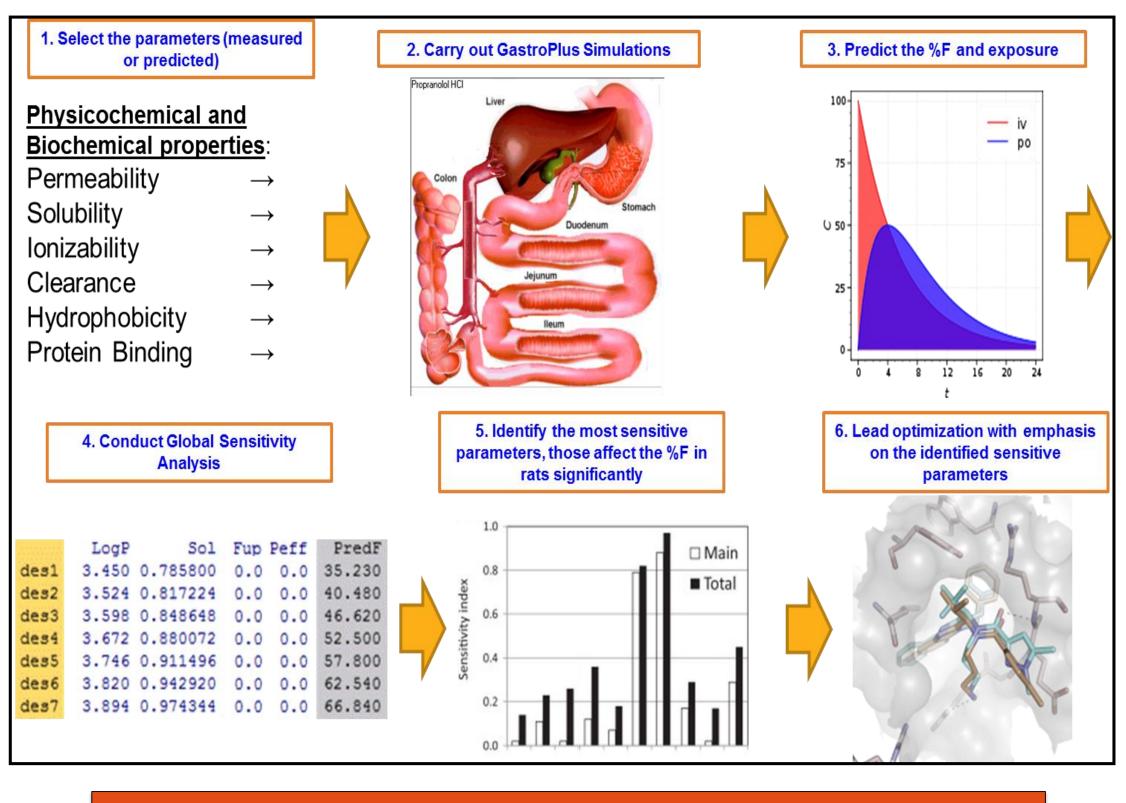
Predicting drug bioavailability using PBPK modeling and Global Sensitivity Analysis NOVARTIS to identify sensitive parameters

Pankaj R. Daga¹, Michael B. Bolger², Ian S. Haworth³, Robert D. Clark², and Eric Martin^{*1} ¹Novartis Institute of Biomedical Research, Emeryville, CA 94608, United States, ²Simulations Plus Inc., Lancaster, CA 93534, United States, ³Department of Pharmacology and Pharmaceutical Sciences, University of Southern California, Los Angeles, CA 90089, United States

Introduction

- ADME modeling in lead optimization typically includes only QSAR/QSPR predictions of physicochemical properties or simple allometric scaling to predict species variation.
- Many physicochemical properties might be modified to improve exposure. Prioritizing is difficult.
- Physiologically-Based Pharmacokinetic (PBPK) modeling, typically applied on individual compounds for clinical trials, gives more accurate and detailed mechanistic results.
- Inputs required for PBPK modeling are the very same properties, that med chemists intend to modify to improve bioavailability
- Predicting clearance is the challenge in modeling whole series, and that was solved with the help of local QSAR for an apparent intrinsic clearance
- Global Sensitivity Analysis (GSA) of PBPK models for whole chemical series in lead opt. could identify the most effective properties to improve drug exposure.

Approach



Conclusions

- > PBPK ADME simulations successfully adapted to lead series:
- Predicting clearance was solved with a local QSAR for "ideal" CL_{fit}
- In 3 cases, >80% of %F predictions within 2X all in silico
- Good local QSAR for CL_{fit} with only 15-20 in vivo %F's

Global Sensitivity Analysis finds key properties:

- Methods developed for GSA of chemical series
- Unique advice for each series:
- DPP4 &HSD1 only CL_{int};
- Kinase: CL_{int} + logD, Sw and RBP
- Specific advice for each compound within series

DPP-4 Inhibitors (Merck)

- ✓ <u>49 Inhibitors</u>
- ✓ <u>RAT in vivo data</u> : %F, CLp
- ✓ <u>Physicochem prop & *in vitro* data</u> : --

11β-HSD1 Inhibitors (AZ)

- ✓ 81 Inhibitors
- ✓ <u>RAT *in vivo* data</u> : %F, CLp
- ✓ <u>Physicochem prop & *in vitro* data</u>: CL_{int(hep)}

Kinase-X inhibitors (In-House)

✓ 63 Compounds

- ✓ <u>RAT in vivo data</u> : %F, CLp, AUC, Cmax
- <u>Physicochem prop & in vitro data</u> : Sol, Perm, PPB, CL_{int(mic)}

Series can be modeled from as few as 15 rat studies

		Global	Local ~15	Local ~35	Loca
	Kinase-X 63 cpd	6% 13 % 16% 2.0 66 %	10 % 8 % 14% 2.1 (18) 68 %	18 % (1.5 (37) 79 %	14%
	HSD1 81 cpd	37 % 30 % 2.9 27%	15 % 9 % 2.6 12 % (18) 64 %	12 % 15 % 1.8 (32) 69 %	16 %
	DPP-4 48 cpd		12 % 8 % 2.0 (15) 80 %	10 % 14 % (1.9 (30) 76 %	10

