



UPPSALA  
UNIVERSITET

# A Population PK Based Model-Integrated BE Platform

Xiaomei Chen

Henrik Bjugård Nyberg

Piyanan Assawasuwannakit

Yevgen Ryznik

Mats O. Karlsson

Andrew C. Hooker, Ph.D.

Professor of Pharmacometrics

Dept. of Pharmacy, Uppsala University

Uppsala, Sweden



# Research projects on utilizing models for bioequivalence assessment at UU in collaboration with FDA

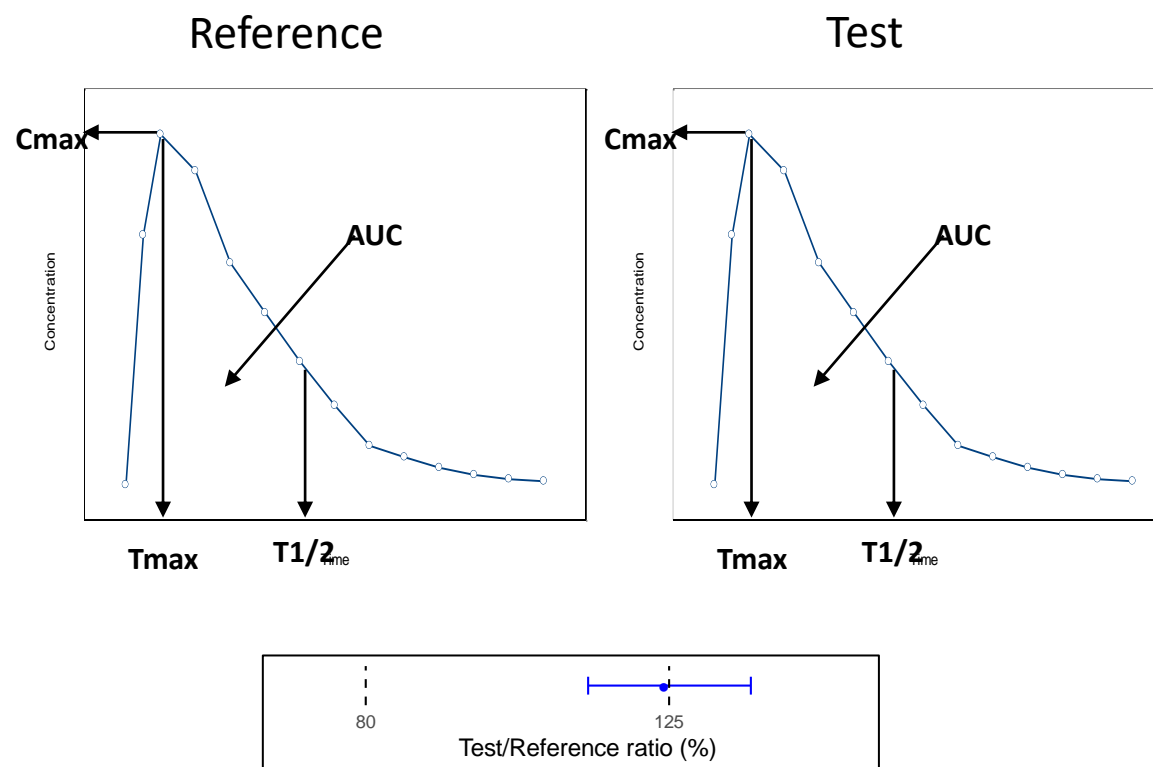
## Funding from Office of Generic Drugs, FDA

- “Development and comparison of model-based bioequivalence analysis methods on sparse data”
- “Model-informed and model-integrated bioequivalence analyses for long-acting injectable products”
- “Model-integrated strategies for bioequivalence evaluation of drugs with high variability and/or long half-life.”

# Standard bioequivalence (BE) studies

- 2x2 crossover designs
- NCA based summary PK metrics (e.g., AUC, C<sub>max</sub>)

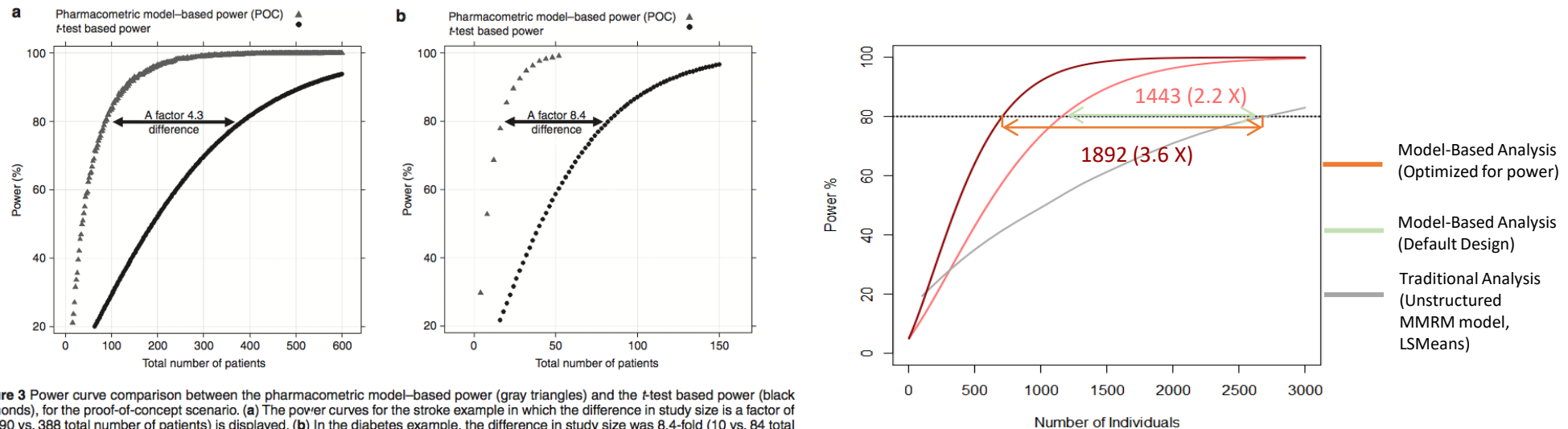
2x2 crossover designs



# Problems for standard BE studies

- NCA analysis not appropriate
- Sparse data
- Drugs with long half-life (e.g. LAI)
  - Long-term BE trial
  - Crossover steady-state studies may be needed in patients
- Highly variable drugs (HVD)
  - BE design needs 3- or 4-way crossover study
  - Estimation of between occasion variability can be biased/imprecise
- Steady-state BE studies
  - Methods for establishing steady state can be inaccurate
- Other
  - Designs can be inefficient
  - Special formulations, e.g. local drug product needs clinical endpoint BE study
  - ...

# Pharmacometric approaches will typically have **higher power** than standard methods

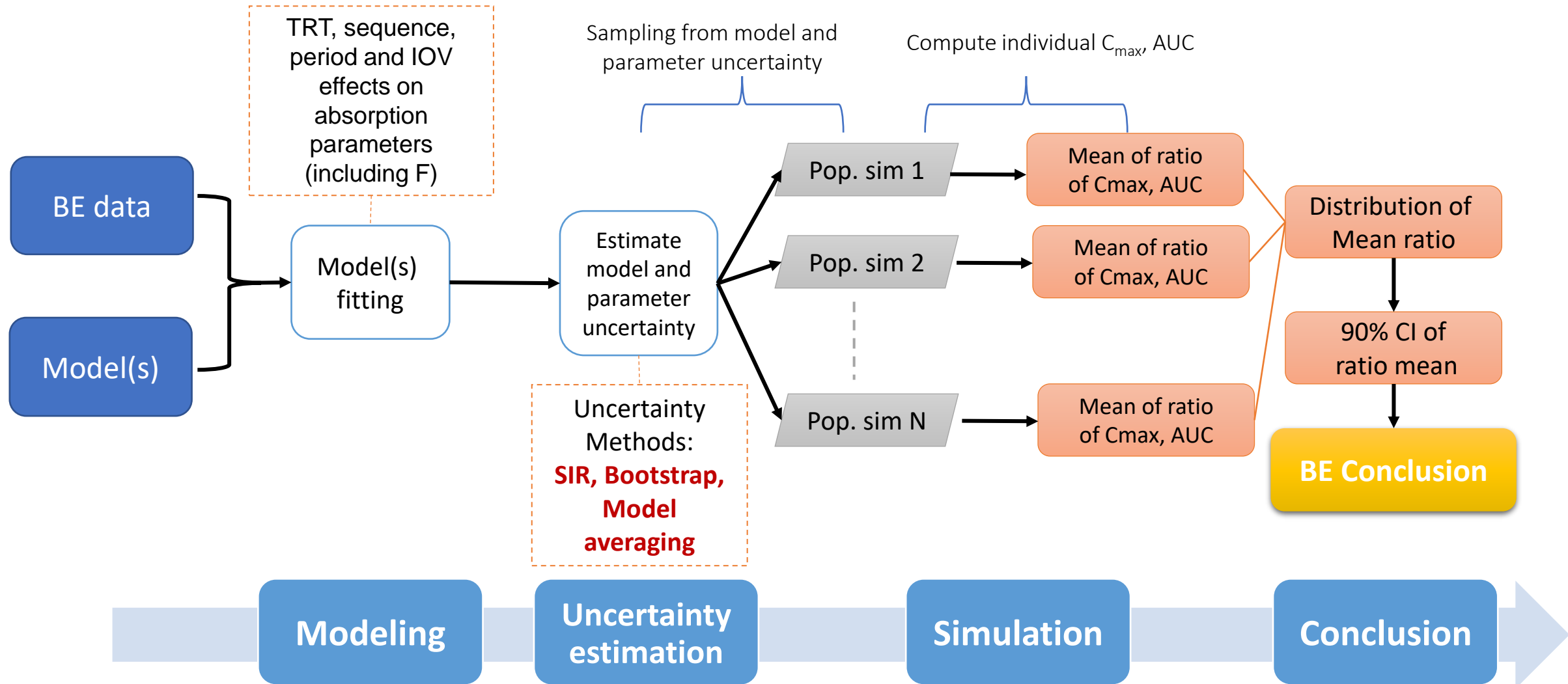


**Figure 3** Power curve comparison between the pharmacometric model-based power (gray triangles) and the t-test based power (black diamonds), for the proof-of-concept scenario. (a) The power curves for the stroke example in which the difference in study size is a factor of 4.3 (90 vs. 388 total number of patients) is displayed. (b) In the diabetes example, the difference in study size was 8.4-fold (10 vs. 84 total number of patients) in favor of the pharmacometric approach.

[Karlsson et al., CPT:PSP, 2013](#)

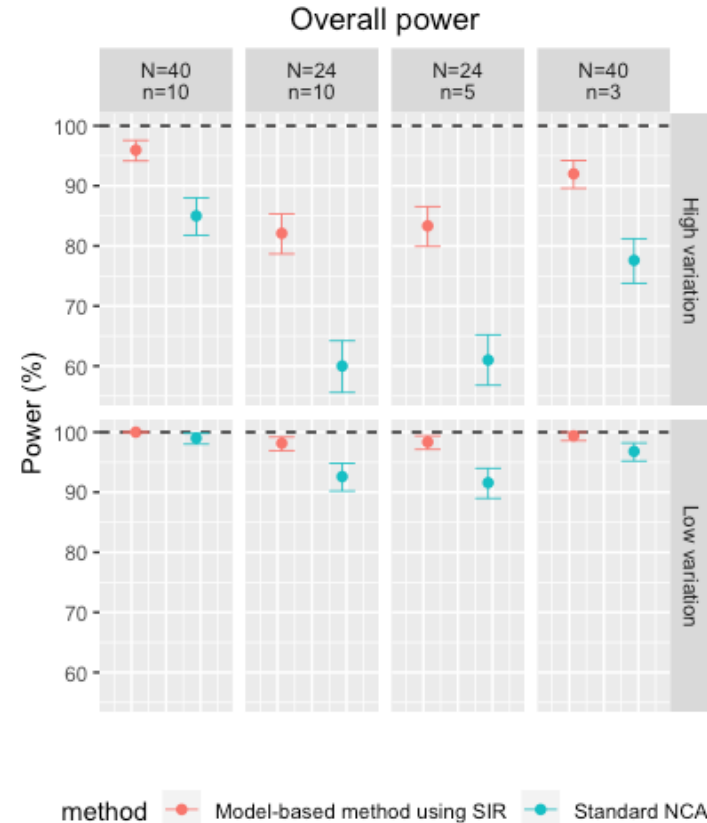
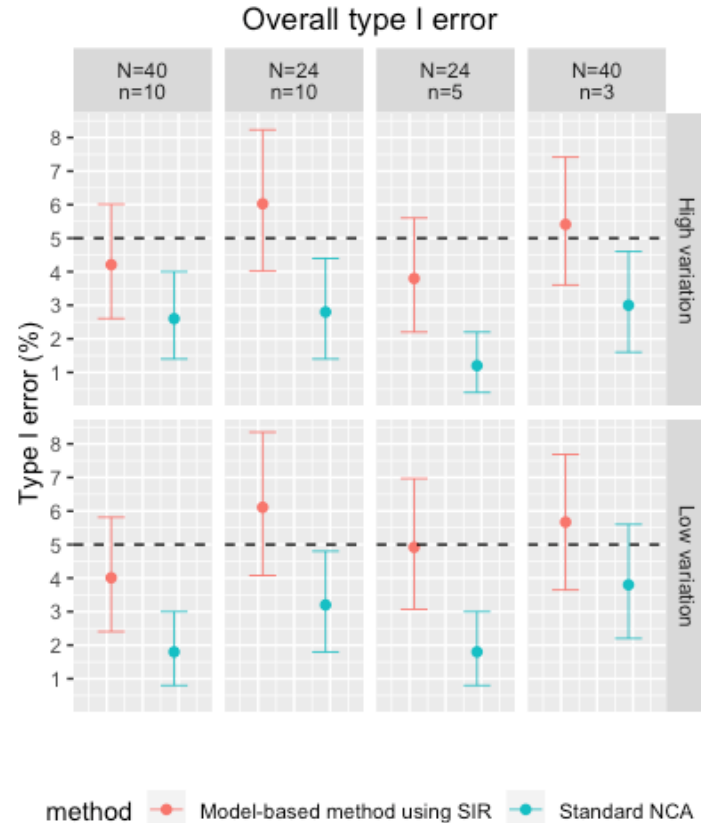
- Hooker *et al.*, ACOP, 2011
- [Ueckert et al., JPKPD, 2013](#)

# Our developed model-integrated BE method



- ACOP 2019, Andrew Hooker, Development and comparison of model-based bioequivalence analysis methods on sparse data.
- ACOP 2019, Xiaomei Chen, Model-based bioequivalence evaluation for ophthalmic products using model averaging approaches.
- ACCP 2019, Mats Karlsson, Development of model-informed bioequivalence evaluation strategies for long-acting injectable products (LAI).

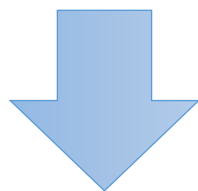
Type I error is controlled for this model-integrated BE method and power is higher (especially with high variation and sparser data)



N = # of individuals, n = # of observations


# Situations where no single PK model may be appropriate for BE analysis

- Identifiability issues
- No prior model




Model Averaging

Avoid estimation bias and overestimation of precision

J Pharmacokinet Pharmacodyn (2017) 44:581–597  
DOI 10.1007/s10928-017-9550-0 

ORIGINAL PAPER


**Model selection and averaging of nonlinear mixed-effect models for robust phase III dose selection**


Yasunori Aoki<sup>1,2</sup>  · Daniel Röshammar<sup>3,4</sup> · Bengt Hamrén<sup>3</sup> · Andrew C. Hooker<sup>1</sup>

Received: 30 June 2016 | Revised: 22 May 2017 | Accepted: 11 June 2017  
DOI: 10.1002/sim.7395

RESEARCH ARTICLE WILEY **Statistics**  
in **Medicine**

**Model averaging for robust assessment of QT prolongation by concentration-response analysis**

A.G. Dosne<sup>1</sup>  | M. Bergstrand<sup>1</sup> | M.O. Karlsson<sup>1</sup> | D. Renard<sup>2</sup> | G. Heimann<sup>2</sup>

*The AAPS Journal* (2018) 20: 56  
DOI: 10.1208/s12248-018-0205-x 

*Research Article*

**Comparison of Model Averaging and Model Selection in Dose Finding Trials Analyzed by Nonlinear Mixed Effect Models**

Simon Buatois,<sup>1,2,3,5</sup> Sebastian Ueckert,<sup>4</sup> Nicolas Frey,<sup>1</sup> Sylvie Retout,<sup>1,2</sup> and France Mentré<sup>3</sup>



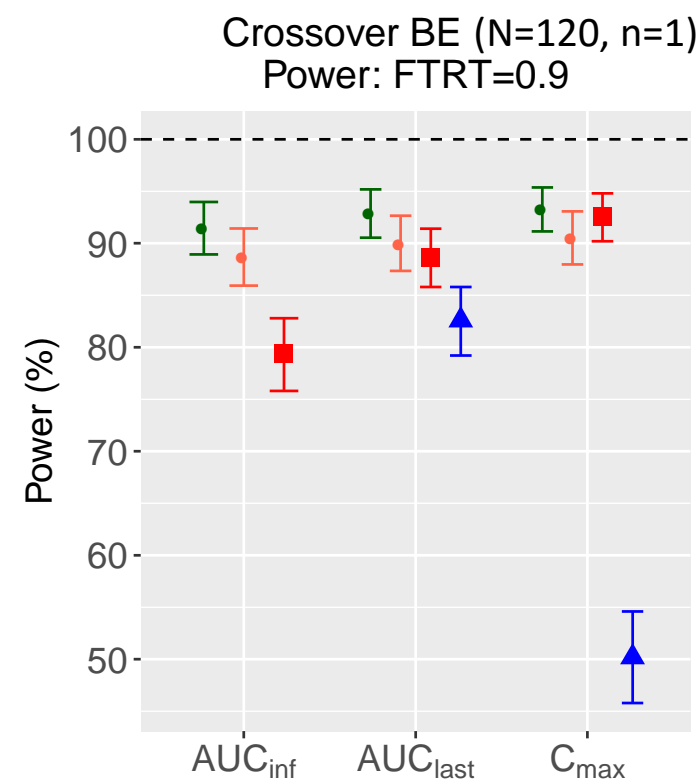
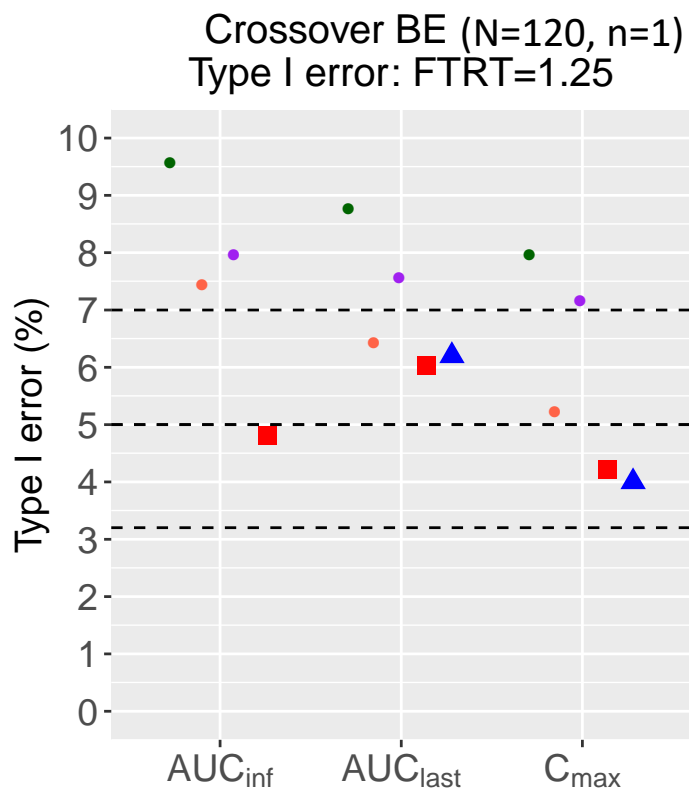
# Model averaging used for cross-over BE study of ophthalmic drugs

## Bootstrap model selection

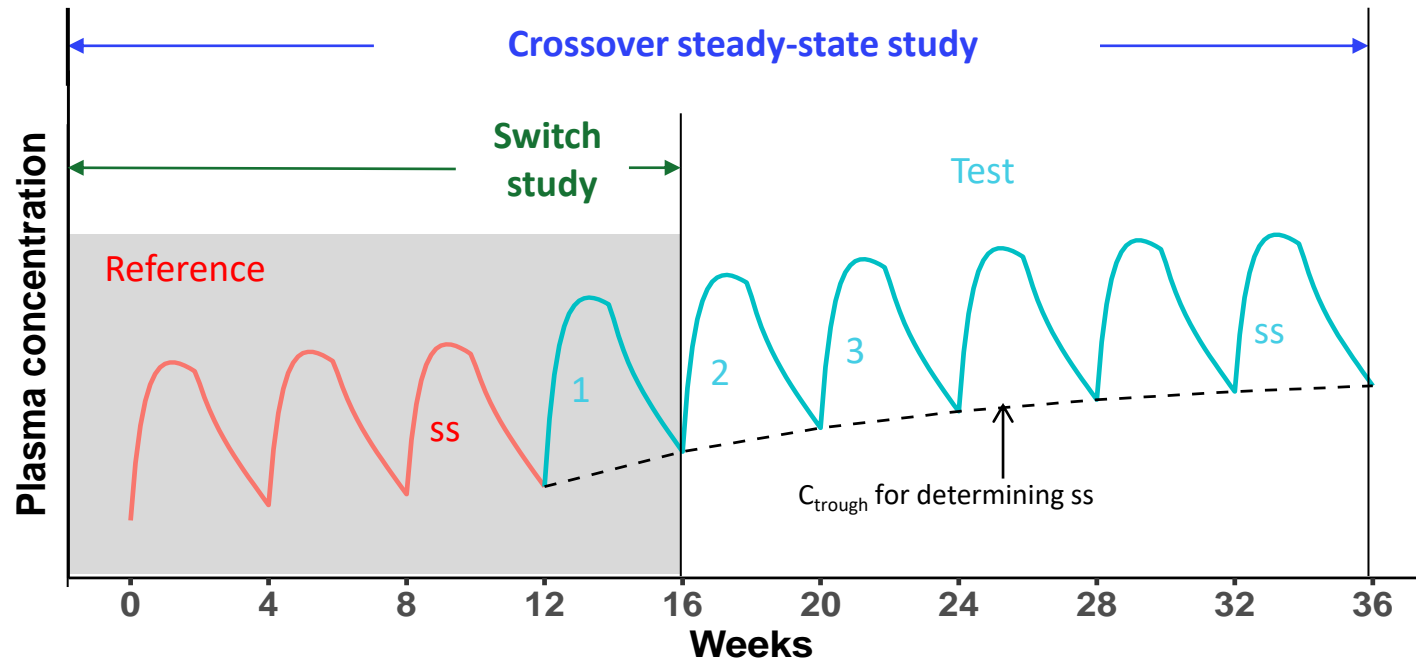
- controls type 1 error for all tests
- Allows for  $AUC_{inf}$  calculations
- Much higher power

method

- Conventional MA-cov matrix
- Conventional MA-SIR
- Conventional MA-bootstrap
- Bootstrap model selection
- Bootstrap NCA



# One potential solution to reduce BE study duration for LAI: use a switch study instead of crossover steady-state



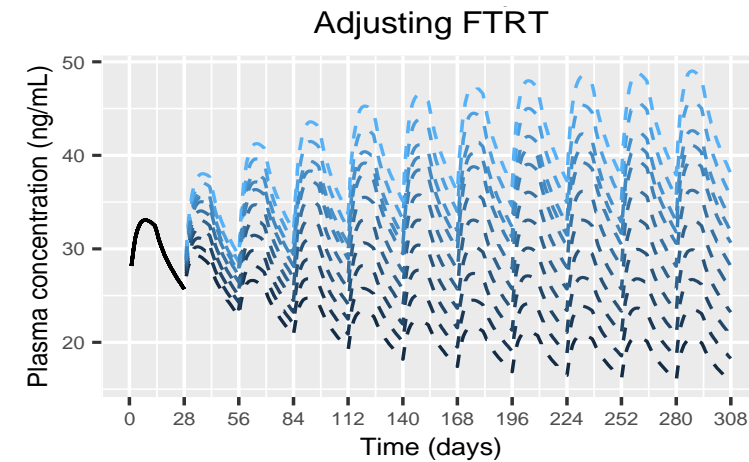
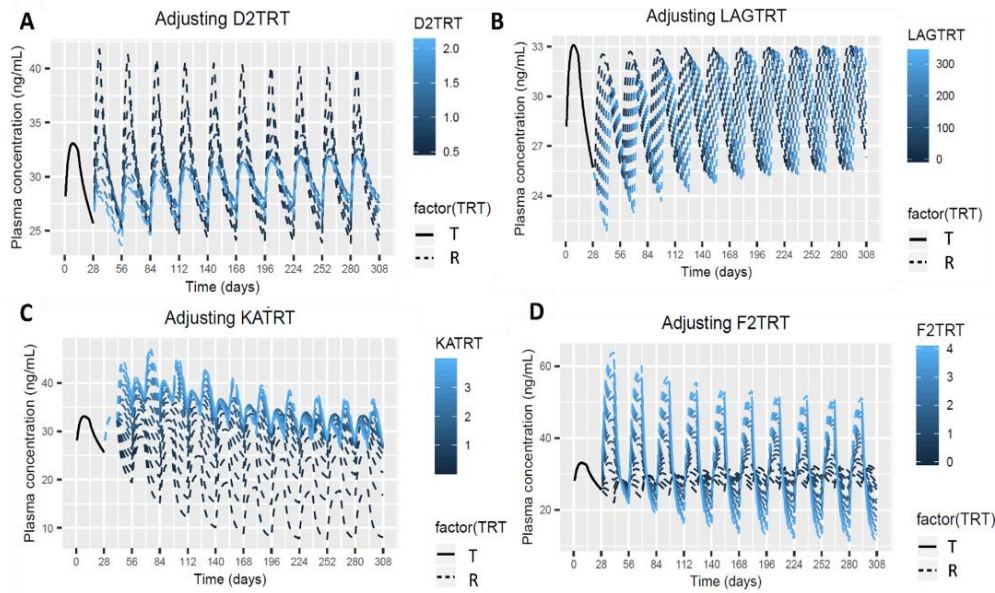
**Model-based approach:** allows you to separate the superposition of test from reference in first period after switch.

**Model-assisted approach:** Use models to simulate studies to determine new BE limits.

**Optimal design approaches** for better BE study design

For more information: <https://complexgenerics.org/LAI2021/>

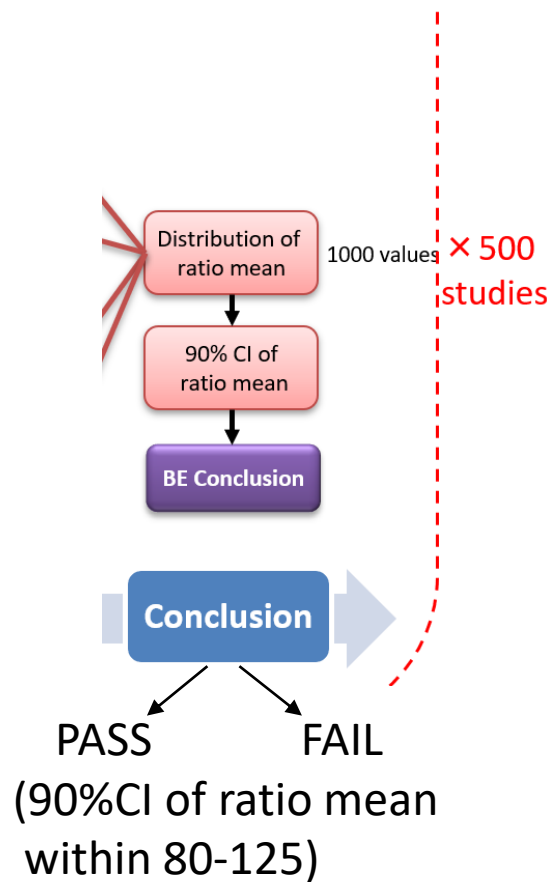
# Simulation of a typical individual



Switch study more sensitive to changes in absorption rate differences

Switch study LESS sensitive to changes in absorption extent differences

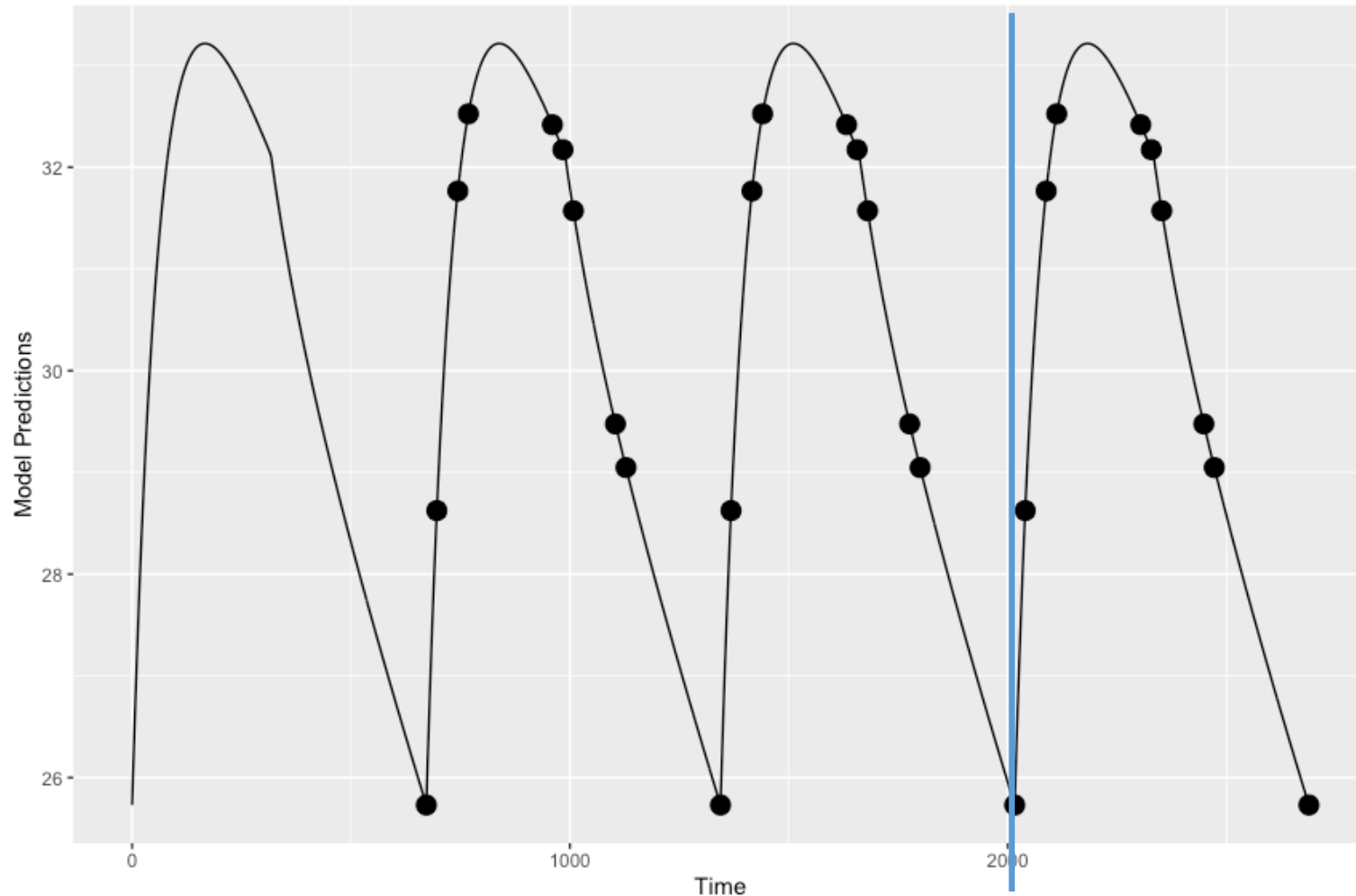
# Power and type I error for model integrated-approach (worst case scenario)



Study design	PK metric	FTRT=1.1,0.9	FTRT=1.25
		N for 80% Power	%Type I error (*95%CI)
Switch	AUC	600	4.66 (3.10-6.38)
	Cmax		4.83 (3.10-6.72)
Crossover SS	AUC	100	2.59 (1.38-3.97)
	Cmax		2.93 (1.72-4.31)

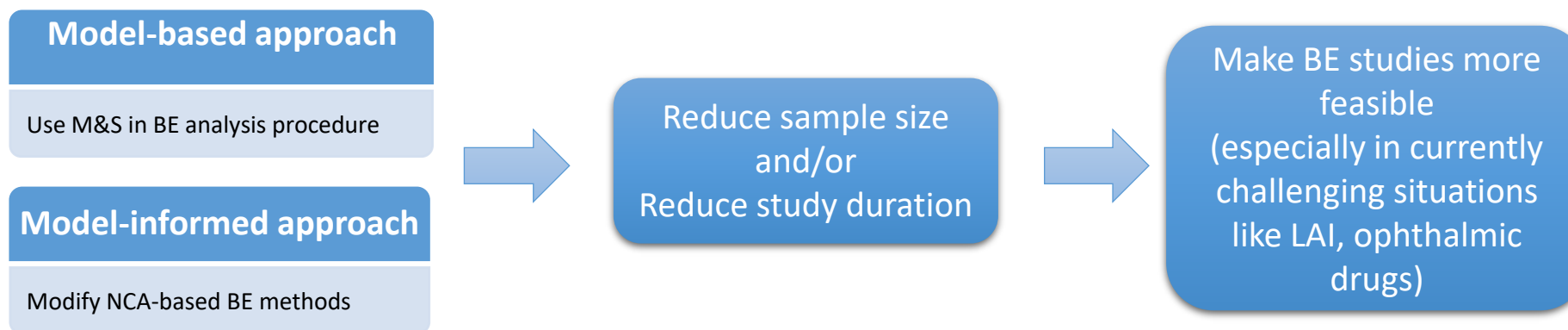
\*95%CI is the 2.5% and 97.5% quantile of the binomial distribution

# Model-integrated design optimization



- Model-integrated BE switch study
- Optimal design (OD) for placement of sample times
- OD based Power evaluation: 10% reduction in number of individuals
- Differences confirmed with SSE based power calculations

# Summary of methods



# Practical implementation – predefining models?

- A model (or a set of models)
  - Previous model based on reference product
  - Potentially build a model in a pre-defined way (current work on automated PK model building ongoing), based on prior/preliminary studies or BE study data (with caution).
- Model must then be adjusted
  - TRT, sequence, period and IOV effects on absorption parameters (including  $F_{rel}$ )

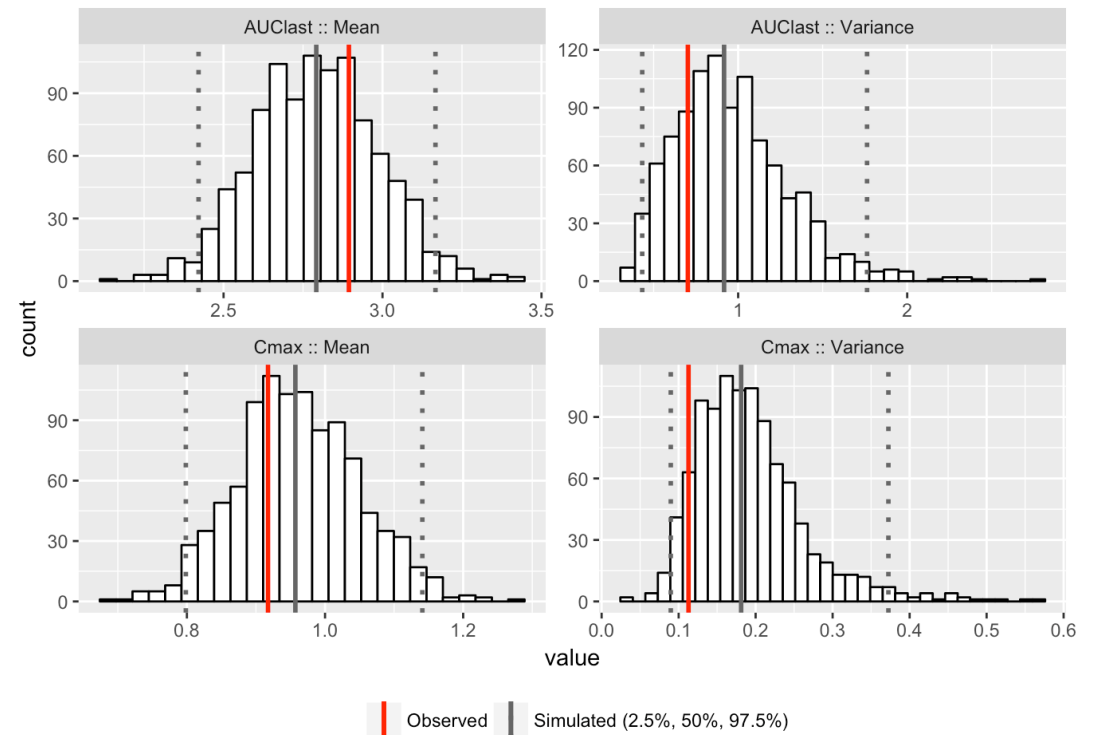
# Availability of models in LAI

- 33 LAI products approved by FDA
- 27 published models for 17 of those products
- Many based on multiple studies from drug development (many subjects with multiple study designs)
  - May not be practically identifiable for a model-integrated BE study analysis



# Model qualification

- Should be identifiable given the study design
  - test using optimal design software, like PopED, <https://andrewhooker.github.io/PopED/>.
- Non-compartmental analysis posterior predictive check of reference data.
  - NCAPPC: <https://cran.r-project.org/package=ncappc>



# Benefits of model sharing

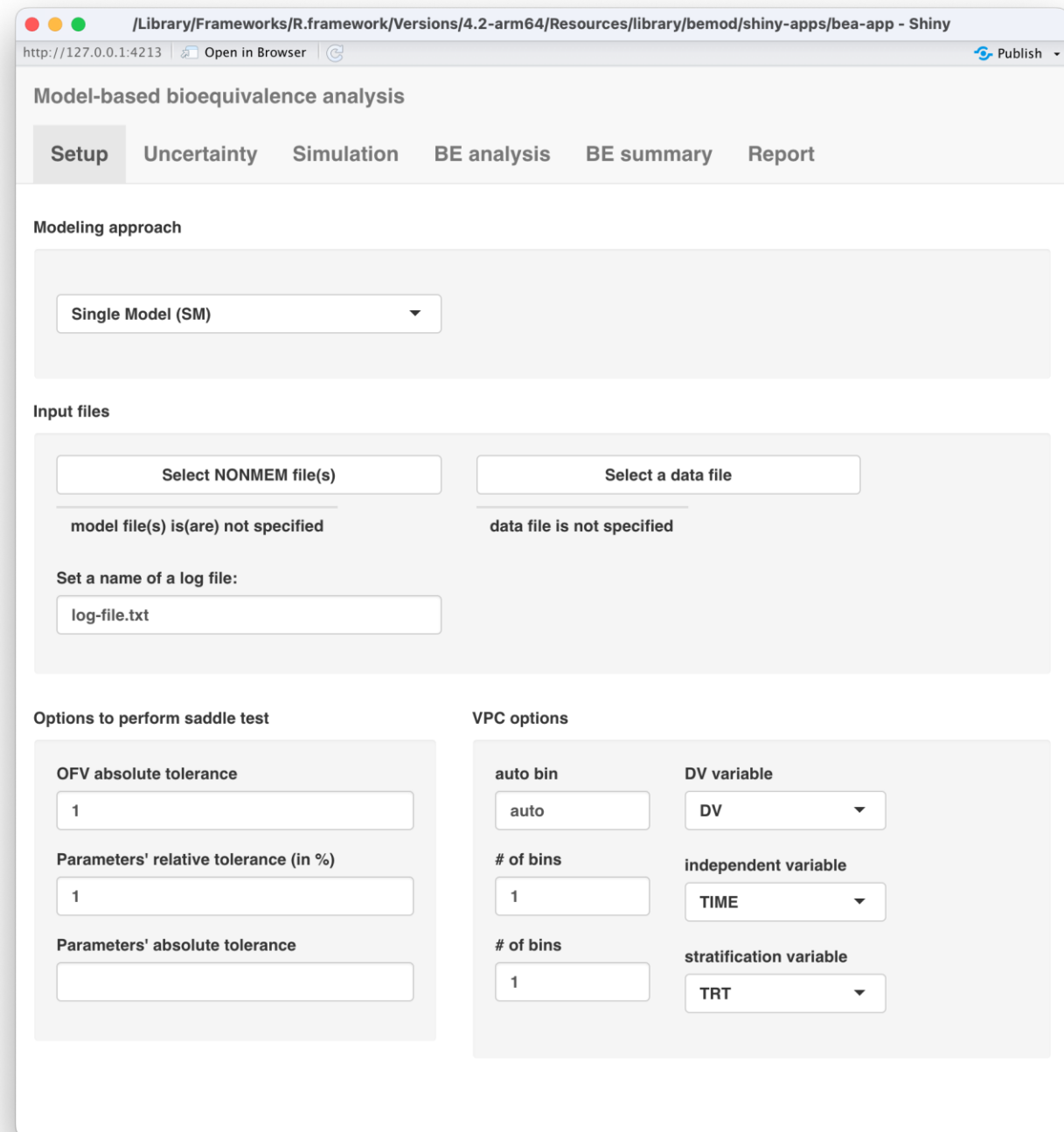
- Model qualification can be done one time and shared for specific types of designs and analyses
- Improved reproducibility and validation of scientific results
- Knowledge propagation: faster development of new science
- Explicit evaluation and verification of models
- Model standardization

# Where would we need a model master file (MMF) and how would it work?

- Acts as a model repository
  - Qualification for specific purposes
    - What was presented in a paper or submission
    - Other purposes (BE)
  - Different levels of qualification
    - Scientific panel approval
    - FDA approval
- Private MMF
  - Not published or available from submission documents
  - Analyses are performed with the model hidden from the user
- Issues
  - Will private MMFs limit scientific discourse / innovation?
  - Investment needed (development/maintenance)
  - IP issues
  - Different modeling languages, file formats, ... How to actually use the information
- Example of an APP for model-integrated BE analysis of a specific LAI (PP1M) on next slides

# R package *bemod*

- Included methods
  - Model-integrated methods
    - single model-based BE method
    - model averaging
    - bootstrap model selection
  - Standard NCA methods
    - Standard linear regression approach
    - Bootstrap NCA
- Ways to run bemod
  - using R scripts
  - using web-based platform created by R shiny
- R package *bemodlai*
  - Depends on *bemod* to perform model-integrated BE methods for LAI
  - PPIM (Paliperidone 1 month) models for model-integrated BE analysis implemented in package
- Available on CRAN shortly



The screenshot shows the Bemod Shiny application interface. The browser address bar indicates the path: /Library/Frameworks/R.framework/Versions/4.2-arm64/Resources/library/bemod/shiny-apps/bea-app - Shiny. The URL is http://127.0.0.1:4213. The application title is "Model-based bioequivalence analysis". The navigation tabs are Setup, Uncertainty, Simulation, BE analysis, BE summary, and Report. The "Setup" tab is active.

**Modeling approach**

Single Model (SM)

**Input files**

Select NONMEM file(s)      Select a data file

model file(s) is(are) not specified      data file is not specified

Set a name of a log file:

log-file.txt

**Options to perform saddle test**

OFV absolute tolerance: 1

Parameters' relative tolerance (in %): 1

Parameters' absolute tolerance:

**VPC options**

auto bin: auto      DV variable: DV

# of bins: 1      independent variable: TIME

# of bins: 1      stratification variable: TRT

# Summary

- Model sharing can increase the quality of scientific work
- For model-integrated BE analysis, a way to share and qualify models for specific products and situations would aid in the practical implementation of the approach

# Acknowledgements

## Funding from FDA

Contracts: HHSF223201710015C, 75F40119C10018

## Colleagues at FDA:

Liang Zhao

Lanyan (Lucy) Fang

Satish Sharan

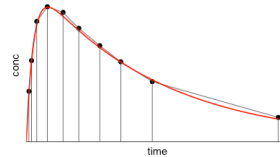
Mark Donnelly

... Many more!

## PM group, Uppsala University

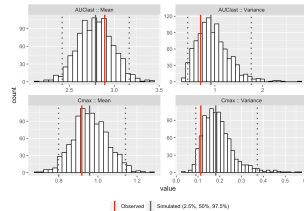
# Software

bemod  
bemodlai



- Model based BE testing
- To be released on CRAN

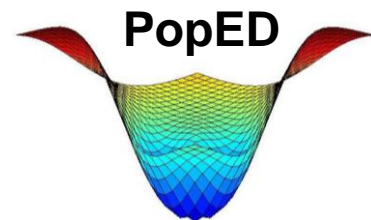
ncappc



- NCA Calculation and Population PK Model Diagnosis
- <https://github.com/UUPharmacometrics/ncappc>



- SIR
- Bootstrap
- <https://uupharmacometrics.github.io/PsN/>



- Optimal experimental design software
- <https://andrewhooker.github.io/PopED/>