

PhysPK

Disruptive software for simulation of physiologically based pharmacokinetic models in individuals and populations

<https://www.physpk.com/>

Physiologically based pharmacokinetic (PBPK)/Pharmacokinetics (PK)/Pharmacodynamics (PD)

version: May-2021

contact: info@physpk.com

Analysis & Models (Unlimited compartments)		Preclinical ADME and Human Studies	
Noncompartmental analysis	✓	First-time-in-human	✓
Compartmental analysis	✓	Single ascending dose	✓
Single-compartment model	✓	Multiple ascending dose	✓
Multi-compartmental models	✓	Drug-drug interaction	✓
M&S individual & population	✓	Thorough QT	✓
Standard PD empirical models	✓	Hepatic impaired	✓
Physiological models	✓	Renal impaired	✓
Population estimation module	✓	Site of absorption	✓
Population validation module	✓	Radiolabeled mass balance	✓
Re-use & export of models & experiments	✓	Exposure-response	
Physiological mechanisms		Characterize drug exposure	✓
Mass conservation - Continuity	✓	Predict dosage requirements	✓
Non-linear elimination	✓	Assess changes in dosage requirements	✓
Phase partition of compounds	✓	Estimate rate of elimination and rate of absorption	✓
Net generation - Reactants	✓	Assess relative bioavailability / bioequivalence	✓
Volumetric capacitance	✓	Characterize intra- and inter-subject variability	✓
Macromolecule and transporter vesicle trafficking	✓	Understand concentration-effect relationships	✓
Quasi-static binding to macromolecules	✓	Establish safety margins and efficacy characteristics	✓
3D/2D/1D spatial region	✓	Dosing simulations (Route administration)	
Membranes and barriers/passive and transporter	✓	Intra-venous (IV)	✓
Multilevel physiological tissues	✓	Extra-basal (EB)	✓
Flow limited tissues	✓	Oral	✓
External devices	✓	Inhaled	✓
Biological activity		Drug reservoir	✓
Transit absorption and liberation structures	✓	Simulation scenarios and studies	
Intrinsic clearances or direct Michaelis – Menten	✓	Computing calculator elements	✓
Metabolism and for carrier-mediated transport	✓	PBPK/PK/PD indices	✓
In Vitro In Vivo Correlation (IVIVC)	✓	Interaction with other external software	✓
Virtual bioequivalence	✓	User-centered design approach	✓
Direct effect PD elements	✓	Graphical user-friendly interface	✓
Pathology/Tissues - oriented WB-PBPK models	✓	Integrated PK study reports	✓
Customized macromolecules database	✓	Standalone PK reports	✓
Customized metabolic network	✓	Data collection and interrogation	✓
General law of mass action kinetics	✓	Dataset generation	✓

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Pharmacokinetics (PK)		Applications	
Complete set of categorized PK components	✓	Connect biological system with pharmacokinetics	✓
Combination of ADME mechanisms and functions	✓	Models of diabetes mellitus & end-stage renal disease	✓
Non-compartmental analysis (NCA) integrated	✓	Absorption and transit gastrointestinal models	✓
Standard PK models parameterized	✓	Tissue PBPK models: kidney, liver, gut and lung	✓
Pharmacodynamics (PD)		Population validation module with Montecarlo	
Direct effect PD elements: Hill, Emax, Linear, etc.	✓	Predictive population validation functions	✓
Cell proliferation – kill models with phases	✓	Goodness of Fit (GoF) plots, Bootstrap & Virtual data	✓
N-compart. delay with different transduction signals	✓	Validation of scientific publications	✓
Indirect response models: Models I, II, III and IV	✓	Users can define new PBPK components	✓
Drag-and-drop PBPK/PK components using ports	✓	Population Estimation (FO, FOCE, FOCEI, ITS, SAEM)	✓
Physiologically based PK (PBPK)		Covariates with variation and real nature	
ADME mechanisms for region given by a set of DAEs	✓	Inter-subject variability with covariance matrix	✓
Standard PBPK tissues (membranes, barriers, etc.)	✓	Validation of the model by epsilon- and eta-shrink.	✓
Drug administration elements	✓	PK/PD/PBPK models as a standalone black box.	✓
Physicochemical in-vivo and vitro properties	✓	Connectivity	
Liberation and absorption	✓	Export the model to Excel	✓
Passive and transporter flow mass	✓	Reuse the model from other software (using APIs)	✓
Quasi-static binding to macromolecules	✓	Define public and private variables for another users	✓
Non-linear metabolism equations	✓	C++ code generation	✓
Customized metabolic networks	✓	Export the model to be executed from the web	✓
Physical laws for continuity of drugs and metabolites	✓	Execute the model remotely using web services	✓
Pressure – vascular flow rates, capacitive laws	✓	Use of csv, xml formats for input/output data	✓
Absorption, transit and liberation coefficients	✓	Use of binary HDF5 format for post-process analysis	✓
User friendly environment		Connection to C, C++ and FORTRAN libraries	✓
Highly intuitive graphics environment	✓	Automatic customization of R Scripts	✓
Drag-and-drop components into a canvas	✓	Target users	
Connection ports to facilitate connections	✓	Pharma industry	✓
Easy to learn OO language to create new components	✓	Academia	✓
Monitor for plotting graphs, histograms, etc.	✓	Healthcare and e-health industry	✓
Easy to model with differential equations	✓	Nutrition industry	✓
Use 1D, 2D and 3D tables for interpolation	✓	Chemical risk analysis companies	✓