A Resource for Extrapolating Toxicokinetic Trends Across Chemicals

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1 Expansion of the Concentration *versus*Time Database

1a) What is the CvTdb?

• The Concentration *versus* Time Database (CvTdb) is a database of standardized time-course data of chemical compound concentrations measured *in vivo* from hundreds of diverse publications. It serves as a platform for assessing PK/TK models on a large set of data. (Sayre, Grulke, and Wambaugh, 2020).

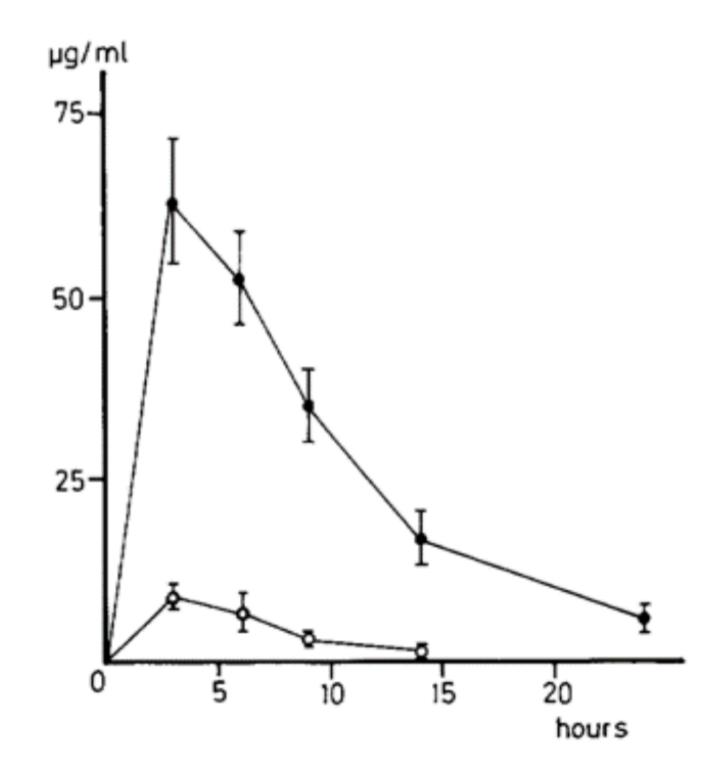


Fig. 1. Plasma concentrations of DEHP (O) and MEHP (\bullet) in rats after single oral administration of 2.8 g/kg DEHP (mean \pm SEM; n=10)

Figure 1: Typical plot from which CvT data is extracted. From Sowa and Steibert (1985).

 The CvTdb contains 389 unique chemicals, including 70 pharmaceuticals (~30%). 101 analytes are present in EPA's ToxCast dataset (~53%).

1b) Integration of Data Shared by Other Institutions

- Showa Pharmaceutical University shared CvT data consisting of over 200 unique compounds (Kamiya *et al.*, 2020; Kamiya *et al.*, 2021).
- If YOU have CvT data, please consider collaborating with us! Visit https://github.com/USEPA/CompTox-PK-CvTdb or email Wambaugh.John@epa.gov

2 Toxicokinetic Trends Across Chemicals

- We can explore trends across chemicals and references using the CvTdb.
- "In PBPK modeling, predictions that are, on average, within a factor of 2 of the experimental data have frequently been considered adequate" (WHO, 2010).
- In Figure 2, 85.1% of replicate timepoint data in the CvTdb is within a factor of two of their respective mean. The "factor of two" rule may not be appropriate if the data itself is spread beyond a factor of two.

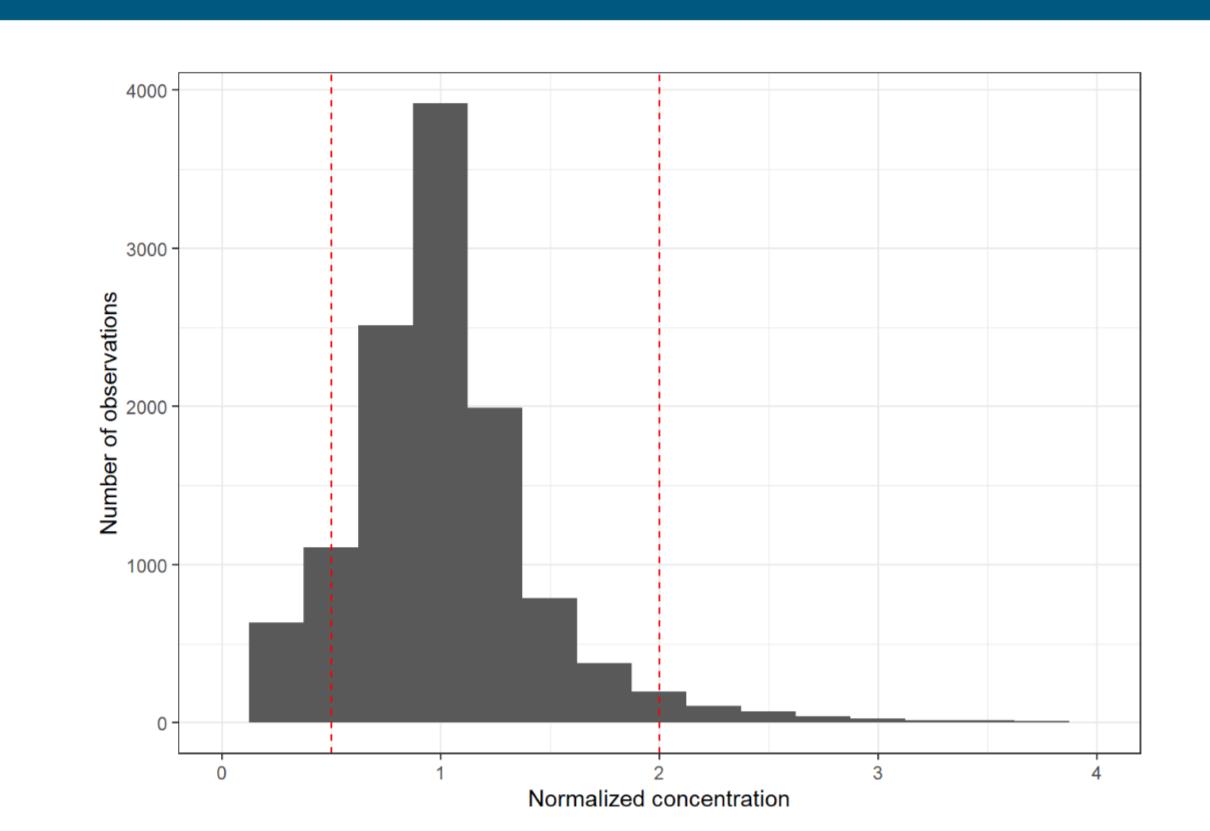


Figure 2: The CvTdb data was grouped into unique combinations of compound/reference/route/dose/timepoint. Groups without replicate timepoints were removed. If all replicate timepoints corresponded to non-detect concentration values, those data were removed. If some, but not all replicate timepoints corresponded to non-detect concentration values, those values were set to equal 0.45 of the minimum value. Each concentration was normalized by the mean concentration of each group.

3 Introducing invivoPKfit

3a) What is invivoPKfit?

 R package that fits 1- and 2- compartment models to CvT data and extrapolates TK parameter values (e.g., half-life, elimination rate, and volume of distribution)

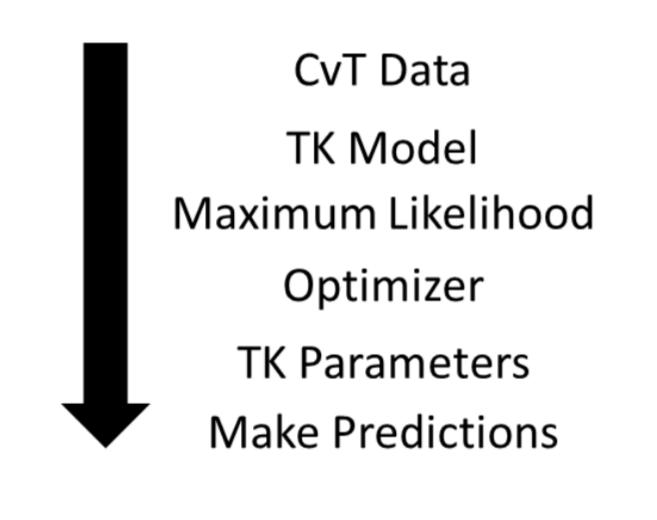
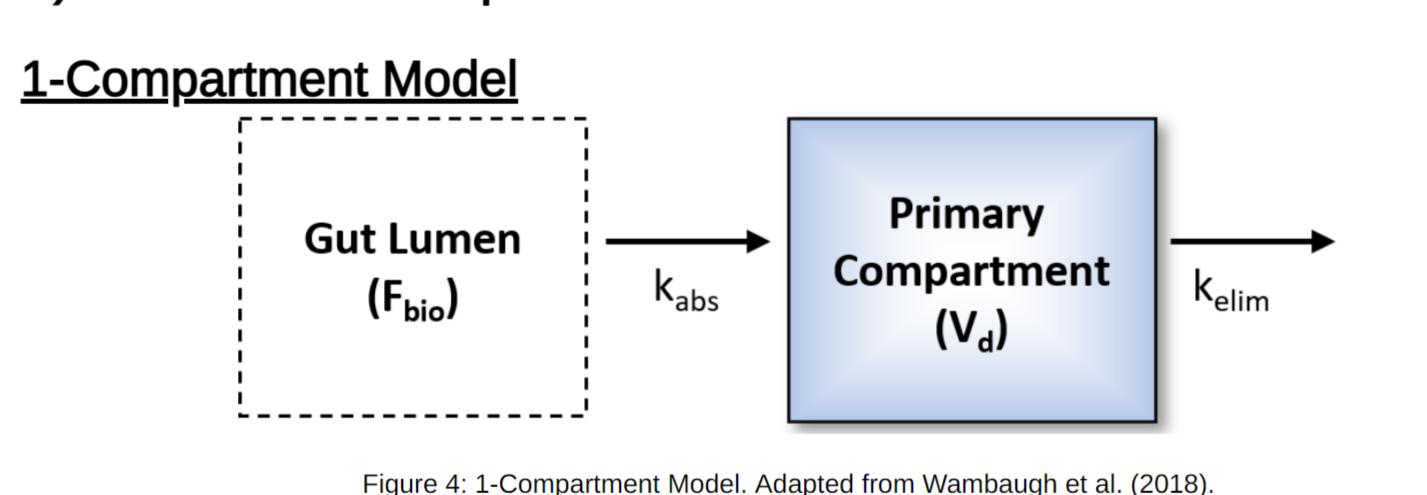


Figure 3: invivoPKfit workflow

3b) TK Model Descriptions



$$C_{iv}(dose,\ t) = rac{dose}{V_d} e^{(-k_{elim}*\ t)}$$
 $F_{bio}*dose = k_{abs}*(e^{-k_{elim}*\ t}-e^{-k_{abs}*\ t})$

• Parameters include V_d (volume of distribution), k_{elim} (elimination rate), k_{abs} (absorption rate; oral only), and F_{bio} (fraction bioavailable; oral only).

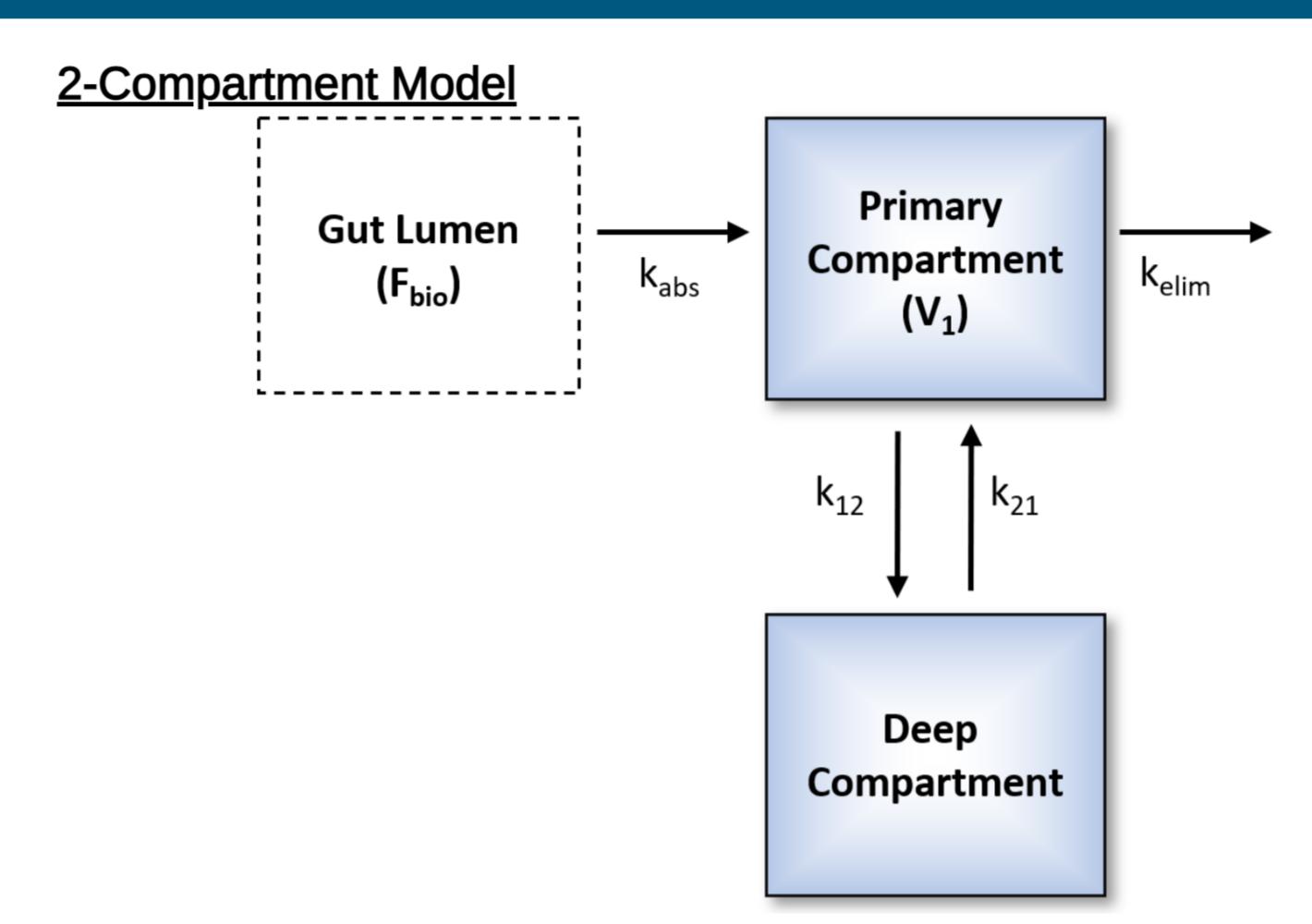


Figure 5: 2-Compartment Model. Adapted from Wambaugh et al. (2018)

$$C_{iv}(dose,\,t)\,=\,A\,*\,e^{-lpha\,*\,t}\,+\,B\,*\,e^{-eta\,*\,t}$$
 $C_{oral}(dose,\,t)\,=\,A\,*\,e^{-lpha\,*\,t}\,+\,B\,*\,e^{-eta\,*\,t}\,+\,C\,*\,e^{-ka\,*\,t}$

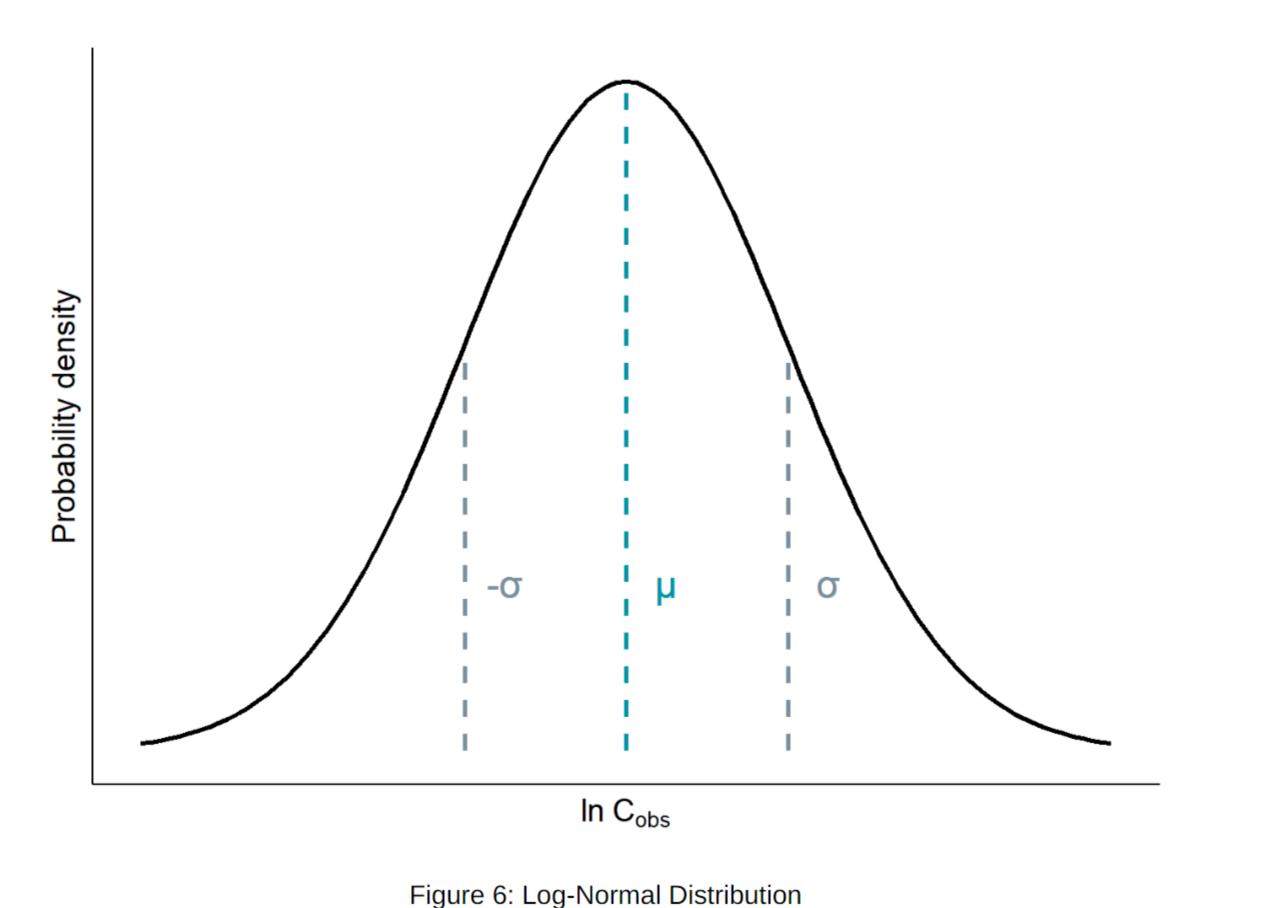
• Parameters include V1 (volume of primary compartment), k_{elim} , k_{12} (distribution rate to deep compartment), k_{21} distribution rate from deep compartment), k_{abs} (oral only), F_{bio} (oral only).

3c) Statistical Model Description

• invivoPKfit calculates the probability of C_{obs} given a PK model $M(p,\,t)$ and a statistical model $S(\sigma)$, where $P=L(C_{obs},\,M,\,S)$, and assumes that C_{obs} are log-normally distributed around the concentrations predicted by $M(p,\,t)$ (Cox and Hinkley, 1979).

$$ln~L(x,~\mu,~\sigma)~=~\Sigma_{i=1,n}lnrac{1}{x\sigma\sqrt{2\pi}}e^{-rac{1}{2}\left(rac{ln~x-\mu)}{\sigma}
ight)^2}$$

$$ln~L(x,~\mu,~\sigma)~=~\Sigma_{i=1,n}lnrac{1}{C_{obs,i}\sigma\sqrt{2\pi}}e^{-rac{1}{2}\left(rac{ln~C_{obs,i}~-~M(p,t_i)}{\sigma}
ight)^2}$$



- The R package, optimx (Nash and Varadhan, 2011; Nash, 2014) optimizes the log-likelihood equation and estimates p and σ .
- We used the Hessian of the likelihood function to estimate standard deviations of the log parameter (Dovi, 1991).

4 invivoPKfit Analyses

4a) Predicted Concentrations

- 63.3% of 16,675 concentrations predicted by the 1-compartment model fit within a factor of two of the observed concentrations.
- 69.1% of 13,097 concentrations predicted by the 2-compartment model fit within a factor of two of the observed concentrations.

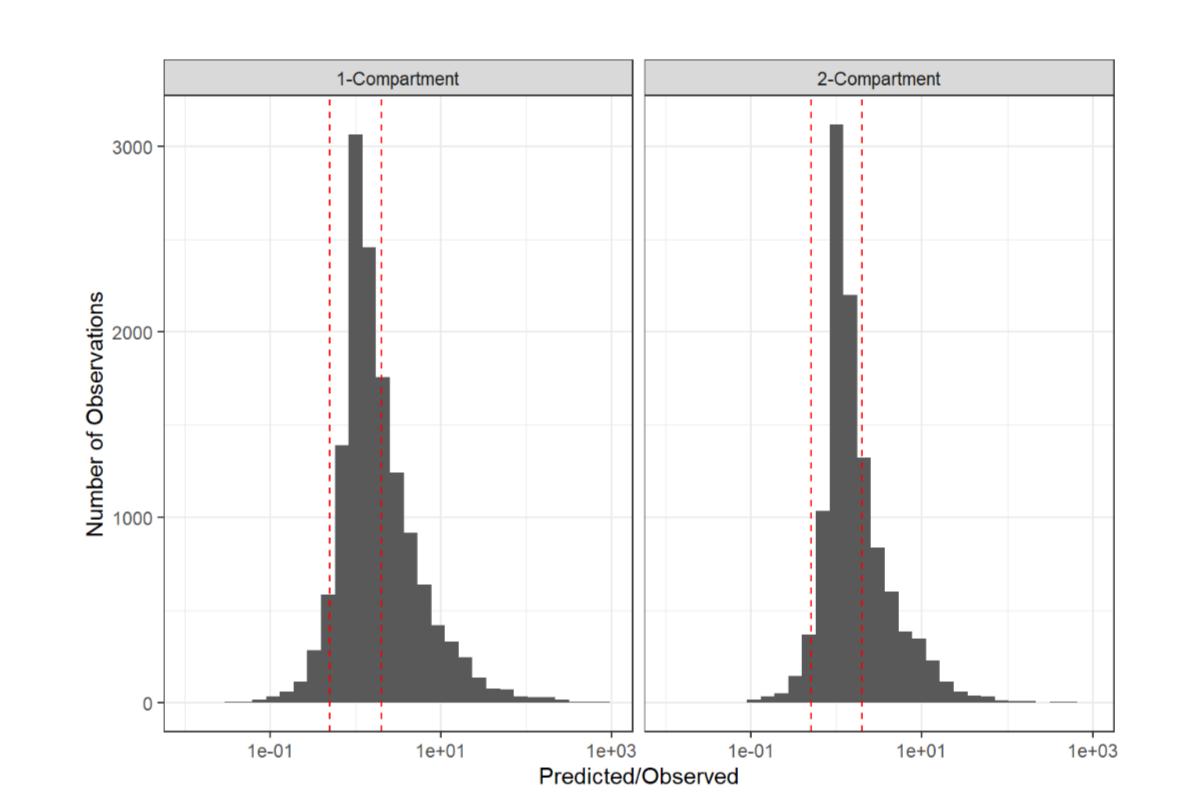


Figure 7: Concentrations were predicted using the estimated model parameters. Predicted concentrations were normalized by observed concentrations, such that C_{pred} / C_{obs} . The red dashed lines mark the 'factor of two' bounds. This plot does not include 'Joint Analysis' fits.

4b) invivoPKfit Performance versus Data Variability

 Can start to gauge how data variability influences the performance of a model

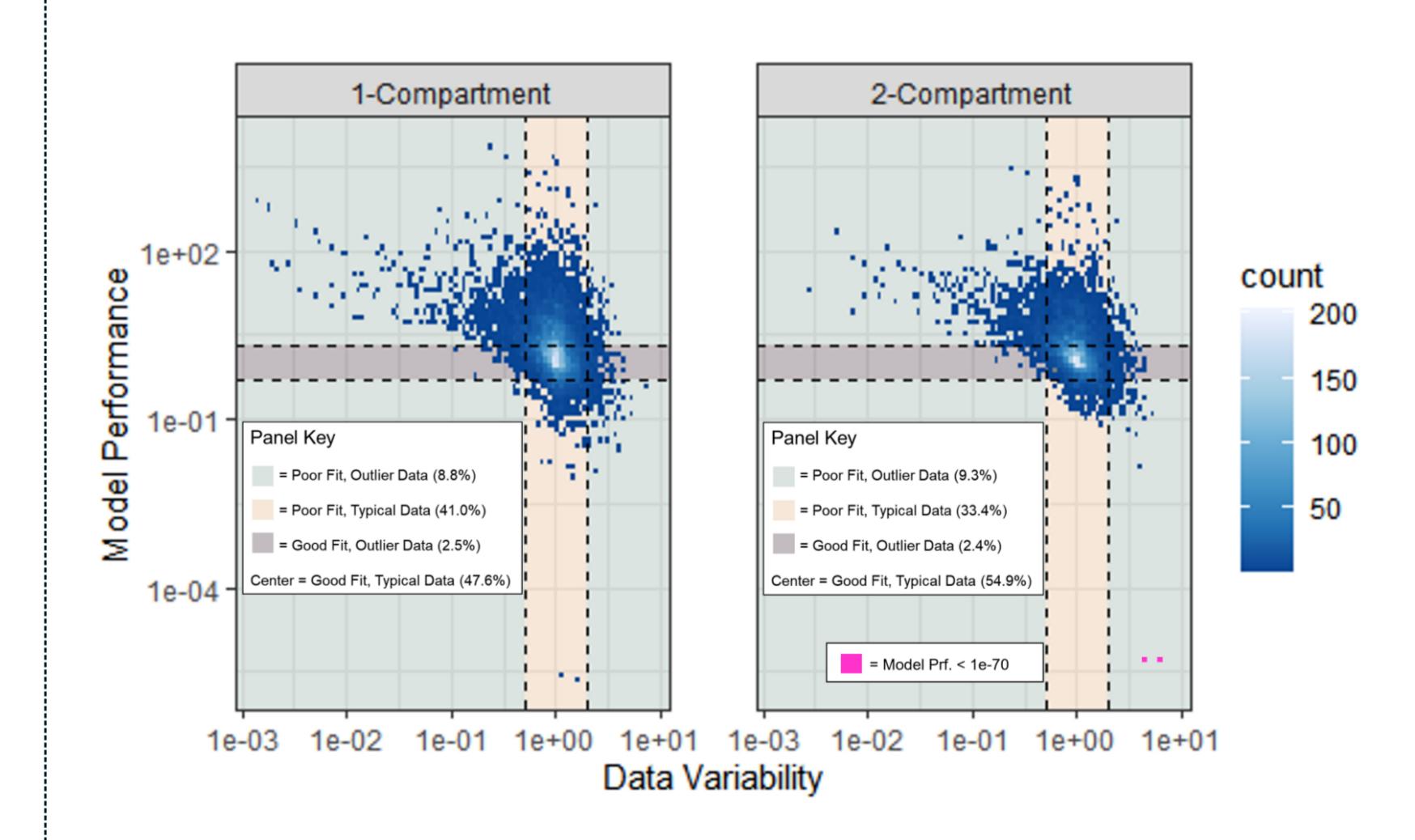


Figure 8: Predicted concentrations were normalized by observed concentrations (see Figure 7), and plotted against observed concentrations normalized by experiment-timpoint specific replicates (see Figure 2). The dashed lines mark the 'factor of 2' bounds f each axis. Sections were assigned based on both the ability of a model to accurately predict an observed concentration and the spread of the observed data. Points colored pink represent concentrations significantly underpredicted by the model.

4c) Diagnosing Poor Fits

 Plotting model predictions against observed data can help determine why a model might fit poorly. A poor fit could indicate 1) a deficiency in the model, 2) an inaccurate curation of data, and/or 3) a deficiency in the experimental collection of data.

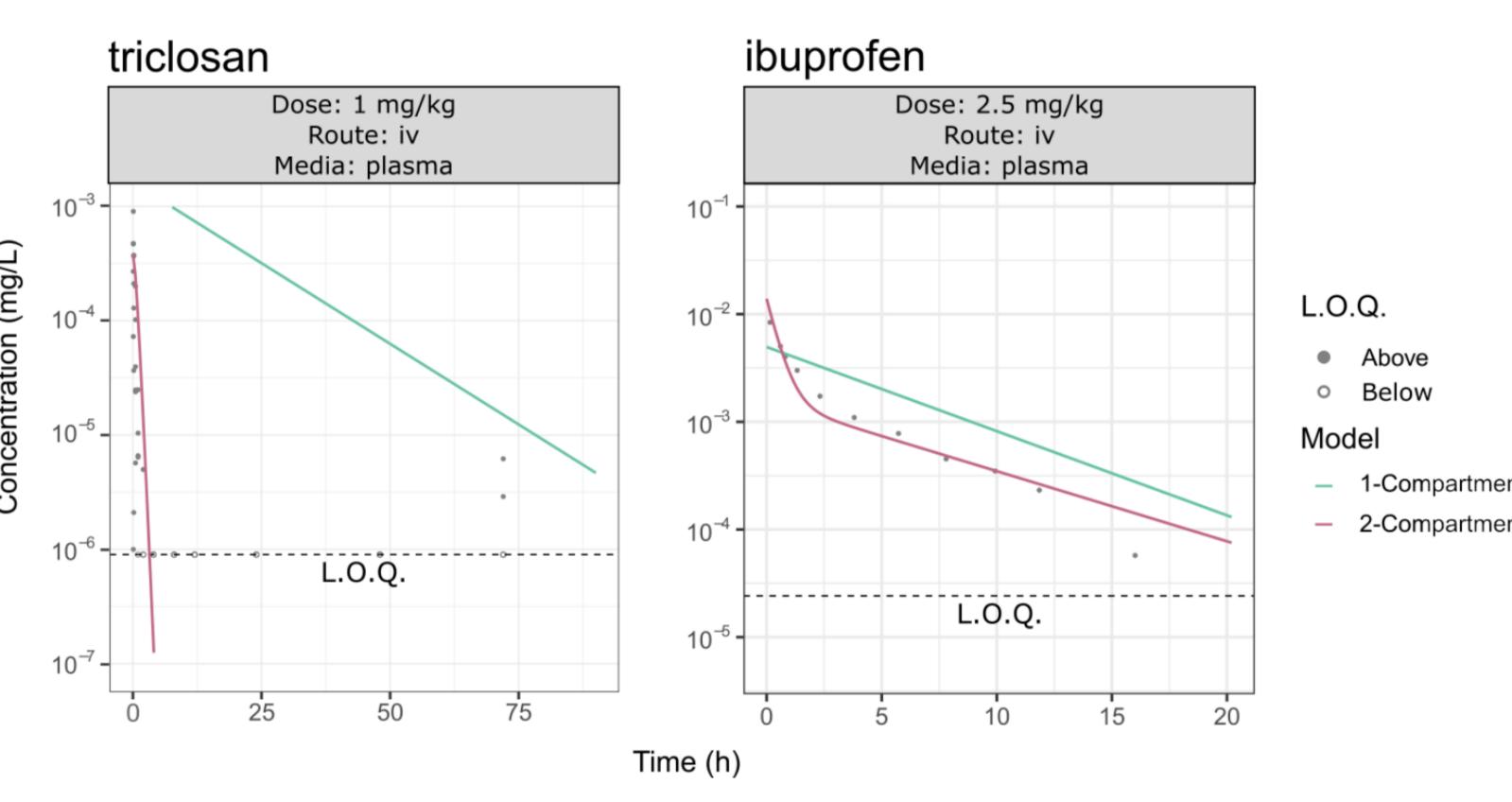


Figure 9: 1-compartment model (green line) and 2-compartment model (red line) fit through CvT data (gray points) Open points represent non-detects that were below the limit of quantitation (L.O.Q.).

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