A → B), v2 (A → C), v3 (C → A), v4 (C → B), and v5 (B → C). Transport reactions include bA (A import) from compartment A to compartment B, bB (B export) from compartment B to compartment A, and bC (C export) from compartment C to compartment B. External components include v1, v2, v3, v4, v5, v6, v7, v8, v9, v10, Km_A, Km_B, Km_C, Vmax_A, Vmax_B, Vmax_C, and scaling factor p.

Table Panel f(x)

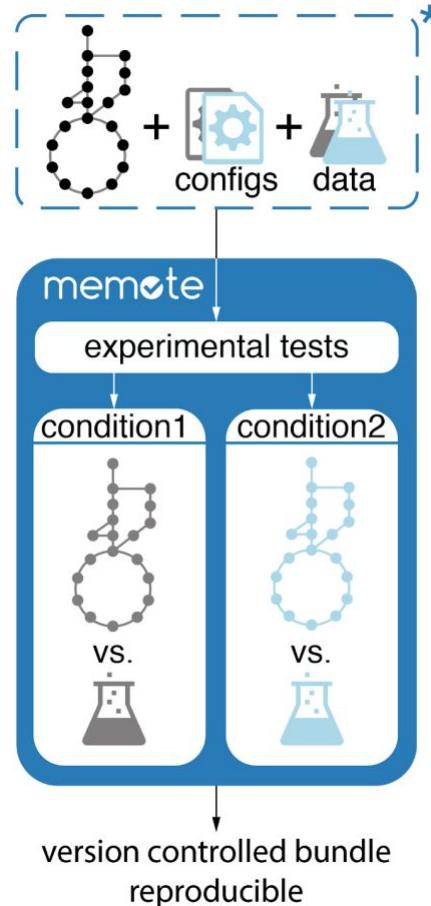
shared name	name	id	sbo	metaid	biomodels.sbo	go	fma	label	value	units	derivedUnits	constant
external compartment	external c...	e	compartment	SBO:0000...	meta_22d897...	GO:0005...	FMA:70022...	external co...	1.0E-6	m3	m^3	<input type="checkbox"/>
cell compartment	cell comp...	c	compartment	SBO:0000...	meta_78b0e7...	GO:0005...	FMA:86846...	cell compar...	1.0E-6	m3	m^3	<input type="checkbox"/>
plasma membrane	plasma m...	m	compartment	SBO:0000...	meta_bcd47...	GO:0005...	FMA:63841...	plasma me...	1.0	m2	m^2	<input type="checkbox"/>
metabolic scaling factor	metabolic s...	scale_f	parameter	SBO:0000...	meta_c63c69...	SBO:000027		Km_C	3.0	µM	mol·km^(-3)	<input checked="" type="checkbox"/>
	Vmax_B	vmax_B	parameter	SBO:0000...	meta_871a28...	SBO:0000186		metabolic s...	1.0E-6	dimensionless	dimensionless	<input checked="" type="checkbox"/>
	Vmax_B	vmax_B	parameter	SBO:0000...	meta_a898f...	SBO:0000186		Vmax_B	2.0	µM_per_s	mol·s^(-1)	<input checked="" type="checkbox"/>
	Vmax_B	vmax_B	parameter	SBO:0000...	meta_351d07...	SBO:0000186		Vmax_B	2.0	µM_per_s	mol·s^(-1)	<input checked="" type="checkbox"/>
	Vmax_V2	vmax_V2	parameter	SBO:0000...	meta_074616...	SBO:0000186		Vmax_V2	5.0	µM_per_s	mol·s^(-1)	<input checked="" type="checkbox"/>
	Vmax_V3	vmax_V3	parameter	SBO:0000...	meta_1e2e9b...	SBO:0000186		Vmax_V3	0.5	µM_per_s	mol·s^(-1)	<input checked="" type="checkbox"/>
	Vmax_V1	vmax_V1	parameter	SBO:0000...	meta_78fe37...	SBO:0000186		Vmax_V1	1.0	µM_per_s	mol·s^(-1)	<input checked="" type="checkbox"/>
	Km_A	Km_A	parameter	SBO:0000...	meta_98f0e1...	SBO:000027		Km_A	1.0	µM	mol·km^(-3)	<input checked="" type="checkbox"/>
	Vmax_V4	vmax_V4	parameter	SBO:0000...	meta_20f045...	SBO:0000186		Vmax_V4	0.5	µM_per_s	mol·s^(-1)	<input checked="" type="checkbox"/>

Node Table Edge Table Network Table

Memory

Model building, quality checks & visualization

- **sbmlutils** – model building, annotation, reports
- **memote** - integrated testing for models and model checks
- **Cy3SBML** – model visualization (data integration)



*matthiaskoenig/sbmlutils: sbmlutils-v0.3.3
(Version v0.3.3)*

M. König. (2019, April 29). Zenodo.
<http://doi.org/10.5281/zenodo.2653495>

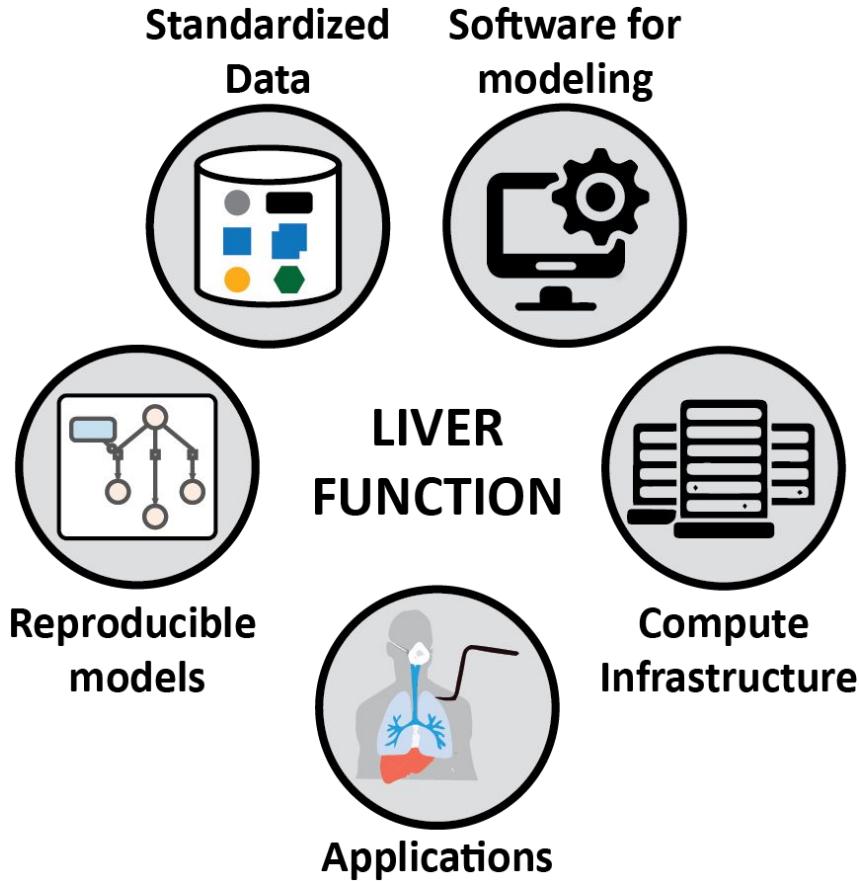
Memote: A community-driven effort towards a standardized genome-scale metabolic model test suite

C Lieven, M Beber, B Olivier, F Bergmann, M Ataman, P Babaei, J Bartell, L Blank, S Chauhan, K Correia, C Diener, A Dräger, B ..., **M. König**, S Klamt, E Klipp, ..., J Wodke, J Xavier, Q Yuan, M Zakhartsev, C Zhang
bioRxiv 350991; doi: 10.1101/350991 Nature Biotechnology [in revision]

*matthiaskoenig/cy3sbml: cy3sbml-v0.2.7
(Version v0.2.7)*

M. König, N. Rodriguez, A. Dräger (2017, November 12). Zenodo.
<http://doi.org/10.5281/zenodo.1145407>

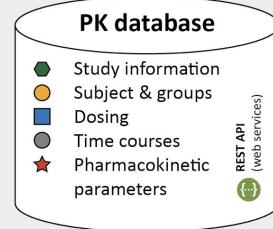
Summary & outlook



Interactive personalized pharmacokinetics models

Pharmacokinetics database

- pharmacokinetics data in standard format
- open source, open access, open data & FAIR
- integration in workflow via REST web services
- annotation to ontologies

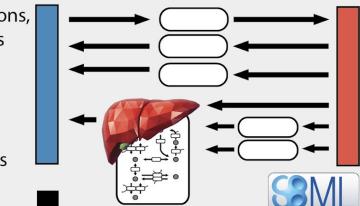


- Pharmacokinetics data for subgroups
- Pharmacokinetics data for individual subjects
- Workflow for data curation

Physiological based pharmacokinetics models

Standard medications, substances & drugs

- caffeine
- paracetamol
- omeprazole
- codeine
- liver function tests (LiMax, galactose)



- Curated and validated models for caffeine, paracetamol, galactose & methacetine
- Stratification & individualization of models
- Standardization (SBML)
- Tools for model building

Frontend

- Interactive computational models (web interface)
- Stratified & individualized simulations
- Integration of clinical data
- Providing view to different stakeholders



- High-performance SBML simulator (libroadrunner)
- Web simulation (tellurium-web)
- Simulation setups (SED-ML)
- Proof-of-principle for stratification & personalization

Patients

- Interactive exploration
- Introduction to pharmacokinetics
- Education (dose, timing, drug-drug interaction, halflife)



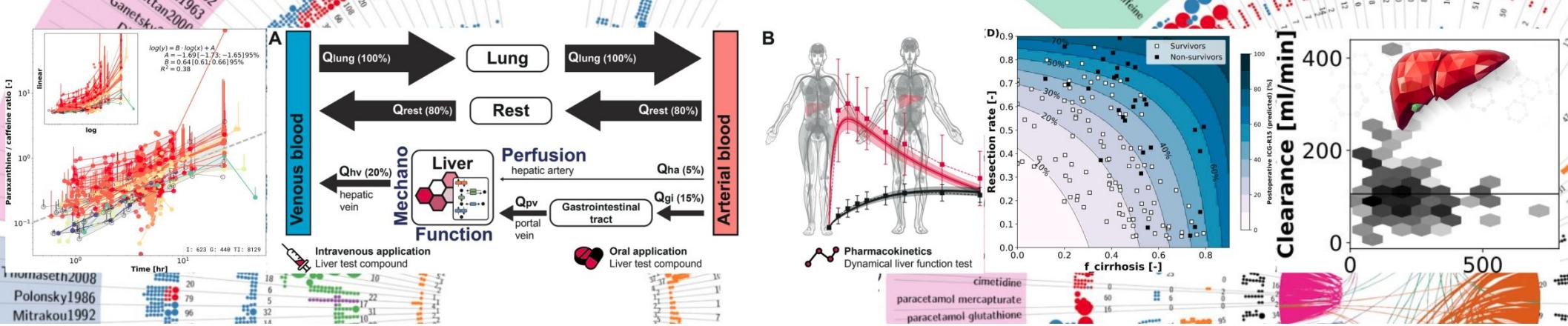
Health-care Professionals

- Risk predictions
- Sensitivities & Specificities, cutoffs
- drug-drug interactions
- Reports



Research

- testing of hypotheses
- sensitivity analysis
- export of models, simulation setups, data sets in standard formats
- improved liver function tests



Dr Matthias König, Systems Medicine of the Liver Lab, Humboldt-University Berlin
<https://livermetabolism.com>



Matthias König
metacetin, caffeine, glucose
Dynamical Liver Function Tests:
LiMAX and Methacetin Breath Test (CYP1A2)



Jan Grzegorzecki
codeine, morphine,
dextromethorphan
Drug-gene interactions.
Pharmacogenetics of CYP2D6 drugs



Yannick Duport
midazolam
Drug-drug interactions. Effect of Inhibitors and Inducers on midazolam clearance



Florian Bartsch
simvastatin, cholesterol
Dosing strategies;
pharmacodynamic effects



Adrian Köller
indocyanine green
Effect of perfusion, protein binding and liver disease (cirrhosis)



Kathleen Green
glucose
Whole-body glucose homeostasis



Janosch Brandhorst
paracetamol
PK model



Sara de Angelis
torasemide
PK/PD model (renal diuresis)



Danny Ke
diazepam,oxazepam
PK model (age & bodyweight)



Sükrü Balcisue
omeprazole
PK/PD model (stomach pH)



Dimitra Eleftheriadou
caffeine, codeine
Data curation



Deepa Maheshvare
glucose
Pancreas in glucose homeostasis

Paula Ogata
metoprolol
PK/PD model (heart rate)

Tutorial: Caffeine

1. Install libroadrunner as python library

pip install libroadrunner

or

conda install libroadrunner

2. Download & extract tutorial zip file

<https://bit.ly/pkpd-tutorial-2022>

3. Open tutorial notebook (jupyter or jupyter lab)

pkpd-tutorial.ipynb

4. Solutions

<https://github.com/matthiaskoenig/pkpd-course>