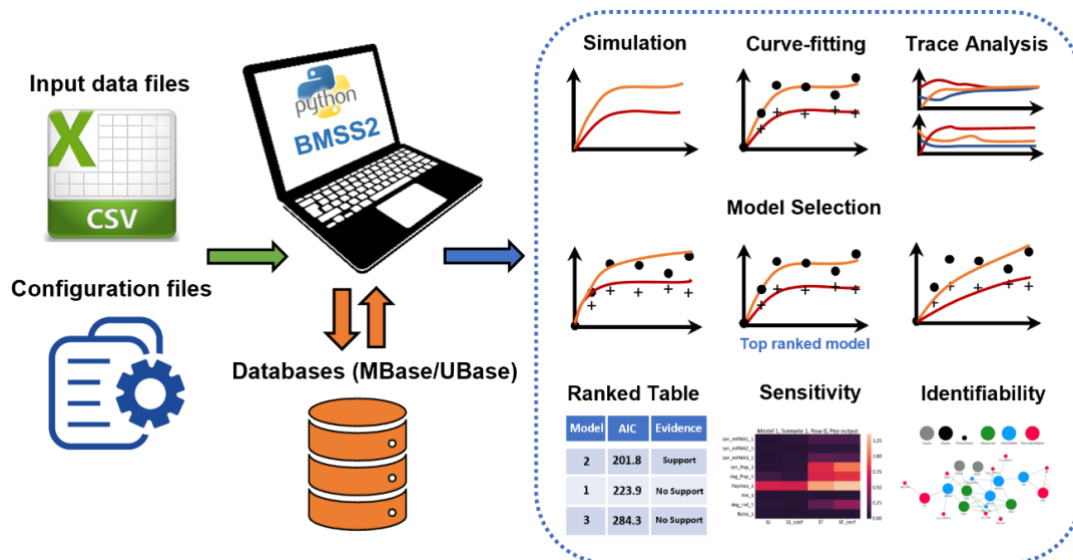# BMSS – An Automated BioModel Selection System for Gene Circuit Designs

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BMSS2.0 *(New!)*

A unified python library for model selection, building, and analysis

Supported Features:

- Automated *model selection* that best balances goodness-of-fit and complexity
- *Database-driven* to allow one to interactively retrieve and store models from/into SQL databases to ensure reproducibility
- Standard *model creation and simulation*
- *Parameter estimation* using *Bayesian Inference* based on Markov chain Monte Carlo and other global optimizers
- Trace analysis for *a posteriori identifiability*
- *A priori structural identifiability* to highlight states to be measured for making parameters identifiable
- Global *sensitivity analysis* to determine sensitive parameters for tuning
- Support parsing of models using *standard file formats* such as SBML, SEDML, and COMBINE archive

The package can be downloaded at https://github.com/EngBioNUS/BMSS2

Note: An extensible web app database listing some of the pre-established models can be found at https://engbio.syncti.org/BMSS2/index.html

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