Title Page

Assessing Liver-to-Plasma Partition Coefficients and In Silico Calculation Methods: When Does the Hepatic Model Matter in PBPK?

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Running Title Page

Model-Dependent Hepatic Partition Coefficients

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ABBREVIATIONS

AUC, area under the curve; \( CL_b \), total blood clearance; \( CL_h \), hepatic clearance; \( CL_{int} \), hepatic intrinsic clearance; CQ, chloroquine; CyA, cyclosporine A; DLZ, diltiazem; DM, dispersion model; DPH, phenytoin; DZP, diazepam; EB, ethoxybenzamide; ER, extraction ratio; FTY720, fingolimod; \( f_{ub} \), unbound fraction in blood; \( f_{up} \), unbound fraction in plasma; HB, hexobarbital; IP, intraperitoneal; IV, intravenous; IVIVE, \textit{in vitro-to-in vivo} extrapolation; \( K_p \), tissue-to-plasma partition coefficient; NIC, nicotine; PBPK, physiologically-based pharmacokinetic; PK, pharmacokinetic; PPN, propranolol; PTM, parallel tube model; PTZ, pentazocine; QD,
quinidine; QSPR, quantitative structure-property relationships; \( R_b \), blood-to-plasma ratio; SS, steady state; TB: tolbutamide; VEM, verapamil; WSM, well-stirred model.
Abstract

The primary models used in pharmacokinetics (PK) to assess hepatic clearance ($CL_h$) are the well-stirred (WSM), parallel tube (PTM), and dispersion model (DM) that differ in their internal flow patterns and assumed unbound liver concentrations. Physiologically-Based Pharmacokinetic (PBPK) models require a hepatic intrinsic clearance ($CL_{int}$) and tissue-to-plasma partition coefficient ($K_p$). Given measured systemic and liver concentration-time profiles, these hepatic models perform similarly but yield model-specific $CL_{int}$ and $K_p$ estimates. This work provides mathematical relationships for the three basic hepatic models and assesses their corresponding PBPK-relevant $K_p$ values with literature-reported single-dose blood and liver concentration-time data of 14 compounds. Model fittings were performed with an open-loop approach where the $CL_h$ and extraction ratio ($ER$) were first estimated from fitting the blood data yielding $CL_{int}$ values for the three hepatic models. The pre-fitted blood data served as forcing input functions to obtain PBPK-operative $K_p$ estimates that were compared with those obtained by the tissue/plasma area ratio (AR), Chen & Gross (C&G) and published in silico methods. The $CL_{int}$ and $K_p$ values for the hepatic models increased with the $ER$ and both showed a rank order being WSM > DM > PTM. Drugs with low $ER$ showed no differences as expected. With model-specific $CL_{int}$ and $K_p$ values, all hepatic models predict the same steady-state $K_p$ ($K_p^{SS}$) that is comparable to those from the AR and C&G methods and reported by direct measurement. All in silico methods performed poorly for most compounds. Hepatic model selection requires cautious application and interpretation in PBPK modeling.

Keywords Hepatic clearance models; Physiologically based pharmacokinetic modeling; Intrinsic clearance; Tissue-to-plasma partition coefficient
Significance Statement

The three hepatic models generate different single-dose (non-steady-state) values of $CL_{int}$ and $K_p$ in PBPK models especially for drugs with high $ER$; however, all $K_p^{ss}$ values expected from constant rate infusion studies were the same. These findings are relevant when using these models for in vitro-to-in vivo extrapolation (IVIVE) where a model-dependent $CL_{int}$ is used to correct measured drug concentrations for depletion of the tissue by metabolism. This model-dependency may also have an impact when assessing the PK/pharmacodynamic relationships when effects relate to assumed hepatic concentrations.
Introduction

Hepatic clearance ($CL_h$) was first extended from the concept of renal clearance by Lewis to describe elimination by the liver (Lewis, 1948). Later, it was further defined as the product of hepatic blood flow ($Q_h$) and extraction ratio ($ER$) (Rowland et al., 1973; Wilkinson and Shand, 1975), and has been one of the most critical parameters in pharmacokinetics (PK) and therapeutic development owing to the pivotal role of liver in eliminating numerous endogenous and exogenous compounds.

The primary models of hepatic elimination in PK to assess and predict the $CL_h$ are the well-stirred (WSM), parallel tube (PTM), and dispersion model (DM) (Bass et al., 1976; Pang and Rowland, 1977; Roberts and Rowland, 1986a; Roberts and Rowland, 1986b). The shared assumptions of these basic hepatic clearance models are that only the unbound drug permeates the hepatocytes; drug distribution into liver is limited by the blood flow without any diffusion barriers; and there is equilibration between drug concentration in the liver and that in the emergent venous blood, i.e., the unbound drug concentration in blood relates to that in the tissue. While the major difference among these models lies in the assumed internal blood flow patterns that result in differing unbound drug concentrations along the sinusoidal flow path within the liver (e.g., bulk flow with infinite mixing creating uniform concentrations for the WSM, plug flow with no mixing resulting in a mono-exponential concentration decline for the PTM, and dispersive flow with some extent of mixing rendering a continuous concentration decline for the DM that lies in between those of the WSM and PTM). Although the WSM is the least physiological, the lesser complexities in math and easier operative feature have made it the most widely used hepatic model for making predictions of the in vivo $CL_h$ using metabolic data obtained from various in vitro systems (in vitro-to-in vivo extrapolation, IVIVE) (Rane et al.,
1977; Houston, 1994; Hallifax et al., 2010) and for applying physiologically-based pharmacokinetic (PBPK) models (Miller et al., 2019).

The WSM has been a vigorous topic of discussion in the PK field in describing the hepatic elimination process and predicting the \textit{in vivo} $CL_h$ by IVIVE (Roberts and Rowland, 1986a; Houston and Carlile, 1997; Iwatsubo et al., 1997; Naritomi et al., 2001; Ito and Houston, 2004; Kilford et al., 2009; Benet et al., 2018; Rowland and Pang, 2018; Pang et al., 2019; Sodhi et al., 2020). Nevertheless, the basic hepatic models remain highly useful as starting points in PK and PBPK in considerations of the hepatic distribution and elimination process for drugs. In practice, PBPK models of hepatic elimination require two important parameters when describing the hepatic disposition of a drug, i.e., the intrinsic clearance ($CL_{\text{int}}$) that reflects the innate ability of the liver to remove the drug from the body by metabolism or excretion with the reference concentration being the unbound drug within the organ and the liver-to-plasma partition coefficient ($K_p$) that represents the extent of drug distribution. Theoretically, given the same measured systemic and liver concentration-time profiles, these hepatic models yield model-specific $CL_{\text{int}}$ and $K_p$ estimates because of the differed intra-organ unbound concentrations. The theoretical expectations of the model dependencies in the $CL_{\text{int}}$ and unbound tissue concentrations have been reviewed (Pang et al., 2019; Rowland et al., 2022). However, there have been no comprehensive comparisons of their applications in PBPK models and the resulting $K_p$ values when assessing \textit{in vivo} time course data. It also remains vague about how to incorporate the more realistic models of hepatic elimination (i.e., PTM and DM) in PBPK.

Values for $K_p$ are needed in operation of PBPK models (as will be shown). The simplest concept of $K_p$ originated with Gillette (Gillette, 1971) who considered it to be the ratio of the fraction of drug unbound in plasma ($f_{up}$) to fraction unbound in tissues ($f_{uT}$). Over time, the complexity of
tissue drug distribution has been appreciated and extended to considerations of binding to various tissue components, lipid partitioning, and ionization with further complications produced by differential permeability, convection, and involvement of transporters (Jusko et al., 2020). Further, when assessed for a clearance organ such as liver, it is well appreciated that the occurrence of metabolism causes partial depletion of the tissue making the experimental measurement of $K_p$ subject to the need for a correction factor based on $Q_h$ and $CL_{int}$ (Chen and Gross, 1979; Jeong and Jusko, 2022). Based on an extended WSM, we previously described how the $K_p$ will also differ based on the experimental approach; the single-dose/non-steady-state (SS) $K_p$ will differ from that obtained under SS conditions ($K_{p,ss}$). It can thus be said that the ‘true’ $K_p$ of the liver is ‘unknowable’ owing to the need for a hepatic model that produces a model-dependent $CL_{int}$ value. Ultimately, $K_p$ values for liver can be generated by various means including model-corrected tissue analyses, fitting experimental data (PBPK models), extrapolation from in vitro tissue dilution studies, or prediction based on physicochemical properties and tissue composition. They often differ with uncertainties regarding the ‘best’ value. This work provides an overview of the assumptions, definitions, and mathematical relationships for the three basic hepatic models and assesses their corresponding $K_p$ values relevant to PBPK models using the published single-dose blood/plasma and liver concentration-time data of 14 flow-limited compounds with liver being the primary site of elimination and exhibiting a wide range of hepatic $ER$. The liver $K_p$ of the model compounds were also estimated by the model-fitted tissue/plasma area ratio (AR) (Gallo et al., 1987), Chen & Gross (C&G) (Chen and Gross, 1979) and published in silico (Poulin and Theil, 2002a; Poulin and Theil, 2002b; Berezhkovskiy, 2004; Rodgers and Rowland, 2006; Lukacova et al., 2008a; Assmus et al., 2017) methods for comparisons.
Theory

The well-acknowledged definition of $CL_h$ is the elimination rate of a drug at steady-state (SS) by the liver divided by the input drug concentration (Rowland, 1972):

$$CL_h = \frac{\text{Elimination rate}}{C_{in}} = \frac{Q_h(C_{in} - C_{out})}{C_{in}} = Q_h ER \tag{1}$$

where $Q_h$ is liver blood flow, $C_{in}$ and $C_{out}$ are the input and output blood concentrations for the liver, and $ER$ is the hepatic extraction ratio.

In PBPK models, for flow-limited substances, the mass balance for the liver is expressed as:

$$V_h \frac{dC_h}{dt} = Q_h(C_{in} - C_{out}) - f_{uh}CL_{int}C_h \tag{2}$$

where $C_h$ is the measured hepatic drug concentration, $V_h$ is the liver volume, $f_{uh}$ is the unbound fraction in the liver, and $CL_{int}$ is the intrinsic clearance representing the intrinsic ability of the liver to remove the drug. In assuming that the free drug hypothesis applies, the $CL_{int}$ acts upon the unbound hepatic drug concentrations, $C_{uh} = f_{uh}C_h$.

At SS, it can be seen from Eqs. 1 and 2 that:

$$\text{Elimination Rate} = CL_hC_{in} = CL_{int}C_{uh} \tag{3}$$

where $CL_h$ and $C_{in}$ are usually model-independent for a drug primarily cleared by the liver, while $CL_{int}$ and $C_{uh}$ differ according to the assumed hepatic CL model.

Hepatic Clearance Models

The three basic hepatic CL models (viz. WSM, PTM and DM) along with their assumptions have been described in detail (Rowland et al., 1973; Pang and Rowland, 1977; Roberts and Rowland, 1986a; Roberts and Rowland, 1986b; Pang et al., 2019; Jusko and Li, 2021). Basically, the internal flow pattern of the liver is assumed to differ with different hepatic models. The dispersion number ($D_N$), which quantifies the degree of axial dispersion of a substance as it transits through the liver is used to differentiate the models.
The WSM assumes that the liver is a single and well-stirred compartment with infinite mixing ($D_N = \infty$), which yields a uniform drug concentration in blood throughout the liver. It is identical to that in blood leaving the liver owing to its instantaneous equilibrium with the liver tissue concentration. Therefore:

$$C_{hb, WSM} = C_{out}$$ (4)

$$C_{uh, WSM} = C_{uhb, WSM} = f_{uh} C_h = f_{ub} C_{hb, WSM} = f_{ub} C_{out}$$ (5)

where $C_{hb, WSM}$ and $C_{uhb, WSM}$ are the total and unbound blood concentrations within the liver for the WSM.

Replacing the $f_{uh} C_h$ term by $f_{ub} C_{out}$ in Eq. 2 under SS conditions gives:

$$Q_h (C_{in} - C_{out}) = f_{ub} C_{L_{int, WSM}} C_{out}$$ (6)

and

$$\frac{C_{out}}{C_{in}} = F_h = \frac{Q_h}{Q_h + f_{ub} C_{L_{int, WSM}}}$$ (7)

where $C_{L_{int, WSM}}$ is the intrinsic clearance for the WSM, $F_h$ is the hepatic availability of a drug, which also equals the oral bioavailability if the drug is exclusively cleared by the liver.

Thus, for the WSM, the mathematical relationship between $ER$ and $f_{ub} C_{L_{int, WSM}}$ can be expressed according to Eq. 7 as:

$$ER = \frac{f_{ub} C_{L_{int, WSM}}}{Q_h + f_{ub} C_{L_{int, WSM}}}$$ (8)

and

$$f_{ub} C_{L_{int, WSM}} = \frac{Q_h ER}{1 - ER}$$ (9)

Subsequently, the well-appreciated equation for calculating $CL_h$ based on the WSM is:

$$CL_h = Q_h \frac{f_{ub} C_{L_{int, WSM}}}{Q_h + f_{ub} C_{L_{int, WSM}}}$$ (10)
The PTM assumes that the liver is comprised of an array of identical and parallel tubes with enzymes distributed evenly in each cross-section of the sinusoidal vascular and perivascular space. No axial spreading ($D_N = 0$) occurs as the drug moves through the liver, resulting in exponentially declining blood concentrations from the inlet to the outlet of the liver. The length-averaged unbound blood concentration in the sinusoid at SS is given by the logarithmic mean of the unbound inlet and outlet concentrations and equals the unbound liver tissue concentration for the PTM:

$$C_{uh,PTM} = C_{uhb,PTM} = \frac{f_{ub}(C_{in} - C_{out})}{\ln(C_{in}/C_{out})} \quad (11)$$

and

$$C_{hb,PTM} = \frac{(C_{in} - C_{out})}{\ln(C_{in}/C_{out})} \quad (12)$$

where $C_{hb,PTM}$ and $C_{uhb,PTM}$ are the total and unbound blood concentrations within the liver for the PTM.

Under SS, combining Eqs. 2 and 12 gives:

$$Q_h(C_{in} - C_{out}) = f_{ub}C_{L_{int,PTM}} \frac{C_{in} - C_{out}}{\ln(C_{in}/C_{out})} \quad (13)$$

and

$$\frac{C_{out}}{C_{in}} = F_h = e^{-\frac{f_{ub}C_{L_{int,PTM}}}{Q_h}} \quad (14)$$

where $C_{L_{int,PTM}}$ is the intrinsic clearance for the PTM.

Based on Eq. 14, the following equations are applicable to the PTM:

$$ER = 1 - e^{-\frac{f_{ub}C_{L_{int,PTM}}}{Q_h}} \quad (15)$$

$$f_{ub}C_{L_{int,PTM}} = -Q_h\ln(1 - ER) \quad (16)$$
\[ CL_h = Q_h \left(1 - e^{-\frac{f_{ub}CL_{int,PTM}}{Q_h}}\right) \]  

(17)

The internal flow pattern of the DM lies between those of the WSM and the PTM, which assumes a dispersive flow with some extent of longitudinal or axial spreading of a substance during the transit through an organ \((0 < D_N < \infty)\). The reported \(D_N\) values for liver range from 0.2 to 0.6 (Diaz-Garcia et al., 1992; Chou et al., 1993; Evans et al., 1993; Oliver et al., 2001). The DM is described by a set of second-order partial differential equations that are defined in time and space, and are only solvable after specifying the boundary conditions (Roberts and Rowland, 1986a). Briefly, it has been shown for the DM that the ratio between \(C_{out}\) and \(C_{in}\) (viz. the hepatic availability \(F_h\)) is identical at SS and following a bolus dose based on the closed boundary conditions \((0 < Z < 1, \text{where } Z \text{ is defined as the distance along the length of the liver})\) (Roberts and Rowland, 1986a; Roberts and Rowland, 1986b) which is given by:

\[ \frac{C_{out}}{C_{in}} = F_h = \frac{4a}{(1+a)^2e^{(a-1)/2D_N}-(1-a)^2e^{-(a+1)/2D_N}} \]  

(18)

Where \(a = (1+4D_NR_N)^{1/2}\), and \(R_N\), the efficiency number that measures the removal rate of substances by liver cells, is given by:

\[ R_N = \frac{f_{ub}CL_{int,DM}P}{Q_h} \]  

(19)

where \(CL_{int,DM}\) is the intrinsic CL for the DM, \(\rho\) is the effective partition coefficient for the unbound drug, defined as:

\[ \rho = \frac{P}{P + CL_{int,DM}} \]  

(20)

where \(P\) is the permeability of the drug to the hepatocyte. In the present analysis, the one-compartment DM (e.g., \(P >> CL_{int,DM}\) when there is no permeability limitation of the drug to the hepatocyte) was assumed for small-molecule lipophilic drugs; Eq. 19 is thus reduced to:

\[ R_N = \frac{f_{ub}CL_{int,DM}}{Q_h} \]  

(21)
Therefore, the $ER$ and $CL_h$ for the DM are:

$$ER = 1 - \frac{4a}{(1+a)^2 e^{-(1-a)/2D_N} - (1-a)^2 e^{-(1+a)/2D_N}}$$  \hspace{1cm} (22)$$

$$CL_h = Q_h (1 - \frac{4a}{(1+a)^2 e^{-(1-a)/2D_N} - (1-a)^2 e^{-(1+a)/2D_N}})$$  \hspace{1cm} (23)$$

Eq. 22 reduces to Eq. 8 with $D_N = \infty$ for the WSM and to Eq. 15 with $D_N = 0$ for PTM, showing that the WSM and the PTM serve as two extremes of the basic hepatic models with the DM being a more general form.

According to Eq.3, the $C_{uh}$ and $C_{uh,b}$ for the DM can be calculated from:

$$C_{uh,DM} = C_{uh,b,DM} = \frac{CL_h C_{in}}{CL_{int,DM}}$$  \hspace{1cm} (24)$$
Materials and Methods

Assessing Liver $CL_{int}$ and $K_p$ in PBPK Models

Model Compounds and Literature Data Sources

The model compounds were selected based on the following criteria:

- Liver is the major eliminating organ
- Extrahepatic clearances are known or assumed to be negligible
- Absorption rates are high
- ER ranges from low to high
- Time courses of blood/plasma and liver concentrations are available from the literature
- Distribution into the liver and access to the hepatic enzymes are flow-limited (high permeability) with minor or negligible transporter involvements

Upon searching the literature, the measured blood or plasma and liver concentration-time data in rats were found for 14 compounds (tolbutamide (TB), cyclosporine A (CyA), chloroquine (CQ), ethoxybenzamide (EB), fingolimod (FTY720), nicotine (NIC), phenytoin (DPH), diazepam (DZP), propranolol (PPN), pentazocine (PTZ), quinidine (QD), verapamil (VEM), diltiazem (DLZ), and hexobarbital (HB)). Concentration versus time data were digitized from the published graphs in the literature (Tables 1 and 2) using GetData Graph Digitizer version 2.26 (http://getdata-graph-digitizer.com/). All in vivo data were obtained from intravenous (IV) bolus studies except that the liver concentration-time profile of CQ was only available after intraperitoneal (IP) bolus administration (Adelusi and Salako, 1982).

Detailed justifications for the selection of model compounds are provided in the Supplemental Methods.

Estimating in vivo Liver $K_p$ of Model Compounds by Hepatic Clearance Models
A piecewise model fitting approach was adopted in which the blood/plasma concentration time data was fitted first and then used as the forcing input function to characterize the liver concentrations as a single organ. This method, also termed an open-loop method or a forcing function approach, was initially proposed (Ebling et al., 1994) to simulate the disposition of thiopental in the rat and was later applied by others (Foster, 1998; Gueorguieva et al., 2004; Cheung et al., 2018).

**Blood/Plasma Concentration-Time Profiles**

For compounds without any blood concentrations \((C_b)\) available, their reported plasma concentrations \((C_p)\) were first converted to \(C_b\) by multiplying by the blood-to-plasma ratio \((R_b)\) before fitting. The \(C_b\)-time data of each drug were fitted by one of the following exponential equations:

\[
C_b = \begin{cases} 
Ae^{-\alpha t} + Be^{-\beta t} & \text{if } C_b \geq C_b0 \\
Ae^{-\alpha t} + Be^{-\beta t} + Ce^{-\gamma t} & \text{if } C_b < C_b0
\end{cases}
\]

\(C_b0 = \text{Dose}/V_b\)  \(\text{Eq. 25}\)

where \(A, B, C\) are the intercepts, \(\alpha, \beta, \gamma\) are the slopes, \(C_b0\) is the initial blood concentration at time 0, and \(V_b\) is the average value of the reported blood volumes in the source literature (78 mL/min/kg).

The total blood clearance \((CL_b)\) and \(ER\) were estimated from:

\[
CL_b = \frac{\text{Dose}}{AUC_b}
\]

\(\text{Eq. 26}\)

and

\[
ER = \frac{CL_b}{Qh}
\]

\(\text{Eq. 27}\)

where \(AUC_b\) is the area under the \(C_b\)-time curves. Eq. 27 assumed that the liver is the only eliminating organ with \(CL_b = CL_h\). Although minor, the contribution of extrahepatic clearance by kidney has been reported for CQ (Liu and Jusko, 2021) and NIC (Plowchalk et al., 1992).
Therefore, the $CL_h$ of these two drugs was estimated by subtracting the reported extrahepatic $CL$ from $CL_b$. The reported $Q_h$ values shown in Table 1 were used for $ER$ calculation except for VEM and DLZ for which the value of 60.82 mL/min/kg (Brown et al., 1997) was applied due to the unavailability of the reported $Q_h$. To allow for fair comparisons among different hepatic models, the same $Q_h$ value of 60.82 mL/min/kg was also used for back calculating the $f_{ub}CL_{int}$ associated with each of the hepatic models as well as the subsequent model fittings of liver data. The estimated $ER$ for each compound was then fixed and used to obtain the model dependent $CL_{int}$ based on Eq. 9 and 16 for the WSM and PTM, as well as the following equation for the DM based on Eq. 21:

$$f_{ub}CL_{int,DM} = R_N Q_h$$

(28)

where $R_N$ was determined from Eq. 22 with a $D_N$ value of 0.6 for the liver (Oliver, 1995; Oliver et al., 2001). The simulated profile of $ER$ vs $R_N$ based on Eq. 22 is displayed in Figure S1.

**Fitting Liver Concentration-Time Data by Hepatic Clearance Models**

Although the assumed internal flow pattern and the resulted unbound tissue and blood concentration within the liver differ, all three basic hepatic clearance models assume perfusion rate-limited distribution and instantaneous equilibrium between the liver tissue $C_h$ ($x$, $t$) and blood $C_{hb}$ ($x$, $t$) concentration at distance $x$ in the liver and time $t$ for flow-limited substances; therefore, the following relationship applies:

$$C_{hb}(x, t) = \frac{R_0C_h(x,t)}{K_p}$$

(29)

where $K_p$ is an apparent value that is also dependent on the assumed hepatic model given the same measured total liver concentration ($C_h$) owing to the model-dependency of $C_{hb}$. 
Since whole liver tissue was collected and homogenized for drug analysis in all the referenced studies, the measured liver concentration at each time point \( t \) is considered as the tissue space-averaged value. Therefore, Eq. 29 becomes the following for all three hepatic models:

\[
C_{hb}(t) = \frac{R_{b}Ch(t)}{K_p}
\]

(30)

Combining Eq. 2, 7 and 30, the change of liver concentrations corresponding to the WSM is given by:

\[
V_h \frac{dC_h}{dt} = Q_h \left( C_{in} - C_{in} \frac{Q_h}{Q_h + f_{ub}CL_{int,WSM}} \right) - f_{ub}CL_{int,WSM} \frac{R_{b}Ch}{K_{p,WSM}}
\]

(31)

where \( C_{in} \) is the previous model-fitted \( C_b \) of each model compound by Eq. 25, \( Q_hC_{in} \) is the forcing input function to fit the liver data and obtain \( K_p \) estimates, and \( V_h \) was assigned a value of 36.6 mL/kg (Brown et al., 1997). Since the liver data of CQ and CyA had been corrected for residual blood, \( V_h \) was adjusted by multiplying the fraction of liver vascular space applied by the source literature (Bernareggi and Rowland, 1991; Kawai et al., 1998; Liu and Jusko, 2021).

Combining Eq. 2, 14 and 30, the concentration changes in the liver corresponding to the PTM are given by:

\[
V_h \frac{dC_h}{dt} = Q_h \left( C_{in} - C_{in} e^{-\frac{f_{ub}CL_{int,PTM}}{Q_h}} \right) - f_{ub}CL_{int,PTM} \frac{R_{b}Ch}{K_{p,PTM}}
\]

(32)

Combining Eq. 2, 18 and 30, the mass balance of liver corresponding to the DM is described by:

\[
V_h \frac{dC_h}{dt} = Q_h \left( C_{in} - C_{in} \frac{4a}{(1+a)^2 a^2 e^{(a-1)/2bN} - (1-a)^2 a^2 e^{-(a+1)/2bN}} \right) - f_{ub}CL_{int,DM} \frac{R_{b}Ch}{K_{p,DM}}
\]

(33)

The liver \( K_p \) values of all compounds except QD and CQ were estimated by fitting the liver concentration-time profiles using Eq. 31-33. In the case of QD and CQ, nonlinear binding in the liver was reported (Harashima et al., 1985; Liu and Jusko, 2021):

\[
C_{bh} = \frac{B_{max}C_{uh}}{K_d + C_{uh}}
\]

(34)
where $C_{bh}$ is the bound concentration of CQ or QD in the liver; $C_{uh}$ and $C_h$ can be calculated from:

$$C_{uh} = C_{uhb} = f_{ub} C_{hb} \quad (35)$$

and

$$C_h = C_{uh} + C_{bh} \quad (36)$$

For simplicity, linear binding of QD in plasma and red blood cells was assumed with the $R_b$ and unbound fraction in the plasma ($f_{up}$) calculated to be 1.52 and 0.325 (Harashima et al., 1985) (Table S2). Therefore, by combining Eq. 30 and 34-36, the concentration-dependent $K_p$ of CQ and QD is expressed by:

$$K_p = f_{ub} R_b (1 + \frac{B_{max}}{K_d+C_{uh}}) = f_{up} (1 + \frac{B_{max}}{K_d+C_{uh}}) \quad (37)$$

where $C_{uh}$ is replaced by Eq. 5 for the WSM, Eq. 11 for the PTM, and Eq. 24 for the DM.

Setting Eq. 31-33 equal to 0 under SS conditions, the $K_p$ associated with each of the hepatic models is:

$$K_{p,WSM} = \frac{C_{h}^{SS}}{C_{in}^{SS}} R_b \left( \frac{Q_h + f_{ub} CL_{int,WSM}}{Q_h} \right)$$

$$= \frac{C_{h}^{SS}}{C_p^{SS}} \left( f_{ub} CL_{int,WSM} \right) \quad (38)$$

$$K_{p,PTM} = \frac{C_{h}^{SS}}{C_{in}^{SS}} \left( \frac{R_b f_{ub} CL_{int,PTM}}{Q_h \left( 1 - e^{-CL_{int,PTM}/Q_h} \right)} \right)$$

$$= \frac{C_{h}^{SS}}{C_p^{SS}} \left( f_{ub} CL_{int,PTM} \right) \quad (39)$$
\[ K_{p,DM} = \frac{c_{h}^{ss}}{c_{in}^{ss}} \left( \frac{R_b f_{ub} CL_{int,DM}}{Q_h \left( 1 - \frac{(a-1)}{(a+1)^2 e^{2DN} - (1-a)^2 e^{-2DN}} \right)} \right) \]

\[ = \frac{c_{h}^{ss}}{c_{p}^{ss}} \left( \frac{f_{ub} CL_{int,DM}}{Q_h ER} \right) \tag{40} \]

where \( C_{h}^{ss}, C_{in}^{ss} \) and \( C_{p}^{ss} \) are the liver, blood and plasma concentrations at SS, and the ratio of \( C_{h}^{ss} \) and \( C_{p}^{ss} \) denotes the measured SS \( K_p \) (\( K_p^{ss} \)).

By replacing the \( C_{h}^{ss}/C_{p}^{ss} \) terms in Eqs. 38-40 by \( K_p^{ss} \), a general relationship between the PBPK non-SS model-operative liver \( K_p \) and the \( K_p^{ss} \) applicable to all three hepatic models is:

\[ K_p^{ss} = K_p \left( \frac{Q_h ER}{f_{ub} CL_{int}} \right) \tag{41} \]

wherein both \( K_p \) and \( CL_{int} \) are model-dependent, but jointly produce the model-independent \( K_p^{ss} \).

Combining Eq. 8 with Eq. 41, \( K_p^{ss} \) can also be expressed as follows for the WSM:

\[ K_p^{ss} = K_{p,WSM} \left( 1 - \frac{f_{ub} CL_{int,WSM}}{Q_h + f_{ub} CL_{int,WSM}} \right) = K_{p,WSM} (1 - ER) \tag{42} \]

**Model Fitting**

The model fittings of blood and liver concentration-time data were performed by nonlinear regression using the maximum likelihood algorithm in ADAPT 5 (Biomedical Simulations Resources, Los Angeles, CA) (D'Argenio et al., 2009). The variance model used was:

\[ V_i = (\sigma_{inter} + \sigma_{slope} Y_i)^2 \tag{43} \]

where \( V_i \) is the variance of the \( i \)th data point; \( Y_i \) is the \( i \)th model-predicted concentration; \( \sigma_{inter} \)

and \( \sigma_{slope} \) are the variance model parameters. Model selection was based on the goodness-of-fit criteria, which included the Akaike Information Criterion (AIC), visual inspection of the fitted profiles, and CV% of the parameter estimates.

The ADAPT code for the model for one compound is provided in the Supplemental Methods.
Liver $K_p$ of Model Compounds Obtained by Other Methods

The liver $K_p$ values were also calculated as follows for comparisons with those estimated by the hepatic clearance models:

1. Reported $K_p^{ss}$ calculated as the SS liver-to-plasma concentration ratio (Table 1).

2. Apparent $K_p$ values calculated from the AR method (Gallo et al., 1987):

$$K_{p,AR} = \frac{AUC_{h,pred}}{AUC_{p,pred}}$$

(44)

where $AUC_{h,pred}$ and $AUC_{p,pred}$ are the areas under the hepatic clearance model-predicted liver and plasma curves (from time 0 to infinity).

3. Apparent $K_p$ values obtained from the terminal slopes of $C_h$- and $C_p$-time data of the model compounds according to the C&G method (Chen and Gross, 1979) for the liver:

$$K_{p,C&G} = \frac{(Q_h + CL_{int,WSM})c_0^h}{c_p^0} = \frac{c_p^0}{c_p^0} + V_G\lambda_G + V_h\lambda_h + V_{SP}\lambda_{SP}$$

(45)

where $c_0^h$ and $\lambda$ are the intercept and slope of the terminal elimination phase of the plasma or tissue concentration-time curve and subscripts $SP$ and $G$ refer to the spleen and gut if available with the assumptions that no metabolism occurs in these two organs. According to Eq. 13 in (Jeong and Jusko, 2022) and the above Eq. 44 (Chen and Gross, 1979), the $K_p^{ss}$ for flow-limited substances can be obtained from $K_{p,C&G}$ in a similar way as the WSM:

$$K_p^{ss} = K_{p,C&G} \left(1 - \frac{f_{ub}CL_{int,WSM}}{Q_h + f_{ub}CL_{int,WSM}}\right) = K_{p,C&G} (1 - ER)$$

(46)

4. Apparent $K_p$ predicted by the in silico methods implemented in the GastroPlus PBPK Simulator (Version 9.8.0002; Simulation Plus Inc., Lancaster, CA) based on the published methods (Poulin and Theil, 2002a; Poulin and Theil, 2002b) (M1), (Berezhkovskiy, 2004) (M2), (Rogers and Rowland, 2006) (M3), and (Lukacova et al.,
2008a) (M4 for all compounds except for CQ). For CQ, M4 refers to the extended Lukacova method that includes lysosomal trapping for basic compounds (Assmus et al., 2017).
Results

Signature Profiles of $CL_h$, $CL_{int}$, $K_p$ in Relation to $ER$

Model simulations were performed using Eq. 1 for $CL_h$, Eq. 9, 16, and 28 for each model $CL_{int}$, and Eq. 38-40 for each model $K_p$ (assuming $f_{ub}$ and $R_b$ all equal to 1) with $ER$ increasing from 0 to 1 to examine the general trend and model-dependencies of these parameters. As shown in Figure 1A, $CL_h$ increased with increasing $ER$ with the upper limit being $Q_h$. The $CL_{int}$ of all hepatic models can exceed $Q_h$, with the rank order being $CL_{int, WSM} > CL_{int, DM} > CL_{int, PTM}$ given the same $ER$. At the low $ER$ range (e.g., 0-0.3), the $CL_{int}$ values of all models are similar and close to the $CL_h$. However, larger differences in $CL_{int}$ were observed at the medium to high $ER$ values (e.g., 0.3 to 1). Like the model-dependent $CL_{int}$, the PBPK-operative $K_p$ also showed increasing trends with increased $ER$ and displayed hepatic model-dependency (Figure 1B), with the WSM $K_p$ being the largest and the PTM $K_p$ being the smallest. The $K_p$ of all three models are close to or larger than the assumed SS $K_p$ value due to different extents of hepatic elimination. For low $ER$ drugs, the hepatic model-specific $K_p$ values are comparable to the SS $K_p$ while larger deviations were seen for high $ER$ drugs.

Liver $K_p$ of the Model Compounds

In applying the hepatic clearance models by the open loop approach, the blood PK data of the model compounds were first fitted by the exponential functions (Eq. 25), with $CL_b$, $ER$ and $f_{ub} CL_{int}$ estimated as secondary parameters based on Eq. 9, 16, and 26-28. These PK parameter estimates are presented in Tables 2 and S1 and the model fittings are displayed in Figure 2. As can be seen, there is good agreement between the observations and model predictions of blood concentrations and the fitted parameters exhibit low CV% values. The $C_b$-time data of CQ after an IP dose were better fitted without an absorption phase as presented. In general, the estimated
$CL_b$ and $ER$ values were comparable to those reported/calculated except that the estimated values were lower for CQ, PTZ, QD and PPN. The estimated $CL_{int}$ values exhibited hepatic model-dependency and increased with increasing $ER$, consistent with the expectations of the $CL_{int}$ profiles shown in Figure 1A.

The unbound blood/tissue concentrations within the liver related to each of the hepatic models were simulated according to Eq. 5, 11, and 24 using VEM as an example (Figure 3). Consistent with theoretical expectations, model-dependencies are observed with the WSM exhibiting the lowest concentrations while those of the PTM are the highest. The unbound liver blood concentrations of all hepatic models are lower than the observed blood concentrations due to depletion by hepatic clearance even when $f_{ub}$ was assumed to be 1. It can be noted that, just as the plasma AUC is determined by Dose/systemic clearance, the hepatic free AUC is determined by Dose/intrinsic clearance. Of course, the latter is model-dependent as shown while the former is not.

Next, the in vivo fitted liver $K_p$ values of the model compounds were estimated by applying the WSM, PTM and DM to the measured liver concentration-time data using the previously model-fitted blood concentration-time data as the forcing input function. The liver $K_p$ and nonlinear tissue binding-related parameters ($B_{max}$ and $K_d$) of QD and CQ were estimated with reasonable CV% values (Table 3) and the liver concentration-time profiles of all compounds were well captured (Figure 2) except for some underpredictions for the early data points of EB and CyA. Nonlinear tissue binding reasonably explained the slower terminal decline in the liver concentrations of QD and CQ as compared to their blood concentrations. Like the $CL_{int}$, the PBPK-operative $K_p$ also differs for the hepatic models with the WSM yielding the highest value while the PTM gives the lowest. Such model-dependency is unnoticeable for low ER drugs but
becomes more remarkable as $ER$ increases. It is evident that the predicted liver concentrations as fitted by different hepatic models were identical although the $CL_{int}$ and $K_p$ values differ. The apparent liver $K_p$ values were also obtained by the AR and C&G methods (Table 3) and compared with those estimated by the WSM (Figure 4). It is important to appreciate the different methods used for estimating $K_p$ values. The $K_{p,C&G}$ values that were corrected for hepatic extraction based on the WSM are comparable with the $K_{p,WSM}$ for most compounds. The $K_{p,AR}$ are uncorrected values that exhibit larger deviations from $K_{p,WSM}$ and $K_{p,C&G}$ as the contribution of hepatic extraction increases. The experimental and GastroPlus-predicted physicochemical properties of all model compounds are summarized in Table S2 and were used for predicting the in silico $K_p$ ($K_{p,exp}$ and $K_{p,pred}$) by the M1 through M4 methods, with the results shown in Table 4 and compared in Figure S2. In general, the predictions by M1 and M2 are similar, while those obtained by M3 and M4 are close to each other. The in silico $K_{p,pred}$ are generally in line with the $K_{p,exp}$ except for those of CQ, HB, CYA and NIC calculated by M3 and M4, and those of DPH predicted by all in silico methods. Overall, regardless of which in silico method was used, the $K_{p,pred}$ and $K_{p,exp}$ differ appreciably from the WSM $K_p$ for most of the compounds (Figure 4).

**Comparisons of the Predicted and Reported Liver $K_p^{ss}$**

To allow for more intuitive comparisons among different prediction methods, the $K_p$ obtained by the hepatic clearance model fittings, C&G method, and in silico methods were converted to their corresponding uncorrected $K_p^{ss}$ using Eq. 41, 42 and 46. With the model-specific sets of $CL_{int}$ and $K_p$, different hepatic models yielded the same $K_p^{ss}$ as expected (Eq. 41). Therefore, a single $K_p^{ss}$ value was listed for all the compounds (Table 3). As can be seen from Figure 5A, the AR $K_p$ and the hepatic model-predicted $K_p^{ss}$ and the C&G method are comparable and within a 2-fold range from the reported in vivo $K_p^{ss}$ for all compounds except for slight underpredictions for PPN.
(predicted/reported $K_p^{ss}$ ratio: 0.34–0.42). In contrast, the *in silico* methods performed poorly (more than 2-fold difference) for most of the compounds with either experimental (Figure 5B) or predicted (Figure 5C) drug properties. Nevertheless, the *in silico* methods performed slightly better when combined with the experimental drug properties, which generated $K_p^{ss}$ predictions within the 2-fold range for TB (M3 and M4), HB (all *in silico* methods), DPH (all *in silico* methods), NIC (M3), PPN (M2) and DZP (M1).

Owing to the nonlinearity in tissue binding, the $K_p^{ss}$ of CQ and QD obtained by different methods were compared separately in Figure S3. The reported and hepatic model predicted $K_p^{ss}$ of CQ and QD were simulated using their corresponding $B_{max}$ and $K_d$ values according to Eq. 5, 7, 25, 37, and 42 with the plasma concentration range of 5–200 ng/mL for CQ and 0.7–5 μg/mL for QD. For CQ, lysosomal trapping along with the appreciable binding to acidic phospholipids in cell membranes have been reported (Allison and Young, 1964; Tietz et al., 1990; Zheng et al., 2011), which are major contributors to the extensive tissue distribution and long terminal half-life of this basic lipophilic molecule. Thus, M4 (Lukacova et al., 2008a) extended with the inclusion of lysosomal sequestration (Assmus et al., 2017) was used specifically for CQ. As shown in Figure S3, the hepatic clearance models slightly underpredict the $K_p^{ss}$ of CQ, with the model-predicted vs reported $K_p^{ss}$ ratio ranging from 0.24–0.48 within the simulated $C_p$ range.

With the incorporation of lysosomal trapping, the *in silico* M4 combined with the experimental drug properties yielded the best $K_p^{ss}$ predictions for CQ among all the methods, followed by the C&G and AR methods, and the *in silico* M3 with the experimental drug properties. The M4 method overpredicted the $K_p^{ss}$ of CQ when the predicted physicochemical properties were used. The reported $K_p^{ss}$ value of CQ measured at the $C_p^{ss}$ of 157 ng/mL (Earle et al., 1948) is about 6-fold higher than that simulated based on the reported tissue binding parameters (Liu and Jusko,
2021) at the same $C_p^{ss}$. In contrast, the hepatic models yielded good $K_p^{ss}$ predictions for QD within the analyzed $C_p$ range. Among all the other methods, the in silico M3 and M4 methods combined with the experimental drug properties also performed reasonably well for predicting the $K_p^{ss}$ of QD. The effects of improper use of $K_p$ on the prediction of liver concentration-time profiles by the WSM were demonstrated using DLZ as an example. Model simulations were performed by decreasing or increasing the previously fitted $K_p,WSM$ to ±2- and 5-fold its normal value, and also with the lowest and highest in silico $K_p$ values (i.e., M1 $K_p,exp$ of 4.33, and M3 $K_p,pred$ of 14.82) (Table 4). As shown in Figure 6, the direct use of a correct $CL_{int,WSM}$ with $K_p$ obtained from sources other than fitting the same in vivo data may result in various degrees of under- and over-predictions of the liver concentrations.
Discussion

The metabolic and biliary excretory capabilities of the liver are fundamental biochemical activities that determine elimination rates of drugs in the complex anatomical and physiological functioning of the hepatic system. Likewise, drugs are ‘bound’ in the liver by multiple mechanisms including reversible and irreversible attachment to macromolecules, lipid partitioning, and ion trapping with differential blood/tissue permeability, transport and convection rates often adding complications (Jusko et al., 2020). The simplest net expression of these complex drug- and organ-specific processes utilized in PK are the organ space-average $\text{CL}_{\text{int}}$ and $K_p$ values. Attempts to measure these properties using in vitro methods unfortunately require a PK model of the liver for in vivo extrapolation (IVIVE). While numerous hepatic clearance models exist, the simple WSM is most commonly utilized in both IVIVE and PBPK. This report explores and compares the operation of the WSM, PTM, and DM in PBPK modeling with a particular focus on resultant $K_p$ values. An overview of the theoretical concepts and mathematical relationships applicable to the basic hepatic models in context of PBPK was presented. The model-dependencies in liver $\text{CL}_{\text{int}}$ have long been appreciated while the properties of the PBPK-operative $K_p$ were explored further and shown to differ among the hepatic models using experimental published data for 14 model compounds and by assessing in silico methodology.

The open-loop approach where the blood/plasma data were pre-fitted and fixed was advantageous for our purposes as we did not have to deal with involvement of organs/tissues other than the liver. When applying the exponential functions to describe the blood PK data, the initial blood concentration was fixed to $\text{Dose}/V_b$ so that the initial distribution space is the blood volume ($V_b$) to create a physiologically plausible initial decline of drug concentrations that
mimics the behavior of full PBPK models as compared to estimating an initial distribution space as with compartment models. This open-loop method was reported to generate comparable $K_p$ estimates as obtained by fitting all tissues simultaneously using a full PBPK model (Gueorguieva et al., 2004). However, the limitation with this approach is that the $CL_{int}$ is highly correlated with $K_p$ resulting in extremely large CV% values when both parameters are estimated simultaneously.

In the present analysis the hepatic model-specific $CL_{int}$ was first estimated from the $CL_b$ or $ER$ by fitting the blood PK data knowing or assuming that the liver is the only clearance organ and then fixed to only estimate the PBPK-operative $K_p$. The calculations of $CL_{int,WSM}$ and $CL_{int,PTM}$ were straightforward (Eq. 9 and 16), while the DM has no explicit solution for the $CL_{int,DM}$ and thus was indirectly calculated (Eq. 28). It was feasible to obtain $R_N$ from a range of $ER$ values with a pre-set $D_N$ value by model simulations using Eq. 22 (see Figure S1) as was similarly done previously (Oliver et al., 2001). The $D_N$ value of 0.6 based on the closed boundary conditions (Oliver, 1995; Oliver et al., 2001) gave reasonable predictions of hepatic availability corresponding to the PTM and WSM extremes when $D_N$ approaches to 0 and infinity as compared to the open or mixed boundary conditions (Roberts and Rowland, 1986a; Roberts and Rowland, 1986b). Reported $Q_h$ values in the literature and commercial software range from 47 to 85 mL/min/kg (Table 1). To make fair comparisons among the models, the $Q_h$ of 60.82 mL/min/kg was chosen (Brown et al., 1997), which is close to the median value of the reported $Q_h$ range used to calculate the model-specific $CL_{int}$ values for all compounds and also used in fitting of liver data. The hepatic model-dependencies in the estimated $CL_{int}$ occurred as expected and are most remarkable for drugs with high $ER$. We show that the PBPK-operative $K_p$ is also dependent on the hepatic model, with the same rank order as for $CL_{int}$. It is expected that if the
lower PTM or DM \( K_p \) value was applied to model fittings based on the WSM, the liver concentrations would be underestimated (Figure 6).

Besides being estimated by fitting plasma and liver profiles with PBPK models, \( K_p \) was obtained by several other means. Using the ratio of SS tissue-to-plasma concentration by constant IV infusion studies or from the tissue/plasma area ratio (AR) from IV bolus studies does not make any assumptions about the tissue model structure and the resulting \( K_p \) values are equivalent for non-eliminating tissues under linear PK conditions. However, for the liver, the experimentally measured \( K_p \) differs from the (unknown) true value and needs to be corrected before utilization in PBPK models. The usual approach for such purpose is application of the WSM \( CL_{int} \) (Houston, 1994) that was presumably done as the basis of the in silico prediction methods. During early drug development when there are no in vivo measurements available, \( K_p \) can also be predicted using in silico quantitative structure-property relationships (QSPR) combined with tissue composition properties using the cited published methods and found in commercial software such as the GastroPlus Simulator (Other software such as SimCyp and PKSim also offer most of these methods.). In this work, the apparent liver \( K_p \) values of all model compounds were calculated using in silico methods. Overall, there were little differences in the \( K_p \) based on in vivo measurements (e.g., hepatic models, AR, and C&G methods) when the \( ER \) is low, while the \( K_{p,AR} \) is smaller than those estimated by the other two methods as \( ER \) increases due to the lack of correction for hepatic elimination. With in silico approaches, compound-specific input parameters (e.g., \( pK_a \), \( LogP \), \( R_b \), and \( f_{up} \)) play important roles in making \( K_p \) predictions. Using experimental and QSPR-predicted physicochemical properties produced comparable in silico \( K_p \) values. The adjusted \( f_{up} \) that improves \( K_p \) predictions of highly lipophilic compounds (Lukacova et al., 2008b) was used. The in silico predicted \( K_p \) values were compared with the WSM \( K_p \) since
they are often utilized in PBPK models with $CL_{int}$ either obtained from \textit{in vitro} or back calculated from the \textit{in vivo} $CL_h$ using the WSM to predict tissue drug disposition. The correlation between the \textit{in silico} and WSM $K_p$ values was not very good for most compounds (Figure 4). Poor agreement was also found for dexamethasone (Song et al., 2020), CQ (Liu and Jusko, 2021), prednisolone (Li et al., 2020), and for many additional compounds (Jeong and Jusko, 2022). Directly using the \textit{in silico} $K_p$ with a WSM $CL_{int}$ may result in poor predictions for the liver concentrations (Figure 6). As shown (Lukacova et al., 2008a), the \textit{in silico} $K_p$ predictions should only be considered approximate. Values for liver are even more prone to error than other tissues owing to the need for correction of measured values for $CL_{int}$.

The limitations of this study are the use of published digitized data and that only the three basic hepatic models assuming perfusion-limitations were compared. Later hepatic models have been expanded to include influences of cell permeability and transporter-mediated clearances (Miyauchi et al., 1987; Kwon and Morris, 1997; Sirianni and Pang, 1997, Jeong and Jusko, 2022). Second-order partial differential equations involving both space and time as needed for the DM (Oliver, 1995; Oliver et al., 2001) were not considered in this analysis since the observed total liver concentration at each time point for all of the study drugs is the tissue space-averaged value. An alternative hepatic model called the series-compartment model was reported to closely approximate the DM where the liver is divided into several compartments connected by blood flow in tandem (Gray and Tam, 1987). It was later extended by considering the hepatic zonation of metabolizing enzymes/transporters (Tirona and Pang, 1996; Abu-Zahra and Pang, 2000) and transporter-associated clearances (Watanabe et al., 2009; Jones et al., 2012; Li et al., 2014; Morse et al., 2017). The assumption that the liver is the only clearance organ may not be perfectly true for some of the selected compounds. However, the main objective of this work is
to assess the hepatic model-dependencies of $CL_{int}$ and the PBPK-operative $K_p$, and how they change with changing $ER$. In any case, if the liver is not fully the elimination organ, the relative values of $K_p$ obtained using the three hepatic models will still differ with the same trend.

Considerable attention has been paid to assessing data from isolated hepatic perfusion studies to identify the “best” model for hepatic clearance (Sodhi et al., 2020), but such assessments have seldom if ever been made using data from PBPK studies. Our report demonstrates how to do this and reveals that the three basic hepatic models that assume different internal concentrations produce differing operative $CL_{int}$ and $K_p$ values especially for drugs with high $ER$ in PBPK-type studies. However, all three models appear to fit liver PK data equally well and such quality of fittings does not serve to discriminate the ‘correct’ model, at least for flow-limited substances.

Our findings are most relevant when using these hepatic models for IVIVE where a model-dependent $CL_{int}$ is needed to correct measured tissue concentrations for depletion by metabolism with the WSM requiring the largest correction factor. Perhaps use of the PTM or DM that entail smaller adjustments would reduce any errors in such corrections. The hepatic model-dependency may also have an impact when assessing the PK/pharmacodynamic relationships when effects relate to assumed hepatic concentrations. Differences in hepatic exposures of presumed unbound drug were found to relate to the expected Dose/intrinsic clearance values (Figure 3).
Authorship Contributions

Participated in research design: Li and Jusko.

Performed data analysis: Li.

Wrote or contributed to the writing of the manuscript: Li and Jusko.
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Footnotes

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Figure Legends

Figure 1. Signature profiles of (A) clearances (\(CL_h\) & \(CL_{int}\)) vs ER, and (B) partition coefficients \(K_p\) vs \(ER\) for the indicated hepatic clearance models. The dashed horizontal lines indicate \(Q_h = 60.82\) mL/min/kg in (A) and \(K_p^{ss} = 1\) in (B).

Figure 2. Blood and liver concentration-time profiles of 14 model compounds. Measured concentrations in blood and liver are indicated by solid symbols in red and black. Black solid lines show the model fittings of the blood data and colored solid lines depict the model fittings of the liver data (WSM: purple, DM: orange, PTM: blue). The estimated \(f_{ab}CL_{int}\) and \(K_p(B_{max}\) and \(K_d\) for CQ and QD) values are listed for each of the model compounds with the same color coding as those for the liver model fittings.

Figure 3. Blood and liver concentration versus time data for verapamil (VEM) with model fittings and predictions. Hepatic clearance model-dependent average unbound liver blood/tissue concentrations simulated according to Eq. 5, 11, and 24 are shown as dashed lines. Closed symbols are measured values, and solid lines depict fittings by hepatic clearance models with the same color coding as those used in Figure 2.

Figure 4. Comparisons of the predicted \(K_p\) by \textit{in silico} methods (A-D), C&G method (E) and AR method (F) with the WSM-estimated \(K_p\). The solid line indicates unity and the dashed lines indicate 2-fold ranges from unity. The black and red symbols in (A-D) represent \textit{in silico} \(K_p^{pred}\) and \(K_p^{exp}\) for each of the compounds.

Figure 5. Comparisons of the predicted \(K_p^{ss}\) by hepatic clearance models, AR method, and C&G method (A), and \textit{in silico} methods (B: \(K_p^{exp}\); C: \(K_p^{pred}\)) with the reported \textit{in vivo} \(K_p^{ss}\). The dashed lines indicate 2-fold ranges from unity. The data are color-coded for each compound and are connected by lines for better visualization.
Figure 6. Effects of changing $K_p$ on predicting the liver concentration-time profiles of DLZ by the WSM. Black circles are measured liver concentrations and color-coded dashed lines indicate model simulations with $K_{p,WSM}$ (26.03, purple), ±2-fold $K_{p,WSM}$ (red), ±5-fold $K_{p,WSM}$ (green), the lowest (M1 $K_{p,exp} = 4.33$, orange) and highest (M3 $K_{p,pred} = 14.82$, pink) in silico $K_p$. In all cases, $f_{ubCL_{int,WSM}}$ was fixed to 397 mL/min/kg.
Tables

Table 1. Literature-reported $Q_h$ (mL/min/kg) and *in vivo* liver $K_{p ss}$ of 14 model compounds.

<table>
<thead>
<tr>
<th>Compound</th>
<th>$Q_h$ (mL/min/kg)$^a$</th>
<th>Reported $K_{p ss}$$^b$</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Chloroquine (CQ)</td>
<td>60.8</td>
<td>420$^c$</td>
<td>(Earle et al., 1948)</td>
</tr>
<tr>
<td>Tolbutamide (TB)</td>
<td>58.9</td>
<td>241~1939$^d$</td>
<td>(Liu and Jusko, 2021)</td>
</tr>
<tr>
<td>Cyclosporine A (CyA)</td>
<td>47.2</td>
<td>16.6</td>
<td>(Bernareggi and Rowland, 1991)</td>
</tr>
<tr>
<td>Ethoxybenzamide (EB)</td>
<td>58.8</td>
<td>1.40</td>
<td>(Lin et al., 1982)</td>
</tr>
<tr>
<td>Fingolimod (FTY720)</td>
<td>47.2</td>
<td>31.4$^e$</td>
<td>(Meno-Tetang et al., 2006)</td>
</tr>
<tr>
<td>Nicotine (NIC)</td>
<td>82.1</td>
<td>7.00</td>
<td>(Plowchalk et al., 1992)</td>
</tr>
<tr>
<td>Pentazocine (PTZ)</td>
<td>50.1</td>
<td>0.47</td>
<td>(Fujio et al., 1983)</td>
</tr>
<tr>
<td>Hexobarbital (HB)</td>
<td>58.8</td>
<td>1.3$^f$</td>
<td>(Igari et al., 1982)</td>
</tr>
<tr>
<td>Phenytoin (DPH)</td>
<td>49.2</td>
<td>0.88$^f$</td>
<td>(Itoh et al., 1988)</td>
</tr>
<tr>
<td>Quinidine (QD)</td>
<td>58.8</td>
<td>5.5~21.4$^d$</td>
<td>(Harashima et al., 1985)</td>
</tr>
<tr>
<td>Propranolol (PPN)</td>
<td>85.0</td>
<td>1.24$^f$</td>
<td>(Shibasaki et al., 1989)</td>
</tr>
<tr>
<td>Diazepam (DZP)</td>
<td>58.8</td>
<td>2.03$^f$</td>
<td>(Igari et al., 1983)</td>
</tr>
</tbody>
</table>
Verapamil (VEM)  NA  10.1  (Yamano et al., 2000)
Diltiazem (DLZ)  NA  3.97  (Yamano et al., 2000)

\( a \) The \( Q_h \) values based on a 250-g rat applied in commercial software are 47.2 mL/min/kg in GastroPlus, 51.7 mL/min/kg in PK-Sim Version 9.1 (http://open-systemspharmacology.org), and 77.4 mL/min/kg in Simcyp (Certara UK Ltd., Simcyp Division, Sheffield, UK; Version 20.1) (Musther et al., 2017).

\( b \) The reported \( K_p^{ss} \) are the ratio of measured liver and plasma concentration at SS unless otherwise indicated.

\( c \) The single \( K_p^{ss} \) value of CQ is based on the \( C_p \) of 157 ng/mL achieved after daily administration of 25 mg CQ to rats for 10 days.

\( d \) The \( K_p^{ss} \) ranges of CQ and QD were obtained from the reported liver \( B_{max} \) and \( K_d \) in the source literature according to Eq. 5, 7, 25, 37, and 42 with the \( C_p \) range of 5~200 ng/mL for CQ and 0.7~5 μg/mL for QD that covers the plasma concentrations in the datasets.

\( e \) The \( K_p^{ss} \) of FTY720 was calculated from the reported PBPK model-estimated \( K_p \) according to Eq. 42.

\( f \) The \( K_p^{ss} \) of HB, DZP, DPH and PPN were obtained from the reported \( K_{p,C&G} \) using Eq. 46.

NA: not available
Table 2. Estimation of $CL_b$ (mL/min/kg), $ER$, and $f_{ub}CL_{int}$ (mL/min/kg) from the blood PK data in rats for the model compounds.

<table>
<thead>
<tr>
<th>Compound $^a$</th>
<th>$ER^b$ Estimated (CV%)</th>
<th>$ER^b$ Reported</th>
<th>$CL_b$ or $CL_h^b$ Estimated (CV%)</th>
<th>$CL_b$ or $CL_h^b$ Reported</th>
<th>$f_{ub}CL_{int}$ (CV%) $^c$ WSM</th>
<th>DM</th>
<th>PTM</th>
</tr>
</thead>
<tbody>
<tr>
<td>TB</td>
<td>0.032 (3.3)</td>
<td>0.03</td>
<td>1.86</td>
<td>1.41</td>
<td>1.99 (3.3)</td>
<td>1.98</td>
<td>1.96</td>
</tr>
<tr>
<td>CQ $^e$</td>
<td>0.033 (7.6)</td>
<td>0.195</td>
<td>2.01</td>
<td>11.5</td>
<td>2.08 (7.8)</td>
<td>2.06</td>
<td>2.04</td>
</tr>
<tr>
<td>CyA</td>
<td>0.06 (1.6)</td>
<td>0.08</td>
<td>2.77</td>
<td>3.7</td>
<td>3.79 (1.7)</td>
<td>3.75</td>
<td>3.68</td>
</tr>
<tr>
<td>EB</td>
<td>0.08 (6.3)</td>
<td>0.12</td>
<td>4.92</td>
<td>7.11</td>
<td>5.55 (4.9)</td>
<td>5.45</td>
<td>5.31</td>
</tr>
<tr>
<td>FTY720</td>
<td>0.17 (7.05)</td>
<td>0.18</td>
<td>7.89</td>
<td>8.28</td>
<td>12.2 (8.5)</td>
<td>11.8</td>
<td>11.1</td>
</tr>
<tr>
<td>NIC</td>
<td>0.39 (3.1)</td>
<td>0.55</td>
<td>29.49</td>
<td>45</td>
<td>38.2 (5.1)</td>
<td>34.3</td>
<td>29.6</td>
</tr>
<tr>
<td>PTZ</td>
<td>0.41 (1.9)</td>
<td>0.82</td>
<td>20.55</td>
<td>41.3</td>
<td>42.2 (3.2)</td>
<td>37.6</td>
<td>32.1</td>
</tr>
<tr>
<td>HB</td>
<td>0.46 (2.7)</td>
<td>0.64</td>
<td>27.33</td>
<td>37.6</td>
<td>52.8 (5)</td>
<td>45.8</td>
<td>38</td>
</tr>
<tr>
<td>DPH</td>
<td>0.55 (2.1)</td>
<td>0.61</td>
<td>26.93</td>
<td>30.1</td>
<td>73.6 (4.7)</td>
<td>61</td>
<td>48.2</td>
</tr>
<tr>
<td>QD $^e$</td>
<td>0.58 (2.1)</td>
<td>0.85</td>
<td>34.2</td>
<td>49.7</td>
<td>84.5 (5)</td>
<td>69.5</td>
<td>53</td>
</tr>
<tr>
<td>PPN</td>
<td>0.59 (3.5)</td>
<td>0.77</td>
<td>49.9</td>
<td>65.7</td>
<td>86.4 (8.5)</td>
<td>69.7</td>
<td>53.8</td>
</tr>
<tr>
<td>DZP</td>
<td>0.66 (5.7)</td>
<td>0.65</td>
<td>38.8</td>
<td>38.22</td>
<td>118 (16.9)</td>
<td>89.8</td>
<td>65.6</td>
</tr>
</tbody>
</table>

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<table>
<thead>
<tr>
<th>Compound</th>
<th>CL\textsubscript{b} (mL/min/kg)</th>
<th>ER (100 mL/min)</th>
</tr>
</thead>
<tbody>
<tr>
<td>VEM</td>
<td>0.7 (1.4)</td>
<td>42.8</td>
</tr>
<tr>
<td></td>
<td>0.75</td>
<td>45.7</td>
</tr>
<tr>
<td></td>
<td>145 (4.6)</td>
<td>105</td>
</tr>
<tr>
<td></td>
<td>74.1 (2.7)</td>
<td></td>
</tr>
<tr>
<td>DLZ</td>
<td>0.87 (2.1)</td>
<td>52.7</td>
</tr>
<tr>
<td></td>
<td>0.85</td>
<td>51.7</td>
</tr>
<tr>
<td></td>
<td>397 (15.7)</td>
<td>213</td>
</tr>
<tr>
<td></td>
<td>123 (6.7)</td>
<td></td>
</tr>
</tbody>
</table>

\textsuperscript{a}Literature sources for the modeling datasets, and the reported/calculated \textit{CL\textsubscript{b}} and \textit{ER} were the same as those in Table 1 except for the following: the modeling datasets of CQ, CyA, EB, and PPN were obtained from (Adelusi and Salako, 1982), (Kawai et al., 1998), (Lin et al., 1978), and (Schneck et al., 1977); the reported/calculated \textit{ER} of HB, DZP, and DLZ were obtained from (Vermeulen et al., 1983), (Igari et al., 1984), and (Naritomi et al., 2001).

\textsuperscript{b}If \textit{ER} was directly available from the literature, \textit{CL\textsubscript{b}} was calculated from \textit{Q\textsubscript{h}}\textit{ER} using the reported \textit{Q\textsubscript{h}} in Table 1 except for VEM for which the \textit{Q\textsubscript{h}} value of 60.82 mL/min/kg (Brown et al., 1997) was used since the reported \textit{Q\textsubscript{h}} was not available from the source literature (Yamano et al., 2000); otherwise, if only the \textit{CL\textsubscript{b}} was reported, \textit{ER} was obtained from \textit{CL\textsubscript{b}}/\textit{Q\textsubscript{h}}. \textit{CL\textsubscript{b}} was assumed to be equal to \textit{CL\textsubscript{h}} for all compounds except for CQ and NIC for which the \textit{CL\textsubscript{h}} were obtained by subtracting their known extrahepatic \textit{CL} from \textit{CL\textsubscript{b}} (Plowchalk et al., 1992; Liu and Jusko, 2021).

\textsuperscript{c}With the estimated \textit{ER}, \textit{f\textsubscript{ub}}\textit{CL\textsubscript{int}} for the WSM, PTM, and DM were calculated using the \textit{Q\textsubscript{h}} of 60.82 mL/min/kg (Brown et al., 1997) according to Eq. 9, 16, and 28; the simulated \textit{R\textsubscript{N}} (Figure S1) were used for the calculation of \textit{f\textsubscript{ub}}\textit{CL\textsubscript{int}} for the DM.

\textsuperscript{d}\textit{CL\textsubscript{b}} have the same CV\% values as those of estimated \textit{ER}.

\textsuperscript{e}The reported/calculated \textit{ER} of CQ was calculated from the reported \textit{Q\textsubscript{h}} and \textit{f\textsubscript{ub}}\textit{CL\textsubscript{int}} (Liu and Jusko, 2021) using Eq. 8, and the calculated \textit{CL\textsubscript{b}} was obtained from \textit{Q\textsubscript{h}}\textit{ER}. For QD, the reported \textit{CL\textsubscript{b}} was calculated from the reported plasma clearance (Harashima et al., 1985) by dividing \textit{R\textsubscript{b}} and the reported \textit{ER} was obtained from \textit{CL\textsubscript{b}}/\textit{Q\textsubscript{h}}.
Table 3. Summary of *in vivo* liver $K_p$ and $K_p^{ss}$ values for the model compounds as obtained by the hepatic clearance models, Area Ratio (AR), and Chen and Gross (C&G) methods.

<table>
<thead>
<tr>
<th>Compound</th>
<th>$ER$</th>
<th>$K_p$ WSM</th>
<th>$K_p$ DM</th>
<th>$K_p$ PTM</th>
<th>$K_p$, C&amp;G</th>
<th>$K_p$, AR</th>
<th>Estimated $K_p^{ss}$</th>
</tr>
</thead>
<tbody>
<tr>
<td>TB</td>
<td>0.032</td>
<td>0.162 (7.8)</td>
<td>0.161 (7.8)</td>
<td>0.159 (7.8)</td>
<td>0.162</td>
<td>0.28</td>
<td>0.157</td>
</tr>
<tr>
<td>CQ</td>
<td>0.033</td>
<td>B$_{max}$=12 (12.8)</td>
<td>B$_{max}$=12 (12.9)</td>
<td>B$_{max}$=12 (12.9)</td>
<td>175.6</td>
<td>169.7</td>
<td>55~470</td>
</tr>
<tr>
<td>CyA</td>
<td>0.06</td>
<td>14.3 (24.7)</td>
<td>14.2 (24.7)</td>
<td>13.9 (24.7)</td>
<td>9.52</td>
<td>13.5</td>
<td>13.5</td>
</tr>
<tr>
<td>EB</td>
<td>0.08</td>
<td>1.15 (20.7)</td>
<td>1.13 (20.6)</td>
<td>1.1 (20.7)</td>
<td>1.43</td>
<td>1.05</td>
<td>1.05</td>
</tr>
<tr>
<td>FTY720</td>
<td>0.17</td>
<td>50.46 (9)</td>
<td>48.67 (9)</td>
<td>46.02 (9)</td>
<td>57.51</td>
<td>41.83</td>
<td>42.02</td>
</tr>
<tr>
<td>NIC</td>
<td>0.39</td>
<td>9.86 (14.3)</td>
<td>8.86 (14.3)</td>
<td>7.65 (14.3)</td>
<td>7.78</td>
<td>6.35</td>
<td>6.06</td>
</tr>
<tr>
<td>PTZ</td>
<td>0.41</td>
<td>0.5 (9.7)</td>
<td>0.48 (9.8)</td>
<td>0.37 (9.7)</td>
<td>0.54</td>
<td>0.36</td>
<td>0.30</td>
</tr>
<tr>
<td>HB</td>
<td>0.46</td>
<td>2.04 (21.8)</td>
<td>1.65 (21.3)</td>
<td>1.46 (21.8)</td>
<td>2.29</td>
<td>1.09</td>
<td>1.09</td>
</tr>
<tr>
<td>DPH</td>
<td>0.55</td>
<td>2.85 (23.4)</td>
<td>2.36 (23.4)</td>
<td>1.87 (23.4)</td>
<td>2.94</td>
<td>1.29</td>
<td>1.29</td>
</tr>
<tr>
<td></td>
<td>QD&lt;sup&gt;c&lt;/sup&gt;</td>
<td>PPN</td>
<td>DZP</td>
<td>VEM</td>
<td>DLZ</td>
<td></td>
<td></td>
</tr>
<tr>
<td>------</td>
<td>----------------</td>
<td>------</td>
<td>------</td>
<td>-----</td>
<td>-----</td>
<td></td>
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<tr>
<td>$B_{\text{max}}$</td>
<td>34.15 (8.9)</td>
<td>33.76 (8.9)</td>
<td>33.8 (8.8)</td>
<td>33.8 (8.8)</td>
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</tr>
<tr>
<td>$K_d$</td>
<td>0.014 (126)</td>
<td>0.017 (130)</td>
<td>0.021 (135)</td>
<td>0.021 (135)</td>
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<tr>
<td>$K_{p,ss}$</td>
<td>97.61</td>
<td>57.8</td>
<td>6.7–43</td>
<td>40.99</td>
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<tr>
<td>$\text{ER}$</td>
<td>57.8</td>
<td>6.7–43</td>
<td>40.99</td>
<td>57.8</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>$\text{Kp}^{ss}$</td>
<td>6.7–43</td>
<td>40.99</td>
<td>57.8</td>
<td>6.7–43</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>$\text{Cp}$ range</td>
<td>5–200 ng/mL</td>
<td>0.7–5 μg/mL</td>
<td>5–200 ng/mL</td>
<td>0.7–5 μg/mL</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

<sup>a</sup> The estimated $ER$ in Table 2 were listed.

<sup>b</sup> The $K_{p,ss}$ were calculated using Eq. 41 for the hepatic models and Eq. 46 for the C&G method except that the values for CQ and QD were simulated by Eq. 5, 7, 25, 37, and 42 with the $C_p$ range of 5–200 ng/mL for CQ and 0.7–5 μg/mL for QD.

<sup>c</sup> The unit of $B_{\text{max}}$ and $K_d$ is μg/mL for both CQ and QD.
Table 4. Prediction of liver $K_p$ of the model compounds by several *in silico* methods incorporated in GastroPlus.

<table>
<thead>
<tr>
<th>Compound</th>
<th>$ER$</th>
<th>$In silico K_{p,, pred}^a$</th>
<th>$In silico K_{p,, exp}^b$</th>
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</thead>
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<tr>
<td></td>
<td></td>
<td>M1</td>
<td>M2</td>
</tr>
<tr>
<td>TB</td>
<td>0.031</td>
<td>2.08</td>
<td>0.68</td>
</tr>
<tr>
<td>CQ</td>
<td>0.033</td>
<td>7.15</td>
<td>12.63</td>
</tr>
<tr>
<td>CyA</td>
<td>0.06</td>
<td>5.60</td>
<td>3.75</td>
</tr>
<tr>
<td>EB</td>
<td>0.08</td>
<td>0.82</td>
<td>0.67</td>
</tr>
<tr>
<td>FTY720</td>
<td>0.17</td>
<td>7.25</td>
<td>8.82</td>
</tr>
<tr>
<td>NIC</td>
<td>0.39</td>
<td>0.80</td>
<td>0.78</td>
</tr>
<tr>
<td>PTZ</td>
<td>0.41</td>
<td>7.10</td>
<td>9.98</td>
</tr>
<tr>
<td>HB</td>
<td>0.46</td>
<td>1.31</td>
<td>0.86</td>
</tr>
<tr>
<td>DPH</td>
<td>0.55</td>
<td>0.99</td>
<td>0.51</td>
</tr>
<tr>
<td>QD</td>
<td>0.58</td>
<td>4.41</td>
<td>3.57</td>
</tr>
<tr>
<td>PPN</td>
<td>0.59</td>
<td>5.44</td>
<td>4.71</td>
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<th>0.66</th>
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<th>1.37</th>
<th>4.13</th>
<th>1.88</th>
<th>1.79</th>
<th>1.79</th>
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</thead>
<tbody>
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<td>DZP</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>VEM</td>
<td>0.7</td>
<td>7.12</td>
<td>10.97</td>
<td>7.49</td>
<td>7.27</td>
<td>6.8</td>
<td>9.02</td>
<td>8.26</td>
<td>7.79</td>
</tr>
<tr>
<td>DLZ</td>
<td>0.87</td>
<td>7.19</td>
<td>8.47</td>
<td>14.82</td>
<td>13.53</td>
<td>4.33</td>
<td>2.49</td>
<td>10.36</td>
<td>7.27</td>
</tr>
</tbody>
</table>

\(^a\) In silico \(K_p\) predicted using the physicochemical properties in the ADMET Predictor™ (Simulations Plus, Inc.) listed in Table S2.

\(^b\) In silico \(K_p\) predicted using the experimentally determined physicochemical properties listed in Table S2.

\(^c\) The M4 \(K_p\) of CQ (357.55) was obtained using the extended Lukacova method that includes lysosomal trapping (Assmus et al., 2017).
Fig. 1
**Fig. 2**

**TB (ER=0.32)**
- $f_{ab}\left CL_{int}/K_p\right$
  - 1.99/0.162
  - 1.98/0.161
  - 1.96/0.159

**CQ (ER=0.33)**
- $f_{ab}\left CL_{int}/B_{max}/K_d\right$
  - 2.08/12/0.008
  - 2.06/12/0.008
  - 2.04/12/0.008

**CyA (ER=0.06)**
- $f_{ab}\left CL_{int}/K_p\right$
  - 3.79/14.3
  - 3.75/14.2
  - 3.68/13.9

**EB (ER=0.08)**
- $f_{ab}\left CL_{int}/K_p\right$
  - 5.55/1.15
  - 5.45/1.13
  - 5.31/1.1

**FTY720 (ER=0.17)**
- $f_{ab}\left CL_{int}/K_p\right$
  - 12.2/50.46
  - 11.8/48.67
  - 11.1/46.02

**NIC (ER=0.39)**
- $f_{ab}\left CL_{int}/K_p\right$
  - 38.2/9.86
  - 34.3/8.86
  - 29.6/7.65

**PTZ (ER=0.41)**
- $f_{ab}\left CL_{int}/K_p\right$
  - 42.2/0.5
  - 37.6/0.48
  - 32.1/0.37

**HB (ER=0.46)**
- $f_{ab}\left CL_{int}/K_p\right$
  - 52.8/2.04
  - 45.8/1.65
  - 38/1.46

**DPH (ER=0.55)**
- $f_{ab}\left CL_{int}/K_p\right$
  - 73.6/2.85
  - 61/2.36
  - 48.2/1.87

**QD (ER=0.58)**
- $f_{ab}\left CL_{int}/B_{max}/K_d\right$
  - 84.5/34.15/0.014
  - 69.5/33.76/0.017
  - 53/33.8/0.021

**PPN (ER=0.59)**
- $f_{ab}\left CL_{int}/K_p\right$
  - 86.4/1.27
  - 69.7/1.03
  - 53.8/0.79

**DZP (ER=0.66)**
- $f_{ab}\left CL_{int}/K_p\right$
  - 118/9.52
  - 89.8/7.24
  - 65.6/5.29

**VEM (ER=0.7)**
- $f_{ab}\left CL_{int}/K_p\right$
  - 145/24.8
  - 105/18
  - 74.1/12.7

**DLZ (ER=0.87)**
- $f_{ab}\left CL_{int}/K_p\right$
  - 397/26.03
  - 213/13.96
  - 123/8.05

*Time (min)*
Fig. 5
Supplemental Materials

**Manuscript number:** DMD-AR-2022-000994R1

**Title:**
Assessing Liver-to-Plasma Partition Coefficients and In Silico Calculation Methods: When Does the Hepatic Model Matter in PBPK?

**Authors:**
Xiaonan Li and William J. Jusko

**Affiliation:**
Department of Pharmaceutical Sciences, State University of New York at Buffalo, 404 Pharmacy Building, Buffalo, New York 14214, USA

**Journal Title:**
Drug Metabolism and Disposition
Supplemental Figures

**Figure S1.** Model simulations of the Extraction Ratio $ER$ vs $R_N$ for the DM according to Eq. 22.
Figure S2. Comparisons of the in silico $K_p$ values obtained using the chemical structure-predicted physicochemical properties ($K_{p, \text{pred}}$) with those calculated using the experimental physicochemical properties ($K_{p, \text{exp}}$).
Figure S3. Comparisons of the predicted $K_{p,s}$ of CQ and QD by hepatic clearance models, AR method, C&G method, and *in silico* methods with their reported $K_{p,s}$ simulated from the published tissue binding parameters in (Liu and Jusko, 2021) and (Harashima et al., 1985) using Eq. 5, 7, 25, 37, and 42. The red solid circle represents the reported $K_{p,s}$ measured at the CQ $C_{p,s}$ of 157 ng/mL by (Earle et al., 1948). The solid black lines indicate a 2-fold range from unity.
**Supplemental Tables**

**Table S1.** Blood PK parameter estimates for the model compounds applying Eq. 25.

<table>
<thead>
<tr>
<th>Compound</th>
<th>Intercepts (CV%)</th>
<th>Slopes (1/min) (CV%)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>A</td>
<td>B</td>
</tr>
<tr>
<td>TB</td>
<td>812.4 (1.6)</td>
<td>213.6 (6.1)</td>
</tr>
<tr>
<td>CQ</td>
<td>127.3 (0.02)</td>
<td>0.387 (8.3)</td>
</tr>
<tr>
<td>CyA</td>
<td>60.34 (0.8)</td>
<td>5.06 (10.5)</td>
</tr>
<tr>
<td>EB</td>
<td>228.4 (0.4)</td>
<td>27.62 (3.5)</td>
</tr>
<tr>
<td>FTY720</td>
<td>3798 (0.3)</td>
<td>44.35 (23.6)</td>
</tr>
<tr>
<td>NIC</td>
<td>1248 (0.15)</td>
<td>34.12 (5.6)</td>
</tr>
<tr>
<td>PTZ</td>
<td>24.07 (0.6)</td>
<td>1.24 (12)</td>
</tr>
<tr>
<td>HB</td>
<td>661.2 (1.3)</td>
<td>88.25 (8.3)</td>
</tr>
<tr>
<td>DPH</td>
<td>115.7 (0.4)</td>
<td>11.84 (3.5)</td>
</tr>
<tr>
<td>QD</td>
<td>377.7 (0.05)</td>
<td>6.91 (2.8)</td>
</tr>
<tr>
<td>PPN</td>
<td>94210 (0.4)</td>
<td>1239 (30.1)</td>
</tr>
<tr>
<td>DZP</td>
<td>15140 (0.5)</td>
<td>205.2 (36.6)</td>
</tr>
<tr>
<td></td>
<td>VEM</td>
<td>DLZ</td>
</tr>
<tr>
<td>------</td>
<td>----------</td>
<td>----------</td>
</tr>
<tr>
<td></td>
<td>62040 (0.1)</td>
<td>61990 (0.2)</td>
</tr>
<tr>
<td></td>
<td>1420 (5.4)</td>
<td>1716 (6.3)</td>
</tr>
<tr>
<td></td>
<td>644.5 (12.8)</td>
<td>392.5 (16.2)</td>
</tr>
<tr>
<td></td>
<td>2.406 (4.1)</td>
<td>2.28 (5.9)</td>
</tr>
<tr>
<td></td>
<td>0.0466 (10.5)</td>
<td>0.0566 (10.3)</td>
</tr>
<tr>
<td></td>
<td>0.0107 (7.6)</td>
<td>0.0105 (10.4)</td>
</tr>
</tbody>
</table>

\(^a\) The units of the intercepts are the same as those of the blood concentrations for each of the model compounds shown in Figure 2. The sum of the intercepts was fixed as Dose/Blood volume \(V_b\).
Table S2. Experimental and predicted compound-specific input parameters for \textit{in silico} $K_p$ prediction by GastroPlus.

<table>
<thead>
<tr>
<th>Compound</th>
<th>Class</th>
<th>pKa</th>
<th>LogP</th>
<th>$R_b$</th>
<th>$f_{up}$ (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>Exp $^a$</td>
<td>Pred $^b$</td>
<td>Exp $^a$</td>
<td>Pred $^b$</td>
</tr>
<tr>
<td>TB</td>
<td>Acid</td>
<td>5.3</td>
<td>5.37, 10.87</td>
<td>2.4</td>
<td>2.27</td>
</tr>
<tr>
<td>CQ</td>
<td>Base</td>
<td>10.1</td>
<td>1.02, 7.25, 9.86</td>
<td>4.63</td>
<td>5.11</td>
</tr>
<tr>
<td>CyA</td>
<td>Neutral</td>
<td>NA</td>
<td>NA</td>
<td>2.90</td>
<td>3.18</td>
</tr>
<tr>
<td>EB</td>
<td>Neutral</td>
<td>NA</td>
<td>11.77</td>
<td>0.80</td>
<td>1.32</td>
</tr>
<tr>
<td>FTY720</td>
<td>Base</td>
<td>8</td>
<td>9.21</td>
<td>5.50</td>
<td>3.72</td>
</tr>
<tr>
<td>NIC</td>
<td>Base</td>
<td>3.04, 7.8</td>
<td>3.05, 8.56</td>
<td>1.17</td>
<td>0.72</td>
</tr>
<tr>
<td>PTZ</td>
<td>Base</td>
<td>8.5</td>
<td>8.16 (Base); 10.34 (Acid)</td>
<td>4.64</td>
<td>4.20</td>
</tr>
<tr>
<td>HB</td>
<td>Acid</td>
<td>8.2</td>
<td>8.17</td>
<td>1.98</td>
<td>1.81</td>
</tr>
<tr>
<td>DPH</td>
<td>Acid</td>
<td>8.33</td>
<td>-2.83, 1.1 (Base); 6.76, 11.4 (Acid)</td>
<td>2.47</td>
<td>1.71</td>
</tr>
</tbody>
</table>
### Table 1: Experimental Values of pKa and LogP

<table>
<thead>
<tr>
<th>Compound</th>
<th>Base</th>
<th>pKa</th>
<th>LogP</th>
</tr>
</thead>
<tbody>
<tr>
<td>QD</td>
<td>8.56</td>
<td>3.87, 7.95</td>
<td>3.44</td>
</tr>
<tr>
<td>PPN</td>
<td>9.45</td>
<td>9.48</td>
<td>3.48</td>
</tr>
<tr>
<td>DZP</td>
<td>3.5</td>
<td>2.96</td>
<td>2.80</td>
</tr>
<tr>
<td>VEM</td>
<td>8.49</td>
<td>8.46</td>
<td>NA</td>
</tr>
<tr>
<td>DLZ</td>
<td>7.7</td>
<td>8.33</td>
<td>2.8</td>
</tr>
</tbody>
</table>

---

**a** The experimental values of pKa and LogP were obtained from (Sangster, 1989; Sangster, 1994; Hansch et al., 1995; Poulin and Theil, 2002; Avdeef, 2003; Rodgers and Rowland, 2006); the literature sources for the experimental $R_b$ and $f_{up}$ are the same as those listed in Tables 1 and 2.

**b** The predicted input parameters were provided by the GastroPlus Simulator based on the chemical structures of the compounds.

**c** The adjusted $f_{up}$ values were given by the GastroPlus simulator based on the experimental and predicted $f_{up}$ and were used for *in silico* $K_p$ prediction.

**d** The listed experimental $R_b$ for CyA is the average of reported values of 1.28 (2.72 mg/kg/day) and 1.18 (2.72 mg/kg/day). The plasma protein binding of FTY720 and QD is nonlinear and the listed experimental $f_{up}$ are the average values of their reported $f_{up}$ ranges.

NA: not applicable or not available.
Supplemental References


Supplemental Methods

Justifications on the Selection of Model Compounds

The assumption that liver is the primary clearance organ of the selected compounds is mainly based on (Bernareggi and Rowland, 1991; Kawai et al., 1998) for Cys A, (Lin et al., 1979; Sugita et al., 1982) for TB, (Igari et al., 1982) for HB, (Naritomi et al., 2001) for DLZ, (Manitpisitkul and Chiou, 1993) for VEM, (Lin et al., 1978) for EB, (Meno-Tetang et al., 2006) for FTY720, (Fujio et al., 1983) for PTZ, (Itoh et al., 1988) for DPH, (Fremstad et al., 1977; Harashima et al., 1985) for QD, (Shibasaki et al., 1989) for PPN, and (Igari et al., 1984) for DZP. For CQ and NIC, $CL_h$ were obtained by subtracting their known extrahepatic $CL$ from $CL_b$ (Plowchalk et al., 1992; Liu and Jusko, 2021).

The in vivo data of all selected compounds except for CQ were obtained from iv bolus studies. It was reported that the contribution of intestinal metabolism is smaller with iv administration than that after oral doses (Pang et al., 2020). Such route-dependent intestinal metabolism has been reported for Cys A (Ducharme et al., 1995), VEM (Darbar et al., 1998), and also QD (Darbar et al., 1997). TB is primarily metabolized by the liver, which has been well supported (McDaniel et al., 1969; Haenen et al., 2002; Fukuno et al., 2018), with the major metabolizing enzyme being CYP2C6 and CYP2C11 in rats and CYP2C9 in humans. Although CYP2C9 is also expressed in human intestine, its protein concentration is about 10-fold less than that in human liver (Lapple et al., 2003). (Scheer et al., 2012) also assessed the hepatic metabolism of tolbutamide by generating mouse models with a deletion of the murine Cyp2c gene cluster and a corresponding humanized model expressing CYP2C9 specifically in the liver.
The $T1/2$ or $CL$ of HB has been frequently used to reflect the hepatic drug-metabolizing enzyme activity owing to the predominant role of liver in the metabolism of HB. It was also reported that the contribution of intestines to the overall metabolism of HB is not significant (van der Graaff et al., 1988).

Theoretically, when a drug is exclusively cleared by the liver, its hepatic availability ($Fh=1-ER$) should be close to the oral bioavailability. This has been confirmed for VEM (Manitpisitkul and Chiou, 1993) and HB (Vermeulen et al., 1983). Given the low systemic $CL$ of Cys A and TB, the contribution of the extrahepatic elimination, if there is any, will not have any significant effect on the estimation of the hepatic model related $CL_{int}$ and $K_p$ in the current analysis.
ADAPT code for blood PK model (QD)

Subroutine SYMBOL
Implicit None

Include 'globals.inc'
Include 'model.inc'

END
Manuscript number: DMD-AR-2022-000994R1

C Enter as Indicated
C
C
NDEqs   =  0   ! Enter # of Diff. Eqs.
NSParam =  3   ! Enter # of System Parameters.
NVparam =  2   ! Enter # of Variance Parameters.
NSecPar =  7   ! Enter # of Secondary Parameters.
NSecOut =  0  ! Enter # of Secondary Outputs (not used).
Ieqsol  =  3  ! Model type: 1 - DIFFEQ, 2 - AMAT, 3 - OUTPUT only.
Descr   = 'QD blood 2CM'

C
C
Enter Symbol for Each System Parameter (eg. Psym(1)='Kel')
C
PSym(1) = 'Cl'
Psym(2) = 'alpha'
Psym(3) = 'beta'

C
C
Enter Symbol for Each Variance Parameter {eg: PVsym(1)='Sigma'}
C
PVsym(1)='Intercept'
PVsym(2)='Sigma'

C
C
Enter Symbol for Each Secondary Parameter {eg: PSsym(1)='CLt'}
C
PSsym(1)='AUCb'
PSsym(2)='CLh'
PSsym(3)='ER'
Subroutine DIFFEQ(T,X,XP)
Implicit None
Include 'globals.inc'
Include 'model.inc'

Real*8 T,X(MaxNDE),XP(MaxNDE)

C
Enter Differential Equations Below  {e.g.  XP(1) = -P(1)*X(1) }  C

C
Return
End

C#........................................................................................................C

PSsym(4)='CLint,WSM'
PSsym(5)='CLint,PTM'
PSsym(6)='AUCp'
PSsym(7)='C2'

C-----------------------------------------------C
C-----------------------------------------------C
C
Return
End

C#........................................................................................................C
Subroutine OUTPUT(Y,T,X)
Implicit None

Include 'globals.inc'
Include 'model.inc'

Real*8 Y(MaxNOE),T,X(MaxNDE)
Real*8 C1,C2,alpha,beta

CC
C Enter Output Equations Below {e.g. Y(1) = X(1)/P(2) }
C----c-----------------------------------

C1 = P(1)
alpha = P(2)
beta = P(3)
C2 = 384.62-C1 !Dose/Vb=384.62

Y(1)=C1*exp(-alpha*T)+C2*exp(-beta*T) ! blood iv

C-------------------------------------
C-------------------------------------

Return
End

C##############################################################
Subroutine VARMOD(V,T,X,Y)
Implicit None

Include 'globals.inc'
Include 'model.inc'
Real*8  V(MaxNOE), T, X(MaxNDE), Y(MaxNOE)
Real*8  Sigma, Intercept

CC
C-------------------------------------------------------------------C
C Enter Variance Model Equations Below                              C
C { e.g. V(1) = (PV(1) + PV(2)*Y(1))**2 }                          C
C-------------------------------------------------------------------C

Intercept=PV(1)
Sigma=PV(2)
V(1)= (PV(1)+PV(2)*Y(1))**2

C-------------------------------------------------------------------C
C
C Return
End

C*************************************************************************

Subroutine COVMOD(Pmean, ICmean, PC)
C Defines any covariate model equations (MLEM, ITS)
Implicit None

Include 'globals.inc'
Include 'model.inc'

Real*8  PC(MaxNCP)
Real*8  Pmean(MaxNSP+MaxNDE), ICmean(MaxNDE)

CC
C-------------------------------------------------------------------C
C Enter # of Covariate Parameters                                  C
C-------------------------------------------------------------------C
NCparam = 0    ! Enter # of Covariate Parameters.

Enter Symbol for Covariate Params {eg: PCsym(1)='CLRenal'}

For the Model Params. that Depend on Covariates Enter the Equation {e.g. Pmean(1) = PC(1)*R(2) }

Return
End

Subroutine POPINIT(PmeanI,ICmeanI,PcovI,ICcovI, PCI)
Initial parameter values for population program parameters (ITS, MLEM)

Implicit None

Include 'globals.inc'
Include 'model.inc'

Integer I,J
Real*8 PmeanI(MaxNSP+MaxNDE), ICmeanI(MaxNDE)
Real*8 PcovI(MaxNSP+MaxNDE,MaxNSP+MaxNDE), ICcovI(MaxNDE,MaxNDE)
Real*8 PCI(MaxNCP)

---

Enter Initial Values for Population Means
{ e.g. PmeanI(1) = 10.0 }

----

Enter Initial Values for Pop. Covariance Matrix (Lower Triang.)
{ e.g. PcovI(2,1) = 0.25 }

----

Enter Values for Covariate Model Parameters
{ e.g. PCI(1) = 2.0 }

----

Return
End

Subroutine PRIOR(Pmean,Pcov,ICmean,ICcov)
C Parameter mean and covariance values for MAP estimation (ID,NPD,STS)
Implicit None

Include 'globals.inc'
Include 'model.inc'

Integer I,J
Real*8 Pmean(MaxNSP+MaxNDE), ICmean(MaxNDE)
Real*8 Pcov(MaxNSP+MaxNDE,MaxNSP+MaxNDE), ICcov(MaxNDE,MaxNDE)

Return
End

Subroutine SPARAM(PS,P,IC)
Implicit None
Include 'globals.inc'

```plaintext
Real*8 PS(MaxNSECP), P(MaxNSP+MaxNDE), IC(MaxNDE)
Real*8 C1,C2,alpha,beta,CLh,Dose,ER,CLint,Qliver,Rb,QliverBrown

C
C Enter Equations Defining Secondary Parameters
C       { e.g. PS(1) = P(1)*P(2) }
C
C1    = P(1)
alpha = P(2)
beta  = P(3)
C2    = 384.62-C1

QliverBrown=60.82
Qliver=58.8 !reported value

Dose=30000 !ug/kg
Rb=1.52

PS(1) = (C1/alpha+C2/beta) !blood AUC
PS(2) = Dose/PS(1) !CLh
PS(3) = PS(2)/(Qliver) !ER
PS(4) = QliverBrown*(PS(3)/(1-PS(3))) !CLint, WSM
PS(5) = -QliverBrown*LOG(1-PS(3)) !CLint, PTM
PS(6) = PS(1)/Rb !plasma AUC
PS(7) = C2

C
C Return
End
```
Subroutine AMAT(A)
Implicit None

Include 'globals.inc'
Include 'model.inc'

Integer I,J
Real*8 A(MaxNDE,MaxNDE)

DO I=1,Ndeqs
  Do J=1,Ndeqs
    A(I,J)=0.0D0
  End Do
End Do

C
C---------------------------------------------------------
C   Enter non zero elements of state matrix {e.g. A(1,1) = -P(1) }  
C---------------------------------------------------------
C
C Return
End

C#************************************************************************C
ADAPT code for the WSM (QD)

C***************************************************************************
C                              ADAPT                                      *
C                           Version 5                                    *
C***************************************************************************
C                          MODEL                                       *
C***************************************************************************
C This file contains Fortran subroutines into which the user must enter the relevant model equations and constants. Consult the User's Guide for details concerning the format for entered equations and definition of symbols.
C***************************************************************************
C       1. Symbol- Parameter symbols and model constants *
C       2. DiffEq- System differential equations           *
C       3. Output- System output equations                *
C       4. Varmod- Error variance model equations         *
C       5. Covmod- Covariate model equations (ITS,MLEM) *
C       6. Popinit- Population parameter initial values (ITS,MLEM) *
C       7. Prior - Parameter mean and covariance values (ID,NPD,STS) *
C       8. Sparam- Secondary parameters                   *
C       9. Amat - System state matrix                     *
C***************************************************************************

CC

Subroutine SYMBOL
Implicit None

Include 'globals.inc'
Include 'model.inc'

CC
C Enter as Indicated

NDEqs = 1 ! Enter # of Diff. Eqs.
NSParam = 2 ! Enter # of System Parameters.
NVParam = 2 ! Enter # of Variance Parameters.
NSecPar = 0 ! Enter # of Secondary Parameters.
NSecOut = 0 ! Enter # of Secondary Outputs (not used).
Ieqsol = 1 ! Model type: 1 - DiffEq, 2 - AMAT, 3 - OUTPUT only.
Descr = 'quinidine liver WSM DE'

PSym(1) = 'Bmax'
PSym(2) = 'Kd'

PVsym(1) = 'Intercept'
PVsym(2) = 'Sigma'

PSym(1) = 'CLt'

C Enter Symbol for Each System Parameter (eg. Psym(1)='Kel')

C Enter Symbol for Each Variance Parameter (eg: PVsym(1)='Sigma')

C Enter Symbol for Each Secondary Parameter (eg: PSym(1)='CLt')
Manuscript number: DMD-AR-2022-000994R1

C
   Return
End

C
#########################################################################
C
Subroutine DIFFEQ(T,X,XP)
Implicit None
Include 'globals.inc'
Include 'model.inc'

Real*8 T,X(MaxNDE),XP(MaxNDE)
Real*8 C1,C2,ka,alpha,beta,Cart,Cout,Bmax,Kd,fup,C3,gamma
Real*8 Qliver,Vliver,Kp,Rb,fub,CLint,ER,psi,Np,Kdp

CC
C
Enter Differential Equations Below {e.g. XP(1) = -P(1)*X(1) } C
C

Bmax=P(1)
Kd=P(2)
Qliver= 60.82  !mL/min/kg
Vliver=36.6  !mL/kg
Rb=1.52
fup=0.325
CLint=84.54

   C1  = 377.7
   C2=6.914
   alpha =1.143
   beta=0.01265
Cart=C1*exp(-alpha*T)+C2*exp(-beta*T) ! blood
Cout=Cart*QLiver/(QLiver+CLInt)
Kp=(Bmax/(Kd+fup*Cout/Rb)+1)*fup
XP(1)=(QLiver* (Cart-Cout)-CLInt*Rb*X(1)/Kp) / Vliver

C---------------------------------------------------------------------C
C---------------------------------------------------------------------C
C
Return
End

C#########################################################################C
Subroutine OUTPUT(Y,T,X)
Implicit None
Include 'globals.inc'
Include 'model.inc'

Real*8 Y(MaxNOE),T,X(MaxNDE)
Real*8 VAd,VBone,VISF_Bone,VISF_Ad,VISFM_Bone,Rb,QK,Cout,Fig
Real*8 C1,C2,alpha,beta,CLInt,Cart,QLiver,ka,Kp,Cuart,Cuout,ER
Real*8 CuLiver,CLiverplasma,NKPA,NKPCBG,KCBG,fub,CLiverblood

C
Enter Output Equations Below  {e.g.  Y(1) = X(1)/P(2) }  
Y(1)=X(1) ! liver
C
C---------------------------------------------------------------------C
C---------------------------------------------------------------------C
C
Subroutine VARMOD(V,T,X,Y)
Implicit None

Include 'globals.inc'
Include 'model.inc'

Real*8 V(MaxNOE),T,X(MaxNDE),Y(MaxNOE)
Real*8 Sigma,Intercept

CCEED------------------------------------------------------------C

Intercept=PV(1)
Sigma=PV(2)
V(1) = (PV(1) + PV(2)*Y(1))**2

CCEED------------------------------------------------------------C

Return
End

Subroutine COVMOD(Pmean, ICmean, PC)
C Defines any covariate model equations (MLEM, ITS)
Implicit None
Include 'globals.inc'
Include 'model.inc'

Real*8 PC(MaxNCP)
Real*8 Pmean(MaxNSP+MaxNDE), ICmean(MaxNDE)

C---------------------------------------------------------------------C
C     Enter # of Covariate Parameters                                 C
C---------------------------------------------------------------------C

NCparam = 0    ! Enter # of Covariate Parameters.
C---------------------------------------------------------------------C
C---------------------------------------------------------------------C
C     Enter Symbol for Covariate Params {eg: PCsym(1)='CLRenal'}        C
C---------------------------------------------------------------------C
C---------------------------------------------------------------------C
C     For the Model Params. that Depend on Covariates Enter the Equation C
C     {e.g. Pmean(1) = PC(1)*R(2) }                                     C
C---------------------------------------------------------------------C

C---------------------------------------------------------------------C
C---------------------------------------------------------------------C
C     Return
C     End
C---------------------------------------------------------------------C
C#
Subroutine POPINIT(PmeanI,ICmeanI,PcovI,ICcovI, PCI)
C Initial parameter values for population program parameters (ITS, MLEM)

Implicit None

Include 'globals.inc'
Include 'model.inc'

Integer I,J
Real*8 PmeanI(MaxNSP+MaxNDE), ICmeanI(MaxNDE)
Real*8 PcovI(MaxNSP+MaxNDE,MaxNSP+MaxNDE), ICcovI(MaxNDE,MaxNDE)
Real*8 PCI(MaxNCP)

C Enter Initial Values for Population Means
{ e.g. PmeanI(1) = 10.0 }

C Enter Initial Values for Pop. Covariance Matrix (Lower Triang.)
{ e.g. PcovI(2,1) = 0.25 }

C Enter Values for Covariate Model Parameters
{ e.g. PCI(1) = 2.0 }

Return
Subroutine PRIOR(Pmean,Pcov,ICmean,ICcov)

C Parameter mean and covariance values for MAP estimation (ID,NPD,STS)
Implicit None

Include 'globals.inc'
Include 'model.inc'

Integer I,J
Real*8 Pmean(MaxNSP+MaxNDE), ICmean(MaxNDE)
Real*8 Pcov(MaxNSP+MaxNDE,MaxNSP+MaxNDE), ICcov(MaxNDE,MaxNDE)

CC
C Enter Nonzero Elements of Prior Mean Vector
C { e.g. Pmean(1) = 10.0 }
CC

CC
C Enter Nonzero Elements of Covariance Matrix (Lower Triang.)
C { e.g. Pcov(2,1) = 0.25 }
CC

C Return
End
Subroutine SPARAM(PS,P,IC)
Implicit None

Include 'globals.inc'

Real*8 PS(MaxNSECP), P(MaxNSP+MaxNDE), IC(MaxNDE)

C
C Enter Equations Defining Secondary Parameters
C     { e.g. PS(1) = P(1)*P(2)  }
C
C
C---c---------------------------------------------------------------------C
C
C Return
End

Subroutine AMAT(A)
Implicit None

Include 'globals.inc'
Include 'model.inc'

Integer I,J
Real*8 A(MaxNDE,MaxNDE)

DO I=1,Ndeqs
Do J=1,Ndeqs
   A(I,J)=0.0D0
End Do
End Do

CC--------------------------------------------------------------------
C             Enter non zero elements of state matrix  {e.g.  A(1,1) = -P(1) } C
C---------------------------------------------------------------C

C--------------------------------------------------------------------
C--------------------------------------------------------------------
C--------------------------------------------------------------------
C Return
C End

C~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~C
ADAPT code for the DM (QD)

******************************************************************************
C                           ADAPT                                     *
C                         Version 5                                    *
C**********************************************************************
C                                                                     *
C                           MODEL                                     *
C                                                                     *
C MODEL
C                                                                     *
C This file contains Fortran subroutines into which the user           *
C must enter the relevant model equations and constants.               *
C Consult the User's Guide for details concerning the format for       *
C entered equations and definition of symbols.                        *
C                                                                 *
C       1. Symbol- Parameter symbols and model constants              *
C       2. DiffEq- System differential equations                     *
C       3. Output- System output equations                           *
C       4. Varmod- Error variance model equations                     *
C       5. Covmod- Covariate model equations (ITS,MLEM)              *
C       6. Popinit- Population parameter initial values (ITS,MLEM)    *
C       7. Prior - Parameter mean and covariance values (ID,NPD,STS) *
C       8. Sparam- Secondary parameters                              *
C       9. Amat - System state matrix                               *
C                                                                 *
C**********************************************************************
C######################################################################C

Subroutine SYMBOL
Implicit None

Include 'globals.inc'
Include 'model.inc'

CC
C Enter as Indicated
C
NDEqs = 1 ! Enter # of Diff. Eqs.
NSParam = 2 ! Enter # of System Parameters.
NVparam = 2 ! Enter # of Variance Parameters.
NSecPar = 0 ! Enter # of Secondary Parameters.
NSecOut = 0 ! Enter # of Secondary Outputs (not used).
Ieqsol = 1 ! Model type: 1 - DIFFEQ, 2 - AMAT, 3 - OUTPUT only.
Descr = 'QD liver DM DE'

PSym(1) = 'Bmax'
PSym(2) = 'Kd'

PVsym(1)='Intercept'
PVsym(2)='Sigma'

PSym(1)='CLt'
Subroutine DIFFEQ(T,X,XP)
Implicit None

Include 'globals.inc'
Include 'model.inc'

Real*8 T,X(MaxNDE),XP(MaxNDE)
Real*8 C1,C2,ka,alpha,beta,Cart,Bmax,Kd,fup,CaveDM
Real*8 Qliver,Vliver,Kp,Rb,fub,CLint,CLh,Cout,a,RN,DN

Bmax=P(1)
Kd=P(2)
CLh=35.3729
Qliver= 60.82  !mL/min/kg
Vliver=36.6  !mL/kg
Rb=1.52
DN=0.6
RN=1.14342
fup=0.325
CLint=69.543
\[ a = (1 + 4 \cdot DN \cdot RN)^0.5 \]
\[
C_1 = 377.7 \\
C_2 = 6.914 \\
\alpha = 1.143 \\
\beta = 0.01265
\]
\[
\text{Cart} = C_1 \cdot \exp(-\alpha \cdot T) + C_2 \cdot \exp(-\beta \cdot T) \quad \text{blood} \\
\text{CaveDM} = \frac{\text{CL}_h \cdot \text{Cart}}{\text{CL}_\text{int}} \quad \text{ave blood conc. in the liver}
\]
\[
\text{Cout} = \text{Cart} \cdot \left(\frac{4 \cdot a}{((a+1)^2) \cdot \exp((a-1)/(2 \cdot DN))} - ((a-1)^2) \cdot \exp(-(a+1)/(2 \cdot DN))\right)
\]
\[
\text{Kp} = \frac{\text{Bmax}/(K_d + \text{CaveDM}/R_b \cdot f_{up}) + 1) \cdot f_{up}}
\]
\[
\text{XP}(1) = \frac{\text{Q}_{\text{Liver}} \cdot (\text{Cart} - \text{Cout}) - \text{CL}_\text{int} \cdot R_b \cdot X(1)/K_p}{V_{\text{Liver}}}
\]

Subroutine OUTPUT(Y,T,X)
Implicit None

Include 'globals.inc'
Include 'model.inc'

Real*8 Y(MaxNOE), T, X(MaxNDE)
Real*8 VA_d, V_Bone, VIF_Bone, VIF_Ad, VIFM_Bone, R_b, QK, Cout, Fig
Real*8 C1, C2, alpha, beta, CLint, Cart, QLiver, ka, Kp, Cuart, Cuout, ER
Real*8 CuLiver, CLiverplasma, NKPA, NKPCBG, KCBG, fub, CLiverblood

C
C   Enter Output Equations Below   {e.g.  Y(1) = X(1)/P(2) }           C
C
Y(1)=X(1)                      ! liver

C
C   Enter Variance Model Equations Below                               C
C         {e.g. V(1) = (PV(1) + PV(2)*Y(1))**2 }                       C
C
Intercept=PV(1)
Sigma=PV(2)
V(1)= (PV(1)+PV(2)*Y(1))**2

C---------------------------------------------------------------------------C
C---------------------------------------------------------------------------C
C
Return
End

C#******************************************************************************C

Subroutine COVMOD(Pmean, ICmean, PC)
C defines any covariate model equations (MLEM, ITS)
Implicit None

Include 'globals.inc'
Include 'model.inc'

Real*8 PC(MaxNCP)
Real*8 Pmean(MaxNSP+MaxNDE), ICmean(MaxNDE)

C
C Enter # of Covariate Parameters
C
NCparam = 0    ! Enter # of Covariate Parameters.
C
C Enter Symbol for Covariate Params {eg: PCsym(1)='CLRenal'}
Subroutine POPINIT(PmeanI, ICmeanI, PcovI, ICcovI, PCI)
C Initial parameter values for population program parameters (ITS, MLEM)
Implicit None
Include 'globals.inc'
Include 'model.inc'

Integer I, J
Real*8 PmeanI(MaxNSP+MaxNDE), ICmeanI(MaxNDE)
Real*8 PcovI(MaxNSP+MaxNDE, MaxNSP+MaxNDE), ICcovI(MaxNDE, MaxNDE)
Real*8 PCI(MaxNCP)

C For the Model Params. that Depend on Covariates Enter the Equation C
{ e.g. Pmean(1) = PC(1)*R(2) }
C

C Return
End

C-------------------------------C
C Enter Initial Values for Population Means
C
{ e.g. Pmean(1) = 10.0 }
C
C-------------------------------C
CC
C------------------
C    Enter Initial Values for Pop. Covariance Matrix (Lower Triang.)    
C                      {  e.g. PcovI(2,1) = 0.25    }                     
C
CC
C------------------
C    Enter Values for Covariate Model Parameters                        
C                      {  e.g. PCI(1) = 2.0    }                         
C
C------------------
C
C
Return
End

Subroutine PRIOR(Pmean,Pcov,ICmean,ICcov)
C Parameter mean and covariance values for MAP estimation (ID,NPD,STS)
C Implicit None

Include 'globals.inc'
Include 'model.inc'

Integer I,J
Real*8 Pmean(MaxNSP+MaxNDE), ICmean(MaxNDE)
Real*8 Pcov(MaxNSP+MaxNDE,MaxNSP+MaxNDE), ICcov(MaxNDE,MaxNDE)
CC
C Enter Nonzero Elements of Prior Mean Vector                             C
C  {  e.g. Pmean(1) = 10.0   }                                           C
C----c------------------------------------------------------------------C

CC
C Enter Nonzero Elements of Covariance Matrix (Lower Triang.)            C
C  {  e.g. Pcov(2,1) = 0.25    }                                       C
C----c------------------------------------------------------------------C

C Return
End

C Subroutine SPARAM(PS,P,IC)
Implicit None

Include 'globals.inc'

Real*8 PS(MaxNSECP), P(MaxNSP+MaxNDE), IC(MaxNDE)

CC
C Enter Equations Defining Secondary Parameters                         C
C  {  e.g. PS(1) = P(1)*P(2)  }                                       C
C----c------------------------------------------------------------------C
Subroutine AMAT(A)
Implicit None

Include 'globals.inc'
Include 'model.inc'

Integer I,J
Real*8 A(MaxNDE,MaxNDE)

DO I=1,Ndeqs
  Do J=1,Ndeqs
    A(I,J)=0.0D0
  End Do
End Do
ADAPT code for the PTM (QD)

**********************************************************************
C                           ADAPT                                     *
C Version 5                                   *
C**********************************************************************
C                                                                     *
C                           MODEL                                     *
C                                                                     *
C This file contains Fortran subroutines into which the user must enter the relevant model equations and constants. Consult the User's Guide for details concerning the format for entered equations and definition of symbols.
C                                                                     *
C       1. Symbol- Parameter symbols and model constants             *
C       2. DiffEq- System differential equations                     *
C       3. Output- System output equations                           *
C       4. Varmod- Error variance model equations                    *
C       5. Covmod- Covariate model equations (ITS,MLEM)              *
C       6. Popinit- Population parameter initial values (ITS,MLEM)   *
C       7. Prior - Parameter mean and covariance values (ID,NPD,STS) *
C       8. Sparam- Secondary parameters                              *
C       9. Amat - System state matrix                               *
C                                                                     *
C**********************************************************************
C##############################################
Subroutine SYMBOL  
Explicit None
   Include 'globals.inc'
   Include 'model.inc'
CC
C Enter as Indicated

C

NDEqs = 1 ! Enter # of Diff. Eqs.
NSParam = 2 ! Enter # of System Parameters.
NVParam = 2 ! Enter # of Variance Parameters.
NSecPar = 0 ! Enter # of Secondary Parameters.
NSecOut = 0 ! Enter # of Secondary Outputs (not used).
Ieqsol = 1 ! Model type: 1 - DIFFEQ, 2 - AMAT, 3 - OUTPUT only.
Descr = 'QD liver PTM DE'

C

PSym(1) = 'Bmax'
PSym(2) = 'Kd'

C

PVsym(1)='Intercept'
PVsym(2)='Sigma'

C

C

C
Subroutine DIFFEQ(T,X,XP)
Implicit None

Include 'globals.inc'
Include 'model.inc'

Real*8 T,X(MaxNDE),XP(MaxNDE)
Real*8 C1,C2,ka,alpha,beta,Cart,Bmax,Kd,Cuart,Cuout,fup
Real*8 Qliver,Vliver,Kp,Rb,fub,CLint,ER,Cout,CuLiver

Bmax=P(1)
Kd=P(2)

Qliver= 60.82  !mL/min/kg
Vliver=36.6  !mL/kg
Rb=1.52
fup=0.325
CLint=52.99

C1 = 377.7
C2=6.914
alpha =1.143
beta=0.01265
Cart=C1*exp(-alpha*T)+C2*exp(-beta*T) ! blood
Cout=Cart*exp(-CLint/Qliver)

CuLiver=((Cart-Cout)/LOG(Cart/Cout))*fup/Rb ! ave.liver unbound plasma

Kp=(Bmax/(Kd+CuLiver)+1)*fup

XP(1)=(Qliver* (Cart-Cout)-CLint*Rb*X(1)/Kp) / Vliver

Subroutine OUTPUT(Y,T,X)
Implicit None
Include 'globals.inc'
Include 'model.inc'

Real*8 Y(MaxNOE),T,X(MaxNDE)
Real*8 VAd,VBone,VISF_Bone,VISF_Ad,VISFM_Bone,Rb,QK,Cout,Fig
Real*8 C1,C2,alpha,beta,CLint,Cart,QLiver,ka,Kp,Cuart,Cuout,ER
Real*8 CuLiver,CLiverplasma,NKPA,NKPCBG,KCBG,fub,CLiverblood

C Enter Output Equations Below  {e.g.  Y(1) = X(1)/P(2) }
Y(1)=X(1) ! liver

C-------------------------------------------------------------
C-----------------------------------------------------------------
C
C Return
End
C
C######################################################################

Subroutine VARMOD(V,T,X,Y)
Implicit None

Include 'globals.inc'
Include 'model.inc'

Real*8 V(MaxNOE),T,X(MaxNDE),Y(MaxNOE)
Real*8 Sigma,Intercept

CCarbon
C-----------------------------------------------------------------
C
Intercept=PV(1)
Sigma=PV(2)
V(1)= (PV(1)+PV(2)*Y(1))**2

C
C-----------------------------------------------------------------
C
Return
End

*****************************************************************************
Subroutine COVMOD(Pmean, ICmean, PC)
C Defines any covariate model equations (MLEM, ITS)
Implicit None

Include 'globals.inc'
Include 'model.inc'

Real*8 PC(MaxNCP)
Real*8 Pmean(MaxNSP+MaxNDE), ICmean(MaxNDE)

NCparam = 0    ! Enter # of Covariate Parameters.

For the Model Params. that Depend on Covariates Enter the Equation
{e.g. Pmean(1) = PC(1)*R(2) }
Subroutine POPINIT(PmeanI,ICmeanI,PcovI,ICcovI, PCI)

C  Initial parameter values for population program parameters (ITS, MLEM)

Implicit None

Include 'globals.inc'
Include 'model.inc'

Integer I,J
Real*8 PmeanI(MaxNSP+MaxNDE), ICmeanI(MaxNDE)
Real*8 PCovI(MaxNSP+MaxNDE,MaxNSP+MaxNDE), ICcovI(MaxNDE,MaxNDE)
Real*8 PCI(MaxNCP)

C Enter Initial Values for Population Means
   { e.g. PmeanI(1) = 10.0  }

C Enter Initial Values for Pop. Covariance Matrix (Lower Triang.)
   { e.g. PCovI(2,1) = 0.25  }
Subroutine PRIOR(Pmean,Pcov,ICmean,ICcov)

Parameter mean and covariance values for MAP estimation (ID,NPD,STS)

Implicit None

Include 'globals.inc'
Include 'model.inc'

Integer I,J
Real*8 Pmean(MaxNSP+MaxNDE), ICmean(MaxNDE)
Real*8 Pcov(MaxNSP+MaxNDE,MaxNSP+MaxNDE), ICcov(MaxNDE,MaxNDE)

Enter Nonzero Elements of Prior Mean Vector

{ e.g. Pmean(1) = 10.0 }

Return
End
Manuscript number: DMD-AR-2022-000994R1

CC
C------------------------------------------------------------------C
C   Enter Nonzero Elements of Covariance Matrix (Lower Triang.)   C
C       {  e.g. Pcov(2,1) = 0.25      }                           C
C------------------------------------------------------------------C

Return
End

C########################################################################C
Subroutine SPARAM(PS,P,IC)
Implicit None
Include 'globals.inc'

Real*8 PS(MaxNSECP), P(MaxNSP+MaxNDE), IC(MaxNDE)

CC
C------------------------------------------------------------------C
C   Enter Equations Defining Secondary Parameters                 C
C       {  e.g. PS(1) = P(1)*P(2)      }                          C
C------------------------------------------------------------------C

C########################################################################C
C
C

52
Subroutine AMAT(A)
Implicit None

Include 'globals.inc'
Include 'model.inc'

Integer I,J
Real*8 A(MaxNDE,MaxNDE)

DO I=1,Ndeqs
  DO J=1,Ndeqs
    A(I,J)=0.0D0
  END DO
END DO

C
C    Enter non zero elements of state matrix {e.g. A(1,1) = -P(1) } C
C
C

Return
End
ADAPT code for simulating the unbound blood/liver concentrations

**********************************************************************
C                           ADAPT
C                         Version 5
C*************************************************************************
C                                                                     *
C                           MODEL                                     *
C                                                                     *
C This file contains Fortran subroutines into which the user must enter the relevant model equations and constants. Consult the User's Guide for details concerning the format for entered equations and definition of symbols.
C                                                                     *
C       1. Symbol- Parameter symbols and model constants            *
C       2. DiffEq- System differential equations                    *
C       3. Output- System output equations                          *
C       4. Varmod- Error variance model equations                    *
C       5. Covmod- Covariate model equations (ITS,MLEM)             *
C       6. Popinit- Population parameter initial values (ITS,MLEM) *
C       7. Prior- Parameter mean and covariance values (ID,NPD,STS) *
C       8. Sparam- Secondary parameters                             *
C       9. Amat - System state matrix                               *
C                                                                     *
C*************************************************************************

Subroutine SYMBOL
Implicit None

Include 'globals.inc'
Include 'model.inc'

CC
NDEqs = 0 ! Enter # of Diff. Eqs.
NSParam = 9 ! Enter # of System Parameters.
NVparam = 2 ! Enter # of Variance Parameters.
NSecPar = 0 ! Enter # of Secondary Parameters.
NSecOut = 0 ! Enter # of Secondary Outputs (not used).
Ieqsol = 3 ! Model type: 1 - DIFFEQ, 2 - AMAT, 3 - OUTPUT only.
Descr = 'unbound liver conc 3CM'

PSym(1) = 'C1'
PSym(2) = 'C2'
Psym(3) = 'alpha'
Psym(4) = 'beta'
Psym(5) = 'C3'
Psym(6) = 'gamma'
PSym(7) = 'ER'
PSym(8) = 'fubCLintDM'
PSym(9) = 'fub'

PVsym(1)='Intercept'
PVsym(2)='Sigma'
CC
C -------------------------------------------------------------C
C Enter Symbol for Each Secondary Parameter {eg: PSym(1)='CLt'} C
C-----c------------------------------------------------------C

C----------------------------------------------------------C
C----------------------------------------------------------C
C
C Return
End

C######################################################CC

Subroutine DIFFEQ(T,X,XP)
Implicit None

Include 'globals.inc'
Include 'model.inc'

Real*8 T,X(MaxNDE),XP(MaxNDE)

CC
C--------------------------------------------------C
C Enter Differential Equations Below {e.g. XP(1) = -P(1)*X(1) } C
C-----c--------------------------------------------------C

C--------------------------------------------------C
C--------------------------------------------------C
C
C Return
Subroutine OUTPUT(Y,T,X)
Implicit None

Include 'globals.inc'
Include 'model.inc'

Real*8 Y(MaxNOE),T,X(MaxNDE)
Real*8 C1,C2,alpha,beta,C3,gamma,fubCLintDM,CLh,ER,Cart,Cout,fub

C1 = P(1)
C2 = P(2)
alpha= P(3)
beta = P(4)
C3=P(5)
gamma=P(6)
ER=P(7)
fubCLintDM=P(8)
fub=P(9)

CLh=60.82*ER

Cart=C1*exp(-alpha*T)+C2*exp(-beta*T)+C3*exp(-gamma*T) ! blood conc
Cout=Cart*(1-ER)

Y(1)=fub*Cout !WSM
Subroutine VARMOD(V,T,X,Y)
Implicit None

Include 'globals.inc'
Include 'model.inc'

Real*8 V(MaxNOE), T, X(MaxNDE), Y(MaxNOE)
Real*8 Sigma, Intercept

Intercept=PV(1)
Sigma=PV(2)
V(1:3)= (PV(1)+PV(2)*Y(1:3))**2

Return
End
Subroutine COVMOD(Pmean, ICmean, PC)
C Defines any covariate model equations (MLEM, ITS)
Implicit None

Include 'globals.inc'
Include 'model.inc'

Real*8 PC(MaxNCP)
Real*8 Pmean(MaxNSP+MaxNDE), ICmean(MaxNDE)

NCparam = 0  ! Enter # of Covariate Parameters

For the Model Params. that Depend on Covariates Enter the Equation C
{e.g. Pmean(1) = PC(1)*R(2) }
Subroutine POPINIT(PmeanI, ICmeanI, PcovI, ICcovI, PCI)
C Initial parameter values for population program parameters (ITS, MLEM)

Implicit None

Include 'globals.inc'
Include 'model.inc'

Integer I, J
Real*8 PmeanI(MaxNSP+MaxNDE), ICmeanI(MaxNDE)
Real*8 PcovI(MaxNSP+MaxNDE,MaxNSP+MaxNDE), ICcovI(MaxNDE,MaxNDE)
Real*8 PCI(MaxNCP)

C Enter Initial Values for Population Means
C { e.g. PmeanI(1) = 10.0 } C
C-----c---------------------------------------------C

C Enter Initial Values for Pop. Covariance Matrix (Lower Triang.) C
C { e.g. PcovI(2,1) = 0.25 } C
C-----c---------------------------------------------C
Subroutine PRIOR(Pmean, Pcov, ICmean, ICcov)

Parameter mean and covariance values for MAP estimation (ID, NPD, STS)

Implicit None

Include 'globals.inc'
Include 'model.inc'

Integer I, J
Real*8 Pmean(MaxNSP+MaxNDE), ICmean(MaxNDE)
Real*8 Pcov(MaxNSP+MaxNDE, MaxNSP+MaxNDE), ICcov(MaxNDE, MaxNDE)

Enter Nonzero Elements of Prior Mean Vector
{ e.g. Pmean(1) = 10.0 }

Subroutine SPARAM(PS,P,IC)
Implicit None

Include 'globals.inc'

Real*8 PS(MaxNSECP), P(MaxNSP+MaxNDE), IC(MaxNDE)
Subroutine AMAT(A)
Implicit None

Include 'globals.inc'
Include 'model.inc'

Integer I,J
Real*8 A(MaxNDE,MaxNDE)

DO I=1,Ndeqs
   Do J=1,Ndeqs
      A(I,J)=0.0D0
   End Do
End Do

C Enter non zero elements of state matrix (e.g. A(1,1) = -P(1) )
C
C Return
End