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Model Parameter Identification Based on Hybrid Metaheuristic Algorithms

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

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

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

Abstract

In this paper, Ant Lion Optimizer (ALO) has been hybridized with Genetic Algorithm (GA) for a model parameter identification problem. When dealing with real-world and large-scale problems, it becomes evident that concentrating on a sole metaheuristic algorithm is rather restrictive. A skilled combination between metaheuristics or other optimization techniques, a so called hybrid metaheuristic, can provide more efficient behaviour and higher flexibility. Hybrid metaheuristics combine the advantages of one algorithm with the strengths of another.

ALO, based on the interaction between antlions and ants in a trap, and GA, based on the mechanics of the nature selection, are two efficient biologically inspired population-based algorithms. To demonstrate the effectiveness of ALO-GA for a real-world problem, parameter identification of an *Escherichia coli* MC4110 fed-batch cultivation process model has been considered. The computational results of the designed algorithm have been compared to the results of various hybridized biologically inspired techniques applied to the same problem. The results clearly show that the proposed algorithm ALO-GA outperforms the considered algorithms.

Hybrid Ant Lion Optimizer-Genetic Algorithm

ALO is a novel metaheuristic swarm-based approach [1] introduced to emulate the hunting behavior of ant lions in nature. This behavior is described by five important phases of hunting ants: random walk, building a trap, trapping ants, sliding the ants towards the antlion, catching the prey and rebuilding the trap.

GA was developed to model adaptation processes using a recombination operator with mutation as a background operator [2]. GA maintains a population of individuals. Each individual represents a potential solution to the problem in consideration. Each solution is evaluated and a new population is formed by selecting more fit individuals. The proposed hybrid algorithm, named ALO-GA, has been designed to improve both the exploration and exploitation and thus to present a powerful and efficient algorithm for real-world numerical optimization problems. As a result, the speed and the precision of the algorithm's convergence are also improved. The pseudo code of the ALO-GA is as follows:

begin
Define the input parameters for both ALO and GA
    % Start ALO
    Initialize the first population of ants and antlions randomly
    Calculate the fitness of ants and antlions
    Find the best antlion and adopt it as the elite (determined optimum)
    for *j:= 1 to size of initial population* Pop_0
        while *the end criterion is not satisfied*
            for *each ant*
                Select an antlion using Roulette wheel
                Update the parameters of the random walk
                Create a random walk and normalize it
                Update the position of the ant
            end for
        Calculate the fitness of all ants
        Replace an antlion with its corresponding ant if it becomes fitter
        Update the elite if an antlion becomes fitter
        end while
        Memorize the best solution for the current iteration in Pop_0
    end for
    % Start GA
        Set the initial population Pop_0 *to the set of best solutions generated by ALO*
        Calculate the value of the fitness function for each individual in Pop_0
    for *i := 1 to MaxGeneration*
          Select individuals Pop_i *from the current population* Pop_{i-1} *in a way that gives advantage to better individuals.*
          Perform crossover with probability p_c
          Perform mutation with probability p_m
          Calculate the value of the fitness function for each individual in Pop_i
    end for
    Rank the solutions, find the current best and memorize
end begin

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:

$$\frac{dX}{dt} = \mu X - \frac{F}{V} X$$

$$\frac{dS}{dt} = -\frac{1}{Y_{S/X}} \mu X + \frac{F}{V}\left(S_{in} - S\right)$$

$$\frac{dV}{dt} = F$$

$$\mu = \frac{\mu_{\max} S}{k_S + S}$$

X – the concentration of the biomass, [g/L],
S – the concentration of the substrate (glucose), [g/L];
F – the feeding rate, [L/h];
V – the volume of the bioreactor, [L];
S_{in} – the initial glucose concentration in the feeding solution, [g/L];
μ – the specific growth rate described by Monod kinetics, [1/h];
μ_{max} – the maximum growth rate, [1/h];
k_S – a saturation constant, [g/L];
$Y_{S/X}$ – an yield coefficient, [-].

Numerical results

The proposed ALO-GA hybrid algorithm has been applied to estimate parameters of an *E. coli* cultivation process model. A series of 30 runs has been conducted due to the stochastic characteristics of the applied algorithm. The average, the best and the worst results of these 30 runs for the criteria value *J* (Table 1) and the model parameters (Table 2) have been observed in order to compare the results of the model parameters' identification. The standard deviation (SD) of the estimates has been also evaluated.

The results (both average and the best), presented in Tables 1 and 2, show that the ALO-GA hybrid algorithm finds the solution with the highest quality, e.g. the smallest objective function value (J = 4.3610). The next best result is achieved by the GA-ACO hybrid algorithm (J = 4.3803).

The model predictions for the biomass and the glucose concentrations, based on the hybrid algorithms estimated sets of model parameters, are compared to the experimental data points of the considered *E. coli* fed-batch cultivation process in Fig. 1 and Fig. 2.

Table 1. Comparison of the objective function values obtained by ALO with published ones [3, 4]

Algorithm	*J*			
	average	best	worst	SD
ACO-GA	4.5765	4.4903	4.6865	0.06916
GA-ACO	4.5706	4.3803	4.6949	0.06325
ACO-FA	4.5196	4.4013	4.6803	0.05914
ALO-GA	**4.4752**	**4.3610**	**4.6617**	**0.04967**

Table 2. Comparison of the parameter estimates obtained by ALO with the published ones [3, 4]

Algorithm	Model parameters					
	$\mu_{\max}$	SD	k_S	SD	$Y_{S/X}$	SD
ACO-GA	0.4976	0.0120	0.0135	0.0023	2.0221	0.0025
GA-ACO	0.4946	0.0121	0.0123	0.0020	2.0204	0.0024
ACO-FA	0.4824	0.0110	0.0114	0.0019	2.0206	0.0021
ALO-GA	**0.5022**	**0.0124**	**0.0146**	**0.0024**	**2.0182**	**0.0020**

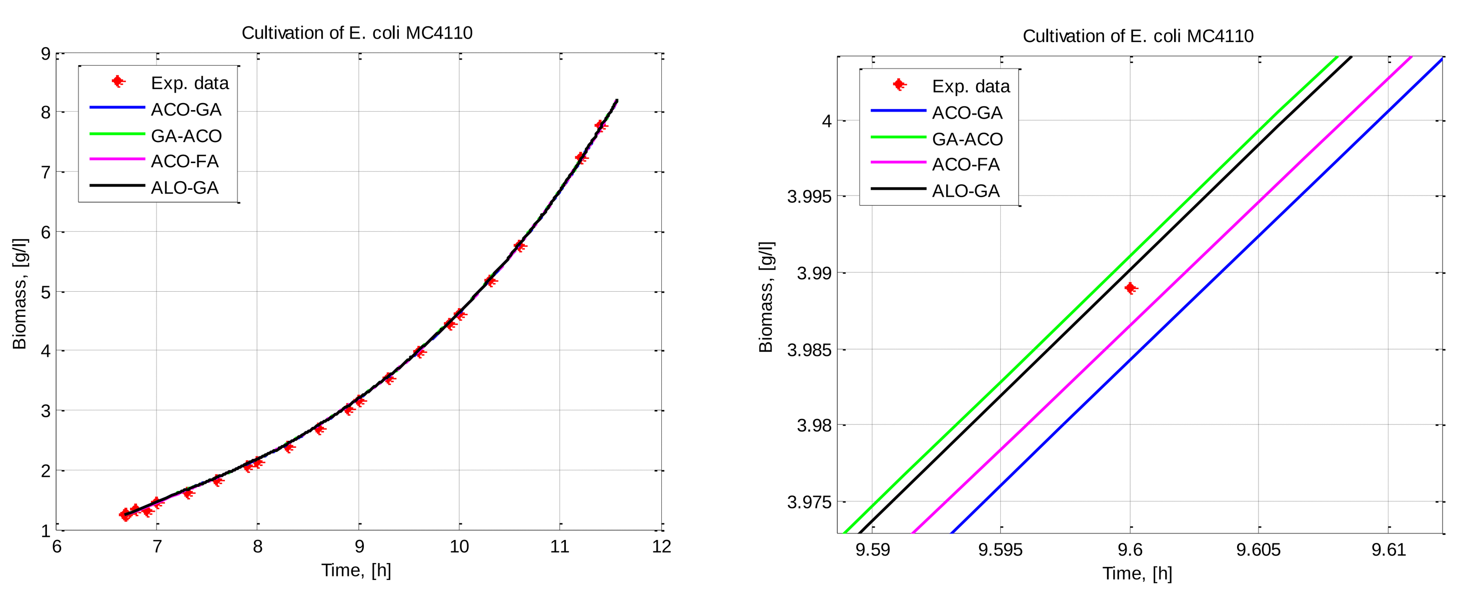

Fig. 1 Time profiles of the process variable biomass: real experimental data and model predicted data

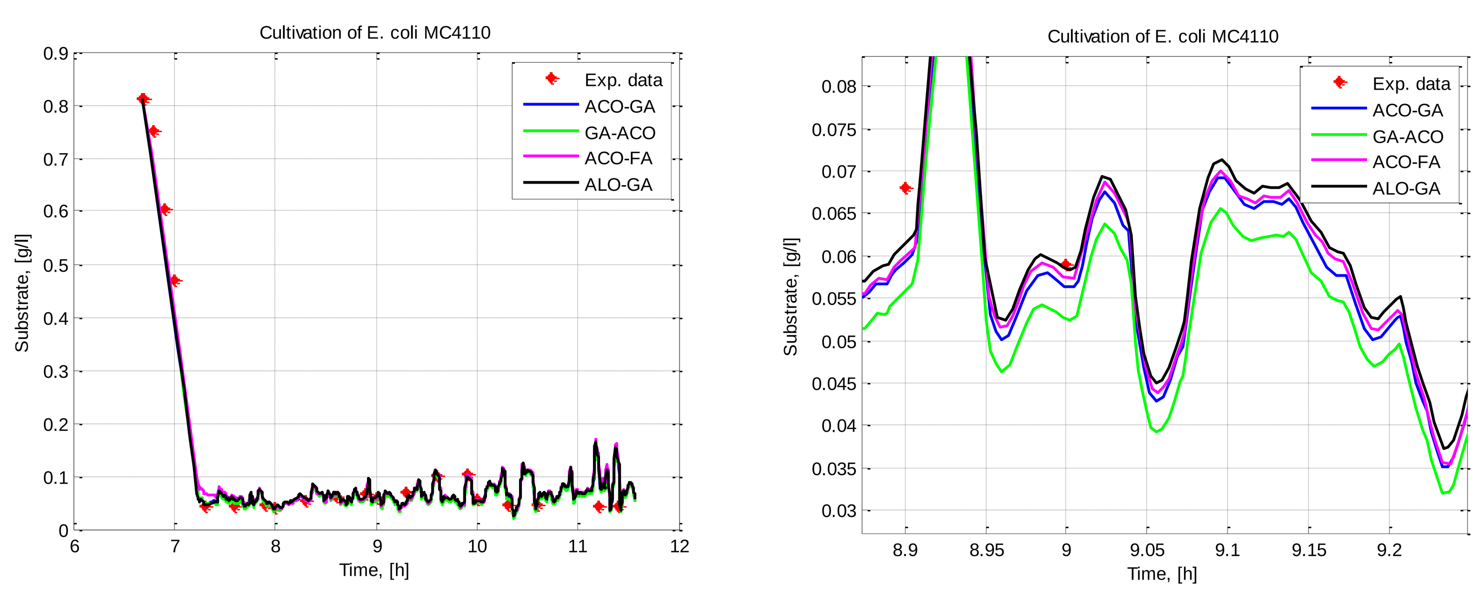

Fig. 2. Time profiles of the process variable substrate: real experimental data and model predicted data

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