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GastroPlus™

PBPK modeling software...
from discovery through development

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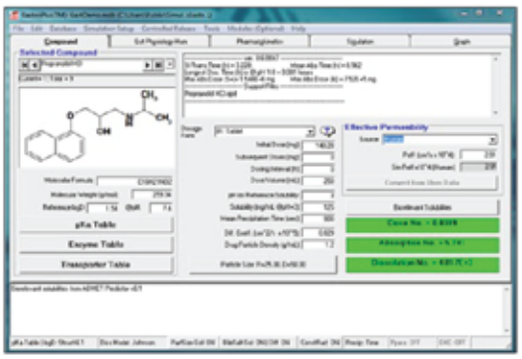
GastroPlus™

Leading the modeling and simulation revolution...

GastroPlus is a mechanistically based simulation software package that simulates intravenous, oral, oral cavity, ocular, inhalation, and dermal/subcutaneous absorption, pharmacokinetics, and pharmacodynamics in humans and animals. This smoothly integrated platform combines a user-friendly interface with powerful science to help you make faster and more informed project decisions!



GastroPlus is by far the most commonly used software of its kind. It has been identified as the #1-ranked program for in vitro - in vivo extrapolation (IVIVE) and has been the focus of several publications from the FDA!

The GastroPlus simulations include:

FOR DISSOLUTION & ABSORPTION -

- The Advanced Compartmental Absorption and Transit (ACAT™) model – only in GastroPlus!
- Physiological gut models for human, dog, rat, mouse, rhesus monkey, cynomolgus monkey, minipig, rabbit and cat – fasted or fed conditions defined
- Vast selection of dosage forms: immediate release, delayed release, controlled release (including dispersed systems, gastric-retention, and more)
- pH-dependent solubility and logD models – ionization effects on dissolution & absorption considered
- Paracellular absorption – estimate paracellular permeability
- Mechanistic effect of bile salts on drug solubility and dissolution
- Enhanced treatment of nanoparticle effects on solubility and dissolution
- Mechanistic models to predict in vivo precipitation
- Options for defining pH-dependent dissolution (Z-factor) and precipitation rates
- Saturable metabolism and/or influx/efflux transport along the GI tract
- Mechanistic deconvolutions and In Vitro - In Vivo correlations (IVIVCs) for various formulations

FOR PHARMACOKINETICS -

- Whole body, physiologically-based pharmacokinetic (PBPK) models defined – including pediatrics
- One-, two-, or three-compartment conventional pharmacokinetic model options available
- Transporter-based IVIVE: automated scaling of permeability across all tissues with PBPK
- Saturable metabolism and transport in liver or any PBPK tissues
- Metabolite tracking – easily link the formation of metabolites with the metabolism of the parent(s) in a single simulation
- Mechanistic treatment of biliary secretion and enterohepatic circulation
- Mechanistic static and dynamic DDI predictions
- Automated PBPK/PD model selection with industry standard pharmacodynamic models

Simulation Modes Available -

- Population Simulator™ – predict likely distributions of PBPK/PD results over different populations
- Parameter Sensitivity Analysis – quickly test sensitivity of results to changes in model parameters
- Batch Simulations – screen compound libraries for bioavailability & PK exposure in different species

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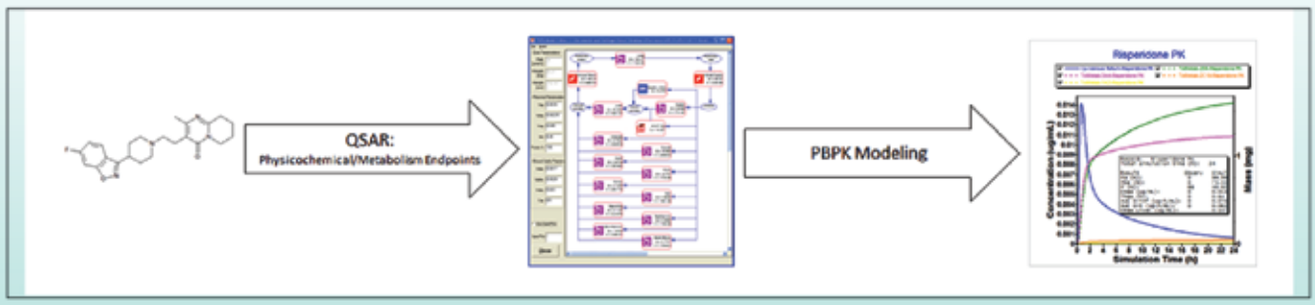
What's New in Version 9.5?

- NEW! PBPK models for antibody-drug conjugates (ADCs)
- NEW! PBPK physiology models for Chinese and hepatic impairment populations
- NEW! Bolus & controlled release models for subcutaneous and intramuscular injections
- Updated! Animal physiology models for non-oral delivery pathways
- Improved! Reporting functions – easy export into Excel spreadsheets
- Upgraded! Automated mechanistic deconvolutions and easier virtual BE simulation setup
- Enhanced! More covariate relationships in Population Simulator
- ... and more!

ADMET Predictor™ Module

CYP metabolism predictions from chemical structure – quickly create full PBPK models in seconds.
The ADMET Predictor™ Module extends the capability of GastroPlus by enabling you to obtain predictions from structure of all physicochemical,pharmacokinetic, and CYP metabolism kinetic parameters required for GastroPlus simulations. The module uses the same models as our best-in-class ADMET Predictor software.



Updated! Enhanced pKa model developed in collaboration with Bayer HealthCare - ALL models retrained with greater accuracy!

This module automatically generates predictions for the following properties:

- CYP metabolism kinetics – Vmax, Km, and CLint
- P-gp and OATP transporter inhibition models (classification)
- Aqueous solubility vs. pH profile
- Biorelevant solubility (FaSSIF, FeSSIF, and FaSSGF)
- logD vs. pH profile
- Rabbit corneal permeability
- Human volume of distribution
- Blood:brain barrier permeation (classification)
- pKa(s)
- Tendency to supersaturate in water
- Diffusion coefficient in water
- Human effective permeability
- Human plasma protein binding
- Human blood:plasma concentration ratio

The ADMET Predictor Module has several critical benefits:

(1) by loading a library of chemical structures, quickly set up a database for screening fraction absorbed & bioavailability – decide which compounds to carry forward into in vivo studies
(2) use the in silico predictions and Parameter Sensitivity Analysis to guide your in vitro studies
(3) begin evaluating different formulation strategies to assess the importance of factors like particle size solubility and dose on absorption

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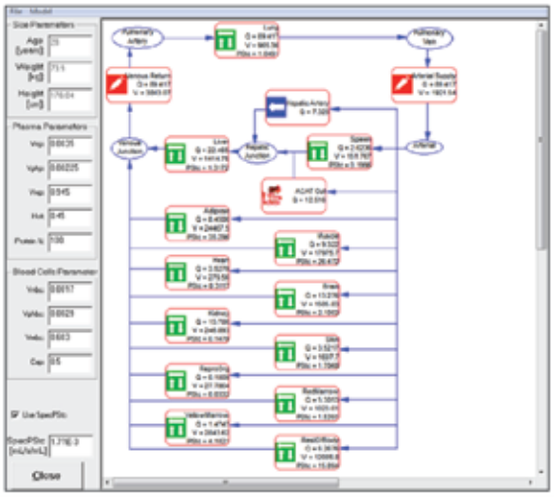
PBPKPlus™ Module Ranked

Ranked #1 in In Vitro-In Vivo Extrapolation (IVIVE) by Pfizer!
(Cole et al., 2nd Asian Pacific Regional ISSX Meeting,
May 2008, Shanghai, China)

Only in GastroPlus! Transporter-based IVIVE: automated scaling of permeability across tissues in the PBPK model



The PBPKPlus Module extends GastroPlus to define a "whole body" PK model, consisting of various tissues. You can easily simulate the distribution & elimination of compound throughout the body and track concentrations in any tissue. Tissues can be defined as needed, or default models can be used with a standard set of compartments:

Adipose	Arterial blood	Brain	Yellow marrow
Gut	Heart	Lungs	Kidney
Muscle	Skin	Red marrow	
Spleen	Reproductive organs	Venous blood	

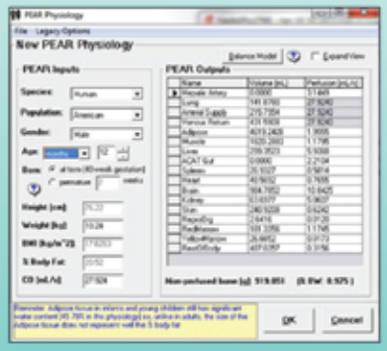
Customize your PBPK model by treating any tissue as either a perfusion-limited or permeability-limited model, and quickly add/delete tissues as needed – all without writing any equations!

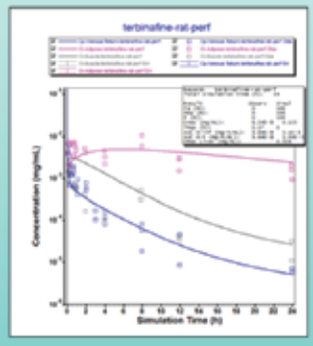
The PBPKPlus Module also provides:

- Generation of physiological model parameters (tissue weights and volumes, composition, perfusion rates, etc...) with our built-in PEAR Physiology™ (Population Estimates for Age-Related Physiology).

Current physiologies are:

- Human (American, Japanese, and NEW! Chinese, Male or Female, based on age)
- Infant/pediatric groups
- NEW! Hepatic impairment
- Rat
- Dog
- Mouse
- Monkey
- Rabbit
- Minipig





- Population simulations based on parameter variances in a sample population – define your own age range, % male vs. female, and the number of "virtual" subjects you wish to create
- Novel methods for estimating tissue partition coefficients from logD, pKa, plasma protein binding and Rbp – only in GastroPlus!
- Physiological model for kidney including glomerular filtration and reabsorption
- Fitting models to in vivo data (plasma/tissue concentrations, amount excreted in urine, etc...)
- Linking of pharmacodynamic effect directly to concentrations in specific tissues
- Mechanistic transport of drug from hepatocytes to bile in liver, modeled either as a linear process or through arrier-mediated transport
- Report-quality plotted output of all time-dependent results in all tissues
- ... and more!

Drug-Drug Interaction (DDI) Module

The DDI Module in GastroPlus allows you to predict drug-drug interactions (DDIs) among drugs and metabolites.

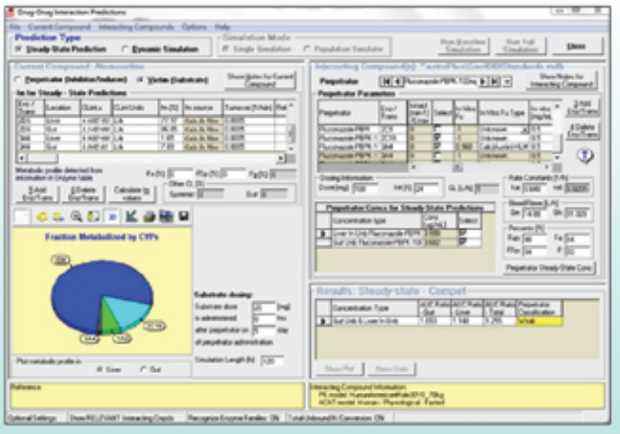
The ability to accurately estimate potential DDIs in silico has several benefits for companies:

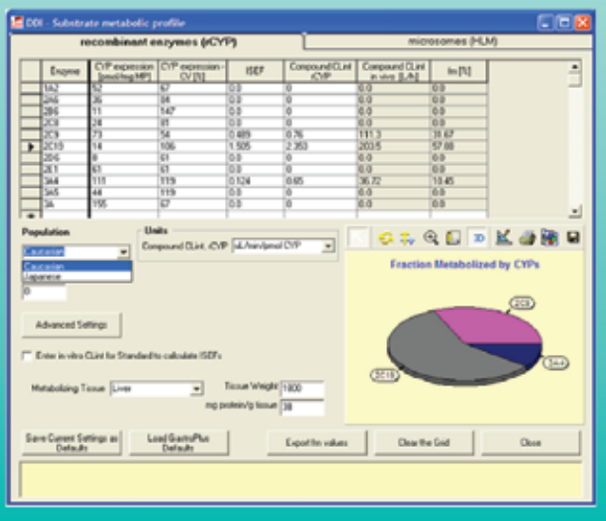
- Explore possible effects on the pharmacology and toxicology of drugs
- Identify species-specific changes to estimate how a drug behaves in animals vs. humans
- Investigate the safety profile of drugs that are co-administered prior to filing regulatory submissions with agencies around the world

With the DDI Module, calculating either steady-state and/or dynamic DDIs is managed through our easy-to-use interface. We provide a database of standard compounds for which all relevant parameters (including reported inhibition/induction constants and full compartmental PK/PBPK models) are defined. Of course, you may predict DDIs among any compounds by simply entering the required inputs. As with other GastroPlus modules, there is no equation or code writing required.

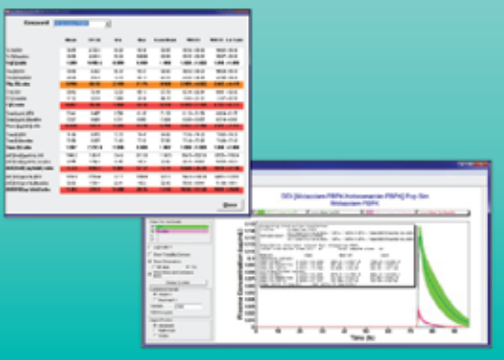
What are some of the advantages to using the DDI Module?

- PBPK models for DDI standard compounds: warfarin and simplified itraconazole
- Population Simulator™ linked with DDI predictions
- Transporter-based drug-drug interactions
- Metabolic and/or transporter induction
- Linked with the industry's #1-ranked dissolution/absorption (ACAT™) model
- Use with either compartmental PK or PBPK models
- Apply competitive and/or time-dependent inhibition kinetics by parent and/or metabolite(s)
- Simulate DDIs for any species
- Account for enzyme expression level differences in various human populations
- Built-in tool to easily calculate the fraction metabolized (fm) from in vitro assays (rCYPs and microsomes are accommodated)





- Incorporate nonlinear gut contributions to DDIs
- Predict the inhibitor effect using simulated concentrations at the site of metabolism (gut, liver,or any PBPK tissue) for dynamic DDI simulations
- Include the effects of multiple substrates on clearance of other substrates metabolized by the same enzyme



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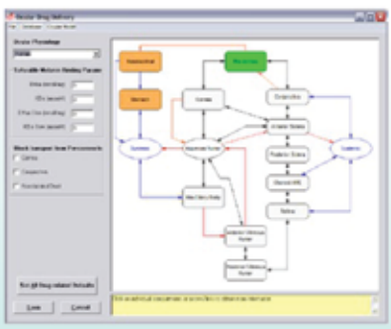
Additional Dosage Routes Module

The Additional Dosage Routes Module in GastroPlus extends the program beyond the traditional oral and intravenous administration routes. With this module, you can simulate drug disposition through additional dosing sites – dermal, intraoral (oral cavity), ocular, pulmonary (intranasal and respiratory), and NEW! intramuscular. These models were all developed in collaboration with top 5 pharmaceutical companies. The ability to predict concentration profiles in different regions of the skin, mouth, eye, lungs, nose, and muscle can help you:

- Explore various formulation/drug delivery options to achieve desired therapeutic effects
- Identify species-specific changes to estimate how a drug is handled in animals vs. humans

With the Additional Dosage Routes Module, simulating concentrations through these sites is managed through our easy-to-use interface. Mechanistic, physiologically-based models are provided for each tissue, for different species. You can also customize your own physiology by entering available information into the program. These models are linked with either compartmental or physiologically-based pharmacokinetics (PBPK) in GastroPlus, so you may predict your drug's distribution and elimination once it enters into the systemic circulation. As with other GastroPlus modules, there is no equation or code writing required.

Ocular Model (Ocular Compartmental Absorption & Transit (OCAT™) Model



- Nonlinear metabolism or transport in any eye tissue!
- Two-site melanin binding options!
- Convective flow incorporated into the ocular disposition model
- Physiology models (human, rabbit, and NEW! monkey)

The ocular model of the Additional Dosage Routes Module provides dosing as:

- Eye drop (topical solution or suspension)
- IVT (intravitreal injection)
- Intravitreal or subconjunctival implants

Some of the processes which can be modeled include:

- Nonlinear metabolism or transport in any eye tissue
- Convective flow incorporated into the ocular
- Two-site melanin binding options
- Predefined physiology models (human, rabbit, and NEW! monkey disposition model

Pulmonary (Intranasal/Respiratory) Model (Pulmonary Compartmental Absorption & Transit (PCAT™) Model

- Nonlinear metabolism or transport in any lung tissue!
- Age-dependent scaling of the pulmonary physiology!
- Physiology models (human, rat, NEW! mouse, and NEW! dog)

The pulmonary model provides dosing via the intranasal or respiratory route as an:

- Immediate release solution
- Immediate release powder

The pulmonary model includes the advanced ICRP 66 deposition model (Smith et al., 1999, LUDEP) for calculating deposition fractions in each compartment of both API and carrier particles. Additionally, you may account for the following processes in your simulations:

- Mucociliary transit
- Nonlinear metabolism or transport in any lung tissue
- Lymphatic transport & systemic absorption
- Age-dependent scaling of the human physiology

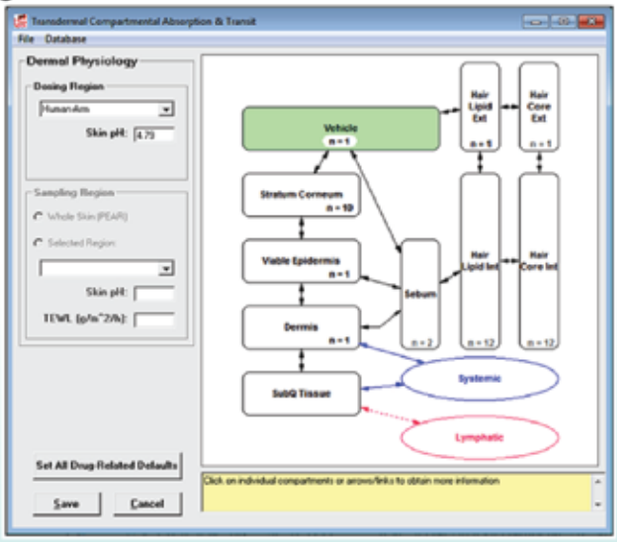
Additional Dosage Routes Module cont.

Dermal/Subcutaneous Model

The Transdermal Compartmental Absorption & Transit (TCAT™) model represents the skin as a collection of the following compartments: stratum corneum, viable epidermis, dermis, subcutaneous tissue, sebum, hair lipid, and hair core. The subcutaneous tissue is also considered. The diagram is shown in the figure below.

The model can simulate a variety of transdermal & subcutaneous dosage forms, specified at different places on the body, including:

- liquid formulations (solutions, lotions, suspensions)
- semi-solid formations (gels, creams, lotions, pastes)
- subcutaneous injections (bolus or controlled release)



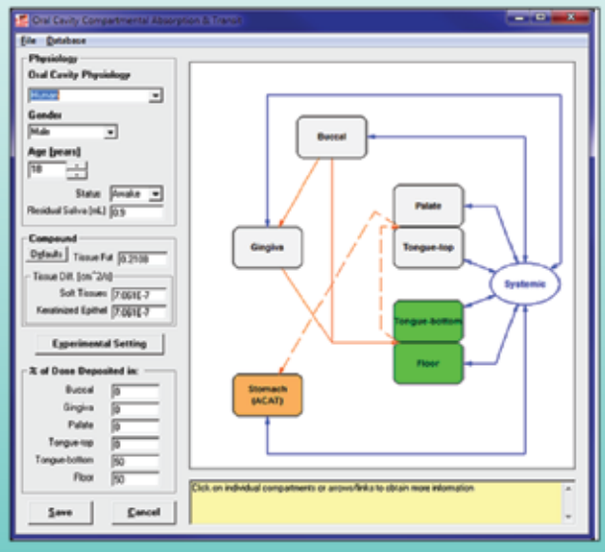
Some of the processes modeled include:

- vehicle evaporation
- absorption from the vehicle into the various tissue regions
- nonlinear metabolism in any tissue region
- systemic circulation and lymphatic absorption

Measured in vivo data for any dermal tissue can be used to compare with simulation results. All standard GastroPlus features, including the Population Simulator and Parameter Sensitivity Analysis, can be used with the dermal model.

Oral Cavity Delivery Model

The Oral Cavity Compartmental Absorption & Transit (OCCAT™) model represents the oral cavity (mouth) as a collection of the following compartments: buccal, gingival, palate, top of the tongue, bottom of the tongue, and mouth floor. The diagram is shown in the figure at right.



The model can simulate a variety of dosage forms including:

- sublingual solutions & tablets
- lingual sprays & supralingual tablets
- controlled release buccal patches

Some of the processes modeled include:

- dissolution & precipitation in the saliva
- diffusion through the oral mucosa
- uptake into systemic circulation
- swallowing of unabsorbed drug

Measured in vivo data for any oral cavity tissue can be used to compare with simulation results. All standard GastroPlus features, including the Population Simulator and Parameter Sensitivity Analysis, can be used with the oral cavity model.

Metabolism and Transporter Module

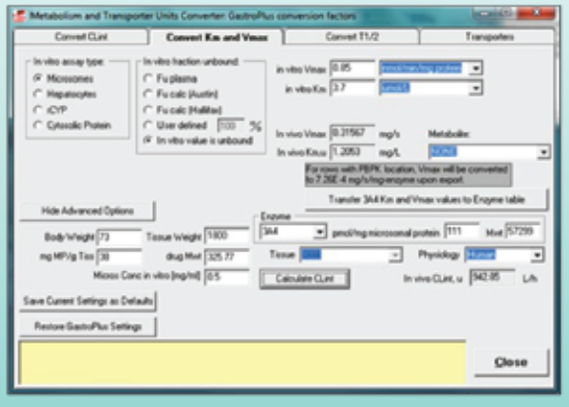
When linked with the upgraded ADMET Predictor™ Module, predict CYP metabolism pathways & kinetics, and have the Enzyme Table automatically populated with the correct locations and units!

Updated! Enzyme and transporter expression levels across species – including UGTs and SULTs!

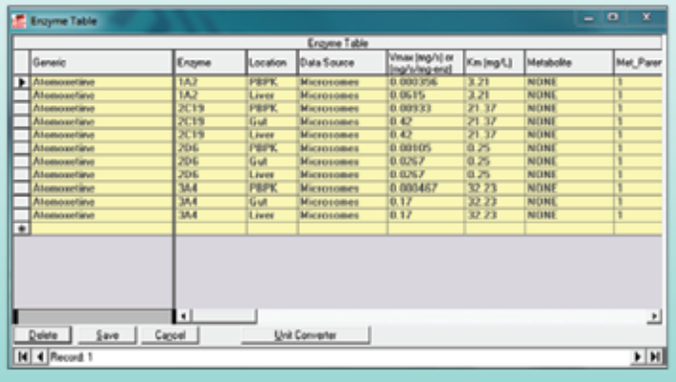
Enhanced! Metabolite tracking options!

The Metabolism and Transporter Module is an optional module that extends the capabilities of GastroPlus to include saturable metabolism and carrier-mediated transport into any compartment (gut, liver, and/or any PBPK tissue), along with metabolite tracking. This module calculates Michaelis-Menten rates for gut and liver (or any PBPK tissue) metabolism and for carrier-mediated transport (influx or efflux) based on input values for Vmax and Km. You can provide Vmax and Km values for each enzyme/transporter independently, or you can lump them into a single effective Vmax and Km, depending on your data. The distribution factors on the Physiology tab are automatically loaded for recognized gut enzymes and transporters, and provide the relative amounts of enzymes or transporters in the various ACAT™ gut model compartments. The Vmax and Km scale factors on the Pharmacokinetics tab are provided to allow fitting nonlinear kinetic models to your data.

The Metabolism and Transporter Module includes a Units Converter for easy transformation of a variety of your in vitro metabolism or transporter kinetic parameters into parameters and units that can be utilized by the GastroPlus model.



The Units Converter window that provides a convenient way of converting in *vitro* measurements to in *vivo* inputs for the GastroPlus model.



Define multiple metabolic/transport pathways, with enzymes and transporters placed into the tissues or organs of your choice!
Also link formation of different metabolics in a single simulation!

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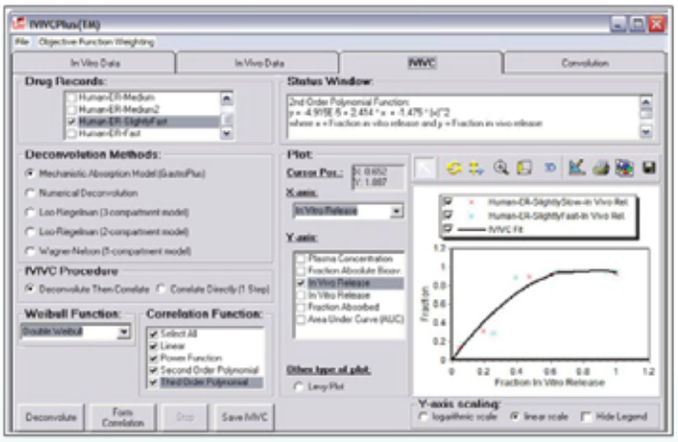
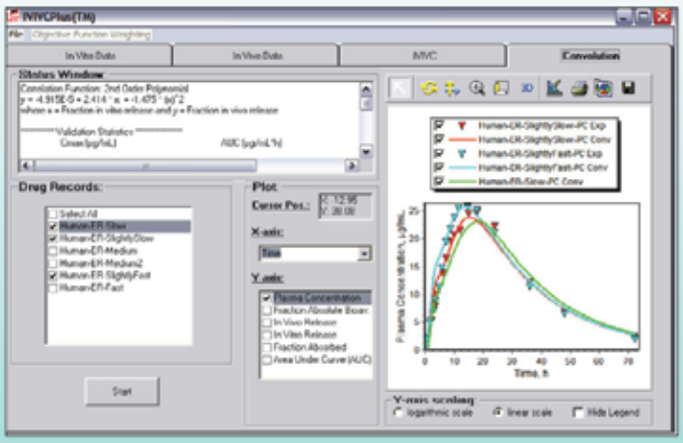
IVIVCPlus™ Module

New article from FDA scientists compare the Mechanistic Absorption deconvolution in GastroPlus vs. traditional methods – conclusion is that GastroPlus provides "greater predictive accuracy" - Mirza et al., Pharm. Res. 2012

IVIVCPlus is an optional add-on module that provides a convenient way to develop a correlation between either *in vitro* release and *in vivo* release or *in vitro* release and absolute bioavailability. The formed correlation can then be used to predict PK profiles for formulations with different *in vitro* release rates.



GastroPlus was the first software program to offer "mechanistic deconvolutions", which deconvolute, or fit, the *in vivo* dissolution vs. time along the gut lumen. An advantage to using the mechanistic deconvolution method is that it can be linked to a PBPK model. We are pleased to validate the mechanistic deconvolution method through a 5-year Research Collaboration Agreement with the U.S. FDA.



IVIVCPlus offers five methods for deconvolution:

1) Mechanistic Absorption Model (GastroPlus)
2) Numerical Deconvolution
3) Loo-Riegelman (2-compartment model)
4) Loo-Riegelman (3-compartment model)
5) Wagner-Nelson (1-compartment model)

The Mechanistic Absorption Model (GastroPlus) deconvolution method directly deconvolutes the *in vivo* release rate. The other four methods are traditional deconvolution methods that calculate the rate of appearance of compound into the systemic circulation. For formulation scientists, the correlation between *in vitro* release and *in vivo* release is much more intuitive and valuable.

Depending on the deconvolution method selected, a correlation can be made between *in vitro* release and *in vivo* release or *in vitro* release and absolute bioavailability. Currently, linear, power, and polynomial (second or third order) functions may be selected for the functional form of the correlation.

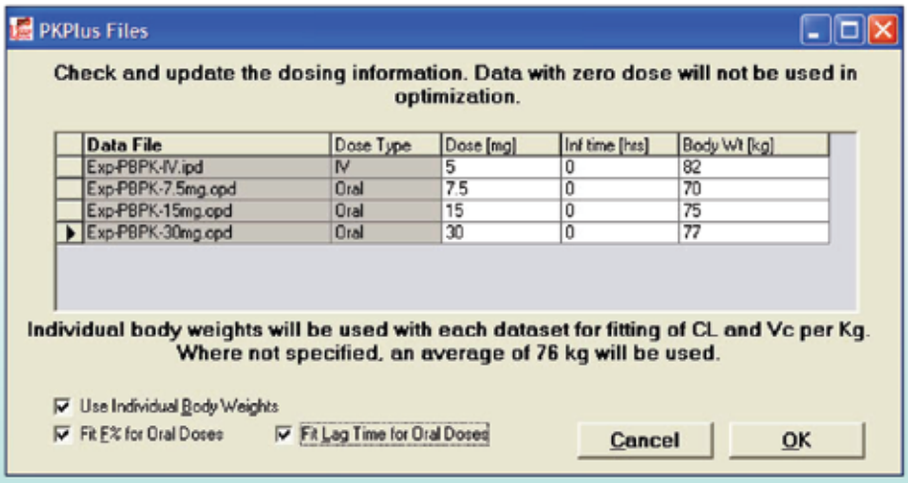
Run Convolutions: The correlation function can be used to calculate an *in vivo* release-time profile or absolute bioavailability-time profile for a new formulation of the compound exhibiting a different *in vitro* release-time profile. A plasma concentration-time profile for the new formulation can be constructed with the calculated *in vivo* release-time or absolute bioavailability-time profile.

Evaluate Validation Statistics: After running a convolution, IVIVCPlus outputs the observed values, predicted values, prediction errors, and mean absolute percent prediction error for both Cmax and AUC. These statistics can be used to evaluate the internal or external predictability of the correlation as described in the FDA's "Guidance for Industry Extended Release Oral Dosage Forms: Development, Evaluation, and Application of *In Vitro/In Vivo* Correlations".

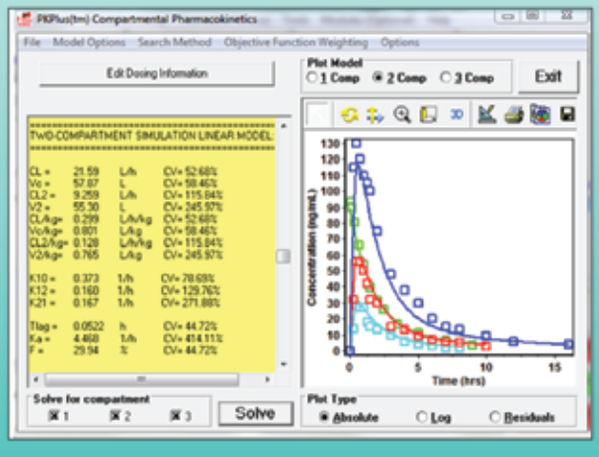
PKPlus™ Module

PKPlus extends GastroPlus to rapidly estimate pharmacokinetic (PK) parameters for non-compartmental analysis (NCA), along with 1-, 2-, & 3-compartment models from IV and oral plasma concentration-time (Cp-time) data, without the need to run full simulations. The fitted parameters include PK parameters, first order absorption rate, bioavailability and absorption lag time (if both IV and oral data are included in fitting). Required inputs are Cp-time profiles, dose, body weight and infusion time (if applicable). Compartmental PK can be fitted to single IV or oral data as well as across multiple Cp-time profiles - IV, oral or combination of IV and oral as well as different dose levels. Linear or saturable clearance models can be selected easily.

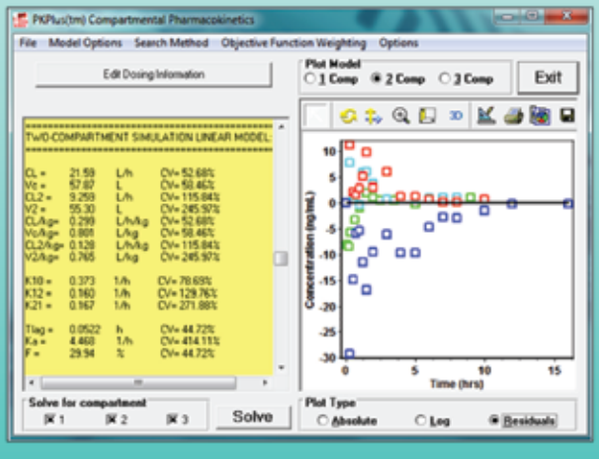
Full statistics, including Akaike Information Criterion and R^2, are provided for all models. Residual information is also captured And can be plotted. Once finished in PKPlus, the parameter values of the selected model can be easily transferred back to the main GastroPlus model, and all model results can be saved into report-quality outputs.



Plotting of absolute, log, and residuals for each model is selected with a mouse click, allowing rapid comparison of models.



2-compartment model for midazolam fitted across IV and three oral doses



Residuals plot for 2-compartment model for midazolam fitted across IV and three oral doses

PDPlus™ Module

Enhanced! Automated model selection – fit across all direct and indirect models, along with phase-nonspecific cell killing options, with a single mouse click!

PDPlus allows you to fit standard pharmacodynamic (PD) models to observed data and use the fitted models to predict PD effect changes due to changes in dose, dosage form, and dosing regimens. The PDPlus module adds the Pharmacodynamics Table, which contains the PD model, the site of PD action, and the parameters that determine the kinetics of the action. Multiple PD models (therapeutic and adverse) can be accommodated for each drug record.

Updated! Easily fit PD models across multiple data sets (e.g, doses)

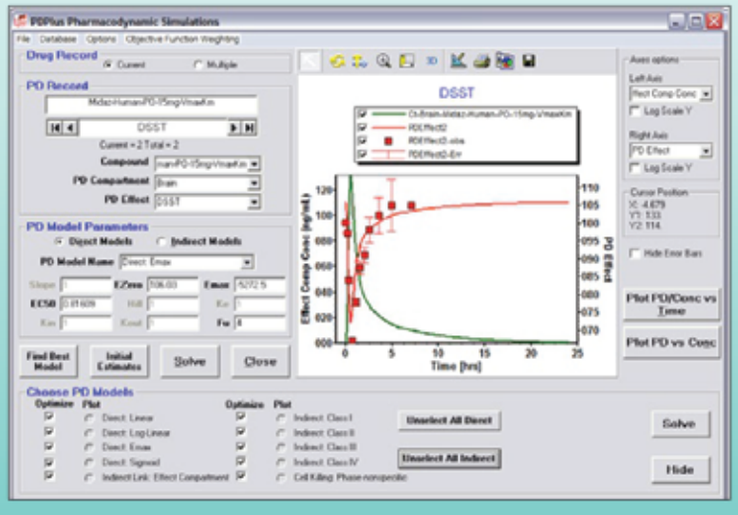
With PDPlus, fitting pharmacodynamic models to observed effect data is quick and easy. You may fit any of the standard PD models:

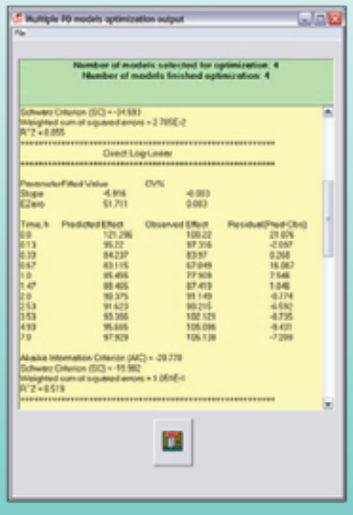
Direct Link: Linear, Log Linear, Emax and Sigmoid Emax

Indirect Link: Class 1, Class 2, Class 3, Class 4

Other: Phase-nonspecific cell killing (for tumor PBPK/PD modeling)

Convenient plotting of both plasma concentration-time and effect vs. time or concentration is provided with absolute and log plots available for each. Plus, all model results can be saved into report-quality outputs.





The effect can be linked directly to drug concentration in a specific tissue to easily perform PBPK/PD modeling.

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Optimization Module

The Optimization Module for GastroPlus extends and enhances the program's basic capabilities in several important ways:

- To automatically fit model parameters to data
- To optimize study designs (e.g., dosing regimens) and dose

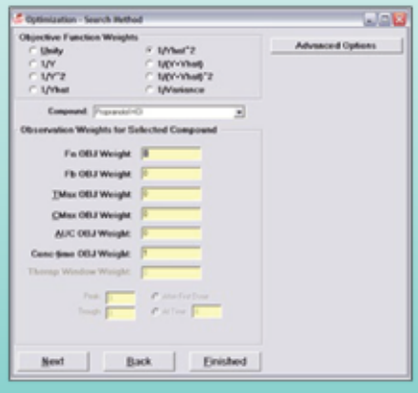
Fitting models to data

One of the most important uses of GastroPlus is to fit absorption, pharmacokinetic, and pharmacodynamic models to observations. In doing so, researchers gain tremendous insight into how their compound is behaving in vivo. When a single set of model parameters can be found that properly describes the observed plasma concentrationtime For all dose levels, a useful model has been obtained. In general, if the model parameters must be changed for each dose level, then something is not being accounted for correctly. The Optimization Module performs the multidimensional search needed to fit model parameters to one or more data sets automatically.

Model fitting can include (but is not limited to):

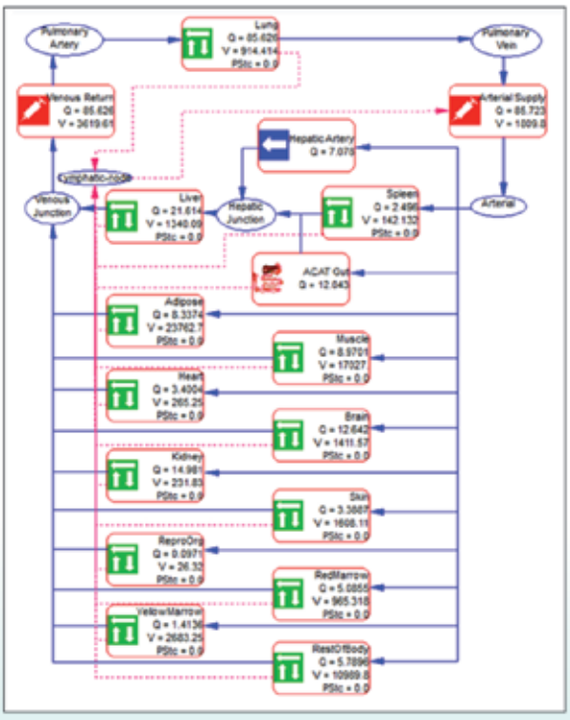
- PBPK model parameters to plasma and/or tissue concentration vs. time data
- Peff and absorption scale factors to determine regional dependencies
- A wide variety of physiological parameters (when necessary)
- Parameters to match profiles of parent drugs or any of their metabolites

Model parameters can be fitted to data for a single record, or across multiple records simultaneously. The program will run one simulation for each record each time it changes the value(s) of one or more model parameters. Typically, hundreds of iterations will be performed, each with N simulations, where N is the number of records whose observations are being used to compare predicted and observed values Objective function weighting is user-defined, and includes the most common weighting schemes.



SimulationsPlus ELECTROLAB

Biologics Module

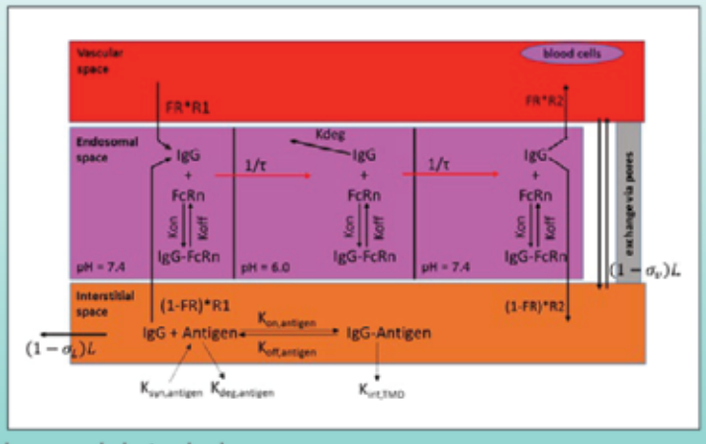


Each organ in the PBPK model is divided into three major compartments representing the vascular, endosomal, and interstitial spaces, as shown in the image at right.

NEW! PBPK models for antibody-drug conjugates (ADCs)

Starting in GastroPlus 9.0, we are pleased to offer PBPK models for large molecules (biologics). The Biologics Module simulates the absorption, distribution, and clearance of biological drugs. In the current implementation, both monoclonal antibodies (mAb) and antibody-drug conjugates (ADCs) administered as an intravenous bolus dose, intravenous infusion, or subcutaneous (SQ) injection can be modeled. As with other GastroPlus modules, there is no equation or code writing required. A schematic diagram of how the different organs are connected to one another is shown at left.

All major organs are connected in an anatomical fashion with plasma flow represented by blue solid arrows and lymph flow by red dashed arrows. The lymph node collects the lymphatic drainage from organs and lymph fluid is returned to the systemic circulation. Each organ in the PBPK model is divided into three major compartments representing the vascular, endosomal, and interstitial spaces, as shown below.



Some of the key processes accounted for in the GastroPlus models include:

- Convective transport and fluid phase endocytosis describing uptake of antibody into the tissue
- mAb-FcRn (neonatal FC receptor) binding & recycling
- Target mediated elimination in the interstitial space to include the influence of specific antigen-mAb interactions on mAb disposition
- Within the endosomal space, the competition for binding to FcRn between endogenous IgG and the therapeutic mAb
- mAb administration by either intravenous (IV) or subcutaneous (SQ) injection
- Complete default physiology parameters for humans – flexibility to create custom species models
- With ADCs, distribution and elimination processes of multiple ADC species with different DAR (drug-to-antibody ratio):
    - o Distribute to peripheral compartments
    - o Cleared by nonspecific clearance
    - o Bind to target receptor, internalize, and be cleared in the cell lysosome

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W5257

Mechanistic Absorption and Physiologically Based Pharmacokinetic Modeling of Itraconazole and Its Application for Drug-Drug Interaction with Midazolam in Adult Populations

Ke X. Szeto, Viera Lukacova, John DiBella, Walter S. Woltosz, and Michael B. Bolger
Simulations Plus, Inc., 42505 10 Street West, Lancaster, CA 93534, USA

Introduction

METHODS

RESULTS

DISCUSSION

CONCLUSIONS

R6307

Physiologically based pharmacokinetic (PBPK) model for prediction of vancomycin pharmacokinetics in children

Lukacova, V. , W.S. Woltosz, M.B. Bolger

Aim

Methods

Results

Conclusions

References

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T3312

Physiologically Based Pharmacokinetic Modeling of Rosuvastatin and Prediction of Transporter-Mediated Drug-Drug Interactions Involving Gemfibrozil

Joyce S. Macwan[1], Viera Lukacova[1], Grazyna Fraczkiewicz[1], Michael B. Bolger[1], Fatemeh Akhlaghi[2], Walter S. Woltosz[1]

PURPOSE

METHODS

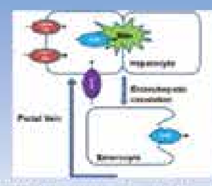

Figure 1.

RESULTS

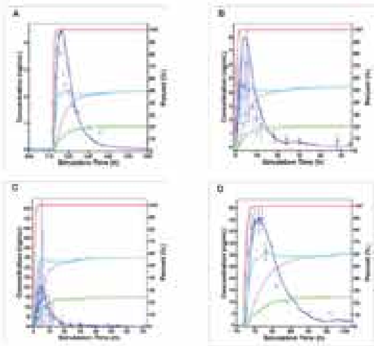

Figure 2.

C_{max} Ratio			AUC Ratio		
Observed	Predicted		Observed	Predicted	
Plasma	Plasma	Muscle	Plasma	Plasma	Muscle
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]

Table 1.

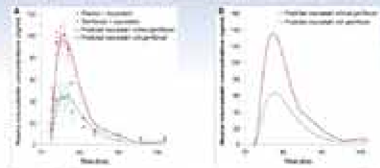

Figure 3.

CONCLUSIONS

REFERENCES

Physiologically Based Pharmacokinetic Modeling of Buspirone and the Effect of Liver Cirrhosis on its Disposition

W5308

Joyce S. Macwan, Grazyna Fraczkiewicz, Viera Lukacova, Michael. B. Bolger, Walter S. Woltosz

Simulations Plus, Inc., 42505 10th Street West, Lancaster, California 93534, USA

PURPOSE

The aim of this work was to develop a physiologically based pharmacokinetic (PBPK) model of buspirone following oral administrations in healthy volunteers, and to extend this model to predict the effects of physiological changes associated with liver cirrhosis in compensated and decompensated hepatic impairment patients.

METHODS

- The GastroPlus™ 8.5 (Simulations Plus, Inc.) Advanced Compartmental Absorption and Transit™ (ACAT™) model and PBPKPlus™ module were used to build the buspirone model for absorption, distribution, and clearance mechanisms.
- Physicochemical and biochemical parameters that predict absorption and distribution were obtained from literature or were predicted from structure with ADMET Predictor™ 6.5 (Simulations Plus, Inc.).
- Human organ weights, volumes, and blood perfusion rates were generated by the Population Estimates for Age-Related (PEAR™) Physiology module.
- Individual tissues were represented as perfusion-limited (blood-flow-limited) models. Tissue/plasma partition coefficients (Kps) were calculated using the Lukacova method [1] from in vitro and in silico physicochemical properties.
- The metabolic clearances of buspirone and its 1-pyrimidinylpiperazine metabolite in gut and liver were estimated from in vitro enzyme kinetic constants for CYP3A4 [2] and CYP2D6 [3], respectively, along with GastroPlus' built-in expression levels for both enzymes in gut and liver.
- The model was validated by comparing simulated and observed plasma concentration-time profiles for the parent drug and its two major metabolites (1-pyrimidinylpiperazine and 6-hydroxybuspirone), obtained after multiple oral administrations of buspirone across several different dose levels (5, 7.5, 15, 20 and 30 mg) in healthy volunteers [4].
- Physiological changes including cardiac output, cytochrome P450 (CYP) enzyme expressions, liver size, hepatic blood flow, renal function, and levels of plasma proteins, all associated with different degrees of severity of liver cirrhosis [5], were incorporated into the PBPK model. Moreover, changes in small intestinal transit time [6] and stomach pH related to liver cirrhosis [7] were included in physiology.
- The final validated model was used to predict concentration-time profiles of buspirone and 1-pyrimidinylpiperazine metabolite in patients with both compensated and decompensated hepatic impairment [8].

RESULTS

- Simulated plasma concentration-time profiles for buspirone and two major metabolites were in close agreement with observed data across multiple dose levels from healthy subjects (**Figure 1**).
- The validated final model, which was extended to predict the effects of liver impairment by incorporating physiological changes associated with different degrees of severity of liver cirrhosis (**Figure 2**), agreed reasonably well with observed data from patients with compensated and decompensated hepatic impairment (**Figure 3**).

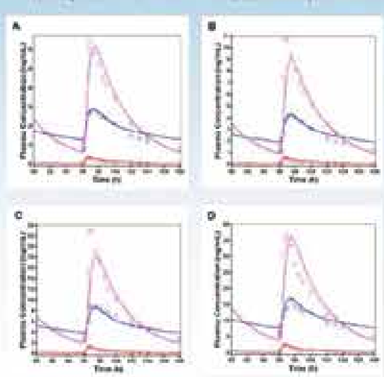

Figure 1. Predicted (lines) and observed (points) Cp-time profiles of buspirone (red), 1-pyrimidinylpiperazine metabolite (blue) and 6-hydroxybuspirone metabolite (pink) in healthy adult volunteers after 9 doses of (A) 5 mg (B) 7.5 mg (C) 15 mg (D) 30 mg buspirone hydrochloride administered once a day.

Figure 2. A default human physiology, created using the PEAR Physiology module was modified by incorporating physiological changes associated with liver cirrhosis.

- Changes in perfusion to organs
  - > Increase cardiac output
  - > Increase hepatic arterial blood flow
  - > Decrease portal blood flow
  - > Increase blood flows in other organs
- Decrease in hematocrit
- Decrease in plasma proteins amount
- Decrease functional liver mass
- Decrease GFR
- Decrease hepatic enzymatic activity

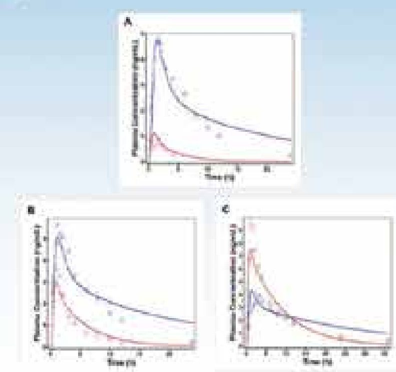

Figure 3. Predicted (lines) and observed (points) Cp-time profiles of buspirone (red) and 1-pyrimidinylpiperazine metabolite (blue) in (A) healthy volunteers (B) compensated (C) decompensated hepatic impairment patients after a single oral administration of 10 mg dose of buspirone hydrochloride.

CONCLUSIONS

- The absorption and pharmacokinetics of buspirone and its metabolites in healthy subjects were accurately simulated using in silico and in vitro data describing the drug's physicochemical and biopharmaceutical characteristics, along with in vitro enzyme kinetics.
- Accounting for physiological changes caused by the disease enabled successful prediction of systemic exposure in patients with different degrees of liver cirrhosis.
- The model indicated that buspirone pharmacokinetics was most sensitive to changes in CYP expression in patients with liver cirrhosis.

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Level A IVIVC Using a Comprehensive Absorption/PBPK Model for Metoprolol

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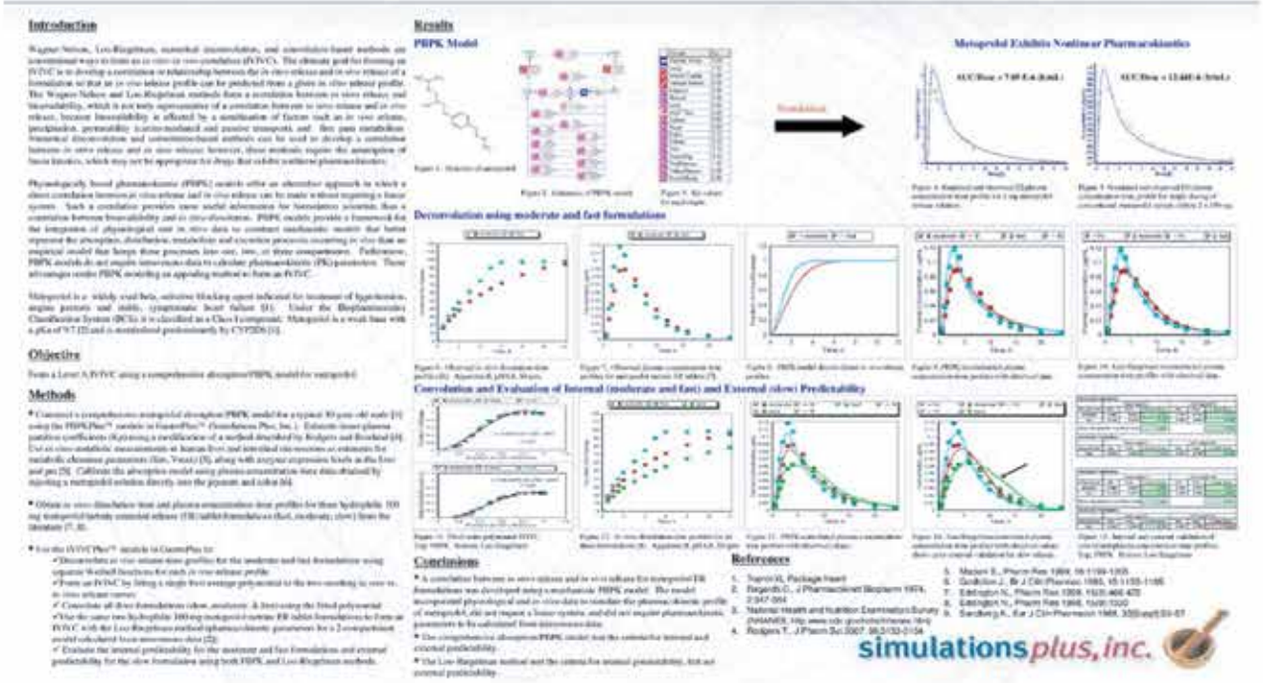

Application of PBPK Modeling to Predict Monoclonal Antibody Disposition after Intravenous and Subcutaneous Administration in Rats and Humans

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PURPOSE

Therapeutic monoclonal antibodies (mAbs) represent a growing segment of the development pipeline in the pharmaceutical industry. Physiologically based pharmacokinetic (PBPK) modeling has been extensively applied in small molecule drug development and has a great potential of helping in the development of mAbs and fusion/mAb derivatives. In this study a comprehensive PBPK model for mAbs was developed to simulate plasma as well as individual tissue concentrations after intravenous (IV) or subcutaneous (SC) administration in preclinical animals and humans.

METHODS

The whole-body PBPK model previously developed in GastroPlus® (Simulations Plus, Inc.) was expanded to include mechanisms related to the disposition and disposition of mAbs. Each organ in the PBPK model is divided into three major compartments representing the vascular, endosomal, and interstitial spaces, as shown in Figure 1.

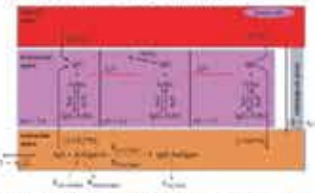


Figure 1: Schematic representation of individual tissue compartments

The following mechanisms are included in the PBPK model:

- Transport of mAb into the tissue interstitial space via convective flow through the paracellular pores in the vascular endothelium
- Uptake of mAb from the vascular and interstitial spaces into the endosomal space via fluid-phase endocytosis
- pH-dependent binding of mAb to FcRn in the endosomal space
- FcRn binding competition between therapeutic mAb and endogenous IgG
- Recycling of mAb to the vascular and interstitial spaces
- Endosomal degradation of the unbound mAb
- Return of mAb from the tissue to the bloodstream through convective transport with lymph flow
- Specific mAb binding to antigen (TMDD)

After IV injection, the mAb was initially distributed in the vascular space of the local tissue/plasma fluids. The local tissue was also divided into three compartments as shown in Figure 1. The same endosomal nonspecific clearance processes were applied to both the systemic clearance and local first-pass clearance after SC administration.

Convective transport through the lymphatic endothelium and fluid-phase endocytosis are the main mechanisms of absorption into the systemic circulation following SC administration of mAb.

The vascular (σ_v) and lymph (σ_L) reflection coefficients, and the fraction of mAb recycled (FR) were obtained from literature (Garg & Balthasar, J Pharmacokinet Pharmacodyn. 34 (2007): 687-709). Other model parameters (pH-dependent mAb-FcRn binding constants, mAb degradation in endosomal space, endosomal uptake, and recycle rates) were fitted using datasets from studies of 14 different antibodies and the reported synthesis rate of endogenous IgG (Junghans, Blood, 90 (1997): 3615-3616; Dare & Cronier, J Immunol, 102 (1969), 1345-1353) for different species. The fitted mAb-FcRn binding constants were within the range of reported in vitro values (Datta-Mannan et al., J Biol Chem, 282 (2007): 1709-1717; Andersen et al., J Biol Chem, 285 (2010) 4826-4836).

RESULTS

The PBPK model for mAbs was used to simulate plasma concentration-time profiles of MEDI-528 in human and Rituximab in rats across different dose levels after IV and SC administration. The simulated profiles were in close agreement with published clinical results (White et al., Clin Ther, 31 (2009), 726-740; Kagan et al., Pharm Res, 29 (2012), 490-499).

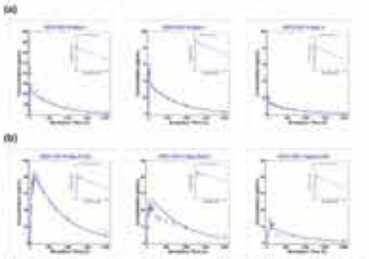


Figure 2: Comparison of simulated (lines) and measured (points) MEDI-528 for 0.3, 3, and 1 mg/kg doses in healthy subjects after IV (a) and SC (b) doses.

Default model parameters for human were used for MEDI-528 simulations.

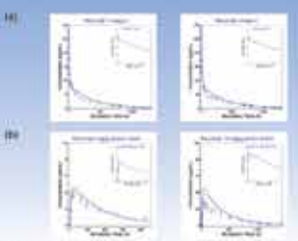
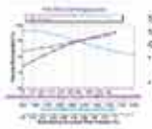


Figure 3: Comparison of simulated (lines) and measured (points) Rituximab for 1 and 10 mg/kg doses in Wistar rats after IV (a) and SC (b) doses.

The association coefficient between Rituximab and rat FcRn was estimated using the data from the 1 mg/kg IV dose. For the simulations of Rituximab in rats after SC administration, an additional linear clearance was included in the local first-pass clearance in addition to the endosomal nonspecific clearance processes and was estimated using the data from the 1 mg/kg SC dose. Other parameters used the default GastroPlus values for rat.



SC bioavailability is sensitive to dose, subcutaneous lymph flow, and effective depot volume

- Bioavailability decreases as dose increases
- Bioavailability increases as the lymph flow or effective depot volume increases

Figure 4: Parameter sensitivity of bioavailability

CONCLUSIONS

- PBPK modeling of mAbs in GastroPlus accurately simulates PK profiles after IV and SC administration
- This model can help to investigate the factors responsible for the systemic disposition of mAbs in preclinical animals and human
- This model could also be applied to assess dose-dependent nonlinear clearance related to TMDD

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