

Genetic Algorithm and Cuckoo Search Hybrid Technique for Parameter Identification of Fermentation Process Model

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Abstract: This paper presents a hybrid scheme based on two population-based metaheuristic techniques, namely genetic algorithm (GA) and cuckoo search (CS). In particular, the hybrid is formed by the application of standard simple genetic algorithms (SGA) and CS, specifically adapted and for first time applied by the authors for the purposes of parameter identification of yeast fed-batch fermentation process model. The parameters of the hybrid technique SGA-CS have been thoroughly explored and tuned to meet the specific peculiarities of the considered here optimization problem. A comparison of SGA, CS and developed hybrid SGA-CS has been performed, outlining the advantages and disadvantages of each algorithm. Additionally, a new modification of SGA-CS hybrid technique, inspired by proven as very effective modification of SGA, working with implementation of main genetic operators in order crossover, mutation and selection, has been here elaborated. Presented modified hybrid technique has been tested, aiming at verification of the obtained promising results of developed SGA-CS technique.

Keywords: Genetic algorithm, Cuckoo search, Hybrid technique, Parameter identification, Fed-batch fermentation process.

Introduction

Metaheuristic techniques play an important role in computational artificial intelligence and has attracted for decades the researchers' attention as a good alternative to the conventional optimization methods. Genetic algorithms (GA) [8], ant colony optimization (ACO) [5], artificial bee colony (ABC) optimization [9], bat algorithm (BA) [22], cuckoo search (CS) [23], particle swarm optimization (PSO) [10] are some of the well-known nature-inspired metaheuristics. They have been developed and tested for solving of wide range optimization problems, among them, parameter identification of fermentation processes models [4, 17], curve data fitting [6], structural optimization problems [7], etc. Since mentioned above algorithms have their own advantages and disadvantages, it became evident that focusing on a sole metaheuristic technique is rather restrictive. A combination between metaheuristic and any other optimization techniques, or between metaheuristic themselves can provide more efficient behaviour and a higher flexibility when solving real-world and large-scale problems [20-22]. In other words, hybrid metaheuristic techniques aim at utilize the strengths of two or more algorithms, e.g. hybrid CS-GA [11], hybrid GA [14], GA and firefly algorithm [16], ACO-GA [18], etc.

The focus of the investigation is on the hybrid scheme between genetic algorithm and cuckoo search – SGA-CS, proposed in [1] for solving benchmark mathematical functions. Here the hybrid is going to be adapted and applied for a first time to a parameter identification of *S. cerevisiae* fed-batch fermentation process model. As it is well-known, fermentation processes (FP) have a numerous specific peculiarities that turned their modelling into rather difficult to be solved task. FP are nonlinear, dynamic systems with interdependent and time-varying process variables. As such, their models have a complex structure (e.g., yeasts [2, 13], yeasts and bacteria [12, 19]) and the choice of an appropriate optimization method for model parameter identification is of a key importance. By themselves, SGA [8] and CS [23] have been proved as a successful tool for parameter identification of fermentation process models of yeasts [3], bacteria [15] and yeasts and bacteria [12]. Thus, the application of SGA-CS hybrid strategy for solving such a complex problem as parameter identification of FP model, seems more promising.

A comparison between SGA, CS and SGA-CS hybrid technique, applied to parameter identification of *S. cerevisiae* fed-batch fermentation process model has been performed in order algorithms' advantages and disadvantages to be outlined. Additionally, a new modification of SGA-CS hybrid technique, inspired by modification of SGA, working with implementation of main genetic operators in order crossover, mutation and selection, has been here elaborated and tested.

Problem formulation

For the purpose of current investigation, a set of real experimental data consisting of on-line measurements of substrate (glucose) and dissolved oxygen, as well as off-line measurements of biomass and ethanol of *S. cerevisiae* fed-batch fermentation process, has been used. The cultivation has been conducted in the *Institute of Technical Chemistry, University of Hannover, Germany*. Full description of process conditions and experimental data can be found in [12].

According to the mass balance and considering mixed oxidative functional state, a mathematical model which describes the dynamics of biomass, substrate, ethanol and dissolved oxygen concentrations of *S. cerevisiae* fed-batch cultivation is commonly described by the following system of non-linear differential equations [12]:

$$\frac{dX}{dt} = \left(\mu_{2S} \frac{S}{S + k_S} + \mu_{2E} \frac{E}{E + k_E} \right) X - \frac{F}{V} X \quad (1)$$

$$\frac{dS}{dt} = -\frac{\mu_{2S}}{Y_{SX}} \frac{S}{S + k_S} X + \frac{F}{V} (S_{in} - S) \quad (2)$$

$$\frac{dE}{dt} = -\frac{\mu_{2E}}{Y_{EX}} \frac{E}{E + k_E} X - \frac{F}{V} E \quad (3)$$

$$\frac{dO_2}{dt} = \left(\frac{\mu_{2E}}{Y_{EX}} \frac{E}{E + k_E} Y_{OE} - \frac{\mu_{2S}}{Y_{SX}} \frac{S}{S + k_S} Y_{OS} \right) X + k_L^{O_2} a(O_2^* - O_2) \quad (4)$$

$$\frac{dV}{dt} = F, \quad (5)$$

where X , S , E , O_2 are respectively the concentrations of biomass, $[g \cdot l^{-1}]$, substrate (glucose), $[g \cdot l^{-1}]$, ethanol, $[g \cdot l^{-1}]$, and dissolved oxygen, $[\%]$; O_2^* – dissolved oxygen saturation concentration, $[\%]$; F – feeding rate, $[h^{-1}]$; V – volume of bioreactor, $[l]$; $k_L^{O_2} a$ – volumetric oxygen transfer coefficient, $[h^{-1}]$; S_{in} – initial glucose concentration in the feeding solution, $[g \cdot l^{-1}]$; μ_{2S} , μ_{2E} – maximum growth rates of substrate and ethanol, $[h^{-1}]$; k_S , k_E – saturation constants of substrate and ethanol, $[g \cdot l^{-1}]$; Y_{ij} – yield coefficients, $[g \cdot g^{-1}]$. All functions in the model (Eqs. (1)-(5)) are continuous and differentiable. Also, all model parameters fulfil the non-zero division requirement.

For the considered here model (Eqs. (1)-(5)), the vector $p = [\mu_{2S}, \mu_{2E}, k_S, k_E, Y_{SX}, Y_{EX}, k_L^{O_2} a, Y_{OS}, Y_{OE}]$, consisting of altogether nine model parameters, is going to be identified.

The optimization criterion, aiming at identification of parameter vector p in order to obtain the best fit to an experimental data set, is defined as mean square deviation between the model output and the experimental data, obtained during the cultivation:

$$J = \sum (Y - Y^*)^2 \rightarrow \min, \quad (6)$$

where Y and Y^* are, respectively, the experimental and model predicted data, $Y = [X, S, E, O_2]$.

Simple genetic algorithms

Genetic algorithm is a widely applied metaheuristic technique, inspired by processes, occurred in the nature. GA works with a set of individuals (chromosomes) called a population. Each of these artificial chromosomes, is composed of binary strings (or genes) of certain length (number of binary digits) and represents a solution of the problem. Each gene contains information for the corresponding parameter.

Simple genetic algorithm, presented for the first time by Goldberg [8], searches a global optimal solution among individuals in one population, using three main genetic operators in a sequence selection, crossover and mutation. The selection is applied for choosing the chromosomes representing better possible solutions according to their own objective function values. The crossover proceeds in order to form new offspring. Mutation is then applied with determinate probability to prevent falling of all solutions into a local optimum of the solved problem. Then the algorithm evaluates the objective function value of the individuals in the current population. According to that the new chromosome is created. The SGA terminate when some termination certain is fulfilled. In this investigation, SGA terminates when a certain number of generations has been reached.

Many modifications of SGA have been elaborated for solving different optimization problems. One of them, developed in [15] and further tested in [2, 4] for parameter identification of *S. cerevisiae* fed-batch fermentation process model, works with implementation of main genetic operators in order crossover, mutation and selection. Modified SGA aims to prevent the destroying of reached good solution by either crossover or mutation or both operators.

Cuckoo search algorithm

The interesting and aggressive breeding behavior of cuckoo species is implemented by Yang and Deb in cuckoo search metaheuristic algorithm for optimization problems solving [23]. In the population based CS algorithm, the eggs in the nest are assumed as a set of candidate

solutions of an optimization problem, while the cuckoo egg is interpreted as a new coming solution. The ultimate goal of the method is to use iteratively these new and potentially better solutions for optimal solution finding of the problem.

Three idealized rules are assumed when standard CS algorithm has been used [23]:

- At a time, each cuckoo lays one egg in a randomly chosen nest;
- The best nests containing high-quality eggs (solutions) will be carried over to the next generations;
- The number of available host nests is fixed, and the probability a host bird to discover egg laid by a cuckoo is $p_a \in (0, 1)$. In this case, the host bird has two possibilities, to throw the egg or simply to abandon the nest and build a new one in a new location.

Further, the last assumption can be approximated by the p_a parameter that gives a possibility n host nests to be replaced with new ones, contain respectively new random solutions. In CS algorithm switching parameter p_a control a balanced combination between local and global explorative random walk. Eqs. (7) and (8) present respectively the local random walk, and the global random walk, carried out using Lévy flights [23]:

$$x_i^{t+1} = x_i^t + \alpha s \otimes H(p_a - \varepsilon) \otimes (x_j^t - x_k^t) \quad (7)$$

$$x_i^{t+1} = x_i^t + \alpha L(s, \lambda) \quad (8)$$

In Eq. (7), x_j^t and x_k^t are two different solutions, selected by random permutation, $H(u)$ is the Heaviside function, ε is a random number drawn from a uniform distribution, s is the step size, $\otimes$ means the entry-wise product of two vectors.

In Eq. (8), the step size scaling factor $\alpha > 0$, and

$$L(s, \lambda) = \frac{\lambda \Gamma(\lambda) \sin(\pi\lambda/2)}{\pi} \frac{1}{s^{1+\lambda}}, (s \gg s_0 > 0). \quad (9)$$

Simple genetic algorithm and cuckoo search hybrid technique

Recently proposed in [1], SGA-CS algorithm is a collaborative combination of two population-based metaheuristic techniques. In the beginning of SGA-CS hybrid algorithm, SGA explores the search space in order to generate solutions. Further, CS uses as initial solution the population obtained by SGA, which is closer to the optimal solution. On the next step, CS explores search space and obtains the best model parameters vector.

The pseudo code of SGA-CS hybrid algorithm, according to [1], is presented in Fig. 1.

Results and discussion

Matlab environment has been used for SGA, CS and SGA-CS algorithms implementations for the purpose of parameter identification of the *S. cerevisiae* fed-batch fermentation model (Eqs. (1)-(5)) with corresponding functions and programs developed. All computations have been performed using Intel Core i3 CPU M 380 @ 2.53GHz, 4 GB Memory (RAM), Windows 8 (64bit) operating system.

SGA and CS algorithm's operators and parameters have been set respectively to [2] and [3] and, for a completeness, they are shortlisted bellow in Table 1.

```
begin
Objective function  $f(\mathbf{x})$ ,  $\mathbf{x} = (x_1, \dots, x_d)^T$ 
Generate random population of  $n$  chromosomes
Define the Cuckoo search parameters
Define the Genetic algorithm parameters
Begin SGA
 $i = 0$ 
Initial population  $P(0)$ 
Evaluate  $P(0)$  fitness
while ( $t < \text{MaxGeneration}$ ) or (stop criterion) do
 $i=i+1$ 
Select  $P(i)$  from  $P(i-1)$ 
Recombine  $P(i)$  with crossover probability
Mutate  $P(i)$  with mutation probability
Evaluate  $P(i)$  fitness
end while
Rank the chromosomes and find the current best
End begin SGA
Begin CS
Initial population of  $n$  host nests = Final best SGA solution
while ( $t < \text{MaxGeneration}$ ) or (stop criterion) do
Get a cuckoo (say  $i$ ) randomly and create a new solution by
Lévy flights
Evaluate its quality or fitness value  $F_i$ 
Choose a nest among  $n$  (say,  $j$ ) randomly
if ( $F_i < F_j$ ),
Replace  $j$  by the new solution  $i$ 
end if
Abandon a fraction  $p_a$  of worse nest
New solutions (nest) are built
Keep the best solution, i.e. nests with quality solutions
Rank the solution and find the current best
end while
Postprocess results and visualization
end
```

Fig. 1 Pseudo code of SGA-CS hybrid technique

As can be seen from Table 1, SGA requires a big number of parameters to be tuned, while CS depends only on two parameters, namely the population size (number of nests) and the probability rate of replacement.

Before proceeding to a hybrid SGA-CS technique, standard SGA and standard CS have been implemented for the purposes of parameter identification of the *S. cerevisiae* fed-batch fermentation model. Thirty independent runs have been performed for each algorithm with operators and parameters of both algorithms as presented in Table 1. Table 2 summarizes the obtained results, presenting the best, worst and mean values of the most representative criterion for the algorithms performance, namely the optimization criterion J and the computational time T .

Table 1. Main SGA and CS operators and parameters

SGA operators	Type
Fitness function	Linear ranking
Selection function	Roulette wheel selection
Crossover function	Double point
Mutation function	Bit inversion
Reinsertion	Fitness-based
SGA parameters	Value
Generation gap	0.8
Crossover probability	0.95
Mutation probability	0.05
Number of generations	100
Number of variables	9
Number of individuals	15
CS parameters	Value
Number of nests	15
Rate of replacement	0.25
Number of generations	100
Number of variables	9

Aiming at an appropriate utilization, and even to gain from the advantages of both SGA and CS algorithms, the hybrid SGA-CS is here adapted and applied for the considered optimization problem. For fine tuning of the hybrid SGA-CS technique's parameters, SGA maximum number of generations have been investigated in details. The results show that SGA finds the optimal solution around the 45-th iteration. Thus, for SGA-CS hybrid algorithm, maximum number of generations has been set to 50. The best, worst and mean values of the optimization criterion J and of the computational time T of the applied SGA-CS hybrid algorithm are also presented in Table 2.

Table 2. Comparison of SGA, CS and SGA-CS performance

Results	SGA		CS		SGA-CS	
	J	T , [s]	J	T , [s]	J	T , [s]
best	0.0221	18.01	0.0221	477.11	0.0221	201.87
worst	0.0225	20.59	0.0222	585.91	0.0221	214.91
average	0.0223	19.08	0.0221	516.81	0.0221	210.90

As seen from Table 2, the values of the optimization criterion obtained with standard genetic algorithm, cuckoo search and hybrid SGA-CS algorithm under identical conditions are very similar. The analysis, based on the averaged values of optimization criterion, show that CS and hybrid SGA-CS yield slightly better results than SGA. Both algorithms give $J = 0.0221$, while SGA reaches $J = 0.0223$. CS algorithm is more reliable than SGA, but at the expense of computational (CPU) time. As shown, SGA is 27 times faster than CS, when applied for parameter identification of *S. cerevisiae* fed-batch fermentation process model.

The results, presented in Table 2, definitely demonstrate the successful combination of the two population-based metaheuristics. SGA-CS is as reliable as CS, but saves almost 60% of the computational time of the algorithm itself. Thus, SGA-CS could be distinguished as a good compromise among the investigated here algorithms.

A verification of obtained promising results from the implementation of SGA-CS hybrid technique to the parameter identification of *S. cerevisiae* fed-batch fermentation process model has been further pursued. For that purpose, the adapted here SGA-CS hybrid technique has been modified in the side of SGA, applying a modified SGA algorithm instead of the standard one. The considered here modification of SGA differs from the standard SGA by the order of implementation of main genetic operators, namely crossover, mutation and selection (the modified algorithm is here denoted as SGAcms). This modification of SGA had been also investigated for the parameter identification of *S. cerevisiae* fed-batch fermentation process model in [16] and had been proved as more reliable than SGA in [5].

As such, SGAcms algorithm has been chosen for hybridization with CS, expecting to improve the model accuracy of SGAcms and the CS algorithm convergence time. The results from the parameter identification of *S. cerevisiae* fed-batch fermentation process model applying consequently SGAcms and SGAcms-CS are presented in Table 3.

Table 3. Comparison of SGAcms and SGAcms-CS performance

Results	SGAcms		SGAcms-CS	
	<i>J</i>	<i>T</i> , [s]	<i>J</i>	<i>T</i> , [s]
best	0.0221	19.88	0.0221	216.95
worst	0.0226	20.82	0.0222	223.39
average	0.0223	20.54	0.0221	220.78

As could be expected, the proposed here modified hybrid SGAcms-CS improves the average value of optimization criterion toward SGAcms, but at the expense of CPU time. But when SGAcms-CS is compared to CS, with respect to CPU time (Table 2), it is obvious that the newly developed hybrid is 2.3 times faster than the CS itself, saving almost 57% of the computational time.

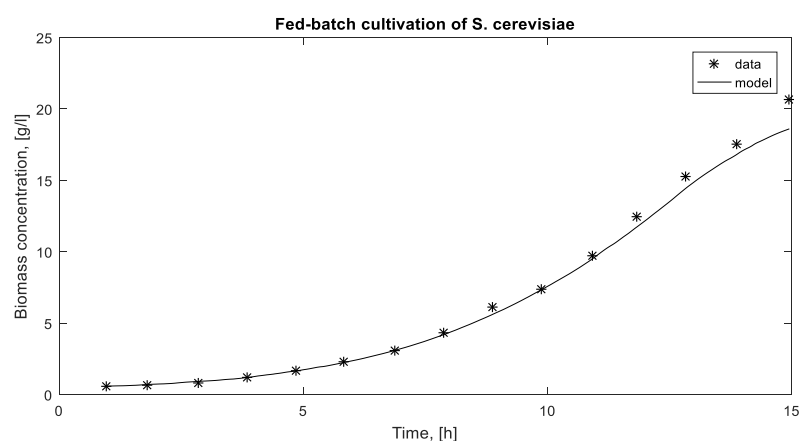
Based on the results presented in Table 2 and Table 3, a comparison of the altogether three metaheuristic algorithms (SGA, SGAcms and CS), and two hybrid algorithms (SGA-CS and herewith developed SGAcms-CS), towards algorithms convergence time and model accuracy has been performed. For the chosen set of the genetic algorithms operators and parameters (Table 1), modified SGAcms reaches almost the same results as the standard SGA. The average value of the optimization criterion is equal for the both investigated here SGA, but the modified SGAcms is slightly slower than the standard one. The win of the competition between adapted SGA-CS and the newly developed SGAcms-CS is on the side of the SGA-CS. Thus, the undisputable leader, distinguished as a good compromise among the five applied in this investigation algorithms, is SGA-CS, which leads to SGA optimization criterion value improvement and saves almost 60% of CS CPU time.

Table 4 presents the best values of optimization criterion *J*, computational time *T* and all nine model parameters when the distinguished SGA-CS hybrid technique is applied to the parameter identification of *S. cerevisiae* fed-batch cultivation.

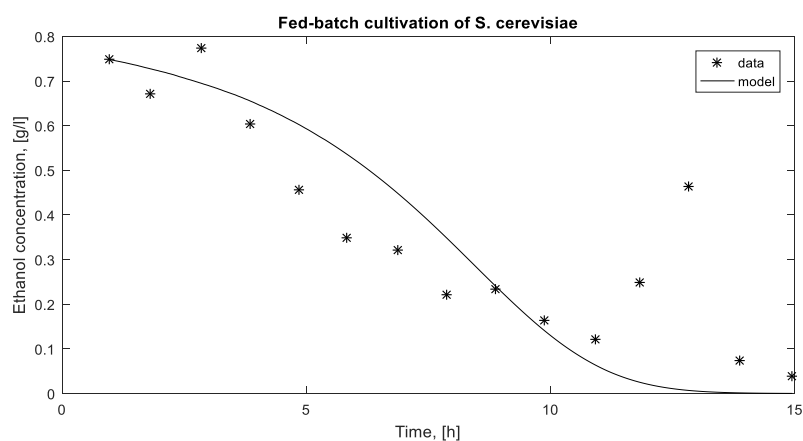
Table 4. Results from model parameter identification procedure when SGA-CS has been applied

J	T [s]	μ_{2S} [h ⁻¹]	μ_{2E} [h ⁻¹]	k_S [g·l ⁻¹]	k_E [g·l ⁻¹]	Y_{SX} [g·g ⁻¹]	Y_{EX} [g·g ⁻¹]	$k_L a$ [h ⁻¹]	Y_{OS} [g·g ⁻¹]	Y_{OE} [g·g ⁻¹]
0.0221	213.37	0.94	0.14	0.12	0.8	0.41	1.92	95.67	753.71	441.34

The workability of SGA-CS hybrid technique for solving such a complex problem as parameter identification of FP process model is demonstrated also in Fig. 2, which presents the results from experimental and model predicted data, respectively, for biomass, ethanol, substrate, and dissolved oxygen.



a)



b)

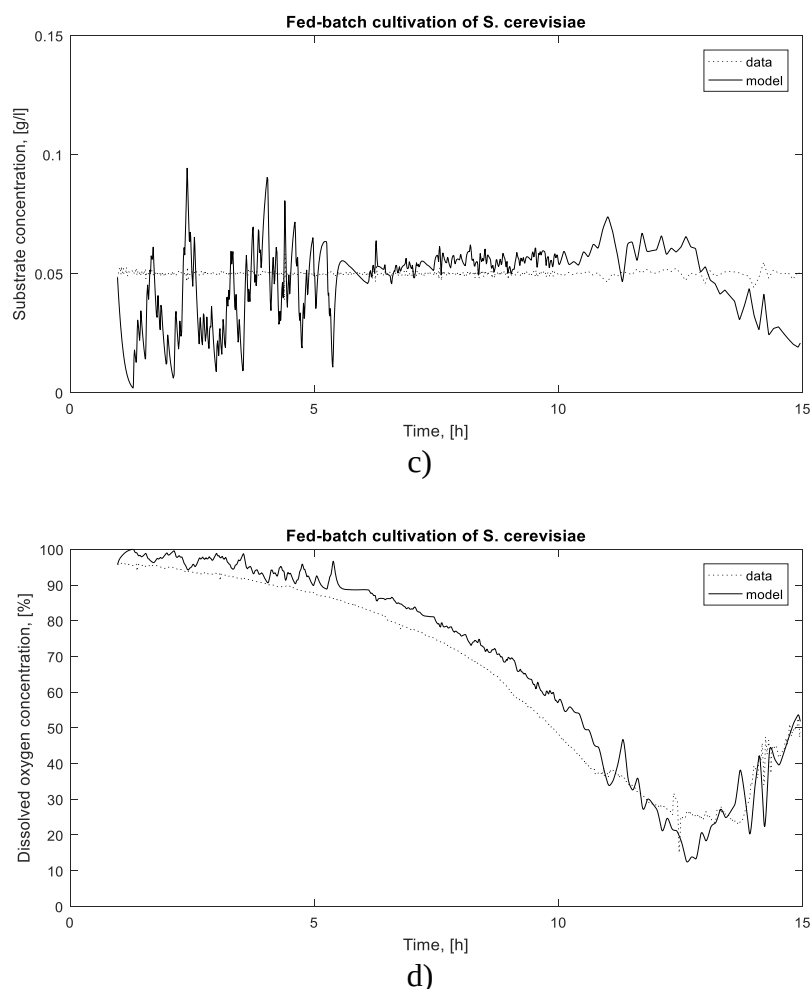


Fig. 2 Experimental and model predicted data for the main process variables: a) biomass; b) ethanol; c) substrate; and d) dissolved oxygen concentrations.

As seen from Table 4 and Fig. 2, adapted SGA-CS is proved as effective tool not only for solving benchmark mathematical functions, but also for real word optimization problem evaluation.

Based on the previous authors' investigations [3, 16], it can be expected that presented here two hybrid techniques of SGA and CS might achieve better results if, e.g., different values of GAs parameters are applied, or if the techniques are implemented to other optimization problems.

Conclusion

In this paper, for a first time a hybrid metaheuristic algorithm SGA-CS, combined advantages of simple genetic algorithm and cuckoo search has been adapted and applied for a parameter identification of non-linear dynamic *S. cerevisiae* fed-batch fermentation process model. After thoroughly conducted comparison between standard SGA, standard CS and hybrid SGA-CS it has been proved that SGA-CS yields better results than SGA toward optimization criterion value and keeps the model accuracy of CS, while saving almost 60% of CS CPU time.

As a step ahead, a verification of the promising obtained results from the adapted SGA-CS has been done by the elaboration of a new SGAcms-CS hybrid modification. It applies a modified SGAcms instead of SGA which implements the main genetic operators in order crossover,

mutation and selection. When applying the SGAcms-CS hybrid technique to a parameter identification of *S. cerevisiae* fed-batch fermentation process model, the results confirm that SGAcms-CS can outperform SGAcms, when the value of optimization criterion is investigated, while saving the CS model accuracy for less CPU time.

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