

A Python/Numpy-based package to support model discrimination and identification

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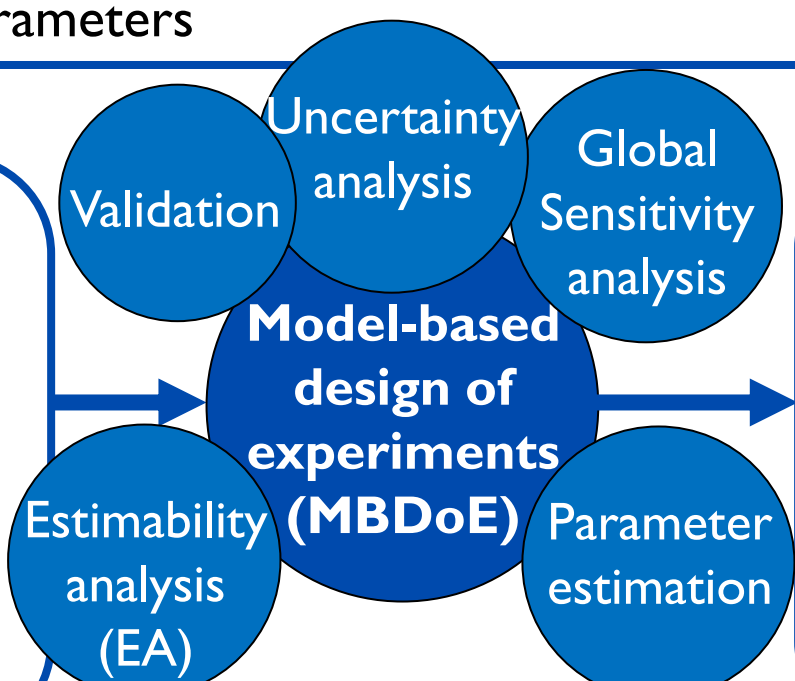


1. INTRODUCTION AND MOTIVATION

- Mechanistic models are cornerstones of optimisation, control, and scale-up in PSE.
- Achieving high fidelity in these structures is challenging during the model identification step. This challenge depends on:
 - Informed selection of the most representative model
 - Precise estimation of model parameters



- Experimental data is often expensive and limited.
- Mechanistic models are often affected by:
 - structural ambiguities
 - parameter correlations



- Model-Based Design of Experiment to maximise information for:
 - Model discrimination [1]
 - Parameter precision (MDDoE-PP) [1]

ISSUE

- MDDoE applications have been limited and mostly in the academic sector.
- The lack of comprehensive and user-friendly packages is one reason hindering its widespread usage. No existing package (e.g. *PYOMO.DOE* [2]) offers a **comprehensive** framework that:
 - Integrates the essential techniques for model discrimination and parameter calibration;
 - Incorporates physical constraints into the design space; and
 - Remains modular and easily interfaces with external simulators.



OBJECTIVE

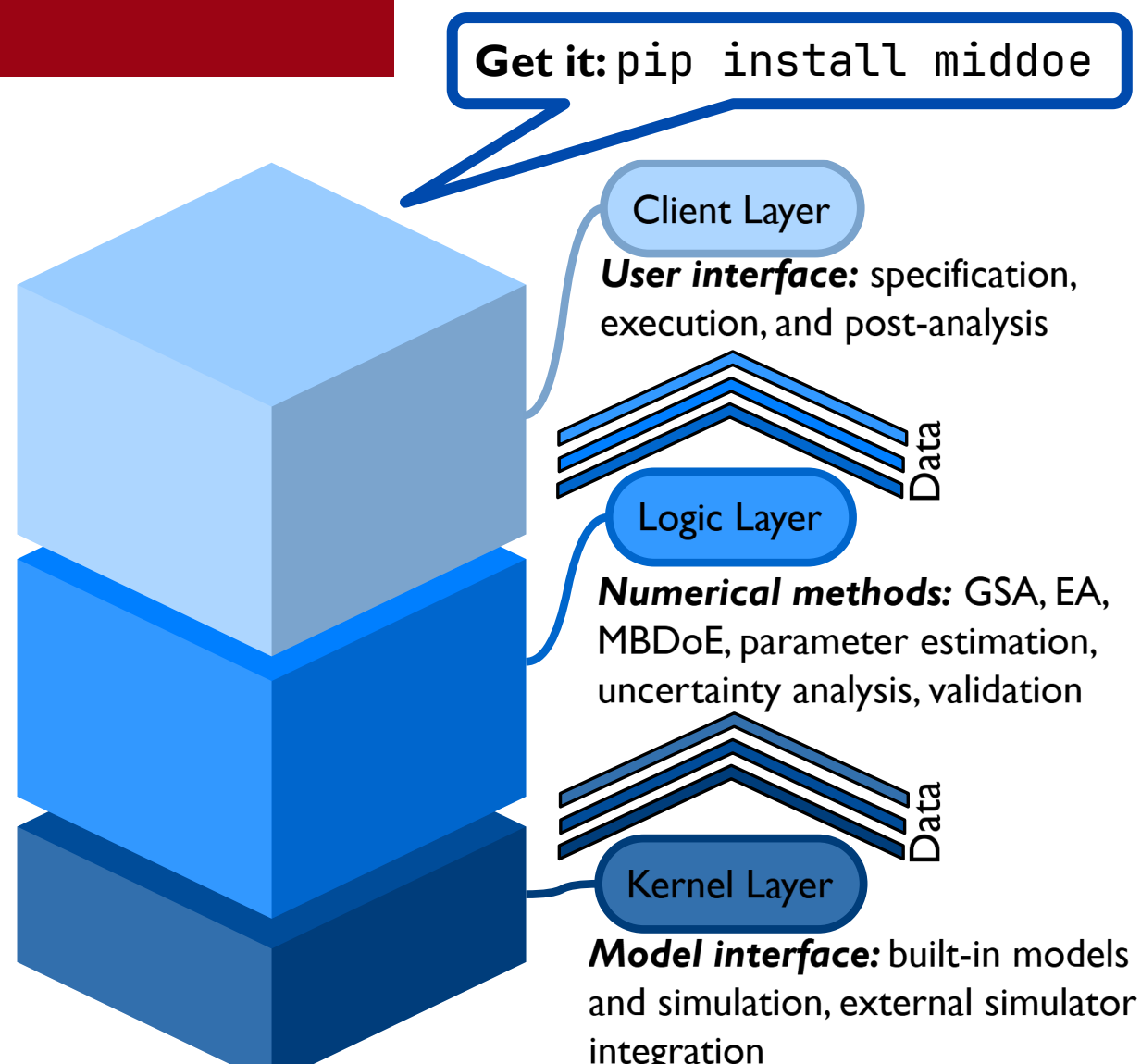
Developing **MDDoE** – Model-(based) Identification, Discrimination, and Design of Experiments – as a comprehensive, user-friendly, and modular open-source tool in *Python* to bridge the gaps in MDDoE digitalisation



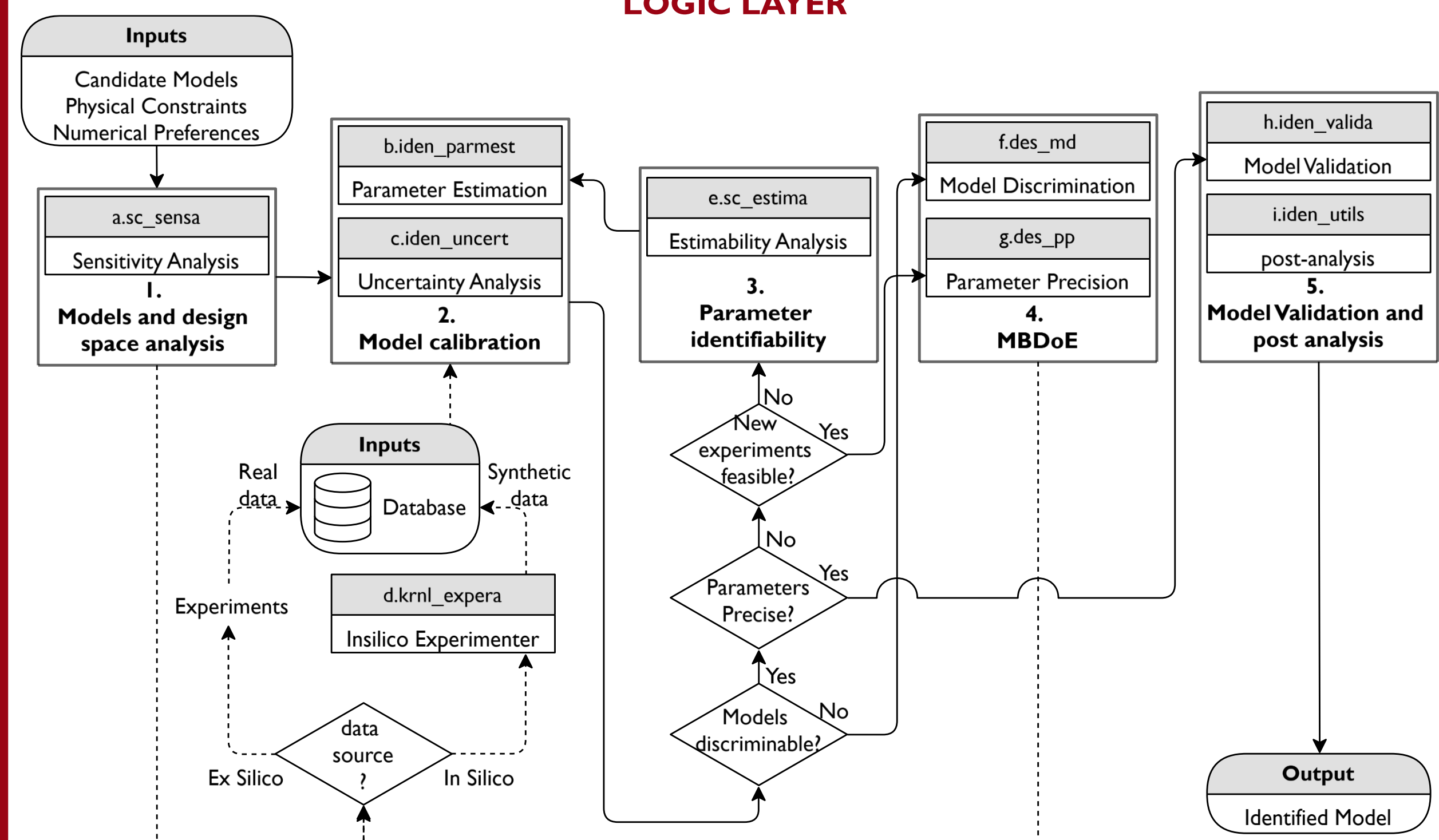
2. MDDoE ARCHITECTURE

- MDDoE** is developed in 3 layers
 - Kernel layer** includes a built-in DAE simulator for stiff/non-stiff systems and custom black-box interfacing.
 - Client layer** is developed for experimenters to run various tasks easily, excluding intensive programming.
 - Logic layer** provides MDDoE and various numerical capabilities to support it.

The **Logic layer** includes supportive techniques for MDDoE, including **GSA-Sobol** and **Estimability Analysis (EA)** [3], used to investigate the parameter space and select unidentifiable parameters



LOGIC LAYER



- MDDoE in **MDDoE** includes **model discrimination** and **parameter precision**, supporting different optimal design objectives.
 - It is capable of handling **non-convexities** in the optimisation core
 - It can embed **physical constraints** into the design space, such as:
 - Control Vector Parametrisations (**CVPs**) for linear and piecewise-constant profiles;
 - Enforced **increasing, decreasing, or relaxed** CVPs;
 - Forced **control/uncontrollable** time spans; and
 - Synchronisation of **sampling** across multiple measurements.

3. CASE STUDY

PROCESS AND SCENARIOS

- An insilico model calibration of Monod model for a semi-batch fermentation reactor in 2 different scenarios:

- Sc1** Experimental data available (2 batches); new experiments cannot be performed
- Sc2** No data available; 4 new experiments can be designed

FORMULATION

$$\frac{\partial y_1(t)}{\partial t} = (r - u_1(t) - \theta_4) \cdot y_1(t)$$

$$\frac{\partial y_2(t)}{\partial t} = -\frac{r \cdot y_1(t)}{\theta_3} \cdot u_1(t)(u_2 - y_2)$$

$$r = \left(\frac{\theta_1 \cdot x_2}{\theta_2 + x_2} \right) \cdot \exp\left(-\frac{x_2}{\theta_5}\right)$$

DESIGN SPACE

| Variable | Range | CVP | Definition |
|-----------|------------|----------|---|
| $y_{1,0}$ | 1 – 10 | — | Biomass initial concentrations |
| $y_{2,0}$ | 1 – 10 | — | Substrate initial concentrations |
| u_1 | 0.05 – 0.2 | Constant | Time-variant dilution rate |
| u_2 | 5 – 35 | Constant | Time-variant feed substrate concentration |

TRUE PARAMETERS

| Parameter | value | Definition |
|------------|-------|-------------------------------|
| θ_1 | 0.31 | Maximum specific growth rate |
| θ_2 | 0.11 | Michaelis constant |
| θ_3 | 0.65 | Yield coefficient |
| θ_4 | 0.25 | Biomass loss rate |
| θ_5 | 5.00 | Substrate inhibition constant |

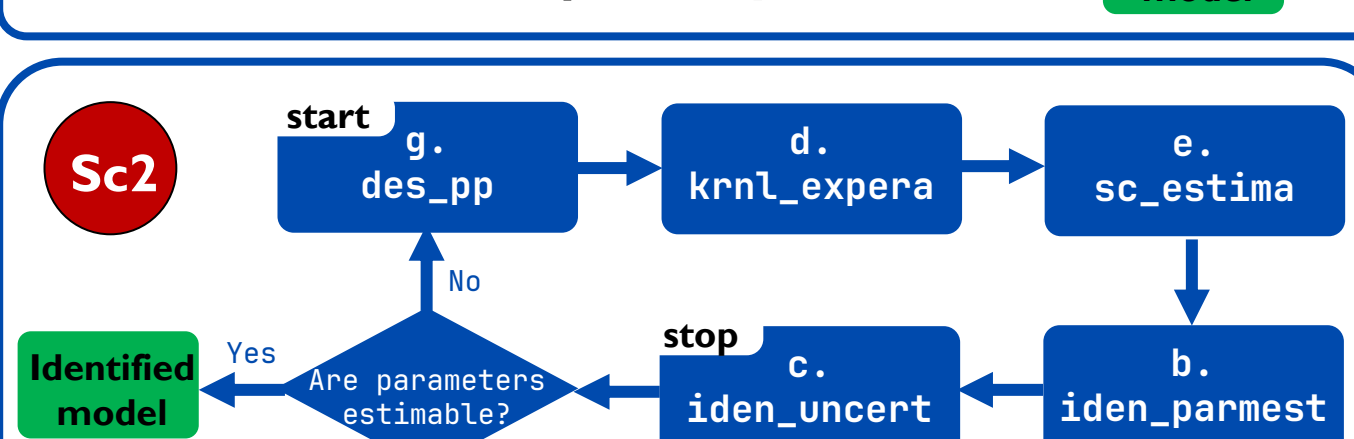
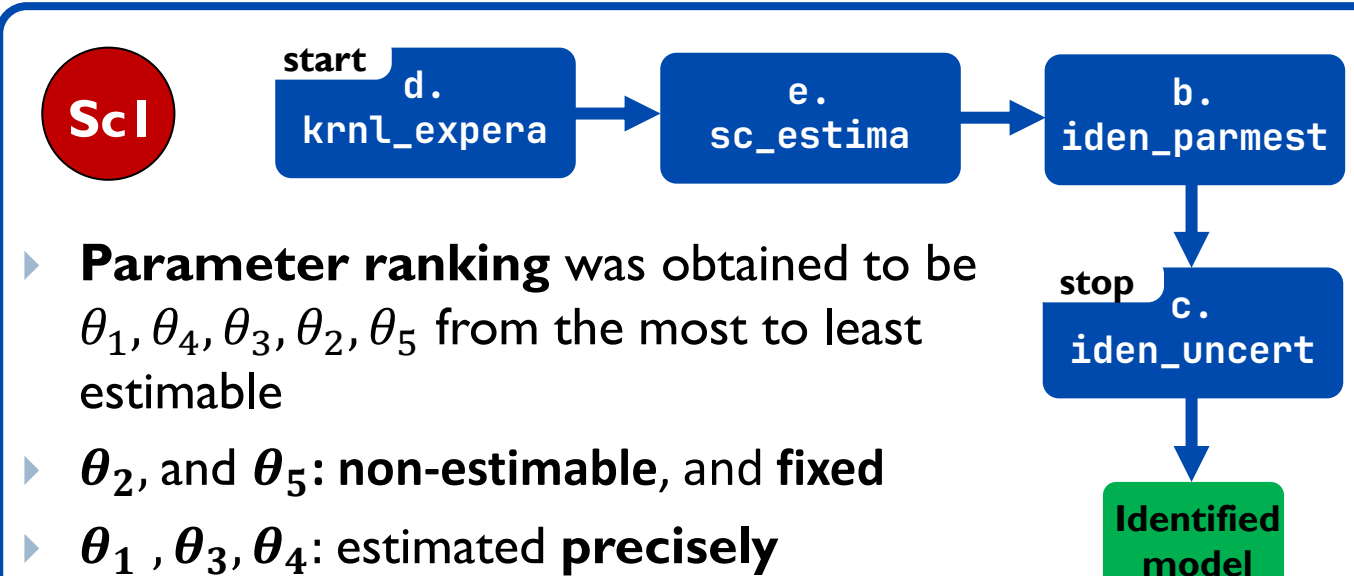
DESIGN CONSTRAINTS

- CVPs have 5 steps, and u_2 is forced to be decreasing.
- Minimum switching/sampling point intervals are 0.5 h.
- Minimum signal perturbation for u_1 , and u_2 are 0.01, and 5.

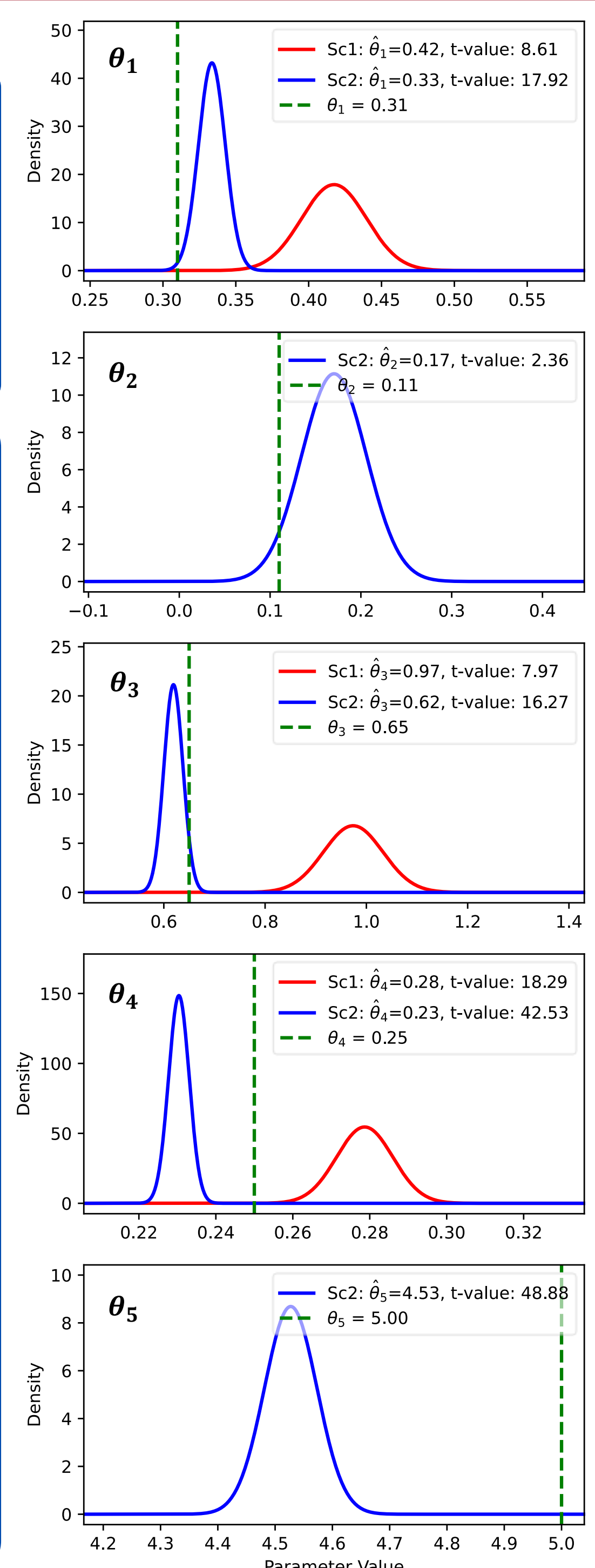
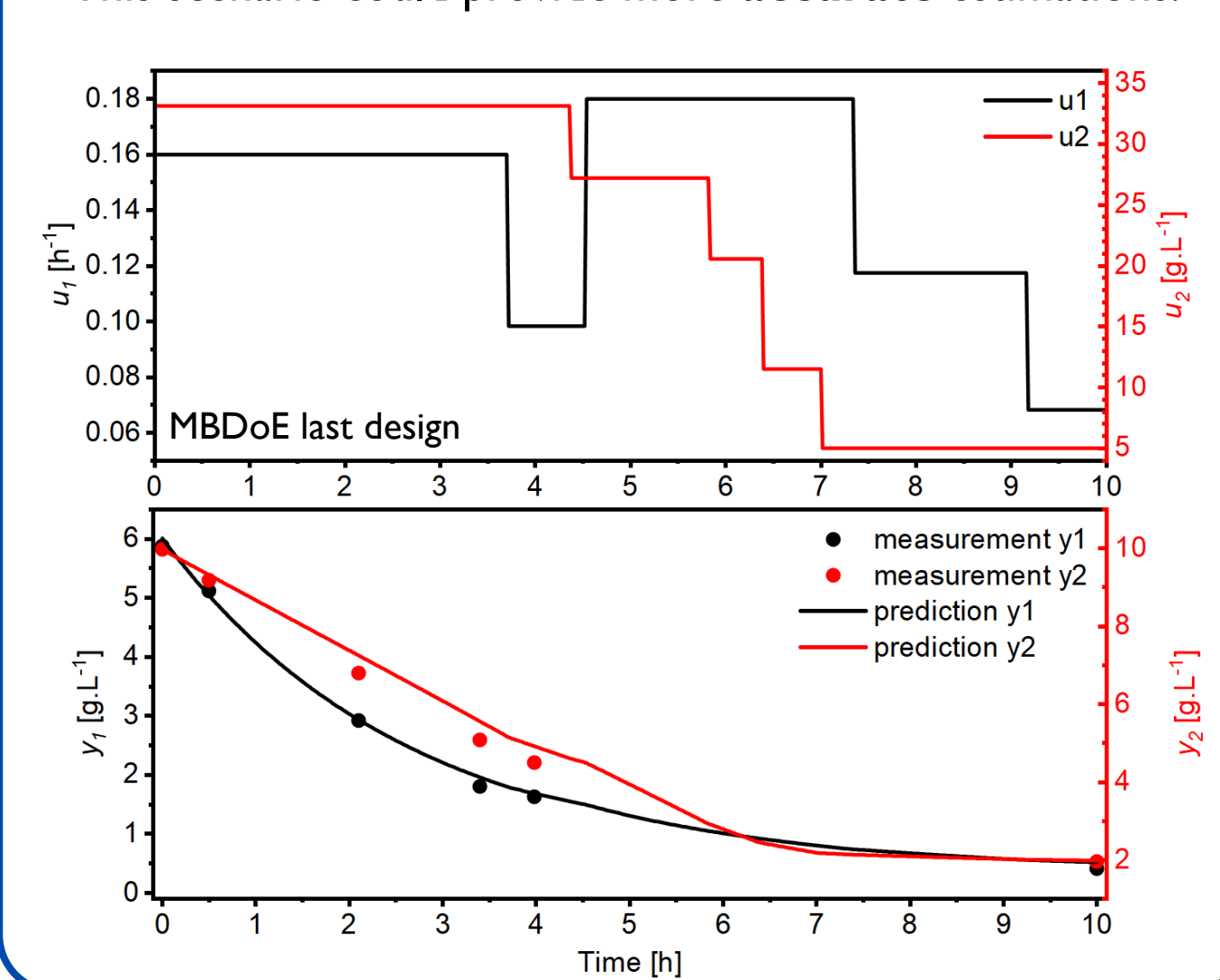
INSILICO EXPERIMENTS

- 6 sampling points per batch
- 10 h process time
- 5% normally distributed relative noise

4. RESULTS



- 4 MDDoE-PP designs were sequentially executed.
- After each design, **EA** identified the estimable parameters.
- Following the 1st experiment, **only** θ_4 was deemed estimable.
- As new experiments were added, more parameters became estimable, and by the 4th experiment, **all** were **precisely** estimated.
- This scenario could provide more **accurate** estimations.



5. CONCLUSIONS

- MDDoE** is a comprehensive *Python* library to accelerate model identification.
- It provides essential steps to support essential numerical techniques by investigating model structure and design space.
- Modular structure enables easy interfacing with external simulators, or using built-in solvers.

6. ACKNOWLEDGEMENT

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7. REFERENCES

- [1] Asprey, S. P. & Macchietto, S. Statistical tools for optimal dynamic model building. *Comput Chem Eng* 24, (2000).
- [2] Wang, J. & Dowling, A. W. Pyomo.DOE: An open-source package for model-based design of experiments in Python. *AIChE Journal* 68, (2022).
- [3] Moshiratabrizi, I., Abdi, K., McMullen, J. P., Wyvratt, B. M. & McAuley, K. B. Parameter estimation and estimability analysis in pharmaceutical models with uncertain inputs. *AIChE Journal* (2023).