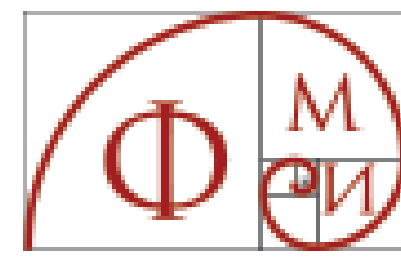


Evolutionary Algorithm Implemented in the Interactive System for Education in Modelling of Bioprocesses

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Abstract

The Interactive System for Education in Modelling and Control of Bioprocesses (InSEMCoBio) has been developed as a dynamic system flexible enough to allow new features to be easily integrated, specifically, additional experimental data for different biotechnological processes, various appropriate kinetic models and optimization algorithms.

The presented research is related to the implementation of a new optimization algorithm in InSEMCoBio. The system has been upgraded with an Evolutionary Algorithm (EA) for parametric identification of available kinetic models based on already integrated experimental data of the *E. coli* MC4110 fed-batch cultivation process. The existing set of operational features and options for graphical visualization of the results has also been updated. The obtained results confirm the workability of the developed software system.

InSEMCoBio allows access to contemporary high-level fundamental knowledge for bioprocesses modelling that can assist teaching programmes in biotechnology and bioengineering. The system could be considered a tool for enhancing education quality by transferring innovative scientific knowledge and technologies to students.

Evolutionary Algorithm

The current state of InSEMCoBio has been extended with an additional metaheuristic algorithm, namely an Evolutionary algorithm (EA) [1]. The algorithm uses computations inspired by the mechanisms of biological evolution.

The procedure has been applied for model parameter identification. It depends on a small set of initial parameters. The initial solution is determined by the values set for the problem parameters. The candidate solutions evolve on each iteration of the algorithm. The quality of these solutions is estimated by a fitness function. Some specific advantages of the procedure are its flexibility and ability to self-adapt in the search for optimum solutions.

From an optimization perspective, EA methodologies are robust and easy to implement. They do not need specific information regarding the objective function (gradient information or smoothness). They have proven their advantages in simple and multimodal optimization problems and have been successfully applied to parameter tuning.

Mathematical Model

The application of the general state space dynamical model to the fed-batch cultivation process of bacteria *E. coli* leads to the following nonlinear differential equation system [2]:

$$\begin{aligned} \frac{dX}{dt} &= \frac{\mu_{\max} S}{k_s + S} X + \frac{F}{V} X & X & \text{– the concentration of the biomass, [g/L],} \\ \frac{dS}{dt} &= -\frac{1}{Y_{S/X}} \frac{\mu_{\max} S}{k_s + S} X + \frac{F}{V} (S_{in} - S) & S & \text{– the concentration of the substrate (glucose), [g/L];} \\ \frac{dV}{dt} &= F & F & \text{– the feeding rate, [L/h];} \\ & & V & \text{– the volume of the bioreactor, [L];} \\ & & S_{in} & \text{– the initial glucose concentration in the feeding solution, [g/L];} \\ & & \mu & \text{– the specific growth rate described by Monod kinetics, [1/h];} \\ & & \mu_{\max} & \text{– the maximum growth rate, [1/h];} \\ & & k_s & \text{– a saturation constant, [g/L];} \\ & & Y_{S/X} & \text{– a yield coefficient, [-].} \end{aligned}$$

Experimental Data

The optimization problem has been solved by exploiting experimental data from an *E. coli* fed-batch cultivation. The data sets were obtained after the fed-batch fermentation process had been carried out at the Institute of Technical Chemistry, University of Hannover, Germany [2]. Online measurements of the substrate (glucose) and offline measurements of biomass were available for both fermentation processes. A flow injection analysis (FIA) system was used for online glucose measurement. The software CAFCA (ANASYSCON, Germany) was applied for FIA system automation and glucose concentration determination. Measurement noise was reduced using an extended continuous-discrete Kalman filter.

Fig. 2c Visualizing the results of the identification procedure in InSEMCoBio

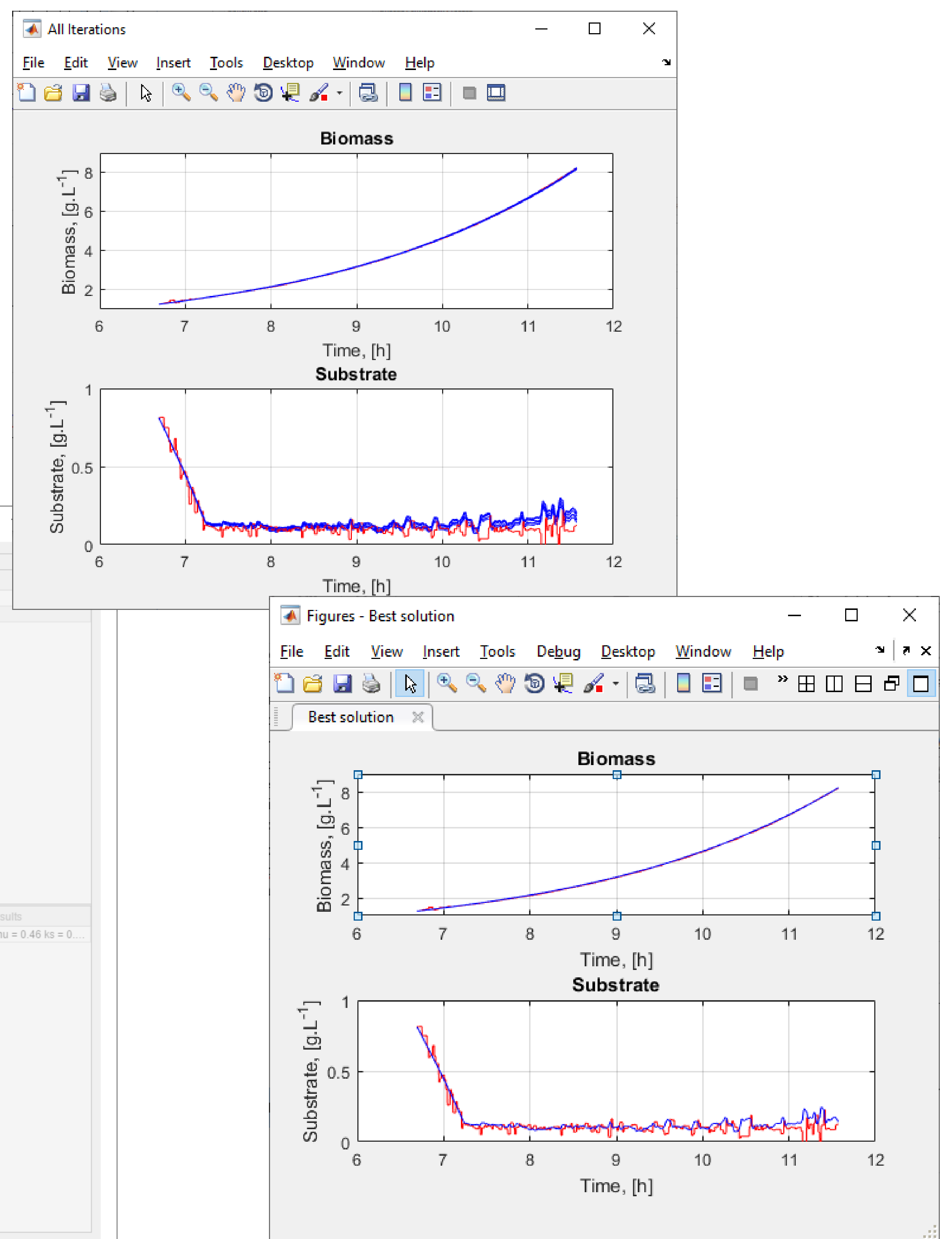
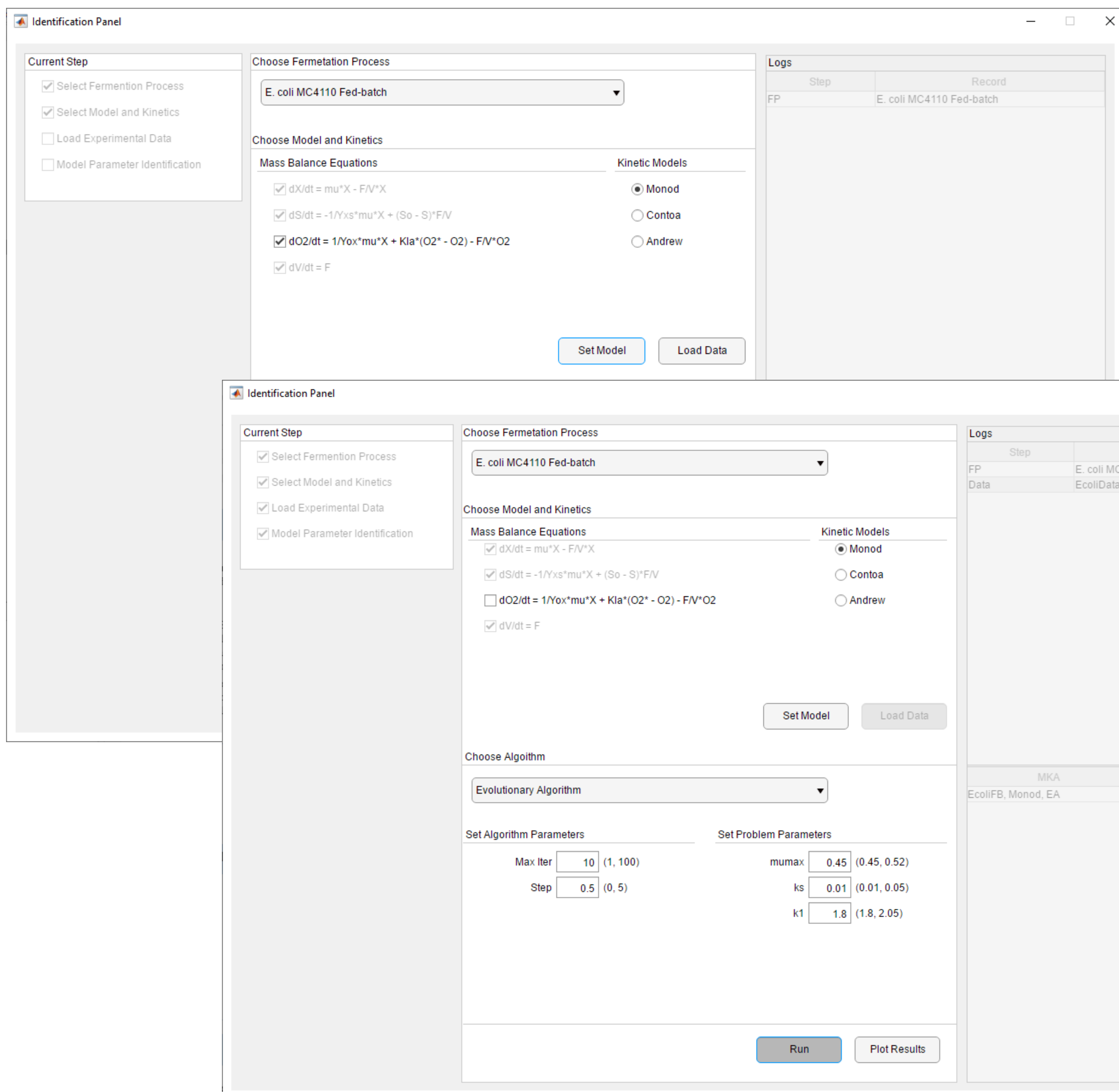


Fig. 2a, b. Setting up a fermentation process model and metaheuristic algorithm parameters in InSEMCoBio



Conclusion

The interactive system InSEMCoBio has been designed to be easily extended. Step by step, the system is developed by integrating new features: new optimization algorithms, new experimental data, specific biotechnological processes, or related kinetic models.

The results of the present research can be summarized in the following way:

1. The implementation of a new optimization algorithm, namely the Evolutionary algorithm, has been integrated into the system.
2. EA has been applied for parametric identification of the *E. coli* MC4110 fed-batch cultivation process model.
3. Real experimental data have been used to validate the system's performance.
4. The extensibility and workability of the developed software system InSEMCoBio have been confirmed.

References

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Further research and work on the system

Two modules have been planned initially as part of the interactive system InSEMCoBio.

The module for model parameter identification of the system is currently under development. It will be further expanded with new hybrid metaheuristic algorithms and different models of cultivation processes.

The following activities are planned for this purpose:

- Integration of models of selected cultivation processes.
- Development of new hybrid metaheuristic algorithms.
- Integration of the newly developed hybrid algorithms into the system.

The work on the system InSEMCoBio will continue further by developing the second module for an adaptive control design.

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