# Simcyp In Vitro Analysis Toolkit (SIVA-Toolkit)

# A User-friendly Tool for Analysis of Complex In Vitro Experimental Data

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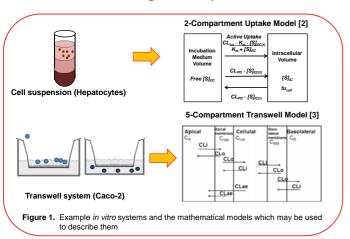
### Complexity of In Vitro Assays

In vitro data analysis in whole cell systems is complex [1] and time consuming, yet accurate data analysis and informed data interpretation are crucial early in the drug development process, especially when In Vitro-In Vivo Extrapolation (IVIVE) approaches are being used.

A number of software tools exist for the analysis of *in vitro* data. However, these tools were developed for broad application and **do not:** 

- support analysis of more complex in vitro experimental systems.
- possess appropriate statistical rigour.
- allow automated IVIVE.

### In Vitro Models (e.g. Transporters)

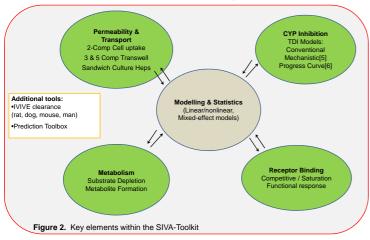


When using whole cell systems (Figure 1) there is a **need to** account for:

- Interplay between metabolic, passive diffusion and active transport processes
- Possible simultaneous time dependent inhibition and competitive inhibition
- Contribution of metabolites to enzyme inhibition
- Nonspecific binding
- Intracellular binding
- Intra & Inter-assay, between donor variability
- Potential outliers

## SIVA-Toolkit - Key Elements

 The SIVA-Toolkit is a user friendly tool for the analysis of complex in vitro experimental data. In vitro assays and associated models included in the SIVA-Toolkit are shown in Figure 2.



#### Importance of In Vitro Transporter Modelling

- Results from two studies [3],[4], showing the impact of modelling on the evaluation of P-glycoprotein (P-gp) kinetics are summarised in Figure 3 and Table 1.
- The likelihood of correctly simulating drug-drug interactions due to P-gp interactions with this compound will be very different if the correct kinetic parameters are not used.

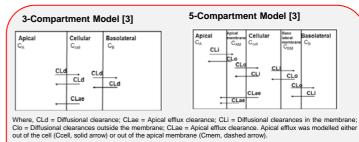


Figure 3. Details of compartmental models used in the evaluation of transporter kinetic parameters by Korzekwa and Nagar [3]

Table 1 Kinetic parameter estimates for P. an mediated transport of Quiniding

Table 1. Killetic parameter estimates for F-gp mediated transport of Quintume			
Quinidine	K <sub>m</sub> (μM) (MDRI-MDCKII)	K <sub>m</sub> (μM) (P-gp induced Caco-2)	Fold Difference in estimated K <sub>m</sub> *
Conventional Michaelis-Menten Model [3]	19.9	4.5	
3-Compartment [4]	0.339	0.234	19 - 59
3-Compartment [3]	0.255	0.228	20 – 78
5-Compartment [3]	0.203	0.175	26 - 100

<sup>\*</sup>Fold difference in estimated  $K_m$  (Michaelis-Menten constant), relative to conventional Michaelis-Menten approach.

### **Advantages of SIVA-Toolkit**

**Specialized -** Specifically designed for drug discovery and early drug development scientists.

**Easy to use-** Provides user-friendly graphical interfaces with predefined library models for currently available *in vitro* assays. Complex data analysis without the need to know a coding language.

**Links to other platforms -** Potential for linkage to other platforms (e.g. Phoenix)

**Statistical rigour** – Ready-made structural models are integrated in a user-friendly manner with powerful nonlinear fitting models in a statistical environment.

**Ease of documentation-** Provides formatted printable reports with a summary of input parameters, experimental details and results.

**Automated IVIVE-** Integration of *in vitro* metabolic clearance data with established IVIVE approaches and physiological scaling factors for extrapolation of hepatic clearance in multiple species (human, dog, rat, mouse).

# References

- [1]. Zamek-Gliszczynski MJ et al., Clin Pharmacol Ther. 2013 Jul;94(1):64-79.
- [2]. Poirier A et al., Drug Metab Dispos. 2008 Dec;36(12):2434-44.
- [3]. Korzekwa K and Nagar S, Pharm Res. 2013 Aug 20. [Epub ahead of print].
- [4]. Tachibana T et al., Pharm Res. 2010 Mar;27(3):442-6.
- [5]. Yang et al., Eur J Pharm Sci. 2007 Jul; 31(3-4):232-41
- [6]. Burt et al., Drug Metab Dispos. 2012 Sep; 40(9): 165-67

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