Modified Simple Genetic Algorithms Improving Convergence Time for the Purposes of Fermentation Process Parameter Identification

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Abstract: - Fermentation processes are characterized with non-linear and time-dependent parameters that make their parameter identification non-trivial task. Failure of conventional optimization methods to yield a satisfactory solution provokes the idea for some stochastic algorithms to be applied. As such, different modifications of simple genetic algorithms (SGA) have been investigated aiming to improve the model accuracy and the algorithm convergence time. For that purpose two new modifications of SGA are developed here. SGA realizations differ from each other in the sequence of implementation of the main genetic operators selection, crossover and mutation. A comparison of the herewith developed two modifications of SGA and standard SGA towards algorithm convergence time and model accuracy is presented for parameter identification of *S. cerevisiae* fed-batch cultivation. The influence of the most important genetic algorithm parameters, namely generation gap, crossover and mutation rates has been investigated, too. Both proposed modifications of SGA produce similar values of the optimization criterion, meanwhile being significantly faster than the standard SGA. Among the considered genetic algorithms parameters, generation gap influences the algorithm calculation time most significantly, saving up to 53% of the time without affecting the model accuracy.

Key-Words: - Genetic algorithms, genetic operators, genetic algorithm parameters, parameter identification, fed-batch fermentation process.

1 Introduction

Fermentation processes (FP) underlie the production of pharmaceuticals, chemicals and enzymes, yeast, foods, beverages, etc. in various industry branches. That is why FP modeling and future optimal control are questions of continued interest. Meanwhile, the modeling and control of FP pose serious challenges to their researchers as they are complex, nonlinear dynamic systems with interdependent and time-varying process parameters. An important step for adequate modeling of non-linear models of FP is the choice of a certain optimization procedure for model parameter identification. Failure of conventional optimization methods such as Nelder-Mead's minimization, sequential quadratic programming, quasi-Newton algorithms (i.e. Broyden, Fletcher, Goldfarb and Shanno), etc. to yield a satisfactory solution [1, 2] provokes the idea for some stochastic

algorithms to be used. Different meta-heuristics methods can be applied to overcome the parameter estimation difficulties [3-5].

As a quite promising stochastic global optimization method, genetic algorithms (GA), originally presented by Holland [6], are widely applied to a variety of complicated cases [7-31]. Among a number of searching tools, GA are one of the methods based on biological evolution and inspired by Darwin's theory of "survival of the fittest". GA are directed random search techniques, based on the mechanics of natural selection and genetics. GA find the global optimal solution in complex multidimensional search space by simultaneously evaluating many points in the parameter space. They require only information concerning the quality of the solution and do not require linearity in the parameters. GA properties, like solving hard problems, noise tolerance, and being easy to interface and hybridize, make them suitable and more workable to different optimization problems, and parameter identification and optimization of fermentation processes, in particular [8, 23-31].

Standard SGA, originally presented in [6], searches a global optimal solution using three main genetic operators in a sequence: selection, crossover and mutation. This algorithm is here denoted as SGA-SCM (coming from selection, crossover, mutation). SGA-SCM starts with selection of chromosomes (a coded parameter set) representing better possible solutions according to their own objective function values. After that, crossover proceeds to form a new offspring. Mutation is then applied with determinate probability aiming to prevent all solutions from falling into a local optimum of the solved problem. GA terminate when some termination criterion is fulfilled, for example: 1) generation number reached; 2) evolution time passed; 3) fitness threshold reached; 4) fitness convergence satisfied; 5) population convergence satisfied; 6) gene convergence satisfied, etc. In this investigation, GA terminates when a certain generation number has been reached. According to [7], the structure of the standard SGA-SCM could be shortly presented as shown in Fig. 1.

Since the basic idea of GA is to imitate the mechanics of natural selection and genetics, one can make an analogy with the processes occurring in nature, saying that the probability that mutation takes place first and then comes crossover is comparable to the probability that both processes occur in a reverse order; or selection to be performed after crossover and mutation, no matter of their order. Following that idea, firstly implemented as a modified genetic algorithm SGA-CMS and applied to parameter identification of *E. coli* cultivation process [8], many modifications of SGA-SCM, concerning the sequence of execution of the main genetic operators, have been developed aiming to improve model accuracy and algorithm convergence time for the purposes of parameter identification of a fed-batch cultivation of *S. cerevisiae* [28-30]. SGA-CMS (crossover, mutation, selection), SGA-SMC (selection, mutation, crossover) and SGA-MCS (mutation, crossover, selection) have been proposed and thoroughly investigated in [30]. Two modifications skipping mutation operator – SGA-SC (selection, crossover) and SGA-CS (crossover, selection) have been also developed and applied [28]. Following the idea that GA imitate natural processes, two new modifications that may possibly occur are herewith proposed – SGA-CSM (crossover, selection, mutation) and SGA-MSC (mutation, selection, crossover).

1. **[Start]**
   Generate random population of *n* chromosomes
2. **[Object function]**
   Evaluate the object function of each chromosome in the populations
3. **[Fitness function]**
   Evaluate the fitness function of each chromosome in the populations
4. **[New population]**
   Create a new population by repeating following steps:
   - 4.1. **[Selection]**
     Select parent chromosomes from the population according to their fitness function
   - 4.2. **[Crossover]**
     Cross over the parents to form new offspring with a crossover probability
   - 4.3. **[Mutation]**
     Mutate new offspring at each locus with a mutation probability
5. **[Replace]**
   Use new generated loop in an old population for a further run of the algorithm
6. **[Test]**
   If the end condition is satisfied, stop and return the best solution in current population
7. **[Loop]**
   Go to step 2.

Fig.1 Structure of standard SGA

There are many operators, functions, parameters and settings in GA that could be specifically implemented in different problems [27-29]. In this study, three of the main GA parameters, namely generation gap (GGAP), crossover (XOVR) and mutation (MUTR) rates are investigated for both proposed SGA modifications. A very big GGAP value does not improve performance of GA, especially regarding how fast the solution will be found. Mutation is randomly applied with low probability, typically in the range 0.01 and 0.1. A higher XOVR introduces new strings more quickly into the population, while a low XOVR may cause stagnation due to the lower exploration rate. Thus and also according to some statements [32], the range of investigated GA parameters is chosen as presented in Table 1.

Table 1. Range of investigated genetic algorithm parameters

GGAP	XOVR	MUTR
0.5	0.65	0.02
0.67	0.75	0.04
0.8	0.85	0.06
0.9	0.95	0.08
-	-	0.1

The aim of this paper is to propose and develop two new possible modifications of SGA, namely SGA-MSC and SGA-CSM. The influence of three of the main GA parameters, namely GGAP, XOVR and MUTR towards model accuracy and algorithm convergence time is thoroughly investigated. A comparison of two newly presented SGA modifications to the standard one SGA-SCM is performed for parameter identification of *S. cerevisiae* fed-batch cultivation.

2 Description of Modified Simple Genetic Algorithms

As one can see in Fig.1 and following the main idea GA to imitate the processes in nature, there is a possibility crossover (sub-step 4.1) to occur before selection (sub-step 4.2). That will lead to a new SGA modification, denoted here as SGA-CSM (crossover, selection, mutation). In such an algorithm the parental genes are combined during the crossover in order to form a new chromosome. After the reproduction, the fitness values for the offspring are calculated and the most fit individuals are selected to replace the parents. Newly created offspring can mutate by a bit changed, when the mutation operator is performed.

In another possible performance the mutation operator occurs first, followed by selection and crossover. This leads to another new SGA modification, denoted here as SGA-MSC (mutation, selection, crossover).

These two newly proposed SGA modifications are thoroughly investigated with respect to model accuracy and algorithm convergence time and applied to parameter identification of *S. cerevisiae* fed-batch cultivation.

3 Parameter Identification of *S. cerevisiae* Fed-batch Cultivation

Experimental data of *S. cerevisiae* fed-batch cultivation is obtained in the *Institute of Technical Chemistry – University of Hannover*, Germany [2]. The cultivation of the yeast *S. cerevisiae* is performed in a 2 l reactor, using a Schatzmann medium. Glucose in feeding solution is 35 g/l. The temperature was controlled at 30°C, the pH at 5.5. The stirrer speed was set to 1200 rpm. Biomass and ethanol were measured off-line, while substrate (glucose) and dissolved oxygen were measured on-line.

Mathematical model of *S. cerevisiae* fed-batch cultivation is commonly described as follows, according to the mass balance [2]:

$$\frac{dX}{dt} = \mu X - \frac{F}{V} X \tag{1}$$

$$\frac{dS}{dt} = -q_S X + \frac{F}{V}\left(S_{in} - S\right) \tag{2}$$

$$\frac{dE}{dt} = q_E X - \frac{F}{V} E \tag{3}$$

$$\frac{dO_2}{dt} = -q_{O_2} X + k_L^{O_2} a\left(O_2^* - O_2\right) \tag{4}$$

$$\frac{dV}{dt} = F \tag{5}$$

where:

X is the concentration of biomass, [g/l];
S – concentration of substrate (glucose), [g/l];
E – concentration of ethanol, [g/l];
O_2 – concentration of oxygen, [%];
O_2^* – dissolved oxygen saturation

concentration, [%];
F – feeding rate, [l/h];
V – volume of bioreactor, [l];
$k_L^{O_2} a$ – volumetric oxygen transfer coefficient, [1/h];
S_{in} – initial glucose concentration in the feeding solution, [g/l];
μ – specific growth rate of biomass, [1/h];
q_S – specific utilization rate of substrate, [1/h];
q_E – specific utilization rate of ethanol, [1/h];
q_{O_2} – specific utilization rate of dissolved oxygen, [1/h].

All functions are continuous and differentiable.

Considered here fed-batch cultivation of *S. cerevisiae* is characterized with keeping glucose concentration equal to or below to its critical level (S_{crit} = 0.05 g/l), sufficient dissolved oxygen $O_2 \geq O_{2crit}$ (O_{2crit} = 18%) and availability of ethanol in the broth. This state corresponds to the so called *mixed oxidative state* (FS II) according to functional state modeling approach [33]. Hence, specific rates in Eqs. (1)-(5) are as follows:

$$\mu = \mu_{2S} \frac{S}{S + k_S} + \mu_{2E} \frac{E}{E + k_E},$$

$$q_S = \frac{\mu_{2S}}{Y_{SX}} \frac{S}{S + k_S},$$

$$q_E = -\frac{\mu_{2E}}{Y_{EX}} \frac{E}{E + k_E}, \quad (6)$$

$$q_{O_2} = q_E Y_{OE} + q_S Y_{OS},$$

where:
μ_{2S} is the maximum growth rate of substrate, [1/h];
μ_{2E} – maximum growth rate of ethanol, [1/h];
k_S – saturation constants of substrate, [g/l];
k_E – saturation constants of ethanol, [g/l];
Y_{ij} – yield coefficients, [g/g].

All model parameters fulfill the non-zero division requirement.

As an optimization criterion, mean square deviation between the model output and the experimental data obtained during cultivation has been used:

$$J_Y = \sum (Y - Y^*)^2 \rightarrow min, \quad (7)$$

where:
Y is the experimental data;
Y^* – model predicted data;
$Y = [X, S, E, O_2]$.

Parameter identification of the model (1)-(6) has been performed using *Genetic Algorithm Toolbox* [34] in *Matlab 7* environment. All the computations are performed using a PC Intel Pentium 4 (2.4 GHz) platform running Windows XP.

The influence of the main GA parameters, namely GGAP, XOVR and MUTR has been examined for two newly introduced modifications of SGA. When one of the parameters GGAP, XOVR or MUTR is investigated according to the values given in Table 1, the basic values for the other two parameters are as follows, according to some statements [32]: GGAP = 0.9, XOVR = 0.85 and MUTR = 0.05.

The values of the GA parameters except for GGAP, XOVR and MUTR and the type of genetic operators are presented in Table 2 and Table 3.

Table 2. Genetic algorithms parameters

Parameter	**Value**
NVAR	9
PRECI	20
NIND	20
MAXGEN	100

where:
NVAR is the number of variables;
PRECI – precision of binary representation;
NIND – number of individuals;
MAXGEN – maximum number of generations.

Table 3. Genetic algorithms operators

Operator	**Type**
Encoding	binary
Reinsertion	fitness-based
Crossover	double point
Mutation	bit inversion
Selection	roulette wheel selection
Fitness function	linear ranking

GA terminate when a certain number of generations is reached, in this case 100. Scalar relative error tolerance *RelTol* is set to $1e^{-4}$, while the vector of

absolute error tolerances (all components) *AbsTol* – to $1e^{-5}$.

3.1 Parameter Identification of *S. cerevisiae* Fed-batch Cultivation applying SGA-SCM

At the beginning of this investigation the standard SGA-SCM has been applied for the purpose of parameter identification of *S. cerevisiae* fed-batch cultivation. The detailed examination of the influence of main genetic algorithm parameters GGAP, XOVR and MUTR has been performed [29], resulting to the statement that GGAP is the most sensitive one. Table 4 demonstrates the influence of GGAP in SGA-SCM to model accuracy and convergence time [29]. Because of the stochastic nature of the GA, several runs have been performed in order of representative results to be achieved. The calculated average values are presented here.

Table 4. Influence of GGAP to model accuracy and convergence time in SGA-SCM

GGAP	**SGA-SCM**	
	J	***t*, s**
0.5	0.0223	43.812
0.67	0.0221	52.797
0.8	0.0221	67.922
0.9	0.0222	70.625

As it is seen from Table 4, the obtained optimization criterion values are very similar. Concerning convergence time, up to almost 38% can be saved using GGAP = 0.5 instead of 0.9 without loss of accuracy. Exploring different values of crossover rate, no such time saving has been accomplished, but it should be pointed out that values of 0.85 for XOVR can be assumed as more appropriate. Only in mutation rate no tendency of influence can be drawn. Thus, after the investigation performed [29], genetic parameter values GGAP = 0.5, XOVR = 0.85 and MUTR = 0.1 are chosen. As a result of parameter identification, applying SGA-SCM, the values of model parameters are shown in Table 5.

Table 5. Parameter identification with SGA-SCM

Parameter	**SGA-SCM (at GGAP = 0.5)**
J	0.0221
CPU time, s	46.5470
μ_{2S}, 1/h	0.94
μ_{2E}, 1/h	0.12
k_S, g/l	0.13
k_E, g/l	0.80
Y_{SX}, g/g	0.41
Y_{EX}, g/g	1.67
$k_L^{O_2}a$, 1/h	65.06
Y_{OS}, g/g	494.89
Y_{OE}, g/g	86.36

Figs.2-5 present results from experimental data and model prediction with SGA-SCM (results not shown in [29]) respectively for the biomass, ethanol, substrate and dissolved oxygen.

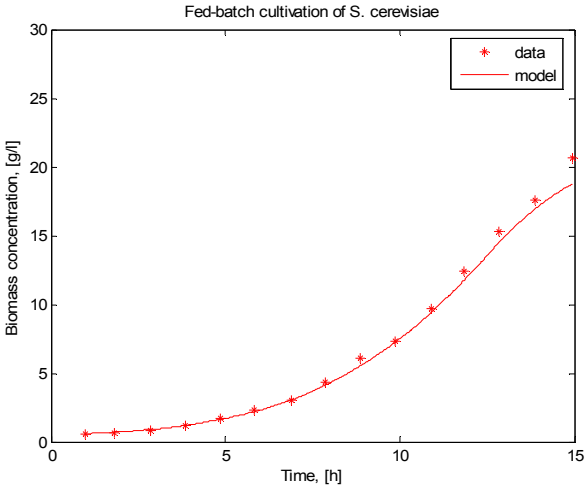

Fig.2 Model prediction with SGA-SCM compared to experimental data, respectively, for the biomass

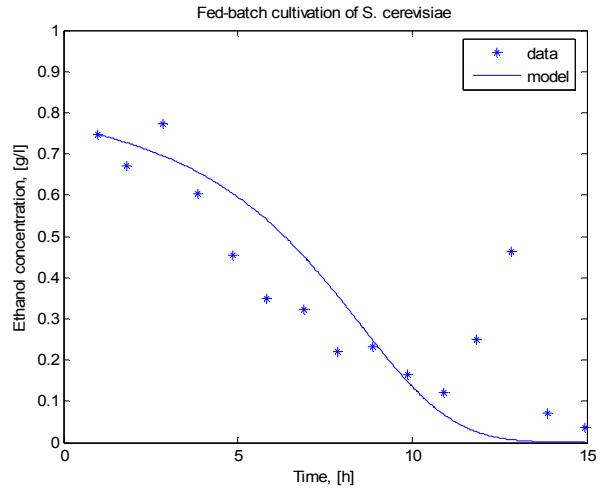

Fig.3 Model prediction with SGA-SCM compared to experimental data, respectively, for the ethanol

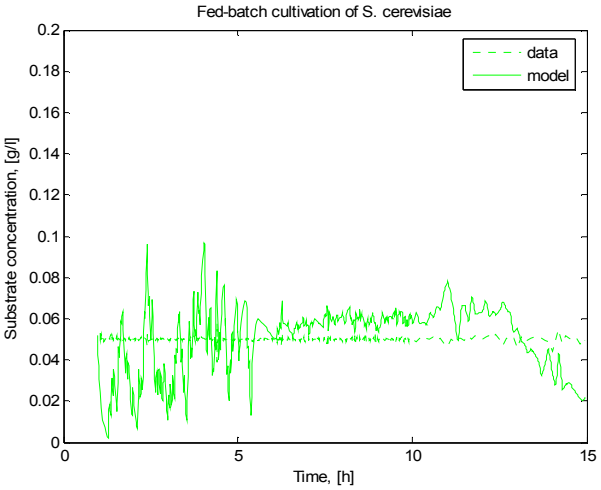

Fig.4 Model prediction with SGA-SCM compared to experimental data, respectively, for the substrate

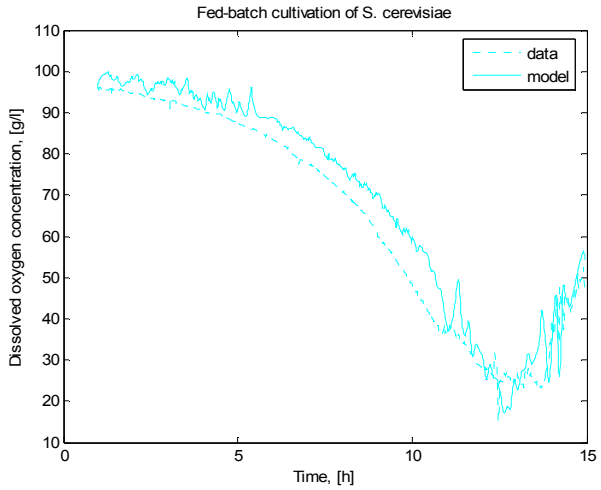

Fig.5 Model prediction with SGA-SCM compared to experimental data, respectively, for the dissolved oxygen

3.2 Parameter Identification of *S. cerevisiae* Fed-batch Cultivation applying SGA-CSM

On the next step of this investigation, the first of the herewith proposed two modifications of SGA-SCM, namely SGA-CSM, has been applied to parameter identification of *S. cerevisiae* fed-batch cultivation. The thorough investigation of three main genetic algorithms parameters GGA, XOVR and MUTR has been fulfilled for the newly presented here SGA-CSM, as performed in [29], Again GGAP has been proven as the most sensitive parameter towards convergence time and model accuracy, while exploring different values of crossover rate no such time saving is realized and no tendency of influence of mutation rate can be drawn. Thus, genetic parameter values GGAP = 0.5, XOVR = 0.85 and MUTR = 0.1 are chosen again. Table 6 demonstrates only the results obtained for the most sensitive parameter GGAP when SGA-CSM has been applied. Again, because of the stochastic nature of the GA, several runs have been performed in order of representative results to be achieved. The calculated average values are presented here.

Table 6. Influence of GGAP to model accuracy and convergence time in SGA-CSM

GGAP	SGA-CSM	
	J	***t*, s**
0.5	0.0224	36.281
0.67	0.0223	39.203
0.8	0.0223	60.313
0.9	0.0235	55.921

A comparison between the proposed modification SGA-CSM and standard SGA-SCM with respect to model accuracy and convergence time has been performed. As shown in Table 4 and Table 6, the optimization criterion values obtained with both kinds of SGA are very similar, varying between 0.0221 and 0.0235, which means about 6% divergence. This fact is promising since the new modification SGA-CSM still ensures high model accuracy. As proven again as the most sensitive among the three investigated parameters concerning the convergence time, GGAP = 0.5 instead of 0.9 ensures saving of 35% computational time without loss of accuracy in SGA-CSM (for comparison – 38% in SGA-SCM). In the same time, SGA-CSM is in all cases significantly faster than the standard

SGA-SCM. If one compares SGA-SCM and SGA-CSM at GGAP = 0.5, the herewith proposed SGA-CMS is 17% faster than SGA-SCM.

Distinguished as the faster algorithm, SGA-CSM is here applied to parameter identification of *S. cerevisiae* fed-batch cultivation. As a result of parameter identification, the values of model parameters are shown in Table 7.

Table 7. Parameter identification with SGA-CSM

Parameter	**SGA-CSM (at GGAP = 0.5)**
J	0.0228
CPU time, s	36.2190
μ_{2S}, 1/h	0.91
μ_{2E}, 1/h	0.12
k_S, g/l	0.09
k_E, g/l	0.70
Y_{SX}, g/g	0.49
Y_{EX}, g/g	2.38
$k_L^{O_2}a$, 1/h	125.39
Y_{OS}, g/g	875.91
Y_{OE}, g/g	98.84

Figs.6-9 present results from experimental data and model prediction with SGA-CSM respectively for the biomass, ethanol, substrate and dissolved oxygen.

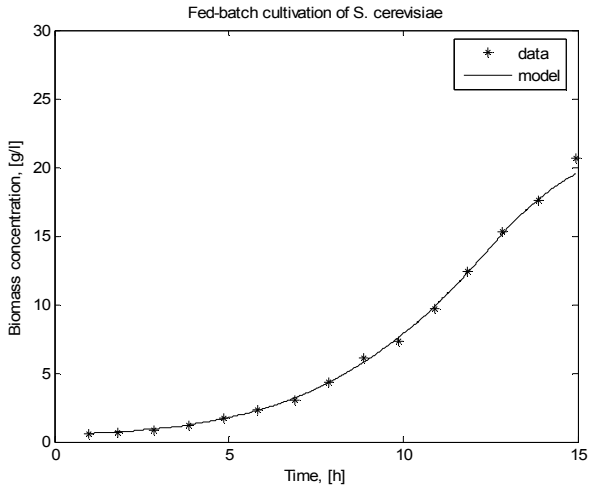

Fig.6 Model prediction with SGA-CSM compared to experimental data, respectively, for the biomass

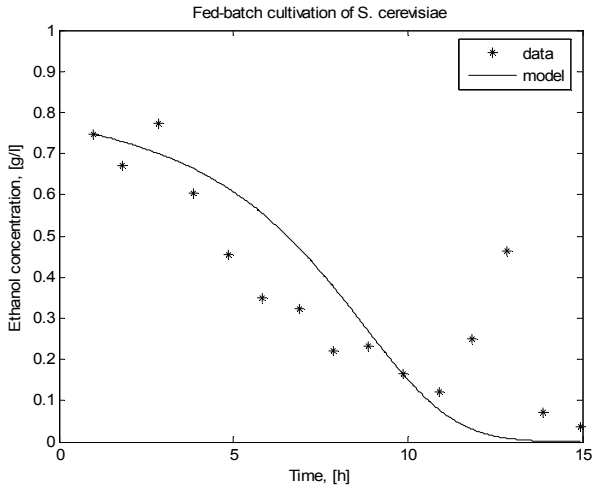

Fig.7 Model prediction with SGA-CSM compared to experimental data, respectively, for the ethanol

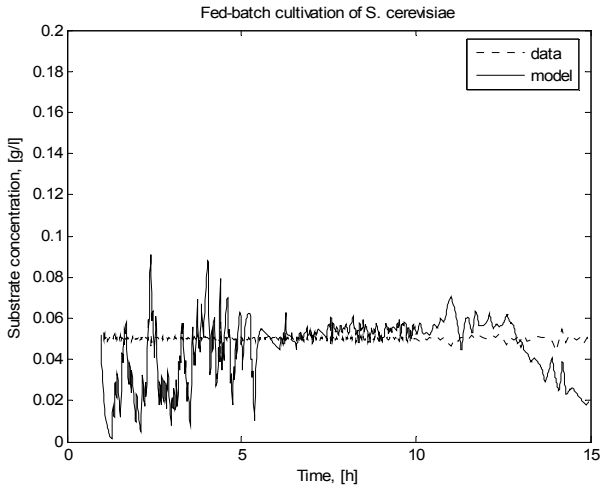

Fig.8 Model prediction with SGA-CSM compared to experimental data, respectively, for the substrate

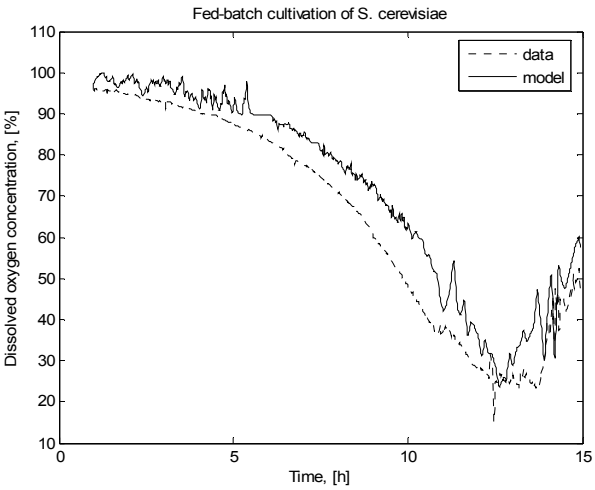

Fig.9 Model prediction with SGA-CSM compared to experimental data, respectively, for the dissolved oxygen

3.3 Parameter Identification of *S. cerevisiae* Fed-batch Cultivation applying SGA-MSC

Further, the second one of the proposed here two modifications of SGA-SCM, namely SGA-MSC, has been applied to parameter identification of *S. cerevisiae* fed-batch cultivation. The thorough investigation of three main genetic algorithms parameters GGAP, XOVR and MUTR has been again performed for SGA-MSC as presented in [29], Again GGAP has been proven as the most sensitive parameter towards convergence time and model accuracy, while exploring different values of crossover rate no such time saving is realized and no tendency of influence of mutation rate can be drawn. Thus, similar to the other two SGA presented here, genetic parameter values GGAP = 0.5, XOVR = 0.85 and MUTR = 0.1 are chosen again. Table 8 demonstrates only the results obtained for the most sensitive parameter GGAP when SGA-MSC has been applied. Again, because of the stochastic nature of the GA, several runs have been performed in order of representative results to be achieved. The calculated average values are presented here.

SGA-MSC still ensures high model accuracy. In the same time, SGA-MSC is faster even than the first modification SGA-CSM and hence faster than the standard SGA-SCM but only for the values of 0.5 and 0.8 for GGAP. As in other modifications [28, 30], it is again demonstrated that there is no loss of model accuracy when the operator mutation is performed first.

Using GGAP = 0.5 instead of 0.9 in SGA-MSC, 53% of the convergence time of the algorithm can be saved without loss of model accuracy. But if one compares SGA-MSC with GGAP = 0.5, as distinguished as the fastest one, to the standard SGA-SCM with recommended GGAP = 0.9 [32], it is almost 2 times faster while saving the model accuracy.

Table 8. Influence of GGAP to model accuracy and convergence time in SGA-MSC

GGAP	**SGA-MSC**	
	J	***t*, s**
0.5	0.0223	36.266
0.67	0.0228	53.547
0.8	0.0223	47.485
0.9	0.0223	77.609

Distinguished as the fastest algorithm, SGA-MSC is here applied to parameter identification of *S. cerevisiae* fed-batch cultivation. As a result of parameter identification, the values of model parameters are shown in Table 9.

Figs.10-13 present results from experimental data and model prediction with SGA-MSC, respectively, for the biomass, ethanol, substrate and dissolved oxygen.

Table 9. Parameter identification with SGA-MSC

Parameter	**SGA-MSC (at GGAP = 0.5)**
J	0.0223
CPU time, s	37.688
μ_{2S}, 1/h	0.91
μ_{2E}, 1/h	0.11
k_S, g/l	0.11
k_E, g/l	0.80
Y_{SX}, g/g	0.44
Y_{EX}, g/g	1.54
$k_L^{O_2}a$, 1/h	120.58
Y_{OS}, g/g	874.40
Y_{OE}, g/g	121.27

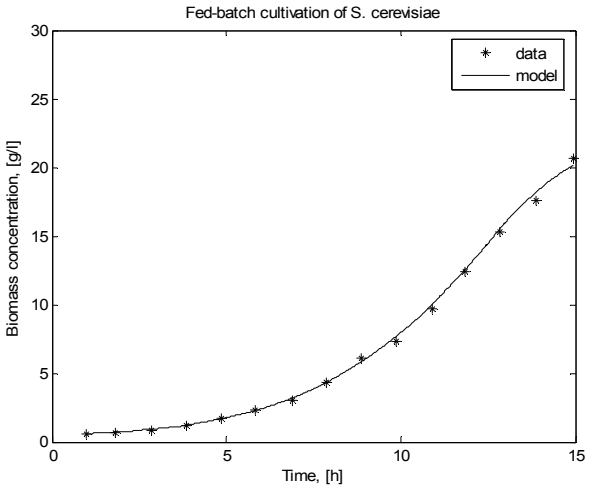

Fig.10 Model prediction with SGA-MSC compared to experimental data, respectively, for the biomass

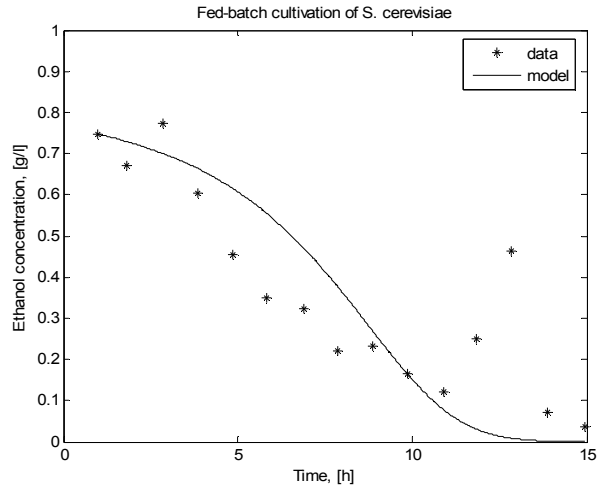

Fig.11 Model prediction with SGA-MSC compared to experimental data, respectively, for the ethanol.

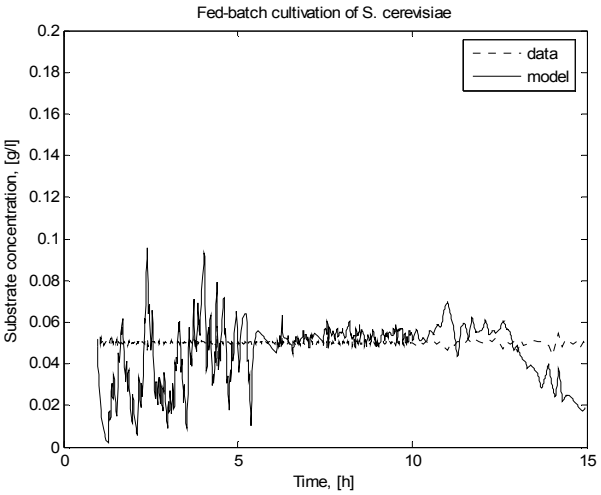

Fig.12 Model prediction with SGA-MSC compared to experimental data, respectively, for the substrate.

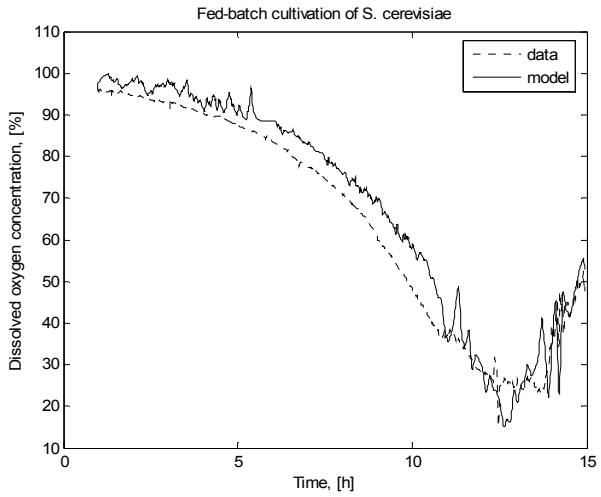

Fig.13 Model prediction with SGA-MSC compared to experimental data, respectively, for the dissolved oxygen.

Presented in this investigation results from the application of newly presented here two modifications of SGA, namely SGA-CSM and SGA-MSC, as well as the standard SGA-SCM for parameter identification of *S. cerevisiae* fed-batch cultivation, show their effectiveness for solving complex nonlinear problems.

4 Analysis and discussion

To answer the spontaneously raised question of how the mere order of execution of the genetic operators can affect the algorithm convergence time, a detailed analysis has been performed of the time needed for execution of each operator in all three considered here SGA.

In the implementation of SGA-SCM, the time for execution of the first operator, namely selection, is about 1.0421 sec, than followed by 0.047 sec for the execution of the crossover operator and 0.031 sec for the mutation operator. Totally, one generation step takes 3.7340 sec.

In the implementation of SGA-CSM, the time for the execution of the first operator – crossover in this case, is about 1.0369 sec, than followed by 0.047 sec for the execution of the selection operator and 0.031 sec for the mutation operator. Totally, one generation step takes 3.5620 sec, which is about 0.172 sec (4.6%) faster than SGA-SMC.

In the implementation of SGA-MSC, the time for the execution of the first operator – mutation in this case, is about 0.9912 sec, than followed by 0.047 sec for the execution of the selection operator and 0.047 sec for the crossover operator. Totally, one generation step takes 3.5940 sec, which is about 0.14 sec (3.7%) faster than SGA-SMC.

The results of the above discussion are summarized in Table 10, presenting the time of execution of different genetic operators in standard SGA-SCM and both its modifications, considered in this investigation.

Table 10. Time for the operators execution in different algorithms ([sec])

	SGA-SMC	**SGA-CSM**	**SGA-MSC**
selection	1.0421	0.047	0.047
crossover	0.047	1.0369	0.047
mutation	0.031	0.031	0.9912
time for 1 generation step	3.7340	3.5620	3.5940

As seen from Table 10, each genetic operator is much slower (more than 20 times for selection and

crossover and more than 30 times for mutation) when it has to be performed first in the corresponding algorithm. Meanwhile, the mutation operator is relatively faster than the other two operators – in about 34%. These facts, superimposing the stochastic nature of GA, mean that merely reordering the operators can lead to a significant decrease of the algorithm convergence time.

If one would like to go deeper in the analysis of the model accuracy degree, *p-values* are supplied in order to follow the experimental modelling techniques: p = 0.6015 for SGA-SCM, p = 0.9319 for SGA-CSM and p = 0.8415 for SGA-MSC. Presented *p-values* prove to the researchers that there are differences between three considered algorithms even though values of objective function seem so close. Additionally, two-way analysis applying *anova* function in MATLAB has been performed for comparing the means of the degree of model accuracy of three considered here SGA at different values of GGAP. Fig.14 presents the results from the *anova* function implementation.

ANOVA Table

Source	SS	df	MS	F	Prob>F
Columns	4.06667e-007	2	2.03333e-007	1.31	0.3379
Rows	3.09167e-007	3	1.03056e-007	0.66	0.6047
Error	9.33333e-007	6	1.55556e-007		
Total	1.64917e-006	11			

Fig.14 Results from the *anova* function implementation for three kinds of SGA

Obtained as a result from the *anova* function *p*-values, namely p = [0.3379 0.6047], show that none of the values of p small enough, hence, there are no significant differences between the three SGA considered here with respect of the degree of model accuracy.

5 Conclusion

In this investigation two newly presented modifications of SGA have been developed and thoroughly examined. The proposed algorithms are with exchanged sequence of the operators selection, crossover and mutation. The influence of some of the main GA parameters, namely generation gap, crossover and mutation rates, has been examined for the herewith considered SGA, aiming to improve the convergence time while preserving high model accuracy. Among the three investigated parameters, the generation gap is the most sensitive one with respect of the convergence time. As a "favourite" among the considered here SGA modifications, SGA-MSC has been distinguished. Using such algorithm up to almost 53% from the calculation time can be saved using GGAP = 0.5 instead of 0.9 without loss of model accuracy. But if one compares SGA-MSC with GGAP = 0.5 to the standard SGA-SCM with recommended GGAP = 0.9, it is almost 2 times faster while saving the model accuracy. The investigation of the different values of crossover and mutation rates shows that no such time saving has been achieved but it should be pointed out that values of 0.85 for crossover rate can be assumed as more appropriate. All modifications of SGA considered here, employing such values of genetic algorithm parameters, show the effectiveness of GA for solving complex nonlinear problems.

For the sake of completeness, the results obtained in applying both herewith proposed modifications have been compared to the results obtained with three other SGA modifications, thoroughly investigated in [29]. Among all five modifications of SGA-SCM, applying different order of three operators, SGA-CSM can be distinguished as the fastest, but not the most accurate one, followed by SGA-MCS [29] and SGA-MSC exhibits comparable values of objective value and convergence time. SGA-CMS is very close to the "leaders", while only SGA-SMC is comparably "slow" to the standard SGA-SCM. As such, some tendency can be outlined, that execution of selection operator at the beginning leads to bigger convergence time for the purposes of fermentation process parameter identification. The same tendency has been observed in SGA-CMS applied to parameter identification of *E. coli* cultivation process [8].

The herewith introduced two new modifications of the standard SGA-SCM have been demonstrated for the purpose of fermentation process parameter identification. Since GA are a stochastic technique widely applied to various optimization problems in different areas, the proposed modifications might be of interest and may help researchers apply GA for solving complex problems.

Acknowledgements

This work is partially supported by National Science Fund of Bulgaria, grant number DID 02-29 and DMU 03-38.

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