



Role of pharmacokinetic modeling and simulation in precision dosing of anticancer drugs

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Abstract: The prospect of precision dosing in oncology is attractive for several reasons. Many anticancer drugs display narrow therapeutic indices, where suboptimal therapy may lead to severe patient outcomes. Clinical study participant recruitment is seldom extended beyond the intended patient population, leading to difficulties in patient recruitment in dedicated clinical trials. The high rate of non-responders and high cost of cancer therapy warrant novel solutions to increase clinical effectiveness and cost-benefit, pharmacokinetic (PK) modeling and model-informed precision dosing (MIPD) can help to maximize these. PK modeling provides a quantitative framework to account for inter-individual variability in drug exposure, the influence of covariates and extrapolation to special populations or drug-drug interactions, using physiologically-based PK (PBPK) modeling. Here we present the current state of PK modeling in precision dosing of anticancer drugs and illustrate its utility, based on an extensive literature review and numerous case examples from both pharmaceutical industry and healthcare focused research. While some great progress has been made in implementing model-informed dosage guidance in the drug label and much research has been carried out to address clinically relevant dosing questions, the uptake of MIPD has been modest in healthcare. The success of PK modeling in industry has been made possible through collaborative efforts between regulators, industry and academia. Collaboration between academia, healthcare and industry, and financial support for research into patient benefit, cost-benefit and clinical effectiveness of these approaches is imperative for wider adaption of PK modeling in precision dosing of anticancer drugs.

Keywords: Population pharmacokinetics (PK); physiologically-based pharmacokinetics (PBPK); modeling; individualized dosing; oncology

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Introduction

In drug development, late phase clinical trials often aim to establish uniform dosing, balancing efficacy and toxicity, across the patient population from a limited set of proposed dosage schemes (1). Dosing of anticancer drugs has traditionally been based on body surface area (BSA) under the assumption that there is a relationship between BSA and

clearance (CL) or volume of distribution (V_d). However, this relationship is in many instances poor and may therefore not accurately reflect the change in drug exposure seen across the population (2-5), meaning variability in drug exposure may remain high at the established dosage regimen (5). This is particularly true when the drug is dosed in a more diverse patient population in clinical practice, such as: complex drug-drug interactions (DDIs), pediatric patients, and

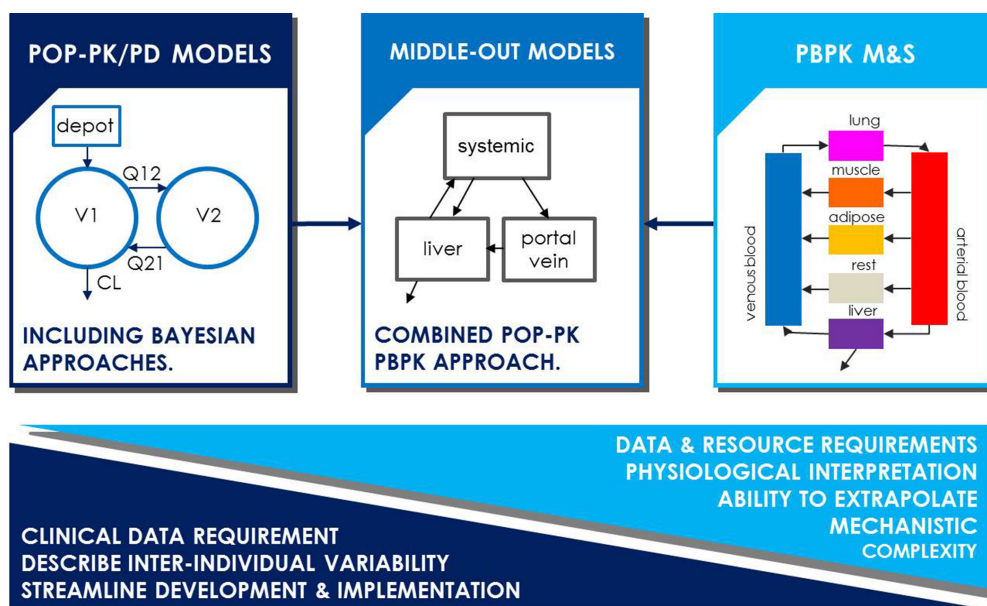


Figure 1 Pharmacokinetic modeling approaches for precision dosing of oncology drugs. Bars indicate the features of the individual and combined techniques.

renally/hepatically impaired or other special populations (6). Explicit dosage recommendations are often absent from the drug label for most special populations at the time of approval (7). These factors contribute to variable clinical practices, where clinicians are challenged to make decisions based on experience and the many times limited literature. Patients with multiple comorbidities/co-medication are therefore at risk of suboptimal pharmacotherapy that may lead to unacceptable levels of toxicity or reduced efficacy (6,8,9). Model-informed precision dosing (MIPD) provides a quantitative framework for achieving the accurate dose for the individual patient through statistical and/or mathematical modeling, such as pharmacokinetic (PK) modeling, by accounting for inter-individual variability (IIV), and other factors that lead to variable drug exposure and/or pharmacodynamic (PD) response (10).

Here we examine the current state of PK modeling in dose individualization of anticancer drugs. The comparative analysis presented here was based on a sample of 393 peer-reviewed publications on PK modeling in oncology (see *Table S1*, in supplementary appendix available online). The dataset should not be considered an exhaustive list of the abundant literature on PK modeling in oncology. Many arguments on precision dosing presented here are part of a much broader discussion on MIPD across therapeutic areas (7,10-12).

The case for MIPD in oncology

The traditional resolution to dose optimization in special populations/DDIs is to carry out dedicated clinical studies. This is however not always feasible in oncology due to patient recruitment issues around dosing drugs in vulnerable populations or patients outside the indicated treatment group (13). Statistical nonlinear-mixed effects (NLME) modeling (population-PK/PD modeling, or pop-PK/PD) aims to describe the IIV in PK parameters using compartmental and increasingly mechanistic models. Physiologically-based PK (PBPK) modeling and simulation (M&S), attribute physiological meaning to PK models by mimicking physiology (inter-compartmental CLs informed by blood flows, volumes based on organ/tissue volumes etc.) in an attempt to better understand the processes that determine drug ADME (absorption, distribution, metabolism and excretion). The combined approach (“middle-out”) accommodates physiological models where model parameters may account for observed IIV in the population sample (see *Figure 1*) (14). Pop-PK/PD and PBPK M&S have gained increasing acceptance in pharmaceutical research and development (R&D) and by regulatory agencies over the last couple of decades to a point where dedicated clinical trials may be substituted/supplemented by modeling, foremost interpolating the

effect of metabolic DDIs (15). It is anticipated that M&S will gain further utility over the coming years as confidence is built in other areas of application, both in pharmaceutical R&D, regulatory submission and clinical practice for dose individualization (7,10,12).

Dose individualization, personalized dosing or precision dosing, may be considered part of the well-recognized paradigm of precision medicine. Precision medicine pursues to personalize prevention, diagnostics and optimal treatment of disease based on individual patient characteristics, e.g., genotyping, renal function and other biomarkers (16). Similarly, precision dosing strives to account for between-patient variability in drug exposure and response to optimize dosing for the individual. This is not a novel idea, carboplatin is the perhaps most famous example in oncology, seeing early adoption of renal function guided dosing (Calvert *et al.* formula) to reduce the risk of hematological toxicity (17). Similarly, PK-based dose adjustment, using therapeutic drug monitoring (TDM), of 5-fluorouracil (5-FU) was shown to produce superior treatment response and reduced toxicity as compared to BSA-guided dosing alone in metastatic colorectal cancer (18).

Precision dosing in cancer therapy is attractive for several reasons. Many anticancer drugs display narrow therapeutic indices, where suboptimal therapy may lead to severe patient outcomes. Clinical study participant recruitment issues accentuates the difficulty of patient recruitment in dedicated clinical trials for special populations and is perhaps part of the reason (as well as accelerated approvals) why there has been an above average adoption of PBPK M&S for new drug applications (NDAs) in oncology to the U.S. Food and Drug Administration (FDA) (19). The relatively high rate of non-responders in cancer treatment together with high cost of cancer therapies warrants alternative approaches to increasing patient benefit and cost-benefit; this may include more effective use of approaches that maximize treatment outcome, such as PK modeling and MIPD (20,21).

Application of PK modeling in oncology

Model-informed drug discovery and development has become established practice in the pharmaceutical industry over the past decades, where today it is employed across drug development to inform internal and regulatory decisions (15,22). In early discovery and pre-clinical development, modeling is used to inform candidate selection, ADME characterization, translation of exposure and effect and more, this includes pop-PK/

PD, PBPK and more mechanistic systems pharmacology/biology approaches. Pop-PK/PD is widely used in clinical development to investigate efficacy, dose selection and dose bridging. PBPK M&S is used clinically for predicting metabolic DDIs, impact of genetic polymorphism, biopharmaceutics effects and extrapolating to special populations (22).

Analysis of peer-reviewed publications using PK modeling in oncology, based on the modeling approach (see *Figure 2*), showed that a majority of studies employed population-based approaches in their data analysis (75%), a subset of these include traditional pop-PK (45%), pop-PK/PD (14%), Bayesian pop-PK (10%) and semi-mechanistic pop-PK/PD (6%). PBPK M&S accounted for 8% of identified studies. In terms of areas of application of PK modeling (see *Figure 3*), the most prominent area of application was investigation of covariates (49%) to account for IIV in PK. This was followed by studies investigating dosing issues (22%), including dose finding and practice based dosing issues. The most studied special populations included pediatric patients (13%), hepatic (3%) and renal impairment (2%). Other investigated special populations included: pregnancy, elderly, and more. Other areas of investigation included: toxicity (18%), dose/PK-efficacy studies (response: 8%), metabolite kinetics (8%), metabolic/transporter genotype/phenotype (6%), DDIs (5%), limited sampling strategies (5%) and more.

In PBPK M&S, predictions of metabolic DDIs and extrapolation to special populations were the perhaps most prominent area of research. This was consistent with common areas of application seen in regulatory submissions where predictions of DDIs tend to dominate due to more well-established body of evidence to support PBPK, guidelines and regulatory acceptance (15,19). There is in other words wide application of PK modeling to address critical questions in dose individualization of oncology drugs.

Population PKs and covariate analysis to aid precision dosing in oncology

Pop-PK/PD aims to describe the observed IIV in drug exposure and response for a given population sample. The method allows estimation of the population mean (θ) and IIV (η) of PK/PD parameters and the remaining residual, or unexplained, variability (ϵ). The approach allows interpolation of drug exposure and response over the observed parameter space through identification of

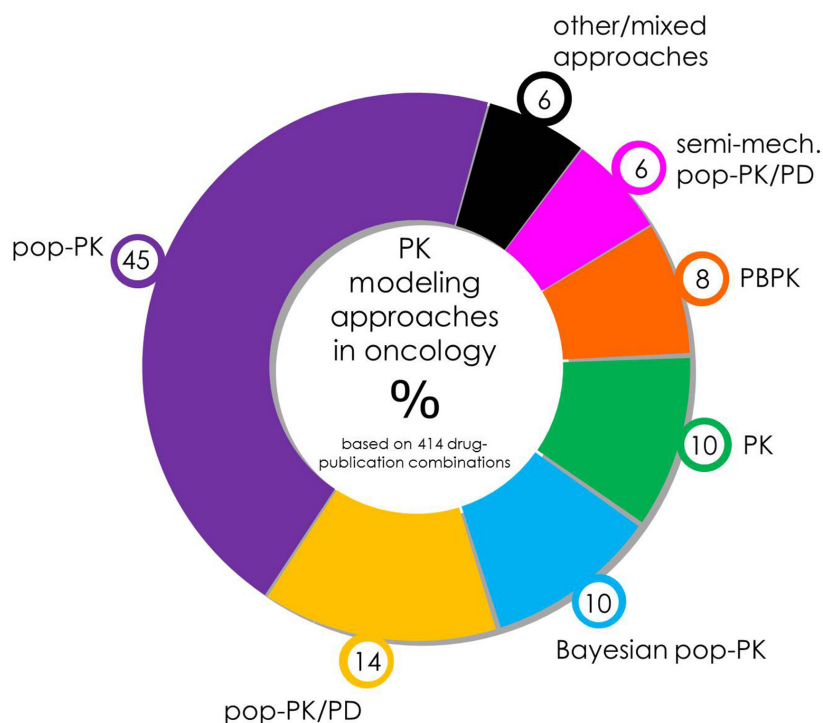


Figure 2 Peer-reviewed publications on pharmacokinetic modeling of oncology drugs categorized based on method of approach (number of publications: 393, number of drug-publication combinations: 414; see supplementary appendix). PK, pharmacokinetic; PD, pharmacodynamic; pop, population-based analysis; semi-mech., semi-mechanistic/semi-physiological; PBPK, physiologically-based pharmacokinetics.

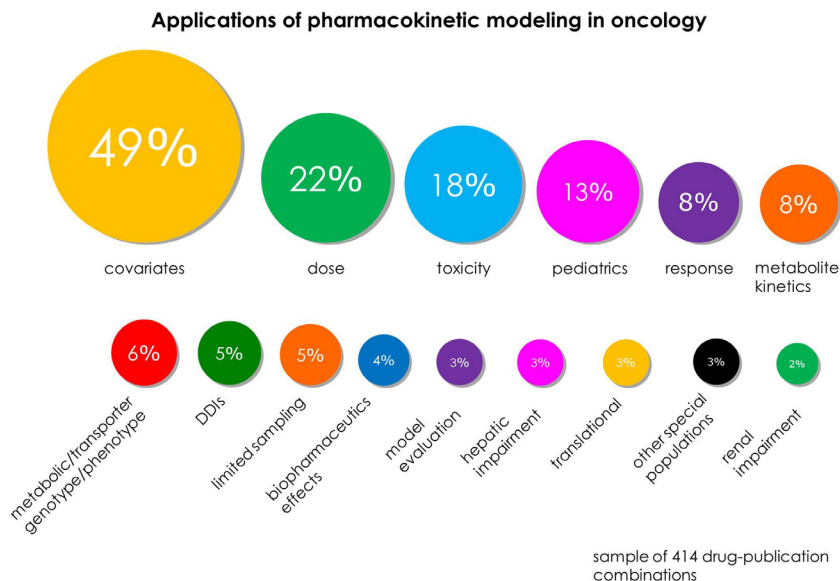


Figure 3 Areas of application of pharmacokinetic modeling in oncology based on a sample of 393 peer-reviewed publications (see supplementary appendix). Circle areas are proportional to frequencies. DDIs, drug-drug interactions.

covariates (demographics, genetic polymorphism and other pathophysiological variables). For example, covariates can be included as either dichotomous [Eq. [1]] or continuous effects [Eq. [2]] on PK parameters, e.g., (23):

$$\theta_{j,i} = \theta_j \times \theta_{Cov,n}^{Cov,i} + \eta_{j,i} \quad [1]$$

$$\theta_{j,i} = \theta_j \times \left(\frac{Cov_i}{Cov} \right)^{\theta_{Cov,n}} + \eta_{j,i} \quad [2]$$

Where mean effect of the n^{th} covariate ($\theta_{Cov,n}$) and IIV of the j^{th} parameter of the i^{th} individual ($\eta_{j,i}$) on population mean (θ_j) determines the individual parameter estimate for the j^{th} parameter ($\theta_{j,i}$), Cov_i is the individual observed covariate and \overline{Cov} the central tendency of the sample population. Significant covariates account for IIV in exposure, meaning that a combined PK-covariate model can forecast individual exposure based on individual biomarker data prior to dosing and refine predictions following sparse PK sampling or TDM. This makes for a powerful tool for precision dosing. Covariate significance can be determined using, e.g., step-wise inclusion based on a predefined statistical criterion (post-hoc p -value testing for difference in objective function), or alternative approaches. Pop-PK-covariate modeling has been successfully employed for oncology drugs to individualize dosing, as included in drug labelling (24,25). Further, there are a number of examples of pop-PK-covariate models that have been used to address dosing issues in clinical practice with some success (see section “PK modeling of anticancer drugs in healthcare”).

Figure 4 shows identified PK covariates for anticancer drugs based on the peer-reviewed literature. The most commonly included covariates were bodyweight (50% of drugs in sample set) and other demographic data [sex (28%), BSA (26%) and age (21%)]. Other common covariates included biomarkers related renal function [creatinine CL (19%), serum creatinine (7%) and estimated glomerular filtration rate (5%)], drug-binding plasma proteins [albumin (17%) and α_1 -acid glycoprotein (AAG, 2%)], cancer type (14%) and concomitant treatment (11%). Other biomarkers of liver function were also reasonably prominent as model covariates, e.g., alanine amino transferase (ALT, 9%), aspartate amino transferase (AST, 6%) and alkaline phosphatase (ALK, 5%) including more. Metabolic genotyping was included for 7% of drugs.

It has been recognized that there is a disparity between the wealth of covariates identified in the literature and the limited number pertaining to the dosage recommendation

in the drug labels of oncology drugs (25). Figure 5 shows factors affecting explicit dose recommendations in the FDA label for selected drugs compared to additional identified PK covariates in the literature. There are many potential explanations for this: covariate selection can be biased (insufficient power, collinearity, etc.), not all statistically significant covariates are clinically relevant, covariates may for example be of obscure meaning and have little physiological/pharmacological relevance (25,32). Further, the identification of significant but low-effect covariates may have little clinical implication. Here, cut-off points have been proposed where covariates may be considered clinically relevant if they explain at least 20% to 30% of IIV (25,33). A lack of communication of research between academia and industry may also affect the difference in the adoption of covariates, suggesting some scope for further individualization of dosing of oncology drugs based on disseminated research (25).

PBPK modeling to inform individualized dosing of anticancer drugs

By assigning physiological meaning to model parameters, PBPK M&S offers a method for quantitative extrapolation of drug exposure from *in vitro* to *in vivo* (IVIVE), between species, across populations and for metabolic/transporter DDIs. In oncology, PBPK M&S has been used extensively for the prediction of DDIs, special populations (renal/hepatic impairment and pediatrics) and biopharmaceutics effects (absorption, formulation, food effects). In fact, some of the earliest examples of PBPK M&S in oncology can be traced back to modeling of chemotherapy agents in the 1970s (34).

There are several factors that explain the wide usage of PBPK in oncology: ethical/safety or recruitment issues, many oncology drugs exhibit narrow therapeutic indices and/or pose risks of severe toxicity and may therefore require more consideration for precision dosing, many anticancer drugs are carried forward through accelerated regulatory approval meaning that studies that have not been carried out in timely fashion may be substituted by PBPK M&S (19). Numerous examples of PBPK M&S of oncology drugs exist in the literature, including for: pediatrics (35-37), biopharmaceutics effects (38), renal impairment (39-41), hepatic impairment (42), metabolic phenotypes/genotypes (43,44) and adherence (44) metabolic/transporter DDIs (45-49), with more examples available in FDA drug labels (50). The current view of FDA regarding PBPK-informed

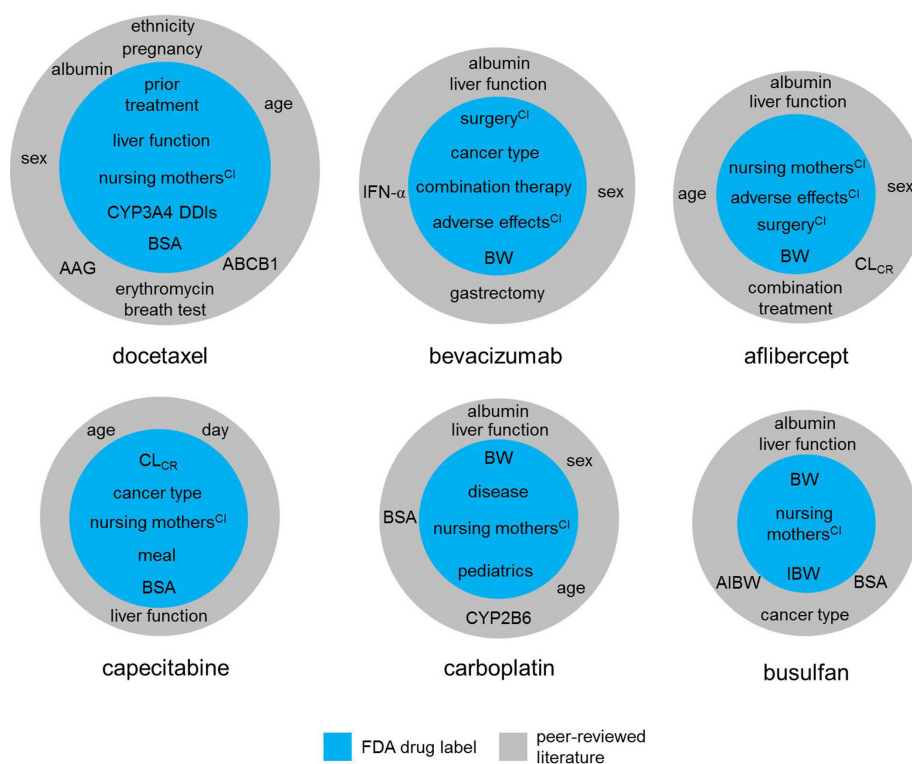


Figure 5 Factors affecting explicit dose recommendations in the FDA drug labels [including contraindications (CI)] of docetaxel (Taxotere[®]), bevacizumab (Avastin[®]), aflibercept (Zaltrap[®]), capecitabine (Xeloda[®]), carboplatin (Teva Pharmaceuticals USA) and busulfan (Busulfex[®]) (blue circles) (26-31). Grey circles indicate additional pharmacokinetic covariates identified in the sampled peer-reviewed literature (see Table S1, supplementary appendix). Exposed circle areas are proportional to the number of factors/covariates. Erythromycin breath test, as surrogate of CYP3A4 activity; liver function, including AST, ALT and more, excluding albumin. AAG, α_1 -acid glycoprotein; AIBW, adjusted IBW; BW, bodyweight; BSA, body surface area; CL_{CR} , creatinine clearance; DDIs, drug-drug interactions; IBW, ideal bodyweight; IFN- α , interferon- α ; AST, aspartate amino transferase; ALT, alanine amino transferase.

dosing, is that sufficient evidence exists to employ verified models for the prediction of metabolic DDIs where the drug is the victim substrate (50). For special populations and biopharmaceutics effects, the jury is still out in the absence of more evidence to support the ability to prospectively and quantitatively predict these effects (50). Here we present selected case examples to illustrate the usefulness of PBPK M&S for dose individualization of anticancer drugs.

Case examples

Ibrutinib—metabolic DDIs

Ibrutinib (Bruton's tyrosine kinase inhibitor; Imbruvica[®]) was granted accelerated approval by the FDA in 2013 (51). The drug is given orally and undergoes extensive first-pass metabolism, mainly via CYP3A4 and to a lesser extent by CYP2D6, whilst undergoing minimal renal CL.

Ketoconazole inhibited 96% of ibrutinib's metabolism in human liver microsomes. A PBPK model was developed to evaluate CYP3A4 DDIs in healthy volunteers with ibrutinib as the victim. The model was validated against clinical DDI studies of ibrutinib in the presence of ketoconazole (strong inhibitor) and rifampin (strong inducer). The PBPK model was then used to interpolate DDI effects of mild, moderate and strong CYP3A4 inducers and inhibitors and used to inform dose guidance in the drug label (52,53).

Sonidegib—bridging DDIs to cancer patients

Sonidegib (Odomzo[®]) is an oral anticancer agent for the treatment of locally advanced basal cell carcinoma. The drug displays low oral bioavailability. *In vitro* drug metabolism studies and clinical DDI trials in the presence of ketoconazole and rifampin were carried to elucidate the metabolic contribution of sonidegib elimination. Co-

administration of ketoconazole led to a 2.25-fold increase in area under the curve (AUC), whereas rifampin produced a 72% reduction in exposure. A PBPK model was developed to bridge the DDI data from healthy volunteers to cancer patients at the ratified dose, to extrapolate to steady state effects and interpolate the effect of moderate/weak CYP3A inhibition/induction. The simulation study showed the effect of the DDIs to be slightly reduced in cancer patients compared to healthy and the interaction magnitude to increase at steady state dosing of sonedegib. The simulated DDI magnitudes and alternative dosing schedules informed dosing recommendations provided in the FDA drug label (54). The study demonstrates the utility of using PBPK M&S to bridge the effect of metabolic DDIs from healthy volunteers to cancer patients.

Alectinib—biopharmaceutics effects

Alectinib [selective anaplastic lymphoma kinase (ALK) inhibitor; Alecenza[®]] underwent accelerated regulatory approval in 2015 because of likely clinical benefit in treating ALK-positive non-small cell lung cancer (55). The drug is a lipophilic basic (pKa ~6–7) displaying poor solubility and moderate oral bioavailability. As alectinib is given orally the pH-dependent solubility may be indicative of potential impact of biopharmaceutics effects. Parrott and co-workers developed a PBPK model to prospectively evaluate food effects and increased gastric pH with esomeprazole. The model predicted a positive food effect and a lack of impact of co-administration of esomeprazole. This was later confirmed in clinical trials, although the magnitude of the food effect was not accurately predicted, potentially due to excipient effects. The absorption model was further refined following confirmatory clinical studies and used to inform dose recommendations on timing of alectinib administration in relation to food intake. Authors stated that these finds were used to inform drug labeling (38).

Docetaxel—pediatric dose bridging

Docetaxel (taxane anticancer drug) is extensively metabolized by CYP3A4, substrate to the efflux transporter P-glycoprotein (P-gp), and active hepatic uptake transporters OATP1B1 and OATP1B3. The drug exhibits dose limiting toxicity in the form of neutropenia. In a retrospective study, a full PBPK model was developed based on adult data and validated against adult data in presence of ketoconazole. The PBPK model was then scaled to pediatrics in order to establish first dose in children assuming a similar exposure-response to adults with the

same indication. A global approach was used where PBPK predictions were fitted using a pop-PK model in order to carry out optimization of sampling times. PBPK predictions of pediatric data gave a reasonable prediction with a 1.4-fold overprediction of CL (37). The study shows proof-of-concept for dose bridging from adults to pediatrics in oncology using PBPK M&S coupled with pop-PK, to inform first-dose-in-children and optimal sampling design.

Impact of physiology of oncology patients on exposure of anticancer drugs

A number of physiological changes have been reported in cancer patients that may impact the PKs of anticancer drugs (such as increased levels of inflammation and altered levels of plasma proteins) (56). With sufficient information, PBPK M&S can facilitate extrapolation of drug exposure to a more clinically relevant oncology population. Cheeti and co-workers developed an oncology PBPK model by altering sex, age, height and weight population distributions, levels of drug-binding plasma proteins (albumin and AAG), and hematocrit to investigate the effect of plasma protein binding on exposure of midazolam (CYP3A probe) and saquinavir (CYP3A probe highly bound to AAG) (57). A similar PBPK model for oncology patients developed by Thai and co-workers was demonstrated to better recover variability in PK profiles and CL of docetaxel compared to when physiology was assumed to remain the same as in healthy (37). In the absence of physiological data, PBPK modeling can also be used to make inferences about physiological parameters based on clinical PK data. Yoshida and co-workers developed a PBPK of irinotecan (topoisomerase I inhibitor) and its metabolites to explore different PK of the drug in cancer patients. Using parameter estimation, the authors could get an indication of the feasible parameter space of irinotecan's CL pathways in cancer patients (58).

PK modeling of anticancer drugs in healthcare

Lately, there has been much debate how PK modeling can be used to aid precision dosing in clinical practice (10,11,59). In an earlier state of the art paper, we proposed a categorization to describe implementation of MIPD in healthcare based on current practices, these were: real-time implementation in healthcare systems, mechanistic modeling and extrapolation and model-derived dose banding (10).

Real-time implementation in healthcare systems refers

to direct implementation of M&S in-line with healthcare, e.g., software tools and integration into electronic health records (EHR). The approach is particularly well-suited for treatments where continuous measurement, such as TDM, is carried out routinely throughout the therapy. Bayesian modeling approaches are particularly well-suited for this approach where feedback-control can be used to update prior parameter estimates and refine individual patient predictions as more data becomes available (10,11). Mechanistic or PBPK models are a powerful tool for allowing extrapolation to for example DDIs or special populations. Despite many examples of application to address dosing in special populations (60), there are few examples of the approach being evaluated in clinical practice (61). This may partly be due to PBPK's reliance on drug-specific and physiological information and its inferior ability to describe IIV compared to pop-PK. This may however change over the coming years, the generation of new proteomic data (62), emergence of "middle-out" modeling (14), and Bayesian PBPK M&S (63) certainly makes PBPK an increasingly viable approach in precision dosing. Model-derived dose banding refers to the use of PK models to develop dosing strategies based on clinically relevant covariates identified during the data analysis. This is perhaps the most practical approach although it potentially may offer less scope for dose individualization compared to other model-based approaches (64-66). Based on previous experiences, work streams have been proposed for how to develop these model-based approaches from conception to implementation in clinical practice. The proposed necessary steps to prove clinical effectiveness of MIPD include: model development, internal validation—to diagnose model misspecifications, external validation—to test performance against a different but related population sample, prospective clinical evaluation—to test the performance of the model-informed approach compared to standard practice, and an implementation phase—for integration into clinical practice (10,67,68). Here follow examples of PK modeling applied to answer clinically relevant dosing issues in oncology (in addition, see *Table 1*). These illustrate both utility and concepts for clinical evaluation and practical implementation in a healthcare.

Case examples

5-FU—metabolic phenotyping

Due to the risk of severe toxicity and a relatively narrow therapeutic index, prediction of toxicity has been widely sought for treatment using thymidylate synthase inhibitor

5-FU (see *Table S1*, supplementary appendix). The drug undergoes metabolism by dihydropyrimidine dehydrogenase (DPD), where DPD deficiency has been linked to an increased risk for toxicity (95). In a retrospective study, van Kuilenburg and co-workers developed a Bayesian pop-PK model, based on population sample of DPD deficient patients and controls. The model described 5-FU CL using nonlinear Michaelis-Menten PK, where DPD deficient patients displayed a 40% reduction in maximum velocity (V_{max}). Using a limited sampling strategy, the DPD phenotype could be determined based on Bayesian estimation of individual V_{max} , AUC or terminal half-life to anticipate the risk of toxicity (69). The approach potentially offers advantages to genotyping where misclassification can occur due to discrepancies in genotype and phenotype.

Carboplatin—Bayesian forecasting of drug exposure

Despite being safer than cisplatin, carboplatin displays dose-limiting bone marrow toxicity. Duffull and co-workers developed a bioanalytical method for measuring carboplatin serum concentrations and a Bayesian pop-PK model with covariates lean bodyweight (LBW) and creatinine CL on CL, and LBW on volumes and inter-compartmental CL based on data from 12 ovarian cancer patients (78). The model was tested prospectively against the Calvert *et al.* formula in an additional 12 patients over two courses. During the first treatment course, the Calvert formula produced less bias compared to the population methods. Following two feedback concentrations the Bayesian method showed superior accuracy for AUC predictions. It was recognized that an updated model may produce better accuracy (79). This was perhaps one of the earliest examples incorporating patient data to update individual priors for prospective predictions (78,79).

Busulfan—strategies for healthcare implementation

Busulfan (alkylating agent) is widely used in combination with cyclophosphamide for conditioning prior to hematopoietic stem cell transplantation. The narrow therapeutic window of busulfan warrants TDM in pediatrics, where up to nine PK samples are taken over the course of a single dose to inform dose adjustments. Hence numerous PK models have been published to address dose individualization of busulfan (see *Table S1*, supplementary appendix).

Neely and co-workers, developed a nonparametric pop-PK model with age (described using a continuous polynomial function), and ideal body weight as covariates

Table 1 Selected examples of pharmacokinetic modeling applied to clinical pharmacotherapy or to solve practice-oriented dosing issues in oncology

Drugs	Aim of modeling	PK modeling approach	Identified covariates	Study approach	Outcomes	References
5-fluorouracil (5-FU)	Develop limited sampling to detect PDP-deficiency	Pop-PK: 2-cmp (V_{max} , K_m)*	Significant difference in V_{max} between DPD-deficient and controls	Development (N=48); validation 1 (N=33)	Limited sampling schedule to identify PDP-deficient patients at risk of toxicity	(69)
Busulfan	Develop and implement PK model to achieve target exposure in HCT children	Bayesian pop-PK: 1-cmp (CL)*	CL; BW, age	Development (N=90); prospective validation 1 (N=21)	Model-based algorithm improved target achievement compared to conventional dosing	(70)
	Examine five different TDM based dosing approaches and implement in EHR	PK: 1/2-cmp	N/A	Development/validation (N=30); software usability testing	Software tool for interpreting TDM was implemented in EHR	(71,72)
	Pediatric dose adjustment based on limited sampling	Bayesian pop-PK: 1-cmp (k_{el})*	Age, IBW	Development (N=53); validation 1 (N=105); validation 2 (N=11); retrospective clinical evaluation (N=20)	Model allowed limited sampling to achieve target concentrations	(73)
	Explore variability in PK in children and young adults to optimize dosing	Pop-PK: 2-cmp (CL)*	CL; BW, day; V_i ; BW	Development (N=245); validation 1 (N=158); prospective clinical evaluation (N=50)	Nomogram based on PK model; dosing scheme led to some residual variability, needing TDM	(64,74,75)
	Evaluate approaches to estimate exposure and clinical outcome in children and young adults	Pop-PK (refitted) (77)	N/A	Evaluation (N=674)	The approach may help optimize target exposure and improve efficacy/toxicity	(76)
Carboplatin	Develop limited sampling strategy	Bayesian pop-PK: 1-cmp (k_{el})*	N/A	Development (N=22); validation 1 (N=15)	Reduced bias and increased precision for AUC estimation using one or two samples	(77)
	Develop Bayesian dose adjustment	Bayesian pop-PK: 2cmp (CL)*	CL; LBW, CL_{CR} ; V_{ss} : LBW; V_i : LBW; CL_{LC} : LBW	Development (N=12); prospective clinical evaluation (N=12)	Model outperformed Calvert formula with two feedback concentrations	(78,79)
	Develop limited sampling strategy	Bayesian pop-PK (CL)*	CL; BW, age, sex, S_{CR} ; V_i ; V_j ; BSA	Development (N=90); validation 1 (N=13); prospective clinical evaluation (N=5)	All patients achieved AUCs close to target using the model-based limited sampling approach	(80)

Table 1 (continued)

Table 1 (continued)

Drugs	Aim of modeling	PK modeling approach	Identified covariates	Study approach	Outcomes	References
Cyclophosphamide	Reduce toxicity in children undergoing HCT	Bayesian pop-PK (CL _{NON} , CL _{IND})*	CL _{NON} ; age	Development (N=147); validation 1 (N=20); prospective clinical evaluation (N=20); (N=50)	A software tool was implemented in clinical practice to individualize dosing in real-time	(81-85)
Docetaxel	Individualize combination of chemotherapy and G-CSF	Semi-mech. pop-PK/PD (k ₆₀)*	N/A	Validation 1 (N=38)	Model has potential to minimize toxicity in individual patients	(86)
Methotrexate	Early detection of impaired elimination	Bayesian pop-PK: 2-cmp (B, β)*	N/A	Development (N=7)	Bayesian limited sampling strategy (two samples) allowed detection of impaired clearance	(87)
	Management of high-dose methotrexate therapy with leucovorin in children/young adults	Bayesian pop-PK: 2-cmp (CL)*	Significant difference in CL between normal and reduced renal function	Development (N=240); retrospective clinical evaluation (N=50)	A clinical software tool was developed, the tool showed reasonable accuracy for predicting exposure	(88,89)
	Dose adjustment of high-dose methotrexate using Bayesian estimation	Bayesian pop-PK: 2cmp (CL)*	N/A	Development (N=33); prospective clinical evaluation (N=42)	Bias and precision was satisfactory, severe toxicities were absent	(90,91)
Pembrolizumab	Evaluate impact of PK modeling on exposure, target engagement and cost	Pop-PK: 2-cmp (CL)* (95)	CL: BW, albumin, baseline tumor burden, eGFR, sex, non-small cell lung cancer; prior ipilimumab, ECOG; V: BW, albumin, sex, prior ipilimumab (95)	Simulation study	Model-derived dose banding can reduce wastage and cost of treatment while maintaining optimal exposure	(66)
Suramin	Develop a rapid loading regimen	Bayesian pop-PK: N/S	N/A	Prospective clinical evaluation (N=13)	Bayesian dosing improved accuracy for achieving target concentrations	(93)
	PK based dose individualization	Bayesian pop-PK: 2/3-cmp (CL)*	N/A	Prospective clinical evaluation (N=18+11); development-model refinement (N=69)	Adaptive-control-with-feedback facilitated precise control of exposure	(94)

* , model elimination parameter(s). BSA, body surface area; BW, bodyweight; CL, clearance; CL_{CR}, creatinine CL; CL_{IND}, inducible CL; CL_{NON}, non-inducible CL; cmp, compartment; DPD, dihydropyrimidine dehydrogenase; ECOG, Eastern Cooperative Oncology Group; eGFR, estimated glomerular filtration rate; EHR, electronic health record; G-CSF, granulocyte colony-stimulating factor; HCT, hematopoietic cell transplant; IBW, ideal BW; k₆₀, elimination rate constant; LBW, lean BW; N, number of study participants; N/A, not applicable; N/S, not stated; PK, pharmacokinetic; PD, pharmacodynamic; pop-PK, population pharmacokinetic modeling; S_{CR}, serum creatinine; TDM, therapeutic drug monitoring; V, volume of distribution; PDP, pyruvate dehydrogenase phosphatase; V_{max}, maximum velocity; K_{mv}, Michaelis constant; Semi-mech., semi-mechanistic/semi-physiological; V₁, volume of first (central) compartment; V₂, volume of second (peripheral) compartment; V_{ss}, volume of distribution at steady state.

on CL and V_d based on a population sample of 53 pediatric patients. An additional two datasets consisting of a total of 116 pediatric patients were then used for model validation and Bayesian updating of priors. The final model was then incorporated into the BestDose™ software platform and blindly tested against an additional 20 patients. The final model allowed target concentration achievement with only two blood samples per adjustment (73).

Abdel-Rahman and co-workers carried out a retrospective evaluation to examine the performance of five different TDM approaches (including non-compartmental and compartmental modeling) to estimate the dose of busulfan in pediatric cancer patients and found considerable discrepancies in dose recommendations (71). Due to observed inefficiencies in the workflow for TDM guided dosing at Children's Mercy Hospital (Kansas City, MO), a clinician-oriented interface was developed around a compartmental model for dose optimization of busulfan based on TDM. The software allowed the use of either a one- or two-compartment model based on a series of quantitative goodness-of-fit criteria implemented within the software. The interface could be accessed through the EHR and was subject to usability testing by healthcare professionals. The research represents a significant step towards bringing MIPD into clinical practice and serves as a proof-of-concept for practical implementation. The authors noted that next steps will focus on quality assurance, predictive performance of the software tool and investigations of model-refinement, including inclusion of covariate effects (72).

Similarly, Long-Boyle and co-workers developed a pop-PK model for busulfan based on retrospective data of 90 pediatric and young adult patients. The final model (CL covariates: actual bodyweight and age) was then implemented in a user-friendly Microsoft Excel-based tool for guiding initial dosing in clinical practice and prospectively evaluated in 21 children. The healthcare tool showed significant improvement in attaining busulfan target concentrations compared to conventional dosing guidelines (70).

As previously mentioned, healthcare implementation of model-based precision dosing may take on different forms; where the previous examples detailed the process of incorporating real-time software tools in healthcare. A more pragmatic approach is the derivation of dose banding based on model optimized dosing regimens. Bartelink and co-workers, developed a two-compartment pop-PK model for busulfan with body weight as a covariate on CL based on 245 pediatric patients. The model was then used to derive

a nomogram for dosing busulfan in clinical practice. The model was externally validated against an additional 158 adult and pediatric patients (64,74). A prospective study was carried out to assess the performance of the model-derived nomogram and the added value of TDM was carried out in 50 pediatric patients undergoing hematopoietic stem cell transplantation. The study concluded that following the model-derived dosing, variability was still significant and therefore TDM was still needed to inform dose optimization (75).

Cyclophosphamide—reduced toxicity and healthcare implementation

Cyclophosphamide (alkylating agent) is given in two doses over two consecutive days as myeloablative preparative treatment before hematopoietic stem cell transplantation. The drug is metabolized to carboxyethylphosphoramide mustard (CEPM) amongst others, where the CEPM is linked to liver toxicity and nonrelapse death. A Bayesian pop-PK model was developed for cyclophosphamide and its metabolites. The model was internally validated and incorporated into an open-source code to allow real-time dose adjustments between the two doses. This was a considerable logistical effort considering the time constraint for bioanalysis and model-derived dose recommendation. A clinical trial was carried out to test the performance of the model-based dosing approach. The approach led to an average total dose reduction of around 9% and a reduction in acute liver and kidney injury with similar overall survival (81-84,96). This case illustrates some of the logistic challenges of real-time implementation of MIPD in clinical practice.

Methotrexate—reduced toxicity and healthcare implementation

Methotrexate (antimetabolite) is used in the treatment of a number of cancers. Due to high IIV in exposure and the risk of toxicity in high-dose methotrexate treatments, the drug is routinely subject to TDM. Barrett and co-workers developed a pop-PK model on TDM data from 240 patients at the Children's Hospital of Philadelphia (Philadelphia, PA), accounting for impaired CL by estimating the probability of a patient belonging to one of the two subgroups. A software dashboard was developed, consisting of a database of patient records, lab data and adverse events management system. The data was then used for Bayesian forecasting of exposure. A user-interface was designed that allowed viewing of TDM data, forecasting

of exposure, the potential risk of toxicity and dose guidance (88). A retrospective study was carried out in 50 pediatric and young adult patients to test the ability of the dashboard to predict future toxicity events to allow earlier recommendations of leucovorin rescue therapy. The study concluded that the dashboard gave reasonably accurate predictions (precision of 12.9%, bias of 2.2%) and could have been used to initiate earlier rescue therapy in 16 of the studied patients, seven patients would have received a larger dose of leucovorin and 37 patients would have received the drug less often. The dashboard can support clinicians in monitoring for risk of toxicity and guide decision making of initiation of rescue therapy (89).

Pembrolizumab—minimizing excess drug wastage

Infused anticancer drugs are sold in vials with a set volume of the drug; however, dosing is often based on body size. This leads to excess drug volumes after dosing a patient which many times are being discarded at the cost of healthcare providers or insurers. It is estimated that the total cost incurred by wastage of the top 20 anticancer drugs amounted to USA dollar (USD) 1.8bn in 2016 in the U.S. alone (97). Pembrolizumab (programmed cell death protein 1 ligand antibody) is currently available as 50-mg vial size in the UK at a licensed dose of 2 mg/kg every 3 weeks. Ogungbenro and co-workers proposed a model-based approach to optimize dose banding to maximize target attainment and minimize wastage. Cost analysis showed that the model-derived dosing strategy could save 16% of the cost of drug treatment compared to dosing by bodyweight by reducing discarded excess volumes of the drug, without altering exposure significantly (66). The work provides an example of how modeling can improve cost-benefit of anticancer treatment.

MIPD in oncology: future challenges

It has been almost 50 years since the first model-based dosing strategies for dose individualization were proposed (98,99). PK modeling has come a long way in supporting dose selection and answering clinically relevant questions in oncology and other disease areas (10,11,59). While academic groups, in collaboration with healthcare professionals, are leading the way for model-based approaches to answer bedside dose individualization, pharmaceutical industry and regulatory agencies have made great strides in model-informed dose guidance in the drug label. It is thought that modeling will gain wider application in clinical practice over

the coming years as precision medicine realizes its potential. For this to happen, there are a number of challenges that need to be met.

At the moment, there is a lack of clinical effectiveness, patient benefit and health economic evidence to support MIPD in healthcare. This is crucial for wider acceptance of MIPD in clinical care. Too many published modeling efforts are concluded following model development, indicating areas of clinical application. Without rigorous validation and clinical evaluation, these models will not see their full utility. Better coordination between academia, industry, healthcare, patient groups, and funding bodies are warranted to support implementation-based research in healthcare.

A prerequisite for precision dosing is the availability of multiple drug dose formulations. For MIPD to gain greater traction, some adjustments to pharmaceutical R&D would be required, with focus earlier in development of precision dosing. Recently, we illustrated how this could work using the “companion tool” approach (10), where a MIPD tool can be considered following candidate selection and developed alongside the drug. Precision dosing can facilitate the advancement of candidate drug that otherwise would be abandoned and there is therefore, in our opinion, great financial incentives to pursue this approach in pharmaceutical industry.

Oncology is an area with a lot to gain from PK modeling based dose individualization. There are however some specific challenges, such as the lack of exposure-effect/toxicity relationship for many new drugs coming to the market. This is of course a prerequisite for PK modeling to be meaningful. The concentration-effect relationship for monoclonal antibodies is poorly understood, where for many of these the dose-efficacy relationship found in clinical trials is flat (100,101). This suggests that current dosing of monoclonal antibodies may not be optimal from an efficacy-cost perspective. Here lies an optimization challenge that can reap financial benefits for healthcare providers and payers, and in the end aid pharmaceutical industry to improve cost-benefit.

Conclusions

Here we present the current state of PK modeling in precision dosing of anticancer drugs. We have illustrated, using published case examples, some of the potential benefits the approach may bring in terms of prospective dosage guidance for DDIs and in special populations, improved attainment of target drug concentration and

reduced risk of toxicity, reducing wastage and scope for improved patient benefit and cost-benefit. While some great progress has been seen in implementation of model-informed dosage guidance in the drug labeling, a collaborative effort from regulators, industry and academia, the uptake has been modest in healthcare. Collaboration between academia, healthcare and industry together with greater financial support for applied research into patient benefit, cost-benefit and clinical effectiveness of model-based dosing approaches is warranted for wider adaptation in healthcare.

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Footnote

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Role of pharmacokinetic modeling and simulation in precision dosing of anticancer drugs

Methods

A literature search was carried out using PubMed (<https://www.ncbi.nlm.nih.gov/pubmed>; 1950–March 2017) to identify a sample set of publications including pharmacokinetic (PK) modeling of anticancer drugs. The inclusion criteria consisted of PK modeling of oncology drugs aimed at either predicting human exposure or based on clinical data. Studies based on pre-clinical data only or pharmacodynamic modeling only were excluded during screening of publications. To capture a broad variety of modeling applications in oncology the search terms included: “physiologically based pharmacokinetic”, “pharmacokinetic”, “PBPK”, “PKPD”, and “pharmacodynamic”, and “model”, “modeling”, and “modelling”, and “oncology”, “cancer”, “anti-cancer”, “tumor”, “tumor”, “anti-tumor” or “anti-tumor”, with filtering based on human species. The search yielded 1,749 publications. Additional publications were identified through references in identified publications, review articles and key literature. The final dataset included 393 publications.

The identified set of publications was categorized based on main and secondary study aims, including:

- ❖ Toxicity: adverse effects/toxicity;
- ❖ Bioequivalence: PK modeling of bioequivalence studies;
- ❖ Biopharmaceutics effects: biopharmaceutics effects, other than food and formulation effects;
- ❖ Covariates: PK covariates, or otherwise included covariates in the model;
- ❖ DDIs: metabolic/transporter drug-drug interactions;
- ❖ Dose: investigating multiple doses, optimal dose, or dose individualization;
- ❖ Efficacy: drug efficacy/response;
- ❖ Ethnicity: differences in PK based on ethnicity;
- ❖ Evaluation/validation: assessment or validation of PK model performance;
- ❖ Food effects: impact of prandial state and/or meal properties on PK;
- ❖ Formulation: impact of formulation on PK;
- ❖ Genotype: metabolic/transporter genotype (and α_1 -acid glycoprotein genotype) effects on PK;
- ❖ Surgery: impact of surgery on PK (including gastric and cytoreductive surgery);
- ❖ Hepatic impairment: PK in hepatically impaired subjects, assessing impact of hepatic impairment on PK;
- ❖ Investigational: main focus to investigate PK of the selected drug;
- ❖ Limited: optimal limited sampling strategies;
- ❖ Metabolite: metabolite PK;
- ❖ Other special populations: PK in other special populations (including: elderly, renal replacement therapy and postmenopausal women);
- ❖ Pediatrics: pediatric drug exposure;
- ❖ Phenotype: metabolic/transporter phenotype effects on PK;
- ❖ Renal impairment: PK in renally impaired subjects, assessing impact of renal impairment on PK;
- ❖ Sex: impact of sex on PK.

Where applicable, identified PK covariates were recorded, either including the full covariate model or a summary of covariates and the PK parameter the effect was modeled on. Additional recording of information included: investigated drug, modeling approach used for development and/or application, and study population(s). Data was analyzed through graphical presentation.

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