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Development of a Whole-Body Physiologically Based Pharmacokinetics Model for Children with Severe Malnutrition

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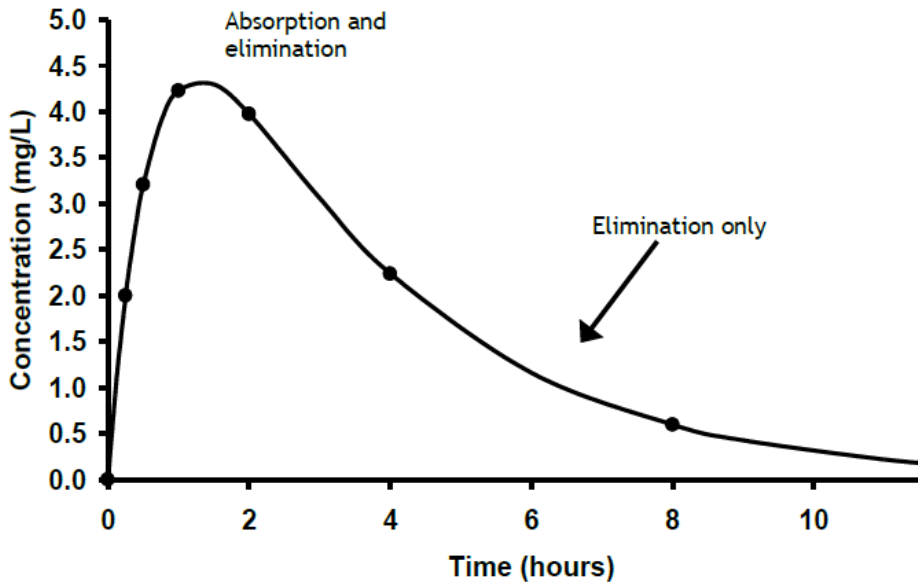
Pharmacokinetics (PK)

- Describes the movement of drugs in and out of the body through the following processes:
 - i. Absorption: the movement of drug from the site of oral or extravascular administration into the systemic circulation
 - ii. Distribution: the reversible transfer of drug between the systemic circulation and the tissues
 - iii. Elimination: the removal of drug from the body by processes such as renal excretion or hepatic metabolism

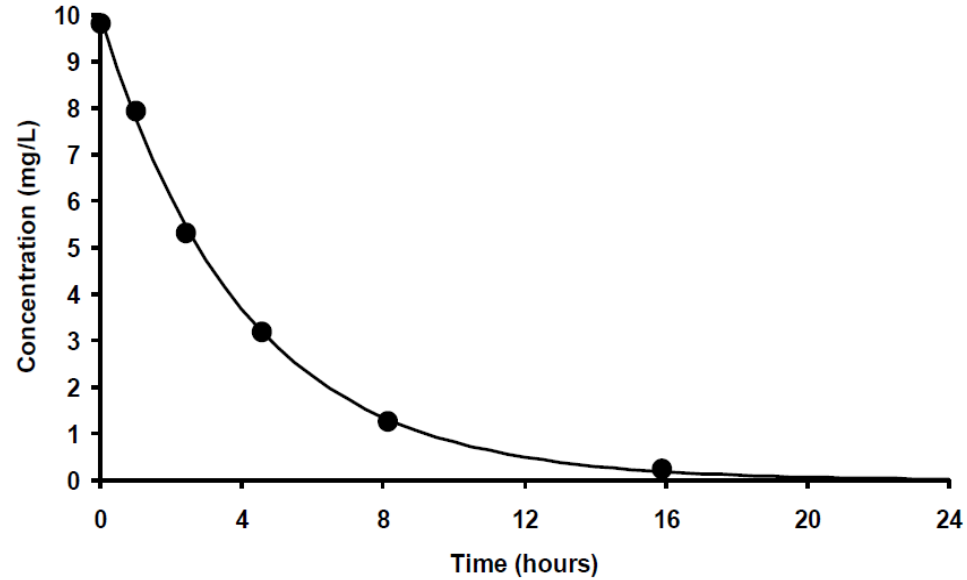


Concentration-time profile

Oral administration



Intravenous administration (IV bolus)





PK model

- Hypothetical structures used to describe and predict the disposition of drugs

For example:

If the desired target range of **Drug X** is 10-20 mg/L

- What loading dose should be used to achieve a serum concentration of 15 mg/L?
- What is the maximum concentration if an oral loading dose of 1000 mg is given?
- What concentration would you expect to measure 8 hours after the dose?



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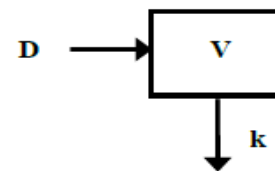
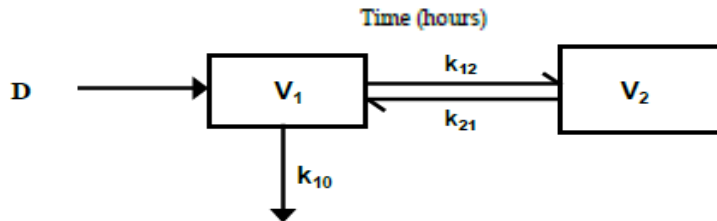
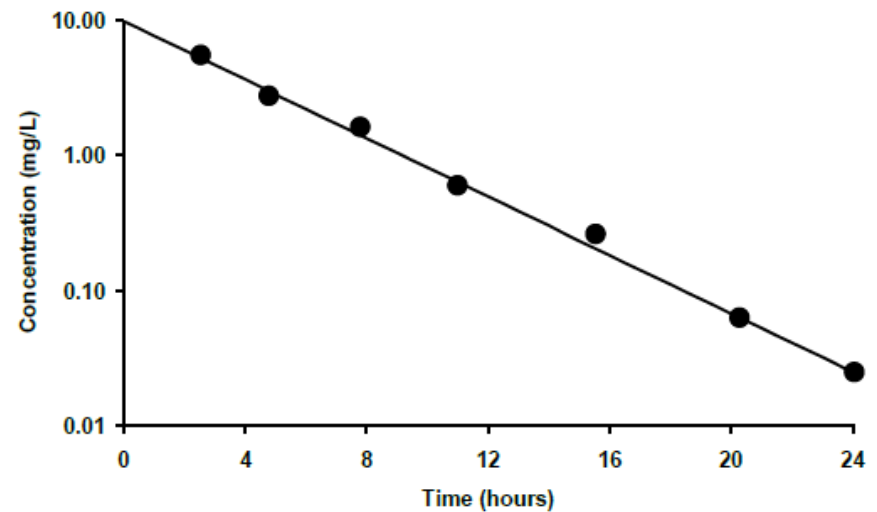
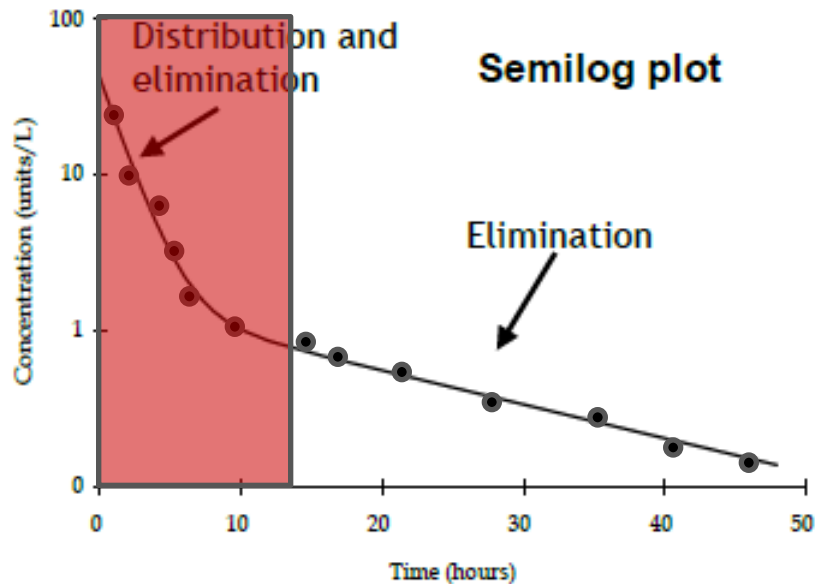
How to develop PK models?

- PK models can be developed by two approaches:
 - i. Empirical approach (traditional method)
 - ii. Mechanistic approach



Empirical approach

- Compartmental model e.g. one- and two-compartment models



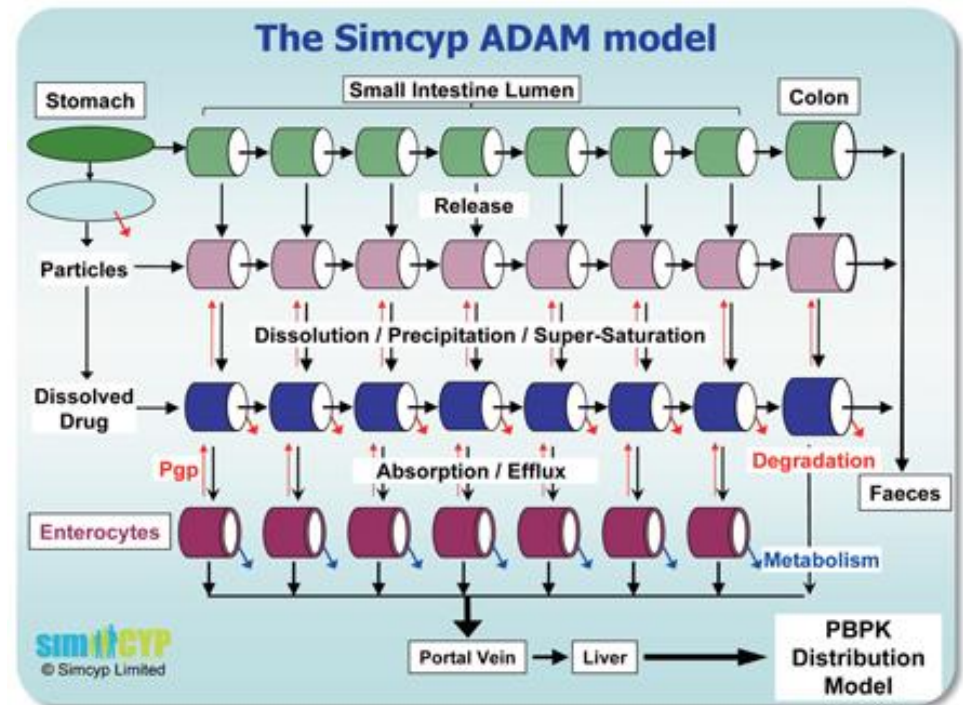
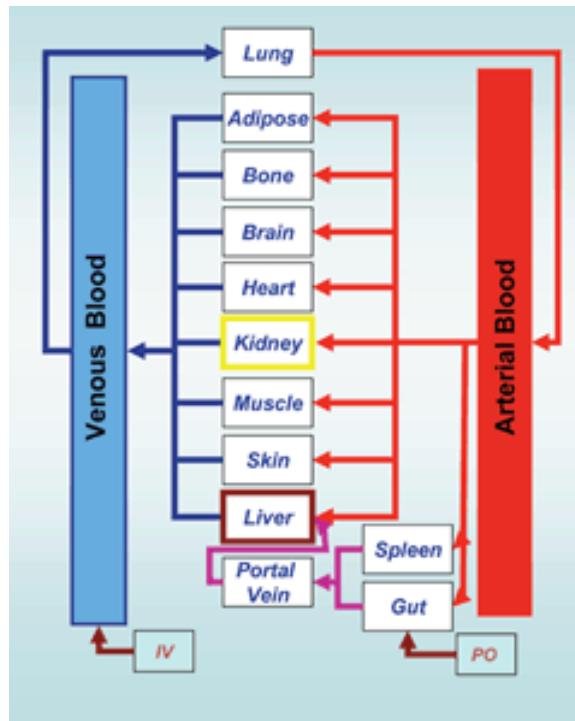
D = dose of the drug
 V = volume of distribution
 k = elimination rate constant

- Simple but the models have no physiological meaning
- Derived from the experimental data (drug concentrations)
- Complexity of the model depends on the data available



Mechanistic approach

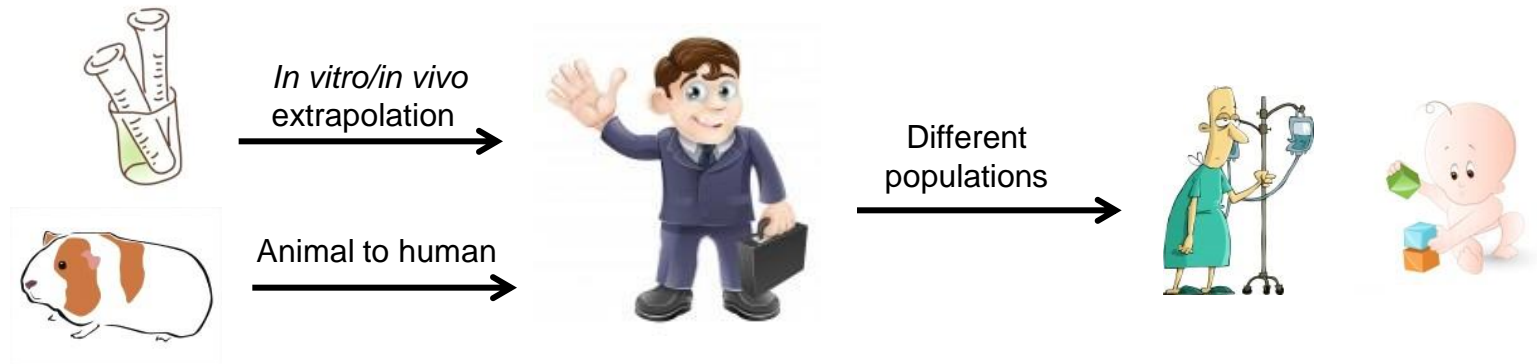
- PK processes of drugs are described by physiologically realistic compartment (anatomy of organism).
- E.g. Whole-body physiologically based pharmacokinetic (PBPK) models, liver metabolism models, absorption model.





Mechanistic approach

- The main use is for predicting drug concentrations with the extrapolation techniques
 - i. Inter-species (e.g. rat to human)
 - ii. Inter-tissue (e.g. plasma to less accessible organs)
 - iii. Inter-route (e.g. IV to oral)
 - iv. Inter-drug (e.g. other drug in the same class)





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Example

A whole-body physiologically based pharmacokinetic (WBPBPK) model for children with severe malnutrition



General method [1]

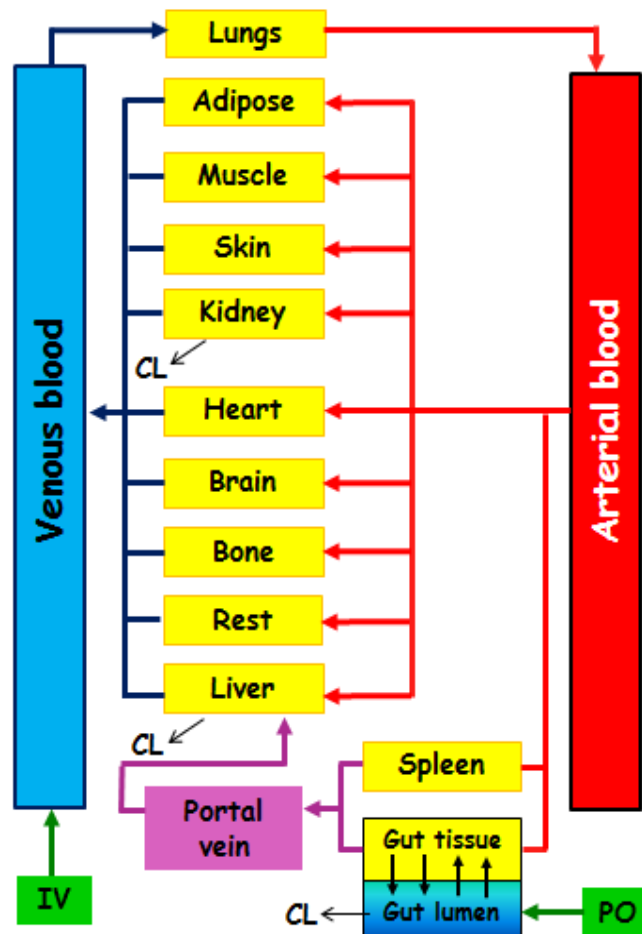
Input parameters

- 1. Drug specific**
 - Tissue:plasma partition coefficient (K_p)
 - LogP, pKa
 - Protein binding (R , f_u)
 - Solubility, Permeability
 - Rate and extent of absorption
 - Clearance
 - Dosage form, particle size
- 2. Species specific**
 - Organ volume
 - Organ blood flow

Trial design

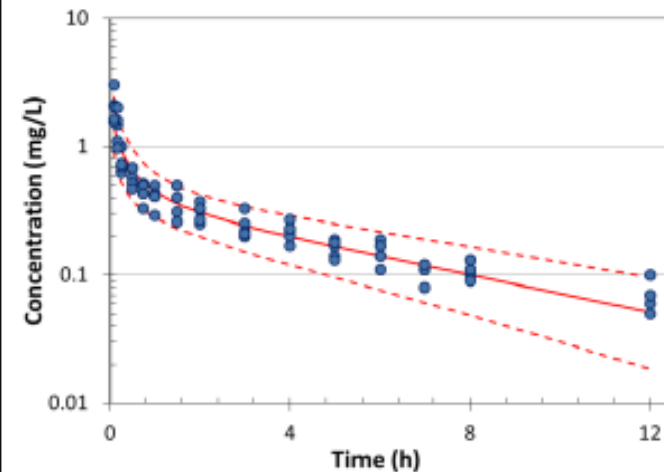
- Dosing regimen
- n doses
- n subjects
- Demographic data

PBPK model



Output

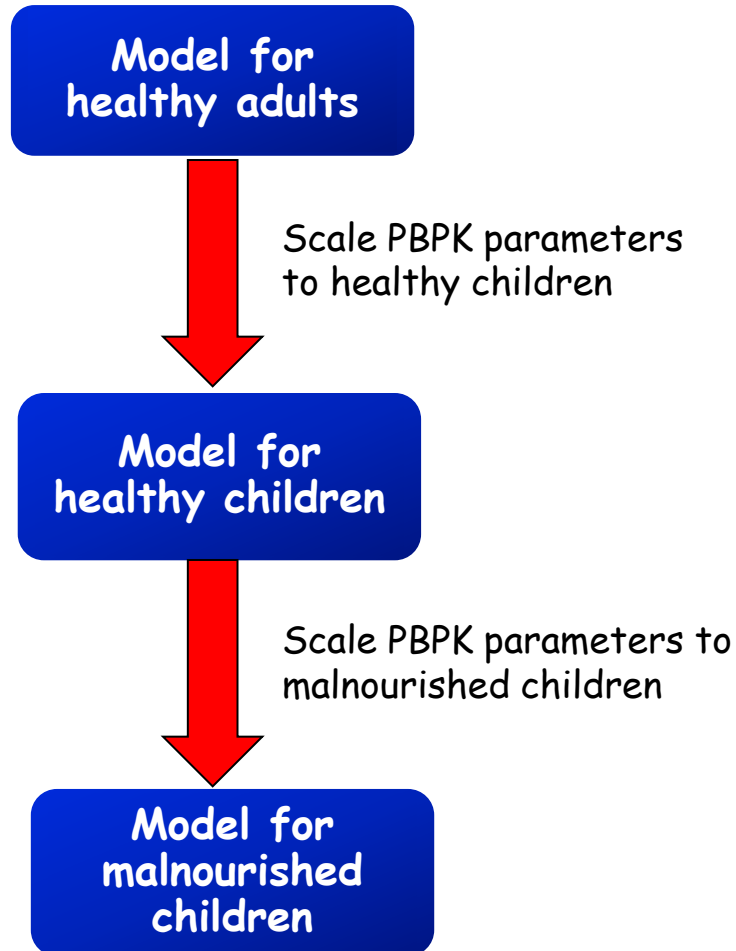
- Incorporate uncertainty and variability
- Simulate n times to obtain median and PIs





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General method [2]

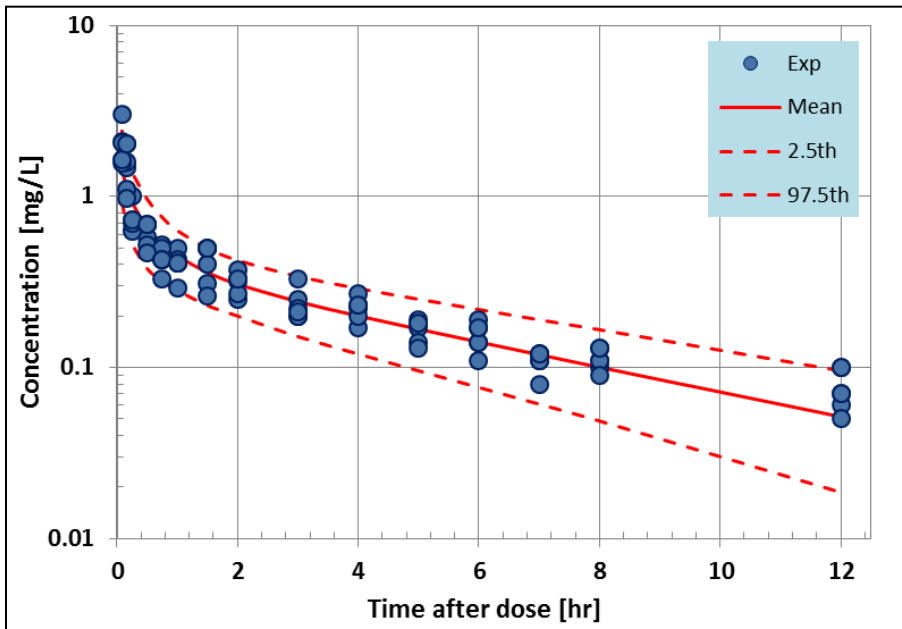




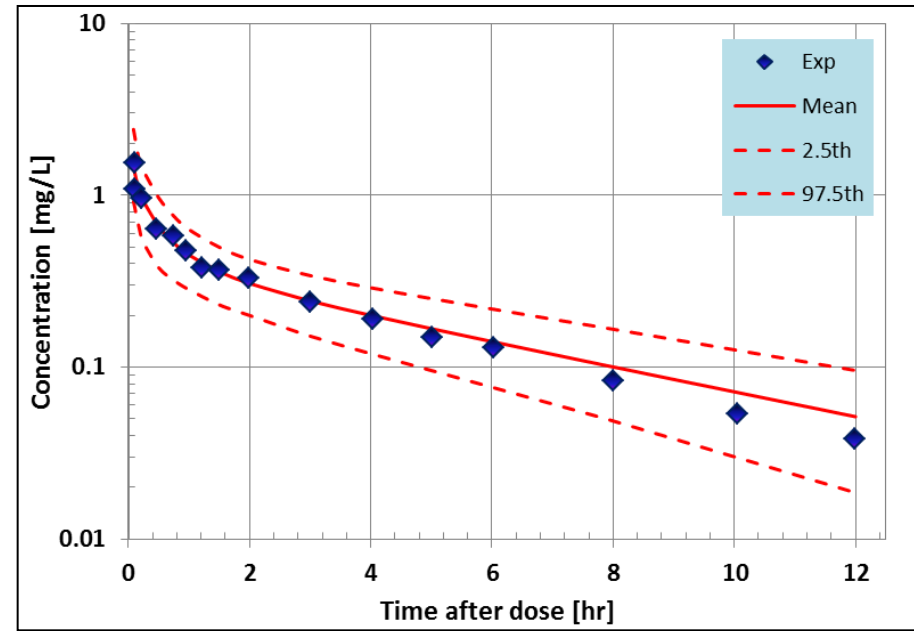
Results: healthy adults

1) IV bolus model (ciprofloxacin 100 mg)

- Observed data
- Mean simulated data
- ⋯ Prediction interval



Wise et al. Pharmacokinetics of intravenously administered ciprofloxacin. *Antimicrob Agents Chemother*, 1984; 26:8-10.

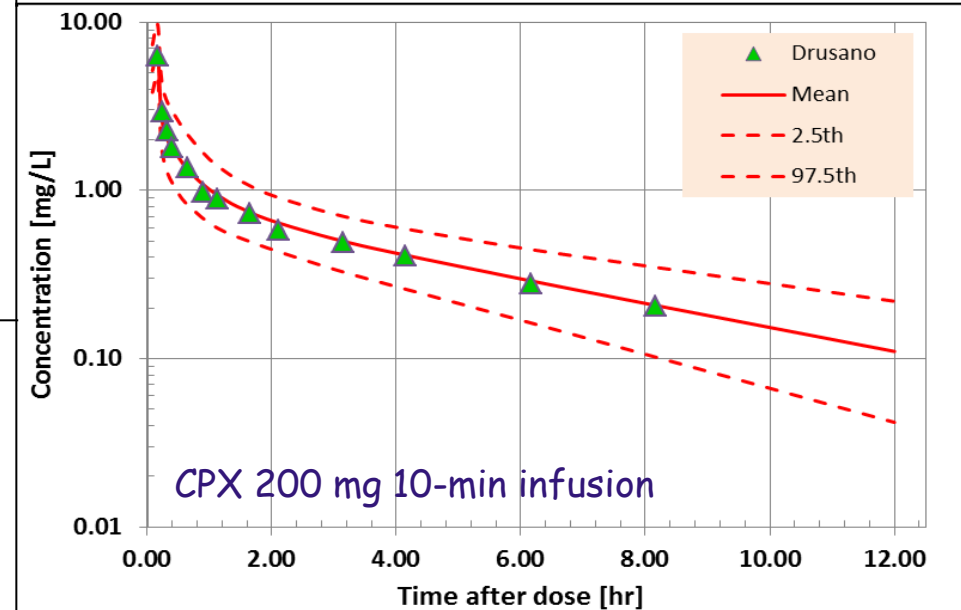
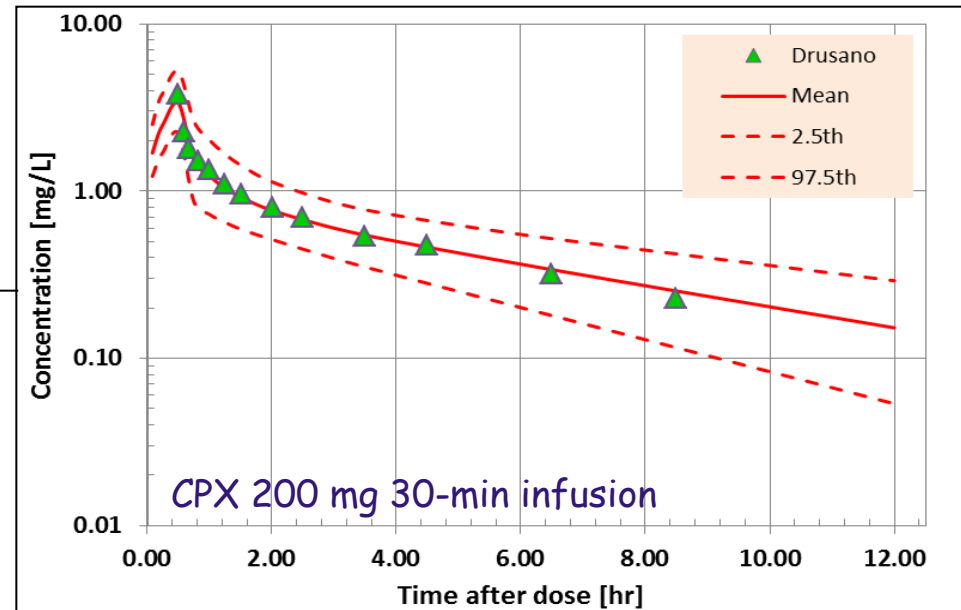
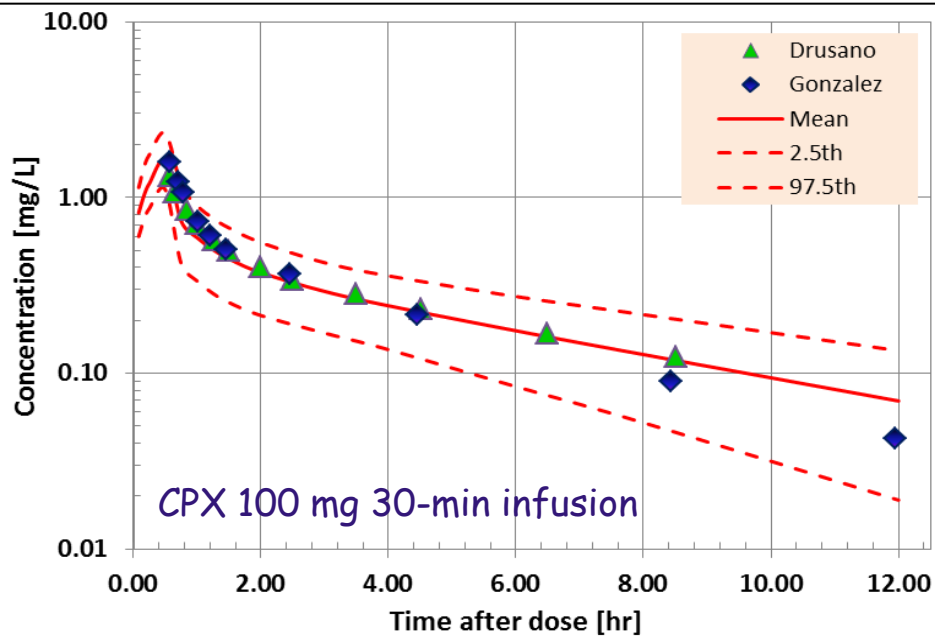


Bergan et al. Pharmacokinetics of ciprofloxacin after intravenous and increasing oral doses. *Eur J Clin Microbiol*, 1986;5: 187-92.



Results: healthy adults

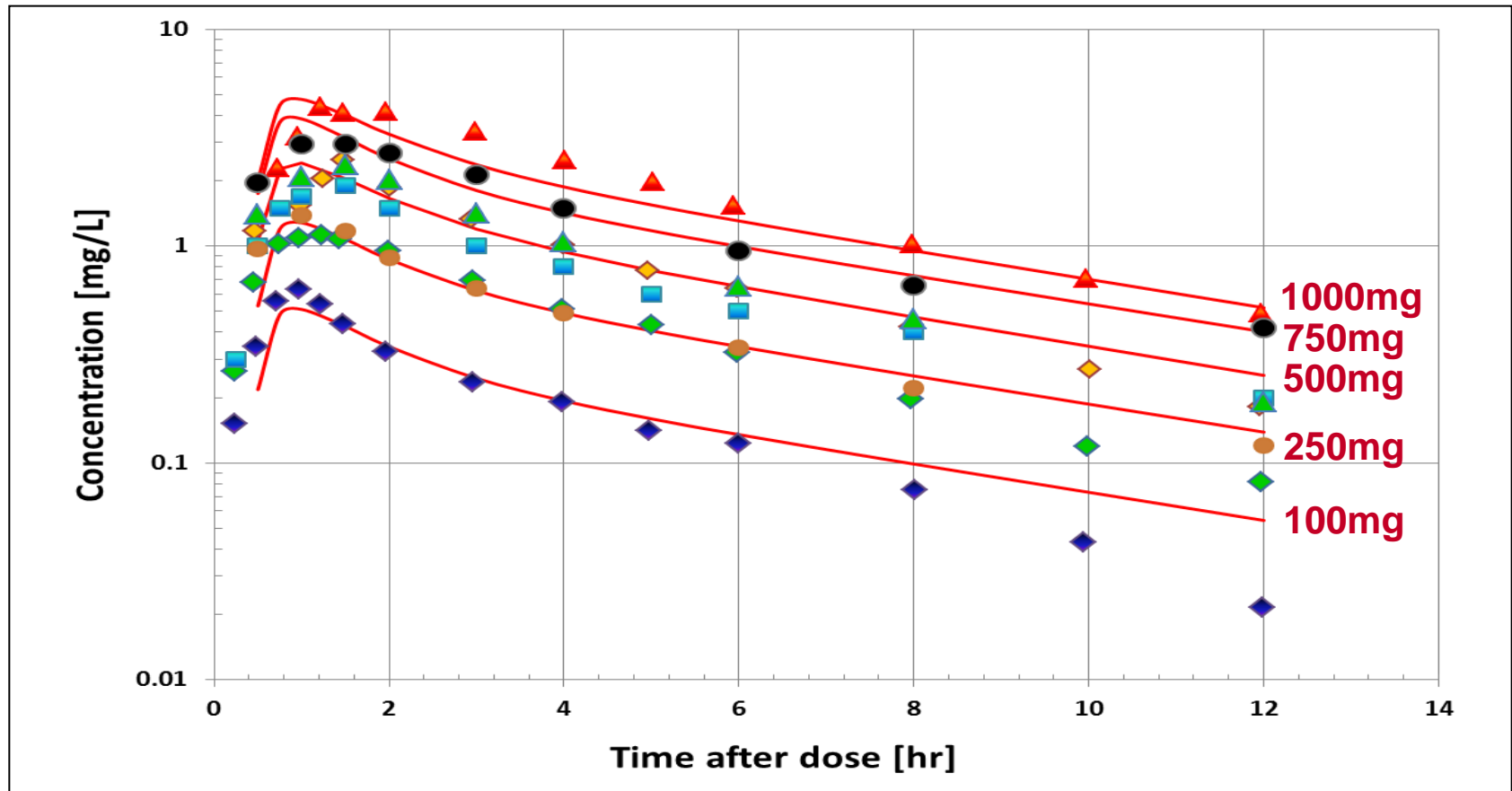
2) IV infusion model





Results: healthy adults

3) Oral model



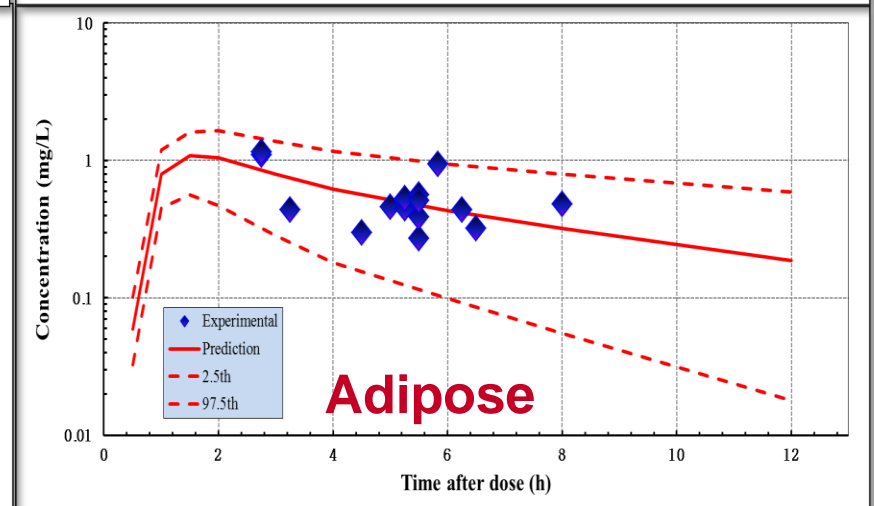
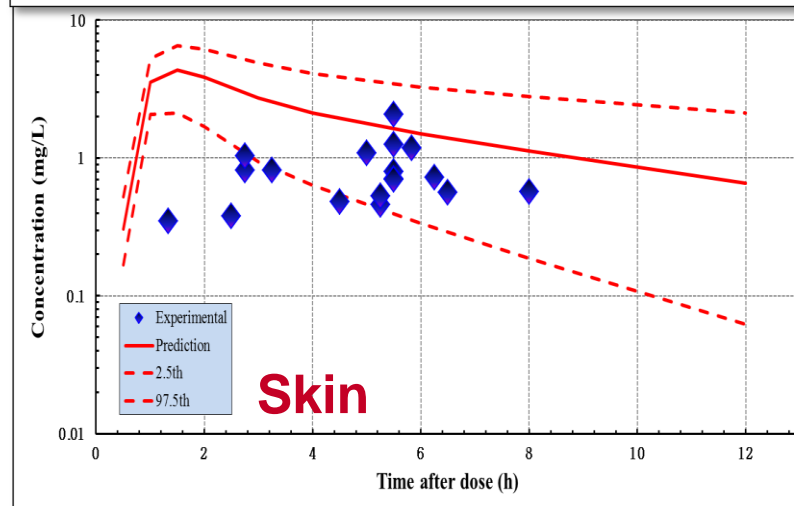
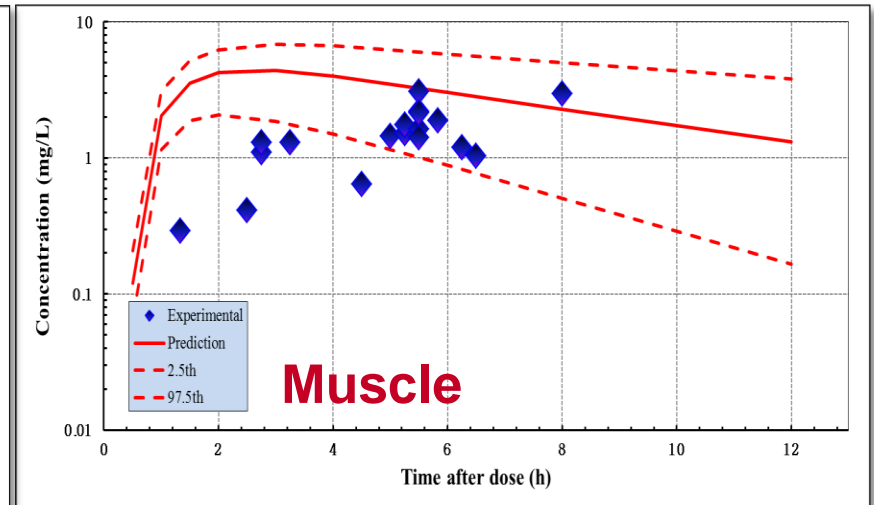
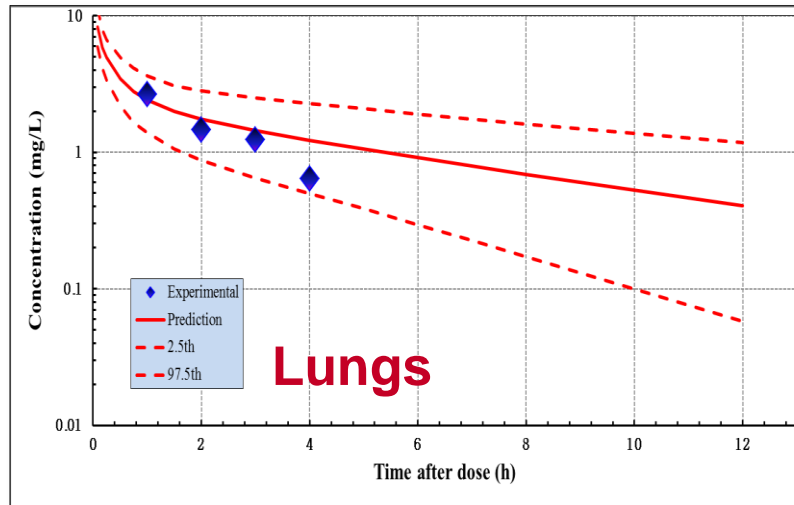
Bergan et al Pharmacokinetics of ciprofloxacin after intravenous and increasing oral doses. Eur J Clin Microbiol, 1986;5:187-92.

Crump, et al Pharmacokinetics and tissue penetration of ciprofloxacin. Antimicrob Agents Chemother, 1983;24:784-6.

Gonzalez et al Multiple-dose pharmacokinetics and safety of ciprofloxacin in normal volunteers. Antimicrob Agents Chemother, 1984;26:741-4.

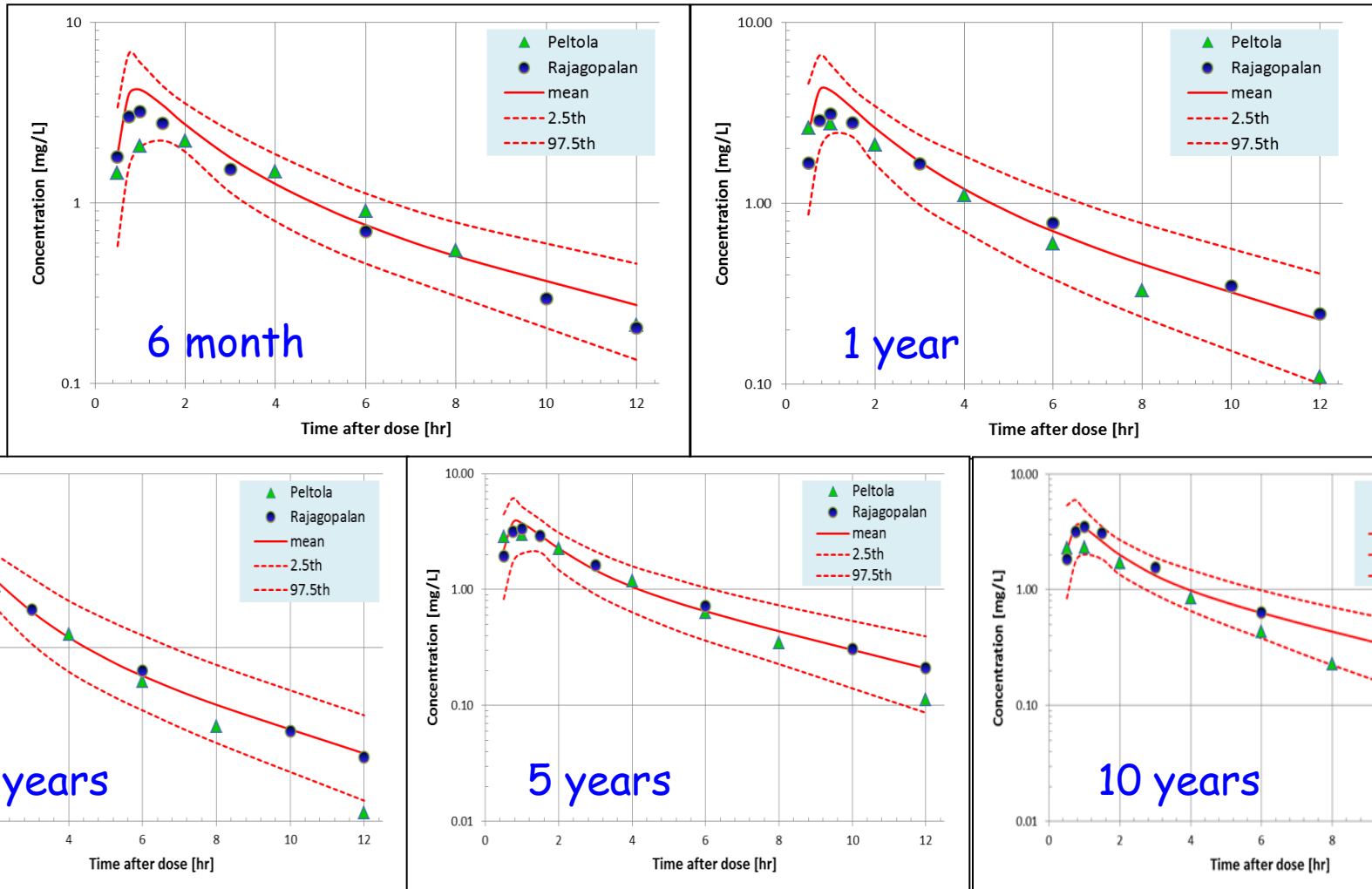


Results: organ concentrations



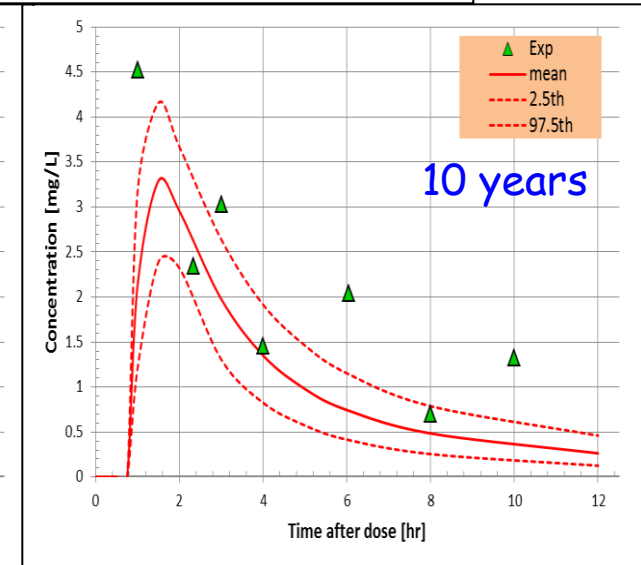
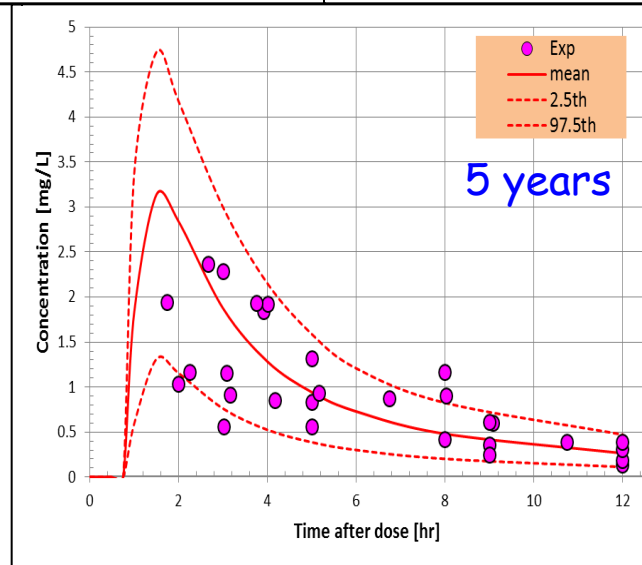
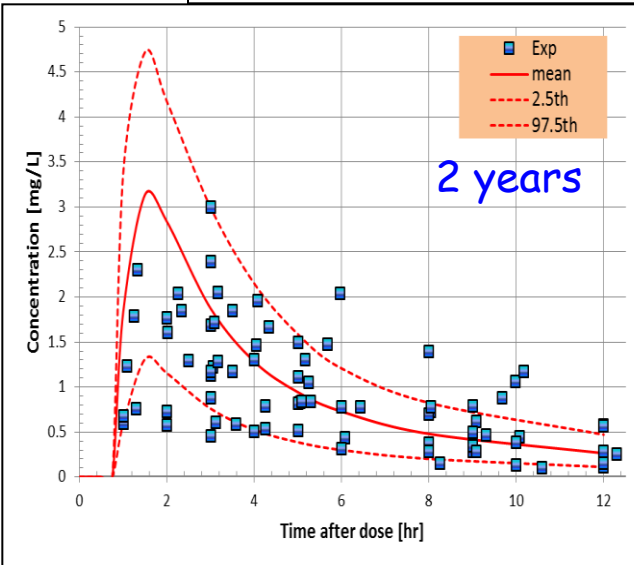
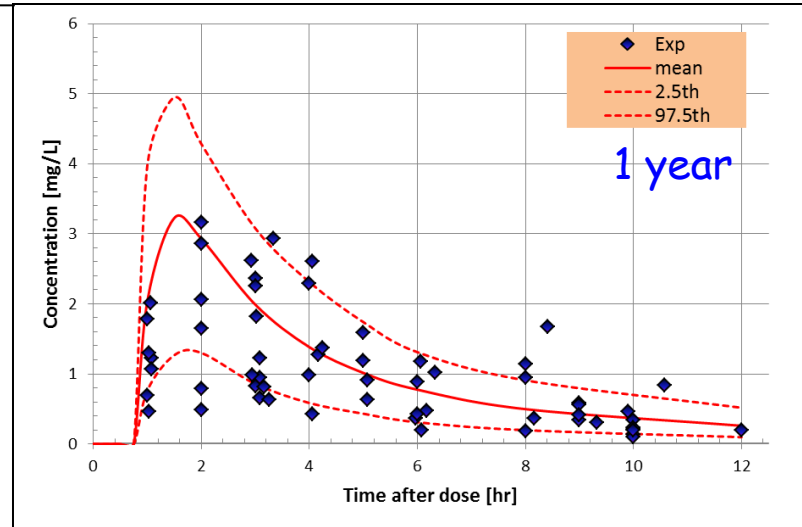
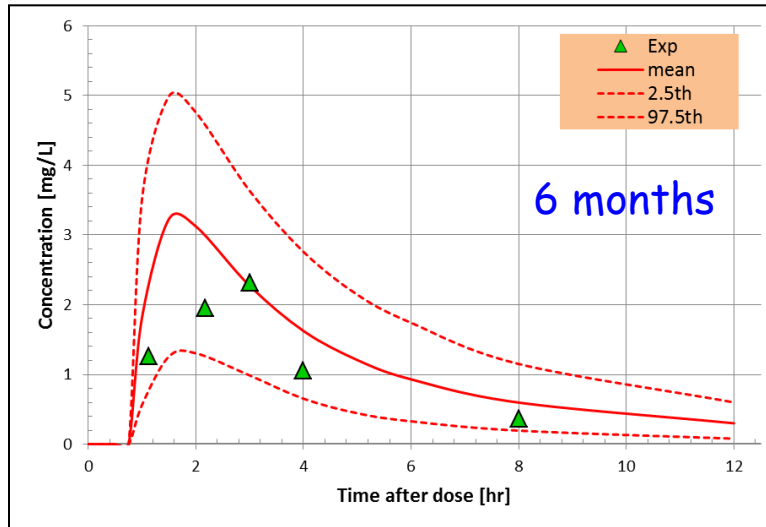


Results: oral model for healthy children





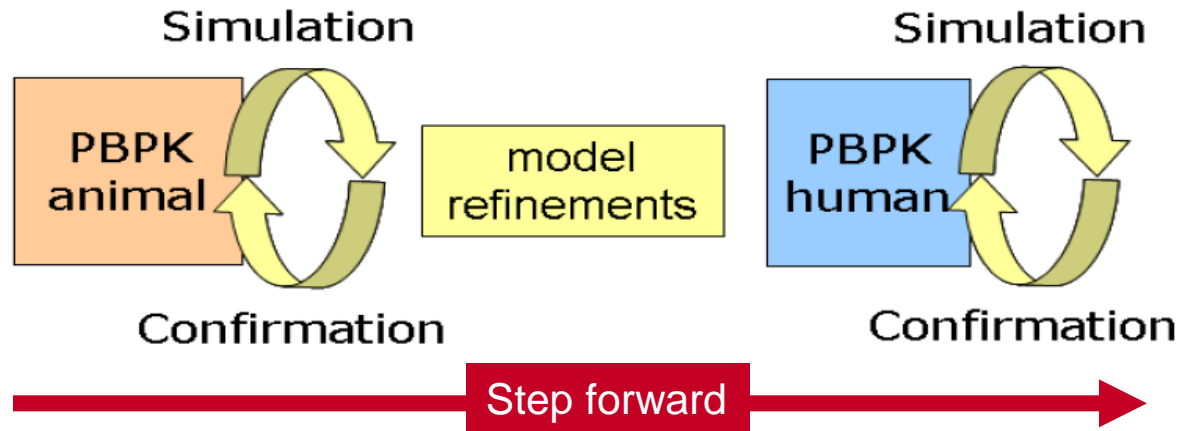
Results: oral model for malnourished children





Application

i. Drug discovery and development: "learn & confirm"



If the model prediction is adequate, then do step forward.

If the model prediction is inadequate, there are some systems that we do not know yet.

ii. Patient care

Predict drug concentrations, efficacy and toxicity for special populations



Program for PBPK simulation

```

Editor - C:\PBPK GUI\Ciprofloxacin.m
579
580 %%-----ODE start-----
581 t=[0 0.083 0.17 0.25 0.5 0.75 1 1.5 2 3 4 5 6 7 8 12];
582 % t=[0:0.01:12];
583 [z, R, b]=matrix(p,n,dose);
584 [t,y]=ode23s('PKmodel',t,z);
585 Conc=y'; %transpose matrix
586 kk=size(Conc); %return array dimension - kk= 1 14
587 m=kk(1,2); %m=14
588 %zint=y(:,m);
589 Concsim=[Concsim; Conc];
590 end
591 Concsim;
592 n_comp=14;
593 ss=size(Concsim);
594 ss1=ss(1,1);
595 M=Concsim;
596
597 for j=1:n_comp
598     for i=j:n_comp:ss1
599         if j==1
600             sim.comp1=M(i,:);
601             K1=[K1;sim.comp1];
602         elseif j==2
603             sim.comp2=M(i,:);
604             K2=[K2;sim.comp2];
605         end
606     end
607 end

Editor - C:\PBPK GUI\samCO.m
1 function [f,ff,smp_BW,smp_CO] = samCO(mean,var)
2 smp_CO=[];
3 smp_CO=normrnd(360,36);
4 sum_all=[];
5 ff=[];
6 while (mean>0)
7     [f,smp_BW] = samBW(mean,var);
8     hh(1)=(f(4)*0.065*smp_CO)/1.8; %liver
9     hh(2)=(f(5)*0.15*smp_CO)/1.1228407; %gut (small+large intestine and stomach)
10    hh(3)=(f(6)*0.03*smp_CO)/0.142315; %spleen
11    hh(4)=(f(7)*0.19*smp_CO)/0.2952381; %kidney
12    hh(5)=(f(8)*0.17*smp_CO)/27.857829; %muscle
13    hh(6)=(f(9)*0.05*smp_CO)/15.8296943; %adipose
14    hh(7)=(f(10)*0.05*smp_CO)/2.9596892; %skin
15    hh(8)=(f(11)*0.04*smp_CO)/0.3203883; %heart
16    hh(9)=(f(12)*0.12*smp_CO)/1.4077670; %brain
17    hh(10)=(f(13)*0.05*smp_CO)/2.7638191; %bone
18    smp_CO;
19    sum_all=sum(hh);
20    if (any(hh<=0))
21        elseif sum_all>=smp_CO
22            ko=1
23        else
24            ff=hh; %ff are organ blood flow
25            break
26    end
    end
    
```

- Written using MATLAB script
- GUI available
- Contained a library of drugs (mainly antibiotics) which is also linked to therapeutic effects.
- Possibly shared for academic uses

Design

Oral (mg)
 IV bolus (mg)
 IV infusion (mg/h)
 Dose (mg) 500

Drug parameters

fu (%)	0.8	CV	10
Ka (/h)	2.5	CV	10
Tlag (h)	0.3	CV	10
F (%)	0.7	CV	10

Body weight

Mean	73
CV	10

Cardiac output

Mean	360
CV	10

Clearance

Renal (L/h)	15	CV	10
Hepatic (L/h)	15	CV	10

Kp models

Poulin&Theil Rodgers&Rowland Willmann

Kp

Arterial	1
Lungs	5.1668
Venous	1
Liver	5.9010
Gut	3.4868
Spleen	4.4056
Adipose	0.5924
Muscle	3.5151
Skin	2.1362
Heart	3.3154
Bone	1.2514
Brain	1.3199
Kidney	6.4090

Organ volumes

Arterial	3.6	CV	10
Lungs	0.4784	CV	10
Venous	1.8	CV	10
Liver	1.8	CV	10
Gut	1.8	CV	10
Spleen	0.1423	CV	10
Adipose	15.8296	CV	10
Muscle	27.8578	CV	10
Skin	2.9569	CV	10
Heart	0.3203	CV	10
Bone	2.7638	CV	10
Brain	1.4077	CV	10
Kidney	0.2952	CV	10

Organ BF (%CO)

Arterial	100
Lungs	100
Venous	100
Liver	6.5
Gut	15
Spleen	3
Adipose	5
Muscle	17
Skin	5
Heart	4
Bone	5
Brain	12
Kidney	19



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Uppsala: Sweden's old capital city (~70 km from Stockholm)





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Back up slides



Model equations

- Mass of the drug in each organ was calculated using Linear ordinary differential equations (LODE)

1) *Non-eliminating organs:*

$$V_{T,i} \frac{dC_{T,i}}{dt} = Q_{T,i} \times \left(C_A - \frac{C_{T,i}}{Kb_i} \right)$$

2) *Eliminating organs (kidney, liver, gut):*

$$V_{T,i} \frac{dC_{T,i}}{dt} = \left[Q_{T,i} \times \left(C_A - \frac{C_{T,i}}{Kb_i} \right) \right] - CL_{int} \times \frac{C_{T,i}}{Kpu_i}$$

C = concentration (mg/L), Q = blood flow (L/h), Kb = tissue:blood partition coefficient, Kpu = tissue:plasma unbound partition coefficient, CL_{int} = intrinsic clearance (L/h), V = volume (L), T = tissue, A = arterial blood, i = each organ in the model



in silico Kp prediction

- Based on in vitro data of i. drug lipophilicity ($\text{LogP}_{\text{O:W}}$), ii. protein binding (f_u , R) and iii. tissue composition

Tissues	Tissue composition (fraction of tissue wet weight)					
	Water	Extracellular water	Intracellular water	Neutral lipids	Neutral phospholipids	Acidic phospholipids
Bone	0.45	0.074	0.0011	0.346	0.100	0.67
Brain	0.78	0.051	0.0565	0.620	0.162	0.40
Gut	0.76	0.0487	0.0163	0.475	0.282	2.41
Heart	0.78	0.0115	0.0166	0.456	0.320	2.25
Kidney	0.76	0.0207	0.0162	0.483	0.273	5.03
Liver	0.73	0.0348	0.0252	0.573	0.161	4.56
Lung	0.78	0.003	0.009	0.446	0.336	3.91
Muscle	0.71	0.022	0.0072	0.630	0.079	2.42
Skin	0.67	0.0284	0.0111	0.291	0.382	1.32
Spleen	0.79	0.0201	0.0198	0.579	0.207	3.18
Adipose	0.15	0.79	0.002	0.017	0.135	0.4
Plasma	0.95	0.0032	0.0021	-	-	-
Blood cells	0.63	0.0012	0.0033	0.603	-	0.57



1) Poulin and Theil method

$$Kp = \frac{\left[P \cdot (V_{nl} + 0.3V_{ph}) + V_w / fu_t + 0.7V_{ph} \right]_{-tissue}}{\left[P \cdot (V_{nl} + 0.3V_{ph}) + V_w / fu_p + 0.7V_{ph} \right]_{-plasma}}$$

2) Rodgers and Rowland method

$$Kpu_{BC} = \left[\frac{(Hct - 1) + R}{fu + Hct} \right]$$

$$X = 10^{pK_{a_{BASE}} - pH_{iw}} + 10^{pH_{iw} - pHa_{ACID}}; Y = 10^{pK_{a_{BASE}} - pH_p} + 10^{pH_p - pHa_{ACID}}; Z = 10^{pK_{a_{BC}} - pH_{iw}} + 10^{pH_{iw} - pHa_{BC}}$$

$$Ka_{AP} = \left[Kpu_{BC} - \left(\frac{1+Z}{1+Y} \cdot V_{iw,BC} \right) - \left(\frac{P \cdot V_{nl,BC} + (0.3P+0.7) \cdot V_{nl,BC}}{1+Y} \right) \right] \cdot \left(\frac{1+Y}{AP_{BC} \cdot Z} \right)$$

$$Kpu = \left[\left(\frac{1+X \cdot V_{iw}}{1+Y} \right) + V_{ew} + \left(\frac{Ka_{AP} \cdot AP \cdot X}{1+Y} \right) + \left(\frac{P \cdot V_{nl} + (0.3P+0.7) \cdot V_{ph}}{1+Y} \right) \right]$$

$P = P_{O:W}$ and $D_{VO:W}$ for lean and adipose tissues, respectively. $D_{VO:W}$ were estimated using linear regression and Henderson-Hasselbalch equations. $Kp = Kpu \cdot fu$

3) Empirical method

$$V_{SS} = V_{plasma} + (V_{BC} \cdot RBC_u \cdot fu) + \sum_{i=1}^n V_{t,i} \times 10^{a_{t,i}} \times \log Kp_{muscle} + b_{tissue,i} \times \log X_{drug} + intercept_{tissue,i}$$