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Interactive System for Education in Modelling of Bioprocesses

Dafina Zoteva[1,2], Olympia Roeva[2], Velislava Lyubenova[3], Maya Ignatova[3]

[1]*Faculty of Mathematics and Informatics,*
Sofia University "St. Kliment Ohridski"
Address: 5 Blvd James Bourchier, 1164 Sofia, Bulgaria
E-mail: dafy.zoteva@gmail.com

[2]*Institute of Biophysics and Biomedical Engineering*
Bulgarian Academy of Sciences
Address: George Bonchev Str., Bl. 105, 1113 Sofia, Bulgaria
E-mail: olympia@biomed.bas.bg

[3]*Department of Mehatronic Bio/Technological Systems,*
Institute of Robotics, Bulgarian Academy of Sciences
Address: George Bonchev Str., Bl. 2, 1113 Sofia, Bulgaria
E-mails: v_lyubenova@ir.bas.bg, maya.ign@gmail.com

Abstract

The presented research is related to the development of an Interactive System for Education in Modelling and Control of Bioprocesses (InSEMCoBio).

The initial state of the software development consists of integrating the available experimental data of the *E. coli* MC4110 fed-batch cultivation process. Relevant kinetic models of the *E. coli* cultivation process have been implemented. The parametric identification of the kinetic models has been conducted with a Genetic Algorithm implemented into the system and adapted for the particular case study. A set of operational features and options for graphical visualization of the results are also available.

The presented software 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.

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

The system: main functional requirements

The development of any software system is preceded by an analysis of its functional and non-functional requirements. For the case of InSEMCoBio they can be shortly summarized in the following way.

The system InSEMCoBio (Fig. 1) targets biotechnology and bioengineering students. Therefore, building up a library with essential fermentation processes to be studied, along with a set of kinetic models describing their dynamics and a database of experimental data, is mandatory.

The mathematical models integrated into the system InSEMCoBio can be employed for different purposes as:

- *Design,* by exploring the impact of the parameters,
- *Research*, by developing and testing hypotheses and gaining new knowledge;
- *Prediction*, by predicting future performance;
- *Process control*, by developing new control strategies;
- *Education*, by exploring new ideas and improving the learning process.

In order to obtain models with high accuracy for the purpose of process control and optimization, appropriate contemporary identification methods need to be integrated into the system.

The computation time during the identification process should be kept to a minimum while an indication that the results are being processed should be provided. Last but not least, it is necessary for the users to be able to compare the resulting optimal models and to validate them with real experimental data.

The main activities and tasks have been identified as a result, as well as their relations.

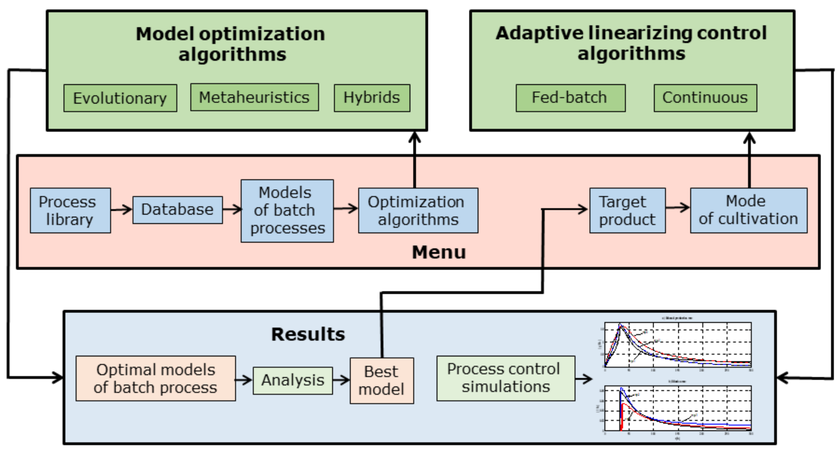

Fig. 1 The concept of the system InSEMCoBio

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The system InSEMCoBio has been developed in MATLAB environment. It consists of two modules: a module for a model parameter identification and a module for an adaptive control design. Currently, the module for a model parameter identification is under development.

The system has a simple user-friendly interface. The main window of the *Identification panel* (Fig. 2a) consists of three panels. The left most panel shows the *Current step* of the identification procedure. The middle panel is where the user controls are located for setting up the model of the fermentation process and the metaheuristic algorithm for the identification procedure. The user defined settings and the results (the parameters estimations) are logged into the information tables in the right panel.

The first step of the identification procedure includes selection of a specific fermentation process. The collection of processes available in the system is shown in the drop-down list *Select a Fermentation process*. When a fermentation process is chosen, appropriate differential equations describing the process are listed in the section *Mass Balance Equations*. There is a checkbox corresponding to each equation. Some of the equations are mandatory for describing the basics of the specified process, therefore, they are selected by default and cannot be unchecked. A set of relevant kinetic models are listed in the section *Kinetic Models*. Exactly one can be specified.

The models are an experts' selection based on literature results taking into account the influence of the main process variables, as well as the physico-chemical variables (temperature, pH, etc.) of the considered processes.

These settings are finalized and confirmed when the button *Set Model* is clicked. The choices of the differential equations and the specific kinetics that describe the process are essential for the next step. They determine the exact experimental data that should be loaded. At this stage real experimental data of bacteria *E. coli* MC4110 fed-batch cultivation process has been integrated into the system.

Currently, the accepted format of the experimental data for each of the fermentation processes available in the system is the .xlsx Excel format. The file should contain data on all possible parameters in the basic and extended models of the corresponding fermentation process. These data are filtered when the model of the process is confirmed so that only the relevant information is used during the identification procedure.

The choice of a kinetic model automatically determines the set of model parameters that have to be identified. The model parametric identification is conducted by metaheuristic algorithms implemented into the InSEMCoBio system, like genetic algorithms, evolutionary algorithm, etc. (Fig. 2b). The set of these metaheuristic algorithms is shown in the drop-down list *Choose algorithm* accessible after loading the experimental data for the model.

Each of the algorithms needs a set of input parameters which are listed upon selecting the corresponding item of the drop-down. The parameters move within certain limits, indicated next to the text field where the value of each parameter, used for the current execution of the optimization algorithm, should be specified. The most appropriate values of the algorithm's parameters, set by experts for the particular cultivation process, are considered as default values.

The model parameter identification is started by the *Run* button. The estimates of the model parameters are obtained as a result, together with their graphical representation. While the results are being processed, the solutions on each iteration of the identification procedure are visualized as a comparison of the real experimental data and the model dynamics (Fig. 2c).

Based on the execution of several identification procedures built into the system InSEMCoBio, the model that most adequately describes the process dynamics can be selected.

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

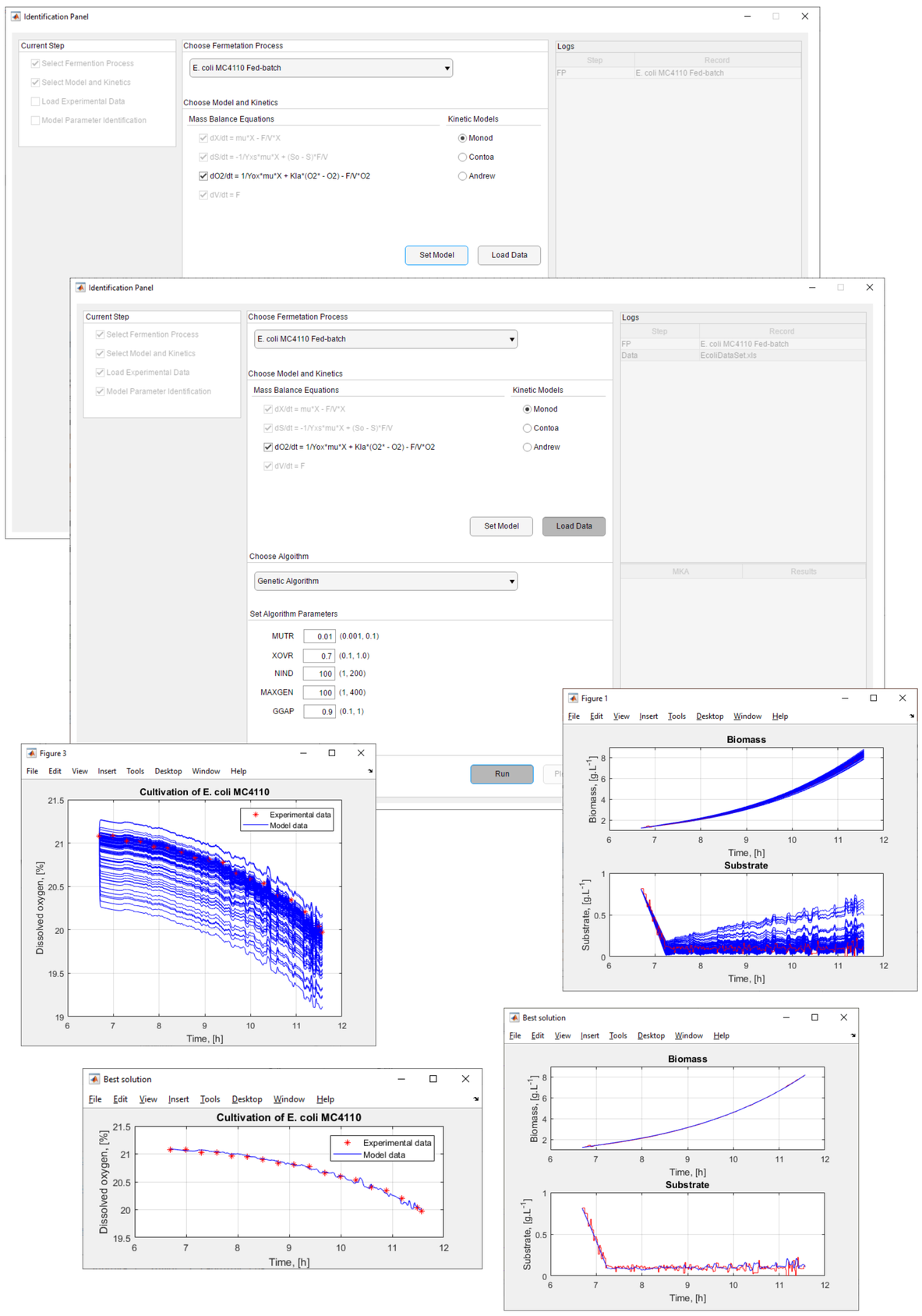

Fig. 2c Visualizing the results of the identification procedure in InSEMCoBio

Conclusion

In a broad perspective, the objective of the system InSEMCoBio is to cover various aspects of the modelling process: selection of an object (yeast or bacteria fermentation), structural (choosing relative kinetic functions), parameter identification (applying appropriate optimization procedures) and model verification.

For the purpose of developing a practical training programme for students, the presented system InSEMCoBio aims to ensure a database collection of real experimental data, a set of essential batch and fed-batch fermentation processes and their mathematical models integrated into the system.

Possible applications of the system are:

- Investigation of a process dynamics;
- Investigation of the influence of kinetic model parameters;
- Investigation of the influence of physiochemical parameters.
- Identification of mathematical models based on different kinetic models and different metaheuristic algorithms.

Further research and work on the system

The module for a model parameter identification of the system InSemCoBio will be expanded with new hybrid metaheuristic algorithms. The following activities are planned for the purpose:

- Comparative analysis of the most commonly used metaheuristic algorithms in case of parameter identification of non-linear cultivation processes models;
- Selection of the most promising metaheuristic algorithms for hybridization;
- Development of new hybrid metaheuristic algorithms;
- Testing the proposed hybridizations on benchmark functions;
- Testing the proposed hybridizations on problems in the field of biotechnology;
- Comparative analysis of the proposed hybrid metaheuristic algorithms with existing metaheuristics or hybrid metaheuristic.
- Integrating the newly developed hybrid algorithms into the system.

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

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