

Where AI and mechanistic PKPD modelling strengthen each other in drug development

Rob van Wijk | Leiden Drug Development Conference, Sept 19th, 2024



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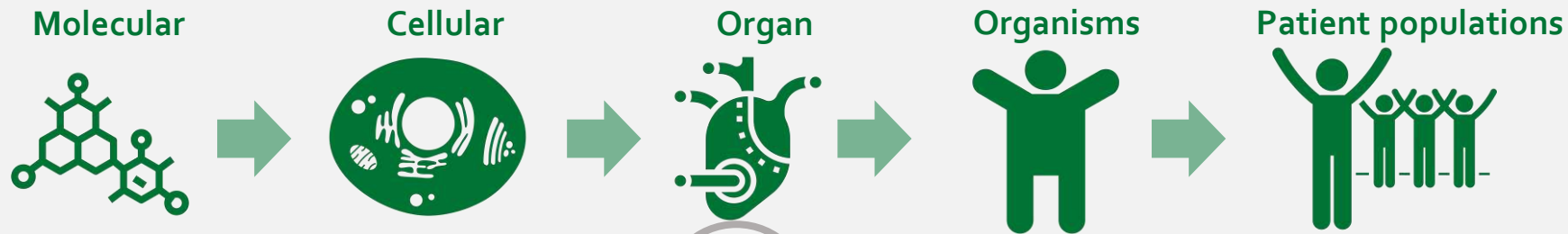
Systems Pharmacology and Pharmacy



Systems Pharmacology and Pharmacy

We aim to develop precision medicine approaches to characterize and predict variation in treatment response and enhance translational drug development strategies.

Systems & clinical pharmacology: Develop systems level understanding of drug action, disease heterogeneity, and inter-individual variation.



Measurement technologies & biomarkers



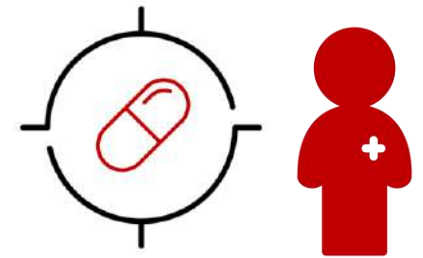
Experimental disease models

PK-PD modeling
Mechanistic modeling

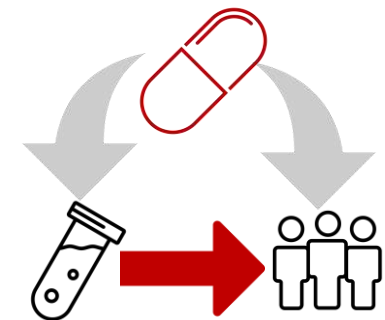


Clinical data & collaborations

Experimental and computational approaches to *translate* measurements and disease models to treatment response in patients.

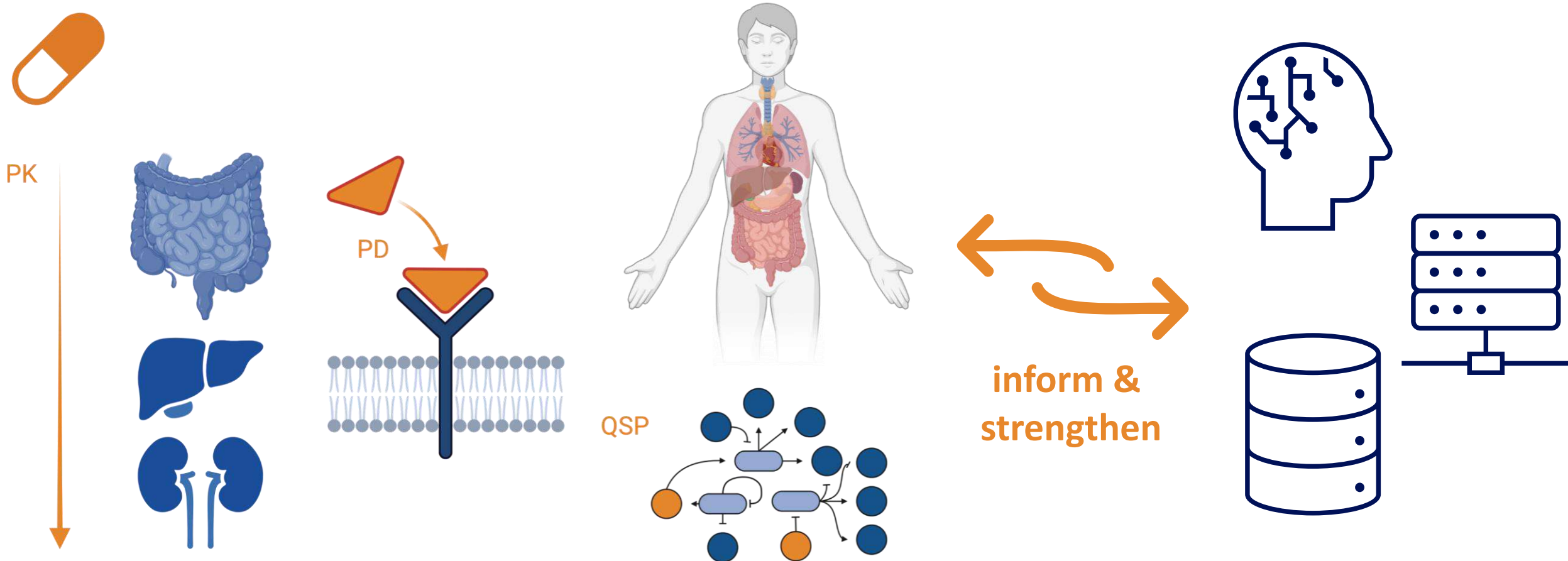


Precision medicine approaches



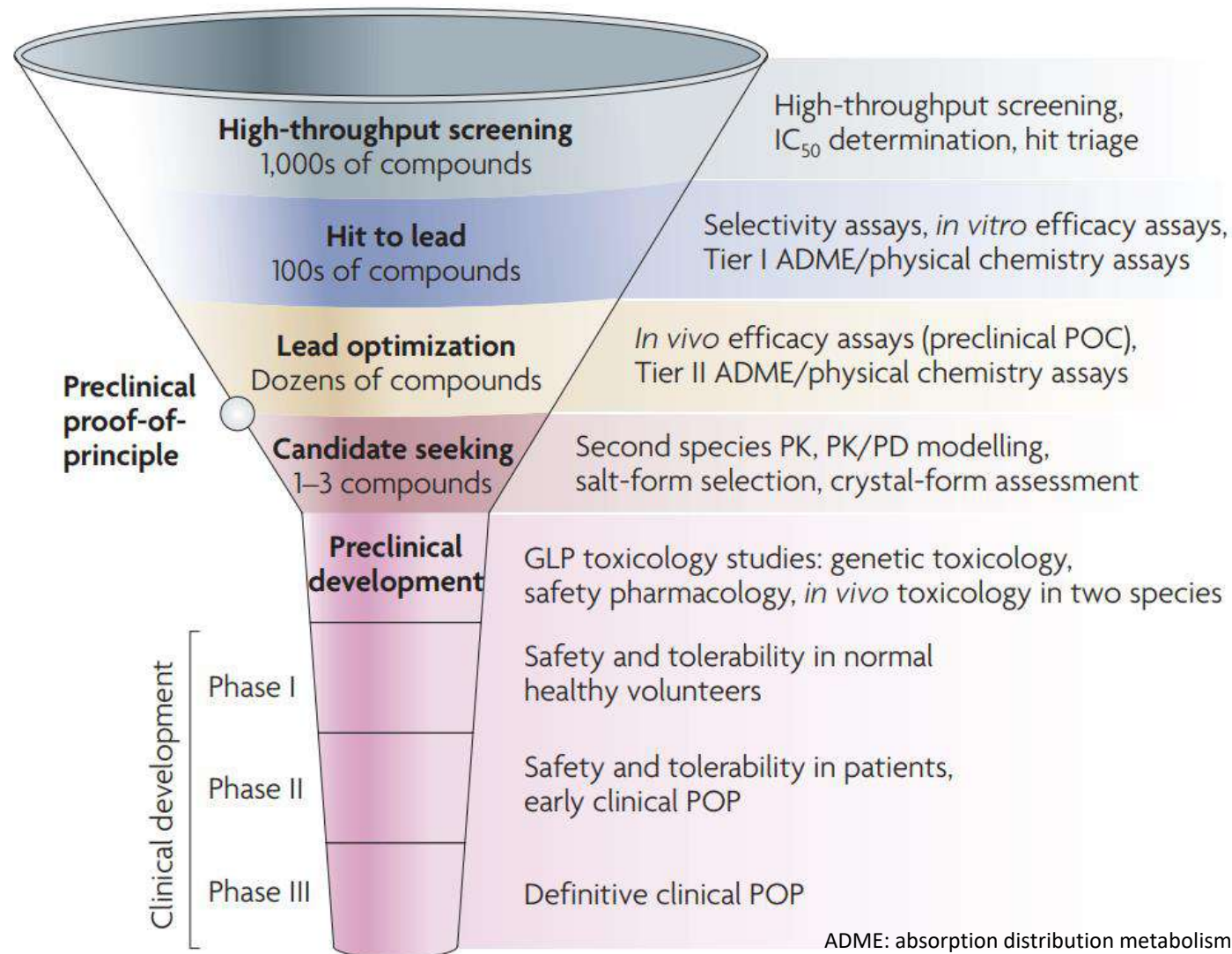
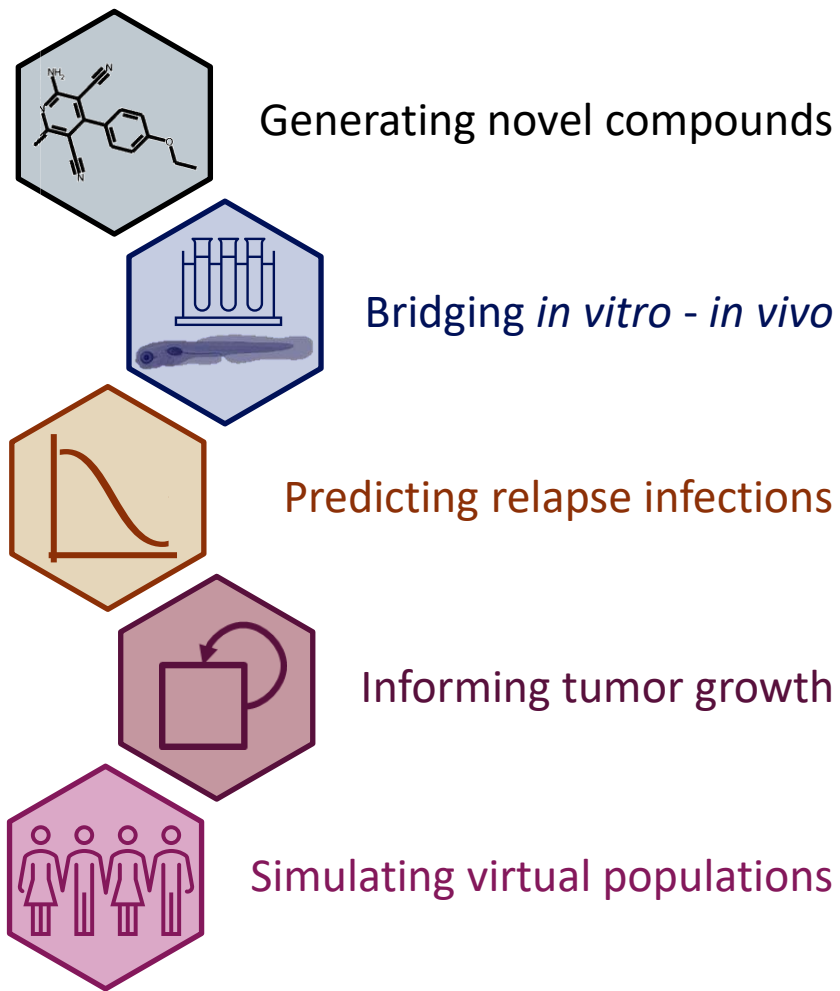
Translational drug development

Mechanistic pharmacological modelling and AI



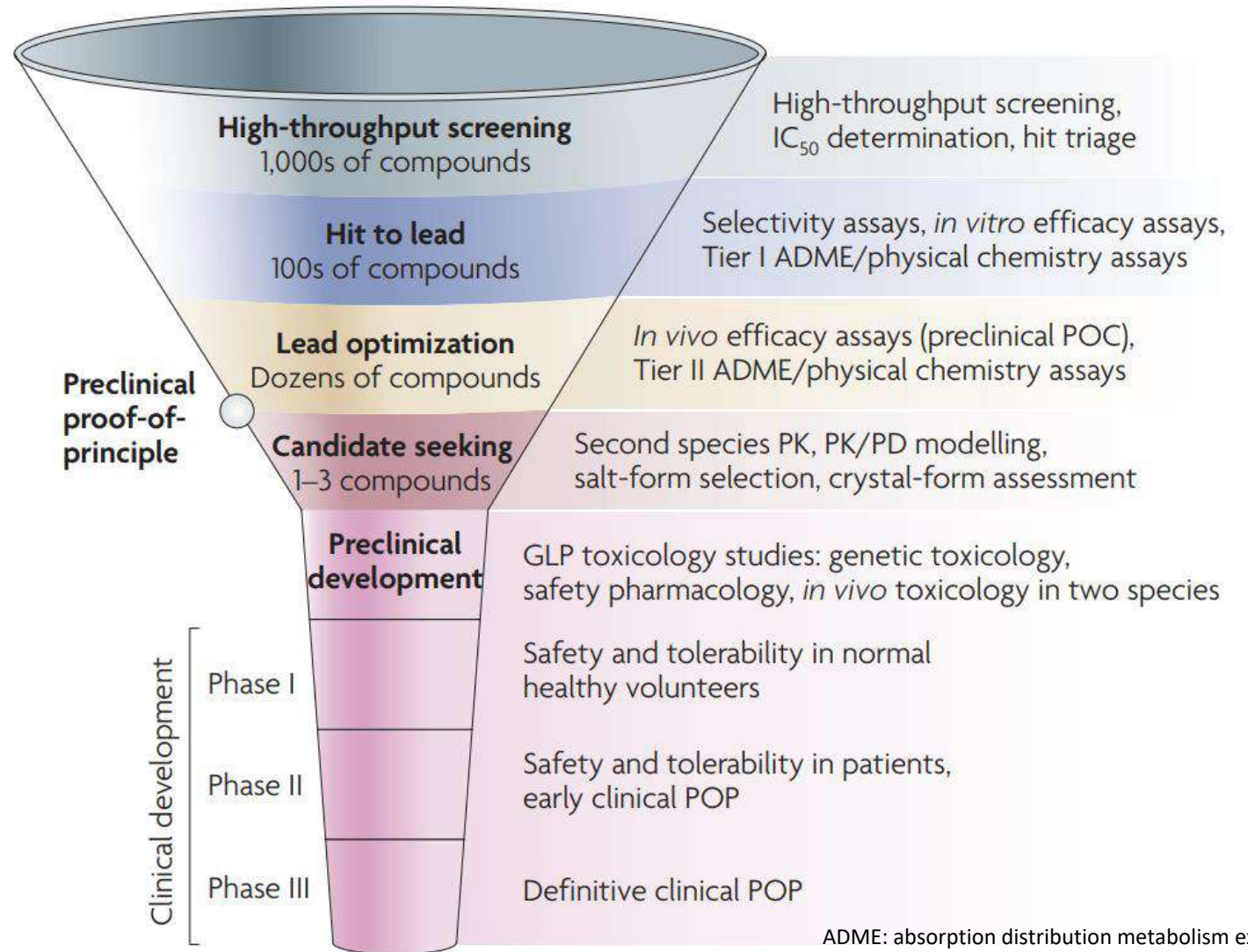
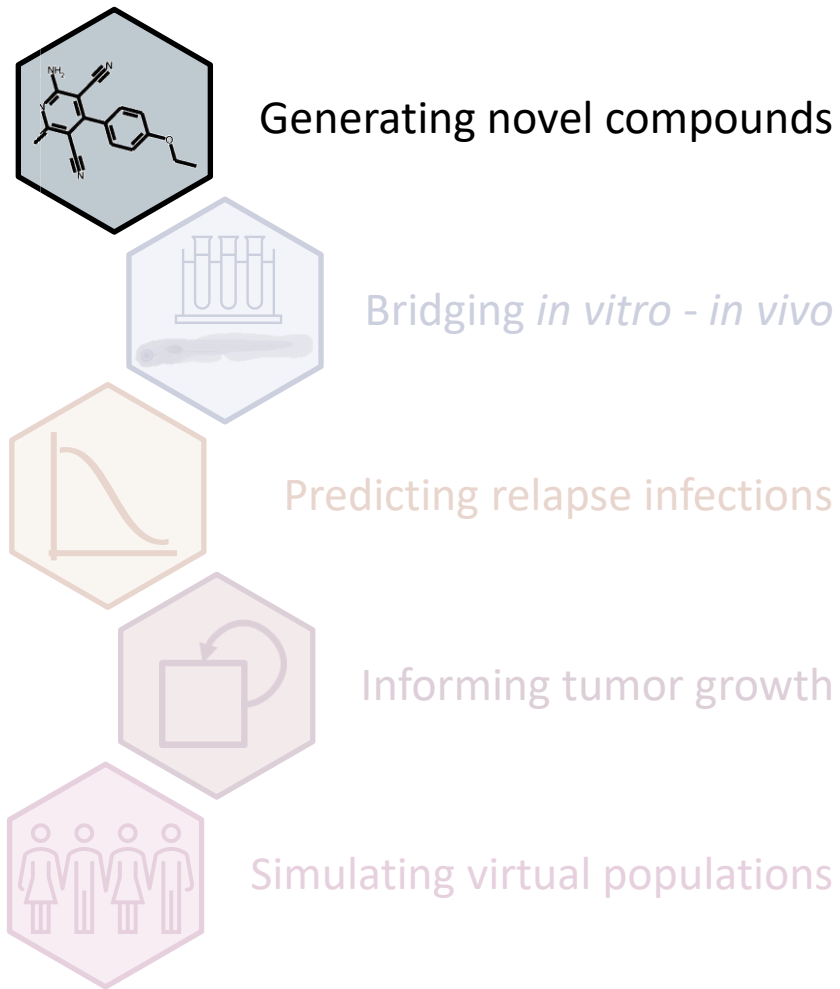
PK: pharmacokinetics, PD: pharmacodynamics
QSP: quantitative systems pharmacology

Model informed drug discovery and development (MID3)



ADME: absorption distribution metabolism excretion
 PK: pharmacokinetics, PD: pharmacodynamics
 POC: proof of concept; POP: proof of principle

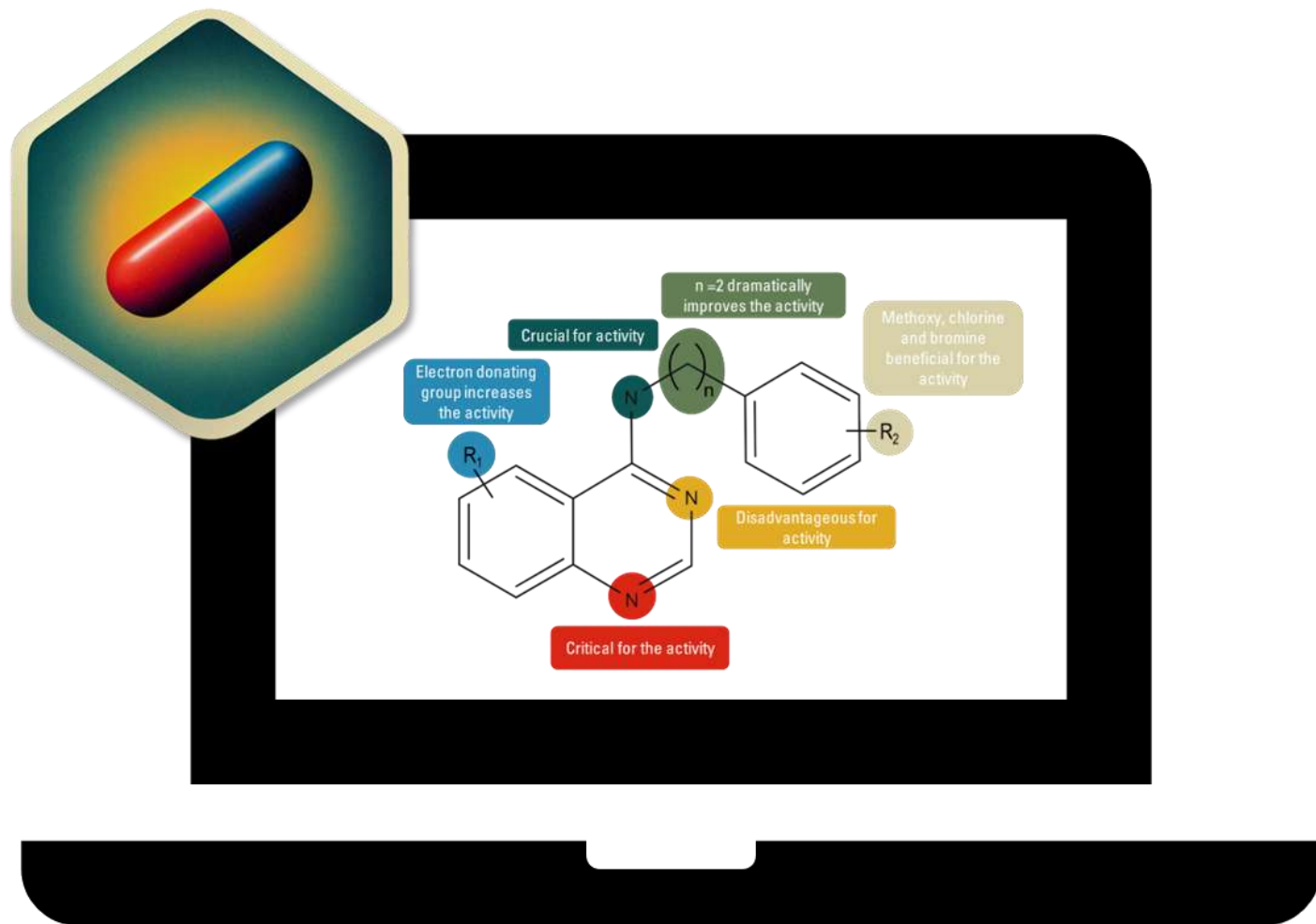
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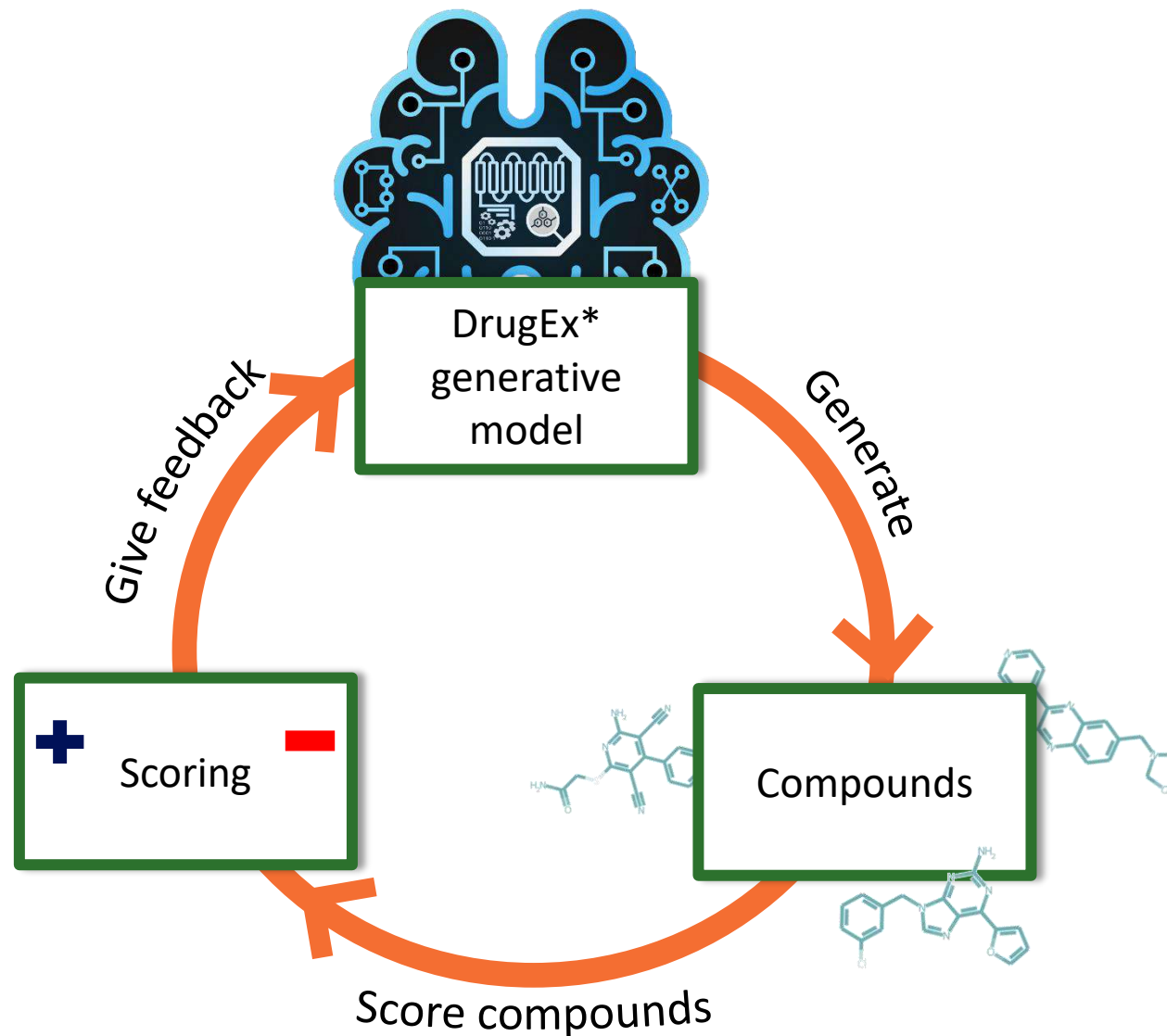
QSPRPRED: A FLEXIBLE OPEN-SOURCE QSPR MODELLING TOOL

Extensive data-preprocessing functionality.
Suitable for building single-task, multi-task
and proteochemometric models.



Helle W. van den Maagdenberg, Martin Šícho, David Araripe, Sohvi Luukkonen, Linde Schoenmaker, Michiel Jaspers, Olivier J. M. Béquignon, Marina Gorostiola González, Remco L. van den Broek, Andrius Bernatavicius, J.G. Coen van Hasselt, Piet H. van der Graaf, and Gerard J. P. van Westen

Learning and confirming cycle in generating novel compounds

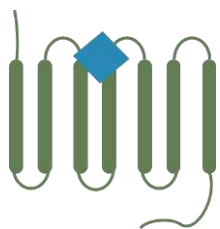


Helle W. van den Maagdenberg

Learning and confirming cycle in generating novel compounds

Scoring

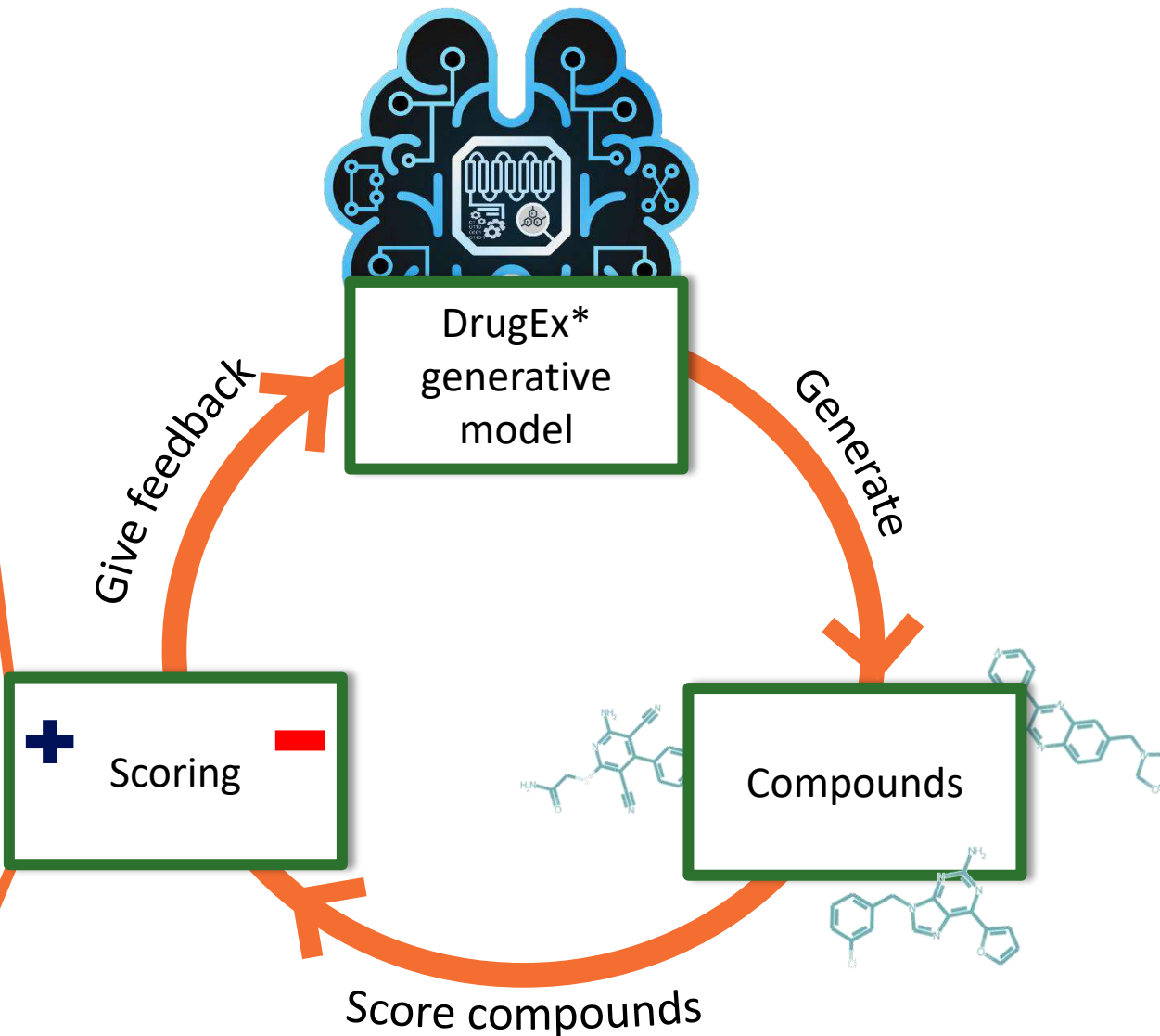
QSPR models for adenosine A_{2A}R binding affinity & human pharmacokinetics



Receptor affinity

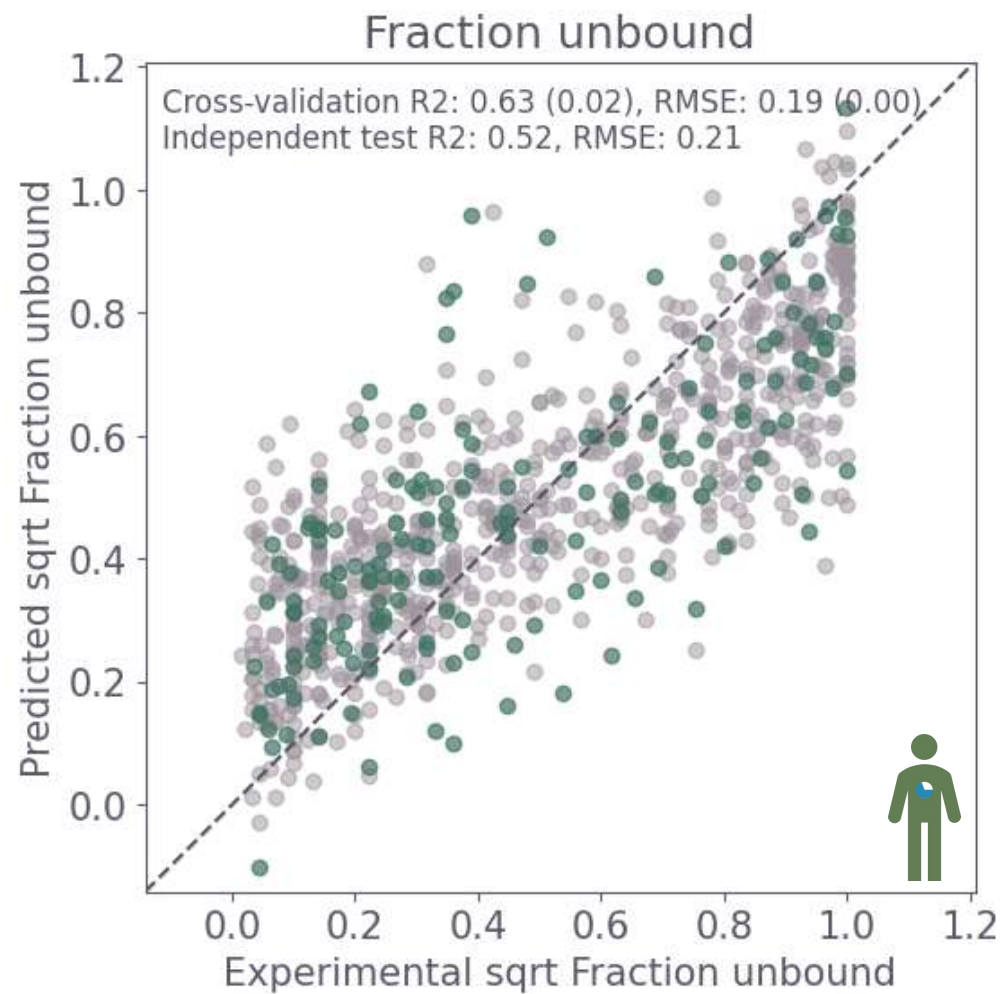
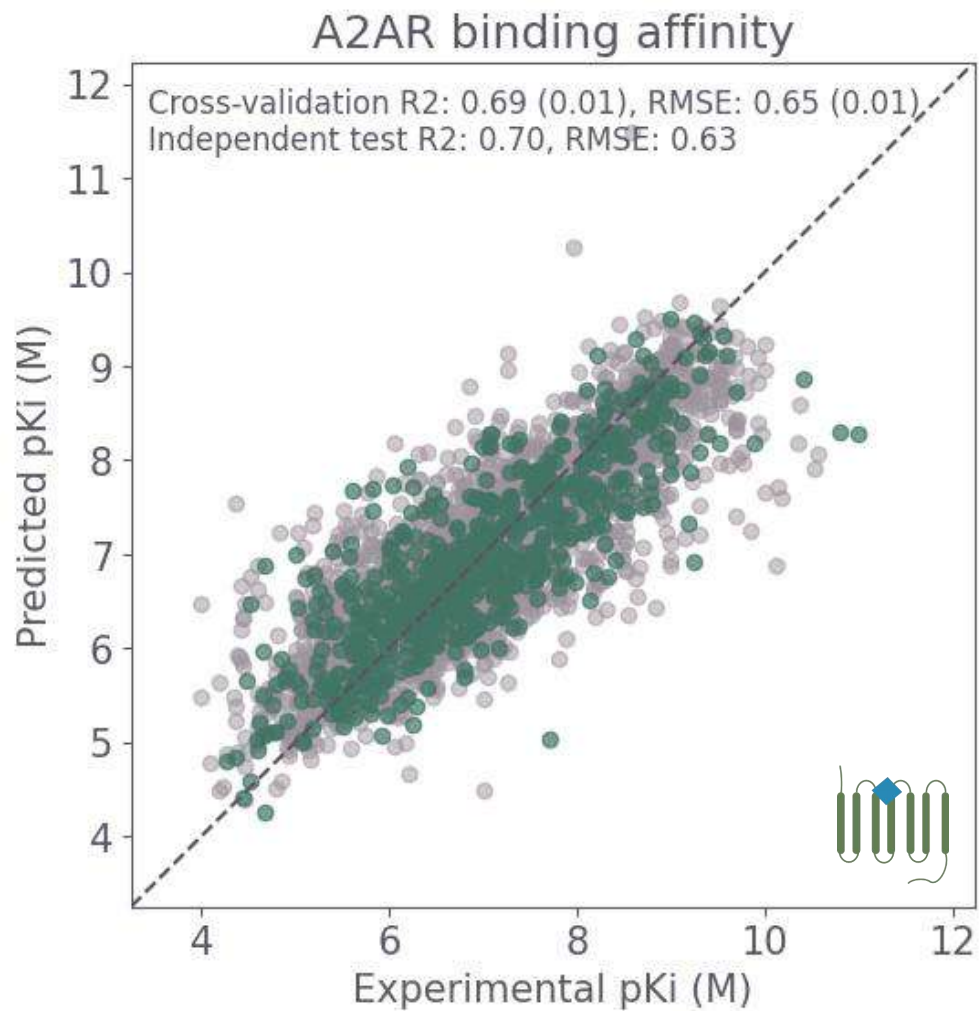


Unbound fraction



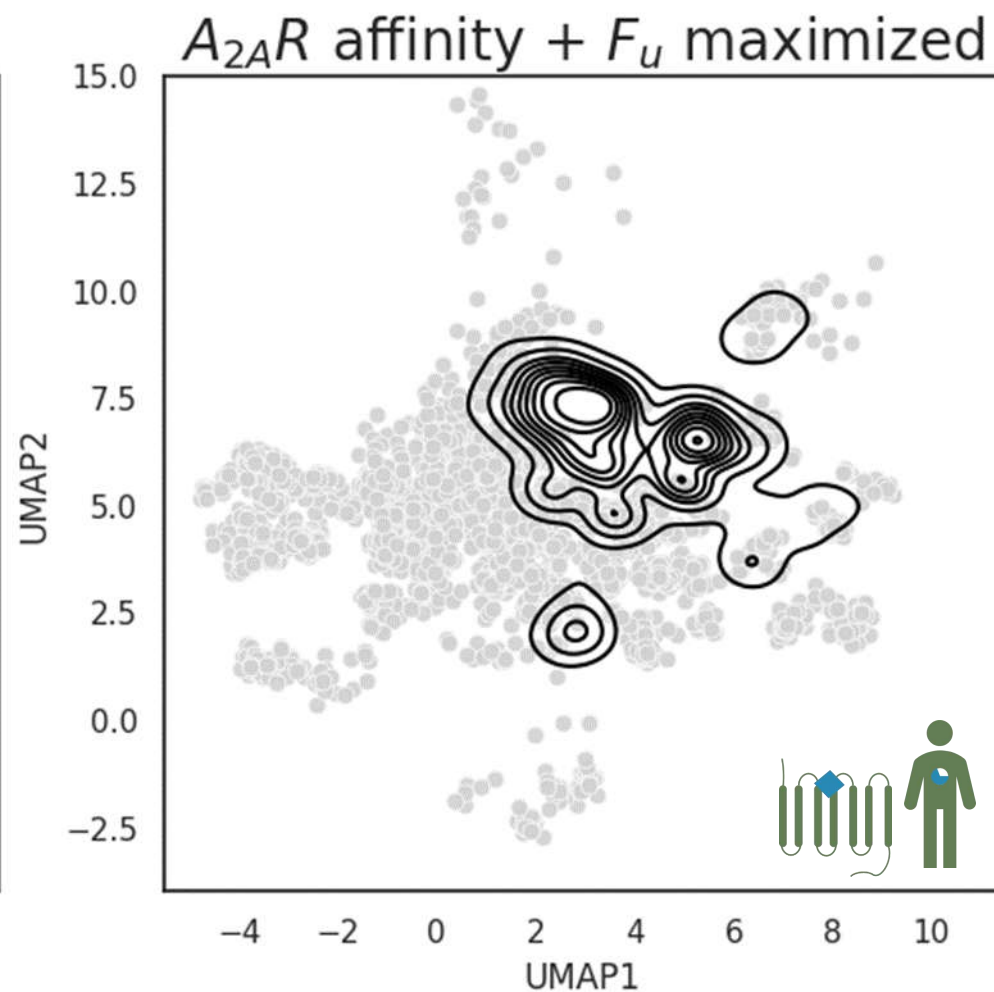
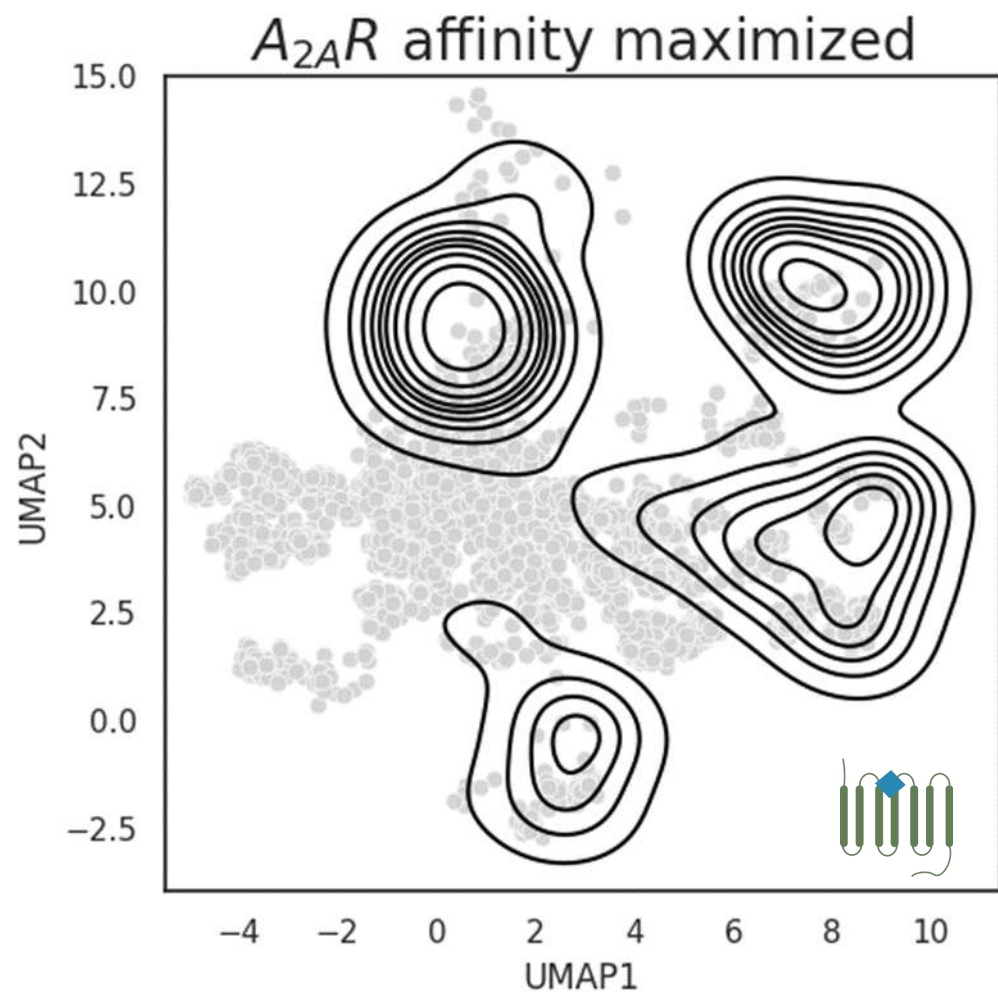
Helle W. van den Maagdenberg

QSPR models trained with QSPRPRED



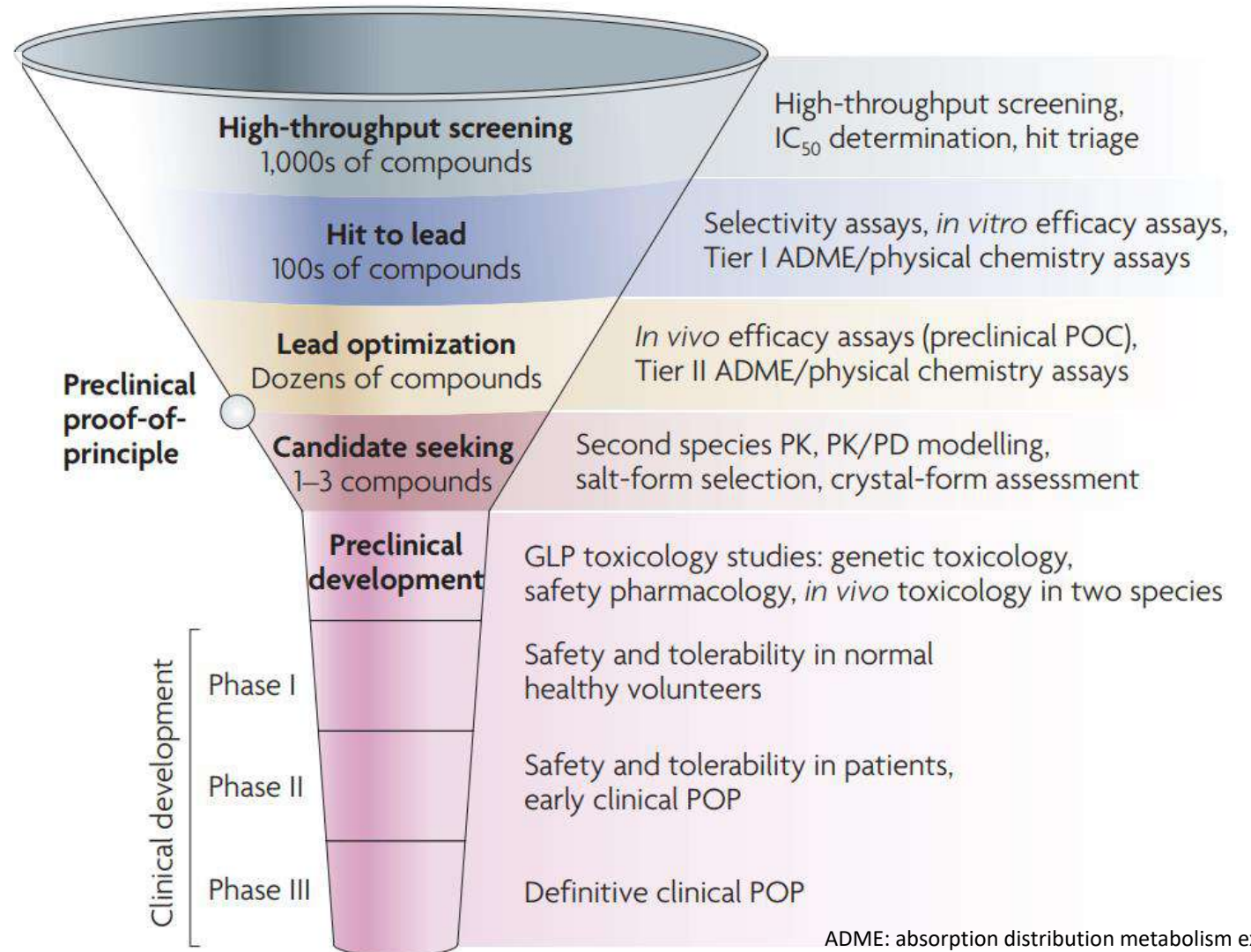
Helle W. van den Maagdenberg

Model-informed novel molecules in chemical space



Helle W. van den Maagdenberg

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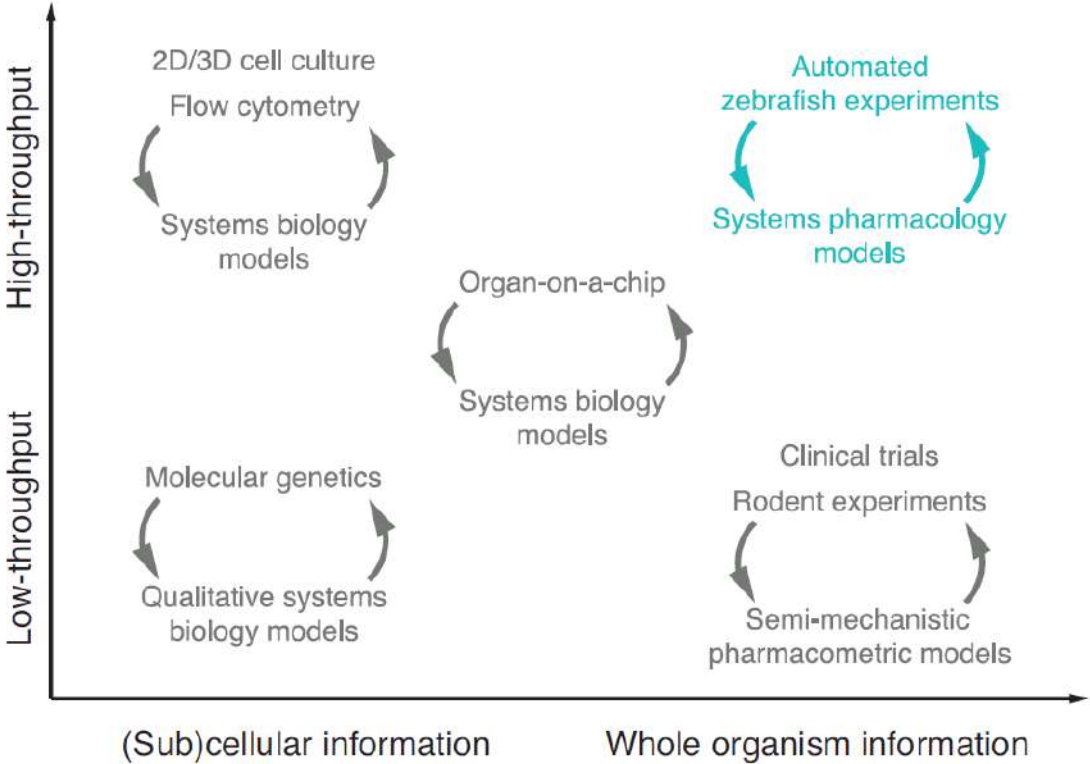
Bridging the in vitro – in vivo gap in drug development



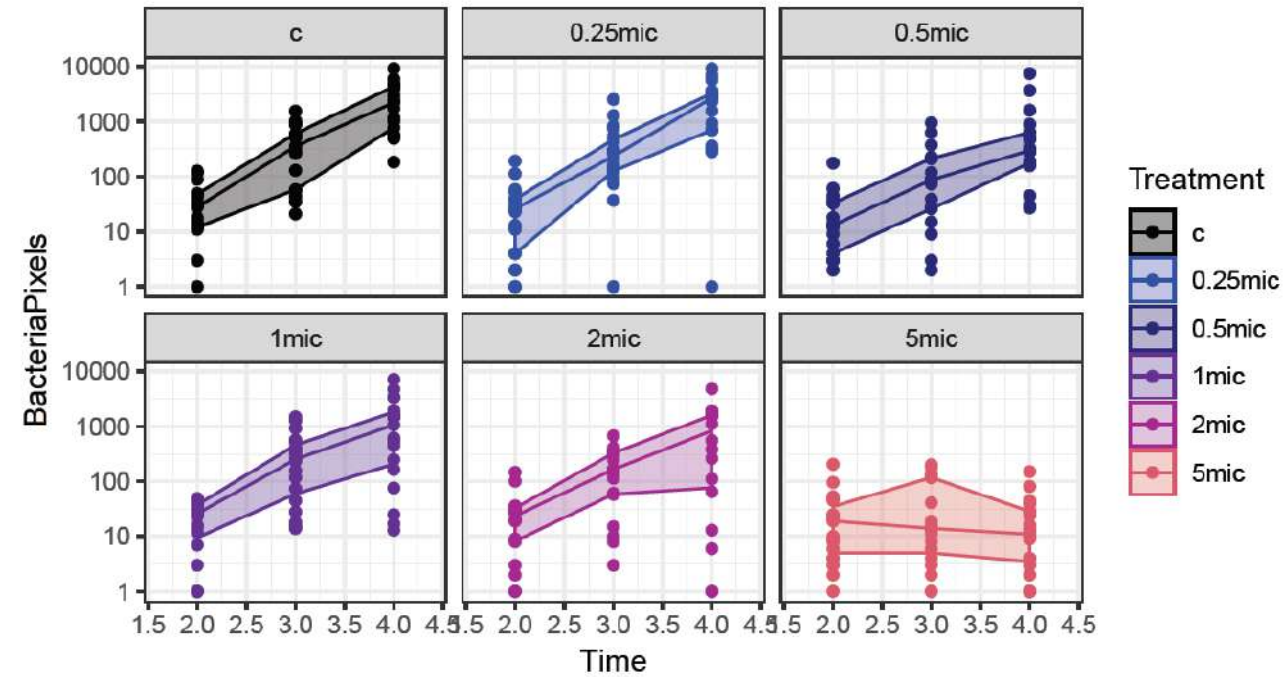
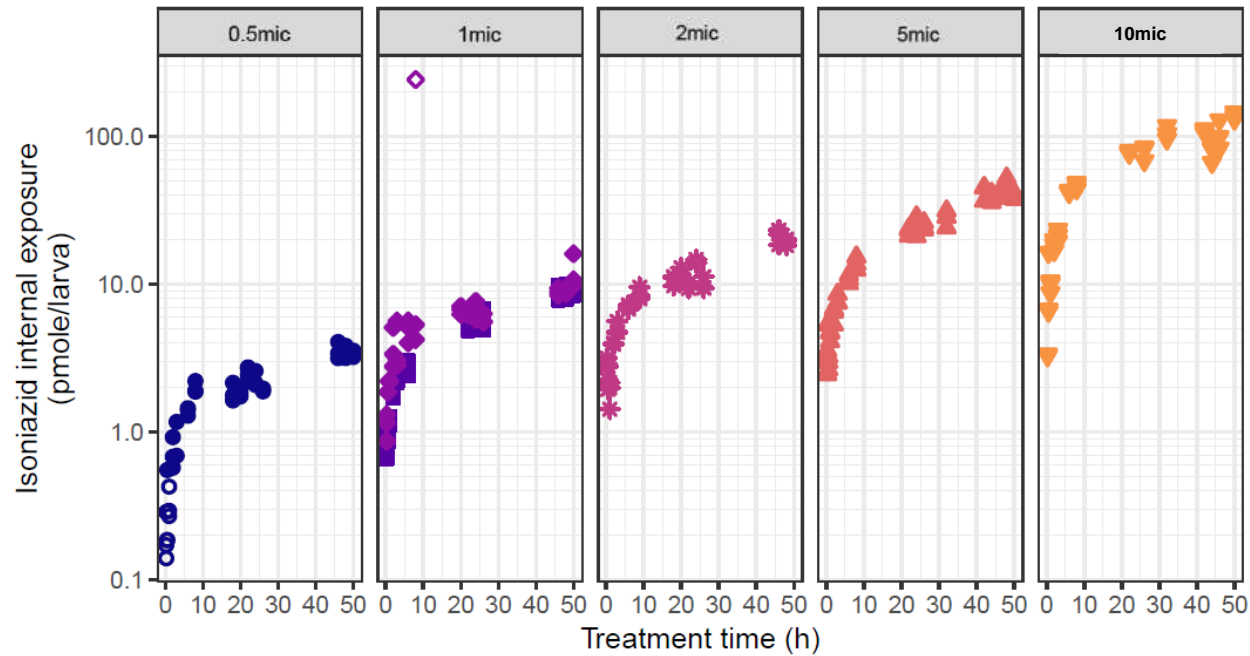
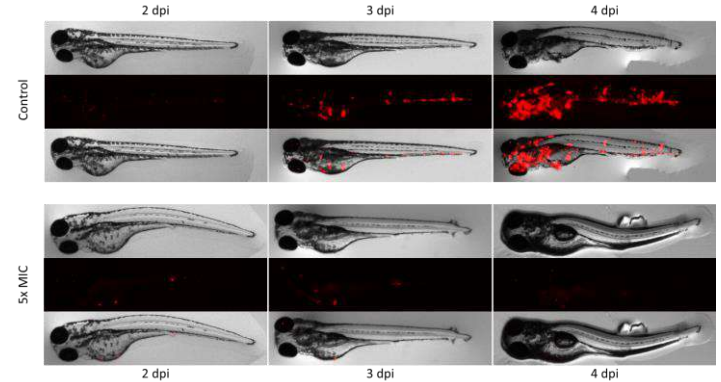
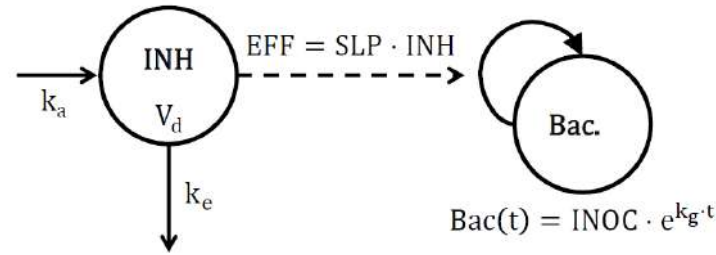
Transparency



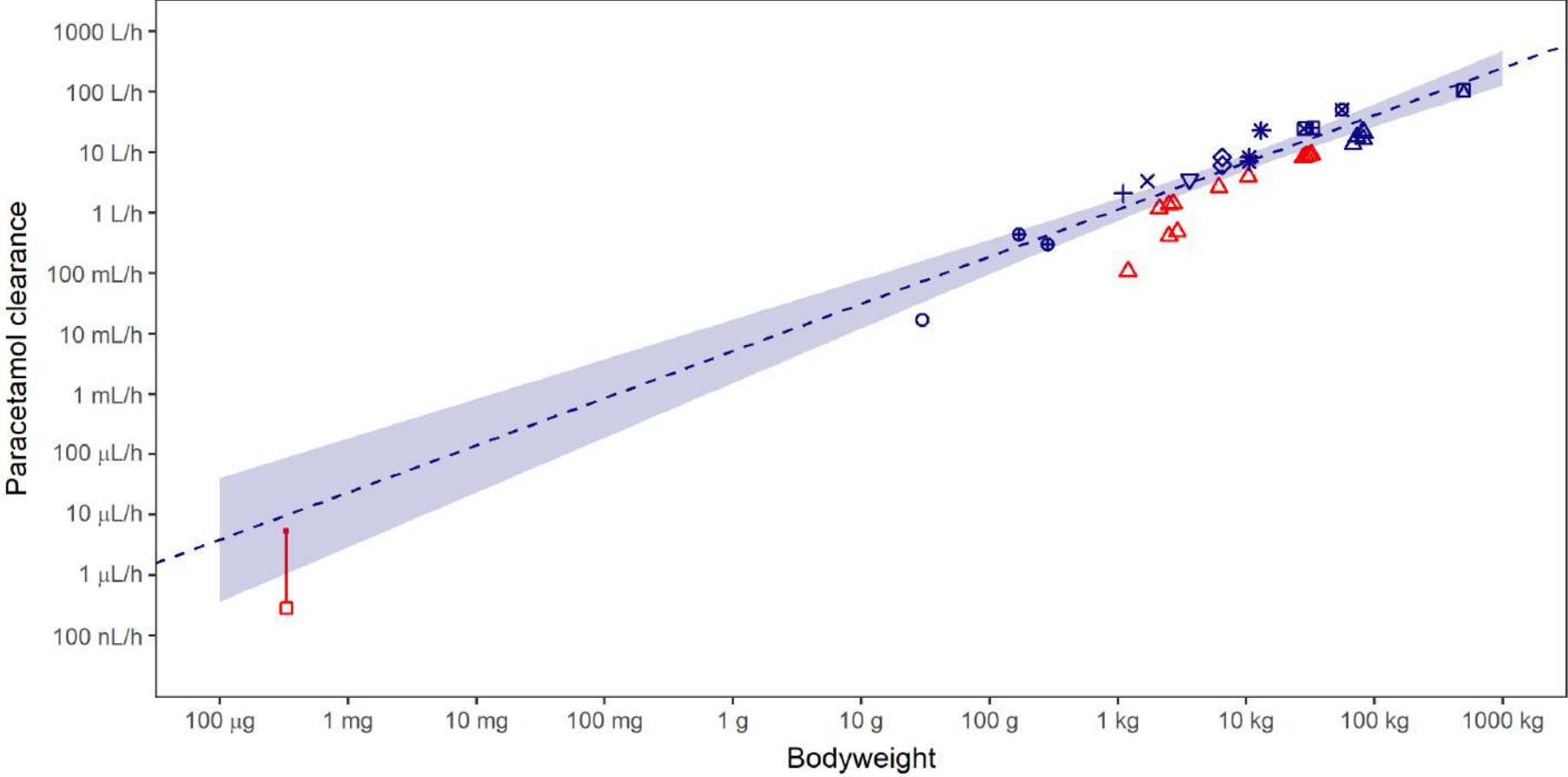
High-throughput (robotics)



High-throughput quantification of PKPD in zebrafish

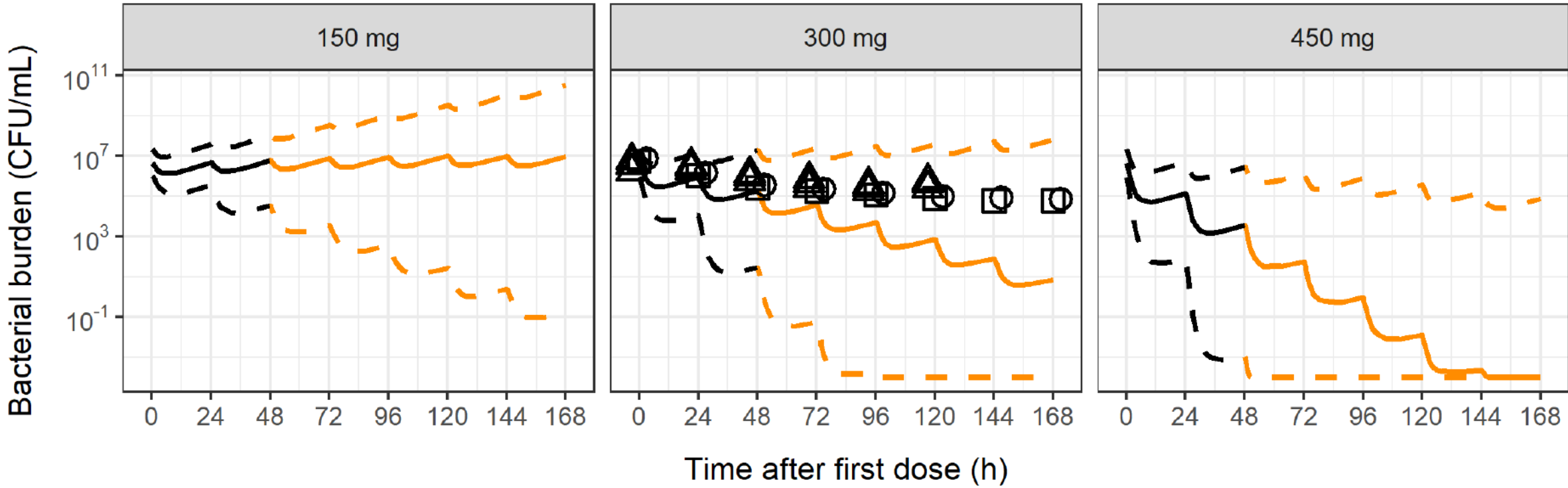


Drug exposure in zebrafish translates to higher vertebrates

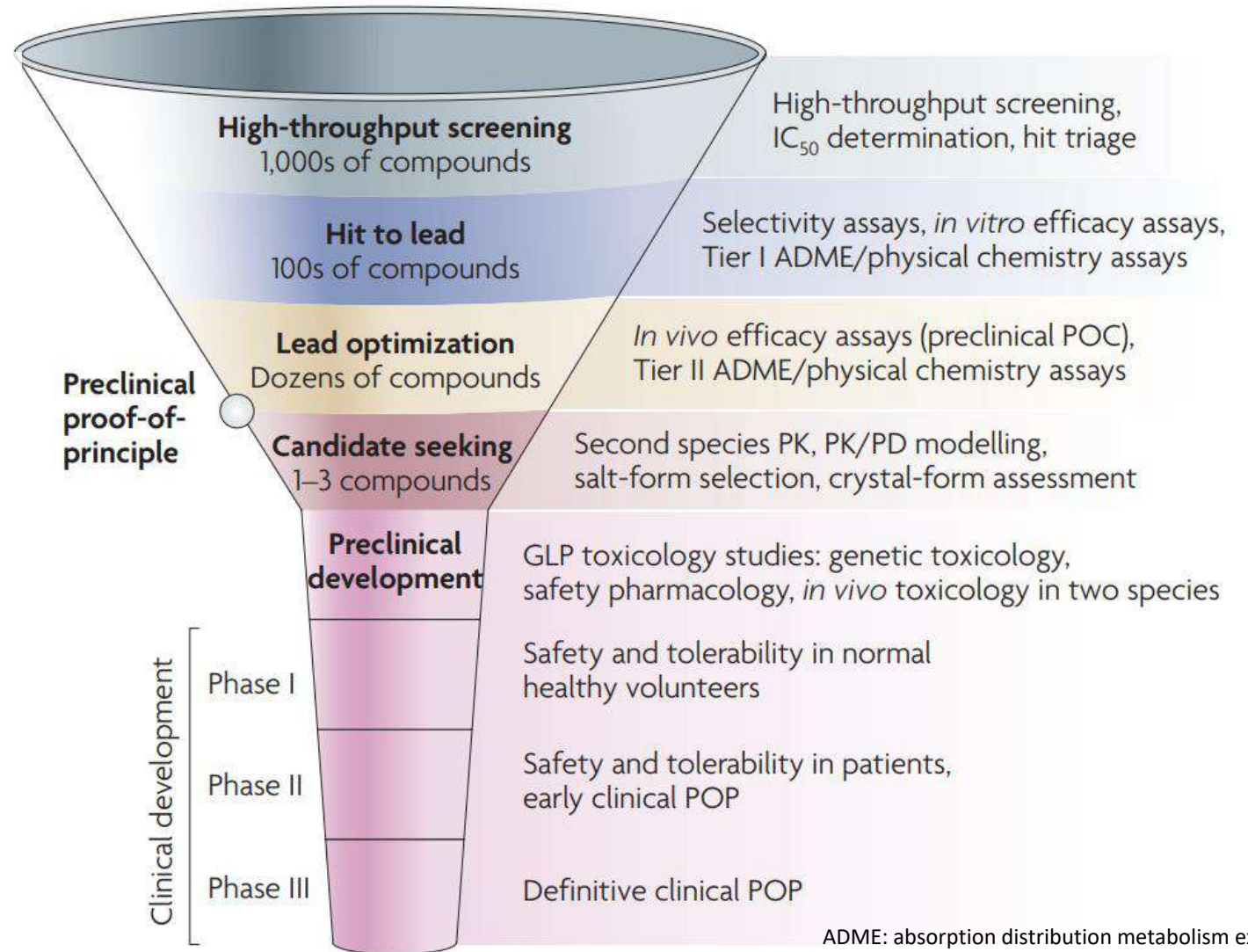
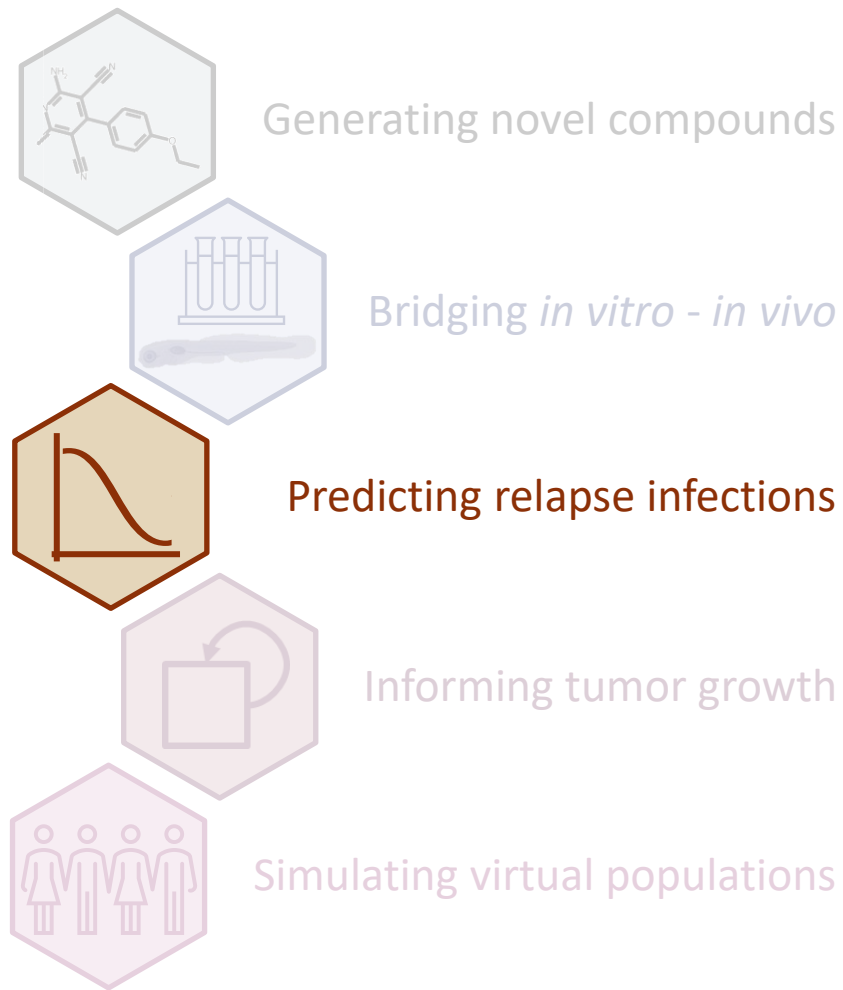


- zebrafish larvae (t=0) △ human (mature) + chicken ◇ cynomolgus monkey ▣ greyhound dog
- zebrafish larvae (t=∞) ○ mouse × turkey * beagle dog ▤ chimpanzee
- △ human (immature) ⊕ rat ▽ rabbit ⊠ pig ▨ horse

Drug efficacy in zebrafish translates to higher vertebrates

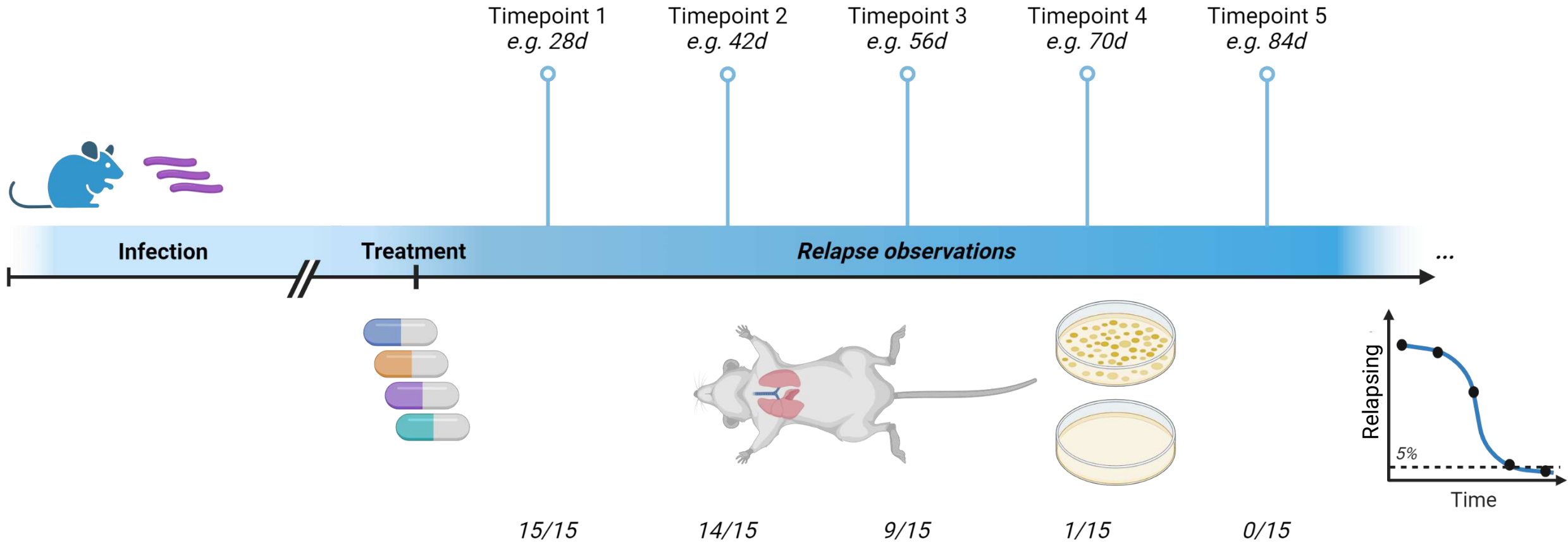


Model informed drug discovery and development (MID3)

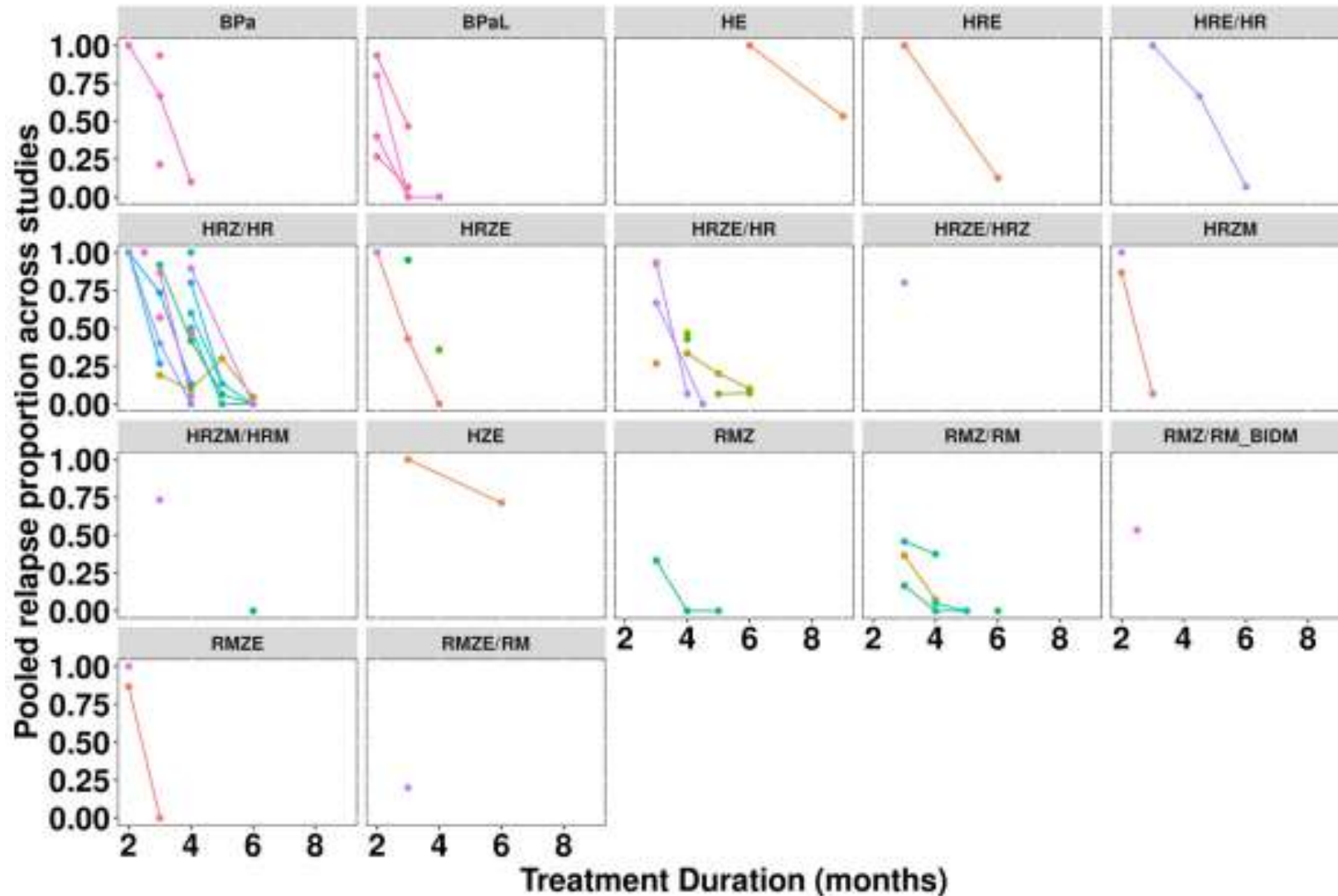


ADME: absorption distribution metabolism excretion
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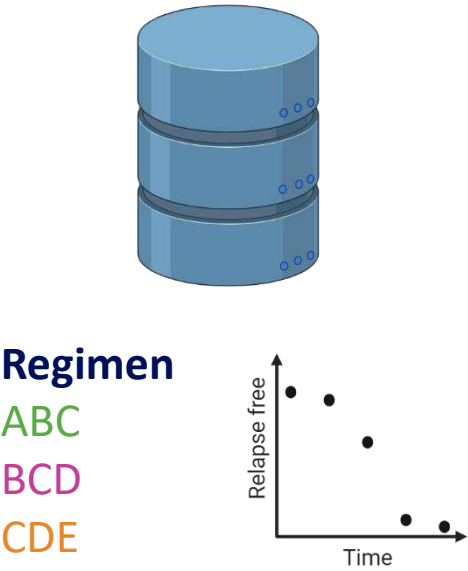
Preclinical experiment of tuberculosis relapse



Relapse data published for different regimens of antibiotics



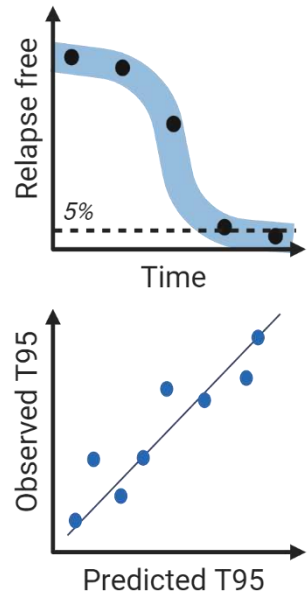
Model-informed ranking of regimens based on relapse



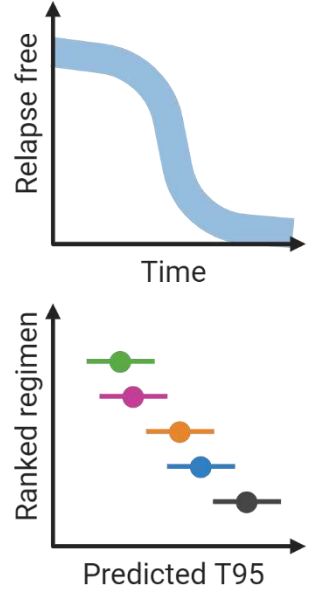
Dataset with (overlapping) regimens



Machine learning (neural networks, random forest)



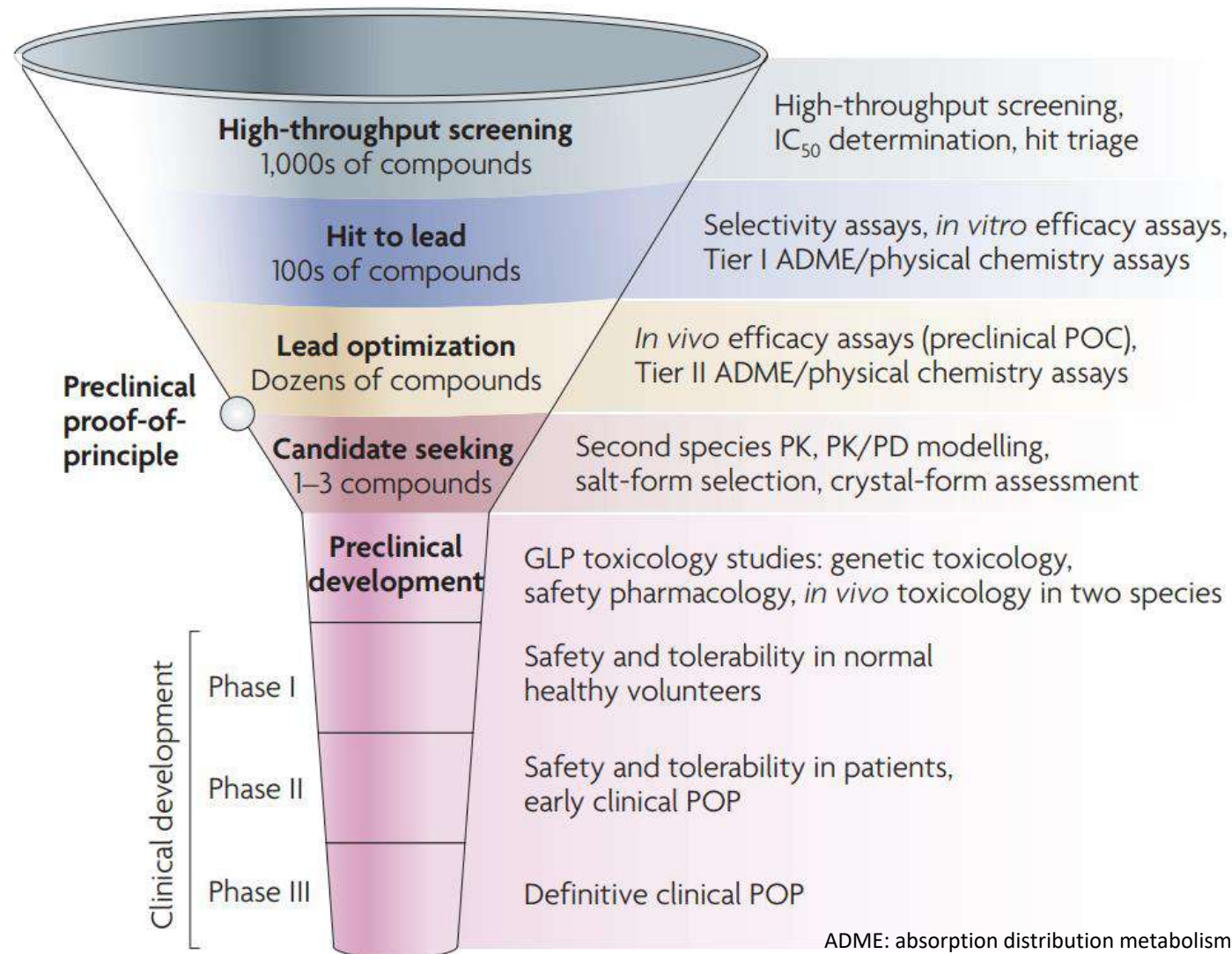
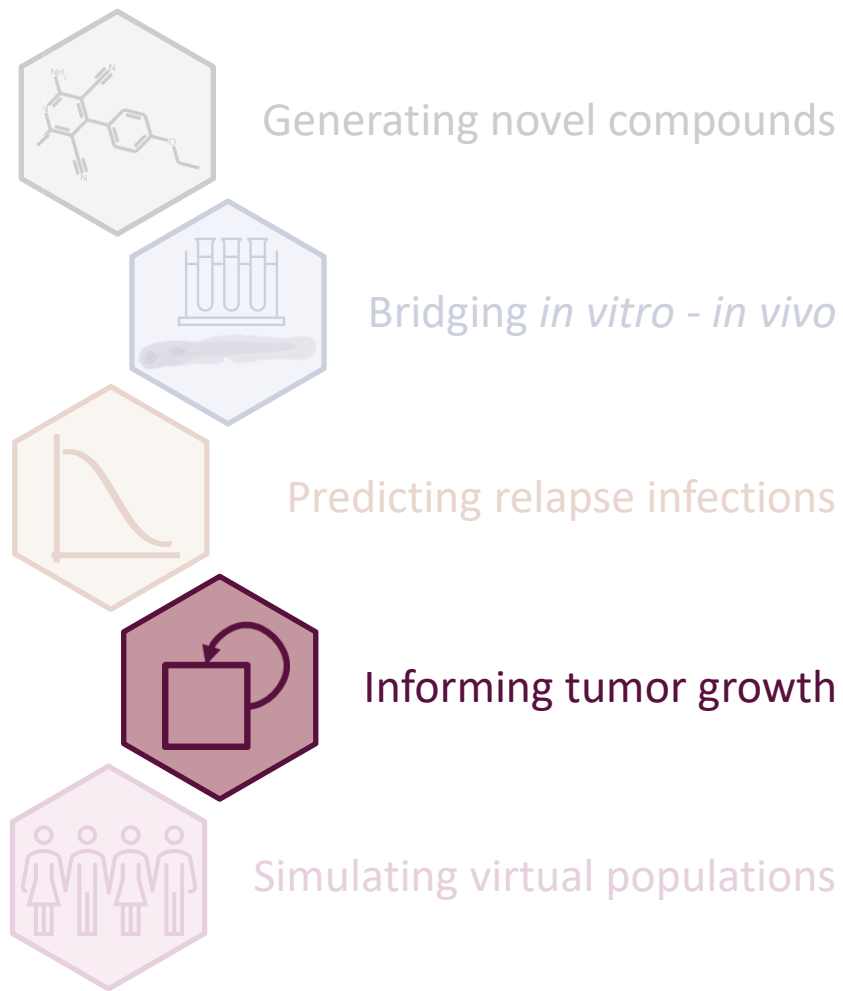
Training and performance



Predicting and ranking novel regimens

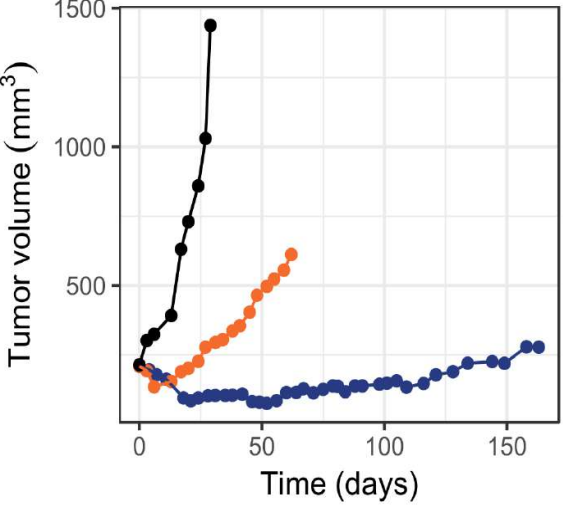
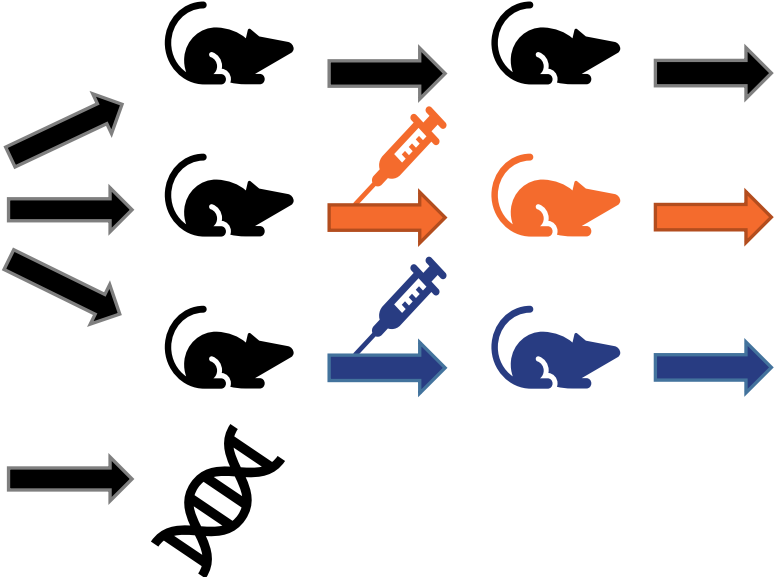
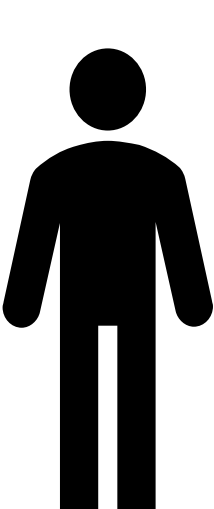
Predict regimen performance based on contribution of individual drug(s)

Model informed drug discovery and development (MID3)

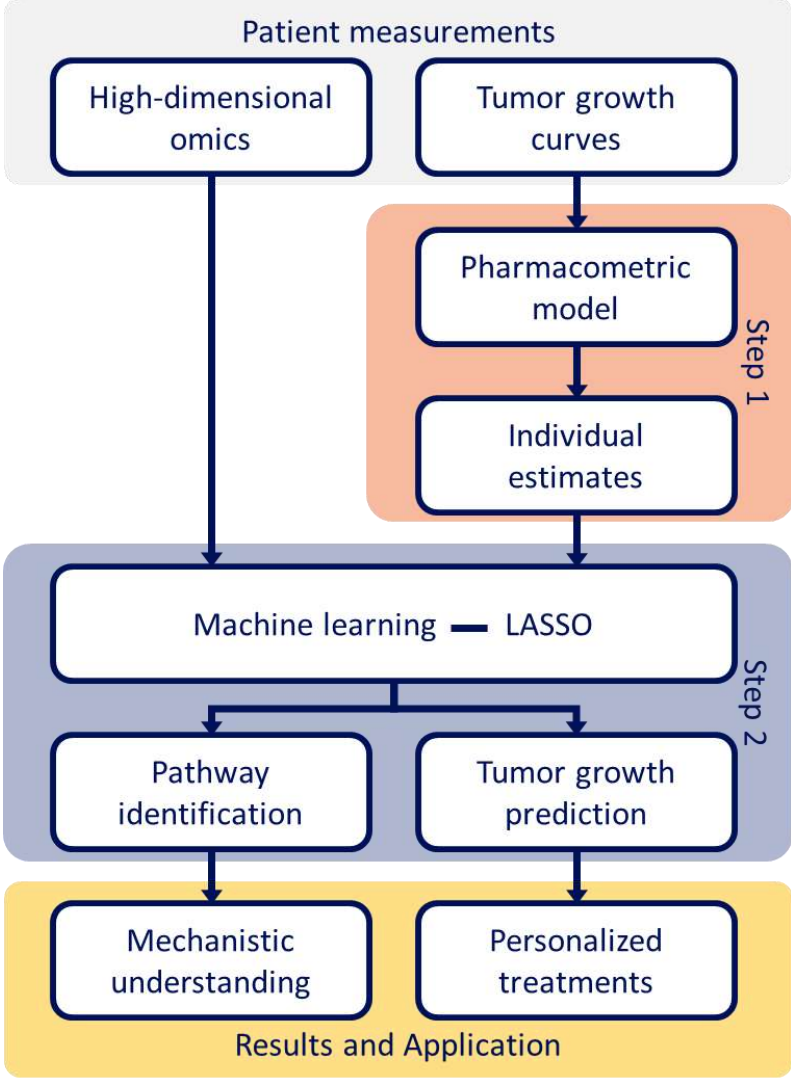


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High-dimensional omics-derived predictors for tumor growth dynamics

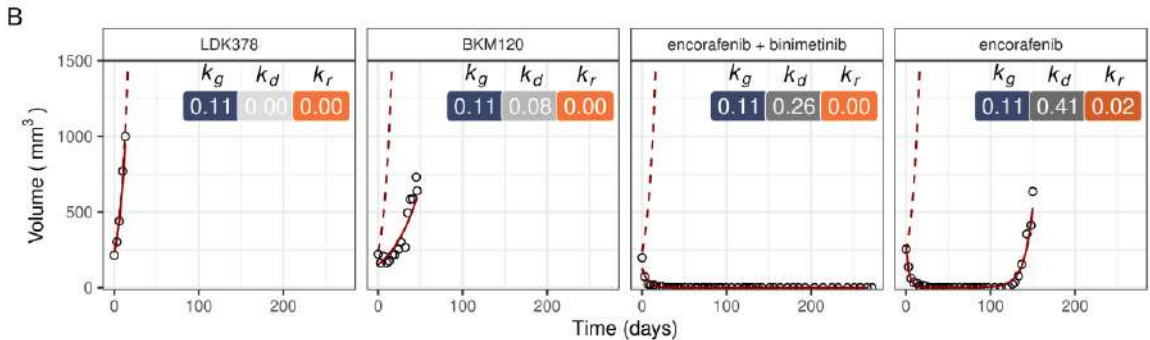
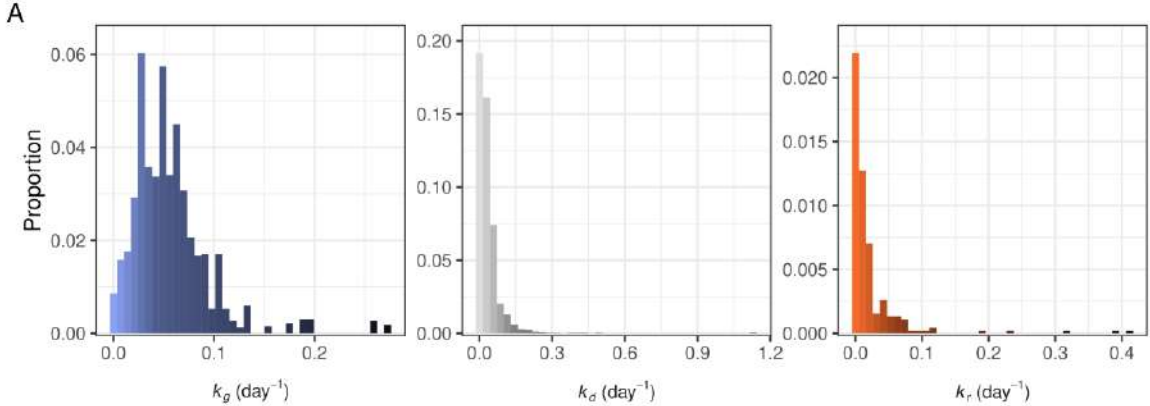


n = 173 patients; n = 2899 mice
 53 treatments
 >22,000 gene expression patterns
 >19,000 copy number variations

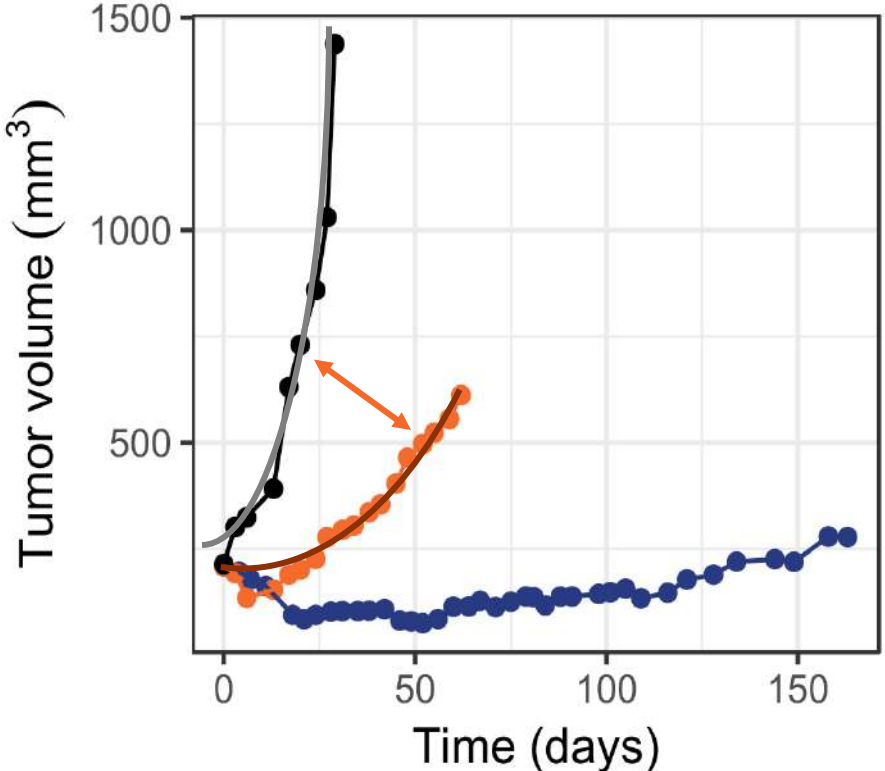


Mechanistic model of tumour growth inhibition

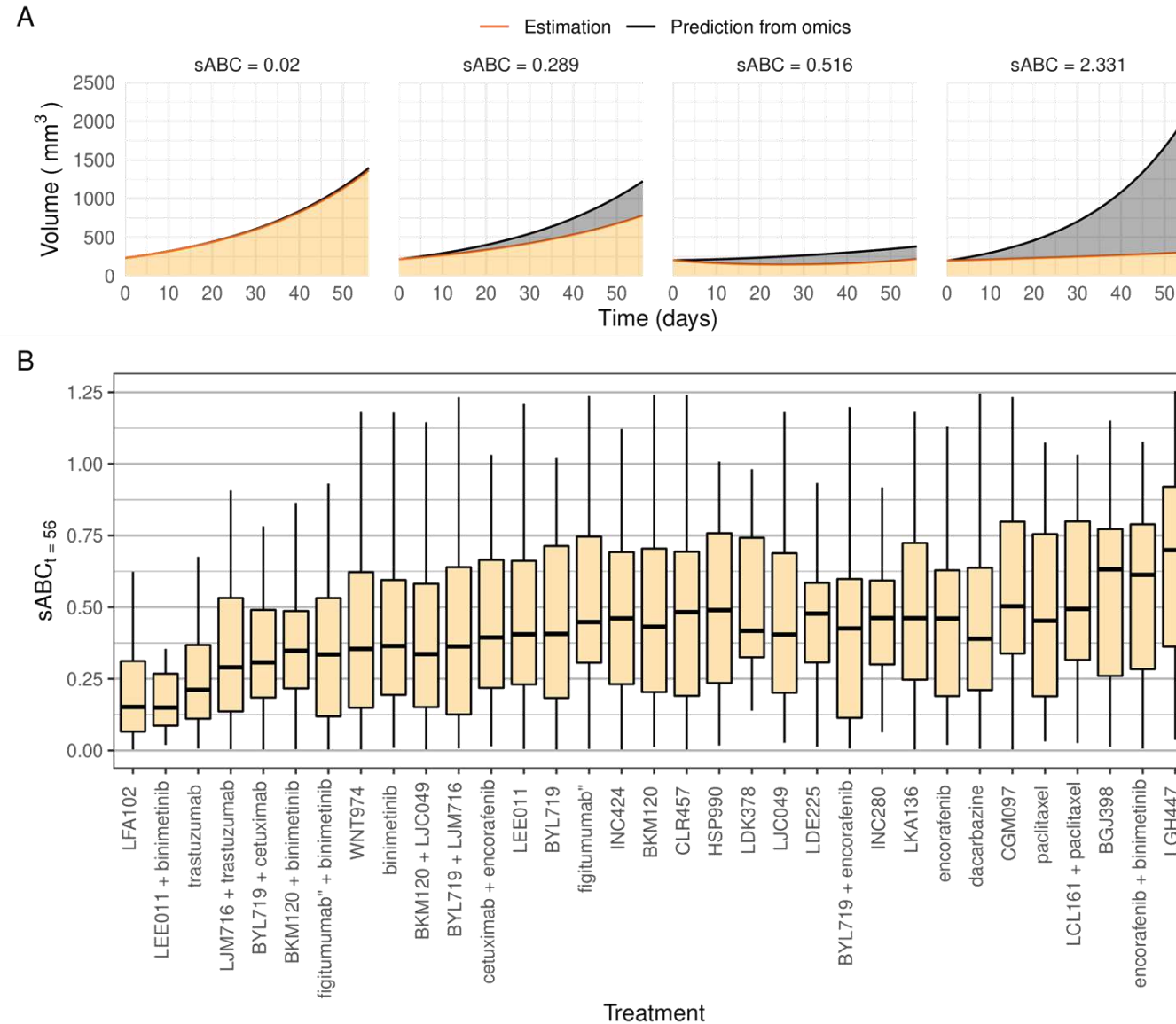
$$\frac{dV(t)}{dt} = K_G V(t) - K_{D,j} V(t) e^{-K_{R,j} t}$$



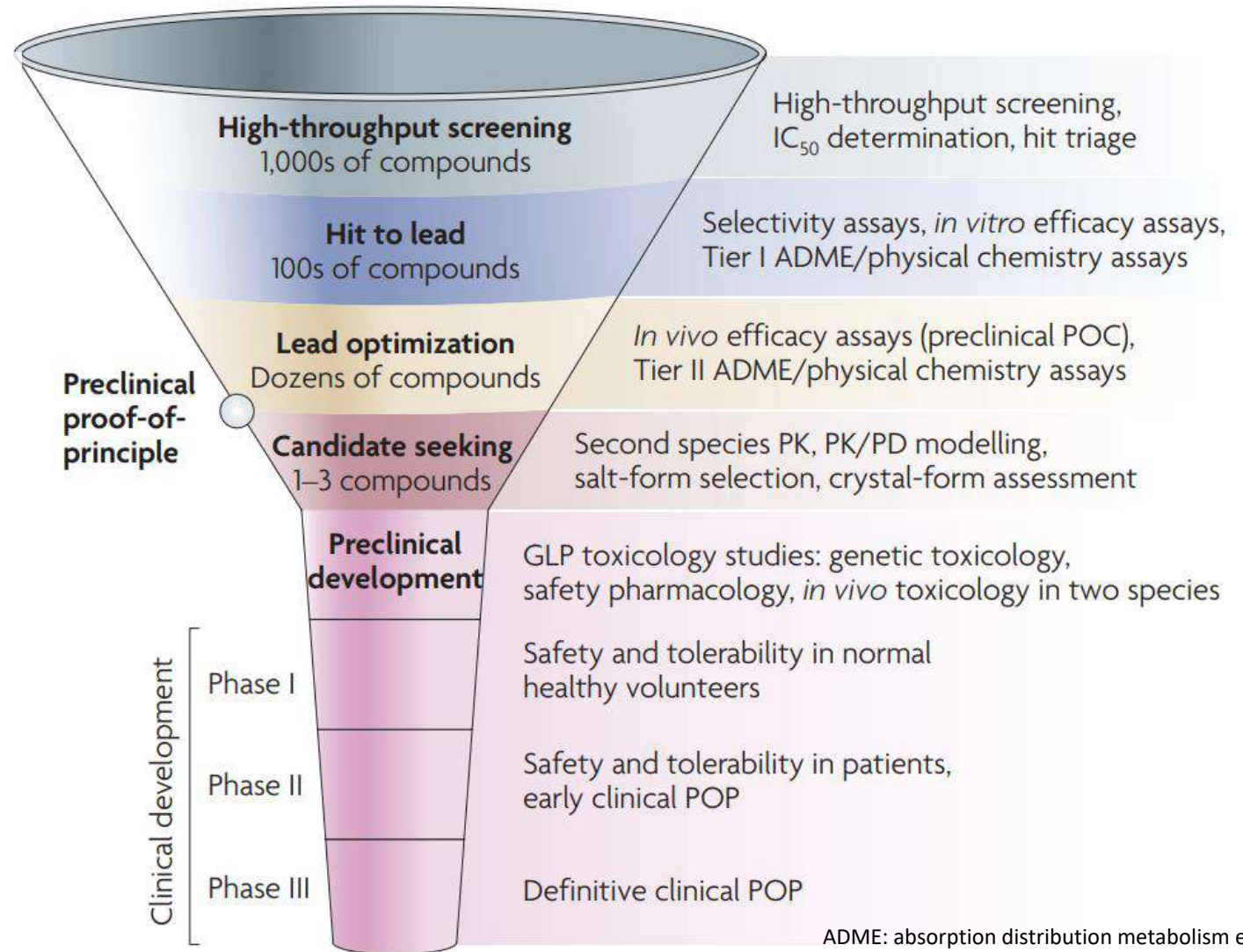
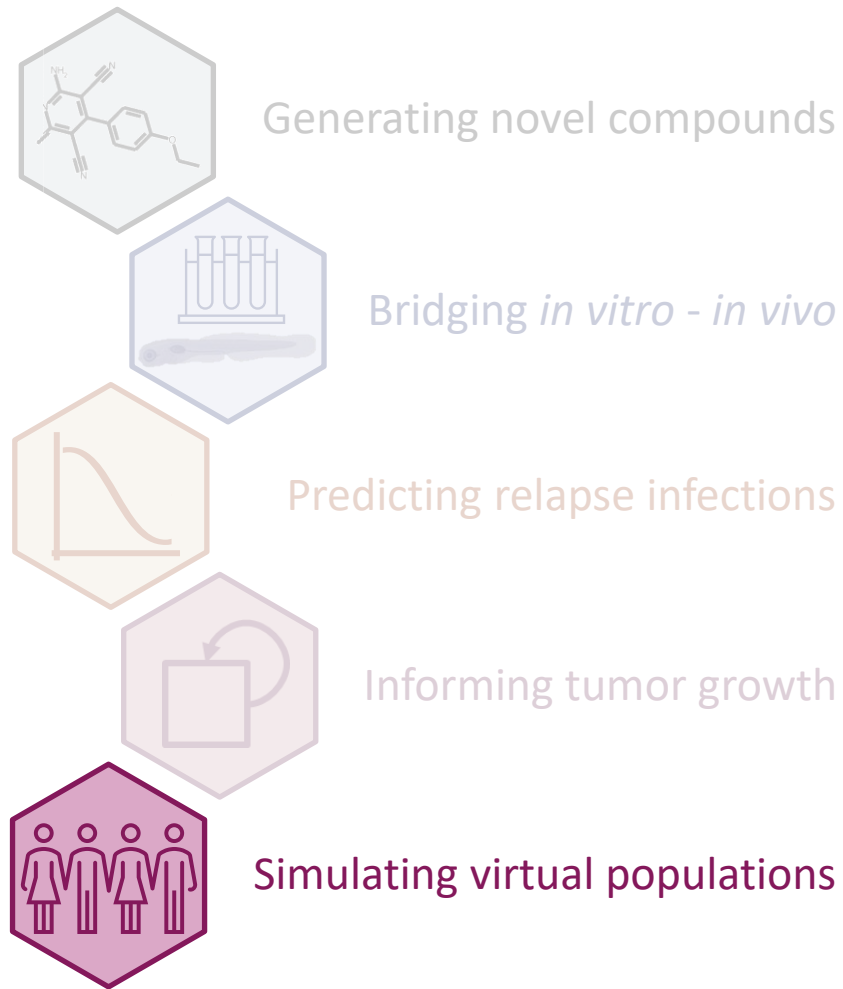
-- Modeled untreated — Modeled treated ○ Observed treated



Individual tumour growth prediction to personalize treatment



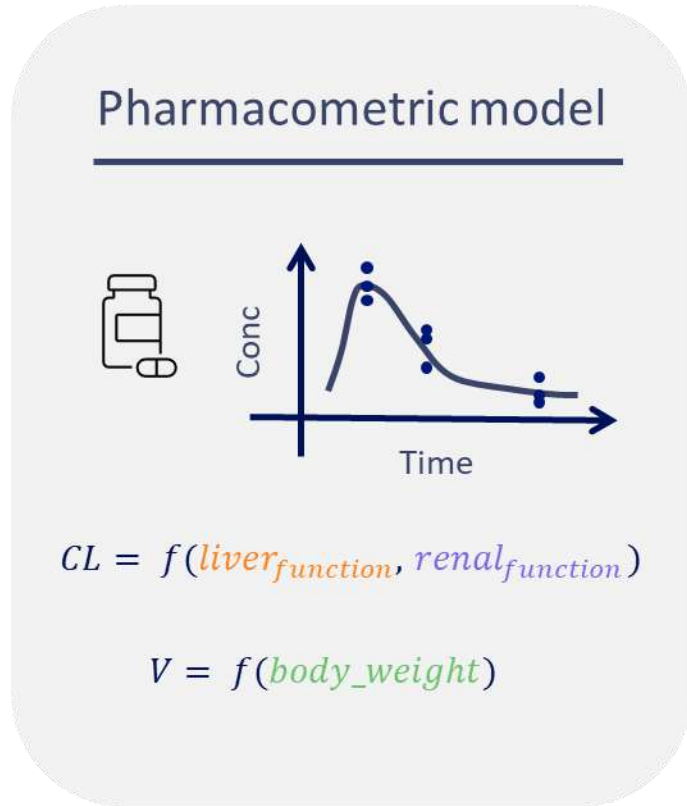
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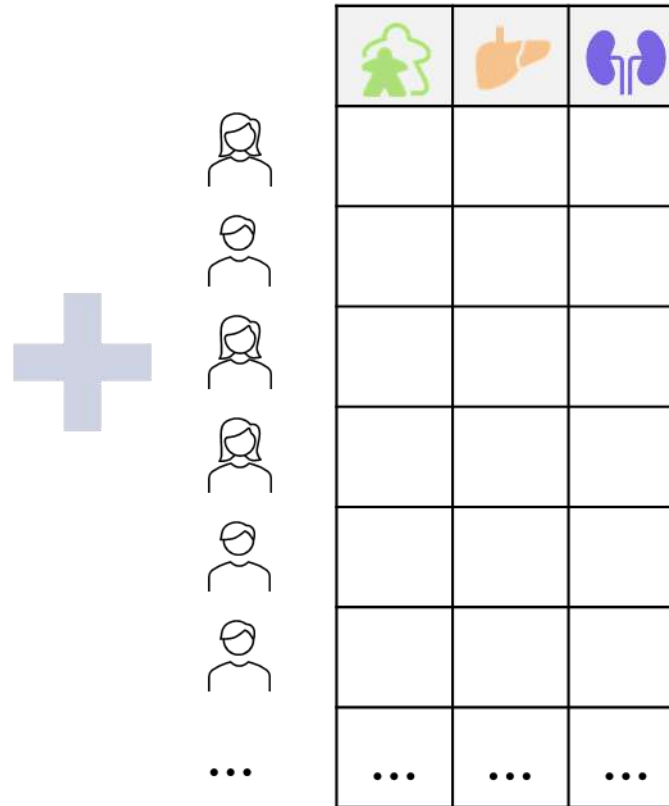
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Simulating trial outcomes in virtual populations

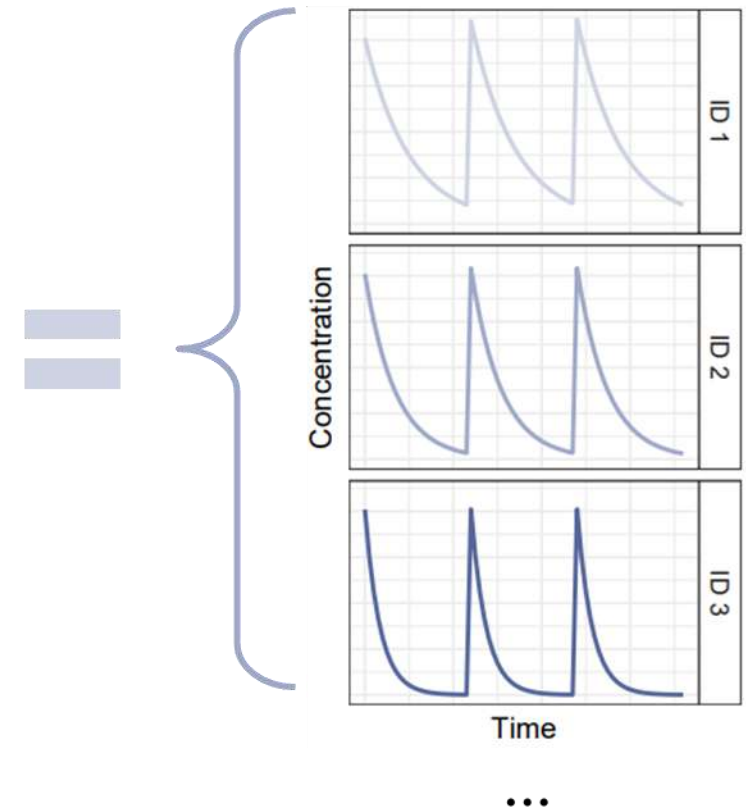
Established model



A set of patient characteristics

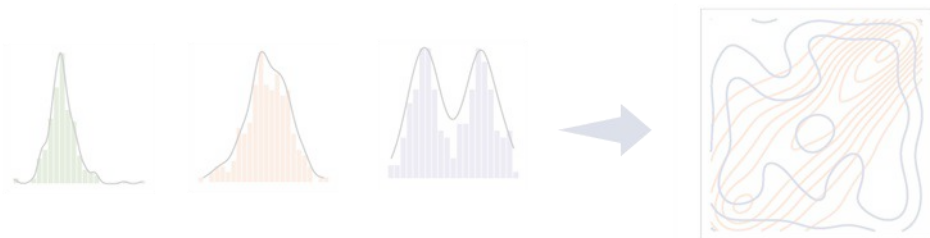


Simulation

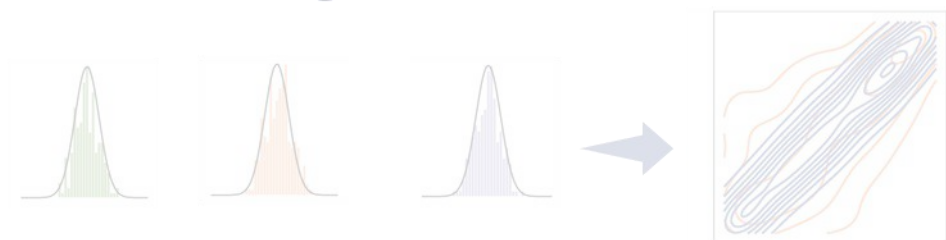


Using copulas (AI) to generate and share realistic virtual populations

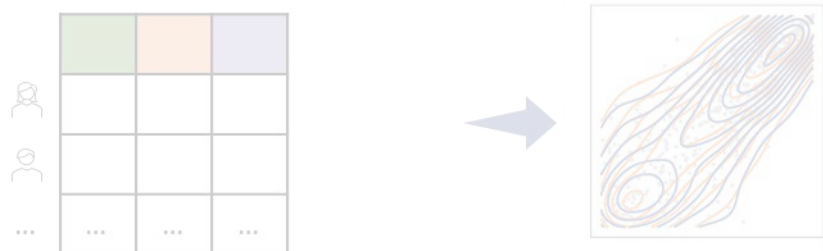
A series of univariate distribution



Multivariate gaussian distribution



Bootstrap (resampling)



Copula, a joint distribution function



Generate realistic VP



Reduce data-sharing barrier

— Observed population — Virtual population

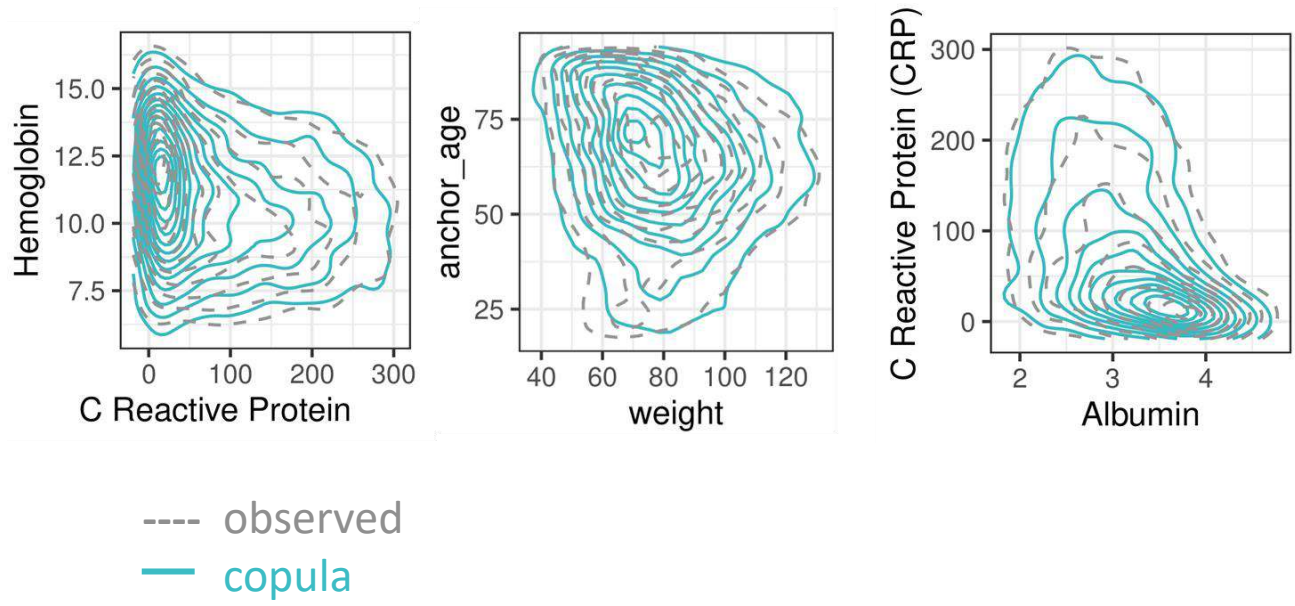
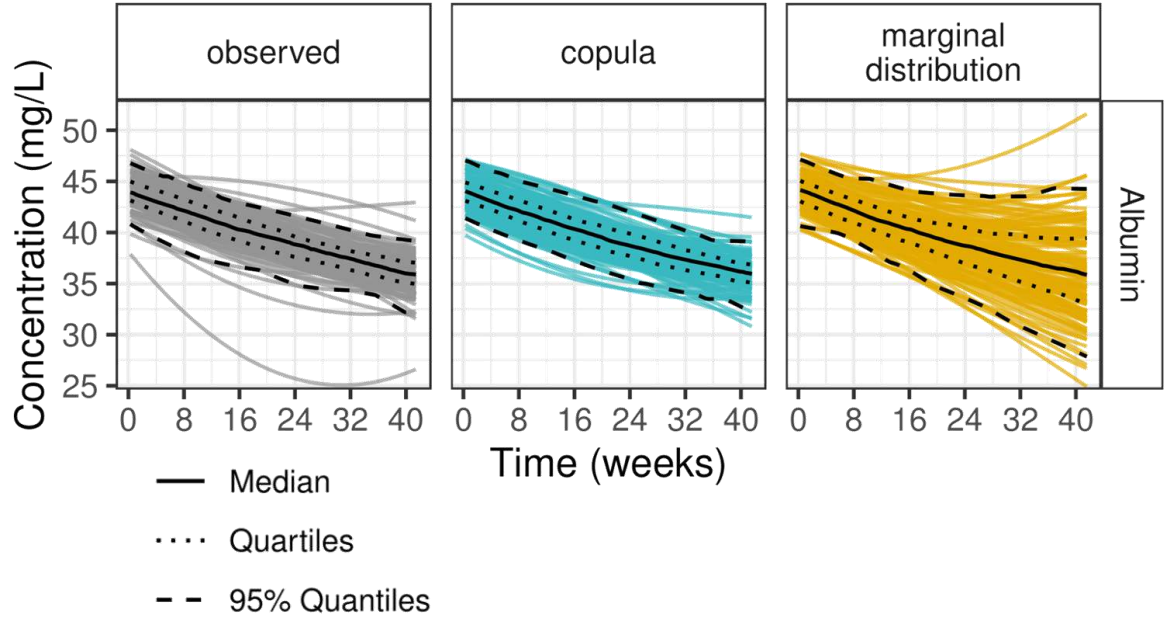
Performance in time-dependent covariates and large data

data Patel, et al. (2013)

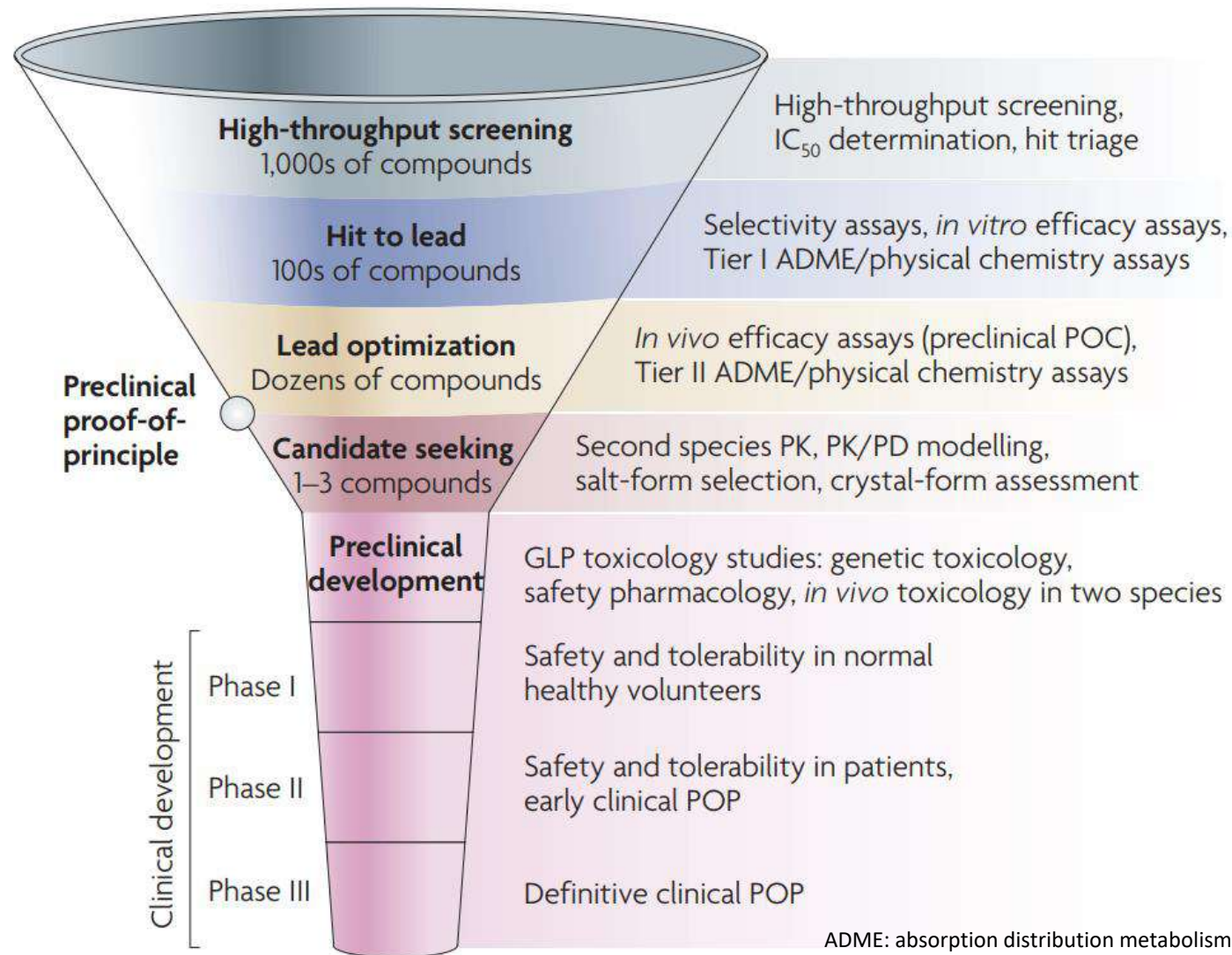
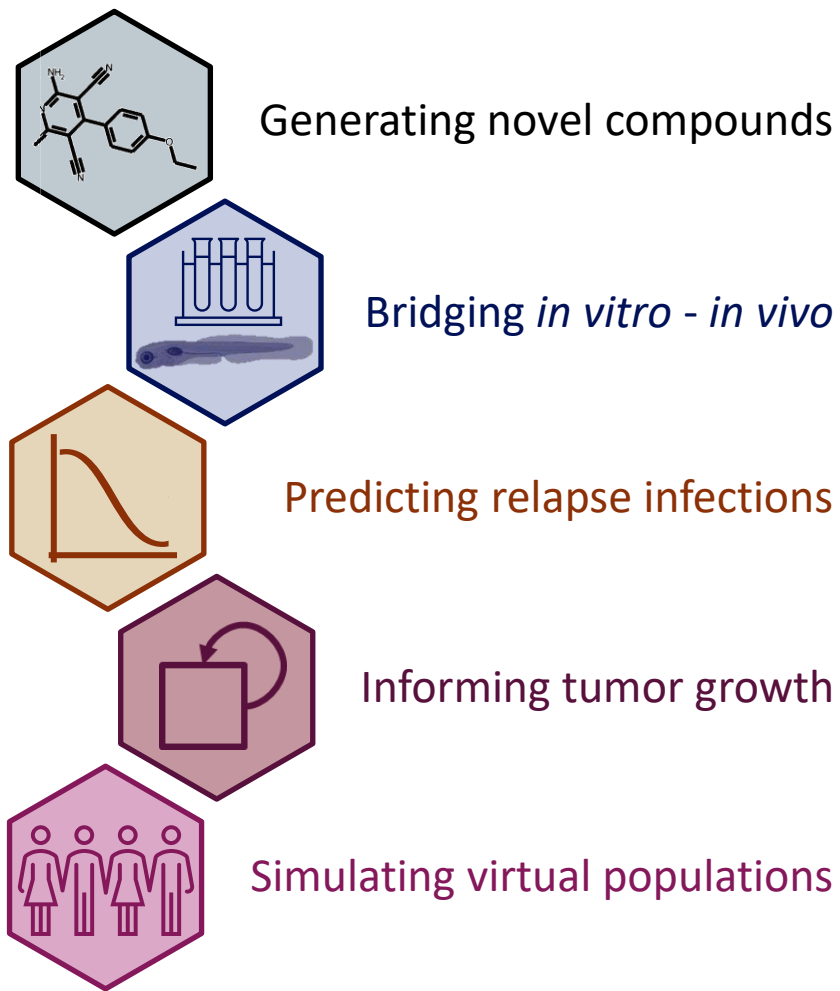
pregnancy, 123 subjects
 6 longitudinal covariates:
 e.g. albumin, bilirubin
 ~14 measurements

data Johnson, et al. (2022)

MIMIC: ICU patients
 30 covariates
 >53.000 patients

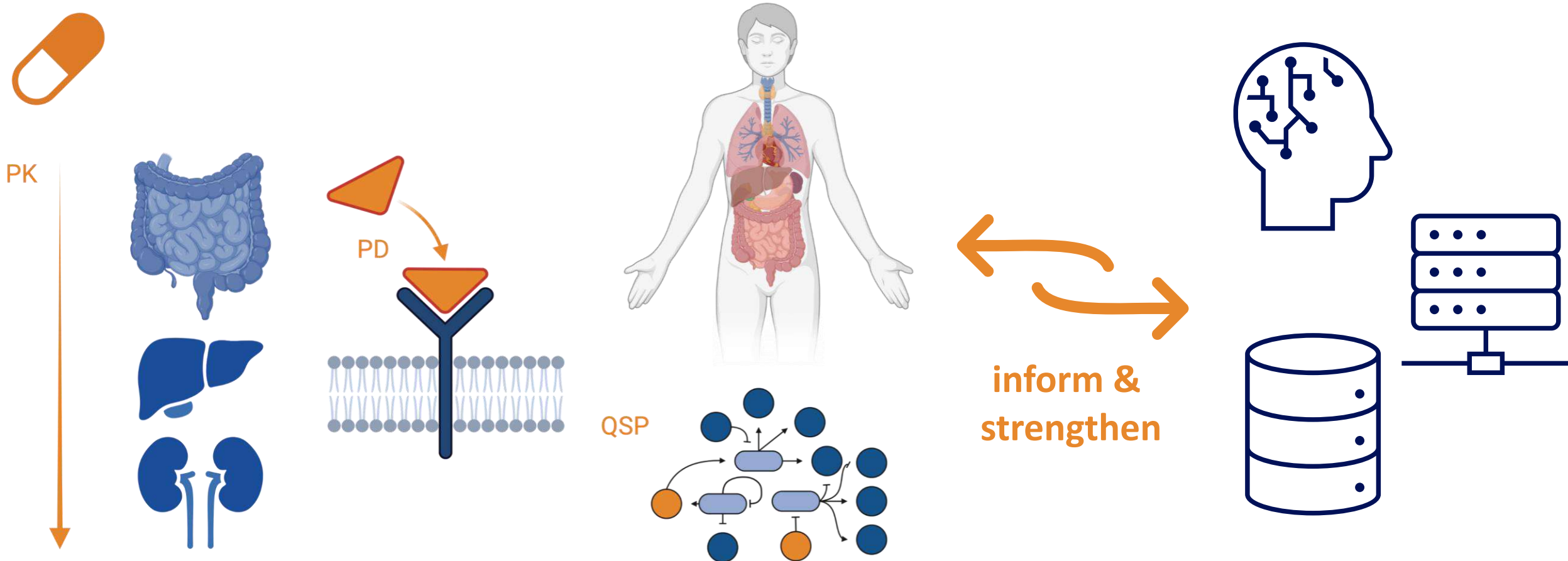


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Mechanistic pharmacological modelling and AI



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Acknowledgments

LACDR | SPP

Laura Zwep
Yuchen Guo
Helle van den Maagdenberg

Translational Immuno-Pharmacology

Collaborators

Leiden University: LUMC, IBL, LIACS
NIH PReDiCTR-TB consortium
University of California, San Francisco
Johns Hopkins University

Graphics

BioRender



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